

Lista de secuencias

<110> JSC "BIOCAD"

<120> Anticuerpo quimérico biespecífico bivalente que comprende un heterodímero basado en CMH o proteínas similares a CMH

<160> 109

<170> BiSSAP 1.3.6

<210> 1

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH clase I HLA-A (alelo A*01:01:01:01)

<400> 1

Gln Arg Thr Asp Pro Pro Lys Thr His Met Thr His His Pro Ile Ser

1. 5 10 15

Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala

20 25 30

Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp

35 40 45

Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys

50 55 60
 Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys
 65 70 75 80
 His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp Glu
 85 90 95
 Leu Ser Ser

<210> 2

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH
 clase I HLA-A (A*02:01:01:01)

<400> 2

Gln Arg Thr Asp Ala Pro Lys Thr His Met Thr His His Ala Val Ser

1. 5 10 15

Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Ser Phe Tyr Pro Ala

20 25 30

Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp

35 40 45

Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys

50 55 60

Trp Ala Ala Val Val Val Pro Ser Gly Gln Glu Gln Arg Tyr Thr Cys

65 70 75 80

His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp Glu

85 90 95

Pro Ser Ser

<210> 3

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH

clase I HLA-A (A*03:01:01:01)

<400> 3

Gln Arg Thr Asp Pro Pro Lys Thr His Met Thr His His Pro Ile Ser

1. 5 10 15

Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala

20 25 30

Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp

35 40 45

Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys

50 55 60

Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys

65 70 75 80

His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp Glu

85 90 95

Leu Ser Ser

<210> 4

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH clase I HLA-A (A*11:01:01:01)

<400> 4

Gln Arg Thr Asp Pro Pro Lys Thr His Met Thr His His Pro Ile Ser

1. 5 10 15

Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala

20 25 30

Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp

35 40 45

Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys

50 55 60

Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys

65 70 75 80

His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp Glu

85 90 95

Leu Ser Ser

<210> 5

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH
clase I HLA-A (A*23:01:01:01)

<400> 5

Gln Arg Thr Asp Pro Pro Lys Thr His Met Thr His His Pro Ile Ser

1. 5 10 15

Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala

20 25 30

Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp

35 40 45

Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys

50 55 60

Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys

65 70 75 80

His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp Glu

85 90 95

Pro Ser Ser

<210> 6

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH
clase I HLA-B (B*07:02:01:01)

<400> 6

Glu Arg Ala Asp Pro Pro Lys Thr His Val Thr His His Pro Ile Ser

1. 5 10 15

Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala

20 25 30

Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp

35 40 45

Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Arg Thr Phe Gln Lys

50 55 60

Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys

65 70 75 80

His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp Glu

85 90 95

Pro Ser Ser

<210> 7

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH
clase I HLA-B (B*08:01:01:01)

<400> 7

Glu Arg Ala Asp Pro Pro Lys Thr His Val Thr His His Pro Ile Ser

1. 5 10 15

Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala

20 25 30

Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp

35 40 45

Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Arg Thr Phe Gln Lys

50 55 60

Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys

65 70 75 80

His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp Glu

85 90 95

Pro Ser Ser

<210> 8

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH
clase I HLA-B (B*13:01:01:01)

<400> 8

Gln Arg Ala Asp Pro Pro Lys Thr His Val Thr His His Pro Ile Ser

1. 5 10 15

Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala

20 25 30

Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp

35 40 45

Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Arg Thr Phe Gln Lys

50 55 60

Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys

65 70 75 80

His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp Glu

85 90 95

Pro Ser Ser

<210> 9

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH
clase I HLA-B (B*14:01:01:01)

<400> 9

Gln Arg Ala Asp Pro Pro Lys Thr His Val Thr His His Pro Ile Ser

1. 5 10 15

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

<210> 10

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH
 clase I HLA-B (B*15:01:01:01)

<400> 10

Gln Arg Ala Asp Pro Pro Lys Thr His Val Thr His His Pro Ile Ser
 1. 5 10 15
 Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala
 20 25 30
 Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp

35 40 45
 Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Arg Thr Phe Gln Lys
 50 55 60
 Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys
 65 70 75 80
 His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp Glu
 85 90 95
 Pro Ser Ser

<210> 11

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH
 clase I HLA-C (C*01:02:01:01)

<400> 11

Gln Arg Ala Glu His Pro Lys Thr His Val Thr His His Pro Val Ser
 1. 5 10 15
 Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Thr
 20 25 30
 Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp
 35 40 45
 Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys
 50 55 60

Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys

65 70 75 80

His Val Gln His Glu Gly Leu Pro Glu Pro Leu Thr Leu Arg Trp Glu

85 90 95

Pro Ser Ser

<210> 12

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH
clase I HLA-C (C*03:02:01)

<400> 12

Gln Arg Ala Glu His Pro Lys Thr His Val Thr His His Pro Val Ser

1. 5 10 15

Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala

20 25 30

Glu Ile Thr Leu Thr Trp Gln Trp Asp Gly Glu Asp Gln Thr Gln Asp

35 40 45

Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys

50 55 60

Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys

65 70 75 80

His Val Gln His Glu Gly Leu Pro Glu Pro Leu Thr Leu Arg Trp Glu

85 90 95

Pro Ser Ser

<210> 13

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH
clase I HLA-C (C*04:01:01:01)

<400> 13

Gln Arg Ala Glu His Pro Lys Thr His Val Thr His His Pro Val Ser

1. 5 10 15

Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala

20 25 30

Glu Ile Thr Leu Thr Trp Gln Trp Asp Gly Glu Asp Gln Thr Gln Asp

35 40 45

Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys

50 55 60

Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys

65 70 75 80

His Val Gln His Glu Gly Leu Pro Glu Pro Leu Thr Leu Arg Trp Lys

85 90 95

Pro Ser Ser

<210> 14

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH clase I HLA-C (C*05:01:01:01)

<400> 14

Gln Arg Ala Glu His Pro Lys Thr His Val Thr His His Pro Val Ser

1. 5 10 15

Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala

20 25 30

Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp

35 40 45

Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys

50 55 60

Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys

65 70 75 80

His Val Gln His Glu Gly Leu Pro Glu Pro Leu Thr Leu Arg Trp Gly

85 90 95

Pro Ser Ser

<210> 15

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH
clase I HLA-C (C*06:02:01:01)

<400> 15

Gln Arg Ala Glu His Pro Lys Thr His Val Thr His His Pro Val Ser

1. 5 10 15

Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala

20 25 30

Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp

35 40 45

Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys

50 55 60

Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys

65 70 75 80

His Val Gln His Glu Gly Leu Pro Glu Pro Leu Thr Leu Arg Trp Glu

85 90 95

Pro Ser Ser

<210> 16

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH
clase I HLA-E (E*01:01:01:01)

<400> 16

Leu His Leu Glu Pro Pro Lys Thr His Val Thr His His Pro Ile Ser

1. 5 10 15

Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala

20 25 30

Glu Ile Thr Leu Thr Trp Gln Gln Asp Gly Glu Gly His Thr Gln Asp

35 40 45

Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys

50 55 60

Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys

65 70 75 80

His Val Gln His Glu Gly Leu Pro Glu Pro Val Thr Leu Arg Trp Lys

85 90 95

Pro Ala Ser

<210> 17

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH

clase I HLA-E (E*01:03:01:01)

<400> 17

Leu His Leu Glu Pro Pro Lys Thr His Val Thr His His Pro Ile Ser

1. 5 10 15

Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala

20 25 30

Glu Ile Thr Leu Thr Trp Gln Gln Asp Gly Glu Gly His Thr Gln Asp

35 40 45

Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys

50 55 60

Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys

65 70 75 80

His Val Gln His Glu Gly Leu Pro Glu Pro Val Thr Leu Arg Trp Lys

85 90 95

Pro Ala Ser

<210> 18

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH

clase I HLA-E (E*01:05)

<400> 18

Leu His Leu Glu Pro Pro Lys Thr His Val Thr His His Pro Ile Ser

1. 5 10 15

Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala

20 25 30

Glu Ile Thr Leu Thr Trp Gln Gln Asp Gly Glu Gly His Thr Gln Asp

35 40 45

Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys

50 55 60

Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys

65 70 75 80

His Val Gln His Glu Gly Leu Pro Glu Pro Val Thr Leu Arg Trp Lys

85 90 95

Pro Ala Ser

<210> 19

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH
clase I HLA-E (E*01:06)

<400> 19

Leu His Leu Glu Pro Pro Lys Thr His Val Thr His His Pro Ile Ser

1. 5 10 15

Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala

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

<210> 20

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH
 clase I HLA-E (E*01:09)

<400> 20

Leu His Leu Glu Pro Pro Lys Thr His Val Thr His His Pro Ile Ser
 1. 5 10 15
 Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala
 20 25 30
 Glu Ile Thr Leu Thr Trp Gln Gln Asp Gly Glu Gly His Thr Gln Asp
 35 40 45

Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys

50 55 60

Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Pro Arg Tyr Thr Cys

65 70 75 80

His Val Gln His Glu Gly Leu Pro Glu Pro Val Thr Leu Arg Trp Lys

85 90 95

Pro Ala Ser

<210> 21

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH
clase I HLA-F (F*01:01:01:01)

<400> 21

Gln Arg Ala Asp Pro Pro Lys Ala His Val Ala His His Pro Ile Ser

1. 5 10 15

Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala

20 25 30

Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Glu Gln Thr Gln Asp

35 40 45

Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys

50 55 60

Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys

65	70	75	80
His Val Gln His Glu Gly Leu Pro Gln Pro Leu Ile Leu Arg Trp Glu			
85	90	95	
Gln Ser Pro			

<210> 22

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH
clase I HLA-F (F*01:02)

<400> 22

Gln Arg Ala Asp Pro Pro Lys Ala His Val Ala His His Pro Ile Ser

1. 5	10	15
------	----	----

Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala

20	25	30
----	----	----

Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Glu Gln Thr Gln Asp

35	40	45
----	----	----

Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys

50	55	60
----	----	----

Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys

65	70	75	80
----	----	----	----

His Val Gln His Glu Gly Leu Pro Gln Pro Leu Ile Leu Arg Trp Glu

85	90	95
----	----	----

Gln Ser Pro

<210> 23

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH clase I HLA-F (F*01:03:01:01)

<400> 23

Gln Arg Ala Asp Pro Pro Lys Ala His Val Ala His His Pro Ile Ser

1. 5 10 15

Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala

20 25 30

Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Glu Gln Thr Gln Asp

35 40 45

Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys

50 55 60

Trp Ala Ala Val Val Val Pro Pro Gly Glu Glu Gln Arg Tyr Thr Cys

65 70 75 80

His Val Gln His Glu Gly Leu Pro Gln Pro Leu Ile Leu Arg Trp Glu

85 90 95

Gln Ser Pro

<210> 24

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH
clase I HLA-F (F*01:04:01:01)

<400> 24

Gln Arg Ala Asp Pro Pro Lys Ala His Val Ala His His Pro Ile Ser

1. 5 10 15

Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala

20 25 30

Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Glu Gln Thr Gln Asp

35 40 45

Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys

50 55 60

Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys

65 70 75 80

His Val Gln His Glu Gly Leu Pro Gln Pro Leu Ile Leu Arg Trp Glu

85 90 95

Gln Ser Pro

<210> 25

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH
clase I HLA-F (F*01:05)

<400> 25

Gln Arg Ala Asp Pro Pro Lys Ala His Val Ala His His Pro Ile Ser

1. 5 10 15

Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala

20 25 30

Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Glu Gln Thr Gln Asp

35 40 45

Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys

50 55 60

Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys

65 70 75 80

His Val Gln His Glu Gly Leu Pro Gln Pro Leu Ile Leu Arg Trp Glu

85 90 95

Gln Ser Leu

<210> 26

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH
clase I HLA-G (G*01:01:01:01)

<400> 26

Gln Arg Ala Asp Pro Pro Lys Thr His Val Thr His His Pro Val Phe

1. 5 10 15

Asp Tyr Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala

20 25 30

Glu Ile Ile Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp

35 40 45

Val Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys

50 55 60

Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys

65 70 75 80

His Val Gln His Glu Gly Leu Pro Glu Pro Leu Met Leu Arg Trp Lys

85 90 95

Gln Ser Ser

<210> 27

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH
clase I HLA-G (G*01:03:01:01)

