

LISTADO DE SECUENCIAS

<110> Regeneron Pharmaceuticals, Inc.

<120> ANTICUERPOS ANTI-TMPRSS6 Y SUS USOS

<130> 728825: RGN9-002PC

<150> 63/187,150

<151> 2011-05-11

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<170> PatentIn versión 3.5

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		Phe	Asn
		Asn	Tyr
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Gly	Met	His	Trp
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Gln	Ala	Pro	Gly
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		Leu	Glu
		Trp	Val
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Gly	Ser	Asn	Glu
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		Ser	Val
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Lys	Gly	Arg	Phe
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Ser	Arg	Asp	Asn
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		Leu	Tyr
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Arg	Ala	Glu	Asp
	90	Thr	Ala
		Val	Tyr
		Tyr	Cys
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Ala	Arg	Asp	Gln
	100	Asp	Tyr
Gly	Gly	Asn	Leu
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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
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Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
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Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Ile Ile Ser Tyr Asp Gly Ser Asn Glu Tyr Tyr Ser Asp Ser Val
50 55 60

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

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

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

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

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
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Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

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

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

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
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			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
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Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
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Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Ser	Thr	Pro	Pro
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Ile	Thr	Phe	Gly	Gln	Gly	Thr	Arg	Leu	Glu	Ile	Lys	Arg	Thr	Val	Ala
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Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

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

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

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

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
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Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
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Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

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

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

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

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

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
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Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
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His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
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ccaggggaagg ggctggagtg ggttggccgt attaaaagca aaactgatag tgggacaaca
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gactacgctg caccctgaa aggcagattc accatctcaa gagatgattc aaaaaacacg
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ctgtatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtaccaca
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Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

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

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Ile Lys Ser Lys Thr Asp Ser Gly Thr Thr
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Thr Thr Val Asp Asn Asp Phe Trp Ser Gly Tyr Tyr Asn Trp Phe Asp
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Pro

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120

ccaggggaagg ggctggagtg ggttggccgt attaaaagca aaactgatag tgggacaaca
180

gactacgctg caccctgaa aggcagattc accatctcaa gagatgattc aaaaaacacg
240

ctgtatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtaccaca
300

gtggataacg atttttggag tggttattat aactggttcg acccctgggg ccaggggaacc
360

ctggtcactg tctcctcagc ctccaccaag ggcccatcgg tcttccccct ggcgcctgc
420

tccaggagca cctccgagag cacagccgcc ctgggctgcc tgggtcaagga ctacttcccc
480

gaaccggtga cgggtgctgtg gaactcaggc gccctgacca gcggcgtgca caccttcccc
540

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600

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660

gacaagagag ttgagtccaa atatgggtccc ccatgcccac cctgcccagc acctgagttc
720

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840

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900

cagttcaaca gcacgtaccg tgtgggcagc gtcctcaccg tctgcacca ggactggctg
960

aacggcaagg agtacaagtg caaggtctcc aacaaaggcc tcccgtcctc catcgagaaa
1020

accatctcca aagccaaagg gcagccccga gagccacagg tgtacaccct gcccccatcc
1080

caggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtaaagg cttctacccc
1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg
1200

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaggctcac cgtggacaag
1260

agcaggtggc aggaggggaa tgtcttctca tgctccgtga tgcattaggc tctgcacaa
1320

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Ala
20 25 30

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

Gly Arg Ile Lys Ser Lys Thr Asp Ser Gly Thr Thr Asp Tyr Ala Ala
50 55 60

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

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

Tyr Cys Thr Thr Val Asp Asn Asp Phe Trp Ser Gly Tyr Tyr Asn Trp
100 105 110

Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
115 120 125

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

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

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

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

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

Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val
210 215 220

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
260 265 270

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
275 280 285

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

290		295		300											
Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu
305					310					315					320
Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser
				325					330					335	
Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro
			340					345					350		
Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln
		355					360					365			
Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala
	370					375					380				
Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr
385					390					395					400
Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu
				405					410					415	
Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser
			420					425					430		
Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser
		435					440					445			
Leu	Ser	Leu	Gly	Lys											
	450														

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120

ccaggggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag tataggctat
180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa gtccctgtat
240

ctgcaaata ga gtggtctgag acctgaggac acggccttgt attattgtgt aaaaagtggg
300

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tca
363

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<400> 42

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

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

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

Leu Gln Met Ser Gly Leu Arg Pro Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Val Lys Ser Gly Phe Tyr Tyr Val Arg Ser Tyr Phe Asp Asn Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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<211> 24
<212> ADN
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<400> 43
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<210> 44
<211> 8
<212> PRT
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<400> 44

Gly Phe Ile Phe Val Asp Tyr Ala
1 5

<210> 45
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<400> 45
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<210> 46
<211> 8
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<400> 46

Ile Ser Trp Asn Ser Gly Ser Ile
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<210> 47

<211> 42

<212> ADN

<213> Secuencia artificial

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<223> Secuencia artificial

<400> 47

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<210> 48

<211> 14

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<400> 48

Val Lys Ser Gly Phe Tyr Tyr Val Arg Ser Tyr Phe Asp Asn
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<211> 339

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120

tggtacctgc ggaagccagg gcagtctcca caactcctga tctatacgct ttcctatcgg
180

gcctctggag tcccagacag gttcagtggc agtggggtcag gcactgattt cacactgaaa
240

atcagtaggg tggaggctga cgatgttgga gtttattact gcatgcaacg tatagagttt
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ccgctcactt tcggcggagg gaccaaggtg gagatcaaa
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<211> 113

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<400> 50

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

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

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

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

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

Ile	Ser	Arg	Val	Glu	Ala	Asp	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Met	Gln
				85					90					95	

Arg	Ile	Glu	Phe	Pro	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile
			100					105					110		

Lys

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<211> 36

<212> ADN
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<400> 52

Gln	Ser	Leu	Leu	Asp	Ser	Asp	Asp	Gly	Asn	Thr	Tyr
1				5					10		

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9

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<400> 54

Thr	Leu	Ser
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<212> ADN
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27

<210> 56
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<400> 56

Met Gln Arg Ile Glu Phe Pro Leu Thr
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120

ccaggggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag tataggctat
180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa gtccctgtat
240

ctgcaaatga gtggtctgag acctgaggac acggccttgt attattgtgt aaaaagtggg
300

ttctattacg ttaggtctta ctttgacaac tggggccagg gaaccctggt caccgtctcc
360

tcagcctcca ccaagggcc atcggtcttc ccctggcgc cctgctccag gagcacctcc
420

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480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc
540

tcaggactct actccctcag cagcgtgggtg accgtgccct ccagcagctt gggcacgaag
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660

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720

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960

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1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct accccagcga catcgccgtg
1140

gagtgggaga gcaatgggca gccggagaa aactacaaga ccacgcctcc cgtgctggac
1200

tccgacggct ctttcttcct ctacagcagg ctcaccgtgg acaagagcag gtggcaggag
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1320

