

SEQUENCE LISTING

<110> Obsidian Therapeutics, Inc.

<120> Linfocitos Infiltrantes Del Tumor Con Interleucina 15 Unida A Membrana Y Usos De Los Mismos

<130> 108407-1291325 (022W01)

<150> 63/153,367

<151> 2021-02-24

<150> 63/139,305

<151> 2021-01-19

<150> 63/226,114

<151> 2021-07-27

<150> 63/244,166

<151> 2021-09-14

<160> 60

<170> PatentIn versión 3.5

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Ser Ile Gly Arg Pro Leu Pro Gly Arg Lys Asn Ile Ile Leu Ser Ser
50 55 60

Gln Pro Gly Thr Asp Asp Arg Val Thr Trp Val Lys Ser Val Asp Glu
65 70 75 80

Ala Ile Ala Ala Cys Gly Asp Val Pro Glu Ile Met Val Ile Gly Gly
85 90 95

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

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

Asn Leu Val Ile Met Gly Lys Lys Thr Trp Phe Ser Ile Pro Glu Lys
50 55 60

Asn Arg Pro Leu Lys Gly Arg Ile Asn Leu Val Leu Ser Arg Glu Leu
65 70 75 80

Lys Glu Pro Pro Gln Gly Ala His Phe Leu Ser Arg Ser Leu Asp Asp
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Ala Leu Lys Leu Thr Glu Gln Pro Glu Leu Ala Asn Lys Val Asp Met
100 105 110

Val Trp Ile Val Gly Gly Ser Ser Val Tyr Lys Glu Ala Met Asn His

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Pro Gly His Leu Lys Leu Phe Val Thr Arg Ile Met Gln Asp Phe Glu				
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Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys Phe
35 40 45

Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val Ala
50 55 60

Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp Tyr
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Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala Thr
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Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu
100 105

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Leu	Asn	Leu	Val	Gln	Asn	Phe	Gln	Met	Lys	His	Glu	Val	Leu	Cys	Arg
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Trp	Ile	Leu	Ser	Val	Lys	Lys	Asn	Tyr	Arg	Lys	Asn	Val	Ala	Tyr	His
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Asn	Trp	Arg	His	Ala	Phe	Asn	Thr	Ala	Gln	Cys	Met	Phe	Ala	Ala	Leu
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Lys	Ala	Gly	Lys	Ile	Gln	Asn	Lys	Leu	Thr	Asp	Leu	Glu	Ile	Leu	Ala
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Leu	Leu	Ile	Ala	Ala	Leu	Ser	His	Asp	Leu	Asp	His	Arg	Gly	Val	Asn
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Asn	Ser	Tyr	Ile	Gln	Arg	Ser	Glu	His	Pro	Leu	Ala	Gln	Leu	Tyr	Cys
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His	Ser	Ile	Met	Glu	His	His	His	Phe	Asp	Gln	Cys	Leu	Met	Ile	Leu
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Asn	Ser	Pro	Gly	Asn	Gln	Ile	Leu	Ser	Gly	Leu	Ser	Ile	Glu	Glu	Tyr
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Lys	Thr	Thr	Leu	Lys	Ile	Ile	Lys	Gln	Ala	Ile	Leu	Ala	Thr	Asp	Leu
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Ala	Leu	Tyr	Ile	Lys	Arg	Arg	Gly	Glu	Phe	Phe	Glu	Leu	Ile	Arg	Lys
		195					200					205			
Asn	Gln	Phe	Asn	Leu	Glu	Asp	Pro	His	Gln	Lys	Glu	Leu	Phe	Leu	Ala
	210					215					220				
Met	Leu	Met	Thr	Ala	Cys	Asp	Leu	Ser	Ala	Ile	Thr	Lys	Pro	Trp	Pro
225					230					235					240

Ile Gln Gln Arg Ile Ala Glu Leu Val Ala Thr Glu Phe Phe Asp Gln
245 250 255

Gly Asp Arg Glu Arg Lys Glu Leu Asn Ile Glu Pro Thr Asp Leu Met
260 265 270

Asn Arg Glu Lys Lys Asn Lys Ile Pro Ser Met Gln Val Gly Phe Ile
275 280 285

Asp Ala Ile Cys Leu Gln Leu Tyr Glu Ala Leu Thr His Val Ser Glu
290 295 300

Asp Cys Phe Pro Leu Leu Asp Gly Cys Arg Lys Asn Arg Gln Lys Trp
305 310 315 320

Gln Ala Leu Ala Glu Gln Gln
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<400> 6

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Trp Leu Asp Asp His Trp Asp Phe Thr Phe Ser Tyr Phe Val Arg Lys
35 40 45