<400> 27

Gln Arg Ala Asp Pro Pro Lys Thr His Val Thr His His Pro Val Phe

1. 5 10 15

Asp Tyr Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala

20 25 30

Glu Ile Ile Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp

35 40 45

Val Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys

50 55 60

Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys

65 70 75 80

His Val Gln His Glu Gly Leu Pro Glu Pro Leu Met Leu Arg Trp Lys

85 90 95

Gln Ser Ser

<210> 28

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH
clase I HLA-G (G*01:04:01:01)

<400> 28

Gln Arg Ala Asp Pro Pro Lys Thr His Val Thr His His Pro Val Phe

1. 5	10	15	
Asp Tyr Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala			
20	25	30	
Glu Ile Ile Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp			
35	40	45	
Val Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys			
50	55	60	
Trp Ala Ala Val Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys			
65	70	75	80
His Val Gln His Glu Gly Leu Pro Glu Pro Leu Met Leu Arg Trp Lys			
85	90	95	
Gln Ser Ser			

<210> 29

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CMH
clase I HLA-G (G*01:06)

<400> 29

Gln Arg Ala Asp Pro Pro Lys Thr His Val Thr His His Pro Val Phe			
1. 5	10	15	
Asp Tyr Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala			
20	25	30	

Glu Ile Ile Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp

35 40 45

Val Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys

50 55 60

Trp Ala Ala Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Met Cys

65 70 75 80

His Val Gln His Glu Gly Leu Pro Glu Pro Leu Met Leu Arg Trp Lys

85 90 95

Gln Ser Ser

<210> 30

<211> 98

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 2$ para el dominio proximal a la membrana de CMH
clase II HLA-DM (HLA-DMA*01:01:01:01)

<400> 30

Ser Arg Gly Phe Pro Ile Ala Glu Val Phe Thr Leu Lys Pro Leu Glu

1. 5 10 15

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

20 25 30

Pro Met Leu Thr Val Asn Trp Gln His His Ser Val Pro Val Glu Gly

35 40 45

Phe Gly Pro Thr Phe Val Ser Ala Val Asp Gly Leu Ser Phe Gln Ala

50 55 60
 Phe Ser Tyr Leu Asn Phe Thr Pro Glu Pro Ser Asp Ile Phe Ser Cys
 65 70 75 80
 Ile Val Thr His Glu Ile Asp Arg Tyr Thr Ala Ile Ala Tyr Trp Val
 85 90 95
 Pro Arg

<210> 31

<211> 100

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\beta 2$ para el dominio proximal a la membrana de CMH
 clase II HLA-DM (HLA-DMB*01:01:01:01)

<400> 31

Arg Thr Arg Pro Pro Ser Val Gln Val Ala Lys Thr Thr Pro Phe Asn

1. 5 10 15

Thr Arg Glu Pro Val Met Leu Ala Cys Tyr Val Trp Gly Phe Tyr Pro

20 25 30

Ala Glu Val Thr Ile Thr Trp Arg Lys Asn Gly Lys Leu Val Met Pro

35 40 45

His Ser Ser Ala His Lys Thr Ala Gln Pro Asn Gly Asp Trp Thr Tyr

50 55 60

Gln Thr Leu Ser His Leu Ala Leu Thr Pro Ser Tyr Gly Asp Thr Tyr

65 70 75 80

Thr Cys Val Val Glu His Ile Gly Ala Pro Glu Pro Ile Leu Arg Asp

85 90 95

Trp Thr Pro Gly

100

<210> 32

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 2$ para el dominio proximal a la membrana de CMH
clase II HLA-DO (HLA-DOA*01:01:01)

<400> 32

Ile Asn Val Pro Pro Arg Val Thr Val Leu Pro Lys Ser Arg Val Glu

1. 5 10 15

Leu Gly Gln Pro Asn Ile Leu Ile Cys Ile Val Asp Asn Ile Phe Pro

20 25 30

Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Gly Gln Thr Val Thr Glu

35 40 45

Gly Val Ala Gln Thr Ser Phe Tyr Ser Gln Pro Asp His Leu Phe Arg

50 55 60

Lys Phe His Tyr Leu Pro Phe Val Pro Ser Ala Glu Asp Val Tyr Asp

65 70 75 80

Cys Gln Val Glu His Trp Gly Leu Asp Ala Pro Leu Leu Arg His Trp

85 90 95

Glu Leu Gln

<210> 33

<211> 100

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\beta 2$ para el dominio proximal a la membrana de CMH clase II HLA-DO (HLA-DOB*01:01:01:01)

<400> 33

Arg Lys Val Gln Pro Glu Val Thr Val Tyr Pro Glu Arg Thr Pro Leu

1. 5 10 15

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

20 25 30

Gly Asp Ile Lys Ile Lys Trp Phe Leu Asn Gly Gln Glu Glu Arg Ala

35 40 45

Gly Val Met Ser Thr Gly Pro Ile Arg Asn Gly Asp Trp Thr Phe Gln

50 55 60

Thr Val Val Met Leu Glu Met Thr Pro Glu Leu Gly His Val Tyr Thr

65 70 75 80

Cys Leu Val Asp His Ser Ser Leu Leu Ser Pro Val Ser Val Glu Trp

85 90 95

Arg Ala Gln Ser

100

<210> 34

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 2$ para el dominio proximal a la membrana de CMH
clase II HLA-DP (HLA-DPA1*01:03:01:01)

<400> 34

Thr Asn Asp Pro Pro Glu Val Thr Val Phe Pro Lys Glu Pro Val Glu

1. 5 10 15

Leu Gly Gln Pro Asn Thr Leu Ile Cys His Ile Asp Lys Phe Phe Pro

20 25 30

Pro Val Leu Asn Val Thr Trp Leu Cys Asn Gly Glu Leu Val Thr Glu

35 40 45

Gly Val Ala Glu Ser Leu Phe Leu Pro Arg Thr Asp Tyr Ser Phe His

50 55 60

Lys Phe His Tyr Leu Thr Phe Val Pro Ser Ala Glu Asp Phe Tyr Asp

65 70 75 80

Cys Arg Val Glu His Trp Gly Leu Asp Gln Pro Leu Leu Lys His Trp

85 90 95

Glu Ala Gln

<210> 35

<211> 100

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\beta 2$ para el dominio proximal a la membrana de CMH
clase II HLA-DP (HLA-DPB1*01:01:01:01)

<400> 35

Arg Arg Val Gln Pro Lys Val Asn Val Ser Pro Ser Lys Lys Gly Pro

1. 5 10 15

Leu Gln His His Asn Leu Leu Val Cys His Val Thr Asp Phe Tyr Pro

20 25 30

Gly Ser Ile Gln Val Arg Trp Phe Leu Asn Gly Gln Glu Thr Ala

35 40 45

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

50 55 60

Ile Leu Val Met Leu Glu Met Thr Pro Gln Gln Gly Asp Val Tyr Ile

65 70 75 80

Cys Gln Val Glu His Thr Ser Leu Asp Ser Pro Val Thr Val Glu Trp

85 90 95

Lys Ala Gln Ser

100

<210> 36

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 2$ para el dominio proximal a la membrana de CMH
clase II HLA-DQ (HLA-DQA1*01:01:01:01)

<400> 36

Thr Asn Glu Val Pro Glu Val Thr Val Phe Ser Lys Ser Pro Val Thr

1. 5 10 15

Leu Gly Gln Pro Asn Thr Leu Ile Cys Leu Val Asp Asn Ile Phe Pro

20 25 30

Pro Val Val Asn Ile Thr Trp Leu Ser Asn Gly Gln Ser Val Thr Glu

35 40 45

Gly Val Ser Glu Thr Ser Phe Leu Ser Lys Ser Asp His Ser Phe Phe

50 55 60

Lys Ile Ser Tyr Leu Thr Phe Leu Pro Ser Ala Asp Glu Ile Tyr Asp

65 70 75 80

Cys Lys Val Glu His Trp Gly Leu Asp Gln Pro Leu Leu Lys His Trp

85 90 95

Glu Pro Glu

<210> 37

<211> 100

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\beta 2$ para el dominio proximal a la membrana de CMH
clase II HLA-DQ (HLA-DQB1*05:01:01:01)

<400> 37

Arg Arg Val Glu Pro Thr Val Thr Ile Ser Pro Ser Arg Thr Glu Ala

1. 5 10 15

Leu Asn His His Asn Leu Leu Ile Cys Ser Val Thr Asp Phe Tyr Pro

20 25 30

Ser Gln Ile Lys Val Arg Trp Phe Arg Asn Asp Gln Glu Glu Thr Ala

35 40 45

Gly Val Val Ser Thr Pro Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln

50 55 60

Ile Leu Val Met Leu Glu Met Thr Pro Gln Arg Gly Asp Val Tyr Thr

65 70 75 80

Cys His Val Glu His Pro Ser Leu Gln Ser Pro Ile Thr Val Glu Trp

85 90 95

Arg Ala Gln Ser

100

<210> 38

<211> 99

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 2$ para el dominio proximal a la membrana de CMH
clase II HLA-DR (HLA-DRA*01:01:01:01)

<400> 38

Thr Asn Val Pro Pro Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu

1. 5 10 15

Leu Arg Glu Pro Asn Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro

20 25 30

Pro Val Val Asn Val Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr

35 40 45

Gly Val Ser Glu Thr Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg

50 55 60

Lys Phe His Tyr Leu Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp

65 70 75 80

Cys Arg Val Glu His Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp

85 90 95

Glu Phe Asp

<210> 39

<211> 100

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\beta 2$ para el dominio proximal a la membrana de CMH
clase II HLA-DR (HLA-DRB1*01:01:01:01)

<400> 39

Arg Arg Val Glu Pro Lys Val Thr Val Tyr Pro Ser Lys Thr Gln Pro

1. 5 10 15

Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser Gly Phe Tyr Pro

20 25 30

Gly Ser Ile Glu Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Lys Ala

35 40 45
 Gly Val Val Ser Thr Gly Leu Ile Gln Asn Gly Asp Trp Thr Phe Gln
 50 55 60
 Thr Leu Val Met Leu Glu Thr Val Pro Arg Ser Gly Glu Val Tyr Thr
 65 70 75 80
 Cys Gln Val Glu His Pro Ser Val Thr Ser Pro Leu Thr Val Glu Trp
 85 90 95
 Arg Ala Arg Ser
 100

<210> 40

<211> 100

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CD1a

<400> 40

Gln Arg Gln Val Lys Pro Glu Ala Trp Leu Ser His Gly Pro Ser Pro
 1. 5 10 15
 Gly Pro Gly His Leu Gln Leu Val Cys His Val Ser Gly Phe Tyr Pro
 20 25 30
 Lys Pro Val Trp Val Met Trp Met Arg Gly Glu Gln Glu Gln Gly
 35 40 45
 Thr Gln Arg Gly Asp Ile Leu Pro Ser Ala Asp Gly Thr Trp Tyr Leu
 50 55 60
 Arg Ala Thr Leu Glu Val Ala Ala Gly Glu Ala Ala Asp Leu Ser Cys

65 70 75 80
 Arg Val Lys His Ser Ser Leu Glu Gly Gln Asp Ile Val Leu Tyr Trp
 85 90 95
 Glu His His Ser
 100