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<210> 58

<211> 448

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<400> 58

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

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

Leu Gln Met Ser Gly Leu Arg Pro Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Val Lys Ser Gly Phe Tyr Tyr Val Arg Ser Tyr Phe Asp Asn Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

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

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

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

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
210 215 220

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

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
260 265 270

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
290 295 300

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

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350

Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

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

Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

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120

tggtacctgc ggaagccagg gcagtctcca caactcctga tctatacgct ttcctatcgg
180

gcctctggag tcccagacag gttcagtggc agtgggtcag gcactgattt cacactgaaa
240

atcagtaggg tggaggctga cgatgttga gtttattact gcatgcaacg tatagagttt
300

ccgctcactt tcggcggagg gaccaaggtg gagatcaaac gaactgtggc tgcaccatct
360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc
420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgcctc
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540

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660

tag
663

<210> 60
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<400> 60

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

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

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

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

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

Ile Ser Arg Val Glu Ala Asp Asp Val Gly Val Tyr Tyr Cys Met Gln
85 90 95

Arg Ile Glu Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 61
<211> 372
<212> ADN
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120

ccaggggaagg ggctggagtg ggtaggtttc attagaagca aagcttatgg tgggacaaca
180

gaatacgccg cgtctgtgaa aggcagattc accatctcaa gagatgattc caaaagcatc
240

gcctatctgc aatgaacag cctgaaaacc gaggacgcag ccatgtatta ctgttctaga
300

gattattacg atattttgac tggttattat ggcgactact ggggccaggg aaccctgggtc
360

accgtctcct ca
372

<210> 62
<211> 124
<212> PRT
<213> Secuencia artificial

<220>
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<400> 62

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

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

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

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

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

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

Tyr Cys Ser Arg Asp Tyr Tyr Asp Ile Leu Thr Gly Tyr Tyr Gly Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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<400> 63
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24

<210> 64
<211> 8
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Gly Phe Asn Phe Gly Asp Tyr Gly
1 5

<210> 65

<211> 30

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<400> 65

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30

<210> 66

<211> 10

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<400> 66

Ile Arg Ser Lys Ala Tyr Gly Gly Thr Thr
1 5 10

<210> 67

<211> 45

<212> ADN

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<210> 68

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<220>

<223> Secuencia artificial

<400> 68

Ser	Arg	Asp	Tyr	Tyr	Asp	Ile	Leu	Thr	Gly	Tyr	Tyr	Gly	Asp	Tyr
1				5					10					15

<210> 69

<211> 321

<212> ADN

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<220>

<223> Secuencia artificial

<400> 69

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60

atcacttgcc gggccagtca gagtattagt agctggttg cctggtatca gcagaaacca
120

gggaaagccc ctaagctcct gatctatcag gcgtctagtt tagaaagtgg ggtcccatca
180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct
240

gaagattttg caacttatta ctgccaacaa tataatagtt attctcggac gttcggccaa
300

gggaccaagg tggaaatcaa a
321

<210> 70

<211> 107

<212> PRT

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<400> 70

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

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

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

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

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

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

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

<210> 71
<211> 18
<212> ADN
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<220>
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<400> 71
cagagtatta gtagctgg
18

<210> 72
<211> 6
<212> PRT
<213> Secuencia artificial

<220>
<223> Secuencia artificial

<400> 72

Gln Ser Ile Ser Ser Trp
1 5

<210> 73
<211> 9
<212> ADN
<213> Secuencia artificial

<220>
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<400> 73

caggcgtct
9

<210> 74
<211> 3
<212> PRT
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<220>
<223> Secuencia artificial

<400> 74

Gln Ala Ser
1

<210> 75
<211> 27
<212> ADN
<213> Secuencia artificial

<220>
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<400> 75
caacaatata atagttattc tcggacg
27

<210> 76
<211> 9
<212> PRT
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<220>
<223> Secuencia artificial

<400> 76

Gln Gln Tyr Asn Ser Tyr Ser Arg Thr
1 5

<210> 77
<211> 1356
<212> ADN
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<220>
<223> Secuencia artificial

<400> 77

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60

tcctgtatag cttctggatt caactttggt gattatggta tgagctgggt ccgccaggct
120

ccaggggaagg ggctggagtg ggtaggtttc attagaagca aagcttatgg tgggacaaca
180

gaatacgccg cgtctgtgaa aggcagattc accatctcaa gagatgattc caaaagcatc
240

gcctatctgc aaatgaacag cctgaaaacc gaggacgcag ccatgtatta ctgttctaga
300

gattattacg atattttgac tggttattat ggcgactact ggggccaggg aaccctggtc
360

accgtctcct cagcctccac caagggccca tcggtcttcc ccctggcgcc ctgctccagg
420

agcacctccg agagcacagc cgccctgggc tgcctgggtca aggactactt ccccgaaccg
480

gtgacggtgt cgtggaactc aggcgccttg accagcggcg tgcacacctt cccggctgtc
540

ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg
600

ggcacgaaga cctacacctg caacgtagat cacaagccca gcaacaccaa ggtggacaag
660

agagttgagt ccaaatatgg tcccccatgc ccaccctgcc cagcacctga gttcctgggg
720

ggaccatcag tcttctgtt cccccaaaa cccaaggaca ctctcatgat ctcccggacc
780

cctgaggtca cgtgcgtggt ggtggacgtg agccaggaag accccgaggt ccagttcaac
840

tgggtacgtg atggcgtgga ggtgcataat gccaaagacaa agccgcggga ggagcagttc
900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaacggc
960

aaggagtaca agtgcaaggc ctccaacaaa ggctccccgt cctccatcga gaaaaccatc
1020

tccaaagcca aagggcagcc ccgagagcca caggtgtaca ccctgcccc atcccaggag
1080

gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta cccagcgac
1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc
1200

gtgctggact ccgacggctc cttcttctc tacagcaggc tcaccgtgga caagagcagg
1260

tggcaggagg ggaatgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac
1320

acacagaagt ccctctccct gtctctgggt aaatga
1356

<210> 78

<211> 451

<212> PRT

<213> Secuencia artificial

<220>

<223> Secuencia artificial

<400> 78

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

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

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

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

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

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

Tyr Cys Ser Arg Asp Tyr Tyr Asp Ile Leu Thr Gly Tyr Tyr Gly Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
115 120 125

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

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

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

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

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn
195 200 205

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

Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln
260 265 270

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Leu Gly Lys
450

<210> 79
<211> 645
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia artificial

<400> 79
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60

atcacttgcc gggccagtca gagtattagt agctggttg cctggtatca gcagaaacca
120

gggaaagccc ctaagctcct gatctatcag gcgtctagtt tagaaagtgg ggtcccatca
180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct
240

gaagatTTTtg caacttatta ctgccaacaa tataatagtt attctcggac gttcggccaa
300

gggaccaagg tggaaatcaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcca
360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taactttctat
420

cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag
480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg
540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc
600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gttag
645

