

1  
SEQUENCE LISTING

<110> F. Hoffmann-La Roche Ag  
Roche Diagnostics GmbH

<120> DNA Polymerases With Increased 3'-Mismatch Discrimination

<130> 26747 WO-HS

<140> Not yet assigned

<141> Not yet assigned

<150> US 61/356,287

<151> 2010-06-18

<160> 42

<170> FastSEQ for windows Version 4.0

<210> 1

<211> 834

<212> PRT

<213> Thermus sp.

<220>

<223> Thermus sp. Z05 DNA polymerase (Z05)

<400> 1

Met	Lys	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu
1				5					10					15	
Val	Asp	Gly	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	
			20				25					30			
Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala
			35				40					45			
Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	Val	Phe
			50			55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu
65				70					75					80	
Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
			85					90					95		
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100				105						110		
Glu	Val	Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys
			115				120					125			
Lys	Ala	Glu	Arg	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg
			130			135					140				
Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	Pro	Glu
145				150					155					160	
Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Lys
			165					170						175	
Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	Ser	Asp
			180				185						190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Lys	Leu
		195				200						205			
Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Ile	Leu	Lys	Asn	Leu	Asp	Arg
			210			215					220				
Val	Lys	Pro	Glu	Ser	Val	Arg	Glu	Arg	Ile	Lys	Ala	His	Leu	Glu	Asp
225				230					235					240	
Leu	Lys	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Ser	Asp	Leu	Pro	Leu
			245					250						255	
Glu	Val	Asp	Phe	Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Arg
			260					265					270		
Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly
			275			280						285			
Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro
			290			295				300					
Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp
305				310						315					320

2

Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Lys	Glu	Gly	Arg	Val	His	Arg
				325					330					335	
Ala	Lys	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val	Arg	Gly
			340					345					350		
Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Asp
		355					360					365			
Leu	Ala	Pro	Ser	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro
	370					375					380				
Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp
385					390					395					400
Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ala	Glu	Arg	Leu	Gln	Gln
				405					410					415	
Asn	Leu	Leu	Glu	Arg	Leu	Lys	Gly	Glu	Glu	Lys	Leu	Leu	Trp	Leu	Tyr
			420					425					430		
Gln	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala
		435					440					445			
Thr	Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Lys	Ala	Leu	Ser	Leu	Glu
	450					455					460				
Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg	Leu	Ala
465					470					475					480
Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu
				485					490					495	
Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Gly	Lys	Thr	Gln	Lys	Thr	Gly
			500					505					510		
Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His
		515					520					525			
Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	Leu	Lys
	530					535					540				
Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Gly	Leu	Val	His	Pro	Arg	Thr	Gly
545					550					555					560
Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu
				565					570					575	
Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Ile	Arg	Thr	Pro	Leu
			580					585					590		
Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu
		595					600					605			
Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu
	610					615					620				
Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile
625					630					635					640
His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Ser	Pro	Glu	Ala	Val
				645					650					655	
Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu
			660					665					670		
Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr
		675					680					685			
Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys
	690					695					700				
Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly
705					710					715					720
Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn
				725					730					735	
Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn
			740					745					750		
Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val
		755					760					765			
Lys	Leu	Phe	Pro	His	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln
	770					775					780				
Val	His	Asp	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu
785					790					795					800
Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala
			805						810					815	
Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala
			820					825					830		
Lys	Gly														

<211> 832  
 <212> PRT  
 <213> Thermus aquaticus

<220>  
 <223> Thermus equaticus DNA polymerase (Taq)

<400> 2  
 Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu  
 1 5 10 15  
 Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly  
 20 25 30  
 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala  
 35 40 45  
 Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val  
 50 55 60  
 Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly  
 65 70 75 80  
 Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu  
 85 90 95  
 Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu  
 100 105 110  
 Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys  
 115 120 125  
 Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp  
 130 135 140  
 Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly  
 145 150 155 160  
 Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro  
 165 170 175  
 Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn  
 180 185 190  
 Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu  
 195 200 205  
 Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu  
 210 215 220  
 Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys  
 225 230 235 240  
 Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val  
 245 250 255  
 Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe  
 260 265 270  
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
 275 280 285  
 Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
 290 295 300  
 Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp  
 305 310 315 320  
 Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro  
 325 330 335  
 Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu  
 340 345 350  
 Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro  
 355 360 365  
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380  
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
 385 390 395 400  
 Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu  
 405 410 415  
 Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu  
 420 425 430  
 Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly  
 435 440 445  
 Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala  
 450 455 460  
 Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His  
 465 470 475 480

Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp  
 Glu Leu Gly Leu 485 Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg  
 Ser Thr Ser 500 Ala Ala Val Leu Glu 505 Ala Leu Arg Glu Ala His Pro Ile  
 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr  
 Tyr 530 Ile Asp Pro Leu Pro 535 Asp Leu Ile His Pro Arg Thr Gly Arg Leu  
 545 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
 Ser Asp Pro Asn 565 Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
 Arg Ile Arg 580 Ala Phe Ile Ala Glu Glu Gly Trp Leu Val Ala  
 Leu Asp Tyr Ser Gln Ile Glu 600 Leu Arg Val Leu Ala His Leu Ser Gly  
 Asp Glu Asn Leu Ile Arg 615 Val Phe Gln Glu Gly Arg Asp Ile His Thr  
 625 Glu Thr Ala Ser Trp 630 Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro  
 Leu Met Arg Arg 645 Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
 Met Ser Ala 660 His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
 Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg  
 Ala Trp Ile Glu Lys Thr 695 Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val  
 705 Glu Thr Leu Phe Gly 710 Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg  
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
 Val Gln Gly Thr Ala Ala Asp 740 Leu Met Lys Leu Ala Met Val Lys Leu  
 Phe Pro Arg Leu Glu Glu Met 755 Gly Ala Arg Met Leu Gln Val His  
 Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala  
 785 Arg Leu Ala Lys Glu 805 Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro  
 Leu Glu Val Glu 820 Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu  
 825 830

<210> 3  
 <211> 830  
 <212> PRT  
 <213> Thermus filiformis

<220>  
 <223> Thermus filiformis DNA polymerase (Tfi)

<400> 3  
 Met Leu Pro Leu Leu Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly  
 1 5 10 15  
 His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu Thr Thr  
 20 25 30  
 Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu  
 35 40 45  
 Leu Lys Ala Leu Lys Glu Asp Gly Glu Val Ala Ile Val Val Phe Asp  
 50 55 60  
 Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala Tyr Lys Ala  
 65 70 75 80  
 Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile  
 85 90 95  
 Lys Glu Leu Val Asp Leu Leu Gly Leu Val Arg Leu Glu Val Pro Gly

			100					105					110		
Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Arg	Lys	Ala	Glu	Arg
		115					120					125			
Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Ser	Ala	Asp	Arg	Asp	Leu	Tyr	Gln
	130					135					140				
Leu	Leu	Ser	Asp	Arg	Ile	His	Leu	Leu	His	Pro	Gly	Gly	Glu	Val	Leu
145					150					155					160
Thr	Pro	Gly	Trp	Leu	Gln	Glu	Arg	Tyr	Gly	Leu	Ser	Pro	Glu	Arg	Trp
			165						170					175	
Val	Glu	Tyr	Arg	Ala	Leu	Val	Gly	Asp	Pro	Ser	Asp	Asn	Leu	Pro	Gly
			180					185					190		
Val	Pro	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Lys	Leu	Leu	Lys	Glu	Trp
		195					200					205			
Gly	Ser	Leu	Glu	Ala	Ile	Leu	Lys	Asn	Leu	Asp	Gln	Val	Lys	Pro	Glu
	210					215					220				
Arg	Val	Trp	Glu	Ala	Ile	Arg	Asn	Asn	Leu	Asp	Lys	Leu	Gln	Met	Ser
225					230					235					240
Leu	Glu	Leu	Ser	Arg	Leu	Arg	Thr	Asp	Leu	Pro	Leu	Glu	Val	Asp	Phe
				245					250					255	
Ala	Lys	Arg	Arg	Glu	Pro	Thr	Gly	Lys	Gly	Leu	Lys	Ala	Phe	Leu	Glu
			260					265					270		
Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu	Glu	Ala
		275					280					285			
Pro	Lys	Glu	Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Gly	Gly	Ala	Phe
	290					295					300				
Leu	Gly	Phe	Leu	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	Leu	Leu
305					310					315					320
Ala	Leu	Ala	Gly	Ala	Lys	Glu	Gly	Arg	Val	His	Arg	Ala	Glu	Asp	Pro
				325					330					335	
Val	Gly	Ala	Leu	Lys	Asp	Leu	Lys	Glu	Ile	Arg	Gly	Leu	Leu	Ala	Lys
			340					345					350		
Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Arg	Glu	Ile	Pro	Pro	Gly
		355					360					365			
Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Gly	Asn	Thr	Asn
	370					375					380				
Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Lys	Glu	Asp	Ala
385					390					395					400
Ala	Ala	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	Trp	Gln	Ala	Leu	Tyr	Pro
				405					410					415	
Arg	Val	Ala	Glu	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	Glu	Val	Glu
			420					425					430		
Arg	Pro	Leu	Ala	Gln	Val	Leu	Ala	His	Met	Glu	Ala	Thr	Gly	Val	Arg
		435					440					445			
Leu	Asp	Val	Pro	Tyr	Leu	Glu	Ala	Leu	Ser	Gln	Glu	Val	Ala		

6

Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser
			660					665					670		
Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ser	Ile	Pro	Tyr	Glu	Glu	Ala	Ala
		675					680					685			
Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg	Ala	Trp
	690					695					700				
Ile	Ala	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Lys	Gly	Tyr	Val	Glu	Thr
705					710					715					720
Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala	Arg	Val	Lys
				725					730					735	
Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val	Gln
			740					745					750		
Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu	Phe	Pro
		755					760					765			
Arg	Leu	Arg	Pro	Leu	Gly	Val	Arg	Ile	Leu	Leu	Gln	Val	His	Asp	Glu
	770					775					780				
Leu	Val	Leu	Glu	Ala	Pro	Lys	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gln	Leu
785					790					795					800
Ala	Lys	Glu	Thr	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ser	Val	Pro	Leu	Glu
				805					810					815	
Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Glu		
			820					825					830		

<210> 4  
 <211> 831  
 <212> PRT  
 <213> Thermus flavus

<220>  
 <223> Thermus flavus DNA polymerase (Tf1)

<400> 4

Met	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val
1				5					10					15	
Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu
			20					25					30		
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
		35					40					45			
Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Val	Val	Val	Val	Val
	50					55				60					
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu	Ala	Tyr
65				70					75						80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
				85					90					95	
Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Val	Arg	Leu	Glu	Val
			100					105					110		
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Arg	Ala
		115					120					125			
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu
	130					135					140				
Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ala	Ile	Leu	His	Pro	Glu	Gly	Tyr
145				150					155						160
Leu	Ile	Thr	Pro	Ala	Trp	Leu	Tyr	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	Glu
				165					170					175	
Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn	Ile
			180					185					190		
Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Gln	Arg	Leu	Ile	Arg
		195					200					205			
Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Phe	Gln	His	Leu	Asp	Gln	Val	Lys
	210					215					220				
Pro	Ser	Leu	Arg	Glu	Lys	Leu	Gln	Ala	Gly	Met	Glu	Ala	Leu	Ala	Leu
225					230					235					240
Ser	Arg	Lys	Leu	Ser	Gln	Val	His	Thr	Asp	Leu	Pro	Leu	Glu	Val	Asp
				245					250					255	
Phe	Gly	Arg	Arg	Arg	Thr	Pro	Asn	Leu	Glu	Gly	Leu	Arg	Ala	Phe	Leu
			260					265					270		

Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu	Glu
		275					280					285			
Gly	Pro	Lys	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala
	290					295					300				
Phe	Leu	Gly	Phe	Ser	Phe	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	Leu
305					310					315					320
Leu	Ala	Leu	Ala	Gly	Ala	Trp	Glu	Gly	Arg	Leu	His	Arg	Ala	Gln	Asp
				325					330					335	
Pro	Leu	Arg	Gly	Leu	Arg	Asp	Leu	Lys	Gly	Val	Arg	Gly	Ile	Leu	Ala
			340					345					350		
Lys	Asp	Leu	Ala	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Asp	Leu	Phe	Pro
	355						360					365			
Glu	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	Thr
	370					375					380				
Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	Asp
385					390					395					400
Ala	Gly	Glu	Arg	Ala	Leu	Leu	Ala	Glu	Arg	Leu	Phe	Gln	Thr	Leu	Lys
				405					410					415	
Glu	Arg	Leu	Lys	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Glu	Glu	Val
			420					425					430		
Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	Arg	Met	Glu	Ala	Thr	Gly	Val
	435						440					445			
Arg	Leu	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	Val	Glu	Ala
	450					455					460				
Glu	Val	Arg	Gln	Leu	Glu	Glu	Val	Phe	Arg	Leu	Ala	Gly	His	Pro	
465					470				475					480	
Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp	Glu
				485					490					495	
Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	Arg	Ser
			500					505					510		
Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile	Val
	515						520					525			
Asp	Arg	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Asn	Thr	Tyr
	530					535					540				
Ile	Asp	Pro	Leu	Pro	Ala	Leu	Val	His	Pro	Lys	Thr	Gly	Arg	Leu	His
545					550					555					560
Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser
				565					570					575	
Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg
			580					585					590		
Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Gly	Trp	Val	Leu	Val	Val	Leu	
	595						600					605			
Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Ser	Gly	Asp	
	610				615					620					
Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr	Gln
625					630					635					640
Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Ser	Pro	Glu	Gly	Val	Asp	Pro	Leu
				645					650					655	
Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met
			660					665					670		
Ser	Ala	His	Arg	Leu	Ser	Gly	Glu	Leu	Ser	Ile	Pro	Tyr	Glu	Glu	Ala
	675						680					685			
Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Tyr	Pro	Lys	Val	Arg	Ala
	690					695					700				
Trp	Ile	Glu	Gly	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	Val	Glu
705					710					715					720
Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala	Arg	Val
				725					730					735	
Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val
			740					745					750		
Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Arg	Leu	Phe
	755						760					765			
Pro	Arg	Leu	Gln	Glu	Leu	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His	Asp
	770					775					780				
Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Asp	Arg	Ala	Glu	Arg	Val	Ala	Ala
785					790					795					800
Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Trp	Pro	Leu	Gln	Val	Pro	Leu
				805					810					815	

Glu Val Glu Val Gly Leu Gly Glu Asp Trp Leu Ser Ala Lys Glu  
820 825 830

<210> 5  
<211> 830  
<212> PRT  
<213> Thermus sp.

<220>  
<223> Thermus sp. sps17 DNA polymerase (Sps17)

<400> 5  
Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly  
1 5 10 15  
His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu Thr Thr  
20 25 30  
Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu  
35 40 45  
Leu Lys Ala Leu Lys Glu Asp Gly Glu Val Ala Ile Val Val Phe Asp  
50 55 60  
Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala Tyr Lys Ala  
65 70 75 80  
Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile  
85 90 95  
Lys Glu Leu Val Asp Leu Leu Gly Leu Val Arg Leu Glu Val Pro Gly  
100 105 110  
Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala Glu Arg  
115 120 125  
Glu Gly Tyr Glu Val Arg Ile Leu Ser Ala Asp Arg Asp Leu Tyr Gln  
130 135 140  
Leu Leu Ser Asp Arg Ile His Leu Leu His Pro Glu Gly Glu Val Leu  
145 150 155 160  
Thr Pro Gly Trp Leu Gln Glu Arg Tyr Gly Leu Ser Pro Glu Arg Trp  
165 170 175  
Val Glu Tyr Arg Ala Leu Val Gly Asp Pro Ser Asp Asn Leu Pro Gly  
180 185 190  
Val Pro Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu Leu Lys Glu Trp  
195 200 205  
Gly Ser Leu Glu Ala Ile Leu Lys Asn Leu Asp Gln Val Lys Pro Glu  
210 215 220  
Arg Val Arg Glu Ala Ile Arg Asn Asn Leu Asp Lys Leu Gln Met Ser  
225 230 235 240  
Leu Glu Leu Ser Arg Leu Arg Thr Asp Leu Pro Leu Glu Val Asp Phe  
245 250 255  
Ala Lys Arg Arg Glu Pro Asp Trp Glu Gly Leu Lys Ala Phe Leu Glu  
260 265 270  
Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Glu Ala  
275 280 285  
Pro Lys Glu Ala Glu Glu Ala Pro Trp Pro Pro Pro Gly Gly Ala Phe  
290 295 300  
Leu Gly Phe Leu Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Leu  
305 310 315 320  
Ala Leu Ala Gly Ala Lys Glu Gly Arg Val His Arg Ala Glu Asp Pro  
325 330 335  
Val Gly Ala Leu Lys Asp Leu Lys Glu Ile Arg Gly Leu Leu Ala Lys  
340 345 350  
Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Arg Glu Ile Pro Pro Gly  
355 360 365  
Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Gly Asn Thr Asn  
370 375 380  
Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Lys Glu Asp Ala  
385 390 395 400  
Ala Ala Arg Ala Leu Ser Glu Arg Leu Trp Gln Ala Leu Tyr Pro  
405 410 415  
Arg Val Ala Glu Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu  
420 425 430  
Arg Pro Leu Ala Gln Val Leu Ala His Met Glu Ala Thr Gly Val Arg



435 440 445  
 Leu Asp Val Pro Tyr Leu Glu Ala Leu Ser Gln Glu Val Ala Phe Glu  
 450 455 460  
 Leu Glu Arg Leu Glu Ala Glu Val His Arg Leu Ala Gly His Pro Phe  
 465 470 475 480  
 Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu  
 485 490 495  
 Gly Leu Pro Pro Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr  
 500 505 510  
 Ser Ala Ala Val Leu Glu Leu Leu Arg Glu Ala His Pro Ile Val Gly  
 515 520 525  
 Arg Ile Leu Glu Tyr Arg Glu Leu Met Lys Leu Lys Ser Thr Tyr Ile  
 530 535 540  
 Asp Pro Leu Pro Arg Leu Val His Pro Lys Thr Gly Arg Leu His Thr  
 545 550 555 560  
 Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp  
 565 570 575  
 Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile  
 580 585 590  
 Arg Lys Ala Phe Ile Ala Glu Glu Gly His Leu Leu Val Ala Leu Asp  
 595 600 605  
 Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu  
 610 615 620  
 Asn Leu Ile Arg Val Phe Arg Glu Gly Lys Asp Ile His Thr Glu Thr  
 625 630 635 640  
 Ala Ala Trp Met Phe Gly Val Pro Pro Glu Gly Val Asp Gly Ala Met  
 645 650 655  
 Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser  
 660 665 670  
 Ala His Arg Leu Ser Gln Glu Leu Ser Ile Pro Tyr Glu Glu Ala Ala  
 675 680 685  
 Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp  
 690 695 700  
 Ile Ala Lys Thr Leu Glu Glu Gly Arg Lys Lys Gly Tyr Val Glu Thr  
 705 710 715 720  
 Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys  
 725 730 735  
 Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln  
 740 745 750  
 Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro  
 755 760 765  
 Arg Leu Arg Pro Leu Gly Val Arg Ile Leu Leu Gln Val His Asp Glu  
 770 775 780  
 Leu Val Leu Glu Ala Pro Lys Ala Arg Ala Glu Glu Ala Ala Gln Leu  
 785 790 795 800  
 Ala Lys Glu Thr Met Glu Gly Val Tyr Pro Leu Ser Val Pro Leu Glu  
 805 810 815  
 Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Ala  
 820 825 830

<210> 6  
 <211> 834  
 <212> PRT  
 <213> Thermus thermophilus

<220>  
 <223> Thermus thermophilus DNA polymerase (Tth)

<400> 6  
 Met Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu  
 1 5 10 15  
 Val Asp Gly His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly  
 20 25 30  
 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala  
 35 40 45  
 Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe  
 50 55 60

Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu
65					70					75					80
Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg
		130				135					140				
Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	Pro	Glu
145				150						155					160
Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165					170						175	
Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	Ser	Asp
		180						185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Lys	Leu
		195					200					205			
Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	Asp	Arg
		210				215					220				
Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	Glu	Asp
225				230						235					240
Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	Pro	Leu
			245						250					255	
Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Arg
			260					265					270		
Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly
		275					280					285			
Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro
		290				295					300				
Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp
305				310						315					320
Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Asp	Gly	Arg	Val	His	Arg
			325						330					335	
Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val	Arg	Gly
			340					345					350		
Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly	Leu	Asp
		355					360					365			
Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro
		370				375					380				
Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp
385				390						395					400
Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	His	Arg
			405					410						415	
Asn	Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp	Leu	Tyr
			420					425					430		
His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala
		435					440					445			
Thr	Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu
		450			455					460					
Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg	Leu	Ala
465				470					475						480
Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu
			485						490					495	
Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Gly	Lys	Thr	Gln	Lys	Thr	Gly
			500					505					510		
Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His
		515					520					525			
Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	Leu	Lys
		530				535					540				
Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	Thr	Gly
545				550						555					560
Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu
			565						570					575	
Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu
			580					585					590		
Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu
		595					600					605			

11

Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu
610						615					620				
Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile
625					630					635					640
His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val
				645					650					655	
Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu
			660					665					670		
Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr
		675					680					685			
Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys
	690					695					700				
Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly
705					710					715					720
Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn
				725					730					735	
Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn
			740					745					750		
Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val
		755					760					765			
Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln
	770					775					780				
Val	His	Asp	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu
785					790					795					800
Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala
				805					810					815	
Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala
			820					825					830		

Lys Gly

<210> 7  
 <211> 834  
 <212> PRT  
 <213> Thermus caldophilus

<220>  
 <223> Thermus caldophilus DNA polymerase (Tca)

