

LISTADO DE SECUENCIAS

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 25 Leu Ser Arg Ala Lys Leu Lys Ala Ser Ser Arg Thr Ser Ala Leu Leu
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 45 Lys Glu Ser Pro His Glu Arg Met His Arg His Ile Glu Leu Ala Trp
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Leu Pro Ala Ser Leu Gly Glu Arg Val Thr Ile Ser Cys Arg Ala Ser
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Gln Ser Ile Ser Asn Ser Leu Ser Trp Phe Gln Gln Lys Pro Asp Gly
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Thr Val Lys Arg Leu Ile Tyr Ser Thr Ser Thr Leu Glu Ser Gly Val
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Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Ser
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Ile Thr Ser Leu Glu Ser Glu Asp Phe Ala Met Tyr Tyr Cys Leu Gln
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Thr Ala Tyr Tyr Ile Ser Trp Ile Arg Gln Thr Ile Gly Gln Gly Leu
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Glu Tyr Val Gly Tyr Ile Asp Met Gly Asn Gly Arg Thr Asn Tyr Asn
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Ala Arg Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
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Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Gly Val Asp Tyr Trp Gly Gln
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Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Gly Val Asp Tyr Trp Gly Gln
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[illegible]

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[illegible]

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40	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	
				165						170					175		
45	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	
				180					185					190			
50	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	
			195					200					205				
55	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	
		210					215					220					
60	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	
	225					230					235					240	
65	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	
					245					250					255		

	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile
	260															
5	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu
	275															
10	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His
	290															
15	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg
	305															
20	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys
	320															
25	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu
	335															
30	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr
	350															
35	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu
	365															
40	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp
	380															
45	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val
	395															
50	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp
	410															
55	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His
	425															
60	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro
	440															
65	Gly	Lys														
	455															
70																
	470															
75																
	485															
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<210> 28
 <211> 1401
 <212> ADN
 <213> artificial

5

<220>
 <223> Secuencia de nucleótido que codifica cR198_H

<400> 28

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15	tgcaaggctt ccggctaccc cgtcaccagc tattatataa gttggataaa gcagacgact	180
	ggacagggcc ttgagtatat tggatatgtt gacatgggaa atggacggac taactacaat	240
	gagaagttca agggcaaggc cacattgact gtagacaaat cctccagcac agccttcatg	300
20	caactcagca gcctgacacc tgacgactct gcggtctatt actgtgcaag ggactccaac	360
	tgggggggtt attactgggg ccaaggagtc atggtcacag tcagctcagc ctccaccaag	420
25	ggcccaagcg tcttccccct ggcaccctcc tccaagagca cctctggcgg cacagccgcc	480
	ctgggctgcc tggtaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc	540
	gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc	600
30	ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac	660
	gtgaatcaca agcccagcaa caccaagggtg gacaagagag ttgagcccaa atcttgtgac	720
35	aaaactcaca catgcccacc ctgcccagca cctgaactcc tgggggggacc ctcagtcttc	780
	ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc	840
	gtggtggttg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc	900
40	gtggaggtgc ataatgcaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg	960
	gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc	1020
45	aaggctctca acaaagccct cccagcccc atcgagaaaa ccatctcaa agccaaaggc	1080
	cagccccggg aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac	1140
	caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg	1200
50	gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac	1260
	ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac	1320
55	gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacca gaagagcctc	1380

tccctgtctc ccggcaaag a

1401

5 <210> 29
 <211> 466
 <212> PRT
 <213> artificial

 10 <220>
 <223> Secuencia de aminoácido de cR198_H
 <400> 29

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

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

 Pro Gly Ser Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Pro Val
 35 40 45

 25 Thr Ser Tyr Tyr Ile Ser Trp Ile Lys Gln Thr Thr Gly Gln Gly Leu
 50 55 60

 30 Glu Tyr Ile Gly Tyr Val Asp Met Gly Asn Gly Arg Thr Asn Tyr Asn
 65 70 75 80

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

 Thr Ala Phe Met Gln Leu Ser Ser Leu Thr Pro Asp Asp Ser Ala Val
 100 105 110

 40 Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Gly Val Asp Tyr Trp Gly Gln
 115 120 125

 45 Gly Val Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 130 135 140

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

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

	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	
				180					185					190			
5	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	
			195					200					205				
10	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	
		210					215					220					
15	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	
	225					230					235					240	
20	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	
					245					250					255		
25	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	
				260					265					270			
30	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	
	290						295					300					
35	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	
	305					310					315					320	
40	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	
					325					330					335		
45	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	
				340					345					350			
50	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	
			355					360					365				
55	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	
	370						375					380					
	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	
	385					390					395					400	

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

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

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

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

Gly Lys
 465

20 <210> 30
 <211> 705
 <212> ADN
 <213> artificial

25 <220>
 <223> Secuencia de nucleótido que codifica hR198_L1

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 atcacctgta gagccagcca gagcatcggc aacagcctga gctgggtcca gcagaaaccc 180
 35 ggcaaggccc ccaagcggct gatctacagc accagcaccc tggaaagcgg cgtgcccagc 240
 agattttctg gcagcggctc cggcaccgac tacaccctga caatcagcag cctgcagccc 300
 40 gaggacttcg ccatgtacta ctgcctgcag ttcgccacct accccgacac ctttggccag 360
 ggcaccaagg tggaaatcaa gcgtacggtg gccgccccct ccgtgttcat cttccccccc 420
 tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taactttctac 480
 45 cccagagagg ccaaggtgca gtggaagggt gacaacgccc tgcagtccgg gaactcccag 540
 gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600
 50 ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660
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55 <210> 31

<211> 234
 <212> PRT
 <213> artificial

5 <220>
 <223> Secuencia de aminoácido de hR198_L1
 <400> 31

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 1 5 10 15

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

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

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

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

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

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

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

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

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

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

55

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

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

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

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

20 <210> 32
 <211> 705
 <212> ADN
 <213> artificial

25 <220>
 <223> Secuencia de nucleótido que codifica hR198_L2

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 gatatccagc tgaccagag ccctagcagc ctgtctgccg gcgtgggcga cagagtgacc 120
 atcacctgta gagccagcca gagcatcggc aacagcctga gctgggtcca gcagaaaccc 180
 ggcaaggccg tgaagcggct gatctacagc accagcaccc tggaaagcgg cgtgcccagc 240
 agattttctg gcagcggctc cggcaccgac tacaccctga caatcagcag cctgcagccc 300
 35 gaggacttcg ccatgtacta ctgcctgcag ttcgccacct accccgacac ctttggccag 360
 ggcaccaagg tggaaatcaa gcgtacggtg gccgcccct ccgtgttcat cttccccccc 420
 40 tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taacttctac 480
 cccagagagg ccaaggtgca gtggaagggt gacaacgccc tgcagtccgg gaactcccag 540
 gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600
 45 ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660
 ctgagctccc ccgtcaccaa gagcttcaac agggggggagt gttag 705

50 <210> 33
 <211> 234
 <212> PRT
 <213> artificial

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<220>

<223> Secuencia de aminoácido de hR198_L2

<400> 33

5 Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
 1 5 10 15
 10 Gly Ala Tyr Gly Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser
 20 25 30
 15 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser
 35 40 45
 20 Ile Gly Asn Ser Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ala Val
 50 55 60
 Lys Arg Leu Ile Tyr Ser Thr Ser Thr Leu Glu Ser Gly Val Pro Ser
 65 70 75 80
 25 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
 85 90 95
 30 Ser Leu Gln Pro Glu Asp Phe Ala Met Tyr Tyr Cys Leu Gln Phe Ala
 100 105 110
 35 Thr Tyr Pro Asp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 115 120 125
 40 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 130 135 140
 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 145 150 155 160
 45 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 165 170 175
 50 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 180 185 190
 55 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 195 200 205

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

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

10 <210> 34
 <211> 705
 <212> ADN
 <213> artificial

<220>
 15 <223> Secuencia de nucleótido que codifica hR198_L3

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 atcacctgta gagccagcca gagcatcggc aacagcctga gctgggtcca gcagaaaccc 180
 25 ggcaaggccc ccaagcggct gatctacagc accagcaccc tggaaagcgg cgtgcccagc 240
 agattttctg gcagcggctc cggcaccgac tacaccctga caatcagcag cctgcagccc 300
 gaggacttcg ccatgtacta ctgcctgcag ttcgccacct tccccgacac ctttggccag 360
 30 ggcaccaagg tggaaatcaa gcgtacggtg gccgccccct ccgtgttcat cttccccccc 420
 tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taactttctac 480
 cccagagagg ccaaggtgca gtggaagggtg gacaacgccc tgcagtccgg gaactcccag 540
 35 gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600
 ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660
 40 ctgagctccc ccgtcaccaa gagcttcaac agggggggagt gttag 705