<210> 41

<211> 97

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CD1b

<400> 41

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

1. 5 10 15

Gly Pro Gly Arg Leu Gln Leu Val Cys His Val Ser Gly Phe Tyr Pro

20 25 30

Lys Pro Val Trp Val Met Trp Met Arg Gly Glu Gln Glu Gln Gln Gly

35 40 45

Thr Gln Leu Gly Asp Ile Leu Pro Asn Ala Asn Trp Thr Trp Tyr Leu

50 55 60

Arg Ala Thr Leu Asp Val Ala Asp Gly Glu Ala Ala Gly Leu Ser Cys

65 70 75 80

Arg Val Lys His Ser Ser Leu Glu Gly Gln Asp Ile Ile Leu Tyr Trp

85 90 95

Arg

<210> 42

<211> 100

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CD1c

<400> 42

His Arg Gln Val Arg Pro Glu Ala Trp Leu Ser Ser Arg Pro Ser Leu

1. 5 10 15

Gly Ser Gly Gln Leu Leu Leu Val Cys His Ala Ser Gly Phe Tyr Pro

20 25 30

Lys Pro Val Trp Val Thr Trp Met Arg Asn Glu Gln Glu Gln Leu Gly

35 40 45

Thr Lys His Gly Asp Ile Leu Pro Asn Ala Asp Gly Thr Trp Tyr Leu

50 55 60

Gln Val Ile Leu Glu Val Ala Ser Glu Glu Pro Ala Gly Leu Ser Cys

65 70 75 80

Arg Val Arg His Ser Ser Leu Gly Gly Gln Asp Ile Ile Leu Tyr Trp

85 90 95

Gly His His Phe

100

<210> 43

<211> 100

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CD1d

<400> 43

Lys Lys Gln Val Lys Pro Lys Ala Trp Leu Ser Arg Gly Pro Ser Pro

1. 5 10 15

Gly Pro Gly Arg Leu Leu Leu Val Cys His Val Ser Gly Phe Tyr Pro

20 25 30

Lys Pro Val Trp Val Lys Trp Met Arg Gly Glu Gln Glu Gln Gln Gly

35 40 45

Thr Gln Pro Gly Asp Ile Leu Pro Asn Ala Asp Glu Thr Trp Tyr Leu

50 55 60

Arg Ala Thr Leu Asp Val Val Ala Gly Glu Ala Ala Gly Leu Ser Cys

65 70 75 80

Arg Val Lys His Ser Ser Leu Glu Gly Gln Asp Ile Val Leu Tyr Trp

85 90 95

Gly Gly Ser Tyr

100

<210> 44

<211> 100

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CD1e

<400> 44

Lys Arg Lys Val Lys Pro Glu Ala Trp Leu Ser Cys Gly Pro Ser Pro

1. 5 10 15

Gly Pro Gly Arg Leu Gln Leu Val Cys His Val Ser Gly Phe Tyr Pro

20 25 30

Lys Pro Val Trp Val Met Trp Met Arg Gly Glu Gln Glu Gln Arg Gly

35 40 45

Thr Gln Arg Gly Asp Val Leu Pro Asn Ala Asp Glu Thr Trp Tyr Leu

50 55 60

Arg Ala Thr Leu Asp Val Ala Ala Gly Glu Ala Ala Gly Leu Ser Cys

65 70 75 80

Arg Val Lys His Ser Ser Leu Gly Gly His Asp Leu Ile Ile His Trp

85 90 95

Gly Gly Tyr Ser

100

<210> 45

<211> 101

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de HFE

<400> 45

Asp Gln Gln Val Pro Pro Leu Val Lys Val Thr His His Val Thr Ser

1. 5 10 15

Ser Val Thr Thr Leu Arg Cys Arg Ala Leu Asn Tyr Tyr Pro Gln Asn

20 25 30

Ile Thr Met Lys Trp Leu Lys Asp Lys Gln Pro Met Asp Ala Lys Glu

35 40 45

Phe Glu Pro Lys Asp Val Leu Pro Asn Gly Asp Gly Thr Tyr Gln Gly

50 55 60

Trp Ile Thr Leu Ala Val Pro Pro Gly Glu Glu Gln Arg Tyr Thr Cys

65 70 75 80

Gln Val Glu His Pro Gly Leu Asp Gln Pro Leu Ile Val Ile Trp Glu

85 90 95

Pro Ser Pro Ser Gly

100

<210> 46

<211> 98

<212> PRT

<213> Secuencia natural

<220>

<223> secuencia de aminoácidos de β 2 universal

microglobulina (β 2M) de CMH clase I o proteínas similares a CMH (CD1,
HFE)

<400> 46

Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala Glu

1. 5 10 15

Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His Pro

20 25 30

Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys

35 40 45

Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu

50 55 60

Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys

65 70 75 80

Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp

85 90 95

Arg Asp

<210> 47

<211> 98

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de β 2 universal

microglobulina (β 2M) de CMH clase I o proteínas similares a CMH (CD1,
HFE) con mutación R12C

<400> 47

Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Cys His Pro Ala Glu

1. 5 10 15

Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His Pro

20 25 30

Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys

35 40 45

Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu

50 55 60

Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys

65 70 75 80

Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp

85 90 95

Arg Asp

<210> 48

<211> 110

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de $\beta 2$ universal

microglobulina ($\beta 2M$) de CMH clase I o proteínas similares a CMH (CD1,

HFE) con mutación R12C + (bisagra) con mutación C220A

<400> 48

Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Cys His Pro Ala Glu

1. 5 10 15

Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His Pro

20 25 30

Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys

35 40 45

Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu

50 55 60

Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys

65 70 75 80

Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp

85 90 95

Arg Asp Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro

100 105 110

<210> 49

<211> 100

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CD1b
con mutación N57C y elongación por 3 aminoácidos GSC en el extremo C terminal

<400> 49

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

1. 5 10 15

Gly Pro Gly Arg Leu Gln Leu Val Cys His Val Ser Gly Phe Tyr Pro

20 25 30

Lys Pro Val Trp Val Met Trp Met Arg Gly Glu Gln Glu Gln Gly

35 40 45

Thr Gln Leu Gly Asp Ile Leu Pro Cys Ala Asn Trp Thr Trp Tyr Leu

50 55 60

Arg Ala Thr Leu Asp Val Ala Asp Gly Glu Ala Ala Gly Leu Ser Cys

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

85 90 95

Arg Gly Ser Cys

100

<210> 50

<211> 99

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CD1b
con mutación N57C y elongación de 2 aminoácidos GS en el extremo C terminal

<400> 50

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

1. 5 10 15

Gly Pro Gly Arg Leu Gln Leu Val Cys His Val Ser Gly Phe Tyr Pro

20 25 30

Lys Pro Val Trp Val Met Trp Met Arg Gly Glu Gln Glu Gln Gly

35 40 45

Thr Gln Leu Gly Asp Ile Leu Pro Cys Ala Asn Trp Thr Trp Tyr Leu

50 55 60

Arg Ala Thr Leu Asp Val Ala Asp Gly Glu Ala Ala Gly Leu Ser Cys

65 70 75 80

Arg Val Lys His Ser Ser Leu Glu Gly Gln Asp Ile Ile Leu Tyr Trp

85 90 95

Arg Gly Ser

<210> 51

<211> 100

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CD1b con mutación N59A y elongación por 3 aminoácidos GSC en el extremo C terminal

<400> 51

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

1. 5 10 15

Gly Pro Gly Arg Leu Gln Leu Val Cys His Val Ser Gly Phe Tyr Pro

20 25 30

Lys Pro Val Trp Val Met Trp Met Arg Gly Glu Gln Glu Gln Gly

35 40 45

Thr Gln Leu Gly Asp Ile Leu Pro Asn Ala Ala Trp Thr Trp Tyr Leu

50 55 60

Arg Ala Thr Leu Asp Val Ala Asp Gly Glu Ala Ala Gly Leu Ser Cys

65 70 75 80

Arg Val Lys His Ser Ser Leu Glu Gly Gln Asp Ile Ile Leu Tyr Trp

85 90 95

Arg Gly Ser Cys

100

<210> 52

<211> 100

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CD1b con mutación N59D y elongación por 3 aminoácidos GSC en el extremo C terminal

<400> 52

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

1. 5 10 15

Gly Pro Gly Arg Leu Gln Leu Val Cys His Val Ser Gly Phe Tyr Pro

20 25 30

Lys Pro Val Trp Val Met Trp Met Arg Gly Glu Gln Glu Gln Gln Gly

35 40 45

Thr Gln Leu Gly Asp Ile Leu Pro Asn Ala Asp Trp Thr Trp Tyr Leu

50 55 60

Arg Ala Thr Leu Asp Val Ala Asp Gly Glu Ala Ala Gly Leu Ser Cys

65 70 75 80

Arg Val Lys His Ser Ser Leu Glu Gly Gln Asp Ile Ile Leu Tyr Trp

85 90 95

Arg Gly Ser Cys

100

<210> 53

<211> 100

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CD1b con mutaciones N57C, N59A y elongación por 3 aminoácidos GSC en el extremo C terminal

<400> 53

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

1. 5 10 15

Gly Pro Gly Arg Leu Gln Leu Val Cys His Val Ser Gly Phe Tyr Pro

20 25 30

Lys Pro Val Trp Val Met Trp Met Arg Gly Glu Gln Glu Gln Gln Gly

35 40 45

Thr Gln Leu Gly Asp Ile Leu Pro Cys Ala Ala Trp Thr Trp Tyr Leu

50 55 60

Arg Ala Thr Leu Asp Val Ala Asp Gly Glu Ala Ala Gly Leu Ser Cys

65 70 75 80

Arg Val Lys His Ser Ser Leu Glu Gly Gln Asp Ile Ile Leu Tyr Trp

85 90 95

Arg Gly Ser Cys

100

<210> 54

<211> 100

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CD1b con mutaciones N57C, N59D y elongación por 3 aminoácidos GSC en el extremo C terminal

<400> 54

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

1. 5 10 15

Gly Pro Gly Arg Leu Gln Leu Val Cys His Val Ser Gly Phe Tyr Pro

20 25 30

Lys Pro Val Trp Val Met Trp Met Arg Gly Glu Gln Glu Gln Gln Gly

35 40 45

Thr Gln Leu Gly Asp Ile Leu Pro Cys Ala Asp Trp Thr Trp Tyr Leu

50 55 60

Arg Ala Thr Leu Asp Val Ala Asp Gly Glu Ala Ala Gly Leu Ser Cys

65 70 75 80

Arg Val Lys His Ser Ser Leu Glu Gly Gln Asp Ile Ile Leu Tyr Trp

85 90 95

Arg Gly Ser Cys

100

<210> 55

<211> 99

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CD1b
con mutaciones N57C, N59A y elongación por 2 aminoácidos GS en
el extremo C terminal

<400> 55

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

1. 5 10 15

Gly Pro Gly Arg Leu Gln Leu Val Cys His Val Ser Gly Phe Tyr Pro

20 25 30

Lys Pro Val Trp Val Met Trp Met Arg Gly Glu Gln Glu Gln Gln Gly

35 40 45

Thr Gln Leu Gly Asp Ile Leu Pro Cys Ala Ala Trp Thr Trp Tyr Leu

50 55 60

Arg Ala Thr Leu Asp Val Ala Asp Gly Glu Ala Ala Gly Leu Ser Cys

65 70 75 80

Arg Val Lys His Ser Ser Leu Glu Gly Gln Asp Ile Ile Leu Tyr Trp

85 90 95

Arg Gly Ser

<210> 56

<211> 99

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CD1b
con mutaciones N57C, N59D y elongación por 2 aminoácidos GS en

el extremo C terminal

<400> 56

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

1. 5 10 15

Gly Pro Gly Arg Leu Gln Leu Val Cys His Val Ser Gly Phe Tyr Pro

20 25 30

Lys Pro Val Trp Val Met Trp Met Arg Gly Glu Gln Glu Gln Gln Gly

35 40 45

Thr Gln Leu Gly Asp Ile Leu Pro Cys Ala Asp Trp Thr Trp Tyr Leu

50 55 60

Arg Ala Thr Leu Asp Val Ala Asp Gly Glu Ala Ala Gly Leu Ser Cys

65 70 75 80

Arg Val Lys His Ser Ser Leu Glu Gly Gln Asp Ile Ile Leu Tyr Trp

85 90 95

Arg Gly Ser

<210> 57

<211> 459

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la primera cadena pesada de candidatos

02-004 y 02-006 (Prolgolimab_VH_HC_hole)

<400> 57

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

1. 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Trp Met Tyr Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Ala Ile Ser Arg Val Asn Ala Lys Asn Thr Met Tyr