Ala Thr Arg Glu Met Val Asn Ala Trp Phe Ala Glu Arg Val His Thr
50 55 60

Ile Pro Val Cys Lys Glu Gly Ile Arg Gly His Thr Glu Ser Cys Ser
65 70 75 80

Cys Pro Leu Gln Gln Ser Pro Arg Ala Asp Asn Ser Ala Pro Gly Thr

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Pro	Thr	Arg	Lys	Ile	Ser	Ala	Ser	Glu	Phe	Asp	Arg	Pro	Leu	Arg	Pro																																											
			100														105														110																											
Ile	Val	Val	Lys	Asp	Ser	Glu	Gly	Thr	Val	Ser	Phe	Leu	Ser	Asp	Ser																																											
			115														120														125																											
Glu	Lys	Lys	Glu	Gln	Met	Pro	Leu	Thr	Pro	Pro	Arg	Phe	Asp	His	Asp																																											
			130														135														140																											
Glu	Gly	Asp	Gln	Cys	Ser	Arg	Leu	Leu	Glu	Leu	Val	Lys	Asp	Ile	Ser																																											
			145														150														155														160													
Ser	His	Leu	Asp	Val	Thr	Ala	Leu	Cys	His	Lys	Ile	Phe	Leu	His	Ile																																											
			165														170														175																											
His	Gly	Leu	Ile	Ser	Ala	Asp	Arg	Tyr	Ser	Leu	Phe	Leu	Val	Cys	Glu																																											
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Asp	Ser	Ser	Asn	Asp	Lys	Phe	Leu	Ile	Ser	Arg	Leu	Phe	Asp	Val	Ala																																											
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Glu	Gly	Ser	Thr	Leu	Glu	Glu	Val	Ser	Asn	Asn	Cys	Ile	Arg	Leu	Glu																																											
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Trp	Asn	Lys	Gly	Ile	Val	Gly	His	Val	Ala	Ala	Leu	Gly	Glu	Pro	Leu																																											
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Asn	Ile	Lys	Asp	Ala	Tyr	Glu	Asp	Pro	Arg	Phe	Asn	Ala	Glu	Val	Asp																																											
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Gln	Ile	Thr	Gly	Tyr	Lys	Thr	Gln	Ser	Ile	Leu	Cys	Met	Pro	Ile	Lys																																											
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Ser	Gly	Asn	Gly	Gly	Thr	Phe	Thr	Glu	Lys	Asp	Glu	Lys	Asp	Phe	Ala																																											
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Ala Tyr Leu Ala Phe Cys Gly Ile Val Leu His Asn Ala Gln Leu Tyr
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Glu Thr Ser Leu Leu Glu Asn Lys Arg Asn Gln Val Leu Leu Asp Leu
325 330 335

Ala Ser Leu Ile Phe Glu Glu Gln Gln Ser Leu Glu Val Ile Leu Lys
340 345 350

Lys Ile Ala Ala Thr Ile Ile Ser Phe Met Gln Val Gln Lys Cys Thr
355 360 365

Ile Phe Ile Val Asp Glu Asp Cys Ser Asp Ser Phe Ser Ser Val Phe
370 375 380

His Met Glu Cys Glu Glu Leu Glu Lys Ser Ser Asp Thr Leu Thr Arg
385 390 395 400

Glu His Asp Ala Asn Lys Ile Asn Tyr Met Tyr Ala Gln Tyr Val Lys
405 410 415

Asn Thr Met Glu Pro Leu Asn Ile Pro Asp Val Ser Lys Asp Lys Arg
420 425 430

Phe Pro Trp Thr Thr Glu Asn Thr Gly Asn Val Asn Gln Gln Cys Ile
435 440 445

Arg Ser Leu Leu Cys Thr Pro Ile Lys Asn Gly Lys Lys Asn Lys Val
450 455 460

Ile Gly Val Cys Gln Leu Val Asn Lys Met Glu Glu Asn Thr Gly Lys
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Val Lys Pro Phe Asn Arg Asn Asp Glu Gln Phe Leu Glu Ala Phe Val
485 490 495

Ile Phe Cys Gly Leu Gly Ile Gln Asn Thr Gln Met Tyr Glu Ala Val
500 505 510

Glu Arg Ala Met Ala Lys Gln Met Val Thr Leu Glu Val Leu Ser Tyr

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His	Ala	Ser	Ala	Ala	Glu	Glu	Glu	Thr	Arg	Glu	Leu	Gln	Ser	Leu	Ala
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Arg	Met	Phe	Thr	Asp	Leu	Asn	Leu	Val	Gln	Asn	Phe	Gln	Met	Lys	His
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Glu	Val	Leu	Cys	Arg	Trp	Ile	Leu	Ser	Val	Lys	Lys	Asn	Tyr	Arg	Lys
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Cys	Leu	Met	Ile	Leu	Asn	Ser	Pro	Gly	Asn	Gln	Ile	Leu	Ser	Gly	Leu
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Ser	Ile	Glu	Glu	Tyr	Lys	Thr	Thr	Leu	Lys	Ile	Ile	Lys	Gln	Ala	Ile
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Leu	Ala	Thr	Asp	Leu	Ala	Leu	Tyr	Ile	Lys	Arg	Arg	Gly	Glu	Phe	Phe
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740 745 750

Glu Leu Phe Leu Ala Met Leu Met Thr Ala Cys Asp Leu Ser Ala Ile
755 760 765

Thr Lys Pro Trp Pro Ile Gln Gln Arg Ile Ala Glu Leu Val Ala Thr
770 775 780

Glu Phe Phe Asp Gln Gly Asp Arg Glu Arg Lys Glu Leu Asn Ile Glu
785 790 795 800

Pro Thr Asp Leu Met Asn Arg Glu Lys Lys Asn Lys Ile Pro Ser Met
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Gln Val Gly Phe Ile Asp Ala Ile Cys Leu Gln Leu Tyr Glu Ala Leu
820 825 830