<400> 7

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

Val 225	Lys	Pro	Glu	Asn	Val 230	Arg	Glu	Lys	Ile	Lys 235	Ala	His	Leu	Glu	Asp 240
Leu	Arg	Leu	Ser	Leu 245	Glu	Leu	Ser	Arg	Val 250	Arg	Thr	Asp	Leu	Pro 255	Leu
Glu	Val	Asp	Leu 260	Ala	Gln	Gly	Arg	Glu 265	Pro	Asp	Arg	Glu	Gly 270	Leu	Arg
Ala	Phe	Leu 275	Glu	Arg	Leu	Glu	Phe 280	Gly	Ser	Leu	Leu	His 285	Glu	Phe	Gly
Leu	Leu 290	Glu	Ala	Pro	Ala	Pro 295	Leu	Glu	Glu	Ala	Pro 300	Trp	Pro	Pro	Pro
Glu 305	Gly	Ala	Phe	Val	Gly 310	Phe	Val	Leu	Ser	Arg 315	Pro	Glu	Pro	Met	Trp 320
Ala	Glu	Leu	Lys	Ala 325	Leu	Ala	Ala	Cys	Arg 330	Asp	Gly	Arg	Val	His 335	Arg
Ala	Ala	Asp	Pro 340	Leu	Ala	Gly	Leu	Lys 345	Asp	Leu	Lys	Glu	Val 350	Arg	Gly
Leu	Leu	Ala 355	Lys	Asp	Leu	Ala	Val 360	Leu	Ala	Ser	Arg	Glu 365	Gly	Leu	Asp
Leu	Val 370	Pro	Gly	Asp	Asp	Pro 375	Met	Leu	Leu	Ala	Tyr 380	Leu	Leu	Asp	Pro
Ser 385	Asn	Thr	Thr	Pro	Glu 390	Gly	Val	Ala	Arg	Arg 395	Tyr	Gly	Gly	Glu	Trp 400
Thr	Glu	Asp	Ala	Ala 405	His	Arg	Ala	Leu	Leu 410	Ser	Glu	Arg	Leu	His 415	Arg
Asn	Leu	Leu	Lys 420	Arg	Leu	Gln	Gly	Glu 425	Lys	Leu	Leu	Trp 430	Leu	Tyr	
His	Glu	Val 435	Glu	Lys	Pro	Leu	Ser 440	Val	Leu	Ala	His 445	Met	Glu	Ala	
Thr	Gly	Val 450	Arg	Leu	Asp	Val 455	Ala	Tyr	Leu	Gln	Ala 460	Leu	Ser	Leu	Glu
Leu 465	Ala	Glu	Glu	Ile	Arg 470	Arg	Leu	Glu	Glu	Glu 475	Val	Phe	Arg	Leu	Ala 480
Gly	His	Pro	Phe	Asn 485	Leu	Asn	Ser	Arg	Asp 490	Gln	Leu	Glu	Arg	Val 495	Leu
Phe	Asp	Glu	Leu 500	Arg	Leu	Pro	Ala	Leu 505	Gly	Lys	Thr	Gln	Lys 510	Thr	Gly
Lys	Arg	Ser 515	Thr	Ser	Ala	Ala	Val 520	Leu	Glu	Ala	Leu	Arg 525	Glu	Ala	His
Pro	Ile 530	Val	Glu	Lys	Ile	Leu 535	Gln	His	Arg	Glu	Leu 540	Thr	Lys	Leu	Lys
Asn 545	Thr	Tyr	Val	Asp	Pro 550	Leu	Pro	Ser	Leu	Val 555	His	Pro	Asn	Thr	Gly 560
Arg	Leu	His	Thr	Arg 565	Phe	Asn	Gln	Thr	Ala 570	Thr	Ala	Thr	Gly	Arg 575	Leu
Ser	Ser	Ser	Asp 580	Pro	Asn	Leu	Gln	Asn 585	Ile	Pro	Val	Arg	Thr 590	Pro	Leu
Gly	Gln	Arg 595	Ile	Arg	Arg	Ala	Phe 600	Val	Ala	Glu	Ala	Gly 605	Trp	Ala	Leu
Val 610	Ala	Leu	Asp	Tyr	Ser	Gln 615	Ile	Glu	Leu	Arg	Val 620	Leu	Ala	His	Leu
Ser 625	Gly	Asp	Glu	Asn	Leu 630	Ile	Arg	Val	Phe	Gln 635	Glu	Gly	Lys	Asp	Ile 640
His	Thr	Gln	Thr	Ala 645	Ser	Trp	Met	Phe	Gly 650	Val	Pro	Pro	Glu	Ala 655	Val
Asp	Pro	Leu	Met 660	Arg	Arg	Ala	Ala	Lys 665	Thr	Val	Asn	Phe	Gly 670	Val	Leu
Tyr	Gly	Met 675	Ser	Ala	His	Arg	Leu 680	Ser	Gln	Glu	Leu	Ala 685	Ile	Pro	Tyr
Glu	Glu	Ala 690	Val	Ala	Phe	Ile 695	Glu	Arg	Tyr	Phe	Gln 700	Ser	Phe	Pro	Lys
Val 705	Arg	Ala	Trp	Ile	Glu 710	Lys	Thr	Leu	Glu	Glu 715	Gly	Arg	Lys	Arg	Gly 720
Tyr	Val	Glu	Thr	Leu 725	Phe	Gly	Arg	Arg	Arg 730	Tyr	Val	Pro	Asp	Leu 735	Asn
Ala	Arg	Val	Lys 740	Ser	Val	Arg	Glu	Ala 745	Ala	Glu	Arg	Met	Ala 750	Phe	Asn
Met	Pro	Val 755	Gln	Gly	Thr	Ala	Ala 760	Asp	Leu	Met	Lys	Leu 765	Ala	Met	Val

Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln
	770					775					780				
Val	His	Asp	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Gly	Ala	Glu	Glu
785					790					795					800
Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala
				805					810					815	
Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala
			820					825					830		
Lys	Gly														

<210> 8  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic DNA polymerase domain motif

<220>  
 <221> VARIANT  
 <222> (6)...(6)  
 <223> Xaa = Ile or Leu

<220>  
 <221> VARIANT  
 <222> (8)...(8)  
 <223> Xaa = Ile, Val or Thr

<220>  
 <221> VARIANT  
 <222> (9)...(9)  
 <223> Xaa = any amino acid other than Arg or Lys

<220>  
 <221> VARIANT  
 <222> (10)...(10)  
 <223> Xaa = Thr, Ser or Leu

<220>  
 <221> VARIANT  
 <222> (11)...(11)  
 <223> Xaa = Pro or Glu

<220>  
 <221> VARIANT  
 <222> (12)...(12)  
 <223> Xaa = Leu or Glu

<400> 8  
 Pro Asn Leu Gln Asn Xaa Pro Xaa Xaa Xaa Xaa Gly  
 1 5 10

<210> 9  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic DNA polymerase domain motif

<220>  
 <221> VARIANT  
 <222> (6)...(6)  
 <223> Xaa = Ile or Leu

<220>

<221> VARIANT  
 <222> (8)...(8)  
 <223> Xaa = Ile, Val or Thr

<220>  
 <221> VARIANT  
 <222> (9)...(9)  
 <223> Xaa = any amino acid other than Arg or Lys

<220>  
 <221> VARIANT  
 <222> (10)...(10)  
 <223> Xaa = Thr or Ser

<220>  
 <221> VARIANT  
 <222> (11)...(11)  
 <223> Xaa = Pro or Glu

<220>  
 <221> VARIANT  
 <222> (12)...(12)  
 <223> Xaa = Leu or Glu

<400> 9  
 Pro Asn Leu Gln Asn Xaa Pro Xaa Xaa Xaa Xaa Xaa Gly  
 1 5 10

<210> 10  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic DNA polymerase domain motif

<220>  
 <221> VARIANT  
 <222> (8)...(8)  
 <223> Xaa = Ile or Val

<220>  
 <221> VARIANT  
 <222> (9)...(9)  
 <223> Xaa = any amino acid other than Arg

<400> 10  
 Pro Asn Leu Gln Asn Ile Pro Xaa Xaa Thr Pro Leu Gly  
 1 5 10

<210> 11  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic DNA polymerase domain motif

<220>  
 <221> VARIANT  
 <222> (9)...(9)  
 <223> Xaa = His, Leu or Ser

<400> 11  
 Pro Asn Leu Gln Asn Ile Pro Ile Xaa Thr Pro Leu Gly  
 1 5 10

<210> 12  
 <211> 31  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic region from polymerase domain of Thermus  
 sp. Z05 DNA polymerase (Z05)

<400> 12  
 Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Ile  
 1 5 10 15  
 Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu  
 20 25 30

<210> 13  
 <211> 31  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic region from polymerase domain of Thermus  
 aquaticus DNA polymerase (Taq)

<400> 13  
 Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val  
 1 5 10 15  
 Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu  
 20 25 30

<210> 14  
 <211> 31  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic region from polymerase domain of Thermus  
 filiformus DNA polymerase (Tfi)

<400> 14  
 Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val  
 1 5 10 15  
 Arg Thr Pro Leu Gly Gln Arg Ile Arg Lys Ala Phe Ile Ala Glu  
 20 25 30

<210> 15  
 <211> 31  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic region from polymerase domain of Thermus  
 flavus DNA polymerase (Tfl)

<400> 15  
 Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val  
 1 5 10 15  
 Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu  
 20 25 30

<210> 16  
 <211> 31  
 <212> PRT

<213> Artificial Sequence

<220>

<223> synthetic region from polymerase domain of Thermus  
sp. Sps17 DNA polymerase (Sps17)

<400> 16

Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val
1				5					10					15	
Arg	Thr	Pro	Leu	Gly	Gln	Arg	Ile	Arg	Lys	Ala	Phe	Ile	Ala	Glu	
			20					25					30		

<210> 17

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic region from polymerase domain of Thermus  
thermophilus DNA polymerase (Tth)

<400> 17

Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val
1				5					10					15	
Arg	Thr	Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	
			20					25					30		

<210> 18

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic region from polymerase domain of Thermus  
caldophilus DNA polymerase (Tca)

<400> 18

Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val
1				5					10					15	
Arg	Thr	Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	
			20					25					30		

<210> 19

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic region from polymerase domain of  
Thermotoga maritima DNA polymerase (Tma)

<400> 19

Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Leu	Pro	Thr
1				5					10					15	
Lys	Ser	Glu	Glu	Gly	Lys	Glu	Ile	Arg	Lys	Ala	Ile	Val	Pro	Gln	
			20					25					30		

<210> 20

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic region from polymerase domain of



## Thermotoga neapolitana DNA polymerase (Tne)

&lt;400&gt; 20

Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Leu	Pro	Thr
1				5					10					15	
Lys	Ser	Glu	Glu	Gly	Lys	Glu	Ile	Arg	Lys	Ala	Ile	Val	Pro	Gln	
			20					25					30		

&lt;210&gt; 21

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> synthetic region from polymerase domain of  
Thermosipho africanus DNA polymerase (Taf)

&lt;400&gt; 21

Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asn	Pro	Asn	Leu	Gln	Asn	Leu	Pro	Thr
1				5					10					15	
Arg	Ser	Glu	Glu	Gly	Lys	Glu	Ile	Arg	Lys	Ala	Val	Arg	Pro	Gln	
			20					25					30		

&lt;210&gt; 22

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic DNA polymerase domain motif

&lt;400&gt; 22

Ala	Ala	Ala	Ala	Ala	Ala
1				5	

&lt;210&gt; 23

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> synthetic region from polymerase domain of  
Deinococcus radiodurans DNA polymerase (Dra)