<210> 35
 <211> 234
 45 <212> PRT
 <213> artificial

<220>
 <223> Secuencia de aminoácido de hR198_L3

50 <400> 35

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

<210> 36
 <211> 705
 <212> ADN
 <213> artificial

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<220>
 <223> Secuencia de nucleótido que codifica hR198_L4

<400> 36
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 gatatccagc tgaccagag ccctagcagc ctgtctgccg gcgtgggcga cagagtgacc 120
 15 atcacctgta gagccagcca gagcatcggc aacagcctga gctgggtcca gcagaaaccc 180
 ggcaaggccg tgaagcggct gatctacagc accagcaccc tggaaagcgg cgtgcccagc 240
 agattttctg gcagcggctc cggcaccgac tacaccctga caatcagcag cctgcagccc 300
 20 gaggacttcg ccatgtacta ctgcctgcag ttcgccacct tccccgacac ctttggccag 360
 ggcaccaagg tggaaatcaa gcgtacggtg gccgccccct ccgtgttcat cttccccccc 420
 tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taacttctac 480
 25 cccagagagg ccaaggtgca gtggaagggtg gacaacgccc tgcagtccgg gaactcccag 540
 gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600
 30 ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660
 ctgagctccc ccgtcaccaa gagcttcaac agggggggagt gttag 705

35

<210> 37
 <211> 234
 <212> PRT
 <213> artificial

40

<220>
 <223> Secuencia de aminoácido de hR198_L4

<400> 37

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

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

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

	Ile	Gly	Asn	Ser	Leu	Ser	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Val	
	50						55					60					
5	Lys	Arg	Leu	Ile	Tyr	Ser	Thr	Ser	Thr	Leu	Glu	Ser	Gly	Val	Pro	Ser	
	65					70					75					80	
10	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	
				85						90					95		
15	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Met	Tyr	Tyr	Cys	Leu	Gln	Phe	Ala	
				100					105					110			
20	Thr	Phe	Pro	Asp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	
			115					120					125				
25	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	
	130						135					140					
30	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	
	145					150					155					160	
35	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	
					165					170					175		
40	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	
				180					185						190		
45	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	
			195					200					205				
50	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	
	210						215					220					
55	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys							
	225					230											
	<210>	38															
	<211>	1401															
	<212>	ADN															
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<223> Secuencia de nucleótido que codifica hR198_H1

<400> 38

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	tgcaaggcct ctggctaccc cgtgaccagc tactacatca gctgggtcag acaggcccca	180
10	ggccagggcc tggaatacat cggctatgtg gacatgggca acggccggac caactacaac	240
	gagaagttca agggcagagc caccctgacc gtggacaaga gcaccagcac cgcctacatg	300
15	gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag agacagcaac	360
	tggggcgtgg actattgggg ccagggcaca ctcgtgaccg tcagctcagc ctccaccaag	420
	ggcccaagcg tcttccccct ggcacctcc tccaagagca cctctggcgg cacagccgcc	480
20	ctgggctgcc tgggtcaagga ctacttcccc gaaccctga ccgtgagctg gaactcaggc	540
	gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc	600
25	ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagacctt catctgcaac	660
	gtgaatcaca agcccagcaa caccaagggtg gacaagagag ttgagcccaa atcttgtgac	720
	aaaactcaca catgcccacc ctgcccagca cctgaactcc tggggggacc ctcagtcttc	780
30	ctcttcccc caaaaccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc	840
	gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc	900
35	gtggaggtgc ataatgcaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg	960
	gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc	1020
	aaggctctca acaaagccct cccagcccc atcgagaaaa ccatctccaa agccaaaggc	1080
40	cagccccggg aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac	1140
	caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg	1200
45	gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac	1260
	ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac	1320
	gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacca gaagagcctc	1380
50	tccctgtctc ccggcaaagt a	1401

<210> 39

<211> 466

55 <212> PRT

<213> artificial

<220>

<223> Secuencia de aminoácido de hR198_H1

5

<400> 39

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
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10

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

15

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

20

Thr Ser Tyr Tyr Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

25

Glu Tyr Ile Gly Tyr Val Asp Met Gly Asn Gly Arg Thr Asn Tyr Asn
65 70 75 80

30

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

35

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

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

40

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

45

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

50

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

55

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

	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
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		210					215					220				
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15	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly
					245					250					255	
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				260					265					270		
25	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu
			275					280					285			
30	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His
	290						295					300				
35	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg
	305					310					315					320
40	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys
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45	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu
				340					345					350		
50	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr
			355					360					365			
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		370					375					380				
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	385					390					395					400
65	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val
					405					410					415	

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

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

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

15 Gly Lys
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 ggccagggcc tggaatacat cggctatgtg gacatgggca acggccggac caactacaac 240
 35 gagaagttca agggcagagc caccctgacc gtggacaaga gcaccagcac cgcctacatg 300
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10 gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac      1260
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   <213> artificial

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25 <220>
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35 Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
   20           25           30

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40 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Pro Val
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45 Thr Ser Tyr Tyr Ile Ser Trp Ile Arg Gln Ala Pro Gly Gln Gly Leu
   50           55           60

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Glu Tyr Ile Gly Tyr Val Asp Met Gly Asn Gly Arg Thr Asn Tyr Asn
65           70           75           80

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50 Glu Lys Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
   85           90           95

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			115					120					125				
10	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	
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15	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	
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20	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	
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25	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	
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30	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	
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35	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	
		210					215					220					
40	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	
		225				230					235					240	
45	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	
					245					250					255		
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				260					265					270			
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60	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	
		290					295					300					
65	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	
	305					310					315					320	

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

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

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

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

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

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

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

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

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

Gly Lys
465

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<223> Secuencia de nucleótido que codifica hR198_H3

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	gcccggttta	agggcagagc	caccctgacc	gtggacaaga	gcaccagcac	cgcttacatg	300
5	gaactgagca	gcctgcggag	cgaggacacc	gccgtgtact	actgcgccag	agacagcaac	360
	tggggcgtgg	actattgggg	ccagggcaca	ctcgtgaccg	tcagctcagc	ctccaccaag	420
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							Trp

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5	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Pro	Val	
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10	Thr	Ala	Tyr	Tyr	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	
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15	Glu	Tyr	Val	Gly	Tyr	Ile	Asp	Met	Gly	Asn	Gly	Arg	Thr	Asn	Tyr	Asn	
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25	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
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30	Tyr	Tyr	Cys	Ala	Arg	Asp	Ser	Asn	Trp	Gly	Val	Asp	Tyr	Trp	Gly	Gln	
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		210					215					220					
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	225					230					235					240	

	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	
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Gly Lys
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25  20      25      30

Pro  Gly  Ala  Ser  Val  Lys  Val  Ser  Cys  Lys  Ala  Ser  Gly  Tyr  Pro  Val
30  35      40      45

Thr  Ala  Tyr  Tyr  Ile  Ser  Trp  Ile  Arg  Gln  Ala  Pro  Gly  Gln  Gly  Leu
35  50      55      60

Glu  Tyr  Val  Gly  Tyr  Ile  Asp  Met  Gly  Asn  Gly  Arg  Thr  Asn  Tyr  Asn
65  65      70      75      80

Ala  Arg  Phe  Lys  Gly  Arg  Ala  Thr  Leu  Thr  Val  Asp  Lys  Ser  Thr  Ser
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Thr  Ala  Tyr  Met  Glu  Leu  Ser  Ser  Leu  Arg  Ser  Glu  Asp  Thr  Ala  Val
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Tyr  Tyr  Cys  Ala  Arg  Asp  Ser  Asn  Trp  Gly  Val  Asp  Tyr  Trp  Gly  Gln
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55

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10	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	
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15	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	
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20	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	
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25	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	
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40	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	
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	305					310					315					320	
55	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	
					325					330					335		
60	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	
				340					345					350			
65	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	
			355					360					365				

