

LISTADO DE SECUENCIAS

<110> UCB Biopharma SRL

<120> ANTICUERPO MULTIESPECIFICO CON ESPECIFICIDAD DE UNIÓN PARA IL-13 E IL-17 HUMANAS

<130> PF0208-WO-PCT

<150> GB 1919061.0

<151> 2019-12-20

<160> 68

<170> Versión PatentIn 3.5

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Thr Ile Thr Tyr Glu Gly Arg Asn Thr Tyr Tyr Arg Asp Ser Val Lys
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Gly

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Pro Pro Gln Tyr Tyr Glu Gly Ser Ile Tyr Arg Leu Trp Phe Ala His
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Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Thr Cys Arg Ala Asp Glu Ser Val Arg Thr Leu
20 25 30

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Trp Ser Asp Pro Trp
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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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20 25 30

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

Ala Thr Ile Thr Tyr Glu Gly Arg Asn Thr Tyr Tyr Arg 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 Val Tyr Tyr Cys
85 90 95

Ala Ser Pro Pro Gln Tyr Tyr Glu Gly Ser Ile Tyr Arg Leu Trp Phe
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Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
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Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Asp	Glu	Ser	Val	Arg	Thr	Leu
			20					25					30		

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

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

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

65					70						75					80
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Thr	Trp	Ser	Asp	Pro	Trp	
				85					90					95		
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	
			100					105					110			
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	
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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	
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Phe	Asn	Arg	Gly	Glu	Cys											
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Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
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Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Asp	Tyr
			20					25					30		

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

Ala	Thr	Ile	Thr	Tyr	Glu	Gly	Arg	Asn	Thr	Tyr	Tyr	Arg	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 Val Tyr Tyr Cys
85 90 95

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

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
115 120 125

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

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
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Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
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Pro Lys Ser Cys
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Lys Ala Ser Gln Asn Ile Asn Glu Asn Leu Asp
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Tyr Thr Asp Ile Leu Gln Thr
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Tyr Gln Tyr Tyr Ser Gly Tyr Thr
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Gly Tyr Ser Phe Thr Ser Tyr Tyr Ile His
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Arg Ile Gly Pro Gly Ser Gly Asp Ile Asn Tyr Asn Glu Lys Phe Lys
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Phe His Tyr Asp Gly Ala Asp
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Asp Ile Gln Met Thr Gln Ser Pro Pro Val Leu Ser Ala Ser Val Gly
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Asp Arg Val Thr Leu Ser Cys Lys Ala Ser Gln Asn Ile Asn Glu Asn
20 25 30

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

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

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

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

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

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180

aggttcagtg gcagtggatc tggtagatg tacacactca ccatcagcag cctgcagcct
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<212> PRT
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Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Lys	Pro	Gly	Ser
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Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe	Thr	Ser	Tyr
		20					25					30			

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

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

Lys Gly Lys Ala Thr Phe Thr Val Asp Lys Tyr Phe Ser Thr Ala Tyr
65 70 75 80

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

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

Thr Val Ser Ser
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cctggacagg gccttgagtg gattgggcgt attggtcctg gaagtggaga tattaattac
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aatgagaagt tcaagggcaa ggccacattt actgtggaca aatatttcag cacagcctac
240

atgcaactca gcagcctgtc acctgaggac actgcggtct tttactgtgc aagatttcac
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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

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

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

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

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

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

Ser

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<400> 27

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

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

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

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

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

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

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

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<400> 28

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

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

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

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

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

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

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

Thr Val Ser Ser
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120

ggcaaggccc ccaagctgct gatctactac accgacatcc tgcagaccgg catcccctcc
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<400> 31

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Ile Asn Glu Asn
20 25 30

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

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

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

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

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

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<400> 32

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

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

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

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

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

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

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

Thr Val Ser Ser
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120

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aggttctccg gctccggctc cggcaccgac tacaccctga ccatctcttc cctgcagccc
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Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

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

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

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

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

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

Ala Arg Phe His Tyr Asp Gly Ala Asp Trp Gly Gln Gly Thr Leu Val

100	105	110
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly		
115	120	125
Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro		
130	135	140
Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys		
145	150	155
Ala Ser Gln Asn Ile Asn Glu Asn Leu Asp Trp Tyr Gln Gln Lys Pro		
165	170	175
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Asp Ile Leu Gln Thr		
180	185	190
Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr		
195	200	205
Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys		
210	215	220
Tyr Gln Tyr Tyr Ser Gly Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu		
225	230	235
		240