&lt;400&gt; 23

Thr	Gly	Arg	Leu	Ser	Ser	Leu	Asn	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Ile
1				5					10					15	
Arg	Ser	Glu	Leu	Gly	Arg	Glu	Ile	Arg	Lys	Gly	Phe	Ile	Ala	Glu	
			20					25					30		

&lt;210&gt; 24

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> synthetic region from polymerase domain of  
Bacillus stearothermophilus DNA polymerase (Bst)

&lt;400&gt; 24

Thr	Gly	Arg	Leu	Ser	Ser	Val	Glu	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Ile
1				5					10					15	
Arg	Leu	Glu	Glu	Gly	Arg	Lys	Ile	Arg	Gln	Ala	Phe	Val	Pro	Ser	
			20					25					30		

<210> 25  
 <211> 31  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic region from polymerase domain of  
 Bacillus caldotenax DNA polymerase (Bca)

<400> 25  
 Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu Gln Asn Ile Pro Ile  
 1 5 10 15  
 Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val Pro Ala  
 20 25 30

<210> 26  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic native consensus motif for region from  
 polymerase domain of bacterial DNA polymerase

<220>  
 <221> VARIANT  
 <222> (6)...(6)  
 <223> Xaa = Ile or Leu

<220>  
 <221> VARIANT  
 <222> (8)...(8)  
 <223> Xaa = Ile, Val or Thr

<220>  
 <221> VARIANT  
 <222> (9)...(9)  
 <223> Xaa = Arg or Lys

<220>  
 <221> VARIANT  
 <222> (10)...(10)  
 <223> Xaa = Thr, Ser or Leu

<220>  
 <221> VARIANT  
 <222> (11)...(11)  
 <223> Xaa = Pro or Glu

<220>  
 <221> VARIANT  
 <222> (12)...(12)  
 <223> Xaa = Leu or Glu

<400> 26  
 Pro Asn Leu Gln Asn Xaa Pro Xaa Xaa Xaa Xaa Xaa Gly  
 1 5 10

<210> 27  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> synthetic polymerase motif corresponding to the  
D580X mutation of Z05, modified Z05 D580 motif

<220>

<221> VARIANT

<222> (7)...(7)

<223> Xaa = Ser or Thr

<220>

<221> VARIANT

<222> (8)...(8)

<223> Xaa = any amino acid other than Asp or Glu

<400> 27

Thr Gly Arg Leu Ser Ser Xaa Xaa Pro Asn Leu Gln Asn  
1 5 10

<210> 28

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic conserved DNA polymerase active site  
motif A

<400> 28

Asp Tyr Ser Gln Ile Glu Leu Arg  
1 5

<210> 29

<211> 893

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic chimeric CS5 DNA polymerase derived from  
N-terminal 5'-nuclease domain of Thermus sp. Z05  
and C-terminal 3'-5' exonuclease and polymerase  
domains of Thermotoga maritima DNA polymerases

<400> 29

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

Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Lys	Leu
		195					200					205			
Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Ile	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Val	Lys	Pro	Glu	Ser	Val	Arg	Glu	Arg	Ile	Lys	Ala	His	Leu	Glu	Asp
225					230					235					240
Leu	Lys	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Ser	Asp	Leu	Pro	Leu
				245					250					255	
Glu	Val	Asp	Phe	Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Arg
			260					265					270		
Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly
		275					280					285			
Leu	Leu	Glu	Glu	Ser	Glu	Pro	Val	Gly	Tyr	Arg	Ile	Val	Lys	Asp	Leu
	290					295					300				
Val	Glu	Phe	Glu	Lys	Leu	Ile	Glu	Lys	Leu	Arg	Glu	Ser	Pro	Ser	Phe
305					310					315					320
Ala	Ile	Asp	Leu	Glu	Thr	Ser	Ser	Leu	Asp	Pro	Phe	Asp	Cys	Asp	Ile
				325					330					335	
Val	Gly	Ile	Ser	Val	Ser	Phe	Lys	Pro	Lys	Glu	Ala	Tyr	Tyr	Ile	Pro
			340					345					350		
Leu	His	His	Arg	Asn	Ala	Gln	Asn	Leu	Asp	Glu	Lys	Glu	Val	Leu	Lys
		355					360					365			
Lys	Leu	Lys	Glu	Ile	Leu	Glu	Asp	Pro	Gly	Ala	Lys	Ile	Val	Gly	Gln
	370					375					380				
Asn	Leu	Lys	Phe	Asp	Tyr	Lys	Val	Leu	Met	Val	Lys	Gly	Val	Glu	Pro
385					390					395					400
Val	Pro	Pro	Tyr	Phe	Asp	Thr	Met	Ile	Ala	Ala	Tyr	Leu	Leu	Glu	Pro
				405					410					415	
Asn	Glu	Lys	Lys	Phe	Asn	Leu	Asp	Asp	Leu	Ala	Leu	Lys	Phe	Leu	Gly
			420					425					430		
Tyr	Lys	Met	Thr	Ser	Tyr	Gln	Glu	Leu	Met	Ser	Phe	Ser	Phe	Pro	Leu
		435					440					445			
Phe	Gly	Phe	Ser	Phe	Ala	Asp	Val	Pro	Val	Glu	Lys	Ala	Ala	Asn	Tyr
	450					455					460				
Ser	Cys	Glu	Asp	Ala	Asp	Ile	Thr	Tyr	Arg	Leu	Tyr	Lys	Thr	Leu	Ser
465					470					475					480
Leu	Lys	Leu	His	Glu	Ala	Asp	Leu	Glu	Asn	Val	Phe	Tyr	Lys	Ile	Glu
				485					490					495	
Met	Pro	Leu	Val	Asn	Val	Leu	Ala	Arg	Met	Glu	Leu	Asn	Gly	Val	Tyr
			500					505					510		
Val	Asp	Thr	Glu	Phe	Leu	Lys	Lys	Leu	Ser	Glu	Glu	Tyr	Gly	Lys	Lys
		515					520					525			
Leu	Glu	Glu	Leu	Ala	Glu	Glu	Ile	Tyr	Arg	Ile	Ala	Gly	Glu	Pro	Phe
	530					535					540				
Asn	Ile	Asn	Ser	Pro	Lys	Gln	Val	Ser	Arg	Ile	Leu	Phe	Glu	Lys	Leu
545					550					555					560
Gly	Ile	Lys	Pro	Arg	Gly	Lys	Thr	Thr	Lys	Thr	Gly	Asp	Tyr	Ser	Thr
				565					570					575	
Arg	Ile	Glu	Val	Leu	Glu	Glu	Leu	Ala	Gly	Glu	His	Glu	Ile	Ile	Pro
			580					585					590		
Leu	Ile	Leu	Glu	Tyr	Arg	Lys	Ile	Gln	Lys	Leu	Lys	Ser	Thr	Tyr	Ile
		595				600						605			
Asp	Ala	Leu	Pro	Lys	Met	Val	Asn	Pro	Lys	Thr	Gly	Arg	Ile	His	Ala
	610					615					620				
Ser	Phe	Asn	Gln	Thr	Gly	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp
625					630					635					640
Pro	Asn	Leu	Gln	Asn	Leu	Pro	Thr	Lys	Ser	Glu	Glu	Gly	Lys	Glu	Ile
				645					650					655	
Arg	Lys	Ala	Ile	Val	Pro	Gln	Asp	Pro	Asn	Trp	Trp	Ile	Val	Ser	Ala
			660					665					670		
Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Ile	Leu	Ala	His	Leu	Ser	Gly	Asp
		675					680					685			
Glu	Asn	Leu	Leu	Arg	Ala	Phe	Glu	Glu	Gly	Ile	Asp	Val	His	Thr	Leu
	690					695					700				
Thr	Ala	Ser	Arg	Ile	Phe	Asn	Val	Lys	Pro	Glu	Glu	Val	Thr	Glu	Glu
705					710					715					720
Met	Arg	Arg	Ala	Gly	Lys	Met	Val	Asn	Phe	Ser	Ile	Ile	Tyr	Gly	Val
				725					730					735	

21

Thr	Pro	Tyr	Gly	Leu	Ser	Val	Arg	Leu	Gly	Val	Pro	Val	Lys	Glu	Ala
			740					745					750		
Glu	Lys	Met	Ile	Val	Asn	Tyr	Phe	Val	Leu	Tyr	Pro	Lys	Val	Arg	Asp
		755					760					765			
Tyr	Ile	Gln	Arg	Val	Val	Ser	Glu	Ala	Lys	Glu	Lys	Gly	Tyr	Val	Arg
	770					775					780				
Thr	Leu	Phe	Gly	Arg	Lys	Arg	Asp	Ile	Pro	Gln	Leu	Met	Ala	Arg	Asp
785					790					795				800	
Arg	Asn	Thr	Gln	Ala	Glu	Gly	Glu	Arg	Ile	Ala	Ile	Asn	Thr	Pro	Ile
			805						810					815	
Gln	Gly	Thr	Ala	Ala	Asp	Ile	Ile	Lys	Leu	Ala	Met	Ile	Glu	Ile	Asp
			820					825					830		
Arg	Glu	Leu	Lys	Glu	Arg	Lys	Met	Arg	Ser	Lys	Met	Ile	Ile	Gln	Val
		835					840					845			
His	Asp	Glu	Leu	Val	Phe	Glu	Val	Pro	Asn	Glu	Glu	Lys	Asp	Ala	Leu
	850					855					860				
Val	Glu	Leu	Val	Lys	Asp	Arg	Met	Thr	Asn	Val	Val	Lys	Leu	Ser	Val
865					870					875					880
Pro	Leu	Glu	Val	Asp	Val	Thr	Ile	Gly	Lys	Thr	Trp	Ser			
				885					890						

<210> 30  
 <211> 893  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> synthetic chimeric CS6 DNA polymerase derived from  
 N-terminal 5'-nuclease domain of Thermus sp. Z05  
 and C-terminal 3'-5' exonuclease and polymerase  
 domains of Thermotoga maritima DNA polymerases

<400> 30

Met	Lys	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu
1				5					10					15	
Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly
			20					25					30		
Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala
			35				40					45			
Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	Val	Phe
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu
65				70						75				80	
Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85				90					95		
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys
			115				120					125			
Lys	Ala	Glu	Arg	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	Pro	Glu
145				150						155				160	
Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Lys
			165					170						175	
Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	Ser	Asp
			180					185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Lys	Leu
		195					200					205			
Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Ile	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Val	Lys	Pro	Glu	Ser	Val	Arg	Glu	Arg	Ile	Lys	Ala	His	Leu	Glu	Asp
225				230						235				240	
Leu	Lys	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Ser	Asp	Leu	Pro	Leu
			245						250				255		
Glu	Val	Asp	Phe	Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Arg
			260					265					270		

Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly
		275					280					285			
Leu	Leu	Glu	Glu	Ser	Glu	Pro	Val	Gly	Tyr	Arg	Ile	Val	Lys	Asp	Leu
	290					295					300				
Val	Glu	Phe	Glu	Lys	Leu	Ile	Glu	Lys	Leu	Arg	Glu	Ser	Pro	Ser	Phe
305					310					315					320
Ala	Ile	Ala	Leu	Ala	Thr	Ser	Ser	Leu	Asp	Pro	Phe	Asp	Cys	Asp	Ile
				325					330					335	
Val	Gly	Ile	Ser	Val	Ser	Phe	Lys	Pro	Lys	Glu	Ala	Tyr	Tyr	Ile	Pro
			340					345					350		
Leu	His	His	Arg	Asn	Ala	Gln	Asn	Leu	Asp	Glu	Lys	Glu	Val	Leu	Lys
		355					360					365			
Lys	Leu	Lys	Glu	Ile	Leu	Glu	Asp	Pro	Gly	Ala	Lys	Ile	Val	Gly	Gln
	370					375					380				
Asn	Leu	Lys	Phe	Asp	Tyr	Lys	Val	Leu	Met	Val	Lys	Gly	Val	Glu	Pro
385					390					395					400
Val	Pro	Pro	Tyr	Phe	Asp	Thr	Met	Ile	Ala	Ala	Tyr	Leu	Leu	Glu	Pro
				405					410					415	
Asn	Glu	Lys	Lys	Phe	Asn	Leu	Asp	Asp	Leu	Ala	Leu	Lys	Phe	Leu	Gly
			420					425					430		
Tyr	Lys	Met	Thr	Ser	Tyr	Gln	Glu	Leu	Met	Ser	Phe	Ser	Phe	Pro	Leu
		435					440					445			
Phe	Gly	Phe	Ser	Phe	Ala	Asp	Val	Pro	Val	Glu	Lys	Ala	Ala	Asn	Tyr
	450					455					460				
Ser	Cys	Glu	Asp	Ala	Asp	Ile	Thr	Tyr	Arg	Leu	Tyr	Lys	Thr	Leu	Ser
465					470					475					480
Leu	Lys	Leu	His	Glu	Ala	Asp	Leu	Glu	Asn	Val	Phe	Tyr	Lys	Ile	Glu
				485					490					495	
Met	Pro	Leu	Val	Asn	Val	Leu	Ala	Arg	Met	Glu	Leu	Asn	Gly	Val	Tyr
			500					505					510		
Val	Asp	Thr	Glu	Phe	Leu	Lys	Lys	Leu	Ser	Glu	Glu	Tyr	Gly	Lys	Lys
		515					520					525			
Leu	Glu	Glu	Leu	Ala	Glu	Glu	Ile	Tyr	Arg	Ile	Ala	Gly	Glu	Pro	Phe
	530					535					540				
Asn	Ile	Asn	Ser	Pro	Lys	Gln	Val	Ser	Arg	Ile	Leu	Phe	Glu	Lys	Leu
545					550					555					560
Gly	Ile	Lys	Pro	Arg	Gly	Lys	Thr	Thr	Lys	Thr	Gly	Asp	Tyr	Ser	Thr
				565					570					575	
Arg	Ile	Glu	Val	Leu	Glu	Glu	Leu	Ala	Gly	Glu	His	Glu	Ile	Ile	Pro
			580					585					590		
Leu	Ile	Leu	Glu	Tyr	Arg	Lys	Ile	Gln	Lys	Leu	Lys	Ser	Thr	Tyr	Ile
		595					600					605			
Asp	Ala	Leu	Pro	Lys	Met	Val	Asn	Pro	Lys	Thr	Gly	Arg	Ile	His	Ala
	610					615					620				
Ser	Phe	Asn	Gln	Thr	Gly	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp
625					630					635					640
Pro	Asn	Leu	Gln	Asn	Leu	Pro	Thr	Lys	Ser	Glu	Glu	Gly	Lys	Glu	Ile
				645					650					655	
Arg	Lys	Ala	Ile	Val	Pro	Gln	Asp	Pro	Asn	Trp	Trp	Ile	Val	Ser	Ala
			660					665					670		
Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Ile	Leu	Ala	His	Leu	Ser	Gly	Asp
		675					680					685			
Glu	Asn	Leu	Leu	Arg	Ala	Phe	Glu	Glu	Gly	Ile	Asp	Val	His	Thr	Leu
	690					695					700				
Thr	Ala	Ser	Arg	Ile	Phe	Asn	Val	Lys	Pro	Glu	Glu	Val	Thr	Glu	Glu
705					710					715					720
Met	Arg	Arg	Ala	Gly	Lys	Met	Val	Asn	Phe	Ser	Ile	Ile	Tyr	Gly	Val
				725					730					735	
Thr	Pro	Tyr	Gly	Leu	Ser	Val	Arg	Leu	Gly	Val	Pro	Val	Lys	Glu	Ala
			740					745					750		
Glu	Lys	Met	Ile	Val	Asn	Tyr	Phe	Val	Leu	Tyr	Pro	Lys	Val	Arg	Asp
		755					760					765			
Tyr	Ile	Gln	Arg	Val	Val	Ser	Glu	Ala	Lys	Glu	Lys	Gly	Tyr	Val	Arg
	770					775					780				
Thr	Leu	Phe	Gly	Arg	Lys	Arg	Asp	Ile	Pro	Gln	Leu	Met	Ala	Arg	Asp
785					790					795					800
Arg	Asn	Thr	Gln	Ala	Glu	Gly	Glu	Arg	Ile	Ala	Ile	Asn	Thr	Pro	Ile
				805					810					815	

Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Glu Ile Asp  
 Arg Glu Leu Lys Glu Arg Lys Met Arg Ser Lys Met Ile Ile Gln Val  
 His Asp Glu Leu Val Phe Glu Val Pro Asn Glu Glu Lys Asp Ala Leu  
 Val Glu Leu Val Lys Asp Arg Met Thr Asn Val Val Lys Leu Ser Val  
 Pro Leu Glu Val Asp Val Thr Ile Gly Lys Thr Trp Ser

<210> 31  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetic error-prone (mutagenic) PCR  
 amplification forward primer

<400> 31  
 ctacctcctg gacccctcca a 21

<210> 32  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetic error-prone (mutagenic) PCR  
 amplification reverse primer

<400> 32  
 ataaccaact ggtagtggcg tgtaa 25

<210> 33  
 <211> 1491  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetic amplicon encoding polymerase domain of Z05  
 D580G DNA polymerase amplified by error-prone (mutagenic)  
 PCR between B1pI and BglII restriction sites

<400> 33  
 ctacctcctg gacccctcca acaccacccc cgaggggggtg gcccggcgct acggggggga 60  
 gtggacggag gacgccgccc accgggccct cctcgtctgag cggctccagc aaaacctctt 120  
 ggaacgcctc aaggagagag aaaagctcct ttggctctac caagaggtgg aaaagcccct 180  
 ctcccgggtc ctggcccaca tggaggccac cggggttaagg ctggacgtgg cctatctaaa 240  
 ggccctttcc ctggagcttg cggaggagat tgcgcgcctc gaggaggagg tcttccgcct 300  
 ggcggggcac ccttcaacc tgaactccc tgaccagcta gagcgggtgc tctttgacga 360  
 gcttaggctt cccgccctgg gcaagacgca aaagacgggg aagcgctcca ccagcgccgc 420  
 ggtgctggag gccctcaggg aggccacccc catcgtggag aagatcctcc agcaccggga 480  
 gctcaccaag ctcaagaaca cctacgtaga cccctccc ggcctcgtcc acccgaggac 540  
 gggccgcctc cacaccgct tcaaccagac agccacggcc acgggaaggc tctctagctc 600  
 cgggcccac ctgcagaata tccccatccg caccctttg ggccagagga tccgccgggc 660  
 ctccgtggcc gaggcgggat gggcggttggg ggcctggac tatagccaga tagagctccg 720  
 ggtcctcgcc cacctctccg gggacgagaa cctgatcagg gtcttccagg aggggaagga 780  
 catccacacc cagaccgcaa gctggatgtt cggcgtctcc ccggaggccg tggaccccct 840  
 gatgcgcccg gcggccaaga cggtgaaact cggcgtcctc tacggcatgt ccgccatag 900  
 gctctccca gacttgcca tcccctacga ggaggcggtg gcctttatag agcgctactt 960  
 ccaagcttc ccaaggtgc gggcctggat agaaaagacc ctggaggagg ggaggaagcg 1020  
 gggctacgtg gaaacctct tcggaagaag gcgctacgtg cccgacctca acgcccgggt 1080  
 gaagagcgtc agggaggccg cggagcgcac gcccttcaac atgcccgtcc agggcaccgc 1140  
 cgccgacctc atgaagctcg ccatggtgaa gctcttcccc cacctccggg agatgggggc 1200  
 ccgcatgctc ctccaggctc acgacgagct cctcctggag gcccccaag cgcgggccga 1260

24

```

ggaggtggcg gctttggcca aggaggccat ggagaaggcc tatcccctcg ccgtgcccct 1320
ggaggtggag gtggggatcg gggaggactg gctttccgcc aagggtgat atcagatctc 1380
cctgattatg cgtcagtcta tgaagaaaaa tcgtatacag atggacgaag agagaatcct 1440
tgtgaattta acagagggtg tagggattac acgccactac cagttgggta t 1491

```

<210> 34  
 <211> 110  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetic wild-type BRAF V600K target polynucleotide

```

<400> 34
agtaaaaata ggtgattttg gtctagctac agtgaaatct cgatggagtg ggtcccatca 60
gtttgaacag ttgtctggat ccattttgtg gatggtaaga attgaggcta 110

```

<210> 35  
 <211> 110  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetic mutant BRAF V600R target polynucleotide

```

<400> 35
agtaaaaata ggtgattttg gtctagctac aaggaaatct cgatggagtg ggtcccatca 60
gtttgaacag ttgtctggat ccattttgtg gatggtaaga attgaggcta 110

```

<210> 36  
 <211> 921  
 <212> PRT  
 <213> Deinococcus radiodurans

<220>  
 <223> Deinococcus radiodurans DNA polymerase (Dra)

```

<400> 36
Met Ala Asp Ala Ser Pro Asp Pro Ser Lys Pro Asp Ala Leu Val Leu
1      5      10
Ile Asp Gly His Ala Leu Ala Phe Arg Ser Tyr Phe Ala Leu Pro Pro
20     25     30
Leu Asn Asn Ser Lys Gly Glu Met Thr Asp Ala Ile Val Gly Phe Met
35     40     45
Lys Leu Leu Leu Arg Leu Ala Arg Gln Lys Ser Asn Gln Val Ile Val
50     55     60
Val Phe Asp Pro Pro Val Lys Thr Leu Arg His Glu Gln Tyr Glu Gly
65     70     75     80
Tyr Lys Ser Gly Arg Ala Gln Thr Pro Glu Asp Leu Arg Gly Gln Ile
85     90     95
Asn Arg Ile Arg Ala Leu Val Asp Ala Leu Gly Phe Pro Arg Leu Glu
100    105    110
Glu Pro Gly Tyr Glu Ala Asp Asp Val Ile Ala Ser Leu Thr Arg Met
115    120    125
Ala Glu Gly Lys Gly Tyr Glu Val Arg Ile Val Thr Ser Asp Arg Asp
130    135    140
Ala Tyr Gln Leu Leu Asp Glu His Val Lys Val Ile Ala Asn Asp Phe
145    150    155    160
Ser Leu Ile Gly Pro Ala Gln Val Glu Glu Lys Tyr Gly Val Thr Val
165    170    175
Arg Gln Trp Val Asp Tyr Arg Ala Leu Thr Gly Asp Ala Ser Asp Asn
180    185    190
Ile Pro Gly Ala Lys Gly Ile Gly Pro Lys Thr Ala Ala Lys Leu Leu
195    200    205
Gln Glu Tyr Gly Thr Leu Glu Lys Val Tyr Glu Ala Ala His Ala Gly
210    215    220
Thr Leu Lys Pro Asp Gly Thr Arg Lys Lys Leu Leu Asp Ser Glu Glu