23

21

<213> artificial
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 <223> Cebador PCR M13 rev largo
 5 <400> 48
 caggaaacag ctatgaccat g 21
 10 <210> 49
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 15 <220>
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 <400> 49
 20 ctcgagttat tcattaggtg aggcgttgag g 31
 <210> 50
 <211> 24
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 25 <213> artificial
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 30 <400> 50
 atggacattc aactgaccca aagc 24
 <210> 51
 35 <211> 24
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 40 <223> Cebador PCR Orai1 CL-FR
 <400> 51
 gataaaaaca ctcggggccg ccac 24
 45 <210> 52
 <211> 63
 <212> ADN
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 50 <220>
 <223> Cebador PCR Orai1 HR-FLAG R
 <400> 52
 55 tcattatttg tcatcgatcat ctttatagtc gaattcttcg ccacgattaa aggatttggt 60

	gac		63
5	<210> 53 <211> 63 <212> ADN <213> artificial		
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15	gac		63
20	<210> 54 <211> 30 <212> ADN <213> artificial		
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30	<210> 55 <211> 705 <212> ADN <213> artificial		
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40	gatatccagc tgaccagag ccctagcagc ctgtctgcc a gcgtgggcga cagagtgacc		120
	atcacctgta gagccagcca gagcatcggc ggcagcctga gctgggtcca gcagaaaccc		180
45	ggcaaggccc ccaagcggct gatctacagc accagcaccc tggaaagcgg cgtgcccagc		240
	agattttctg gcagcggctc cggcaccgac tacaccctga caatcagcag cctgcagccc		300
50	gaggacttcg ccatgtacta ctgcctgcag ttcgccatct tccccgacag ctttggccag		360
	ggcaccaagg tggaaatcaa gcgtacggtg gccgccccct ccgtgttcat cttccccccc		420
	tccgacgagc agctgaagtc cggcaccgcc tccgtgggtg gctgctgaa taactttctac		480
55	cccagagagg ccaaggtgca gtggaagggtg gacaacgccc tgcagtccgg gaactcccag		540

gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600
 ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660
 5 ctgagctccc ccgtcaccaa gagcttcaac agggggggagt gttag 705

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 <211> 234
 10 <212> PRT
 <213> artificial

<220>
 <223> Secuencia de aminoácido de hR198_LG1
 15 <400> 56

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 1 5 10 15
 20

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

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser
 35 40 45
 30

Ile Gly Gly Ser Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro
 50 55 60
 35

Lys Arg Leu Ile Tyr Ser Thr Ser Thr Leu Glu Ser Gly Val Pro Ser
 65 70 75 80
 40

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
 85 90 95
 45

Ser Leu Gln Pro Glu Asp Phe Ala Met Tyr Tyr Cys Leu Gln Phe Ala
 100 105 110
 50

Ile Phe Pro Asp Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 115 120 125
 55

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 130 135 140
 145

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

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

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

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

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

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

20 <210> 57
<211> 705
<212> ADN
<213> artificial

25 <220>
<223> Secuencia de nucleótido que codifica hR198_LG2

30 <400> 57
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atcacctgtc acgccagcca gaacatcggc ggcagcctga gctgggtcca gcagaaaccc 180
35 ggcaaggccc ccaagcggct gatctacctg accagcaccg tggactgggg cgtgcccagc 240
agattttctg gcagcggctc cggcaccgac tacaccctga caatcagcag cctgcagccc 300
40 gaggacttcg ccatgtacta ctgcctgcag ttcgccatct tccccgacag ctttggccag 360
ggcaccaagg tggaaatcaa gcgtacggtg gccgccccct ccgtgttcat cttccccccc 420
tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taactttctac 480
45 cccagagagg ccaaggtgca gtggaagggt gacaacgccc tgcagtccgg gaactcccag 540
gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600
50 ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660
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55 <210> 58

<211> 234
 <212> PRT
 <213> artificial

5 <220>
 <223> Secuencia de aminoácido de hR198_LG2
 <400> 58

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 1 5 10 15

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

20 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys His Ala Ser Gln Asn
 35 40 45

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

25 Lys Arg Leu Ile Tyr Leu Thr Ser Thr Leu Asp Trp Gly Val Pro Ser
 65 70 75 80
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
 85 90 95

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

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

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

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

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

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

55

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

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

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

15 <210> 59
 <211> 705
 <212> ADN
 <213> artificial

20 <220>
 <223> Secuencia de nucleótido que codifica hR198_LG3

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 25 atcacctgtc acgccagccg gaacatcggc ggcagcctga gctgggtcca gcagaaaccc 180
 ggcaaggccc ccaagcggct gatctacctg accagcagcc tggactgggg cgtgcccagc 240
 30 agattttctg gcagcggctc cggcaccgac tacaccctga caatcagcag cctgcagccc 300
 gaggacttcg ccatgtacta ctgcctgcag ttcgccatct tccccgacag ctttggccag 360
 ggcaccaagg tggaaatcaa gcgtacggtg gccgccccct ccgtgttcat cttccccccc 420
 35 tccgacgagc agctgaagtc cggcaccgcc tccgtgggtg gcctgctgaa taactttctac 480
 cccagagagg ccaaggtgca gtggaagggt gacaacgccc tgcagtccgg gaactcccag 540
 40 gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600
 ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660
 ctgagctccc ccgtcaccaa gagcttcaac aggggggagt gttag 705
 45

<210> 60
 <211> 234
 <212> PRT
 50 <213> artificial

<220>
 <223> Secuencia de aminoácido de hR198_LG3

55 <400> 60

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	1				5					10					15		
5	Gly	Ala	Tyr	Gly	Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	
				20					25					30			
10	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	His	Ala	Ser	Arg	Asn	
			35					40					45				
15	Ile	Gly	Gly	Ser	Leu	Ser	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	
		50					55					60					
20	Lys	Arg	Leu	Ile	Tyr	Leu	Thr	Ser	Ser	Leu	Asp	Trp	Gly	Val	Pro	Ser	
	65					70					75					80	
25	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	
					85					90					95		
30	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Met	Tyr	Tyr	Cys	Leu	Gln	Phe	Ala	
				100					105					110			
35	Ile	Phe	Pro	Asp	Ser	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	
			115					120					125				
40	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	
		130					135					140					
45	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	
	145					150					155					160	
50	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	
					165					170					175		
55	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	
				180					185					190			
60	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	
			195					200					205				
65	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	
		210					215					220					

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

5 <210> 61
<211> 1401
<212> ADN
<213> artificial

10 <220>
<223> Secuencia de nucleótido que codifica hR198_HG1

<400> 61

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gtgcagctgg tgcagtctgg cgccgaagtg aagaaaccag gcgccagcgt gaagggtgtcc 120
tgcaaggcct ctggctaccc cgtgaccgcc tactacatca gctgggtcag acaggcccca 180

20 ggccagggcc tggaatacgt gggctacatc gacatgggca acggccggac cgactacaac 240
gcccggttta agggcagagc caccctgacc gtggacaaga gcaccagcac cgcctacatg 300
gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag agacagcaac 360

25 tggggcgccg actattgggg ccagggcaca ctcgtgaccg tcagctcagc ctccaccaag 420
ggcccaagcg tcttccccct ggcaccctcc tccaagagca cctctggcgg cacagccgcc 480

30 ctgggctgcc tgggtcaagga ctacttcccc gaaccctga ccgtgagctg gaactcaggc 540
gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 600
ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660

35 gtgaatcaca agcccagcaa caccaagggtg gacaagagag ttgagcccaa atcttgtgac 720
aaaactcaca catgcccacc ctgcccagca cctgaactcc tggggggacc ctcagtcttc 780

40 ctcttcccc caaaaccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 840
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900
gtggaggtgc ataatgcaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 960

45 gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020
aaggctctca acaaagccct cccagcccc atcgagaaaa ccatctccaa agccaaaggc 1080

50 cagccccggg aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac 1140
caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200
gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac 1260

55

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ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac      1320
gtctttctcat gctccgtgat gcatgaggct ctgcacaacc actacaccca gaagagcctc      1380
5  tccctgtctc ccggcaaatg a                                              1401

<210> 62
<211> 466
10 <212> PRT
    <213> artificial

<220>
<223> Secuencia de aminoácido de hR198_HG1
15 <400> 62

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

25 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Pro Val
   35          40          45