Thr His Val Ser Glu Asp Cys Phe Pro Leu Leu Asp Gly Cys Arg Lys
835 840 845

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35 40 45

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

Ala Phe Asn Val Glu Phe Asp Asp Ser Gln Asp Lys Ala Val Leu Lys
65 70 75 80

Gly Gly Pro Leu Asp Gly Thr Tyr Arg Leu Ile Gln Phe His Phe His
85 90 95

Trp Gly Ser Leu Asp Gly Gln Gly Ser Glu His Thr Val Asp Lys Lys
100 105 110

Lys Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Thr Lys Tyr Gly
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Ile Phe Leu Lys Val Gly Ser Ala Lys Pro Gly Leu Gln Lys Val Val
145 150 155 160

Asp Val Leu Asp Ser Ile Lys Thr Lys Gly Lys Ser Ala Asp Phe Thr
165 170 175

Asn Phe Asp Pro Arg Gly Leu Leu Pro Glu Ser Leu Asp Tyr Trp Thr
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Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Leu Glu Cys Val Thr Trp
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1200

tagtcatgat tctatgtaat gtaaaccaga aaaaataaat gttcatgatt tcaagatgtt
1260

atattaaaga aaaactttta aaattattat atatttatag caaagttatc ttaaatatga
1320

attctgttgt aatttaatga cttttgaatt acagagatat aaatgaagta ttatctgtaa
1380

aaattgttat aattagagtt gtgatacaga gtatatattcc attcagacaa tatatcataa
1440

cttaataaat attgtatattt agatatattc tctaataaaa ttcagaattc ta
1492

<210> 9
<211> 595
<212> PRT
<213> Homo Sapiens

<400> 9

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

Ile	Pro	Leu	Glu	Arg	Pro	Leu	Gly	Glu	Val	Tyr	Leu	Asp	Ser	Ser	Lys
		35					40					45			

Pro	Ala	Val	Tyr	Asn	Tyr	Pro	Glu	Gly	Ala	Ala	Tyr	Glu	Phe	Asn	Ala
	50					55					60				

Ala Ala Ala Ala Asn Ala Gln Val Tyr Gly Gln Thr Gly Leu Pro Tyr
65 70 75 80

Gly Pro Gly Ser Glu Ala Ala Ala Phe Gly Ser Asn Gly Leu Gly Gly
85 90 95

Phe Pro Pro Leu Asn Ser Val Ser Pro Ser Pro Leu Met Leu Leu His
100 105 110

Pro Pro Pro Gln Leu Ser Pro Phe Leu Gln Pro His Gly Gln Gln Val
115 120 125

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

Gly Pro Pro Ala Phe Tyr Arg Pro Asn Ser Asp Asn Arg Arg Gln Gly
145 150 155 160

Gly Arg Glu Arg Leu Ala Ser Thr Asn Asp Lys Gly Ser Met Ala Met
165 170 175

Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr Ala
180 185 190

Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe
195 200 205

Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala Thr
210 215 220

Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys
225 230 235 240

Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile Arg
245 250 255

Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg Asp
260 265 270

Asp Gly Glu Gly Arg Gly Glu Val Gly Ser Ala Gly Asp Met Arg Ala

275					280					285					
Ala	Asn	Leu	Trp	Pro	Ser	Pro	Leu	Met	Ile	Lys	Arg	Ser	Lys	Lys	Asn
	290					295					300				
Ser	Leu	Ala	Leu	Ser	Leu	Thr	Ala	Asp	Gln	Met	Val	Ser	Ala	Leu	Leu
305					310					315					320
Asp	Ala	Glu	Pro	Pro	Ile	Leu	Tyr	Ser	Glu	Tyr	Asp	Pro	Thr	Arg	Pro
				325					330					335	
Phe	Ser	Glu	Ala	Ser	Met	Met	Gly	Leu	Leu	Thr	Asn	Leu	Ala	Asp	Arg
			340					345					350		
Glu	Leu	Val	His	Met	Ile	Asn	Trp	Ala	Lys	Arg	Val	Pro	Gly	Phe	Val
		355					360					365			
Asp	Leu	Thr	Leu	His	Asp	Gln	Val	His	Leu	Leu	Glu	Cys	Ala	Trp	Leu
	370					375					380				
Glu	Ile	Leu	Met	Ile	Gly	Leu	Val	Trp	Arg	Ser	Met	Glu	His	Pro	Gly
385					390					395					400
Lys	Leu	Leu	Phe	Ala	Pro	Asn	Leu	Leu	Leu	Asp	Arg	Asn	Gln	Gly	Lys
				405					410					415	
Cys	Val	Glu	Gly	Met	Val	Glu	Ile	Phe	Asp	Met	Leu	Leu	Ala	Thr	Ser
			420					425					430		
Ser	Arg	Phe	Arg	Met	Met	Asn	Leu	Gln	Gly	Glu	Glu	Phe	Val	Cys	Leu
		435					440					445			
Lys	Ser	Ile	Ile	Leu	Leu	Asn	Ser	Gly	Val	Tyr	Thr	Phe	Leu	Ser	Ser
	450					455					460				
Thr	Leu	Lys	Ser	Leu	Glu	Glu	Lys	Asp	His	Ile	His	Arg	Val	Leu	Asp
465					470					475					480
Lys	Ile	Thr	Asp	Thr	Leu	Ile	His	Leu	Met	Ala	Lys	Ala	Gly	Leu	Thr
				485					490					495	

Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser
500 505 510

His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met
515 520 525

Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu
530 535 540

Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val
545 550 555 560

Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser
565 570 575

His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro
580 585 590

Ala Thr Val
595

<210> 10
<211> 22
<212> PRT
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 10

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Ser Gly Ala Arg Cys
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<210> 11
<211> 66
<212> ADN
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 11
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60

cggtgt
66

<210> 12
<211> 114
<212> PRT
<213> Homo Sapiens

<400> 12

Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
1 5 10 15

Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
20 25 30

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
35 40 45

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
50 55 60

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
65 70 75 80

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
85 90 95

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
100 105 110

Thr Ser

<210> 13
<211> 342
<212> ADN
<213> Homo Sapiens

<400> 13

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attgatgcca cgctgtacac agaaagcgat gtgcatccta gctgtaaggt gacagcgatg
120

aagtgttttc ttttggagct gcaggttaatt agtcttgagt ccggcgatgc cagcattcat
180

gataccgtag aaaacttgat tatcctggcc aacaattctc tgtcctcaaa cggaaacgta
240

accgagagcg gttgtaaaga atgtgaagaa ctggaagaaa agaacatcaa ggagtttctg
300

caatcattcg ttcacatcgt acaaatgttc ataaatacgt ca
342

<210> 14
<211> 30
<212> PRT
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 14

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

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
20 25 30

<210> 15
<211> 90
<212> ADN
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 15
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ggaagtggaa gcggtagtgg gtctggatct
90

<210> 16

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

<220>
<223> Construcción sintética

<400> 16

Lys Gln Glu His Phe Pro Asp Asn
1 5

<210> 17
<211> 24
<212> ADN
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 17
aaacaagagc actttcctga taac
24

<210> 18
<211> 21
<212> PRT
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 18

Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly Ile Phe
1 5 10 15

Val Ile Cys Cys Leu
20

<210> 19
<211> 63
<212> ADN
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 19

ctgttgccga gctgggcatg tacgcttata agtgtaaacg gcatctttgt aatatgctgt
60

ctg
63

<210> 20
<211> 25
<212> PRT
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 20

Thr Tyr Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg
1 5 10 15

Leu Arg Arg Glu Ser Val Arg Pro Val
20 25

<210> 21
<211> 75
<212> ADN
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 21
acctactgct tcgcaccaag gtgccgggag agaaggagaa atgaaagact gagaagggag
60

agcgtgagac ctgtg
75

<210> 22
<211> 25
<212> PRT
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 22

Thr Tyr Cys Phe Ala Pro Arg Cys Arg Glu Arg Ala Arg Asn Glu Arg
1 5 10 15

Leu Arg Arg Glu Thr Val Arg Pro Val
20 25

<210> 23
<211> 75
<212> ADN
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 23
acctactgct tcgcaccaag gtgccgggag agagcaagaa atgaaagact gagaaggag
60

accgtgagac ctgtg
75

<210> 24
<211> 2
<212> PRT
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 24

Gly Ser
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<210> 25
<211> 6
<212> ADN
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 25
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6

<210> 26
<211> 208
<212> PRT
<213> Secuencia artificial

<220>

<223> Construcción sintética

<400> 26

Ser His His Trp Gly Tyr Gly Lys His Asn Gly Pro Glu His Trp His
1 5 10 15

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

Asp Thr His Thr Ala Lys Tyr Asp Pro Ser Leu Lys Pro Leu Ser Val
35 40 45

Ser Tyr Asp Gln Ala Thr Ser Leu Arg Ile Leu Asn Asn Gly His Ala
50 55 60

Phe Asn Val Glu Phe Asp Asp Ser Gln Asp Lys Ala Val Leu Lys Gly
65 70 75 80

Gly Pro Leu Asp Gly Thr Tyr Arg Leu Ile Gln Phe His Phe His Trp
85 90 95

Gly Ser Leu Asp Gly Gln Gly Ser Glu His Thr Val Asp Lys Lys Asp
100 105 110

Ser Ile Lys Thr Lys Gly Lys Ser Ala Asp Phe Thr Asn Phe Asp Pro
115 120 125

Arg Gly Leu Leu Pro Glu Ser Leu Asp Tyr Trp Thr Tyr Pro Gly Ser
130 135 140

Leu Thr Thr Pro Pro Leu Leu Glu Cys Val Thr Trp Ile Val Leu Lys
145 150 155 160

Glu Pro Ile Ser Val Ser Ser Glu Gln Val Leu Lys Phe Arg Lys Leu
165 170 175

Asn Phe Asn Gly Glu Gly Glu Pro Glu Glu Leu Met Val Asp Asn Trp
180 185 190

Arg Pro Ala Gln Pro Leu Lys Asn Arg Gln Ile Lys Ala Ser Phe Lys
195 200 205

<210> 27
<211> 777
<212> ADN
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 27
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60