```



225	Asn	Val	Lys	Phe	Ser	His	Asp	Leu	Ser	Cys	Met	Val	Thr	Asp	Leu	Pro
					245					250						
	Leu	Asp	Ile	Glu	Phe	Gly	Val	Arg	Arg	Leu	Pro	Asp	Asn	Pro	Leu	Val
				260					265					270		
	Thr	Glu	Asp	Leu	Leu	Thr	Glu	Leu	Glu	Leu	His	Ser	Leu	Arg	Pro	Met
			275					280					285			
	Ile	Leu	Gly	Leu	Asn	Gly	Pro	Glu	Gln	Asp	Gly	His	Ala	Pro	Asp	Asp
		290					295					300				
	Leu	Leu	Glu	Arg	Glu	His	Ala	Gln	Thr	Pro	Glu	Glu	Asp	Glu	Ala	Ala
		305				310					315					320
	Ala	Leu	Pro	Ala	Phe	Ser	Ala	Pro	Glu	Leu	Ala	Glu	Trp	Gln	Thr	Pro
				325						330					335	
	Ala	Glu	Gly	Ala	Val	Trp	Gly	Tyr	Val	Leu	Ser	Arg	Glu	Asp	Asp	Leu
				340					345					350		
	Thr	Ala	Ala	Leu	Leu	Ala	Ala	Ala	Thr	Phe	Glu	Asp	Gly	Val	Ala	Arg
			355					360					365			
	Pro	Ala	Arg	Val	Ser	Glu	Pro	Asp	Glu	Trp	Ala	Gln	Ala	Glu	Ala	Pro
		370					375					380				
	Glu	Asn	Leu	Phe	Gly	Glu	Leu	Leu	Pro	Ser	Asp	Lys	Pro	Leu	Thr	Lys
		385				390					395					400
	Lys	Glu	Gln	Lys	Ala	Leu	Glu	Lys	Ala	Gln	Lys	Asp	Ala	Glu	Lys	Ala
				405					410						415	
	Arg	Ala	Lys	Leu	Arg	Glu	Gln	Phe	Pro	Ala	Thr	Val	Asp	Glu	Ala	Glu
				420					425					430		
	Phe	Val	Gly	Gln	Arg	Thr	Val	Thr	Ala	Ala	Ala	Ala	Lys	Ala	Leu	Ala
			435					440					445			
	Ala	His	Leu	Ser	Val	Arg	Gly	Thr	Val	Val	Glu	Pro	Gly	Asp	Asp	Pro
		450				455					460					
	Leu	Leu	Tyr	Ala	Tyr	Leu	Leu	Asp	Pro	Ala	Asn	Thr	Asn	Met	Pro	Val
		465				470				475						480
	Val	Ala	Lys	Arg	Tyr	Leu	Asp	Arg	Glu	Trp	Pro	Ala	Asp	Ala	Pro	Thr
				485					490						495	
	Arg	Ala	Ala	Ile	Thr	Gly	His	Leu	Val	Arg	Glu	Leu	Pro	Pro	Leu	Leu
				500					505					510		
	Asp	Asp	Ala	Arg	Arg	Lys	Met	Tyr	Asp	Glu	Met	Glu	Lys	Pro	Leu	Ser
			515					520					525			
	Gly	Val	Leu	Gly	Arg	Met	Glu	Val	Arg	Gly	Val	Gln	Val	Asp	Ser	Asp
		530					535					540				
	Phe	Leu	Gln	Thr	Leu	Ser	Ile	Gln	Ala	Gly	Val	Arg	Leu	Ala	Asp	Leu
		545				550				555						560
	Glu	Ser	Gln	Ile	His	Glu	Tyr	Ala	Gly	Glu	Phe	His	Ile	Arg	Ser	
				565					570					575		
	Pro	Lys	Gln	Leu	Glu	Thr	Val	Leu	Tyr	Asp	Lys	Leu	Glu	Leu	Ala	Ser
				580					585					590		
	Ser	Lys	Lys	Thr	Lys	Leu	Thr	Gly	Gln	Arg	Ser	Thr	Ala	Val	Ser	Ala
			595					600					605			
	Leu	Glu	Pro	Leu	Arg	Asp	Ala	His	Pro	Ile	Ile	Pro	Leu	Val	Leu	Glu
		610					615					620				
	Phe	Arg	Glu	Leu	Asp	Lys	Leu	Arg	Gly	Thr	Tyr	Leu	Asp	Pro	Ile	Pro
		625				630				635						640
	Asn	Leu	Val	Asn	Pro	His	Thr	Gly	Arg	Leu	His	Thr	Thr	Phe	Ala	Gln
				645					650					655		
	Thr	Ala	Val	Ala	Thr	Gly	Arg	Leu	Ser	Leu	Asn	Pro	Asn	Leu	Gln	
			660						665				670			
	Asn	Ile	Pro	Ile	Arg	Ser	Glu	Leu	Gly	Arg	Glu	Ile	Arg	Lys	Gly	Phe
			675					680					685			
	Ile	Ala	Glu	Asp	Gly	Phe	Thr	Leu	Ile	Ala	Ala	Asp	Tyr	Ser	Gln	Ile
		690					695					700				
	Glu	Leu	Arg	Leu	Leu	Ala	His	Ile	Ala	Asp	Asp	Pro	Leu	Met	Gln	Gln
		705				710				715						720
	Ala	Phe	Val	Glu	Gly	Ala	Asp	Ile	His	Arg	Arg	Thr	Ala	Ala	Gln	Val
				725						730					735	
	Leu	Gly	Leu	Asp	Glu	Ala	Thr	Val	Asp	Ala	Asn	Gln	Arg	Arg	Ala	Ala
			740						745					750		
	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu
			755					760					765			
	Ser	Asn	Asp	Leu	Gly	Ile	Pro	Tyr	Ala	Glu	Ala	Ala	Thr	Phe	Ile	Glu

26

770	Ile	Tyr	Phe	Ala	Thr	Tyr	Pro	Gly	Ile	Arg	Arg	Tyr	Ile	Asn	His	Thr
785	Leu	Asp	Phe	Gly	Arg	Thr	His	Gly	Tyr	Val	Glu	Thr	Leu	Tyr	Gly	Arg
	Arg	Arg	Tyr	Val	Pro	Gly	Leu	Ser	Ser	Arg	Asn	Arg	Val	Gln	Arg	Glu
	Ala	Glu	Glu	Arg	Leu	Ala	Tyr	Asn	Met	Pro	Ile	Gln	Gly	Thr	Ala	Ala
	Asp	Ile	Met	Lys	Leu	Ala	Met	Val	Gln	Leu	Asp	Pro	Gln	Leu	Asp	Ala
	Ile	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His	Asp	Glu	Leu	Leu	Ile	Glu
	Ala	Pro	Leu	Asp	Lys	Ala	Glu	Gln	Val	Ala	Ala	Leu	Thr	Lys	Lys	Val
	Met	Glu	Asn	Val	Val	Gln	Leu	Lys	Val	Pro	Leu	Ala	Val	Glu	Val	Gly
	Thr	Gly	Pro	Asn	Trp	Phe	Asp	Thr	Lys							

<210> 37

<211> 892

<212> PRT

<213> Thermosipho africanus

<220>

<223> Thermosipho africanus DNA polymerase (Taf)

<400> 37

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

27

Asp	Lys	Leu	Lys	Lys	Leu	Ala	Glu	Glu	Ile	Glu	Lys	Tyr	Lys	Thr	Phe
305					310					315					320
Ser	Ile	Asp	Thr	Glu	Thr	Thr	Ser	Leu	Asp	Pro	Phe	Glu	Ala	Lys	Leu
				325					330					335	
Val	Gly	Ile	Ser	Ile	Ser	Thr	Met	Glu	Gly	Lys	Ala	Tyr	Tyr	Ile	Pro
			340					345					350		
Val	Ser	His	Phe	Gly	Ala	Lys	Asn	Ile	Ser	Lys	Ser	Leu	Ile	Asp	Lys
		355					360					365			
Phe	Leu	Lys	Gln	Ile	Leu	Gln	Glu	Lys	Asp	Tyr	Asn	Ile	Val	Gly	Gln
	370					375					380				
Asn	Leu	Lys	Phe	Asp	Tyr	Glu	Ile	Phe	Lys	Ser	Met	Gly	Phe	Ser	Pro
385					390					395					400
Asn	Val	Pro	His	Phe	Asp	Thr	Met	Ile	Ala	Ala	Tyr	Leu	Leu	Asn	Pro
				405					410					415	
Asp	Glu	Lys	Arg	Phe	Asn	Leu	Glu	Glu	Leu	Ser	Leu	Lys	Tyr	Leu	Gly
			420					425					430		
Tyr	Lys	Met	Ile	Ser	Phe	Asp	Glu	Leu	Val	Asn	Glu	Asn	Val	Pro	Leu
		435					440					445			
Phe	Gly	Asn	Asp	Phe	Ser	Tyr	Val	Pro	Leu	Glu	Arg	Ala	Val	Glu	Tyr
	450					455					460				
Ser	Cys	Glu	Asp	Ala	Asp	Val	Thr	Tyr	Arg	Ile	Phe	Arg	Lys	Leu	Gly
465					470					475					480
Arg	Lys	Ile	Tyr	Glu	Asn	Glu	Met	Glu	Lys	Leu	Phe	Tyr	Glu	Ile	Glu
				485					490					495	
Met	Pro	Leu	Ile	Asp	Val	Leu	Ser	Glu	Met	Glu	Leu	Asn	Gly	Val	Tyr
			500					505					510		
Phe	Asp	Glu	Glu	Tyr	Leu	Lys	Glu	Leu	Ser	Lys	Lys	Tyr	Gln	Glu	Lys
		515					520					525			
Met	Asp	Gly	Ile	Lys	Glu	Lys	Val	Phe	Glu	Ile	Ala	Gly	Glu	Thr	Phe
	530					535					540				
Asn	Leu	Asn	Ser	Ser	Thr	Gln	Val	Ala	Tyr	Ile	Leu	Phe	Glu	Lys	Leu
545					550					555					560
Asn	Ile	Ala	Pro	Tyr	Lys	Lys	Thr	Ala	Thr	Gly	Lys	Phe	Ser	Thr	Asn
				565					570					575	
Ala	Glu	Val	Leu	Glu	Glu	Leu	Ser	Lys	Glu	His	Glu	Ile	Ala	Lys	Leu
			580					585					590		
Leu	Leu	Glu	Tyr	Arg	Lys	Tyr	Gln	Lys	Leu	Lys	Ser	Thr	Tyr	Ile	Asp
		595					600					605			
Ser	Ile	Pro	Leu	Ser	Ile	Asn	Arg	Lys	Thr	Asn	Arg	Val	His	Thr	Thr
	610					615					620				
Phe	His	Gln	Thr	Gly	Thr	Ser	Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asn	Pro
625					630					635					640
Asn	Leu	Gln	Asn	Leu	Pro	Thr	Arg	Ser	Glu	Glu	Gly	Lys	Glu	Ile	Arg
				645					650					655	
Lys	Ala	Val	Arg	Pro	Gln	Arg	Gln	Asp	Trp	Trp	Ile	Leu	Gly	Ala	Asp
			660					665					670		
Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Val	Ser	Lys	Asp	Glu
		675					680					685			
Asn	Leu	Leu	Lys	Ala	Phe	Lys	Glu	Asp	Leu	Asp	Ile	His	Thr	Ile	Thr
	690					695				700					
Ala	Ala	Lys	Ile	Phe	Gly	Val	Ser	Glu	Met	Phe	Val	Ser	Glu	Gln	Met
705					710					715					720
Arg	Arg	Val	Gly	Lys	Met	Val	Asn	Phe	Ala	Ile	Ile	Tyr	Gly	Val	Ser
				725					730					735	
Pro	Tyr	Gly	Leu	Ser	Lys	Arg	Ile	Gly	Leu	Ser	Val	Ser	Glu	Thr	Lys
			740					745					750		
Lys	Ile	Ile	Asp	Asn	Tyr	Phe	Arg	Tyr	Tyr	Lys	Gly	Val	Phe	Glu	Tyr
		755					760					765			
Leu	Lys	Arg	Met	Lys	Asp	Glu	Ala	Arg	Lys	Lys	Gly	Tyr	Val	Thr	Thr
	770					775					780				
Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Ile	Pro	Gln	Leu	Arg	Ser	Lys	Asn	Gly
785					790					795					800
Asn	Arg	Val	Gln	Glu	Gly	Glu	Arg	Ile	Ala	Val	Asn	Thr	Pro	Ile	Gln
				805					810					815	
Gly	Thr	Ala	Ala	Asp	Ile	Ile	Lys	Ile	Ala	Met	Ile	Asn	Ile	His	Asn
			820					825					830		
Arg	Leu	Lys	Lys	Glu	Asn	Leu	Arg	Ser	Lys	Met	Ile	Leu	Gln	Val	His
		835					840					845			