30 Thr Ala Tyr Tyr Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
   50          55          60

35 Glu Tyr Val Gly Tyr Ile Asp Met Gly Asn Gly Arg Thr Asp Tyr Asn
   65          70          75          80

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

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

50 Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Gly Ala Asp Tyr Trp Gly Gln
   115         120         125

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

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

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	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	
					165					170						175	
5	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	
				180					185						190		
10	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	
			195					200						205			
15	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	
		210					215					220					
20	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	
		225				230					235					240	
25	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	
					245					250					255		
30	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	
				260					265					270			
35	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	
			275					280					285				
40	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	
		290					295					300					
45	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	
		305				310					315					320	
50	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	
					325					330					335		
55	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	
				340					345					350			
60	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	
			355					360					365				
65	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	
		370					375					380					

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

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

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

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

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

20 Gly Lys
465

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25    <210> 63
      <211> 1401
      <212> ADN
      <213> artificial
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30 <220>
 <223> Secuencia de nucleótido que codifica hR198 HG2

<400> 63
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gtgcagctgg tgcagtctgg cgccgaagtg aagaaaccag gcgccagcgt gaaggtgtcc 120

tqcaaggcct ctggctaccc catcaccgcc tactacatca gctgggtcag acaggcccca 180

40 ggccagggcc tggaaatcgt gggctacatc qacatgggca acggccggac cgactacaac 240

ggccggttta agggcagagc caccctgacc gtggacaaga gcaccagcac cgcctacatg 300

gaactgaqca gcctgcqgaq cqaggacacc gccgtgtact actgcqccaq agacaqcaac 360

tggggagccg actattgggg ccagggcaca ctcgtgaccg tcagctcagc ctccaccaag 420

ggcccaagcg tcttccccct ggcaccctcc tccaagaqca cctctggcgg cacagccgcc 480

50 ctgggctgcc tgggtcaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 600

ctcagcagcg tgggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660

55

gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 720
 aaaactcaca catgcccacc ctgcccagca cctgaactcc tgggggggacc ctgagtcttc 780
 5 ctcttccccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 840
 gtgggtggtg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900
 10 gtggaggtgc ataatgcaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 960
 gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020
 aaggtctcca acaaagccct ccagccccc atcgagaaaa ccatctccaa agccaaaggc 1080
 15 cagccccggg aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac 1140
 caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatgc cgtggagtgg 1200
 gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac 1260
 20 ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 1320
 gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacca gaagagcctc 1380
 25 tccctgtctc ccggcaaag a 1401

<210> 64
 <211> 466
 30 <212> PRT
 <213> artificial
 <220>
 <223> Secuencia de aminoácido de hR198_HG2
 35 <400> 64

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

	Gly	Arg	Phe	Lys	Gly	Arg	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Thr	Ser	
					85					90					95		
5	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
				100					105					110			
10	Tyr	Tyr	Cys	Ala	Arg	Asp	Ser	Asn	Trp	Gly	Ala	Asp	Tyr	Trp	Gly	Gln	
			115					120					125				
15	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	
		130					135					140					
20	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	
	145					150					155					160	
25	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	
					165					170					175		
30	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	
				180					185					190			
35	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	
			195					200					205				
40	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	
		210					215					220					
45	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	
						230					235					240	
50	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	
					245					250					255		
55	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	
				260					265					270			
60	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	
			275					280					285				
65	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	
		290					295					300					

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

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

10

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

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

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

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

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

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
30 420 425 430

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

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

40 Gly Lys
465

45	<210>	65
	<211>	1401
	<212>	ADN
	<213>	artificial

50 <220>
 <223> Secuencia de nucleótido que codifica hR198_HG3

55 <400> 65
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	gtgcagctgg tgcagtctgg cgccgaagtg aagaaaccag gcgccagcgt gaaggtgtcc	120
	tgcaaggcct ctggctaccc catcaccgcc tactacatca gctgggtcag acaggcccca	180
5	ggccagggcc tggaatacgt gggctacatc gacatgggca acggccggac cgactacaac	240
	atgcggttta agggcagagc caccctgacc gtggacaaga gcaccagcac cgcctacatg	300
10	gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag agacagcaac	360
	tggggcgccg actattgggg ccagggcaca ctcgtgaccg tcagctcagc ctccaccaag	420
	ggcccaagcg tcttccccct ggcaccctcc tccaagagca cctctggcgg cacagccgcc	480
15	ctgggctgcc tggtaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc	540
	gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc	600
20	ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac	660
	gtgaatcaca agcccagcaa caccaagggtg gacaagagag ttgagcccaa atcttgtgac	720
	aaaactcaca catgcccacc ctgcccagca cctgaactcc tggggggacc ctcagtcttc	780
25	ctcttcccc caaaaccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc	840
	gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc	900
30	gtggaggtgc ataatgcaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg	960
	gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc	1020
	aagggtctcca acaaagccct cccagcccc atcgagaaaa ccatctccaa agccaaaggc	1080
35	cagccccggg aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac	1140
	caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg	1200
40	gagagcaatg gccagccga gaacaactac aagaccaccc ctcccgtgct ggactccgac	1260
	ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac	1320
	gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacca gaagagcctc	1380
45	tccctgtctc ccggcaaag a	1401

<210> 66

<211> 466

50 <212> PRT

<213> artificial

<220>

<223> Secuencia de aminoácido de hR198_HG3

55

<400> 66

5 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 1 5 10 15
 Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30
 10 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Pro Ile
 35 40 45
 15 Thr Ala Tyr Tyr Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60
 20 Glu Tyr Val Gly Tyr Ile Asp Met Gly Asn Gly Arg Thr Asp Tyr Asn
 65 70 75 80
 25 Met Arg Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
 85 90 95
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 100 105 110
 30 Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Gly Ala Asp Tyr Trp Gly Gln
 115 120 125
 35 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 130 135 140
 40 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 145 150 155 160
 45 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 165 170 175
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 180 185 190
 50 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 195 200 205
 55

	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	
	210						215					220					
5	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	
	225					230					235					240	
10	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	
					245					250					255		
15	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	
				260					265					270			
20	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	
			275					280					285				
25	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	
	290						295					300					
30	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	
					325					330					335		
35	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	
				340					345					350			
40	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	
			355					360					365				
45	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	
	385					390					395					400	
50	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	
					405					410					415		
55	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	
				420					425					430			

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

5

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

10 Gly Lys
 465

15 <210> 67
 <211> 1401
 <212> ADN
 <213> artificial

20 <220>
 <223> Secuencia de nucleótido que codifica hR198_H4-LALA

<400> 67
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 tgcaaggcct ctggctaccc cgtgaccgcc tactacatca gctggatcag acaggcccca 180
 30 ggccagggcc tggaatacgt gggctacatc gacatgggca acggccggac caactacaac 240
 gcccggttta agggcagagc caccctgacc gtggacaaga gcaccagcac cgcctacatg 300
 gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag agacagcaac 360
 35 tggggcgctgg actattgggg ccagggcaca ctcgtgaccg tcagctcagc ctccaccaag 420
 ggcccaagcg tcttccccct ggcaccctcc tccaagagca cctctggcgg cacagccgcc 480
 ctgggctgcc tggtaagga ctacttcccc gaaccctga ccgtgagctg gaactcaggc 540
 40 gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 600
 ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagacctt catctgcaac 660
 45 gtgaatcaca agcccagcaa caccaagggt gacaagagag ttgagcccaa atcttgtgac 720
 aaaactcaca catgcccacc ctgcccagca cctgaagccg cggggggacc ctcagtcttc 780
 50 ctcttcccc caaaaccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 840
 gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900
 gtggaggtgc ataatgcaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 960
 55 gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020

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aaggctctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggc      1080
cagccccggg aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac      1140
5  caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg      1200
gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac      1260
10 ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac      1320
gtctttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacca gaagagcctc      1380
tccctgtctc ccggcaaata a                                     1401

15  <210> 68
    <211> 466
    <212> PRT
    <213> artificial
20  <220>
    <223> Secuencia de aminoácido de hR198_H4-LALA

25  <400> 68
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1      5      10      15

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

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

40  Thr Ala Tyr Tyr Ile Ser Trp Ile Arg Gln Ala Pro Gly Gln Gly Leu
      50      55      60

45  Glu Tyr Val Gly Tyr Ile Asp Met Gly Asn Gly Arg Thr Asn Tyr Asn
      65      70      75      80

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

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

55  Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Gly Val Asp Tyr Trp Gly Gln
      115      120      125