65 70 75 80

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

85 90 95

Ala Arg Asp Glu Gly Gly Gly Thr Gly Trp Gly Val Leu Lys Asp Trp

100 105 110

Pro Tyr Gly Leu Asp Ala Trp Gly Gln Gly Thr Leu Val Thr Val Ser

115 120 125

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

130 135 140

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp

145 150 155 160

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr

165 170 175

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr

180 185 190

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

195 200 205

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp

210 215 220

Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro

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

245 250 255
Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val Thr

260 265 270
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn

275 280 285
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg

290 295 300
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val

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

325 330 335
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys

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

355 360 365
Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe

370 375 380
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

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

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

420 425 430
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr

435 440 445
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

450 455

<210> 58

<211> 214

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la primera cadena ligera de candidatos

02-004 y 02-006 (Progolimab_VL_CK)

<400> 58

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

1. 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Asn Val

20 25 30

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

35 40 45

Arg Asp Ser Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser

50 55 60

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

65 70 75 80

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

85 90 95

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

100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly

115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala

130 135 140
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys
 210

<210> 59

<211> 452

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la segunda cadena pesada de candidatos
 02-004 y 02-009 (Ocrelizumab_VH_b2m_Fc_knob)

<400> 59

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

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

50 55 60

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

65 70 75 80

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

85 90 95

Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp

100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ile Gln Arg Thr Pro Lys

115 120 125

Ile Gln Val Tyr Ser Arg His Pro Ala Glu Asn Gly Lys Ser Asn Phe

130 135 140

Leu Asn Cys Tyr Val Ser Gly Phe His Pro Ser Asp Ile Glu Val Asp

145 150 155 160

Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys Val Glu His Ser Asp Leu

165 170 175

Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe

180 185 190

Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys Arg Val Asn His Val Thr

195 200 205

Leu Ser Gln Pro Lys Ile Val Lys Trp Asp Arg Asp Glu Pro Lys Ser

210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala

225 230 235 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu

245 250 255

Tyr Ile Thr Arg Glu Pro Glu Val Thr Cys Val Val Val Asp Val Ser

260 265 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu

275 280 285
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr

290 295 300
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn

305 310 315 320
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro

325 330 335
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln

340 345 350
Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val

355 360 365
Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val

370 375 380
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro

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

405 410 415
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val

420 425 430
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu

435 440 445
Ser Pro Gly Lys

450

<210> 60

<211> 206

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la segunda cadena ligera de candidatos

02-004 y 02-009 (Ocrelizumab_VL_CD1b)

<400> 60

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 Ser Ser Val Ser Tyr Met

20 25 30

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

35 40 45

Ala Pro Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser

50 55 60

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

65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Phe Asn Pro Pro Thr

85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gln Arg Gln Val Lys Pro

100 105 110

Glu Ala Trp Leu Ser Ser Gly Pro Ser Pro Gly Pro Gly Arg Leu Gln

115 120 125

Leu Val Cys His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val Met

130 135 140

Trp Met Arg Gly Glu Gln Glu Gln Gln Gly Thr Gln Leu Gly Asp Ile

145 150 155 160

Leu Pro Asn Ala Asn Trp Thr Trp Tyr Leu Arg Ala Thr Leu Asp Val

165 170 175

Ala Asp Gly Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His Ser Ser

180 185 190
Leu Glu Gly Gln Asp Ile Ile Leu Tyr Trp Arg Gly Ser Cys

195 200 205

<210> 61

<211> 452

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la primera cadena pesada de candidatos
02-005 y 02-008 (Ocrelizumab_VH_ HC_hole)

<400> 61

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1. 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20 25 30

Asn Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

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

85 90 95

Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp

100 105 110

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

115 120 125

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

130 135 140

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

145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro

165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr

180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn

195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser

210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala

225 230 235 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu

245 250 255

Tyr Ile Thr Arg Glu Pro Glu Val Thr Cys Val Val Val Asp Val Ser

260 265 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu

275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr

290 295 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn

305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro

325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln

340 345 350
Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val

355 360 365
Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val

370 375 380
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro

385 390 395 400
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr

405 410 415
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val

420 425 430
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu

435 440 445
Ser Pro Gly Lys

450

<210> 62

<211> 213

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la primera cadena ligera de candidatos
02-005 y 02-008 (Ocrelizumab_VL_CK)

<400> 62

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 Ser Ser Val Ser Tyr Met

20 25 30

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

35 40 45

Ala Pro Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser

50 55 60

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

65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Phe Asn Pro Pro Thr

85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro

100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr

115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys

130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu

145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser

165 170 175

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

180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe

195 200 205

Asn Arg Gly Glu Cys

210

<210> 63

<211> 459

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la segunda cadena pesada de candidatos

02-005 y 02-007 (Prolgolimab_VH_b2m_Fc_knob)

<400> 63

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

1. 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Trp Met Tyr Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Ala Ile Ser Arg Val Asn Ala Lys Asn Thr Met Tyr

65 70 75 80

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

85 90 95

Ala Arg Asp Glu Gly Gly Gly Thr Gly Trp Gly Val Leu Lys Asp Trp

100 105 110

Pro Tyr Gly Leu Asp Ala Trp Gly Gln Gly Thr Leu Val Thr Val Ser

115 120 125

Ser Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala

130 135 140

Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His

145 150 155 160

Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu

165 170 175

Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr

180 185 190

Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala

195 200 205

Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp

210 215 220

Asp Arg Asp Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro

225 230 235 240

Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro

245 250 255

Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val Thr

260 265 270

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn

275 280 285

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg

290 295 300

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val

305 310 315 320

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser

325 330 335

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys

340 345 350

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp

355 360 365

Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe

370 375 380

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

385 390 395 400
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 405 410 415
 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 420 425 430
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 435 440 445
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 450 455

<210> 64

<211> 207

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la segunda cadena ligera de candidatos
 02-005 y 02-007 (Prolgolimab_VL_CD1b)

<400> 64

Gln Pro Val Leu Thr Gln Pro Leu Ser Val Ser Val Ala Leu Gly Gln
 1. 5 10 15
 Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Asn Val
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45
 Arg Asp Ser Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60

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

<210> 65

<211> 454

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la segunda cadena pesada de candidatos

02-006 y 02-008 (Anti-CSF1R_VH_b2m_Fc_knob)

<400> 65

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Arg Pro Gly Gly

1. 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Glu Phe Thr Phe Asp Asp Tyr

20 25 30

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

35 40 45

Ser Ala Ile Ser Trp Asn Gly Gly Ser Thr Asn Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys

85 90 95

Ala Ser Thr Val Glu Val Ala His Arg Arg Leu Tyr Lys Tyr Leu Glu

100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ile Gln Arg Thr

115 120 125

Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala Glu Asn Gly Lys Ser

130 135 140

Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His Pro Ser Asp Ile Glu

145 150 155 160

Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys Val Glu His Ser

165 170 175

Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu Leu Tyr Tyr Thr

180 185 190

Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys Arg Val Asn His

195 200 205

Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp Arg Asp Glu Pro

210 215 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu

225 230 235 240

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp

245 250 255

Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val Thr Cys Val Val Val Asp

260 265 270

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

275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn

290 295 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp

305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro

325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu

340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn

355 360 365

Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile

370 375 380

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

385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys

405 410 415

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

420 425 430

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

435 440 445

Ser Leu Ser Pro Gly Lys

450

<210> 66

<211> 208

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la segunda cadena ligera de candidatos

02-006 y 02-008 (Anti-CSF1R_VL_CD1b)

<400> 66

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

1. 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val

20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr

35 40 45

Gly Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser

50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly

65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ile Ser Ser Asp His

85 90 95

Val Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Gln Arg Gln Val

100 105 110

Lys Pro Glu Ala Trp Leu Ser Ser Gly Pro Ser Pro Gly Pro Gly Arg

115 120 125

Leu Gln Leu Val Cys His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp
 130 135 140
 Val Met Trp Met Arg Gly Glu Gln Glu Gln Gln Gly Thr Gln Leu Gly
 145 150 155 160
 Asp Ile Leu Pro Asn Ala Asn Trp Thr Trp Tyr Leu Arg Ala Thr Leu
 165 170 175
 Asp Val Ala Asp Gly Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His
 180 185 190
 Ser Ser Leu Glu Gly Gln Asp Ile Ile Leu Tyr Trp Arg Gly Ser Cys
 195 200 205

<210> 67

<211> 454

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la primera cadena pesada de candidatos

02-007 y 02-009 (Anti-CSF1R_VH_HC_hole)

<400> 67

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Arg Pro Gly Gly
 1. 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Glu Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45
Ser Ala Ile Ser Trp Asn Gly Gly Ser Thr Asn Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95
Ala Ser Thr Val Glu Val Ala His Arg Arg Leu Tyr Lys Tyr Leu Glu
100 105 110
Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
115 120 125
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
130 135 140
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145 150 155 160
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
165 170 175
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
180 185 190
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
195 200 205
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro
210 215 220
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225 230 235 240
Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
245 250 255
Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val Thr Cys Val Val Val Asp
260 265 270

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

275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn

290 295 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp

305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro

325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu

340 345 350

Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn

355 360 365

Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile

370 375 380

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

385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys

405 410 415

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

420 425 430

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

435 440 445

Ser Leu Ser Pro Gly Lys

450

<210> 68

<211> 215

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la primera cadena ligera de candidatos

02-007 y 02-009 (Anti-CSF1R_VL_CK)

<400> 68

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

1. 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val

20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr

35 40 45

Gly Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser

50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly

65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ile Ser Ser Asp His

85 90 95

Val Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Arg Thr Val Ala

100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser

115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu

130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser

145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu

165 170 175

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

180 185 190

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

195 200 205

Ser Phe Asn Arg Gly Glu Cys

210 215

<210> 69

<211> 459

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la cadena pesada de los candidatos 03-001,
03-005 y 03-006, que comprende microglobulina β 2 universal
(β 2M) con mutación R12C

<400> 69

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

1. 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Trp Met Tyr Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Ala Ile Ser Arg Val Asn Ala Lys Asn Thr Met Tyr

65 70 75 80

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

85 90 95

Ala Arg Asp Glu Gly Gly Gly Thr Gly Trp Gly Val Leu Lys Asp Trp

100 105 110

Pro Tyr Gly Leu Asp Ala Trp Gly Gln Gly Thr Leu Val Thr Val Ser

115 120 125

Ser Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Cys His Pro Ala

130 135 140

Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His

145 150 155 160

Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu

165 170 175

Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr

180 185 190

Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala

195 200 205

Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp

210 215 220

Asp Arg Asp Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro

225 230 235 240

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro

245 250 255

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

260 265 270

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn

275 280 285

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg

290 295 300

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val

305 310 315 320
 Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 325 330 335
 Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 340 345 350
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
 355 360 365
 Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 370 375 380
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 385 390 395 400
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 405 410 415
 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 420 425 430
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 435 440 445
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 450 455

<210> 70

<211> 459

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la cadena pesada de los candidatos 03-003
 y 03-004, que comprende microglobulina β 2 universal (β 2M)

<400> 70

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

1. 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Trp Met Tyr Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Ala Ile Ser Arg Val Asn Ala Lys Asn Thr Met Tyr

65 70 75 80

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

85 90 95

Ala Arg Asp Glu Gly Gly Gly Thr Gly Trp Gly Val Leu Lys Asp Trp

100 105 110

Pro Tyr Gly Leu Asp Ala Trp Gly Gln Gly Thr Leu Val Thr Val Ser

115 120 125

Ser Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala

130 135 140

Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His

145 150 155 160

Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu

165 170 175

Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr

180 185 190

Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala

195 200 205

Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp

210	215	220	
Asp Arg Asp Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro			
225	230	235	240
Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro			
245	250	255	
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr			
260	265	270	
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn			
275	280	285	
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg			
290	295	300	
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val			
305	310	315	320
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser			
325	330	335	
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys			
340	345	350	
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu			
355	360	365	
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe			
370	375	380	
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu			
385	390	395	400
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe			
405	410	415	
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly			
420	425	430	
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr			
435	440	445	

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

450

455

<210> 71

<211> 459

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la cadena pesada de los candidatos 03-002, 03-007 y 03-008, que comprende microglobulina β 2 universal (β 2M) con mutación R12C y (bisagra) con mutación C220A