Ile Lys

<210> 36
 <211> 726
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> secuencia recombinante

<400> 36
 gaggtgcagc tgggtgcagtc cggcgccgag gtgaagaagc cgggtcctc cgtgaagggtg
 60

tcctgcaagg cctccggcta ctcttcacc tcctactaca tccactgggt gaggcaggcc
 120

cccgccagg gcctggagt gatgggcagg atcgccccg gctccggcga catcaactac
180

aacgagaagt tcaagggcag ggccaccttc accgtggaca agtccacctc caccgcctac
240

atggagctgt cctccctgag gtccgaggac accgccgtgt actactgcgc caggttccac
300

tacgacggcg ccgactgggg ccagggcacc ctggtgaccg tgtcctccgg aggtggcggg
360

tctggcgggtg gcggttccgg tggcgggtgga tcgggaggtg gcggttctga catccagatg
420

accagtccc cctcctccct gtccgcctcc gtgggcgaca gggtgaccat cacctgcaag
480

gcctcccaga acatcaacga gaacctggac tgggtaccagc agaagcccgg caaggccccc
540

aagctgctga tctactacac cgacatcctg cagaccggca tcccctccag gttctccggc
600

tccggctccg gcaccgacta caccctgacc atctcctccc tgcagcccga ggacttcgcc
660

acctactact gctaccagta ctactccggc tacaccttcg gccagggcac caagctggag
720

atcaag
726

<210> 37
<211> 242
<212> PRT
<213> Secuencia artificial

<220>
<223> secuencia recombinante

<400> 37

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

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

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

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

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

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

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

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
130 135 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
145 150 155 160

Ala Ser Gln Asn Ile Asn Glu Asn Leu Asp Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Asp Ile Leu Gln Thr
180 185 190

Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
195 200 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
210 215 220

Tyr Gln Tyr Tyr Ser Gly Tyr Thr Phe Gly Cys Gly Thr Lys Leu Glu
225 230 235 240

Ile Lys

<210> 38
<211> 726
<212> ADN
<213> Secuencia artificial

<220>
<223> secuencia recombinante

<400> 38
gaggtgcagc tgggtgcagtc cggcgccgag gtgaagaagc cgggtcctc cgtgaagggtg
60

tcttgcaagg cctccggcta ctcttcacc tcctactaca tccactgggt gaggcaggcc
120

cccggccagt gcctggagtg gatgggcagg atcggtcccg gctccggcga catcaactac
180

aacgagaagt tcaagggcag ggccaccttc accgtggaca agtccacctc caccgcctac
240

atggagctgt cctccctgag gtccgaggac accgccgtgt actactgcgc caggttccac
300

tacgacggcg ccgactgggg ccagggcacc ctggtgaccg tgcctccgg aggtggcgggt
360

tctggcgggtg gcggttccgg tggcgggtgga tcgggaggtg gcggttctga catccagatg
420

accagtccc cctcctccct gtccgcctcc gtgggcgaca gggtgaccat cacctgcaag
480

gcctcccaga acatcaacga gaacctggac tggtagcagc agaagcccg caaggccccc
540

aagctgctga tctactacac cgacatctg cagaccggca tcccctccag gttctccggc
600

tccggctccg gcaccgacta caccctgacc atctcctccc tgcagcccga ggacttcgcc
660

acctactact gctaccagta ctactccggc tacaccttcg gctgcggcac caagctggag
720

atcaag
726

<210> 39
<211> 12
<212> PRT
<213> Secuencia artificial

<220>
<223> secuencia recombinante

<400> 39

Gln Ser Ser Pro Ser Val Trp Ser Asn Phe Leu Ser
1 5 10

<210> 40
<211> 7
<212> PRT
<213> Secuencia artificial

<220>
<223> secuencia recombinante

<400> 40

Glu Ala Ser Lys Leu Thr Ser
1 5

<210> 41
<211> 11
<212> PRT
<213> Secuencia artificial

<220>
<223> secuencia recombinante

<400> 41

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

<210> 42
<211> 10
<212> PRT
<213> Secuencia artificial

<220>
<223> secuencia recombinante

<400> 42

Gly Ile Asp Leu Ser Asn Tyr Ala Ile Asn
1 5 10

<210> 43
<211> 16
<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia recombinante