attgccaagg gagagcgcca gtcccctggt gacatcgaca ctcatacagc caagtatgac
120

ccttcctga agcccctgtc tgtttcctat gatcaagcaa cttccctgag aatcctcaac
180

aatggtcatg ctttcaacgt ggagtttgat gactctcagg acaaagcagt gctcaaggga
240

ggaccctgg atggcactta cagattgatt cagtttcact ttcactgggg ttcacttgat
300

ggacaagggt cagagcatatc tgtggataaa aagaaatatg ctgcagaact tcacttggtt
360

cactggaaca ccaaatatgg ggattttggg aaagctgtgc agcaacctga tggactggcc
420

gttctaggta tttttttgaa ggttggcagc gctaaaccgg gccatcagaa agttgttgat
480

gtgctggatt ccattaaaac aaagggcaag agtgctgact tcactaactt cgatcctcgt
540

ggcctccttc ctgaatccct ggattactgg acctaccag gctcactgac caccctcct
600

cttctggaat gtgtgacctg gattgtgctc aaggaacca tcagcgtcag cagcgagcag
660

gtgttgaaat tccgtaaact taacttcaat ggggaggggtg aaccgaaga actgatgggtg
720

gacaactggc gcccagctca gccactgaag aacaggcaaa tcaaagcttc cttcaaa
777

<210> 28
<211> 222
<212> PRT

<213> Secuencia artificial

<220>

<223> Construcción sintética

<400> 28

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

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

Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr
35 40 45

Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys
50 55 60

Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser
65 70 75 80

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

Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu
100 105 110

Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile
115 120 125

Val Gln Met Phe Ile Asn Thr Ser Gly Ser Gly Ser Gly Ser Gly Ser
130 135 140

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
145 150 155 160

Gly Ser Gly Ser Gly Ser Lys Gln Glu His Phe Pro Asp Asn Leu Leu
165 170 175

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

Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg
195 200 205

Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val Gly Ser
210 215 220

<210> 29

<211> 666

<212> ADN

<213> Secuencia artificial

<220>

<223> Construcción sintética

<400> 29

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60

cgggtgtaatt gggtaaattgt tatcagtgat ctcaagaaga tagaggatct catccagtcc
120

atgcatattg atgccacgct gtacacagaa agcgatgtgc atcctagctg taagggtgaca
180

gcgatgaagt gttttctttt ggagctgcag gtaattagtc ttgagtccgg cgatgccagc
240

attcatgata ccgtagaaaa cttgattatc ctggccaaca attctctgtc ctcaaacgga
300

aacgtaaccg agagcggttg taaagaattgt gaagaactgg aagaaaagaa catcaaggag
360

tttctgcaat cattcgttca catcgtacaa atgttcataa atacgtcagg atctggttct
420

ggttccggaa gtggatctgg ttcaggggtcc ggtagtggat ctgggtcagg aagtggaagc
480

ggtagtgggt ctggatctaa acaagagcac tttcctgata acctgttgcc gagctgggag
540

attacgttta tcagtgtaaa cggcatcttt gtaatatgct gtctgacctg ctgcttcgca
600

ccaaggtgcc gggagagaag gagaaatgaa agactgagaa gggagagcgt gagacctgtg
660

ggatcc
666

<210> 30
<211> 430
<212> PRT
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 30

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

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

Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr
35 40 45

Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys
50 55 60

Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser
65 70 75 80

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

Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu
100 105 110

Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile
115 120 125

Val Gln Met Phe Ile Asn Thr Ser Gly Ser Gly Ser Gly Ser Gly Ser
130 135 140

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
145 150 155 160

Gly Ser Gly Ser Gly Ser Lys Gln Glu His Phe Pro Asp Asn Leu Leu
165 170 175

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

Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg
195 200 205

Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val Gly Ser Ser His
210 215 220

His Trp Gly Tyr Gly Lys His Asn Gly Pro Glu His Trp His Lys Asp
225 230 235 240

Phe Pro Ile Ala Lys Gly Glu Arg Gln Ser Pro Val Asp Ile Asp Thr
245 250 255

His Thr Ala Lys Tyr Asp Pro Ser Leu Lys Pro Leu Ser Val Ser Tyr
260 265 270

Asp Gln Ala Thr Ser Leu Arg Ile Leu Asn Asn Gly His Ala Phe Asn
275 280 285

Val Glu Phe Asp Asp Ser Gln Asp Lys Ala Val Leu Lys Gly Gly Pro
290 295 300

Leu Asp Gly Thr Tyr Arg Leu Ile Gln Phe His Phe His Trp Gly Ser
305 310 315 320

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

Lys Thr Lys Gly Lys Ser Ala Asp Phe Thr Asn Phe Asp Pro Arg Gly
340 345 350

Leu Leu Pro Glu Ser Leu Asp Tyr Trp Thr Tyr Pro Gly Ser Leu Thr
355 360 365

Thr Pro Pro Leu Leu Glu Cys Val Thr Trp Ile Val Leu Lys Glu Pro
370 375 380

Ile Ser Val Ser Ser Glu Gln Val Leu Lys Phe Arg Lys Leu Asn Phe

385 390 395 400

Asn Gly Glu Gly Glu Pro Glu Glu Leu Met Val Asp Asn Trp Arg Pro
405 410 415

Ala Gln Pro Leu Lys Asn Arg Gln Ile Lys Ala Ser Phe Lys
420 425 430

<210> 31
<211> 1443
<212> ADN
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 31
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60