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	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	
	130						135					140					
5	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	
	145					150					155					160	
10	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	
					165					170					175		
15	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	
				180					185					190			
20	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	
			195					200					205				
25	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	
	210						215					220					
30	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	
	225					230					235					240	
35	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala	Gly	Gly	
					245					250					255		
40	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	
				260					265					270			
45	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	
			275					280					285				
50	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	
	290						295					300					
55	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	
	305					310					315					320	
60	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	
					325					330					335		
65	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	
				340					345					350			

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

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

10 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 385 390 395 400
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 405 410 415

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

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

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

Gly Lys
 465

30 <210> 69
 <211> 1401
 <212> ADN
 <213> artificial

35 <220>
 <223> Secuencia de nucleótido que codifica hR198_HG1-LALA

40 <400> 69
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 gtgcagctgg tgcagtctgg cgccgaagtg aagaaaccag gcgccagcgt gaaggtgtcc 120
 tgcaaggcct ctggctaccc cgtgaccgcc tactacatca gctgggtcag acaggcccca 180
 45 ggccagggcc tggaatacgt gggctacatc gacatgggca acggccggac cgactacaac 240
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 50 gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag agacagcaac 360
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 ggcccaagcg tcttccccct ggcaccctcc tccaagagca cctctggcgg cacagccgcc 480
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ctgggctgcc tggtaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc      540
gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc      600
5  ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagacctt catctgcaac      660
gtgaatcaca agcccagcaa caccaagggt gacaagagag ttgagcccaa atcttgtgac      720
10  aaaactcaca catgcccacc ctgcccagca cctgaagccg cgggggggacc ctcagtcttc      780
ctcttcccc caaaaccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc      840
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc      900
15  gtggaggtgc ataatgcaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg      960
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc     1020
20  aaggtctcca acaaagccct cccagcccc atcgagaaaa ccatctccaa agccaaaggc     1080
cagccccggg aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac     1140
caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg     1200
25  gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac     1260
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac     1320
30  gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacca gaagagcctc     1380
tccctgtctc ccggcaaattg a                                             1401

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35  <210> 70
    <211> 466
    <212> PRT
    <213> artificial

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40  <220>
    <223> Secuencia de aminoácido de hR198_HG1-LALA

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    <400> 70

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

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

```

```

55  Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Pro Val
    35           40           45

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

<213> artificial

<220>

5 <223> Secuencia de nucleótido que codifica Señal secretora de cadena pesada humana y Región constante IgG2 humana

<400> 71

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	ggcccttccg tggtccctct ggccccttgt agccgttcca ccagcgagtc caccgccgcc	180
15	cttggtgtgc tgggtgaagga ctacttcctt gagcctgtga ccgtgagctg gaactccgga	240
	gcccttacca gcggcgtgca caccttcctt gccgtgctgc agtccagcgg cctttactcc	300
	ctgagctccg tggtgaccgt gcctagctcc aacttcggca cccaaaccta cacctgtaac	360
20	gtggaccaca agcctagcaa caccaagggtg gacaagaccg tggagcgtaa gtgttggtg	420
	gagtgtcctc ctgtcctgc cctcctgtg gccggacctt ccgtgttctt tttccctcct	480
25	aagcctaagg acaccctgat gatcagccgt acccctgagg tgacctgtgt ggtggtggac	540
	gtgtcccacg aggaccctga ggtgcagttc aactggtacg tggacggcgt ggaggtgcac	600
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35	cctcaagtgt acacccttcc tcctagccgt gaggagatga ccaagaacca agtgtccctt	840
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	caacctgaga acaactacaa gaccaccctt cctatgcttg acagcgacgg ctcttcttc	960
40	ctgtacagca agctgaccgt ggacaagtcc cgttggcaac aaggcaacgt gttcagctgt	1020
	tccgtgatgc acgaggccct gcacaaccac tacacccaaa agagcctttc cctgagccct	1080
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<210> 72

<211> 1395

<212> ADN

50 <213> artificial

<220>

<223> Secuencia de nucleótido que codifica Cadena pesada de 2C1.1

55 <400> 72

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5	tgcgctgtgt	acggaggcag	cttcagcggc	tactactggt	cctggatccg	gcagccccct	180
	ggcaagggcc	tggaatggat	cggcgagatc	gaccacagcg	gcagcaccaa	ctacaacccc	240
10	gccctgaagt	cccggctgac	catcagcgtg	gacaccagca	agaaccagtt	cagcctgaag	300
	ctgagcagcg	tgacagccgc	cgacaccgcc	gtgtactact	gtgccagagc	cggcagcggc	360
	ggctacgagg	attggttcga	tccttggggc	cagggcaccc	tggtgaccgt	cagctcagcc	420
15	agcaccaagg	gcccttccgt	gttcctctg	gccccttgta	gccgttcac	cagcgagtcc	480
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20	aactccggag	cccttaccag	cggcgtgcac	accttccctg	ccgtgctgca	gtccagcggc	600
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30	gtggtggacg	tgtcccacga	ggaccctgag	gtgcagttca	actggtacgt	ggacggcgtg	900
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	gtgtccgtgc	ttaccgtggt	gcaccaagac	tggctgaacg	gcaaggagta	caagtgtaa	1020
35	gtgagcaaca	agggacttcc	tgcccctatc	gagaagacca	tctccaagac	caagggccaa	1080
	cctcgtgagc	ctcaagtgt	cacccttcct	cctagccgtg	aggagatgac	caagaaccaa	1140
40	gtgtccctta	cctgtctggt	gaagggcttc	taccctagcg	acatcgccgt	ggagtgggag	1200
	tccaacggac	aacctgagaa	caactacaag	accacccctc	ctatgcttga	cagcgacggc	1260
	tccttcttcc	tgtacagcaa	gctgaccgtg	gacaagtccc	gttggcaaca	aggcaacgtg	1320
45	ttcagctgtt	ccgtgatgca	cgaggccctg	cacaaccact	acacccaaaa	gagcctttcc	1380
	ctgagccctg	gaaag					1395
50	<210>	73					
	<211>	465					
	<212>	PRT					
	<213>	artificial					
55	<220>						

<223> Secuencia de aminoácido de Cadena pesada de 2C1.1

<400> 73

5	Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp	1	5	10	15
10	Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Gln	Trp	Gly	Ala	Gly	Leu	Leu	Lys	20	25	30	
15	Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Ala	Val	Tyr	Gly	Gly	Ser	Phe	35	40	45	
20	Ser	Gly	Tyr	Tyr	Trp	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	50	55	60	
25	Glu	Trp	Ile	Gly	Glu	Ile	Asp	His	Ser	Gly	Ser	Thr	Asn	Tyr	Asn	Pro	65	70	75	80
30	Ala	Leu	Lys	Ser	Arg	Leu	Thr	Ile	Ser	Val	Asp	Thr	Ser	Lys	Asn	Gln	85	90	95	
35	Phe	Ser	Leu	Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	100	105	110	
40	Tyr	Cys	Ala	Arg	Ala	Gly	Ser	Gly	Gly	Tyr	Glu	Asp	Trp	Phe	Asp	Pro	115	120	125	
45	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	130	135	140	
50	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	145	150	155	160
55	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	165	170	175	
60	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	180	185	190	
65	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	195	200	205	

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

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

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

10 Lys
 465

15 <210> 74
 <211> 739
 <212> ADN
 <213> artificial

20 <220>
 <223> Secuencia de nucleótido que codifica Cadena ligera de 2C1.1

<400> 74
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 cagtccgtgc tgaccagcc tccttccgtg tctggcgccc ctggccagag agtgaccatc 120
 25 agctgtaccg gcagcagcag caacatcgga gccggctaca acgtgactg gtatcagcag 180
 ttccccgga ccgacccaa gctgctgac tacgtgtaca acatccggcc cagcggcgtg 240
 30 cccgaccggt tttctggcag cagaagcggc acaagcgcca gcctggccat caccggcctg 300
 cagaccgagg acgaggcca ctactactgc cagagctacg acagcagcct gagcggcgtg 360
 gtgttcggcg gaggcaccaa gctgacagtg ctgggccagc ccaaggccaa ccccaccgtg 420
 35 accctgttcc cccaagcag cgaggaactg caggccaaca aggccaccct ggtgtgcctg 480
 atcagcgact tctaccctgg cgccgtgaca gtggcctgga aggccgatgg atctcccggtg 540
 40 aaggccggcg tggaaccac caagcccagc aagcagagca acaacaata cgccgccagc 600
 agctacctga gcctgacccc cgagcagtgg aagtcccacc ggtcctacag ctgccaggtg 660
 acacacgagg gcagcacctg ggaaaagacc gtggcccca ccgagtgcag ctaggggccc 720
 45 gtttaaacgg gggaggcta 739