<210> 80

<211> 214

<212> PRT

<213> Secuencia artificial

<220>

<223> Secuencia artificial

<400> 80

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Arg

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
 210

<210> 81

<211> 378

<212> ADN

<213> Secuencia artificial

<220>

<223> Secuencia artificial

<400> 81

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 60

tcctgtgcag cctctggagt cactttcagt aacgtctgga tgagttgggt ccgccagggt
 120

ccaggggaagg ggctggaatg gggtggccgt attaaaagca aaactgatgg tgggacaaca
 180

gactacgctg caccctgaa aggcagattt accatctcaa aagatgattc aaaaaatacg
240

ttgttcctgc aaatgaacag cctgaaaacc gaagacacag ccgtgtatta ctgtaccaca
300

gagaccggcg atttttggag tggttattat cctcgcttcc agcactgggg ccagggcacc
360

ctggtcaccg tctcctca
378

<210> 82

<211> 126

<212> PRT

<213> Secuencia artificial

<220>

<223> Secuencia artificial

<400> 82

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

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

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

Gly Arg Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr Asp Tyr Ala Ala
50 55 60

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

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

Tyr Cys Thr Thr Glu Thr Gly Asp Phe Trp Ser Gly Tyr Tyr Pro Arg
100 105 110

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

<210> 83
<211> 24
<212> ADN
<213> Secuencia artificial

<220>
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<400> 83
ggagtcactt tcagtaacgt ctgg
24

<210> 84
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> Secuencia artificial

<400> 84

Gly Val Thr Phe Ser Asn Val Trp
1 5

<210> 85
<211> 30
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia artificial

<400> 85
attaaaagca aaactgatgg tgggacaaca
30

<210> 86
<211> 10
<212> PRT
<213> Secuencia artificial

<220>
<223> Secuencia artificial

<400> 86

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

<210> 87
<211> 51
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia artificial

<400> 87
accacagaga ccggcgattt ttggagtggg tattatcctc gcttccagca c
51

<210> 88
<211> 17
<212> PRT
<213> Secuencia artificial

<220>
<223> Secuencia artificial

<400> 88

Thr	Thr	Glu	Thr	Gly	Asp	Phe	Trp	Ser	Gly	Tyr	Tyr	Pro	Arg	Phe	Gln
1				5					10					15	

His

<210> 89
<211> 324
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia artificial

<400> 89
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60

atcacttgcc gggcaagtca gtatattagc acctatttaa attggtatca gcagaaacca
120

gggaaagccc ctagcctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca
180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct
240

gaagattttg catcttactc ctgtcaacag agttacagta cccctccgta cacttttggc
300

caggggacca agctggagat caaa
324

<210> 90
<211> 108
<212> PRT
<213> Secuencia artificial

<220>
<223> Secuencia artificial

<400> 90

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

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

Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Ser	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	Ser	Tyr	Ser	Cys	Gln	Gln	Ser	Tyr	Ser	Thr	Pro	Pro
				85					90					95	

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

<210> 91
<211> 18
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia artificial

<400> 91

cagtatatta gcacctat
18

<210> 92
<211> 6
<212> PRT
<213> Secuencia artificial

<220>
<223> Secuencia artificial

<400> 92

Gln Tyr Ile Ser Thr Tyr
1 5

<210> 93
<211> 30
<212> ADN
<213> Secuencia artificial

<220>
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<400> 93
caacagagtt acagtacccc tccgtacact
30

<210> 94
<211> 10
<212> PRT
<213> Secuencia artificial

<220>
<223> Secuencia artificial

<400> 94

Gln Gln Ser Tyr Ser Thr Pro Pro Tyr Thr
1 5 10

<210> 95
<211> 1362
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia artificial

<400> 95

gaggtgcagc tgggtggagtc tggggggaggc ttggtaaagc ctgggggggtc cctgagagtc
60

tcctgtgcag cctctggagt cactttcagt aacgtctgga tgagttgggt ccgccagggt
120

ccaggggaagg ggctggaatg ggttggccgt attaaaagca aaactgatgg tgggacaaca
180

gactacgctg caccctgaa aggcagattt accatctcaa aagatgattc aaaaaatacg
240

ttgttcctgc aaatgaacag cctgaaaacc gaagacacag ccgtgtatta ctgtaccaca
300

gagaccggcg atttttggag tggttattat cctcgcttcc agcactgggg ccagggcacc
360

ctggtcaccg tctcctcagc ctccaccaag ggcccatcgg tcttccccct ggcgcctgc
420

tccaggagca cctccgagag cacagccgcc ctgggctgcc tggtaagga ctacttcccc
480

gaaccggtga cgggtgctg gaactcaggc gccctgacca gcggcgtgca caccttcccc
540

gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc
600

agcttgggca cgaagaccta cacctgcaac gtagatcaca agcccagcaa caccaagggtg
660

gacaagagag ttgagtccaa atatgggtccc ccatgcccac cctgcccagc acctgagttc
720

ctgggggggac catcagtctt cctgttcccc ccaaaacca aggacactct catgatctcc
780

cggacccctg aggtcacgtg cgtgggtggtg gacgtgagcc aggaagacct cgagggtccag
840

ttcaactggt acgtggatgg cgtggagggtg cataatgcc aagacaaagcc gcgggaggag
900

cagttcaaca gcacgtaccg tgtgggtcagc gtcctcaccg tctgcacca ggactggctg
960

aacggcaagg agtacaagtg caaggtctcc aacaaaggcc tcccgtcctc catcgagaaa
1020

accatctcca aagccaaagg gcagccccga gagccacagg tgtacacct gcccccattc
1080

caggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctacccc
1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg
1200

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaggctcac cgtggacaag
1260

agcagggtggc aggaggggaa tgtcttctca tgctccgtga tgcattgaggc tctgcacaac
1320

cactacacac agaagtcctt ctccctgtct ctgggtaaatt ga
1362

<210> 96

<211> 453

<212> PRT

<213> Secuencia artificial

<220>

<223> Secuencia artificial

<400> 96

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

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

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

Gly Arg Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr Asp Tyr Ala Ala
50 55 60

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

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

Tyr Cys Thr Thr Glu Thr Gly Asp Phe Trp Ser Gly Tyr Tyr Pro Arg
100 105 110

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

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

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

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

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

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

Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val
210 215 220

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
260 265 270

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
290 295 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
325 330 335

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Leu Gly Lys
450

<210> 97
<211> 648
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia artificial

<400> 97
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60

atcacttgcc gggcaagtca gtatattagc acctatttaa attggtatca gcagaaacca
120

gggaaagccc ctagcctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca
180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct
240

gaagattttg catcttactc ctgtcaacag agttacagta cccctccgta cacttttggc
300

caggggacca agctggagat caaacgaact gtggctgcac catctgtctt catcttcccg
360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc
420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc
480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg
540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag
600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgtttag
648