cgggtgtaatt gggtaaattgt tatcagtgat ctcaagaaga tagaggatct catccagtcc
120

atgcatattg atgccacgct gtacacagaa agcgatgtgc atcctagctg taagggtgaca
180

gcgatgaagt gttttctttt ggagctgcag gtaattagtc ttgagtccgg cgatgccagc
240

attcatgata ccgtagaaaa cttgattatc ctggccaaca attctctgtc ctcaaacgga
300

aacgtaaccg agagcggttg taaagaatgt gaagaactgg aagaaaagaa catcaaggag
360

tttctgcaat cattcgttca catcgtacaa atgttcataa atacgtcagg atctggttct
420

ggttccggaa gtggatctgg ttcaggggtcc ggtagtggat ctgggtcagg aagtggaagc
480

ggtagtgggt ctggatctaa acaagagcac tttcctgata acctgttgcc gagctgggag
540

attacgttta tcagtgtaaa cggcatcttt gtaatatgct gtctgacctg ctgcttcgca
600

ccaaggtgcc gggagagaag gagaaatgaa agactgagaa gggagagcgt gagacctgtg
660

ggatcctccc atcactgggg gtacggcaaa cacaacggac ctgagcactg gcataaggac
720

ttccccattg ccaagggaga ggcgcagtc cctgttgaca tcgacactca tacagccaag
780

tatgaccctt ccctgaagcc cctgtctgtt tcctatgac aagcaacttc cctgagaatc
840

ctcaacaatg gtcattgctt caacgtggag ttgatgact ctcaggacaa agcagtgtc
900

aagggaggac ccctggatgg cacttacaga ttgattcagt ttcactttca ctgggggtca
960

cttgatggac aagggttcaga gcatactgtg gataaaaaga aatatgctgc agaacttcac
1020

ttggttcact ggaacaccaa atatggggat tttgggaaag ctgtgcagca acctgatgga
1080

ctggccgttc taggtatattt tttgaagggtt ggcagcgcta aaccgggcca tcagaaagtt
1140

gttgatgtgc tggattccat taaaacaaag ggcaagagtg ctgacttcac taacttcgat
1200

cctcgtggcc tccttcctga atccctggat tactggacct acccaggctc actgaccacc
1260

cctcctcttc tggaatgtgt gacctggatt gtgctcaagg aaccatcag cgtcagcagc
1320

gagcaggtgt tgaaattccg taaacttaac ttcaatgggg aggggtgaacc cgaagaactg
1380

atgggtggaca actggcgccc agctcagcca ctgaagaaca ggcaaataca agcttccttc
1440

aaa
1443

<210> 32
<211> 51
<212> ADN
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 32
atgtggctgc agtctctgct cctcttgggg actgtcgcct gttctatttc a
51

<210> 33
<211> 17
<212> PRT
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 33

Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile
1 5 10 15

Ser

<210> 34
<211> 399
<212> ADN
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 34
caaggacagg atcgacatat gattcggatg cgccaactga tagatatagt cgatcaactc
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aagaattatg tgaatgactt ggtccctgag tttctgccgg ctccagagga cgttgaaaca
120

aactgtgaat ggtcagcggtt ttcattgtttt caaaaggcac agtcaagtc cgccaataca
180

ggcaataacg agcggattat aaatgtctca attaaaaagc tcaagcgcaa acccccttca
240

acgaatgctg gtcgccgcca gaaacacagg ttgacctgtc cctcctgtga ctcatagag
300

aagaaacctc ccaaggaatt tctcgaacgc tttaagtcac tcttgcagaa gatgattcat
360

cagcattga gtagccggac acatggttca gaggatagt
399

<210> 35
<211> 133
<212> PRT

<213> Secuencia artificial

<220>

<223> Construcción sintética

<400> 35

Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile
1 5 10 15

Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu
20 25 30

Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser
35 40 45

Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu
50 55 60

Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser
65 70 75 80

Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys
85 90 95

Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys
100 105 110

Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr His
115 120 125

Gly Ser Glu Asp Ser
130

<210> 36

<211> 36

<212> ADN

<213> Secuencia artificial

<220>

<223> Construcción sintética

<400> 36

gagtctaagt atggcccacc gtgtcccccc tgccca
36

<210> 37
<211> 12
<212> PRT
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 37

Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro
1				5				10			

<210> 38
<211> 651
<212> ADN
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 38

gcacctgagt tcctcggagg cccctctgta ttctgtttc ccccaaagcc caaggatact
60

cttatgatct cacgcactcc ggaagtaacc tgcgtggtgg tggatgtgag tcaggaagac
120

cccgaagtcc agtttaattg gtacgtggac ggggttgagg tacataacgc caaaacgaaa
180

cctcgggagg agcaattcaa ttccacttac cgggttgat cagtcctgac tgtactgcat
240

caagattggc tcaacgggaa agagtacaag tgtaaggta gtaataaagg gctgccgtct
300

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360

ctgccaccct ctcaggagga gatgactaaa aaccaagtgt cactgacctg ccttgtaag
420

ggtttttacc catctgatat agcagtagag tgggaatcca atggacagcc agagaacaat
480

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540

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<210> 39

<211> 217

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<223> Construcción sintética

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Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
115 120 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
130 135 140

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145 150 155 160

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

Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Leu Gly Lys
210 215

<210> 40
<211> 66
<212> ADN
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<223> Construcción sintética

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<210> 41
<211> 22
<212> PRT
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 41

Met Ala Leu Ile Val Leu Gly Gly Val Ala Gly Leu Leu Leu Phe Ile
1 5 10 15

Gly Leu Gly Ile Phe Phe
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<210> 42
<211> 9
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<213> Secuencia artificial

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<223> Construcción sintética

<400> 42

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9

<210> 43

<211> 3

<212> PRT

<213> Secuencia artificial

<220>

<223> Construcción sintética

<400> 43

Gly Ser Gly

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<210> 44

<211> 57

<212> ADN

<213> Secuencia artificial

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<223> Construcción sintética