50 <210> 75
 <211> 237
 <212> PRT
 <213> artificial

55 <220>
 <223> Secuencia de aminoácido de Cadena ligera de 2C1.1

<400> 75

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 1 5 10 15
 Gly Ala Tyr Gly Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly
 20 25 30
 10 Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn
 35 40 45
 15 Ile Gly Ala Gly Tyr Asn Val His Trp Tyr Gln Gln Phe Pro Arg Thr
 50 55 60
 20 Asp Pro Lys Leu Leu Ile Tyr Val Tyr Asn Ile Arg Pro Ser Gly Val
 65 70 75 80
 25 Pro Asp Arg Phe Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala
 85 90 95
 Ile Thr Gly Leu Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser
 100 105 110
 30 Tyr Asp Ser Ser Leu Ser Gly Val Val Phe Gly Gly Gly Thr Lys Leu
 115 120 125
 35 Thr Val Leu Gly Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro
 130 135 140
 40 Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu
 145 150 155 160
 45 Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp
 165 170 175
 Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln
 180 185 190
 50 Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu
 195 200 205
 55

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly
 210 215 220

5 Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
 225 230 235

10 <210> 76
 <211> 1395
 <212> ADN
 <213> artificial

15 <220>
 <223> Secuencia de nucleótido que codifica Cadena pesada de 5H3.1

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20 gtgcagctgg tgcagtctgg cgccgaagtg aagaaacctg gcgctagcgt gaaggtgtcc 120
 tgcaaggcca gcggctacac cttcaccgac tactacatga actgggtgcg ccaggctcca 180

25 ggacagggcc tggaatggat gggctggatc aacccaaca gcggcggcac caaatacgcc 240
 cagaaattcc agggcagagt gaccatgacc cgggacacca gcatccggac cgcctacatg 300

30 gaactgagcc ggctgagaag cgacgacacc gccgtgtact actgcgccag agagtacggc 360
 ggcaacagcg attggttcga cccttggggc cagggcaccc tggtgaccgt cagctcagcc 420

35 agcaccaagg gcccttcctg gttccctctg gccccttgta gccgttcac cagcgagtcc 480
 accgccgccc ttggctgtct ggtgaaggac tacttccctg agcctgtgac cgtgagctgg 540

40 aactccggag cccttaccag cggcgtgcac accttccctg ccgtgctgca gtccagcggc 600
 ctttactccc tgagctccgt ggtgaccgtg cctagctcca acttcggcac ccaaactac 660

45 acctgtaacg tggaccacaa gcctagcaac accaaggtgg acaagaccgt ggagcgtaag 720
 tgttgtgtgg agtgtcctcc ttgtcctgcc cctcctgtgg ccggaccttc cgtgttcctt 780

50 ttccctccta agcctaagga caccctgatg atcagccgta cccctgaggt gacctgtgtg 840
 gtggtggacg tgtcccacga ggaccctgag gtgcagttca actggtacgt ggacggcgtg 900

55 gaggtgcaca acgccaagac caagcctcgt gaggagcaat tcaacagcac cttccgtgtg 960
 gtgtccgtgc ttaccgtggg gcaccaagac tggctgaacg gcaaggagta caagtgtgag 1020
 gtgagcaaca agggacttcc tgcccctatc gagaagacca tctccaagac caagggccaa 1080
 cctcgtgagc ctcaagtgtg cacccttcct cctagccgtg aggagatgac caagaaccaa 1140

gtgtccctta cctgtctggt gaagggcttc taccctagcg acatcgccgt ggagtgggag 1200
 tccaacggac aacctgagaa caactacaag accacccttc ctatgcttga cagcgacggc 1260
 5 tccttcttcc tgtacagcaa gctgaccgtg gacaagtccc gttggcaaca aggcaacgtg 1320
 ttcagctgtt ccgtgatgca cgaggccctg cacaaccact acacccaaaa gagcctttcc 1380
 ctgagccctg gaaag 1395

10

<210> 77

<211> 465

<212> PRT

15 <213> artificial

<220>

<223> Secuencia de aminoácido de Cadena pesada de 5H3.1

20 <400> 77

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

25

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

30

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

35

Thr Asp Tyr Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60

40

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

45

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

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

50

Tyr Tyr Cys Ala Arg Glu Tyr Gly Gly Asn Ser Asp Trp Phe Asp Pro
 115 120 125

55

	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	
	130						135					140					
5	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	
	145					150					155					160	
10	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	
					165					170					175		
15	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	
				180					185					190			
20	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	
			195					200					205				
25	Thr	Val	Pro	Ser	Ser	Asn	Phe	Gly	Thr	Gln	Thr	Tyr	Thr	Cys	Asn	Val	
		210					215					220					
30	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Pro	Val	Ala	Gly	Pro	
					245					250					255		
35	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	
				260					265					270			
40	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	
			275					280					285				
45	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	
		290					295					300					
50	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Val	
	305					310					315					320	
55	Val	Ser	Val	Leu	Thr	Val	Val	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	
					325					330					335		
60	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ala	Pro	Ile	Glu	Lys	
				340					345					350			

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

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

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

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

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

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

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

30 Lys
465

	<210>	78
	<211>	742
35	<212>	ADN
	<213>	artificial

<220>
<223> Secuencia de nucleótido que codifica Cadena ligera de 5H3.1

<400> 78
atgggtgctgc agaccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60

cagtccgtgc tgaccagcc tccttccgtg tctggcgccc ctggccagag agtgaccatc 120

agctgtaccg gcagcagcag caacatcggg gctggatacg acgtgcactg gtatcagcag 180

ctgcccggca ccgcccccaa gctgctgac tacggcaaca gcaaccggcc cagcggcgctg 240

50 cccgatagat tcagcggcag caagagcggc accagcgcca gcctggccat taccggactg 300

caggccgagg acgaggccga ctactactgc cagagctacg acaaccggct gagcgacagc 360

55 gtggtgatcg gcggaggcac caagctggcc gtgcaggac agcccaaggc caaccccacc 420

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gtgaccctgt tcccccaag cagcgaggaa ctgcaggcca acaaggccac cctgggtgtgc      480
ctgatcagcg acttctaccc tggcgccgtg acagtggcct ggaaggccga tggatctccc      540
5  gtgaaggccg gcgtggaaac caccaagccc agcaagcaga gcaacaacaa atacgccgcc      600
   agcagctacc tgagcctgac ccccagcag tggaagtccc accggtccta cagctgccag      660
10  gtgacacacg agggcagcac cgtggaaaag accgtggccc ccaccgagtg cagctagggg      720
   cccgtttaaa cgggggaggc ta                                             742

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15  <210> 79
   <211> 238
   <212> PRT
   <213> artificial

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20  <220>
   <223> Secuencia de aminoácido de Cadena ligera de 5H3.1
   <400> 79

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

```

```

30  Gly Ala Tyr Gly Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly
   20           25           30

```

```

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

```

```

40  Ile Gly Ala Gly Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr
   50           55           60

```

```

45  Ala Pro Lys Leu Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val
   65           70           75           80

```

```

50  Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala
   85           90           95

```

```

55  Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser
   100          105          110

```