Asp	Glu	Leu	Val	Phe	Glu	Val	Pro	Asp	Asn	28 Glu	Leu	Glu	Ile	Val	Lys
850						855				860					
Asp	Leu	Val	Arg	Asp	Glu	Met	Glu	Asn	Ala	Val	Lys	Leu	Asp	Val	Pro
865					870					875					880
Leu	Lys	Val	Asp	Val	Tyr	Tyr	Gly	Lys	Glu	Trp	Glu				
				885					890						

<210> 38  
 <211> 893  
 <212> PRT  
 <213> Thermotoga maritima

<220>  
 <223> Thermotoga maritima DNA polymerase (Tma)

<400>	38														
Met	Ala	Arg	Leu	Phe	Leu	Phe	Asp	Gly	Thr	Ala	Leu	Ala	Tyr	Arg	Ala
1				5					10					15	
Tyr	Tyr	Ala	Leu	Asp	Arg	Ser	Leu	Ser	Thr	Ser	Thr	Gly	Ile	Pro	Thr
			20					25					30		
Asn	Ala	Thr	Tyr	Gly	Val	Ala	Arg	Met	Leu	Val	Arg	Phe	Ile	Lys	Asp
		35					40					45			
His	Ile	Ile	Val	Gly	Lys	Asp	Tyr	Val	Ala	Val	Ala	Phe	Asp	Lys	Lys
	50					55					60				
Ala	Ala	Thr	Phe	Arg	His	Lys	Leu	Leu	Glu	Thr	Tyr	Lys	Ala	Gln	Arg
65					70					75					80
Pro	Lys	Thr	Pro	Asp	Leu	Leu	Ile	Gln	Gln	Leu	Pro	Tyr	Ile	Lys	Lys
				85					90					95	
Leu	Val	Glu	Ala	Leu	Gly	Met	Lys	Val	Leu	Glu	Val	Glu	Gly	Tyr	Glu
			100					105					110		
Ala	Asp	Asp	Ile	Ile	Ala	Thr	Leu	Ala	Val	Lys	Gly	Leu	Pro	Leu	Phe
		115					120					125			
Asp	Glu	Ile	Phe	Ile	Val	Thr	Gly	Asp	Lys	Asp	Met	Leu	Gln	Leu	Val
	130					135					140				
Asn	Glu	Lys	Ile	Lys	Val	Trp	Arg	Ile	Val	Lys	Gly	Ile	Ser	Asp	Leu
145					150					155					160
Glu	Leu	Tyr	Asp	Ala	Gln	Lys	Val	Lys	Glu	Lys	Tyr	Gly	Val	Glu	Pro
				165					170					175	
Gln	Gln	Ile	Pro	Asp	Leu	Leu	Ala	Leu	Thr	Gly	Asp	Glu	Ile	Asp	Asn
			180					185					190		
Ile	Pro	Gly	Val	Thr	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Val	Gln	Leu	Leu
		195					200					205			
Glu	Lys	Tyr	Lys	Asp	Leu	Glu	Asp	Ile	Leu	Asn	His	Val	Arg	Glu	Leu
	210					215					220				
Pro	Gln	Lys	Val	Arg	Lys	Ala	Leu	Leu	Arg	Asp	Arg	Glu	Asn	Ala	Ile
225					230					235					240
Leu	Ser	Lys	Lys	Leu	Ala	Ile	Leu	Glu	Thr	Asn	Val	Pro	Ile	Glu	Ile
				245					250					255	
Asn	Trp	Glu	Glu	Leu	Arg	Tyr	Gln	Gly	Tyr	Asp	Arg	Glu	Lys	Leu	Leu
		260						265					270		
Pro	Leu	Leu	Lys	Glu	Leu	Glu	Phe	Ala	Ser	Ile	Met	Lys	Glu	Leu	Gln
		275					280					285			
Leu	Tyr	Glu	Glu	Ser	Glu	Pro	Val	Gly	Tyr	Arg	Ile	Val	Lys	Asp	Leu
	290					295					300				
Val	Glu	Phe	Glu	Lys	Leu	Ile	Glu	Lys	Leu	Arg	Glu	Ser	Pro	Ser	Phe
305					310					315					320
Ala	Ile	Asp	Leu	Glu	Thr	Ser	Ser	Leu	Asp	Pro	Phe	Asp	Cys	Asp	Ile
				325					330					335	
Val	Gly	Ile	Ser	Val	Ser	Phe	Lys	Pro	Lys	Glu	Ala	Tyr	Tyr	Ile	Pro
			340					345					350		
Leu	His	His	Arg	Asn	Ala	Gln	Asn	Leu	Asp	Glu	Lys	Glu	Val	Leu	Lys
	355						360					365			
Lys	Leu	Lys	Glu	Ile	Leu	Glu	Asp	Pro	Gly	Ala	Lys	Ile	Val	Gly	Gln
	370					375					380				
Asn	Leu	Lys	Phe	Asp	Tyr	Lys	Val	Leu	Met	Val	Lys	Gly	Val	Glu	Pro
385					390					395					400
Val	Pro	Pro	Tyr	Phe	Asp	Thr	Met	Ile	Ala	Ala	Tyr	Leu	Leu	Glu	Pro

29

Asn	Glu	Lys	Lys	405 Phe	Asn	Leu	Asp	410 Asp	Leu	Ala	Leu	Lys	415 Phe	Leu	Gly
Tyr	Lys	Met	420 Thr	Ser	Tyr	Gln	Glu	425 Leu	Met	Ser	Phe	Ser	430 Phe	Pro	Leu
Phe	Gly	Phe	435 Ser	Phe	Ala	Asp	Val	440 Pro	Val	Glu	Lys	445 Ala	Ala	Asn	Tyr
Ser	Cys	Glu	450 Asp	Ala	Asp	Ile	Thr	455 Tyr	Arg	Leu	Tyr	460 Lys	Thr	Leu	Ser
465 Leu	Lys	Leu	His	470 Glu	Ala	Asp	Leu	475 Glu	Asn	Val	Phe	480 Tyr	Lys	Ile	Glu
Met	Pro	Leu	Val	485 Asn	Val	Leu	Ala	490 Arg	Met	Glu	Leu	495 Asn	Gly	Val	Tyr
Val	Asp	Thr	500 Glu	Phe	Leu	Lys	Lys	505 Leu	Ser	Glu	Glu	510 Tyr	Gly	Lys	Lys
Leu	Glu	Glu	515 Leu	Ala	Glu	Glu	Ile	520 Tyr	Arg	Ile	Ala	525 Gly	Glu	Pro	Phe
Asn	Ile	Asn	530 Ser	Pro	Lys	Gln	Val	535 Ser	Arg	Ile	Leu	540 Phe	Glu	Lys	Leu
545 Gly	Ile	Lys	550 Pro	Arg	Gly	Lys	Thr	555 Thr	Lys	Thr	Gly	560 Asp	Tyr	Ser	Thr
Arg	Ile	Glu	565 Val	Leu	Glu	Glu	Leu	570 Ala	Gly	Glu	His	575 Glu	Ile	Ile	Pro
Leu	Ile	Leu	580 Glu	Tyr	Arg	Lys	Ile	585 Gln	Lys	Leu	Lys	590 Ser	Thr	Tyr	Ile
Asp	Ala	Leu	595 Pro	Lys	Met	Val	Asn	600 Pro	Lys	Thr	Gly	605 Arg	Ile	His	Ala
610 Ser	Phe	Asn	615 Gln	Thr	Gly	Thr	Ala	620 Thr	Gly	Arg	Leu	625 Ser	Ser	Ser	Asp
625 Pro	Asn	Leu	630 Gln	Asn	Leu	Pro	Thr	635 Lys	Ser	Glu	Glu	640 Gly	Lys	Glu	Ile
Arg	Lys	Ala	645 Ile	Val	Pro	Gln	Asp	650 Pro	Asn	Trp	Trp	655 Ile	Val	Ser	Ala
Asp	Tyr	Ser	660 Gln	Ile	Glu	Leu	Arg	665 Ile	Leu	Ala	His	670 Leu	Ser	Gly	Asp
Glu	Asn	Leu	675 Leu	Arg	Ala	Phe	Glu	680 Glu	Gly	Ile	Asp	685 Val	His	Thr	Leu
Thr	Ala	Ser	690 Arg	Ile	Phe	Asn	Val	700 Lys	Pro	Glu	Glu	705 Val	Thr	Glu	Glu
705 Met	Arg	Arg	710 Ala	Gly	Lys	Met	Val	715 Asn	Phe	Ser	Ile	720 Ile	Tyr	Gly	Val
Thr	Pro	Tyr	725 Gly	Leu	Ser	Val	Arg	730 Leu	Gly	Val	Pro	735 Val	Lys	Glu	Ala
Glu	Lys	Met	740 Ile	Val	Asn	Tyr	Phe	745 Val	Leu	Tyr	Pro	750 Lys	Val	Arg	Asp
Tyr	Ile	Gln	755 Arg	Val	Val	Ser	Glu	760 Ala	Lys	Glu	Lys	765 Gly	Tyr	Val	Arg
Thr	Leu	Phe	770 Gly	Arg	Lys	Arg	Asp	775 Ile	Pro	Gln	Leu	780 Met	Ala	Arg	Asp
785 Arg	Asn	Thr	790 Gln	Ala	Glu	Gly	Glu	795 Arg	Ile	Ala	Ile	800 Asn	Thr	Pro	Ile
Gln	Gly	Thr	805 Ala	Ala	Asp	Ile	Ile	810 Lys	Leu	Ala	Met	815 Ile	Glu	Ile	Asp
Arg	Glu	Leu	820 Lys	Glu	Arg	Lys	Met	825 Arg	Ser	Lys	Met	830 Ile	Ile	Gln	Val
His	Asp	Glu	835 Leu	Val	Phe	Glu	Val	840 Pro	Asn	Glu	Glu	845 Lys	Asp	Ala	Leu
Val	Glu	Leu	850 Val	Lys	Asp	Arg	Met	855 Thr	Asn	Val	Val	860 Lys	Leu	Ser	Val
865 Pro	Leu	Glu	870 Val	Asp	Val	Thr	Ile	875 Gly	Lys	Thr	Trp	880 Ser			
			885					890							