<400> 44

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57

<210> 45

<211> 19

<212> PRT

<213> Secuencia artificial

<220>

<223> Construcción sintética

<400> 45

Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn

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15

Pro Gly Pro

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<220>
<223> Construcción sintética

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120

ttggccgcgg cttgtgcagt gtttcttgct tgcccgtggg cagttagcgg tgctcgcga
180

tctcccggaa gcgcggcgag tcctcgactc agggaaggtc cggagctgag cccagatgac
240

ccgcgcggtt tgctggacct ccgccaagga atgttcgctc aactcgttgc gcaaaacgta
300

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360

acaggcggac tcagttacaa ggaggatact aaggaactgg tagtcgctaa ggctggggta
420

tactacgtgt tctttcaact cgaactgaga agggtggttg cgggagaagg atctggaagt
480

gtatctctcg ccctgcacct ccaaccctc agaagtgccg ccggagcggc cgcccttgcc
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660

cgggcgaggc acgcttgga actcacaaa ggtgcgacgg ttctcggctt gtttagggtt
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<210> 47
<211> 254
<212> PRT
<213> Secuencia artificial

<220>

<223> Construcción sintética

<400> 47

Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro
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Pro Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu Val
20 25 30

Ala Gly Leu Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe
35 40 45

Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser
50 55 60

Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp
65 70 75 80

Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val
85 90 95

Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp
100 105 110

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

Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe
130 135 140

Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser
145 150 155 160

Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala
165 170 175

Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala
180 185 190

Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala
195 200 205

Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His
210 215 220

Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val
225 230 235 240

Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
245 250

<210> 48
<211> 3
<212> ADN
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 48
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3

<210> 49
<211> 2040
<212> ADN
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 49
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120

gtgaatgact tggtcctga gtttctgccg gctccagagg acgttgaaac aaactgtgaa
180

tggtcagcgt tttcatgttt tcaaaaggca cagctcaagt ccgccaatac aggcaataac
240

gagcggatta taaatgtctc aattaataag ctcaagcgca aacccccttc aacgaatgct
300

ggtcgccgcc agaaacacag gttgacctgt ccctcctgtg actcatacga gaagaaacct
360

cccaaggaat ttctcgaacg ctttaagtca ctcttcgaga agatgattca tcagcacttg
420

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660

acgaaacctc gggaggagca attcaattcc acttaccggg ttgtatcagt cctgactgta
720

ctgcatcaag attggctcaa cgggaaagag tacaagtgtg aggttagtaa taaagggtg
780

ccgtctagta ttgagaaaac gatcagtaag gctaaagggc agccaagaga gccacaagta
840

tataccctgc caccctctca ggaggagatg actaaaaacc aagtgtcact gacctgcctt
900

gttaagggtt tttacccatc tgatatagca gtagagtggg aatccaatgg acagccagag
960

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1080

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1320

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<211> 679

<212> PRT

<213> Secuencia artificial

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<223> Construcción sintética

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Ser Gln Gly Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp
20 25 30

Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe
35 40 45

Leu Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe
50 55 60

Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn
65 70 75 80

Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro
85 90 95

Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser
100 105 110

Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe
115 120 125

Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr
130 135 140

His Gly Ser Glu Asp Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
145 150 155 160

Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
165 170 175

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
180 185 190

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
195 200 205

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
210 215 220

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
225 230 235 240

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
245 250 255

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
260 265 270

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

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
290 295 300

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
305 310 315 320

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
325 330 335

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
340 345 350

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
355 360 365

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Met Ala Leu Ile Val
370 375 380

Leu Gly Gly Val Ala Gly Leu Leu Leu Phe Ile Gly Leu Gly Ile Phe
385 390 395 400

Phe Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp
405 410 415

Val Glu Glu Asn Pro Gly Pro Met Glu Tyr Ala Ser Asp Ala Ser Leu
420 425 430

Asp Pro Glu Ala Pro Trp Pro Pro Ala Pro Arg Ala Arg Ala Cys Arg
435 440 445

Val Leu Pro Trp Ala Leu Val Ala Gly Leu Leu Leu Leu Leu Leu
450 455 460

Ala Ala Ala Cys Ala Val Phe Leu Ala Cys Pro Trp Ala Val Ser Gly
465 470 475 480

Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly
485 490 495

Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln
500 505 510

Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly
515 520 525

Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr
530 535 540

Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys
545 550 555 560

Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val
565 570 575

Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro
580 585 590

Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu
595 600 605

Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly
610 615 620

Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His
625 630 635 640

Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr
645 650 655

Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro
660 665 670

Ser Pro Arg Ser Glu Gly Ser
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<211> 9772
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<223> Construcción sintética

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120

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180

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240

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360

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420

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480

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1080

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1980

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<211> 259

<212> PRT

<213> Secuencia artificial

<220>

<223> Construcción sintética

<400> 55

Ser His His Trp Gly Tyr Gly Lys His Asn Gly Pro Glu His Trp His
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Lys Asp Phe Pro Ile Ala Lys Gly Glu Arg Gln Ser Pro Val Asp Ile
20 25 30