```

   Tyr Asp Asn Arg Leu Ser Asp Ser Val Val Ile Gly Gly Gly Thr Lys
   115          120          125

```

55

Leu Ala Val Gln Gly Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe
130 135 140

5 Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys
145 150 155 160

10 Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala
165 170 175

Asp Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys
180 185 190

15

Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro
195 200 205

Glu Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu

210 215 220

25 Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
225 230 235

30	<210>	80
	<211>	1433
	<212>	ADN
	<213>	artificial

35 <223> Secuencia de nucleótido que codifica Cadena pesada de 10F8

<400> 80
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40 cgcctcccaga tgggtgctgt ctcaagtgca gctgcagcag tctggcgccg aactcgtgcg 120

gcctggaagc agcgtgaaga tcagctgcaa ggccagcggc tacgccttcc ggtcctactg 180

gatgaactgg gtcaagcaga gaccaggcca gggcctggaa tggatcgccc acatctatcc 240

cgccgacggc gacaccaact acaacggcaa gttcaagggc aaggccaccc tgaccgccga 300

caagaqcagc agcacagcct acatgcagct gtccagcctg accagcgaag acagcgcctt 360

50 gtacctgtgt ggcagagggc gacacaaccgt ggtggtggat tattggggcc agggcaccac 420

actgaccgtg tccagcgcca agaccacccc cccatctgtg tatectctgg cccctggatc 480

tgccgcccag accaacagca tggtcaccct gggctgcctc gtgaagggct acttcctga 540

55

gcctgtgacc gtgacctgga acagcggctc tctgtctagc ggcgtgcaca cctttccagc 600
 cgtgctgcag agcgacctgt acaccctgag cagctccgtg accgtgccta gcagcacctg 660
 5 gcctagcgag acagtgcctt gcaacgtggc ccaccctgcc agctctacca aggtggacaa 720
 gaaaatcgtg ccccgaggact gcggctgcaa gccctgtatc tgtaccgtgc ccgaggtgtc 780
 10 ctccgtgttc atcttccac ccaagcccaa ggacgtgctg accatcacc tgacacccaa 840
 agtgacatgt gtggtggtgg acatcagcaa ggacgacccc gaggtgcagt tcagttggtt 900
 cgtggacgac gtggaagtgc acacagccca gaccagccc agagaggaa agttcaacag 960
 15 caccttcaga agcgtgtccg agctgcccac catgcaccag gactggctga acggcaaaga 1020
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 gaccaagggc agaccaagg ccccccaggt gtacacaatc cccccacca aagaacagat 1140
 20 ggccaaggac aaggtgtccc tgacctgcat gatcaccgat ttcttcccag aggacatcac 1200
 cgtggaatgg cagtggaacg gccagccgc cgagaactac aagaacaccc agcctatcat 1260
 25 ggacaccgac ggcagctact tcgtgtacag caagctgaac gtgcagaagt ccaactggga 1320
 ggccggcaac accttcacct gtagcgtgct gcacgagggc ctgcacaatc accacaccga 1380
 30 gaagtcctg tcccacagcc ccggcaaatg agtttaaacg ggggaggcta act 1433

<210> 81

<211> 461

<212> PRT

35 <213> artificial

<220>

<223> Secuencia de aminoácido de Cadena pesada de 10F8

40 <400> 81

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

45

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

50

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

55

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

	Glu	Trp	Ile	Gly	His	Ile	Tyr	Pro	Gly	Asp	Gly	Asp	Thr	Asn	Tyr	Asn	
	65					70					75					80	
5	Gly	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	
					85					90					95		
10	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	
				100					105					110			
15	Tyr	Leu	Cys	Gly	Arg	Gly	Gly	Thr	Thr	Val	Val	Val	Asp	Tyr	Trp	Gly	
			115					120					125				
20	Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser	Ala	Lys	Thr	Thr	Pro	Pro	Ser	
		130					135					140					
25	Val	Tyr	Pro	Leu	Ala	Pro	Gly	Ser	Ala	Ala	Gln	Thr	Asn	Ser	Met	Val	
	145					150					155					160	
30	Thr	Leu	Gly	Cys	Leu	Val	Lys	Gly	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	
					165					170					175		
35	Val	Leu	Gln	Ser	Asp	Leu	Tyr	Thr	Leu	Ser	Ser	Ser	Val	Thr	Val	Pro	
			195					200					205				
40	Ser	Ser	Thr	Trp	Pro	Ser	Glu	Thr	Val	Thr	Cys	Asn	Val	Ala	His	Pro	
		210					215					220					
45	Ala	Ser	Ser	Thr	Lys	Val	Asp	Lys	Lys	Ile	Val	Pro	Arg	Asp	Cys	Gly	
	225					230					235					240	
50	Cys	Lys	Pro	Cys	Ile	Cys	Thr	Val	Pro	Glu	Val	Ser	Ser	Val	Phe	Ile	
					245					250					255		
55	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Val	Leu	Thr	Ile	Thr	Leu	Thr	Pro	Lys	
				260					265					270			
60	Val	Thr	Cys	Val	Val	Val	Asp	Ile	Ser	Lys	Asp	Asp	Pro	Glu	Val	Gln	
			275					280					285				

[illegible]

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      ccggacccgg aagaactacc tggcctggta tcagcagaag cccggccagt cccccaagct      240
5    gctgatctac tgggccagca ccagagaaag cggcgtgccc gatagattca ccggcagcgg      300
      ctctggcacc gacttcaccc tgacaatcag cagcgtgcag gccgaggacc ttgctgtgta      360
10   ctactgcaag cagagctaca acctgccctg gaccttcggc ggaggcacca agctggaaat      420
      caagagagcc gacgccgctc ccaccgtgtc catctttcca cctagcagcg agcagctgac      480
      cagcggcgga gctagcgtcg tgtgcttcct gaacaacttc taccccaagg acatcaacgt      540
15   gaagtggaag atcgacggca gcgagcggca gaacggcgtg ctgaatagct ggaccgacca      600
      ggacagcaag gactccacct acagcatgtc cagcaccctg accctgacca aggacgagta      660
20   cgagcggcac aacagctaca catgcgaggc caccacaag accagcacct ccccatcgt      720
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      <211> 240
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      <223> Secuencia de aminoácido de Cadena ligera de 10F8

30   <400> 83

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

40   Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
      35              40              45

45   Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
      50              55              60

      Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
      65              70              75              80

50   Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
      85              90              95

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	Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr	
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5	Tyr Cys Lys Gln Ser Tyr Asn Leu Pro Trp Thr Phe Gly Gly Gly Thr	
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10	Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe	
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15	Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys	
	145 150 155 160	
20	Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile	
	165 170 175	
25	Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln	
	180 185 190	
30	Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr	
	195 200 205	
35	Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His	
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10	tgagcctgtg accgtgacct ggaacagcgg ctctctgtct agcggcgtgc acacctttcc	600
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	gttcgtggac gacgtggaag tgcacacagc ccagacccag cccagagagg aacagttcaa	960
	cagcaccttc agaagcgtgt ccgagctgcc catcatgcac caggactggc tgaacggcaa	1020
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	Pro	Gly	Ser	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ala	Phe	
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5	Ser	Ser	Tyr	Trp	Met	Asn	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	
		50					55					60					
10	Glu	Trp	Ile	Gly	His	Ile	Tyr	Pro	Gly	Asp	Gly	Asp	Thr	Asn	Tyr	Asn	
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15	Gly	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	
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25	Tyr	Phe	Cys	Ala	Arg	Ser	Gly	Arg	Leu	Arg	Phe	Ala	Met	Asp	Tyr	Trp	
			115					120					125				
30	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Ala	Lys	Thr	Thr	Pro	Pro	
		130					135					140					
35	Ser	Val	Tyr	Pro	Leu	Ala	Pro	Gly	Ser	Ala	Ala	Gln	Thr	Asn	Ser	Met	
	145					150				155						160	
40	Val	Thr	Leu	Gly	Cys	Leu	Val	Lys	Gly	Tyr	Phe	Pro	Glu	Pro	Val	Thr	
					165					170					175		
45	Val	Thr	Trp	Asn	Ser	Gly	Ser	Leu	Ser	Ser	Gly	Val	His	Thr	Phe	Pro	
				180					185					190			
50	Ala	Val	Leu	Gln	Ser	Asp	Leu	Tyr	Thr	Leu	Ser	Ser	Ser	Val	Thr	Val	
			195					200					205				
55	Pro	Ser	Ser	Thr	Trp	Pro	Ser	Glu	Thr	Val	Thr	Cys	Asn	Val	Ala	His	
		210					215					220					
60	Pro	Ala	Ser	Ser	Thr	Lys	Val	Asp	Lys	Lys	Ile	Val	Pro	Arg	Asp	Cys	
		225				230					235					240	
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<220>

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ccggacccgg aagaactacc tggcctggta tcagcagaag cccggccagt cccccaagct 240

15

gctgatctac tgggccagca ccagagaaaag cggcgtgccc gatagattca ccggcagcgg 300

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gcggcacaac agctacacat gcgaggccac ccacaagacc agcacctccc ccatcgtgaa 720

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<223> Secuencia de aminoácido de Cadena ligera de 14F74

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Gly Ala Tyr Gly Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala
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50

Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
35 40 45

55

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

	Pro	Ser	Ser	Thr	Trp	Pro	Ser	Glu	Thr	Val	Thr	Cys	Asn	Val	Ala	His
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5	Pro	Ala	Ser	Ser	Thr	Lys	Val	Asp	Lys	Lys	Ile	Val	Pro	Arg	Asp	Cys
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15	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Val	Leu	Thr	Ile	Thr	Leu	Thr	Pro
				260					265					270		
20	Lys	Val	Thr	Cys	Val	Val	Val	Asp	Ile	Ser	Lys	Asp	Asp	Pro	Glu	Val
			275					280					285			
25	Gln	Phe	Ser	Trp	Phe	Val	Asp	Asp	Val	Glu	Val	His	Thr	Ala	Gln	Thr
		290					295					300				
30	Gln	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Ser	Val	Ser	Glu
	305					310					315					320
35	Leu	Pro	Ile	Met	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Phe	Lys	Cys