<400> 71

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

1. 5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Trp Met Tyr Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

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

50

55

60

Lys Gly Arg Phe Ala Ile Ser Arg Val Asn Ala Lys Asn Thr Met Tyr

65

70

75

80

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

85

90

95

Ala Arg Asp Glu Gly Gly Gly Thr Gly Trp Gly Val Leu Lys Asp Trp

100

105

110

Pro Tyr Gly Leu Asp Ala Trp Gly Gln Gly Thr Leu Val Thr Val Ser

115 120 125

Ser Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Cys His Pro Ala

130 135 140

Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His

145 150 155 160

Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu

165 170 175

Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr

180 185 190

Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala

195 200 205

Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp

210 215 220

Asp Arg Asp Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro

225 230 235 240

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro

245 250 255

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

260 265 270

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn

275 280 285

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg

290 295 300

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val

305 310 315 320

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser

325 330 335

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys

340 345 350
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
 355 360 365
 Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 370 375 380
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 385 390 395 400
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 405 410 415
 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 420 425 430
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 435 440 445
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 450 455

<210> 72

<211> 207

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la cadena ligera del candidato 03-001,
 que comprende $\alpha 3$ para el dominio proximal a la membrana de CD1b con mutación N57C

<400> 72

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

1. 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Asn Val
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45
 Arg Asp Ser Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60
 Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Ala Gln Ala Gly
 65 70 75 80
 Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Thr Ala Val
 85 90 95
 Phe Gly Thr Gly Thr Lys Leu Thr Val Leu Gln Gln Arg Gln Val Lys
 100 105 110
 Pro Glu Ala Trp Leu Ser Ser Gly Pro Ser Pro Gly Pro Gly Arg Leu
 115 120 125
 Gln Leu Val Cys His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val
 130 135 140
 Met Trp Met Arg Gly Glu Gln Glu Gln Gln Gly Thr Gln Leu Gly Asp
 145 150 155 160
 Ile Leu Pro Cys Ala Asn Trp Thr Trp Tyr Leu Arg Ala Thr Leu Asp
 165 170 175
 Val Ala Asp Gly Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His Ser
 180 185 190
 Ser Leu Glu Gly Gln Asp Ile Ile Leu Tyr Trp Arg Gly Ser Cys
 195 200 205

<210> 73

<211> 206

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la cadena ligera del candidato 03-002,
que comprende $\alpha 3$ para el dominio proximal a la membrana de CD1b con mutación N57C

<400> 73

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

1. 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Asn Val

20 25 30

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

35 40 45

Arg Asp Ser Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser

50 55 60

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

65 70 75 80

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

85 90 95

Phe Gly Thr Gly Thr Lys Leu Thr Val Leu Gln Gln Arg Gln Val Lys

100 105 110

Pro Glu Ala Trp Leu Ser Ser Gly Pro Ser Pro Gly Pro Gly Arg Leu

115 120 125

Gln Leu Val Cys His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val

130 135 140

Met Trp Met Arg Gly Glu Gln Glu Gln Gln Gly Thr Gln Leu Gly Asp

145 150 155 160

Ile Leu Pro Cys Ala Asn Trp Thr Trp Tyr Leu Arg Ala Thr Leu Asp

165 170 175

Val Ala Asp Gly Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His Ser

180 185 190

Ser Leu Glu Gly Gln Asp Ile Ile Leu Tyr Trp Arg Gly Ser

195 200 205

<210> 74

<211> 207

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la cadena ligera del candidato 03-003,

que comprende $\alpha 3$ para el dominio proximal a la membrana de CD1b con mutación N59A

<400> 74

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

1. 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Asn Val

20 25 30

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

35 40 45

Arg Asp Ser Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser

50 55 60

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

65 70 75 80

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

85 90 95

Phe Gly Thr Gly Thr Lys Leu Thr Val Leu Gln Gln Arg Gln Val Lys

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

<210> 75

<211> 207

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la cadena ligera del candidato 03-004,
 que comprende $\alpha 3$ para el dominio proximal a la membrana de CD1b con mutación N59D

<400> 75

Gln Pro Val Leu Thr Gln Pro Leu Ser Val Ser Val Ala Leu Gly Gln
 1. 5 10 15
 Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Asn Val
 20 25 30

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

35 40 45

Arg Asp Ser Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser

50 55 60

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

65 70 75 80

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

85 90 95

Phe Gly Thr Gly Thr Lys Leu Thr Val Leu Gln Gln Arg Gln Val Lys

100 105 110

Pro Glu Ala Trp Leu Ser Ser Gly Pro Ser Pro Gly Pro Gly Arg Leu

115 120 125

Gln Leu Val Cys His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val

130 135 140

Met Trp Met Arg Gly Glu Gln Glu Gln Gln Gly Thr Gln Leu Gly Asp

145 150 155 160

Ile Leu Pro Asn Ala Asp Trp Thr Trp Tyr Leu Arg Ala Thr Leu Asp

165 170 175

Val Ala Asp Gly Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His Ser

180 185 190

Ser Leu Glu Gly Gln Asp Ile Ile Leu Tyr Trp Arg Gly Ser Cys

195 200 205

<210> 76

<211> 207

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la cadena ligera del candidato 03-005,
que comprende $\alpha 3$ para el dominio proximal a la membrana de CD1b con mutaciones N57C,
N59A

<400> 76

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

1. 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Asn Val

20 25 30

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

35 40 45

Arg Asp Ser Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser

50 55 60

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

65 70 75 80

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

85 90 95

Phe Gly Thr Gly Thr Lys Leu Thr Val Leu Gln Gln Arg Gln Val Lys

100 105 110

Pro Glu Ala Trp Leu Ser Ser Gly Pro Ser Pro Gly Pro Gly Arg Leu

115 120 125

Gln Leu Val Cys His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val

130 135 140

Met Trp Met Arg Gly Glu Gln Glu Gln Gln Gly Thr Gln Leu Gly Asp

145 150 155 160

Ile Leu Pro Cys Ala Ala Trp Thr Trp Tyr Leu Arg Ala Thr Leu Asp

165 170 175

Val Ala Asp Gly Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His Ser

180 185 190
Ser Leu Glu Gly Gln Asp Ile Ile Leu Tyr Trp Arg Gly Ser Cys

195 200 205

<210> 77

<211> 207

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la cadena ligera del candidato 03-006,
que comprende $\alpha 3$ para el dominio proximal a la membrana de CD1b con mutaciones N57C,
N59D

<400> 77

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

1. 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Asn Val

20 25 30

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

35 40 45

Arg Asp Ser Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser

50 55 60

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

65 70 75 80

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

85 90 95

Phe Gly Thr Gly Thr Lys Leu Thr Val Leu Gln Gln Arg Gln Val Lys

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

<210> 78

<211> 206

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la cadena ligera del candidato 03-007,
 que comprende $\alpha 3$ para el dominio proximal a la membrana de CD1b con mutaciones N57C,
 N59A

<400> 78

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

1. 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Asn Val

20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45
 Arg Asp Ser Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60
 Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Ala Gln Ala Gly
 65 70 75 80
 Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Thr Ala Val
 85 90 95
 Phe Gly Thr Gly Thr Lys Leu Thr Val Leu Gln Gln Arg Gln Val Lys
 100 105 110
 Pro Glu Ala Trp Leu Ser Ser Gly Pro Ser Pro Gly Pro Gly Arg Leu
 115 120 125
 Gln Leu Val Cys His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val
 130 135 140
 Met Trp Met Arg Gly Glu Gln Glu Gln Gln Gly Thr Gln Leu Gly Asp
 145 150 155 160
 Ile Leu Pro Cys Ala Ala Trp Thr Trp Tyr Leu Arg Ala Thr Leu Asp
 165 170 175
 Val Ala Asp Gly Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His Ser
 180 185 190
 Ser Leu Glu Gly Gln Asp Ile Ile Leu Tyr Trp Arg Gly Ser
 195 200 205

<210> 79

<211> 206

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de la cadena ligera del candidato 03-008,
que comprende $\alpha 3$ para el dominio proximal a la membrana de CD1b con mutaciones N57C,
N59D

<400> 79

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

1. 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Asn Val

20 25 30

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

35 40 45

Arg Asp Ser Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser

50 55 60

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

65 70 75 80

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

85 90 95

Phe Gly Thr Gly Thr Lys Leu Thr Val Leu Gln Gln Arg Gln Val Lys

100 105 110

Pro Glu Ala Trp Leu Ser Ser Gly Pro Ser Pro Gly Pro Gly Arg Leu

115 120 125

Gln Leu Val Cys His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val

130 135 140

Met Trp Met Arg Gly Glu Gln Glu Gln Gln Gly Thr Gln Leu Gly Asp

145 150 155 160

Ile Leu Pro Cys Ala Asp Trp Thr Trp Tyr Leu Arg Ala Thr Leu Asp

165 170 175

Val Ala Asp Gly Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His Ser

180 185 190

Ser Leu Glu Gly Gln Asp Ile Ile Leu Tyr Trp Arg Gly Ser

195 200 205

<210> 80

<211> 1377

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido
de la primera cadena pesada de candidatos 02-004 y 02-006
(Prolgolimab_VH_HC_hole)

<400> 80

caggttcagc tgggtgcagtc tgggggaggc ttgggtgcagc ctgggggggtc tctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctactgga tgtattgggt ccgccagggt 120

ccaggggaagg ggctcgagtg ggtctcagct attgatactg gtggtggtag gacatactat 180

gcagactccg tgaagggccg gttcgccatc tccagagtca acgccaagaa cacaatgtat 240

ctgcaaata acagcctgag agccgaggac acggccgtgt attactgtgc gagagatgaa 300

ggcgggggta cgggttgggg tgttttgaag gattggccct acggcttgga cgcatggggc 360

caggggaccc tggtcaccgt ctctcagct agcaccaagg gcccatcggg cttccccctg 420

gcaccctcct ccaagagcac ctctgggggc acagcggccc tgggctgcct ggtcaaggac 480

tacttccccg aaccggtgac ggtgtcgtgg aactcaggcg ccctgaccag cggcgtgcac 540

accttcccgg ctgtcctaca gtcctcagga ctctactccc tcagcagcgt ggtgaccgtg 600

ccctccagca gcttgggcac ccagacctac atctgcaacg tgaatcaca gccagcaac 660

accaaggtgg acaagagagt tgagccaaa tcttgtaga aaactcacac atgccaccg 720

tgcccagcac ctgaagccgc agggggaccg tcagtcttcc tttcccccc aaaaccaag 780

gacaccctct acatcacccg ggagcctgag gtcacatgcg tgggtgtgga cgtgagccac 840

gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatccaag 900

acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc 960

ctgcaccagg actggctgaa tggcaaggag tacaagtga aggtctcaa caaagccctc 1020

ccagcccca tcgagaaaac catctcaaa gccaaagggc agccccgaga accacaggtg 1080

tgaccctgc cccatcccg ggatgagctg accaagaacc aggtcagcct gtctgcgcc 1140

gtcaaaggct tctatcccag cgacatgcc gtggagtggg agagcaatgg gcagccggag 1200

aacaactaca agaccagcc tccgtgctg gactccgacg gtccttctt cctcgtcagc 1260

aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1320

catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtcccc gggtaaa 1377

<210> 81

<211> 642

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido
de la primera cadena ligera de los candidatos 02-004 y 02-006
(Prolgolimab_VL_CK)

<400> 81

cagcctgtgc tgactcagcc actctcagtgc tcagtggccc tgggacagac ggccaggatt 60

acctgtgggg gaaacaacat tggaagtaaa aatgtgcact ggtaccagca gaagccaggc 120

caggcccctg tgctgggtcat ctatagggat agcaaccggc cctctgggat ccctgagcga 180

ttctctggct ccaactcggg gaacacggcc accctgacca tcagcagagc ccaagccggg 240

gatgaggctg actattactg tcagggtgtg gacagcagca ctgtgtctt cggaactggg 300

accaagctga ccgtcctaca gcgtacggtg gctgcacat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 82

<211> 1356

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido
de la segunda cadena pesada de candidatos 02-004 y 02-009
(Ocrelizumab_VH_b2m_Fc_knob)

