

P057712C0 Sequence listing - corrected
Sequence Listing

<110> Consejo Superior De Investigaciones Cientificas (CSIC)

<120> PHAGE PHI 29 DNA POLYMERASE CHIMERA

<130> 53044

<160> 19

<170> PatentIn version 3.5

<210> 1

<211> 572

<212> PRT

<213> Bacteriophage phi-29

<400> 1

Met Pro Arg Lys Met Tyr Ser Cys Asp Phe Glu Thr Thr Thr Lys Val
1 5 10 15

Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile Glu Asp His
20 25 30

Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met Ala Trp Val
35 40 45

Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys Phe Asp Gly
50 55 60

Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys Trp Ser Ala
65 70 75 80

Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg Met Gly Gln
85 90 95

Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys Arg Lys Ile
100 105 110

His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe Pro Val Lys
115 120 125

Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly Asp Ile Asp
130 135 140

Tyr His Lys Glu Arg Pro Val Gly Tyr Lys Ile Thr Pro Glu Glu Tyr
145 150 155 160

Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Arg Leu Leu Ile
165 170 175

Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser Asp Ser Leu
180 185 190

Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys Lys Val Phe
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P057712CO Sequence listing - corrected

195

200

205

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

Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys Glu Ile Gly
225 230 235 240

Glu Gly Met Val Phe Asp Val Asn Ser Leu Tyr Pro Ala Gln Met Tyr
245 250 255

Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu Gly Lys Tyr
260 265 270

Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile Arg Cys Glu
275 280 285

Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile Lys Arg Ser
290 295 300

Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly Gly Glu Ile
305 310 315 320

Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met Lys Glu His
325 330 335

Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys Phe Lys Ala
340 345 350

Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr Tyr Ile Lys
355 360 365

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

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

Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu Gly Glu Glu
405 410 415

Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe Ile Thr Ala
420 425 430

Trp Ala Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys Tyr Asp Arg
435 440 445

Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly Thr Glu Ile
450 455 460

Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu Gly Tyr Trp
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P057712C0 Sequence listing - corrected
 465 470 475 480

Ala His Glu Ser Thr Phe Lys Arg Val Lys Tyr Leu Arg Gln Lys Thr
 485 490 495

Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys Leu Val Glu
 500 505 510

Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val Lys Cys Ala
 515 520 525

Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu Asn Phe Lys
 530 535 540

Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln Val Pro Gly
 545 550 555 560

Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys
 565 570

<210> 2
 <211> 984
 <212> PRT
 <213> Methanopyrus kandleri
 <400> 2

Met Ala Leu Val Tyr Asp Ala Glu Phe Val Gly Ser Glu Arg Glu Phe
 1 5 10 15

Glu Glu Glu Arg Glu Thr Phe Leu Lys Gly Val Lys Ala Tyr Asp Gly
 20 25 30

Val Leu Ala Thr Arg Tyr Leu Met Glu Arg Ser Ser Ser Ala Lys Asn
 35 40 45

Asp Glu Glu Leu Leu Glu Leu His Gln Asn Phe Ile Leu Leu Thr Gly
 50 55 60

Ser Tyr Ala Cys Ser Ile Asp Pro Thr Glu Asp Arg Tyr Gln Asn Val
 65 70 75 80

Ile Val Arg Gly Val Asn Phe Asp Glu Arg Val Gln Arg Leu Ser Thr
 85 90 95

Gly Gly Ser Pro Ala Arg Tyr Ala Ile Val Tyr Arg Arg Gly Trp Arg
 100 105 110

Ala Ile Ala Lys Ala Leu Asp Ile Asp Glu Glu Asp Val Pro Ala Ile
 115 120 125

Glu Val Arg Ala Val Lys Arg Asn Pro Leu Gln Pro Ala Leu Tyr Arg
 130 135 140

P057712CO Sequence listing - corrected

Ile Leu Val Arg Tyr Gly Arg Val Asp Leu Met Pro Val Thr Val Asp
145 150 155 160

Glu Val Pro Pro Glu Met Ala Gly Glu Phe Glu Arg Leu Ile Glu Arg
165 170 175

Tyr Asp Val Pro Ile Asp Glu Lys Glu Glu Arg Ile Leu Glu Ile Leu
180 185 190

Arg Glu Asn Pro Trp Thr Pro His Asp Glu Ile Ala Arg Arg Leu Gly
195 200 205

Leu Ser Val Ser Glu Val Glu Gly Glu Lys Asp Pro Glu Ser Ser Gly
210 215 220

Ile Tyr Ser Leu Trp Ser Arg Val Val Val Asn Ile Glu Tyr Asp Glu
225 230 235 240

Arg Thr Ala Lys Arg His Val Lys Arg Arg Asp Arg Leu Leu Glu Glu
245 250 255

Leu Tyr Glu His Leu Glu Glu Leu Ser Glu Arg Tyr Leu Arg His Pro
260 265 270

Leu Thr Arg Arg Trp Ile Val Glu His Lys Arg Asp Ile Met Arg Arg
275 280 285

Tyr Leu Glu Gln Arg Ile Val Glu Cys Ala Leu Lys Leu Gln Asp Arg
290 295 300

Tyr Gly Ile Arg Glu Asp Val Ala Leu Cys Leu Ala Arg Ala Phe Asp
305 310 315 320

Gly Ser Ile Ser Met Ile Ala Thr Thr Pro Tyr Arg Thr Leu Lys Asp
325 330 335

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

Leu Ala Thr Leu Ile Asp Glu His Gly Leu Ser Pro Asp Ala Ala Asp
355 360 365

Glu Leu Ile Glu His Phe Glu Ser Ile Ala Gly Ile Leu Ala Thr Asp
370 375 380

Leu Glu Glu Ile Glu Arg Met Tyr Glu Glu Gly Arg Leu Ser Glu Glu
385 390 395 400

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

P057712CO Sequence listing - corrected

Glu Gly Val Gly Arg Lys Thr Ala Glu Arg Leu Leu Arg Ala Phe Gly
420 425 430

Asn Pro Glu Arg Val Lys Gln Leu Ala Arg Glu Phe Glu Ile Glu Lys
435 440 445

Leu Ala Ser Val Glu Gly Val Gly Glu Arg Val Leu Arg Ser Leu Val
450 455 460

Pro Gly Tyr Ala Ser Leu Ile Ser Ile Arg Gly Ile Asp Arg Glu Arg
465 470 475 480

Ala Glu Arg Leu Leu Lys Lys Tyr Gly Gly Tyr Ser Lys Val Arg Glu
485 490 495

Ala Gly Val Glu Glu Leu Arg Glu Asp Gly Leu Thr Asp Ala Gln Ile
500 505 510

Arg Glu Leu Lys Gly Leu Lys Thr Leu Glu Ser Ile Val Gly Asp Leu
515 520 525

Glu Lys Ala Asp Glu Leu Lys Arg Lys Tyr Gly Ser Ala Ser Ala Val
530 535 540

Arg Arg Leu Pro Val Glu Glu Leu Arg Glu Leu Gly Phe Ser Asp Asp
545 550 555 560

Glu Ile Ala Glu Ile Lys Gly Ile Pro Lys Lys Leu Arg Glu Ala Phe
565 570 575

Asp Leu Glu Thr Ala Ala Glu Leu Tyr Glu Arg Tyr Gly Ser Leu Lys
580 585 590

Glu Ile Gly Arg Arg Leu Ser Tyr Asp Asp Leu Leu Glu Leu Gly Ala
595 600 605

Thr Pro Lys Ala Ala Ala Glu Ile Lys Gly Pro Glu Phe Lys Phe Leu
610 615 620

Leu Asn Ile Glu Gly Val Gly Pro Lys Leu Ala Glu Arg Ile Leu Glu
625 630 635 640

Ala Val Asp Tyr Asp Leu Glu Arg Leu Ala Ser Leu Asn Pro Glu Glu
645 650 655

Leu Ala Glu Lys Val Glu Gly Leu Gly Glu Glu Leu Ala Glu Arg Val
660 665 670

Val Tyr Ala Ala Arg Glu Arg Val Glu Ser Arg Arg Lys Ser Gly Arg
675 680 685

P057712C0 Sequence listing - corrected

Gln Glu Arg Ser Glu Glu Glu Trp Lys Glu Trp Leu Glu Arg Lys Val
690 695 700

Gly Glu Gly Arg Ala Arg Arg Leu Ile Glu Tyr Phe Gly Ser Ala Gly
705 710 715 720

Glu Val Gly Lys Leu Val Glu Asn Ala Glu Val Ser Lys Leu Leu Glu
725 730 735

Val Pro Gly Ile Gly Asp Glu Ala Val Ala Arg Leu Val Pro Gly Tyr
740 745 750

Lys Thr Leu Arg Asp Ala Gly Leu Thr Pro Ala Glu Ala Glu Arg Val
755 760 765

Leu Lys Arg Tyr Gly Ser Val Ser Lys Val Gln Glu Gly Ala Thr Pro
770 775 780