Asp Thr His Thr Ala Lys Tyr Asp Pro Ser Leu Lys Pro Leu Ser Val
35 40 45

Ser Tyr Asp Gln Ala Thr Ser Leu Arg Ile Leu Asn Asn Gly His Ala
50 55 60

Phe Asn Val Glu Phe Asp Asp Ser Gln Asp Lys Ala Val Leu Lys Gly
65 70 75 80

Gly Pro Leu Asp Gly Thr Tyr Arg Leu Ile Gln Phe His Phe His Trp
85 90 95

Gly Ser Leu Asp Gly Gln Gly Ser Glu His Thr Val Asp Lys Lys Lys
100 105 110

Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Thr Lys Tyr Gly Asp
115 120 125

Phe Gly Lys Ala Val Gln Gln Pro Asp Gly Leu Ala Val Leu Gly Ile
130 135 140

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

Val Leu Asp Ser Ile Lys Thr Lys Gly Lys Ser Ala Asp Phe Thr Asn
165 170 175

Phe Asp Pro Arg Gly Leu Leu Pro Glu Ser Leu Asp Tyr Trp Thr Tyr
180 185 190

Pro Gly Ser Leu Thr Thr Pro Pro Leu Leu Glu Cys Val Thr Trp Ile
195 200 205

Val Leu Lys Glu Pro Ile Ser Val Ser Ser Glu Gln Val Leu Lys Phe
210 215 220

Arg Lys Leu Asn Phe Asn Gly Glu Gly Glu Pro Glu Glu Leu Met Val
225 230 235 240

Asp Asn Trp Arg Pro Ala Gln Pro Leu Lys Asn Arg Gln Ile Lys Ala
245 250 255

Ser Phe Lys

<210> 56
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<223> Construcción sintética

<400> 56

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

Ile Asp Thr His Thr Ala Lys Tyr Asp Pro Ser Leu Lys Pro Leu Ser
35 40 45

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

Ala Phe Asn Val Glu Phe Asp Asp Ser Gln Asp Lys Ala Val Leu Lys
65 70 75 80

Gly Gly Pro Leu Asp Gly Thr Tyr Arg Leu Ile Gln Phe His Phe His
85 90 95

Trp Gly Ser Leu Asp Gly Gln Gly Ser Glu His Thr Val Asp Lys Lys
100 105 110

Lys Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Thr Lys Tyr Gly
115 120 125

Asp Phe Gly Lys Ala Val Gln Gln Pro Asp Gly Leu Ala Val Leu Gly
130 135 140

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

Asp Val Leu Asp Ser Ile Lys Thr Lys Gly Lys Ser Ala Asp Phe Thr
165 170 175

Asn Phe Asp Pro Arg Gly Leu Leu Pro Glu Ser Leu Asp Tyr Trp Thr
180 185 190

Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Leu Glu Cys Val Thr Trp
195 200 205

Ile Val Leu Lys Glu Pro Ile Ser Val Ser Ser Glu Gln Val Leu Lys
210 215 220

Phe Arg Lys Leu Asn Phe Asn Gly Glu Gly Glu Pro Glu Glu Leu Met
225 230 235 240

Val Asp Asn Trp Arg Pro Ala Gln Pro Leu Lys Asn Arg Gln Ile Lys
245 250 255

Ala Ser Phe Lys
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<210> 57
<211> 259
<212> PRT
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<400> 57

Ser His His Trp Gly Tyr Gly Lys His Asn Gly Pro Glu His Trp His
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Lys Asp Phe Pro Ile Ala Lys Gly Glu Arg Gln Ser Pro Val Asp Ile
20 25 30

Asp Thr His Thr Ala Lys Tyr Asp Pro Ser Leu Lys Pro Leu Ser Val
35 40 45

Ser Tyr Asp Gln Ala Thr Asn Leu Arg Ile Leu Asn Asn Gly His Ala
50 55 60

Phe Asn Val Glu Phe Asp Asp Ser Gln Asp Lys Ala Val Leu Lys Gly
65 70 75 80

Gly Pro Leu Asp Gly Thr Tyr Arg Leu Ile Gln Phe His Phe His Trp
85 90 95

Gly Ser Leu Asp Gly Gln Gly Ser Glu His Thr Val Asp Lys Lys Lys
100 105 110

Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Thr Lys Tyr Gly Asp
115 120 125

Phe Gly Lys Ala Val Gln Gln Pro Asp Gly Leu Ala Val Leu Gly Ile
130 135 140

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

Val Leu Asp Ser Ile Lys Thr Lys Gly Lys Ser Ala Asp Phe Thr Asn
165 170 175

Phe Asp Pro Arg Gly Leu Leu Pro Glu Ser Leu Asp Tyr Trp Thr Tyr
180 185 190

Pro Gly Ser Leu Thr Thr Pro Pro Leu Leu Glu Cys Val Thr Trp Ile
195 200 205

Val Leu Lys Glu Pro Ile Ser Val Ser Ser Glu Gln Val Leu Lys Phe
210 215 220

Arg Lys Leu Asn Phe Asn Gly Glu Gly Glu Pro Glu Glu Leu Met Val
225 230 235 240

Asp Asn Trp Arg Pro Ala Gln Pro Leu Lys Asn Arg Gln Ile Lys Ala
245 250 255

Ser Phe Lys

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<211> 18
<212> PRT
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 58

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
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His Ser

<210> 59
<211> 48
<212> PRT
<213> Secuencia artificial

<220>
<223> Construcción sintética

<400> 59

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

Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala
35 40 45

<210> 60
<211> 33
<212> PRT
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<223> Construcción sintética

<400> 60

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			20					25					30		

Ala