<400> 82

gaagtccaat tagtagaatc aggcggcggc ttagtgcaac ccggtggctc actgcgtttg 60

agctgtgctg ctatgggcta tacctttacg tcctacaaca tgcatgggtg gagacaagca 120

cctggcaagg gtctcgaatg ggtaggcgct atctatccag gaaatggtga cacctcttac 180

aaccagaagt ttaagggctg ctttaccatc tcggtcgata agagcaagaa caccctgtac 240

ctacagatga attcggtacg ggagaggac acagccgtct attactgcgc tcgggtggtg 300

tattactcca actcttactg gtacttcgac gttggggcc agggaactct tgtgaccgtg 360

agctctatcc aacgcacacc aaagatccag gtctattcgc ggcatccggc agaaaacgga 420

aagagtaact tcctgaactg ctatgtatcg ggctttcatc caagtatat cgagggtggac 480

ctgctgaaga acggagagag aatcgagaag gtggaacact cggacctgag cttctccaag 540

gactggagtt tctacctgct gtactatacc gagttcacc cgacagaaaa ggacgaatac 600

gcatgtcggg tcaatcatgt caccctgagt cagccgaaaa tcgtaaagtg ggatcgggac 660

gagcccaaat ctgtgacaa aactcacaca tgcccaccgt gccagcacc tgaagccgct 720

ggggggaccgt cagtcttctt cttccccca aaaccaagg acaccctcta catcaccggg 780

gaacctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 840

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 900

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 960

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1020

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatgccgg 1080

gatgagctga ccaagaacca ggtcagcctg tggcgcctgg tcaaaggctt ctatcccagc 1140

gacatgccg tggagtggga gagcaatggg cagccggaga acaactaaa gaccacgcct 1200

cccgtgctgg actccgacgg ctcttcttc ctctatagca agctcacctg ggacaagagc 1260

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1320

tacacgcaga agagcctctc cctgtccccg ggtaaa 1356

<210> 83

<211> 618

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido
de la segunda cadena ligera de los candidatos 02-004 y 02-009
(Ocrelizumab_VL_CD1b)

<400> 83

gacattcaaa tgaccaatc gccatcttcg ctttcagctt cggtaggaga tcgcgtaacc 60

attacatgcc gggcctcgtc ttcggtctcg tacatgcatt ggtatcagca aaaaccagga 120

aaagctcca aaccctgat ctacgaccc tctaactgg cttctggcgt cccgtcgagg 180

tttcgggtt ctggctctgg cacagacttt acactacca tctcgtcgt gcagccagag 240

gattttgcca cctactactg tcagcaatgg tctttaatc caccaacatt cggccagggg 300

accaaagtag aaatcaaaca gagacagggt aaaccagagg catggctaag ttctggacct 360

tcacctggac ctggtagatt acaattagta tgtcatgtgt cgggatttta tcctaaacct 420

gtttgggtca tgtggatgag gggcgagcaa gagcagcaag gaacacagtt aggcgacatc 480

ctgccgaatg caaactggac atggtactta agagcaaccc tggatgtagc ggacggcgaa 540

gccgctggat tatcgtgccg ggtaaagcat tcgtcgtgg agggccaaga cataatactc 600

tattggcgcg gtagttgc 618

<210> 84

<211> 1356

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido

de la primera cadena pesada de candidatos 02-005 y 02-008

(Ocrelizumab_VH_ HC_hole)

<400> 84

gaagtccaat tagtagaatc aggcggcggc ttagtgcaac ccggtggctc actgcgtttg 60

agctgtgctg ctagtggcta tacctttacg tcctacaaca tgcattgggt gagacaagca 120

cctggcaagg gtctcgaatg ggtaggcgct atctatccag gaaatgggtga cacctcttac 180

aaccagaagt ttaagggctg ctttaccatc tcggtcgata agagcaagaa caccctgtac 240

ctacagatga attcgttacg ggcagaggac acagccgtct attactgcgc tcgggtggta 300

tattactcca actcttactg gtacttcgac gtttggggcc agggaactct tgtgaccgtg 360

agctctgcta gcaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc 420

tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480

gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca cttcccggc tgcctacag 540

tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600

cagacctaca tctgcaacgt gaatcacaag ccagcaaca ccaaggtgga caagagagtt 660

gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaagccgca 720

gggggaccgt cagtcttctt cttccccca aaaccaagg acaccctcta catcaccgg 780

gagcctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 840

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 900

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 960

ggcaaggagt acaagtgcaa ggtctcaac aaagccctcc cagcccccat cgagaaaacc 1020

atctccaaag ccaaagggca gccccgagaa ccacaggtgt gcaccctgcc cccatcccgg 1080

gatgagctga ccaagaacca ggtcagcctg tctgcgccg tcaaaggctt ctatcccagc 1140

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactaaa gaccacgcct 1200

cccgtgctgg actccgacgg ctcttcttc ctcgtcagca agctcaccgt ggacaagagc 1260

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1320

tacacgcaga agagcctctc cctgtccccg ggtaaa 1356

<210> 85

<211> 639

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido
de la primera cadena ligera de los candidatos 02-005 y 02-008

(Ocrelizumab_VL_CK)

<400> 85

gacattcaaa tgaccaatc gccatcttcg ctttcagctt cggtaggaga tcgcgtaacc 60

attacatgcc gggcctcgtc ttcggtctcg tacatgcatt ggtatcagca aaaaccagga 120

aaagctcca aaccctgat ctacgcacc tctaacctgg cttctggcgt cccgtcgagg 180

tttcggggtt ctggctctgg cacagacttt acacttacca tctcgtcgt gcagccagag 240

gattttgcca cctactactg tcagcaatgg tctttaatc caccaacatt cggccagggg 300

accaaagtag aatcaaacg tacggtggct gcacatctg tttcatctt cccgcatct 360

gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc 420

agagaggcca aagtacagt gaaggtggat aacgccctcc aatcgggtaa ctcccaggag 480

agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg 540

agcaaagcag actacagaaa acacaaagtc tacgcctgcg aagtcacca tcagggcctg 600

agctcgcccg tcacaaagag cttcaacagg ggagagtgt 639

<210> 86

<211> 1377

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido
de la segunda cadena pesada de candidatos 02-005 y 02-007
(Prolgolimab_VH_b2m_Fc_knob)

<400> 86

caggttcagc tgggtcagtc tgggggaggc ttgggtcagc ctggggggtc tctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctactgga tgtattgggt ccgccagggt 120

ccaggggaagg ggctcgagtg ggtctcagct attgatactg gtggtggtag gacatactat 180

gcagactccg tgaagggccg gttcgccatc tccagagtca acgccaagaa cacaatgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagatgaa 300

ggcgggggta cgggttgggg tgttttgaag gattggccct acggccttga cgcatggggc 360

caggggaccc tggtcaccgt ctctcaatc caacgcacac caaagatcca ggtctattcg 420

cggcatccgg cagaaaacgg aaagagtaac ttctgaact gctatgtatc gggctttcat 480

ccaagtgata tcgaggtgga cctgctgaag aacggagaga gaatcgagaa ggtggaacac 540

tcggacctga gcttctcaa ggactggagt ttctacctgc tgtactatac cgagttcacc 600

ccgacagaaa aggacgaata cgcattgctg gtcaatcatg tcacctgag tcagccgaaa 660

atcgtaaagt gggatcggga cgagcccaaa tcttgtaga aaactcacac atgccaccg 720

tgccagcac ctgaagccg tgggggaccg tcagtcttc tctcccc aaaccaag 780

gacacctct acatcacccg ggaacctgag gtacatgctg tgggtggga cgtgagccac 840

gaagacctg aggtcaagtt caactggtag gtggacggc tggaggtgca taatccaag 900

acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctaccgtc 960

ctgcaccagg actggctgaa tggcaaggag tacaagtga aggtctcaa caaagccctc 1020

ccagcccca tcgagaaaac catctcaaa gccaaagggc agccccgaga accacaggtg 1080

tacacctgc cccatgccg ggatgagctg accaagaacc aggtcagcct gtggtgcctg 1140

gtcaaaggct tctatcccag cgacatgcc gtggagtggg agagcaatgg gcagccggag 1200

aacaactaca agaccagcc tccgtgctg gactccgac gctcctctt cctctatagc 1260

aagtcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1320

catgaggctc tgcacaacca ctacgcag aagagcctct cctgtcccc gggtaaa 1377

<210> 87

<211> 621

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido

de la segunda cadena ligera de los candidatos 02-005 y 02-007

(Prolgolimab_VL_CD1b)

<400> 87

cagcctgtgc tgactcagcc actctcagtg tcagtggccc tgggacagac ggccaggatt 60

acctgtgggg gaaacaacat tggaagtaaa aatgtgcact ggtaccagca gaagccaggc 120

caggcccctg tgctgggtcat ctatagggat agcaaccggc cctctgggat ccctgagcga 180

ttctctggct ccaactcggg gaacacggcc accctgacca tcagcagagc ccaagccggg 240

gatgaggctg actattactg tcagggtggtg gacagcagca ctgctgtctt cggaactggg 300

accaagctga ccgtcctaca gcagagacag gttaaaccag aggcatggct aagttctgga 360

ccttcacctg gacctggtag attacaatta gtatgtcatg tgtcgggatt ttatcctaaa 420

cctgtttggg tcatgtggat gaggggag caagagcagc aaggaacaca gtaggcgac 480

atcctgccga atgcaaaactg gacatggtac ttaagagcaa ccctggatgt agcggacggc 540

gaagccgctg gattatcgtg ccgggtaaag cattcgtcgc tggagggccca agacataata 600

ctctattggc gcggtagttg c

621

<210> 88

<211> 1362

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido
de la segunda cadena pesada de candidatos 02-006 y 02-008
(Anti-CSF1R_VH_b2m_Fc_knob)

<400> 88

caagtcagtg ttgtagaaag cggcggaggt ttggttaggc ccggaggcag cctgagatta 60

tcctgtgcag caagcgagtt cacttttgat gactatgcga tgagttgggt gcgacaagct 120

cctggaaagg gattggaatg ggtgtcagcg atctcatgga atggcggatc aactaactac 180

gcagattctg tcaagggcag gttaccatc tcccgggata acgcaaagaa tagtctgtac 240

cttcaaatga acagtctcgc cgctgaggac actgccttat attattgcgc aagcactgtg 300

gaagtagccc accgacggtt gtataagtac ctccaagtat ggggtcaggg aacactggtc 360

acagtaagct caatccaacg cacaccaaag atccaggtct attcgcggca tccggcagaa 420

aacggaaaga gtaacttct gaactgctat gtatcgggct ttcaccaag tgatcgcag 480

gtggacctgc tgaagaacgg agagagaatc gagaaggagg aacactcgga cctgagcttc 540

tccaaggact ggagtttcta cctgctgtac tataccgagt tcaccccgac agaaaaggac 600

gaatacgcat gtcgggtcaa tcatgtcacc ctgagtcagc cgaaaatcgt aaagtgggat 660

cgggacgagc ccaaattctg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 720

gccgctgggg gaccgtcagt cttcctctc ccccaaaaac ccaaggacac cctctacatc 780

acccgggaac ctgaggtcac atgcgtgggtg gtggacgtga gccacgaaga ccctgaggtc 840

aaattcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 900

gagcagtaca acagcacgta ccgtgtgggtc agcgtcctca ccgtcctgca ccaggactgg 960

ctgaatggca aggagtacaa gtgcaagggtc tccaacaaag ccctcccagc ccccatcgag 1020

aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 1080

tgccgggatg agctgaccaa gaaccagggtc agcctgtggt gcctgggtcaa aggcttctat 1140

cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cgagaacaa ctacaagacc 1200

acgcctcccg tgctggactc cgacggctcc ttcttctct atagcaagct caccgtggac 1260

aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1320

aaccactaca cgcagaagag cctctccctg tccccgggta aa 1362

<210> 89

<211> 624

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido
de la segunda cadena ligera de los candidatos 02-006 y 02-008
(Anti-CSF1R_VL_CD1b)