					325					330					335	
40	Arg	Val	Asn	Ser	Ala	Ala	Phe	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser
				340					345					350		
45	Lys	Thr	Lys	Gly	Arg	Pro	Lys	Ala	Pro	Gln	Val	Tyr	Thr	Ile	Pro	Pro
			355					360					365			
50	Pro	Lys	Glu	Gln	Met	Ala	Lys	Asp	Lys	Val	Ser	Leu	Thr	Cys	Met	Ile
	370						375					380				
55	Thr	Asp	Phe	Phe	Pro	Glu	Asp	Ile	Thr	Val	Glu	Trp	Gln	Trp	Asn	Gly
	385					390					395					400
60	Gln	Pro	Ala	Glu	Asn	Tyr	Lys	Asn	Thr	Gln	Pro	Ile	Met	Asp	Thr	Asp
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65	Gly	Ser	Tyr	Phe	Val	Tyr	Ser	Lys	Leu	Asn	Val	Gln	Lys	Ser	Asn	Trp
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 25 ccggacccgg aagaactacc tggcctggta tcagcagaag cccggccagt cccccaagct 240
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 cagcaaggac tccacctaca gcatgtccag caccctgacc ctgaccaagg acgagtacga 660
 40 gcggcacaac agctacacat gcgaggccac ccacaagacc agcacctccc ccatcgtgaa 720
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50 <220>
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				20					25					30			
10	Val	Ser	Ala	Gly	Glu	Lys	Val	Thr	Met	Ser	Cys	Lys	Ser	Ser	Gln	Ser	
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		50					55					60					
20	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	
	65					70					75					80	
25	Glu	Ser	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	
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50	Leu	Asn	Asn	Phe	Tyr	Pro	Lys	Asp	Ile	Asn	Val	Lys	Trp	Lys	Ile	Asp	
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55	Gly	Ser	Glu	Arg	Gln	Asn	Gly	Val	Leu	Asn	Ser	Trp	Thr	Asp	Gln	Asp	
				180					185					190			
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65	Asp	Glu	Tyr	Glu	Arg	His	Asn	Ser	Tyr	Thr	Cys	Glu	Ala	Thr	His	Lys	
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Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
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35 <220>
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 1 5 10

<210> 95
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 25 <210> 98
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 40 <210> 99
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 <212> PRT
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 45 <400> 99

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 1 5

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Leu Gln Phe Ala Thr Tyr Pro Asp Thr
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Gly

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Gly

15

<210> 109

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25

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<210> 111

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tgcaaggcct ctggctaccc cgtgaccagc tactacatca gctggatcag acaggcccca 180

55

ggccagggcc tggaatggat cggctatgtg gacatgggca acggccggac caactacaac 240

gagaagttca agggcagagc caccctgacc gtggacaaga gcaccagcac cgcctacatg 300
 gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag agacagcaac 360
 5 tggggcgtgg actattgggg ccagggcaca ctctgtgaccg tcagctcagc ctccaccaag 420
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 10 ctgggctgcc tggtaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc 540
 gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 600
 ctgagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660
 15 gtgaatcaca agcccagcaa caccaagggtg gacaagagag ttgagcccaa atcttgtgac 720
 aaaactcaca catgcccacc ctgcccagca cctgaactcc tggggggacc ctgagtcttc 780
 ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 840
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 25 gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020
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 gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac 1260
 35 ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 1320
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<210> 112
 <211> 466
 <212> PRT
 45 <213> artificial

<220>
 <223> Secuencia de aminoácido de hR198_H0

50 <400> 112
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				20					25					30			
5	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Pro	Val	
			35					40					45				
10	Thr	Ser	Tyr	Tyr	Ile	Ser	Trp	Ile	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	
		50					55					60					
15	Glu	Trp	Ile	Gly	Tyr	Val	Asp	Met	Gly	Asn	Gly	Arg	Thr	Asn	Tyr	Asn	
	65					70				75						80	
20	Glu	Lys	Phe	Lys	Gly	Arg	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Thr	Ser	
					85					90					95		
25	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
				100					105					110			
30	Tyr	Tyr	Cys	Ala	Arg	Asp	Ser	Asn	Trp	Gly	Val	Asp	Tyr	Trp	Gly	Gln	
			115					120					125				
35	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	
		130					135					140					
40	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	
	145					150					155					160	
45	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	
					165					170					175		
50	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	
				180					185					190			
55	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	
			195					200					205				
60	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	
		210					215					220					
65	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	
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[illegible]

465

5 <210> 113
 <211> 1401
 <212> ADN
 <213> artificial

10 <220>
 <223> Secuencia de nucleótido que codifica hR198_H5

<400> 113
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 tgcaaggcct ctggctaccc cgtgaccgcc tactacatca gctggatcag acaggcccca 180
 20 ggccagggcc tggaatggat cggctacatc gacatgggca acggccggac caactacaac 240
 gcccggttta agggcagagc caccctgacc gtggacaaga gcaccagcac cgcctacatg 300
 gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag agacagcaac 360
 25 tggggcgtgg actattgggg ccagggcaca ctcgtgaccg tcagctcagc ctccaccaag 420
 ggcccaagcg tcttccccct ggcacctcc tccaagagca cctctggcgg cacagccgcc 480
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 30 gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 600
 ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660
 35 gtgaatcaca agcccagcaa caccaagggtg gacaagagag ttgagccaa atcttgtgac 720
 aaaactcaca catgcccacc ctgcccagca cctgaactcc tggggggacc ctcagtcttc 780
 ctcttcccc caaaaccaa ggacacctc atgatctccc ggacctctga ggtcacatgc 840
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 gtggaggtgc ataatgcaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 960
 45 gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020
 aaggtctcca acaaagccct cccagcccc atcgagaaaa ccatctcaa agccaaaggc 1080
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<210> 114

<211> 466

<212> PRT

<213> artificial

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<220>

<223> Secuencia de aminoácido de hR198_H5

<400> 114

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
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Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

25

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

30

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

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

35

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

40

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

45

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

50

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

55

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

	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	
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5	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	
				180					185					190			
10	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	
			195					200					205				
15	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	
		210					215					220					
20	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	
		225				230					235					240	
25	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	
					245					250					255		
30	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	
				260					265					270			
35	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	
		275						280					285				
40	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	
		290					295					300					
45	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	
		305				310					315					320	
50	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	
					325					330					335		
55	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	
				340					345					350			
60	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	
			355					360					365				
65	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	
		370					375					380					

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

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

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

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

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

Gly Lys
 465

25 <210> 115
 <211> 48
 <212> PRT
 <213> Homo sapiens

30 <400> 115

Ser Gly Ser Gly Phe Leu Pro Leu Lys Lys Gln Pro Gly Gln Pro Arg
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35 Pro Thr Ser Lys Pro Pro Ala Ser Gly Ala Ala Ala Asn Val Ser Thr
 20 25 30

40 Ser Gly Ile Thr Pro Gly Gln Ala Ala Ala Ile Ala Ser Thr Thr Ile
 35 40 45

45 <210> 116
 <211> 11
 <212> PRT
 <213> Rattus rattus

<400> 116

50 Arg Ala Ser Gln Ser Ile Ser Asn Ser Leu Ser
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