<210> 98

<211> 215

<212> PRT

<213> Secuencia artificial

<220>

<223> Secuencia artificial

<400> 98

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

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

Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Ser	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 Ser Tyr Ser Cys Gln Gln Ser Tyr Ser Thr Pro Pro

85

90

95

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

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

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

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

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

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

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

Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 99

<211> 372

<212> ADN

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<223> Secuencia artificial

<400> 99

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tcctgtgcag cctctggatt caccttttagt agctatgcca tgacctgggt ccgccaggct
 120

ccaggggaagg ggctggagtg ggtctcagct attagtggta gtgatactag cacatactac
 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgttt
240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaacatcaa
300

gattacgatt tttctacta ctactccgct atggacgtct ggggccaagg gaccacggtc
360

accgtctcct ca
372

<210> 100

<211> 124

<212> PRT

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<220>

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<400> 100

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 Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Asp Thr Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys His Gln Asp Tyr Asp Phe Ser Tyr Tyr Tyr Ser Ala Met Asp
100 105 110

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

<210> 101
<211> 24
<212> ADN
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<220>
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<400> 101
ggattcacct ttagtagcta tgcc
24

<210> 102
<211> 8
<212> PRT
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<220>
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<400> 102

Gly Phe Thr Phe Ser Ser Tyr Ala
1 5

<210> 103
<211> 24
<212> ADN
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<400> 103
attagtggta gtgatactag caca
24

<210> 104
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
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<400> 104

Ile Ser Gly Ser Asp Thr Ser Thr
1 5

<210> 105
<211> 51
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia artificial

<400> 105
gcgaaacatc aagattacga tttttcctac tactactccg ctatggacgt c
51

<210> 106
<211> 17
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<220>
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<400> 106

Ala	Lys	His	Gln	Asp	Tyr	Asp	Phe	Ser	Tyr	Tyr	Tyr	Ser	Ala	Met	Asp
1				5					10					15	

Val

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<211> 321
<212> ADN
<213> Secuencia artificial

<220>
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<400> 107
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60

atcacttgtc gggcgagtca ggatttcaac agctggtag cctggatatca gcagaaacca
120

gggaaagccc ctaaactcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca
180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct
240

gaagattttg cgacttacta ttgtcagcag actgacagtt tccattcac ttttggccct
300

gggaccaaag tggatatcaa a
321

<210> 108
<211> 107
<212> PRT
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<220>
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<400> 108

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

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

Leu	Ala	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	Thr	Asp	Ser	Phe	Pro	Phe
				85					90					95	

Thr	Phe	Gly	Pro	Gly	Thr	Lys	Val	Asp	Ile	Lys
			100					105		

<210> 109
<211> 18
<212> ADN
<213> Secuencia artificial

<220>
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<400> 109

caggatttca acagctgg
18

<210> 110
<211> 6
<212> PRT
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<220>
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<400> 110

Gln Asp Phe Asn Ser Trp
1 5

<210> 111
<211> 27
<212> ADN
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<400> 111
cagcagactg acagtttccc attcact
27

<210> 112
<211> 9
<212> PRT
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<220>
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<400> 112

Gln Gln Thr Asp Ser Phe Pro Phe Thr
1 5

<210> 113
<211> 1356
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia artificial

<400> 113

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60

tcctgtgcag cctctggatt cacctttagt agctatgccca tgacctgggt ccgccagggt
120

ccaggggaagg ggctggagtg ggtctcagct attagtggta gtgatactag cacatactac
180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cagctgtttt
240

ctgcaaatac acagcctgag agccgaggac acggccgtat attactgtgc gaaacatcaa
300

gattacgatt tttcctacta ctactccgct atggacgtct ggggccaagg gaccacggtc
360

accgtctcct cagcctccac caagggccca tcggtcttcc ccctggcgcc ctgctccagg
420

agcacctccg agagcacagc cgccctgggc tgcctgggtca aggactactt ccccgaaaccg
480

gtgacggtgt cgtggaactc aggcgccttg accagcggcg tgcacacctt cccggctgtc
540

ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg
600

ggcacgaaga cctacacctg caacgtagat cacaagccca gcaacaccaa ggtggacaag
660

agagttgagt ccaaatatgg tcccccatgc ccaccctgcc cagcacctga gttcctgggg
720

ggaccatcag tcttctgtt cccccaaaa cccaaggaca ctctcatgat ctcccggacc
780

cctgaggtca cgtgcgtggt ggtggacgtg agccaggaag accccgaggt ccagttcaac
840

tggtacgtgg atggcgtgga ggtgcataat gccaaagaaa agccgcggga ggagcagttc
900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaacggc
960

aaggagtaca agtgcaaggc ctccaacaaa ggctcccggt cctccatcga gaaaaccatc
1020

tccaaagcca aagggcagcc ccgagagcca caggtgtaca ccctgcccc atcccaggag
1080

gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta cccagcgac
1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc
1200

gtgctggact ccgacggctc cttcttctc tacagcaggc tcaccgtgga caagagcagg
1260

tggcaggagg ggaatgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac
1320

acacagaagt ccctctccct gtctctgggt aaatga
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<210> 114

<211> 451

<212> PRT

<213> Secuencia artificial

<220>

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<400> 114

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 Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Asp Thr Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys His Gln Asp Tyr Asp Phe Ser Tyr Tyr Tyr Ser Ala Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys
115 120 125

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

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

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

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

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn
195 200 205

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

Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln
260 265 270

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Leu Gly Lys
450

<210> 115
<211> 645
<212> ADN
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<220>
<223> Secuencia artificial

<400> 115
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atcacttgtc gggcgagtca ggatttcaac agctggtag cctggtatca gcagaaacca
120

gggaaagccc ctaaactcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca
180

aggttcagcg gcagtggatc tgggacagat ttactctca ccatcagcag cctgcagcct
240

gaagatTTTtg cgacttacta ttgtcagcag actgacagtt tccattcac ttttggccct
300

gggaccaaag tggatatcaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcca
360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taactttctat
420

cccagagagg ccaaagtaca gtggaagggtg gataacgcc tccaatcggg taactcccag
480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg
540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc
600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gttag
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<210> 116

<211> 214

<212> PRT

<213> Secuencia artificial

<220>

<223> Secuencia artificial

<400> 116

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

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

Leu	Ala	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 Thr Asp Ser Phe Pro Phe