<400> 43

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

<210> 44

<211> 13

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia recombinante

<400> 44

Thr	Val	Pro	Gly	Tyr	Ser	Thr	Ala	Pro	Tyr	Phe	Asp	Leu
1				5					10			

<210> 45

<211> 110

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia recombinante

<400> 45

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

Asp	Arg	Val	Thr	Ile	Thr	Cys	Gln	Ser	Ser	Pro	Ser	Val	Trp	Ser	Asn
			20					25					30		

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

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

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

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

Ser Asp Thr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 46
<211> 121
<212> PRT
<213> Secuencia artificial

<220>
<223> secuencia recombinante

<400> 46

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

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

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

Gly Ile Ile Trp Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys
50 55 60

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 47
<211> 330
<212> ADN

<213> Secuencia artificial

<220>

<223> secuencia recombinante

<400> 47

gatattcaga tgacgcaatc accttcgagc gtatccgcct cggaggaga cagggtgaca
60

atcacttgtc agtcatcccc ctcatctgg agcaactttt tgtcatggta tcagcagaag
120

cccgaaagg ctccgaaatt gctgatctac gaggcacga agttgacgag cgggtgtacca
180

agcagattct ccggttcggg gtcgggaact gacttcaccc ttacgatctc atcgctgcag
240

ccggaggatt ttgcgaccta ctactgtggg ggtgggtatt cgtcgatttc cgacacaaca
300

ttcgggggcg gcacgaaagt ggaaatcaag
330

<210> 48

<211> 363

<212> ADN

<213> Secuencia artificial

<220>

<223> secuencia recombinante

<400> 48

gaagtgcagt tgctggagtc aggtggagg ctggtgcagc ccggaggatc gctgcggttg
60

tcattgcgcg tgctccggtat tgatttgtcc aattacgcca tcaattgggt acgccaagcg
120

ccagggaagg gccttgagtg gattggcatc atctgggcgt cggggacgac cttttatgct
180

acttgggcca aaggaagatt cacaatctcc cgagacaact cgaagaacac cgtgtatctt
240

caaatgaact cgctcagggc cgaggacag gcggtctact actgtgcacg gacagtgccg
300

ggttattcaa cggcacctta ctttgatctt tggggccagg ggaccctcgt gactgtctca
360

agt
363

<210> 49
<211> 110
<212> PRT
<213> Secuencia artificial

<220>
<223> secuencia recombinante

<400> 49

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

Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn
20 25 30

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

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

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

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

Ser Asp Thr Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 50
<211> 121
<212> PRT
<213> Secuencia artificial

<220>
<223> secuencia recombinante

<400> 50

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

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

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

Gly Ile Ile Trp Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys
50 55 60

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 51
<211> 330
<212> ADN
<213> Secuencia artificial

<220>
<223> secuencia recombinante

<400> 51
gatattcaga tgacgcaatc accttcgagc gtatccgcct cgggtgggaga cagggtgaca
60

atcacttgtc agtcatcccc ctcagtctgg agcaactttt tgtcatggta tcagcagaag
120

cccggaaagg ctccgaaatt gctgatctac gaggcacga agttgacgag cgggtgtacca
180

agcagattct ccggttcggg gtcgggaact gacttcaccc ttacgatctc atcgctgcag
240

ccggaggatt ttgcgaccta ctactgtggg ggtgggtatt cgtcgatttc cgacacaaca
300

ttcgggtgcg gcacgaaagt ggaaatcaag
330

<210> 52
<211> 363
<212> ADN
<213> Secuencia artificial

<220>
<223> secuencia recombinante

<400> 52
gaagtgcagt tgctggagtc aggtggaggg ctggtgcagc ccggaggatc gctgcggttg
60

tcatgcgcgg tgtccggtat tgatttgtcc aattacgcca tcaattgggt acgccaagcg
120

ccagggaagt gccttgagtg gattggcatc atctgggcgt cggggacgac cttttatgct
180

acttgggcca aaggaagatt cacaatctcc cgagacaact cgaagaacac cgtgtatctt
240

caaatgaact cgctcagggc cgaggacacg gcggtctact actgtgcacg gacagtgccg
300

ggttattcaa cggcacctta ctttgatctt tggggccagg ggaccctcgt gactgtctca
360

agt
363

<210> 53
<211> 251
<212> PRT
<213> Secuencia artificial

<220>
<223> secuencia recombinante

<400> 53

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

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

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

Gly Ile Ile Trp Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys
50 55 60

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
130 135 140

Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val
145 150 155 160

Thr Ile Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn Phe Leu Ser
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Glu
180 185 190