Asp Glu Leu Arg Glu Leu Gly Leu Gly Asp Ala Lys Ile Ala Arg Ile
785 790 795 800

Leu Gly Leu Arg Ser Leu Val Asn Lys Arg Leu Asp Val Asp Thr Ala
805 810 815

Tyr Glu Leu Lys Arg Arg Tyr Gly Ser Val Ser Ala Val Arg Lys Ala
820 825 830

Pro Val Lys Glu Leu Arg Glu Leu Gly Leu Ser Asp Arg Lys Ile Ala
835 840 845

Arg Ile Lys Gly Ile Pro Glu Thr Met Leu Gln Val Arg Gly Met Ser
850 855 860

Val Glu Lys Ala Glu Arg Leu Leu Glu Arg Phe Asp Thr Trp Thr Lys
865 870 875 880

Val Lys Glu Ala Pro Val Ser Glu Leu Val Arg Val Pro Gly Val Gly
885 890 895

Leu Ser Leu Val Lys Glu Ile Lys Ala Gln Val Asp Pro Ala Trp Lys
900 905 910

Ala Leu Leu Asp Val Lys Gly Val Ser Pro Glu Leu Ala Asp Arg Leu
915 920 925

Val Glu Glu Leu Gly Ser Pro Tyr Arg Val Leu Thr Ala Lys Lys Ser
930 935 940

Asp Leu Met Arg Val Glu Arg Val Gly Pro Lys Leu Ala Glu Arg Ile
945 950 955 960

P057712C0 Sequence listing - corrected

Arg Ala Ala Gly Lys Arg Tyr Val Glu Glu Arg Arg Ser Arg Arg Glu
965 970 975

Arg Ile Arg Arg Lys Leu Arg Gly
980

<210> 3
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> dominio H de la topoisomerasa V de Methanopyrus kandleri
<400> 3

Trp Lys Glu Trp Leu Glu Arg Lys Val Gly Glu Gly Arg Ala Arg Arg
1 5 10 15

Leu Ile Glu Tyr Phe Gly Ser Ala Gly Glu Val Gly Lys Leu Val Glu
20 25 30

Asn Ala Glu Val Ser Lys Leu Leu Glu Val Pro Gly Ile Gly Asp Glu
35 40 45

Ala Val Ala Arg Leu Val Pro Gly
50 55

<210> 4
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> dominio I de la topoisomerasa V de Methanopyrus kandleri
<400> 4

Tyr Lys Thr Leu Arg Asp Ala Gly Leu Thr Pro Ala Glu Ala Glu Arg
1 5 10 15

Val Leu Lys Arg Tyr Gly Ser Val Ser Lys Val Gln Glu Gly Ala Thr
20 25 30

Pro Asp Glu Leu Arg Glu Leu Gly Leu Gly Asp Ala Lys Ile Ala Arg
35 40 45

Ile Leu Gly
50

<210> 5
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

P057712C0 Sequence listing - corrected

<223> secuencia aminoacídica conectora

<400> 5

Ala Tyr Asp Val Gly Ala
1 5

<210> 6

<211> 6

<212> PRT

<213> Artificial Sequence

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<223> secuencia aminoacídica conectora

<400> 6

Gly Thr Gly Ser Gly Ala
1 5

<210> 7

<211> 34

<212> DNA

<213> Artificial Sequence

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<223> cebador 3

<400> 7

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34

<210> 8

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> cebador 1

<400> 8

gcgtatgatg tgggcgccgg

20

<210> 9

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> cebador 2

<400> 9

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38

<210> 10

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> secuencia aminoacídica conectora

<400> 10

P057712C0 Sequence listing - corrected

Gly Thr Gly Ser Gly Ala
1 5

<210> 11
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> cebador 4

<400> 11
ccgtctccgg gagctgcatg tg 22

<210> 12
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> cebador 5

<400> 12
ggcgcccaca tcatacgctt tgattgtgaa tgtgtcatca acc 43

<210> 13
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> cebador 6

<400> 13
ggcgccagag ccggtgcctt tgattgtgaa tgtgtcatca acc 43

<210> 14
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleótido de 15 pares de bases

<400> 14
gatcacagtg agtac 15

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleótido de 21 pares de bases

<400> 15
tctattgtac tcactgtgat c 21

<210> 16
<211> 17
<212> DNA
<213> Artificial Sequence

P057712C0 Sequence listing - corrected

<220>		
<223>	cebador	
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<211>	22	
<212>	DNA	
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<400>	17	
	ccgtctccgg gagctgcatg tg	22
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<211>	26	
<212>	DNA	
<213>	Artificial Sequence	
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<400>	18	
	ccggatgaca gcaggcagtg acagtc	26
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<213>	Artificial Sequence	
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