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

Gln Ala Cys Glu Val Asn Leu Thr Leu Asp Asn Arg Leu Asp Ser Gln
260 265 270

Gly Val Leu Ser Thr Pro Tyr Phe Pro Ser Tyr Tyr Ser Pro Gln Thr
275 280 285

His Cys Ser Trp His Leu Thr Val Pro Ser Leu Asp Tyr Gly Leu Ala
290 295 300

Leu Trp Phe Asp Ala Tyr Ala Leu Arg Arg Gln Lys Tyr Asp Leu Pro
305 310 315 320

Cys Thr Gln Gly Gln Trp Thr Ile Gln Asn Arg Arg Leu Cys Gly Leu
325 330 335

Arg Ile Leu Gln Pro Tyr Ala Glu Arg Ile Pro Val Val Ala Thr Ala
340 345 350

Gly Ile Thr Ile Asn Phe Thr Ser Gln Ile Ser Leu Thr Gly Pro Gly
355 360 365

Val Arg Val His Tyr Gly Leu Tyr Asn Gln Ser Asp Pro Cys Pro Gly
370 375 380

Glu Phe Leu Cys Ser Val Asn Gly Leu Cys Val Pro Ala Cys Asp Gly
385 390 395 400

Val Lys Asp Cys Pro Asn Gly Leu Asp Glu Arg Asn Cys Val Cys Arg
405 410 415

Ala Thr Phe Gln Cys Lys Glu Asp Ser Thr Cys Ile Ser Leu Pro Lys
420 425 430

Val Cys Asp Gly Gln Pro Asp Cys Leu Asn Gly Ser Asp Glu Glu Gln
435 440 445

Cys Gln Glu Gly Val Pro Cys Gly Thr Phe Thr Phe Gln Cys Glu Asp
450 455 460

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

465					470						475				480
Cys	Arg	Asp	Gly	Ser	Asp	Glu	Glu	His	Cys	Asp	Cys	Gly	Leu	Gln	Gly
				485					490					495	
Pro	Ser	Ser	Arg	Ile	Val	Gly	Gly	Ala	Val	Ser	Ser	Glu	Gly	Glu	Trp
			500					505					510		
Pro	Trp	Gln	Ala	Ser	Leu	Gln	Val	Arg	Gly	Arg	His	Ile	Cys	Gly	Gly
		515					520					525			
Ala	Leu	Ile	Ala	Asp	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	Cys	Phe	Gln
	530					535						540			
Glu	Asp	Ser	Met	Ala	Ser	Thr	Val	Leu	Trp	Thr	Val	Phe	Leu	Gly	Lys
545					550					555					560
Val	Trp	Gln	Asn	Ser	Arg	Trp	Pro	Gly	Glu	Val	Ser	Phe	Lys	Val	Ser
				565					570					575	
Arg	Leu	Leu	Leu	His	Pro	Tyr	His	Glu	Glu	Asp	Ser	His	Asp	Tyr	Asp
			580					585					590		
Val	Ala	Leu	Leu	Gln	Leu	Asp	His	Pro	Val	Val	Arg	Ser	Ala	Ala	Val
		595					600					605			
Arg	Pro	Val	Cys	Leu	Pro	Ala	Arg	Ser	His	Phe	Phe	Glu	Pro	Gly	Leu
	610					615					620				
His	Cys	Trp	Ile	Thr	Gly	Trp	Gly	Ala	Leu	Arg	Glu	Gly	Gly	Pro	Ile
625					630					635					640
Ser	Asn	Ala	Leu	Gln	Lys	Val	Asp	Val	Gln	Leu	Ile	Pro	Gln	Asp	Leu
				645					650					655	
Cys	Ser	Glu	Val	Tyr	Arg	Tyr	Gln	Val	Thr	Pro	Arg	Met	Leu	Cys	Ala
			660					665					670		
Gly	Tyr	Arg	Lys	Gly	Lys	Lys	Asp	Ala	Cys	Gln	Gly	Asp	Ala	Gly	Gly
		675					680					685			

Pro Leu Val Cys Lys Ala Leu Ser Gly Arg Trp Phe Leu Ala Gly Leu
690 695 700

Val Ser Trp Gly Leu Gly Cys Gly Arg Pro Asn Tyr Phe Gly Val Tyr
705 710 715 720

Thr Arg Ile Thr Gly Val Ile Ser Trp Ile Gln Gln Val Val Thr Glu
725 730 735

Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly Gly Glu Gln Lys Leu Ile
740 745 750