Ala Ser Lys Leu Thr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
195 200 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
210 215 220

Phe Ala Thr Tyr Tyr Cys Gly Gly Gly Tyr Ser Ser Ile Ser Asp Thr
225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
245 250

<210> 54

<211> 753
<212> ADN
<213> Secuencia artificial

<220>
<223> secuencia recombinante

<400> 54
gaagtgcagt tgctggagtc aggtggaggg ctggtgcagc ccggaggatc gctgcggttg
60

tcatgcgcgg tgtccggtat tgatttgtcc aattacgcca tcaattgggt acgccaagcg
120

ccaggggaagg gccttgagtg gattggcatc atctgggcgt cggggacgac cttttatgct
180

acttgggcca aaggaagatt cacaatctcc cgagacaact cgaagaacac cgtgtatctt
240

caaatgaact cgctcagggc cgaggacacg gcggtctact actgtgcacg gacagtgccg
300

ggttattcaa cggcacctta ctttgatctt tggggccagg ggaccctcgt gactgtctca
360

agtggaggtg gcggttcttg cgggtggcgt tccggtggcg gtggatcggg aggtggcgg
420

tctgatattc agatgacgca atcaccttcg agcgtatccg cctcgggtggg agacaggggtg
480

acaatcactt gtcagtcac cccctcagtc tggagcaact ttttgtcatg gtatcagcag
540

aagcccggaa aggctccgaa attgctgac tacgaggcat cgaagttgac gagcgggtga
600

ccaagcagat tctccggttc ggggtcggga actgaattca cccttacgat ctcatcgctg
660

cagccggagg attttgcgac ctactactgt gggggtgggt attcgtcgat ttccgacaca
720

acattcgggg gcggcacgaa agtggaatc aag
753

<210> 55
<211> 251
<212> PRT
<213> Secuencia artificial

<220>

<223> secuencia recombinante

<400> 55

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

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

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

Gly Ile Ile Trp Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys
50 55 60

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
130 135 140

Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val
145 150 155 160

Thr Ile Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn Phe Leu Ser
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Glu
180 185 190

Ala Ser Lys Leu Thr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
195 200 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
210 215 220

Phe Ala Thr Tyr Tyr Cys Gly Gly Gly Tyr Ser Ser Ile Ser Asp Thr
225 230 235 240

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
245 250

<210> 56

<211> 753

<212> ADN

<213> Secuencia artificial

<220>

<223> secuencia recombinante

<400> 56

gaagtgcagt tgctggagtc aggtggaggg ctggtgcagc ccggaggatc gctgcggttg
60

tcatgcgcgg tgtccggtat tgatttgtcc aattacgcca tcaattgggt acgccaagcg
120

ccagggaagt gccttgagtg gattggcatc atctgggcgt cggggacgac cttttatgct
180

acttgggcca aaggaagatt cacaatctcc cgagacaact cgaagaacac cgtgtatctt
240

caaatgaact cgctcagggc cgaggacacg gcggtctact actgtgcacg gacagtgccg
300

ggttattcaa cggcacctta ctttgatctt tggggccagg ggaccctcgt gactgtctca
360

agtggaggtg gcggttctgg cgggtggcgg tccggtggcg gtggatcggg aggtggcgg
420

tctgatattc agatgacgca atcaccttcg agcgtatccg cctcgggtggg agacagggtg
480

acaatcactt gtcagtcatc cccctcagtc tggagcaact tttgtcatg gtatcagcag
540

aagcccggaa aggctccgaa attgctgac tacgaggcat cgaagttgac gagcgggtga
600

ccaagcagat tctccggttc ggggtcggga actgacttca cccttacgat ctcatcgctg
660

cagccggagg attttgcgac ctactactgt ggggggtgggt attcgtcgat ttccgacaca
720

acattcgggt gcggcacgaa agtggaatc aag
753

<210> 57

<211> 492

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia recombinante

<400> 57

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 Phe Thr Phe Ser Asp Tyr
20 25 30