<400> 89

caggcagggc tgactcagcc accctcgggtg tcagtggccc caggacagac ggccaggatt 60

accgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc 120

caggcccctg tgctggctgt ctatggtgat agcgaccggc cctcagggat ccctgagcga 180

ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaagccggg 240

gatgaggccg actattactg tcaggtgtgg gatattagta gtgatcatgt ggtattcggc 300

ggagggaccc agctcaccgt ttacagaga caggtaaac cagaggcatg gctaagttct 360

ggaccttcac ctggacctgg tagattacaa ttagtatgtc atgtgtcggg attttatcct 420

aaacctgttt gggcatgtg gatgaggggc gagcaagagc agcaaggaac acagttaggc 480

gacatcctgc cgaatgcaaa ctggacatgg tacttaagag caaccctgga ttagcggac 540

ggcgaagccg ctggattatc gtgccgggta aagcattcgt cgctggaggg ccaagacata 600

atactctatt ggcgcggtag ttgc 624

<210> 90

<211> 1362

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido
de la primera cadena pesada de candidatos 02-007 y 02-009
(Anti-CSF1R_VH_HC_hole)

<400> 90

caagtccagt tggtagaaag cggcggaggt ttggttaggc ccggaggcag cctgagatta 60

tcctgtgcag caagcgagtt cacttttgat gactatgcga tgagttgggt gcgacaagct 120

cctggaaagg gattggaatg ggtgtcagcg atctcatgga atggcggatc aactaactac 180

gcagattctg tcaagggcag gtttaccatc tcccgggata acgcaaagaa tagtctgtac 240

cttcaaatga acagtctgcg cgctgaggac actgccttat attattgcgc aagcactgtg 300

gaagtagccc accgacgggt gtataagtac ctggaagtat ggggtcaggg aacactggtc 360

acagtaagct cagctagcac caagggccca tcggtcttcc ccctggcacc ctctccaag 420

agcacctctg ggggcacagc ggccctgggc tgcctgttca aggactactt cccgaaccg 480

gtgacgggtg cgtggaactc aggcgccttg accagcggcg tgcacacctt cccggctgtc 540

ctacagtctt caggactcta ctcctcagc agcgtggtga ccgtgccctc cagcagcttg 600

ggcaccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 660

agagttgagc ccaaattctg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 720

gccgcagggg gaccgtcagt cttcctcttc ccccaaaac ccaaggacac cctctacatc 780

accggggagc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 840

aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 900

gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtctgca ccaggactgg 960

ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 1020

aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtgcac cctgccccca 1080

tcccgggatg agctgaccaa gaaccaggctc agcctgtcct gcgccgtcaa aggcttctat 1140

cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1200

acgcctcccg tgctggactc cgacggctcc ttcttctcg tcagcaagct caccgtggac 1260

aagagcaggc ggcagcaggg gaacgtcttc tcattgtccg tgatgcatga ggctctgcac 1320

aaccactaca cgcagaagag cctctccctg tccccgggta aa 1362

<210> 91

<211> 645

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido
de la primera cadena ligera de los candidatos 02-007 y 02-009
(Anti-CSF1R_VL_CK)

<400> 91

caggcagggc tgactcagcc accctcgggtg tcagtggccc caggacagac ggccaggatt 60

acctgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc 120

caggcccctg tgctggctgt ctatggtgat agcgaccggc cctcagggat ccctgagcga 180

ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaagccggg 240

gatgaggccg actattactg tcaggtgtgg gatattagta gtgatcatgt ggtattcggc 300

ggagggaccc agctcaccgt ttacgtacg gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> 92

<211> 1377

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido

de cadena pesada de candidatos 03-001 y 03-005,

que comprende microglobulina $\beta 2$ universal ($\beta 2M$) con mutación

R12C

<400> 92

caggttcagc tggcgcagtc tgggggaggc ttggtgcagc ctgggggggc tctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctactgga tgtattgggt ccgccaggtt 120

ccaggggaagg ggctcgagtg ggtctcagct attgatactg gtggtggtag gacatactat 180

gcagactccg tgaagggccg gttcccatc tccagagtca acgccaagaa cacaatgtat 240

ctgcaaata acagcctgag agccgaggac acggccgtgt attactgtgc gagagatgaa 300

ggcgggggta cgggttgggg tgtttgaag gattggccct acggcttgga cgcatggggc 360

caggggaccc tggtcaccgt ctctcaatc caacgcacac caaagatcca ggtctattcg 420

tgccatccgg cagaaaacgg aaagagtaac ttctgaact gctatgtatc gggctttcat 480

ccaagtata tcgaggtgga cctgtgaag aacggagaga gaatcgagaa ggtggaacac 540

tcggacctga gcttctcaa ggactggagt ttctacctgc tgtactatac cgagttcacc 600

ccgacagaaa aggacgaata cgcatgtcgg gtcaatcatg tcaccctgag tcagccgaaa 660

atcgtaaagt gggatcggga cgagcccaaa tcttgtaga aaactcacac atgccaccg 720

tgtccagcac ctgaactcct ggggggaccg tcagtcttcc tttccccc aaaaccaag 780

gacacctca tgatctccc gaccctgag gtcacatgc tgggtgtgga cgtgagccac 840

gaagaccctg aggtcaagtt caactggtag gtggacggcg tggaggtgca taatgccaag 900

acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc 960

ctgcaccagg actggctgaa tggcaaggag tacaagtga aggtctccaa caaagccctc 1020

ccagccccca tcgagaaaac catctccaaa gccaaagggc agccccgaga accacaggtg 1080

tacaccctgc ccccatcccg ggaggagatg accaagaacc aggtcagcct gacctgcctg 1140

gtcaaaggct tctatcccag cgacatgcc gtggagtggg agagcaatgg gcagccggag 1200

aacaactaca agaccagcc tccgtgctg gactccgacg gctccttctt cctctatagc 1260

aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1320

catgaggctc tgcacaacca ctacacgcag aaaagcctct ccctgtcccc gggtaaa 1377

<210> 93

<211> 1377

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido

de cadena pesada de candidatos 03-003 y 03-004,

que comprende microglobulina $\beta 2$ universal ($\beta 2M$)

<400> 93

caggttcagc tgggtcagtc tgggggaggc ttggtgcagc ctggggggtc tctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctactgga tgtattgggt ccgccaggtt 120

ccaggggaagg ggctcgagtg ggtctcagct attgatactg gtggtggtag gacatactat 180

gcagactccg tgaagggccg gttcgccatc tccagagtca acgccaagaa cacaatgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagatgaa 300

ggcgggggta cgggttgggg tgtttgaag gattggccct acggcttga cgcatggggc 360

caggggaccc tggtcaccgt ctctcaatc caacgcacac caaagatcca ggtctattcg 420

cgcatccgg cagaaaacgg aaagagtaac ttctgaact gctatgtatc gggctttcat 480

ccaagtgata tcgaggtgga cctgtgaag aacggagaga gaatcgagaa ggtggaacac 540

tcggacctga gcttctcaa ggactggagt ttctacctgc tgtactatac cgagttcacc 600

ccgacagaaa aggacgaata cgcatgtcgg gtcaatcatg tcaccctgag tcagccgaaa 660

atcgtaaagt gggatcgga cgagcccaa tcttgtaga aaactcacac atgccaccg 720

tgtccagcac ctgaactct ggggggaccg tcagtcttc tttccccc aaaaccaag 780

gacaccctca tgatctcccg gaccctgag gtcacatgcg tgggtgtgga cgtgagccac 840

gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag 900

acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc 960

ctgcaccagg actggctgaa tggcaaggag tacaagtga aggtctcaa caaagccctc 1020

ccagccccc tcgagaaaac catctcaaa gccaaagggc agccccgaga accacaggtg 1080

tacaccctgc ccccatcccg ggaggagatg accaagaacc aggtcagcct gacctgcctg 1140

gtcaaaggct tctatcccag cgacatgcc gtggagtggg agagcaatgg gcagccggag 1200

aacaactaca agaccacgcc tccgtgctg gactccgacg gctccttct cctctatagc 1260

aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1320

catgaggctc tgcacaacca ctacacgcag aaaagcctct ccctgtcccc gggtaaa 1377

<210> 94

<211> 1377

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido

de cadena pesada de candidatos 03-002, 03-007 y
03-008, que comprende microglobulina $\beta 2$ universal ($\beta 2M$) con
mutación R12C y bisagra con mutación C220A

<400> 94

caggttcagc tgggtcagtc tgggggaggc ttgggtcagc ctggggggtc tctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctactgga tgtattgggt ccgccaggtt 120

ccaggaagg ggctcagtg ggtctcagct attgatactg gtggtggtag gacatactat 180

gcagactccg tgaagggccg gttcgccatc tccagagtca acgccaagaa cacaatgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagatgaa 300

ggcgggggta cgggttgggg tgttttgaag gattggccct acggcttga cgcatggggc 360

caggggaccc tggtcaccgt ctctcaatc caacgcacac caaagatcca ggtctattcg 420

tgccatccgg cagaaaacgg aaagagtaac ttctgaact gctatgtatc gggctttcat 480

ccaagtgata tcgaggtgga cctgctgaag aacggagaga gaatcgagaa ggtggaacac 540

tcggacctga gcttctcaa ggactggagt ttctacctgc tgtactatac cgagttcacc 600

ccgacagaaa aggacgaata cgcattgctg gtcaatcatg tcaccctgag tcagccgaaa 660

atcgtaaagt gggatcgga cgagcccaaa tctgccgaca aaactcacac atgccaccg 720

tgcccagcac ctgaactcct ggggggaccg tcagtcttcc tcttcccc aaacccaag 780

gacacctca tgatctccg gacctctgag gtcacatgcg tgggtggtgga cgtgagccac 840

gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag 900

acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc 960

ctgcaccagg actggctgaa tggcaaggag tacaagtgc aggtctcaa caaagccctc 1020

ccagcccca tcgagaaaac catctccaaa gccaaaggcg agccccgaga accacaggtg 1080

tacacctgc ccccatccg ggaggagatg accaagaacc aggtcagcct gacctgcctg 1140

gtcaaaggct tctatcccag cgacatcgcc gtggagtggg agagcaatgg gcagccggag 1200

aacaactaca agaccagcc tccgtgctg gactccgacg gctccttctt cctctatagc 1260

aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1320

catgaggctc tgcacaacca ctacacgag aaaagcctct ccctgtcccc gggtaaa 1377

<210> 95

<211> 621

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido
de cadena ligera del candidato 03-001, que comprende
 $\alpha 3$ para el dominio proximal a la membrana de CD1b con mutación N57C

<400> 95

cagcctgtgc tgactcagcc actctcagtg tcagtggccc tgggacagac ggccaggatt 60

acctgtgggg gaaacaacat tggaagtaaa aatgtgcact ggtaccagca gaagccaggc 120

caggcccctg tgctggtcat ctatagggat agcaaccggc cctctgggat ccctgagcga 180

ttctctggct ccaactcggg gaacacggcc accctgacca tcagcagagc ccaagccggg 240

gatgaggctg actattactg tcaggtgtgg gacagcagca ctgctgtctt cggaactggg 300

accaagctga ccgtcctaca gcagagacag gttaaaccag aggcatggct aagttctgga 360

ccttcacctg gacctgtag attacaatta gtatgtcatg tgtcgggatt ttatcctaaa 420

cctgtttggg tcattgtgat gaggggcgag caagagcagc aaggaacaca gtaggcgac 480

atcctgccgt gcgcaactg gacatggtac ttaagagcaa ccctggatgt agcggacggc 540

gaagccgctg gattatcgtg ccgggtaaag cattcgtcgc tggagggcca agacataata 600

ctctattggc gcggtagttg c

621

<210> 96

<211> 618

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido
de cadena ligera del candidato 03-002, que comprende
 $\alpha 3$ para el dominio proximal a la membrana de CD1b con mutación N57C