Ser Glu Glu Asp Leu His His His His His His
755 760

<210> 118

<211> 759

<212> PRT

<213> Secuencia artificial

<220>

<223> Secuencia artificial

<400> 118

Lys Ala Glu Val Thr Val Ser Gln Val Tyr Ser Gly Ser Leu Arg Val
1 5 10 15

Leu Asn Arg His Phe Ser Gln Asp Leu Gly Arg Arg Glu Ser Ile Ala
20 25 30

Phe Arg Ser Glu Ser Ala Lys Ala Gln Lys Met Leu Gln Glu Leu Val
35 40 45

Ala Ser Thr Arg Leu Gly Thr Tyr Tyr Asn Ser Ser Ser Val Tyr Ser
50 55 60

Phe Gly Glu Gly Pro Leu Thr Cys Phe Phe Trp Phe Ile Leu Asp Ile
65 70 75 80

Pro Glu Tyr Gln Arg Leu Thr Leu Ser Pro Glu Val Val Arg Glu Leu
85 90 95

Leu Val Asp Glu Leu Leu Ser Asn Ser Ser Thr Leu Ala Ser Tyr Lys
100 105 110

Thr Glu Tyr Glu Val Asp Pro Glu Gly Leu Val Ile Leu Glu Ala Ser
115 120 125

Val Asn Asp Ile Val Val Leu Asn Ser Thr Leu Gly Cys Tyr Arg Tyr
130 135 140

Ser Tyr Val Asn Pro Gly Gln Val Leu Pro Leu Lys Gly Pro Asp Gln
145 150 155 160

Gln Thr Thr Ser Cys Leu Trp His Leu Gln Gly Pro Glu Asp Leu Met
165 170 175

Ile Lys Val Arg Leu Glu Trp Thr Arg Val Asp Cys Arg Asp Arg Val
180 185 190

Ala Met Tyr Asp Ala Ala Gly Pro Leu Glu Lys Arg Leu Ile Thr Ser
195 200 205

Val Tyr Gly Cys Ser Arg Gln Glu Pro Val Met Glu Val Leu Ala Ser
210 215 220

Gly Ser Val Met Ala Val Val Trp Lys Lys Gly Met His Ser Tyr Tyr
225 230 235 240

Asp Pro Phe Leu Leu Ser Val Lys Ser Val Ala Phe Gln Asp Cys Gln
245 250 255

Val Asn Leu Thr Leu Glu Gly Arg Leu Asp Thr Gln Gly Phe Leu Arg
260 265 270

Thr Pro Tyr Tyr Pro Ser Tyr Tyr Ser Pro Ser Thr His Cys Ser Trp
275 280 285

His Leu Thr Val Pro Ser Leu Asp Tyr Gly Leu Ala Leu Trp Phe Asp
290 295 300

Ala Tyr Ala Leu Arg Arg Gln Lys Tyr Asn Arg Leu Cys Thr Gln Gly

305					310						315				320
Gln	Trp	Met	Ile	Gln	Asn	Arg	Arg	Leu	Cys	Gly	Phe	Arg	Thr	Leu	Gln
				325					330					335	
Pro	Tyr	Ala	Glu	Arg	Ile	Pro	Met	Val	Ala	Ser	Asp	Gly	Val	Thr	Ile
			340					345					350		
Asn	Phe	Thr	Ser	Gln	Ile	Ser	Leu	Thr	Gly	Pro	Gly	Val	Gln	Val	Tyr
		355					360					365			
Tyr	Ser	Leu	Tyr	Asn	Gln	Ser	Asp	Pro	Cys	Pro	Gly	Glu	Phe	Leu	Cys
	370					375					380				
Ser	Val	Asn	Gly	Leu	Cys	Val	Pro	Ala	Cys	Asp	Gly	Ile	Lys	Asp	Cys
385					390					395					400
Pro	Asn	Gly	Leu	Asp	Glu	Arg	Asn	Cys	Val	Cys	Arg	Ala	Met	Phe	Gln
				405					410					415	
Cys	Gln	Glu	Asp	Ser	Thr	Cys	Ile	Ser	Leu	Pro	Arg	Val	Cys	Asp	Arg
			420					425					430		
Gln	Pro	Asp	Cys	Leu	Asn	Gly	Ser	Asp	Glu	Glu	Gln	Cys	Gln	Glu	Gly
		435					440					445			
Val	Pro	Cys	Gly	Thr	Phe	Thr	Phe	Gln	Cys	Glu	Asp	Arg	Ser	Cys	Val
	450					455					460				
Lys	Lys	Pro	Asn	Pro	Glu	Cys	Asp	Gly	Gln	Ser	Asp	Cys	Arg	Asp	Gly
465					470					475					480
Ser	Asp	Glu	Gln	His	Cys	Asp	Cys	Gly	Leu	Gln	Gly	Leu	Ser	Ser	Arg
				485					490					495	
Ile	Val	Gly	Gly	Thr	Val	Ser	Ser	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala
			500					505					510		
Ser	Leu	Gln	Ile	Arg	Gly	Arg	His	Ile	Cys	Gly	Gly	Ala	Leu	Ile	Ala
		515					520					525			

Asp Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met
530 535 540

Ala Ser Pro Lys Leu Trp Thr Val Phe Leu Gly Lys Met Arg Gln Asn
545 550 555 560

Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu Phe Leu
565 570 575

His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val Ala Leu Leu
580 585 590

Gln Leu Asp His Pro Val Val Tyr Ser Ala Thr Val Arg Pro Val Cys
595 600 605

Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly Gln His Cys Trp Ile
610 615 620

Thr Gly Trp Gly Ala Gln Arg Glu Gly Gly Pro Val Ser Asn Thr Leu
625 630 635 640

Gln Lys Val Asp Val Gln Leu Val Pro Gln Asp Leu Cys Ser Glu Ala
645 650 655

Tyr Arg Tyr Gln Val Ser Pro Arg Met Leu Cys Ala Gly Tyr Arg Lys
660 665 670

Gly Lys Lys Asp Ala Cys Gln Gly Asp Ala Gly Gly Pro Leu Val Cys
675 680 685

Arg Glu Pro Ser Gly Arg Trp Phe Leu Ala Gly Leu Val Ser Trp Gly
690 695 700

Leu Gly Cys Gly Arg Pro Asn Phe Phe Gly Val Tyr Thr Arg Val Thr
705 710 715 720

Arg Val Ile Asn Trp Ile Gln Gln Val Leu Thr Glu Gln Lys Leu Ile
725 730 735

Ser Glu Glu Asp Leu Gly Gly Glu Gln Lys Leu Ile Ser Glu Glu Asp

740

745

750

Leu His His His His His His
755

<210> 119

<211> 763

<212> PRT

<213> Secuencia artificial

<220>

<223> Secuencia artificial

<400> 119

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

Arg Val Leu Asn Arg His Phe Ser Gln Asp Leu Thr Arg Arg Glu Ser
20 25 30

Ser Ala Phe Arg Ser Glu Thr Ala Lys Ala Gln Lys Met Leu Lys Glu
35 40 45

Leu Ile Ala Ser Thr Arg Leu Gly Thr Tyr Tyr Asn Ser Ser Ser Val
50 55 60

Tyr Ser Phe Gly Glu Gly Pro Leu Thr Cys Phe Phe Trp Phe Ile Leu
65 70 75 80

Gln Ile Pro Glu His Arg Arg Leu Met Leu Ser Pro Glu Val Val Gln
85 90 95

Ala Leu Leu Val Glu Glu Leu Leu Ser Thr Val Asn Ser Ser Ala Ala
100 105 110

Val Pro Tyr Arg Ala Glu Tyr Glu Val Asp Pro Glu Gly Leu Val Ile
115 120 125

Leu Glu Ala Ser Val Lys Asp Ile Ala Ala Leu Asn Ser Thr Leu Gly
130 135 140

Cys Tyr Arg Tyr Ser Tyr Val Gly Gln Gly Gln Val Leu Arg Leu Lys

145		150		155		160									
Gly	Pro	Asp	His	Leu	Ala	Ser	Ser	Cys	Leu	Trp	His	Leu	Gln	Gly	Pro
				165					170					175	
Glu	Asp	Leu	Met	Leu	Lys	Leu	Arg	Leu	Glu	Trp	Thr	Leu	Ala	Glu	Cys
			180					185					190		
Arg	Asp	Arg	Leu	Ala	Met	Tyr	Asp	Val	Ala	Gly	Pro	Leu	Glu	Lys	Arg
		195					200					205			
Leu	Ile	Thr	Ser	Val	Tyr	Gly	Cys	Ser	Arg	Gln	Glu	Pro	Val	Val	Glu
	210					215					220				
Val	Leu	Ala	Ser	Gly	Ala	Ile	Met	Ala	Val	Val	Trp	Lys	Lys	Gly	Leu
225					230					235					240
His	Ser	Tyr	Tyr	Asp	Pro	Phe	Met	Leu	Ser	Val	Gln	Ser	Val	Val	Phe
				245					250					255	
Gln	Ala	Cys	Glu	Val	Asn	Leu	Thr	Leu	Asp	Asp	Arg	Leu	Asp	Ser	Gln
			260					265					270		
Gly	Val	Leu	Ser	Thr	Pro	Tyr	Phe	Pro	Ser	Tyr	Tyr	Ser	Pro	Arg	Thr
		275					280					285			
His	Cys	Ser	Trp	His	Leu	Thr	Val	Pro	Ser	Leu	Asp	Tyr	Gly	Leu	Ala
	290					295					300				
Leu	Trp	Phe	Asp	Ala	Tyr	Ala	Leu	Arg	Arg	Gln	Lys	Tyr	Asp	Leu	Pro
305					310					315					320
Cys	Thr	Gln	Gly	Gln	Trp	Thr	Ile	Gln	Asn	Arg	Arg	Leu	Cys	Gly	Leu
				325					330					335	
Arg	Ile	Leu	Gln	Pro	Tyr	Ala	Glu	Arg	Ile	Pro	Val	Val	Ala	Thr	Ala
			340					345					350		
Gly	Ile	Thr	Ile	Asn	Phe	Thr	Ser	Gln	Ile	Ser	Leu	Thr	Gly	Pro	Gly
		355					360					365			