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

Ala Thr Ile Thr Tyr Glu Gly Arg Asn Thr Tyr Tyr Arg 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 Val Tyr Tyr Cys
85 90 95

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

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
115 120 125

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

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
180 185 190

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

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
210 215 220

Pro Lys Ser Cys Ser Gly Gly Gly Gly Thr Gly Gly Gly Gly Ser Glu
225 230 235 240

Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
245 250 255

Leu Arg Leu Ser Cys Ala Val Ser Gly Ile Asp Leu Ser Asn Tyr Ala
260 265 270

Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly
275 280 285

Ile Ile Trp Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys Gly
290 295 300

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln
305 310 315 320

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

Thr Val Pro Gly Tyr Ser Thr Ala Pro Tyr Phe Asp Leu Trp Gly Gln
340 345 350

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
355 360 365

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
370 375 380

Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr
385 390 395 400

Ile Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn Phe Leu Ser Trp
405 410 415

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Glu Ala
420 425 430

Ser Lys Leu Thr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
435 440 445

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
450 455 460

Ala Thr Tyr Tyr Cys Gly Gly Gly Tyr Ser Ser Ile Ser Asp Thr Thr
465 470 475 480

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr
485 490

<210> 58

<211> 1476

<212> ADN

<213> Secuencia artificial

<220>

<223> secuencia recombinante

<400> 58

gaagttcagc tggtcgagtc tggaggtggc cttgtccaac ctggagggag cctgcgtctc
60

tcttgtgcag caagcggatt cacgttttct gattacaata tggcttgggt tagacaggca
120

ccgggtaagg gccttgaatg ggttgcgacg attacatacg aaggcagaaa tacctattac
180

agggactcag taaaagggcg gtttaccata agccgagata atgctaaaaa cagtctgtat
240

ttgcaaatga acagcctacg agctgaagac actgccgtgt attactgcgc gagtccacct
300

cagtattatg aaggatcaat ctatcgctc tggttcgac attggggaca ggggaccctt
360

gtgacagtct cgagtgcgtc cacaaagggc ccatcgggtct tccccctggc accctcctcc
420

aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa
480

ccagtgcgg tgtcgtggaa ctcaagggtc ctgaccagcg gcgttcacac cttcccggct
540

gtcctacagt cttcaggact ctactccctg agcagcgtgg tgaccgtgcc ctccagcagc
600

ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtcgat
660

aagaaagttg agcccaaata ttgtagcggg ggcgggtggc ccggaggtgg cggttcagaa
720

gtgcagttgc tggagtcagg tggagggctg gtgcagcccg gaggatcgct gcggttgtca
780

tgcgcgggtg ccggtattga tttgtccaat tacgccatca attgggtacg ccaagcgcca
840

gggaagggcc ttgagtggat tggcatcacc tgggcgtcgg ggacgacctt ttatgtact
900

tgggccaag gaagattcac aatctcccga gacaactcga agaacaccgt gtatcttcaa
960

atgaactcgc tcagggccga ggacacggcg gtctactact gtgcacggac agtgccgggt
1020

tattcaacgg caccttactt tgatctttgg ggccagggga ccctcgtgac tgtctcaagt
1080

ggaggtggcg gttctggcgg tggcggttcc ggtggcgggt gatcgggagg tggcggttct
1140

gatattcaga tgacgcaatc accttcgagc gtatccgcct cgggtgggaga cagggtgaca
1200

atcacttgtc agtcatcccc ctcaagtctg agcaactttt tgtcatggta tcagcagaag
1260

cccggaagagg ctccgaaatt gctgatctac gaggcacga agttgacgag cgggtgtacca
1320

agcagattct ccggttcggg gtcgggaact gacttcaccc ttacgatctc atcgctgcag
1380

ccggaggatt ttgcgaccta ctactgtggg ggtgggtatt cgtcgatttc cgacacaaca
1440

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1476

<210> 59

<211> 492

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia recombinante

<400> 59

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
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Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Asp	Tyr
			20					25					30		

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

Ala	Thr	Ile	Thr	Tyr	Glu	Gly	Arg	Asn	Thr	Tyr	Tyr	Arg	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	Val	Tyr	Tyr	Cys
				85					90					95	