<400> 96

cagcctgtgc tgactcagcc actctcagtgc tcagtggtccc tgggacagac ggccaggatt 60

acctgtgggg gaaacaacat tggaagtaaa aatgtgcact ggtaccagca gaagccaggc 120

caggcccctg tgctggtcat ctataggat agcaaccggc cctctgggat ccctgagcga 180

ttctctggct ccaactcggg gaacacggcc accctgacca tcagcagagc ccaagccggg 240

gatgaggctg actattactg tcaggtgtgg gacagcagca ctgctgtctt cggaactggg 300

accaagctga ccgtcctaca gcagagacag gttaaaccag aggcatggct aagttctgga 360

ccttcacctg gacctgtag attacaatta gtatgtcatg tgtcgggatt ttatcctaaa 420

cctgtttggg tcattgtgat gaggggagag caagagcagc aaggaacaca gtaggcgac 480

atcctgccgt gcgcaactg gacatgttac ttaagagcaa ccctggatgt agcggacggc 540

gaagccgctg gattatcgtg ccgggtaaag cattcgtcgc tggagggcca agacataata 600

ctctattggc gcggtagt 618

<210> 97

<211> 621

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido
de cadena ligera del candidato 03-003, que comprende
 α 3 para el dominio proximal a la membrana de CD1b con mutación N59A

<400> 97

cagcctgtgc tgactcagcc actctcagtg tcagtggccc tgggacagac ggccaggatt 60

acctgtgggg gaaacaacat tggaagtaaa aatgtgcact ggtaccagca gaagccaggc 120

caggcccctg tgctgggtcat ctatagggat agcaaccggc cctctgggat ccctgagcga 180

ttctctggct ccaactcggg gaacacggcc accctgacca tcagcagagc ccaagccggg 240

gatgaggctg actattactg tcaggtgtgg gacagcagca ctgctgtctt cggaactggg 300

accaagctga ccgtcctaca gcagagacag gttaaaccag aggcattggct aagttctgga 360

ccttcacctg gacctgtag attacaatta gtatgtcatg tgtcgggatt ttatcctaaa 420

cctgtttggg tcatgtggat gaggggag caagagcagc aaggaacaca gtaggcgac 480

atcctgccga atgcagcctg gacatggtac ttaagagcaa ccctggatgt agcggacggc 540

gaagccgctg gattatcgtg ccgggtaaag cattcgtcgc tggagggcca agacataata 600

ctctattggc gcggtagttg c 621

<210> 98

<211> 621

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido

de cadena ligera del candidato 03-004, que comprende

α3 para el dominio proximal a la membrana de CD1b con mutación N59D

<400> 98

cagcctgtgc tgactcagcc actctcagtgc tcagtggccc tgggacagac ggccaggatt 60

acctgtgggg gaaacaacat tggaagtaaa aatgtgcact ggtaccagca gaagccaggc 120

caggcccctg tgctggtcat ctataggat agcaaccggc cctctgggat ccctgagcga 180

ttctctggct ccaactcggg gaacacggcc accctgacca tcagcagagc ccaagccggg 240

gatgaggctg actattactg tcaggtgtgg gacagcagca ctgctgtctt cggaactggg 300

accaagctga ccgtcctaca gcagagacag gttaaaccag aggcatggct aagttctgga 360

ccttcacctg gacctggtag attacaatta gtatgtcatg tgtcgggatt ttatcctaaa 420

cctgtttggg tcatgtggat gaggggag caagagcagc aaggaacaca gtaggcgac 480

atcctgccga atgcagactg gacatggtac ttaagagcaa ccctggatgt agcggacggc 540

gaagccgctg gattatctg cgggtaaag cattcgtcg tggagggcc agacataata 600

ctctattggc gcggtagtg c 621

<210> 99

<211> 621

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido

de cadena ligera del candidato 03-005, que comprende

α3 para el dominio proximal a la membrana de CD1b con mutaciones N57C, N59A

<400> 99

cagcctgtgc tgactcagcc actctcagtg tcagtggccc tgggacagac ggccaggatt 60

acctgtgggg gaaacaacat tggaagtaaa aatgtgcact ggtaccagca gaagccaggc 120

caggcccctg tgctggtcat ctatagggat agcaaccggc cctctgggat ccctgagcga 180

ttctctggct ccaactcggg gaacacggcc accctgacca tcagcagagc ccaagccggg 240

gatgaggctg actattactg tcagggtggtg gacagcagca ctgctgtctt cggaactggg 300

accaagctga ccgtcctaca gcagagacag gttaaaccag aggcatggct aagttctgga 360

ccttcacctg gacctgtag attacaatta gtatgtcatg tgtcgggatt ttatcctaaa 420

cctgtttggg tcatgtggat gaggggag caagagcagc aaggaacaca gtaggcgac 480

atcctgccgt gcgcagcctg gacatggtac ttaagagcaa ccctggatgt agcggacggc 540

gaagccgctg gattatcgtg ccgggtaaag cattcgtcgc tggagggcca agacataata 600

ctctattggc gcggtagttg c 621

<210> 100

<211> 621

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido
de cadena ligera del candidato 03-006, que comprende
α3 para el dominio proximal a la membrana de CD1b con mutaciones N57C, N59D

<400> 100

cagcctgtgc tgactcagcc actctcagtgc tcagtggccc tgggacagac ggccaggatt 60

acctgtgggg gaaacaacat tggaagtaaa aatgtgcact ggtaccagca gaagccaggc 120

caggcccctg tgctgtgcat ctatagggat agcaaccggc cctctgggat ccctgagcga 180

ttctctggct ccaactcggg gaacacggcc accctgacca tcagcagagc ccaagccggg 240

gatgaggctg actattactg tcaggtgtgg gacagcagca ctgctgtctt cggaactggg 300

accaagctga ccgtctaca gcagagacag gttaaaccag aggcatggct aagttctgga 360

ccttcacctg gacctggtag attacaatta gtatgtcatg tgtcgggatt ttatcctaaa 420

cctgtttggg tcattgtgat gaggggag caagagcagc aaggaacaca gtaggcgac 480

atcctgccgt gcgcagactg gacatggtac ttaagagcaa ccctggatgt agcggacggc 540

gaagccgctg gattatcgtg ccgggtaaag cattcgtcgc tggagggcca agacataata 600

ctctattggc gcggtagttg c

621

<210> 101

<211> 618

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido
de cadena ligera del candidato 03-007, que comprende
α3 para el dominio proximal a la membrana de CD1b con mutaciones N57C, N59A

<400> 101

cagcctgtgc tgactcagcc actctcagtg tcagtggccc tgggacagac ggccaggatt 60

acctgtgggg gaaacaacat tggaagtaaa aatgtgcact ggtaccagca gaagccaggc 120

caggcccctg tgctggtcat ctatagggat agcaaccggc cctctgggat ccctgagcga 180

ttctctggct ccaactcggg gaacacggcc accctgacca tcagcagagc ccaagccggg 240

gatgaggctg actattactg tcaggtgtgg gacagcagca ctgctgtctt cggaactggg 300

accaagctga ccgtcctaca gcagagacag gttaaaccag aggcattggct aagtcttggg 360

ccttcacctg gacctgtag attacaatta gtatgtcatg tgtcgggatt ttatcctaaa 420

cctgtttggg tcattgtgat gaggggcgag caagagcagc aaggaacaca gtaggcgac 480

atcctgccgt gcgcagcctg gacatggtag ttaagagcaa ccctggatgt agcggacggc 540

gaagccgctg gattatcgtg ccgggtaaag cattcgtcgc tggagggcca agacataata 600

ctctattggc gcggtagt 618

<210> 102

<211> 618

<212> ADN

<213> Secuencia artificial

<220>

<223> Ácido nucleico que codifica la secuencia de aminoácido

de cadena ligera del candidato 03-008, que comprende

α 3 para el dominio proximal a la membrana de CD1b con mutaciones N57C, N59D

<400> 102

cagcctgtgc tgactcagcc actctcagtgc tcagtggccc tgggacagac ggccaggatt 60

acctgtgggg gaaacaacat tggaagtaaa aatgtgcact ggtaccagca gaagccaggc 120

caggcccctg tgctggatcat ctatagggat agcaaccggc cctctgggat ccctgagcga 180

ttctctggct ccaactcggg gaacacggcc accctgacca tcagcagagc ccaagccggg 240

gatgaggctg actattactg tcaggtgtgg gacagcagca ctgctgtctt cggaactggg 300

accaagctga ccgtcctaca gcagagacag gttaaaccag aggcattggct aagttctgga 360

ccttcacctg gacctgtag attacaatta gtatgtcatg tgcggggatt ttatcctaaa 420

cctgtttggg tcatgtggat gaggggag caagagcagc aaggaacaca gtaggcgac 480

atcctgccgt gcgcagactg gacatggtac ttaagagcaa ccctggatgt agcggacggc 540

gaagccgctg gattatcgtg ccgggtaaag cattcgtcg tgaggggcca agacataata 600

ctctattggc gcggtagt 618

<210> 103

<211> 129

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos del dominio variable de cadena pesada
del anticuerpo Prolgolimab (Prolgolimab_VH)

<400> 103

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

1. 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Trp Met Tyr Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val

35 40 45
 Ser Ala Ile Asp Thr Gly Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Ala Ile Ser Arg Val Asn Ala Lys Asn Thr Met Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Glu Gly Gly Gly Thr Gly Trp Gly Val Leu Lys Asp Trp
 100 105 110
 Pro Tyr Gly Leu Asp Ala Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 115 120 125
 Ser

<210> 104

<211> 107

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos del dominio variable de cadena liviana
 del anticuerpo Prolgolimab (Prolgolimab_VL)

<400> 104

Gln Pro Val Leu Thr Gln Pro Leu Ser Val Ser Val Ala Leu Gly Gln
 1. 5 10 15
 Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Asn Val
 20 25 30

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

35 40 45

Arg Asp Ser Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser

50 55 60

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

65 70 75 80

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

85 90 95

Phe Gly Thr Gly Thr Lys Leu Thr Val Leu Gln

100 105

<210> 105

<211> 122

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos del dominio variable de cadena pesada
del anticuerpo Ocrelizumab (Ocrelizumab_VH)

<400> 105

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1. 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20 25 30

Asn Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

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

85 90 95

Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp

100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 106

<211> 106

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos del dominio variable de cadena liviana
del anticuerpo Ocrelizumab (Ocrelizumab_VL)

<400> 106

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1. 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met

20 25 30

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

35 40 45

Ala Pro Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser

50 55 60

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

65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Phe Asn Pro Pro Thr

85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

<210> 107

<211> 124

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos del dominio variable de cadena pesada
del anticuerpo contra CSF1R (Anti-CSF1R_VH)

<400> 107

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Arg Pro Gly Gly

1. 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Glu Phe Thr Phe Asp Asp Tyr

20 25 30

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

35 40 45

Ser Ala Ile Ser Trp Asn Gly Gly Ser Thr Asn Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys

85 90 95
Ala Ser Thr Val Glu Val Ala His Arg Arg Leu Tyr Lys Tyr Leu Glu
100 105 110
Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 108

<211> 108

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos del dominio variable de cadena liviana
del anticuerpo contra CSF1R (Anti-CSF1R_VL)

<400> 108

Gln Ala Gly Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1. 5 10 15
Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
20 25 30
His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
35 40 45
Gly Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80
Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ile Ser Ser Asp His
85 90 95

Val Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu

100

105

<210> 109

<211> 100

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia de aminoácidos de $\alpha 3$ para el dominio proximal a la membrana de CD1b
con elongación de GSC en el extremo terminal C

<400> 109

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

1. 5

10

15

Gly Pro Gly Arg Leu Gln Leu Val Cys His Val Ser Gly Phe Tyr Pro

20

25

30

Lys Pro Val Trp Val Met Trp Met Arg Gly Glu Gln Glu Gln Gly

35

40

45

Thr Gln Leu Gly Asp Ile Leu Pro Asn Ala Asn Trp Thr Trp Tyr Leu

50

55

60

Arg Ala Thr Leu Asp Val Ala Asp Gly Glu Ala Ala Gly Leu Ser Cys

65

70

75

80

Arg Val Lys His Ser Ser Leu Glu Gly Gln Asp Ile Ile Leu Tyr Trp

85

90

95

Arg Gly Ser Cys

100