Val Arg Val His Tyr Gly Leu Tyr Asn Gln Ser Asp Pro Cys Pro Gly
370 375 380

Glu Phe Leu Cys Ser Val Asn Gly Leu Cys Val Pro Ala Cys Asp Gly
385 390 395 400

Val Lys Asp Cys Pro Asn Gly Leu Asp Glu Arg Asn Cys Val Cys Arg
405 410 415

Ala Thr Phe Gln Cys Gln Glu Asp Ser Thr Cys Ile Ser Leu Leu Lys
420 425 430

Val Cys Asp Gly Gln Pro Asp Cys Leu Asn Gly Ser Asp Glu Glu Arg
435 440 445

Cys Gln Glu Gly Val Pro Cys Gly Thr Phe Thr Phe Gln Cys Glu Asp
450 455 460

Gln Ser Cys Val Lys Lys Pro Asn Pro Gln Cys Asp Gly Arg Pro Asp
465 470 475 480

Cys Arg Asp Gly Ser Asp Glu Gln His Cys Asp Cys Gly Leu Gln Gly
485 490 495

Pro Ser Ser Arg Ile Val Gly Gly Ala Val Ser Ser Glu Gly Glu Trp
500 505 510

Pro Trp Gln Ala Ser Leu Gln Val Arg Gly Arg His Ile Cys Gly Gly
515 520 525

Ala Leu Ile Ala Asp Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln
530 535 540

Glu Asp Ser Met Ala Ser Pro Ala Leu Trp Thr Val Phe Leu Gly Lys
545 550 555 560

Val Trp Gln Asn Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser
565 570 575

Arg Leu Leu Leu His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp

580	585	590
Val Ala Leu Leu Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val		
595	600	605
Arg Pro Val Cys Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly Leu		
610	615	620
His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly Pro Thr		
625	630	635
Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro Gln Asp Leu		
645	650	655
Cys Ser Glu Ala Tyr Arg Tyr Gln Val Thr Pro Arg Met Leu Cys Ala		
660	665	670
Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln Gly Asp Ala Gly Gly		
675	680	685
Pro Leu Val Cys Lys Ala Leu Ser Gly Arg Trp Phe Leu Ala Gly Leu		
690	695	700
Val Ser Trp Gly Leu Gly Cys Gly Arg Pro Asn Tyr Phe Gly Val Tyr		
705	710	715
Thr Arg Ile Thr Gly Val Ile Gly Trp Ile Gln Gln Val Val Thr Glu		
725	730	735
Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly Gly Glu Gln Lys Leu Ile		
740	745	750
Ser Glu Glu Asp Leu His His His His His His		
755	760	

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Ser His Phe Phe Glu Pro Gly Leu His Cys Trp
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<211> 26

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Leu Val Ser Trp Gly Leu Gly Cys Gly Arg Pro Asn Tyr Phe Gly Val
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Tyr Thr Arg Ile Thr Gly Val Ile Ser Trp
20 25

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Leu Ile Thr Ser Thr Arg Leu Gly Thr
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Gly Glu Trp Pro Trp Gln Ala Ser Leu
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Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln Asn Ser
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Arg Trp Pro Gly Glu Val Ser Phe Lys
20 25

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<211> 21
<212> PRT
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<400> 125

Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly Pro Ile Ser Asn Ala
1 5 10 15

Leu Gln Lys Val Asp
20

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<211> 811
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<400> 126

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

Pro Glu Gly Met Phe Lys Ala Cys Glu Asp Ser Lys Arg Lys Ala Arg

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

Leu Lys Leu Arg Leu Glu Trp Thr Leu Ala Glu Cys Arg Asp Arg Leu
260 265 270

Ala Met Tyr Asp Val Ala Gly Pro Leu Glu Lys Arg Leu Ile Thr Ser
275 280 285

Val Tyr Gly Cys Ser Arg Gln Glu Pro Val Val Glu Val Leu Ala Ser
290 295 300

Gly Ala Ile Met Ala Val Val Trp Lys Lys Gly Leu His Ser Tyr Tyr
305 310 315 320

Asp Pro Phe Val Leu Ser Val Gln Pro Val Val Phe Gln Ala Cys Glu
325 330 335

Val Asn Leu Thr Leu Asp Asn Arg Leu Asp Ser Gln Gly Val Leu Ser
340 345 350

Thr Pro Tyr Phe Pro Ser Tyr Tyr Ser Pro Gln Thr His Cys Ser Trp
355 360 365

His Leu Thr Val Pro Ser Leu Asp Tyr Gly Leu Ala Leu Trp Phe Asp
370 375 380

Ala Tyr Ala Leu Arg Arg Gln Lys Tyr Asp Leu Pro Cys Thr Gln Gly
385 390 395 400

Gln Trp Thr Ile Gln Asn Arg Arg Leu Cys Gly Leu Arg Ile Leu Gln
405 410 415

Pro Tyr Ala Glu Arg Ile Pro Val Val Ala Thr Ala Gly Ile Thr Ile
420 425 430

Asn Phe Thr Ser Gln Ile Ser Leu Thr Gly Pro Gly Val Arg Val His
435 440 445

Tyr Gly Leu Tyr Asn Gln Ser Asp Pro Cys Pro Gly Glu Phe Leu Cys
450 455 460

Ser Val Asn Gly Leu Cys Val Pro Ala Cys Asp Gly Val Lys Asp Cys

465		470		475		480									
Pro	Asn	Gly	Leu	Asp	Glu	Arg	Asn	Cys	Val	Cys	Arg	Ala	Thr	Phe	Gln
				485					490					495	
Cys	Lys	Glu	Asp	Ser	Thr	Cys	Ile	Ser	Leu	Pro	Lys	Val	Cys	Asp	Gly
			500					505					510		
Gln	Pro	Asp	Cys	Leu	Asn	Gly	Ser	Asp	Glu	Glu	Gln	Cys	Gln	Glu	Gly
		515					520					525			
Val	Pro	Cys	Gly	Thr	Phe	Thr	Phe	Gln	Cys	Glu	Asp	Arg	Ser	Cys	Val
	530					535					540				
Lys	Lys	Pro	Asn	Pro	Gln	Cys	Asp	Gly	Arg	Pro	Asp	Cys	Arg	Asp	Gly
545					550					555					560
Ser	Asp	Glu	Glu	His	Cys	Asp	Cys	Gly	Leu	Gln	Gly	Pro	Ser	Ser	Arg
				565					570					575	
Ile	Val	Gly	Gly	Ala	Val	Ser	Ser	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala
			580					585					590		
Ser	Leu	Gln	Val	Arg	Gly	Arg	His	Ile	Cys	Gly	Gly	Ala	Leu	Ile	Ala
		595					600					605			
Asp	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	Cys	Phe	Gln	Glu	Asp	Ser	Met
	610					615					620				
Ala	Ser	Thr	Val	Leu	Trp	Thr	Val	Phe	Leu	Gly	Lys	Val	Trp	Gln	Asn
625					630					635					640
Ser	Arg	Trp	Pro	Gly	Glu	Val	Ser	Phe	Lys	Val	Ser	Arg	Leu	Leu	Leu
				645					650					655	
His	Pro	Tyr	His	Glu	Glu	Asp	Ser	His	Asp	Tyr	Asp	Val	Ala	Leu	Leu
			660					665					670		
Gln	Leu	Asp	His	Pro	Val	Val	Arg	Ser	Ala	Ala	Val	Arg	Pro	Val	Cys
		675					680					685			

Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly Leu His Cys Trp Ile
690 695 700

Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly Pro Ile Ser Asn Ala Leu
705 710 715 720

Gln Lys Val Asp Val Gln Leu Ile Pro Gln Asp Leu Cys Ser Glu Val
725 730 735

Tyr Arg Tyr Gln Val Thr Pro Arg Met Leu Cys Ala Gly Tyr Arg Lys
740 745 750

Gly Lys Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
755 760 765

Lys Ala Leu Ser Gly Arg Trp Phe Leu Ala Gly Leu Val Ser Trp Gly
770 775 780

Leu Gly Cys Gly Arg Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr
785 790 795 800

Gly Val Ile Ser Trp Ile Gln Gln Val Val Thr
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<212> ADN
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<220>
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<400> 127
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120

ttactcttcc actccaaaag gatgcccggtg gccgaggccc cccaggtggc tggcggggcag
180

ggggacggag gtgatggcga ggaagcggag ccggagggga tgttcaaggc ctgtgaggac
240

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420

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480

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600

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660

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780

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1080

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1440

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3209

<210> 128

<211> 800

<212> PRT

<213> Secuencia artificial

<220>

<223> Secuencia artificial

<400> 128

Met Pro Val Ala Lys Ala Pro Gln Val Ala Gly Gly Gln Gly Asp Gly

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

Lys Gly Pro Asp His Leu Ala Ser Ser Cys Leu Trp His Leu Gln Gly
225 230 235 240

Pro Glu Asp Leu Met Leu Lys Leu Arg Leu Glu Trp Thr Leu Ala Glu
245 250 255

Cys Arg Asp Arg Leu Ala Met Tyr Asp Val Ala Gly Pro Leu Glu Lys
260 265 270

Arg Leu Ile Thr Ser Val Tyr Gly Cys Ser Arg Gln Glu Pro Val Val
275 280 285

Glu Val Leu Ala Ser Gly Ala Ile Met Ala Val Val Trp Lys Lys Gly
290 295 300

Leu His Ser Tyr Tyr Asp Pro Phe Met Leu Ser Val Gln Ser Val Val
305 310 315 320

Phe Gln Ala Cys Glu Val Asn Leu Thr Leu Asp Asp Arg Leu Asp Ser
325 330 335

Gln Gly Val Leu Ser Thr Pro Tyr Phe Pro Ser Tyr Tyr Ser Pro Arg
340 345 350

Thr His Cys Ser Trp His Leu Thr Val Pro Ser Leu Asp Tyr Gly Leu
355 360 365

Ala Leu Trp Phe Asp Ala Tyr Ala Leu Arg Arg Gln Lys Tyr Asp Leu
370 375 380

Pro Cys Thr Gln Gly Gln Trp Thr Ile Gln Asn Arg Arg Leu Cys Gly
385 390 395 400

Leu Arg Ile Leu Gln Pro Tyr Ala Glu Arg Ile Pro Val Val Ala Thr
405 410 415

Ala Gly Ile Thr Ile Asn Phe Thr Ser Gln Ile Ser Leu Thr Gly Pro
420 425 430

Gly Val Arg Val His Tyr Gly Leu Tyr Asn Gln Ser Asp Pro Cys Pro

435								440									445
Gly	Glu	Phe	Leu	Cys	Ser	Val	Asn	Gly	Leu	Cys	Val	Pro	Ala	Cys	Asp		
450						455					460						
Gly	Val	Lys	Asp	Cys	Pro	Asn	Gly	Leu	Asp	Glu	Arg	Asn	Cys	Val	Cys		
465					470					475					480		
Arg	Ala	Thr	Phe	Gln	Cys	Gln	Glu	Asp	Ser	Thr	Cys	Ile	Ser	Leu	Leu		
				485					490					495			
Lys	Val	Cys	Asp	Gly	Gln	Pro	Asp	Cys	Leu	Asn	Gly	Ser	Asp	Glu	Glu		
			500					505					510				
Arg	Cys	Gln	Glu	Gly	Val	Pro	Cys	Gly	Thr	Phe	Thr	Phe	Gln	Cys	Glu		
		515					520					525					
Asp	Gln	Ser	Cys	Val	Lys	Lys	Pro	Asn	Pro	Gln	Cys	Asp	Gly	Arg	Pro		
530						535					540						
Asp	Cys	Arg	Asp	Gly	Ser	Asp	Glu	Gln	His	Cys	Asp	Cys	Gly	Leu	Gln		
545					550				555						560		
Gly	Pro	Ser	Ser	Arg	Ile	Val	Gly	Gly	Ala	Val	Ser	Ser	Glu	Gly	Glu		
				565					570					575			
Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	Val	Arg	Gly	Arg	His	Ile	Cys	Gly		
			580					585					590				
Gly	Ala	Leu	Ile	Ala	Asp	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	Cys	Phe		
	595						600					605					
Gln	Glu	Asp	Ser	Met	Ala	Ser	Pro	Ala	Leu	Trp	Thr	Val	Phe	Leu	Gly		
610						615					620						
Lys	Val	Trp	Gln	Asn	Ser	Arg	Trp	Pro	Gly	Glu	Val	Ser	Phe	Lys	Val		
625					630					635					640		
Ser	Arg	Leu	Leu	Leu	His	Pro	Tyr	His	Glu	Glu	Asp	Ser	His	Asp	Tyr		
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Val Arg Pro Val Cys Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly
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Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly Pro
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Thr Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro Gln Asp
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Leu Cys Ser Glu Ala Tyr Arg Tyr Gln Val Thr Pro Arg Met Leu Cys
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Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln Gly Asp Ser Gly
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Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg Trp Phe Leu Ala Gly
755 760 765

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

Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly Gln His Cys Trp Ile
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Tyr Arg Tyr Gln Val Ser Pro Arg Met Leu Cys Ala Gly Tyr Arg Lys
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