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

Ala	His	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr
		115					120					125			

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

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
180 185 190

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

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
210 215 220

Pro Lys Ser Cys Ser Gly Gly Gly Gly Thr Gly Gly Gly Gly Ser Glu
225 230 235 240

Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
245 250 255

Leu Arg Leu Ser Cys Ala Val Ser Gly Ile Asp Leu Ser Asn Tyr Ala
260 265 270

Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Ile Gly
275 280 285

Ile Ile Trp Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys Gly
290 295 300

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln
305 310 315 320

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

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

340	345	350
Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly		
355	360	365
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met		
370	375	380
Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr		
385	390	395
Ile Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn Phe Leu Ser Trp		
405	410	415
Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Glu Ala		
420	425	430
Ser Lys Leu Thr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser		
435	440	445
Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe		
450	455	460
Ala Thr Tyr Tyr Cys Gly Gly Gly Tyr Ser Ser Ile Ser Asp Thr Thr		
465	470	475
Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Arg Thr		
485	490	

<210> 60

<211> 1476

<212> ADN

<213> Secuencia artificial

<220>

<223> secuencia recombinante

<400> 60

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120

ccgggtaagg gccttgaatg ggttgcgacg attacatacg aaggcagaaa tacctattac
180

agggactcag taaaagggcg gtttaccata agccgagata atgctaaaaa cagtctgtat
240

ttgcaaatga acagcctacg agctgaagac actgccgtgt attactgcgc gagtccacct
300

cagtattatg aaggatcaat ctatcgctc tggttcgac attggggaca ggggaccctt
360

gtgacagtct cgagtgcgtc cacaaagggc ccatcgggtct tccccctggc accctcctcc
420

aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa
480

ccagtgcagg tgtcgtggaa ctgaggtgcc ctgaccagcg gcgttcacac cttcccggct
540

gtcctacagt cttcaggact ctactccctg agcagcgtgg tgaccgtgcc ctccagcagc
600

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660

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720

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780

tgcgcggtgt ccggtattga tttgtccaat tacgccatca attgggtacg ccaagcgcca
840

gggaagtgcc ttgagtggat tggcatcatc tgggcgtcgg ggacgacctt ttatgctact
900

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960

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1020

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1080

ggaggtggcg gttctggcgg tggcggttcc ggtggcgggt gatcgggagg tggcggttct
1140

gatattcaga tgacgcaatc accttcgagc gtatccgcct cgggtgggaga cagggtgaca
1200

atcacttgtc agtcatcccc ctcatgtctgg agcaactttt tgtcatggta tcagcagaag
1260

cccgaaagg ctccgaaatt gctgatctac gaggcacga agttgacgag cgggtgtacca
1320

agcagattct ccggttcggg gtcgggaact gacttcaccc ttacgatctc atcgctgcag
1380

ccggaggatt ttgcgaccta ctactgtggg ggtgggtatt cgtcgatttc cgacacaaca
1440

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1476

<210> 61
<211> 469
<212> PRT
<213> Secuencia artificial

<220>
<223> secuencia recombinante

<400> 61

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
210 215 220

Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
225 230 235 240

Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser
245 250 255

Tyr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
260 265 270

Met Gly Arg Ile Gly Pro Gly Ser Gly Asp Ile Asn Tyr Asn Glu Lys
275 280 285

Phe Lys Gly Arg Ala Thr Phe Thr Val Asp Lys Ser Thr Ser Thr Ala
290 295 300

Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr
305 310 315 320

Cys Ala Arg Phe His Tyr Asp Gly Ala Asp Trp Gly Gln Gly Thr Leu
325 330 335

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
340 345 350

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
355 360 365

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

Lys Ala Ser Gln Asn Ile Asn Glu Asn Leu Asp Trp Tyr Gln Gln Lys
385 390 395 400

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Asp Ile Leu Gln
405 410 415

Thr Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
420 425 430

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
435 440 445

Cys Tyr Gln Tyr Tyr Ser Gly Tyr Thr Phe Gly Gln Gly Thr Lys Leu
450 455 460

Glu Ile Lys Arg Thr
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<210> 62
<211> 1407
<212> ADN
<213> Secuencia artificial

<220>
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120

ggtaaagctc ctaaactgct catctatctg gtgtccaact cggagatagg tgtgccagat
180

cggtttagtg ggtctggttc aggcactgat ttcagactga ccatatcatc tctacagcca
240

gaggacttcg ccacatatta ctgtcagcaa acctggagtg acccgtggac tttcggccag
300

ggcactaaag tagaaattaa acgtacggtg gccgctccct ccgtgttcat cttcccaccc
360

tccgacgagc agctgaagtc cggcaccgcc tccgtcgtgt gcctgctgaa caacttctac
420

ccccgcgagg ccaaggtgca gtggaaggtg gacaacgccc tgcagtccgg caactcccag
480

gaatccgtca ccgagcagga ctccaaggac agcacctact ccctgtcctc caccctgacc
540

ctgtccaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc
600

ctgtccagcc ccgtgaccaa gtccttcaac cggggcgagt gcagcgggtgg cgggtggctcc
660

ggaggtggcg gttcagaggt gcagctggtg cagtccggcg ccgaggtgaa gaagcccggc
720

tcctccgtga aggtgtcctg caaggcctcc ggctactcct tcacctccta ctacatccac
780

tgggtgaggc agggcccccg ccagggcctg gagtggatgg gcaggatcgg ccccggtccc
840

ggcgacatca actacaacga gaagttcaag ggcagggcca cttcacctg ggacaagtcc
900

acctccaccg cctacatgga gctgtcctcc ctgaggtccg aggacaccgc cgtgtactac
960

tgcgccaggt tccactacga cggcgccgac tggggccagg gcaccctggt gaccgtgtcc
1020

tccggaggtg gcggttcttg cgggtggcgg tccggtggcg gtggatcggg aggtggcgg
1080

tctgacatcc agatgacca gtccccctcc tccctgtccg cctccgtggg cgacaggggt
1140

accatcacct gcaaggcctc ccagaacatc aacgagaacc tggactggta ccagcagaag
1200

cccggcaagg cccccaagct gctgatctac tacaccgaca tcctgcagac cggcatcccc
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1380

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1407

<210> 63

<211> 469

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia recombinante

<400> 63

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

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

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

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

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

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala
		100						105					110		

Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly
		115					120					125			

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
210 215 220

Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
225 230 235 240

Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser
245 250 255

Tyr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp
260 265 270

Met Gly Arg Ile Gly Pro Gly Ser Gly Asp Ile Asn Tyr Asn Glu Lys
275 280 285

Phe Lys Gly Arg Ala Thr Phe Thr Val Asp Lys Ser Thr Ser Thr Ala
290 295 300

Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr
305 310 315 320

Cys Ala Arg Phe His Tyr Asp Gly Ala Asp Trp Gly Gln Gly Thr Leu
325 330 335

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

340

345

350

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
 355 360 365

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

Lys Ala Ser Gln Asn Ile Asn Glu Asn Leu Asp Trp Tyr Gln Gln Lys
 385 390 395 400

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Asp Ile Leu Gln
 405 410 415

Thr Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
 420 425 430

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
 435 440 445

Cys Tyr Gln Tyr Tyr Ser Gly Tyr Thr Phe Gly Cys Gly Thr Lys Leu
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Glu Ile Lys Arg Thr
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<210> 64

<211> 1407

<212> ADN

<213> Secuencia artificial

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<223> secuencia recombinante

<400> 64

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ggtaaagctc ctaaactgct catctatctg gtgtccaact cggagatagg tgtgccagat
 180

cggttttagtg ggtctggttc aggcactgat ttcagactga ccataatcatc tctacagcca
240

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420

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480

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600

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720

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780

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1200

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1260

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1320

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1380

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1407

<210> 65
<211> 11
<212> PRT
<213> Secuencia artificial

<220>
<223> secuencia recombinante

<400> 65

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
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<210> 66
<211> 20
<212> PRT
<213> Secuencia artificial

<220>
<223> secuencia recombinante

<400> 66

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
20

<210> 67
<211> 11
<212> PRT
<213> Secuencia artificial

<220>
<223> secuencia recombinante

<400> 67

Ser Gly Gly Gly Gly Thr Gly Gly Gly Gly Ser
1 5 10

<210> 68
<211> 20
<212> PRT
<213> Secuencia artificial

<220>
<223> secuencia recombinante

<400> 68

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
20