<210> 39  
 <211> 893  
 <212> PRT  
 <213> Thermotoga neopolitana

&lt;220&gt;

&lt;223&gt; Thermotoga neopolitana DNA polymerase (Tne)

&lt;400&gt; 39

Met	Ala	Arg	Leu	Phe	Leu	Phe	Asp	Gly	Thr	Ala	Leu	Ala	Tyr	Arg	Ala
1				5					10					15	
Tyr	Tyr	Ala	Leu	Asp	Arg	Ser	Leu	Ser	Thr	Ser	Thr	Gly	Ile	Pro	Thr
			20					25					30		
Asn	Ala	Val	Tyr	Gly	Val	Ala	Arg	Met	Leu	Val	Lys	Phe	Ile	Lys	Glu
		35					40					45			
His	Ile	Ile	Pro	Glu	Lys	Asp	Tyr	Ala	Ala	Val	Ala	Phe	Asp	Lys	Lys
	50					55					60				
Ala	Ala	Thr	Phe	Arg	His	Lys	Leu	Leu	Val	Ser	Asp	Lys	Ala	Gln	Arg
65					70					75					80
Pro	Lys	Thr	Pro	Ala	Leu	Leu	Val	Gln	Gln	Leu	Pro	Tyr	Ile	Lys	Arg
				85				90						95	
Leu	Ile	Glu	Ala	Leu	Gly	Phe	Lys	Val	Leu	Glu	Leu	Glu	Gly	Tyr	Glu
			100					105					110		
Ala	Asp	Asp	Ile	Ile	Ala	Thr	Leu	Ala	Val	Arg	Ala	Ala	Arg	Phe	Leu
		115					120					125			
Met	Arg	Phe	Ser	Leu	Ile	Thr	Gly	Asp	Lys	Asp	Met	Leu	Gln	Leu	Val
	130					135					140				
Asn	Glu	Lys	Ile	Lys	Val	Trp	Arg	Ile	Val	Lys	Gly	Ile	Ser	Asp	Leu
145					150					155					160
Glu	Leu	Tyr	Asp	Ser	Lys	Lys	Val	Lys	Glu	Arg	Tyr	Gly	Val	Glu	Pro
				165					170					175	
His	Gln	Ile	Pro	Asp	Leu	Leu	Ala	Leu	Thr	Gly	Asp	Asp	Ile	Asp	Asn
			180					185					190		
Ile	Pro	Gly	Val	Thr	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Val	Gln	Leu	Leu
		195					200					205			
Gly	Lys	Tyr	Arg	Asn	Leu	Glu	Tyr	Ile	Leu	Glu	His	Ala	Arg	Glu	Leu
	210					215					220				
Pro	Gln	Arg	Val	Arg	Lys	Ala	Leu	Leu	Arg	Asp	Arg	Glu	Val	Ala	Ile
225					230					235					240
Leu	Ser	Lys	Lys	Leu	Ala	Thr	Leu	Val	Thr	Asn	Ala	Pro	Val	Glu	Val
				245					250					255	
Asp	Trp	Glu	Glu	Met	Lys	Tyr	Arg	Gly	Tyr	Asp	Lys	Arg	Lys	Leu	Leu
			260					265					270		
Pro	Ile	Leu	Lys	Glu	Leu	Glu	Phe	Ala	Ser	Ile	Met	Lys	Glu	Leu	Gln
		275					280					285			
Leu	Tyr	Glu	Glu	Ala	Glu	Pro	Thr	Gly	Tyr	Glu	Ile	Val	Lys	Asp	His
	290					295					300				
Lys	Thr	Phe	Glu	Asp	Leu	Ile	Glu	Lys	Leu	Lys	Glu	Val	Pro	Ser	Phe
305					310					315					320
Ala	Leu	Asp	Leu	Glu	Thr	Ser	Ser	Leu	Asp	Pro	Phe	Asn	Cys	Glu	Ile
				325					330					335	
Val	Gly	Ile	Ser	Val	Ser	Phe	Lys	Pro	Lys	Thr	Ala	Tyr	Tyr	Ile	Pro
			340					345					350		
Leu	His	His	Arg	Asn	Ala	His	Asn	Leu	Asp	Glu	Thr	Leu	Val	Leu	Ser
		355					360					365			
Lys	Leu	Lys	Glu	Ile	Leu	Glu	Asp	Pro	Ser	Ser	Lys	Ile	Val	Gly	Gln
	370					375					380				
Asn	Leu	Lys	Tyr	Asp	Tyr	Lys	Val	Leu	Met	Val	Lys	Gly	Ile	Ser	Pro
385					390					395					400
Val	Tyr	Pro	His	Phe	Asp	Thr	Met	Ile	Ala	Ala	Tyr	Leu	Leu	Glu	Pro
				405					410					415	
Asn	Glu	Lys	Lys	Phe	Asn	Leu	Glu	Asp	Leu	Ser	Leu	Lys	Phe	Leu	Gly
			420					425					430		
Tyr	Lys	Met	Thr	Ser	Tyr	Gln	Glu	Leu	Met	Ser	Phe	Ser	Ser	Pro	Leu
		435					440					445			
Phe	Gly	Phe	Ser	Phe	Ala	Asp	Val	Pro	Val	Asp	Lys	Ala	Ala	Glu	Tyr
	450					455					460				
Ser	Cys	Glu	Asp	Ala	Asp	Ile	Thr	Tyr	Arg	Leu	Tyr	Lys	Ile	Leu	Ser
465					470					475					480
Met	Lys	Leu	His	Glu	Ala	Glu	Leu	Glu	Asn	Val	Phe	Tyr	Arg	Ile	Glu
				485					490					495	
Met	Pro	Leu	Val	Asn	Val	Leu	Ala	Arg	Met	Glu	Phe	Asn	Trp	Val	Tyr
			500					505					510		

31

Val	Asp	Thr	Glu	Phe	Leu	Lys	Lys	Leu	Ser	Glu	Glu	Tyr	Gly	Lys	Lys
		515					520					525			
Leu	Glu	Glu	Leu	Ala	Glu	Lys	Ile	Tyr	Gln	Ile	Ala	Gly	Glu	Pro	Phe
		530				535					540				
Asn	Ile	Asn	Ser	Pro	Lys	Gln	Val	Ser	Asn	Ile	Leu	Phe	Glu	Lys	Leu
545					550					555					560
Gly	Ile	Lys	Pro	Arg	Gly	Lys	Thr	Thr	Lys	Thr	Gly	Asp	Tyr	Ser	Thr
				565					570					575	
Arg	Ile	Glu	Val	Leu	Glu	Glu	Ile	Ala	Asn	Glu	His	Glu	Ile	Val	Pro
			580					585						590	
Leu	Ile	Leu	Glu	Phe	Arg	Lys	Ile	Leu	Lys	Leu	Lys	Ser	Thr	Tyr	Ile
		595					600					605			
Asp	Thr	Leu	Pro	Lys	Leu	Val	Asn	Pro	Lys	Thr	Gly	Arg	Phe	His	Ala
	610					615					620				
Ser	Phe	His	Gln	Thr	Gly	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp
625					630					635					640
Pro	Asn	Leu	Gln	Asn	Leu	Pro	Thr	Lys	Ser	Glu	Glu	Gly	Lys	Glu	Ile
				645					650					655	
Arg	Lys	Ala	Ile	Val	Pro	Gln	Asp	Pro	Asp	Trp	Trp	Ile	Val	Ser	Ala
			660					665					670		
Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Ile	Leu	Ala	His	Leu	Ser	Gly	Asp
		675					680					685			
Glu	Asn	Leu	Val	Lys	Ala	Phe	Glu	Glu	Gly	Ile	Asp	Val	His	Thr	Leu
	690					695					700				
Thr	Ala	Ser	Arg	Ile	Tyr	Asn	Val	Lys	Pro	Glu	Glu	Val	Asn	Glu	Glu
705					710					715					720
Met	Arg	Arg	Val	Gly	Lys	Met	Val	Asn	Phe	Ser	Ile	Ile	Tyr	Gly	Val
				725					730					735	
Thr	Pro	Tyr	Gly	Leu	Ser	Val	Arg	Leu	Gly	Ile	Pro	Val	Lys	Glu	Ala
			740					745					750		
Glu	Lys	Met	Ile	Ile	Ser	Tyr	Phe	Thr	Leu	Tyr	Pro	Lys	Val	Arg	Ser
		755					760					765			
Tyr	Ile	Gln	Gln	Val	Val	Ala	Glu	Ala	Lys	Glu	Lys	Gly	Tyr	Val	Arg
	770					775					780				
Thr	Leu	Phe	Gly	Arg	Lys	Arg	Asp	Ile	Pro	Gln	Leu	Met	Ala	Arg	Asp
785					790					795					800
Lys	Asn	Thr	Gln	Ser	Glu	Gly	Glu	Arg	Ile	Ala	Ile	Asn	Thr	Pro	Ile
				805					810					815	
Gln	Gly	Thr	Ala	Ala	Asp	Ile	Ile	Lys	Leu	Ala	Met	Ile	Asp	Ile	Asp
			820					825					830		
Glu	Glu	Leu	Arg	Lys	Arg	Asn	Met	Lys	Ser	Arg	Met	Ile	Ile	Gln	Val
		835					840					845			
His	Asp	Glu	Leu	Val	Phe	Glu	Val	Pro	Asp	Glu	Glu	Lys	Glu	Glu	Leu
	850					855					860				
Val	Asp	Leu	Val	Lys	Asn	Lys	Met	Thr	Asn	Val	Val	Lys	Leu	Ser	Val
865					870					875					880
Pro	Leu	Glu	Val	Asp	Ile	Ser	Ile	Gly	Lys	Ser	Trp	Ser			
				885					890						

<210> 40

<211> 876

<212> PRT

<213> Bacillus stearothermophilus

<220>

<223> Bacillus stearothermophilus DNA polymerase (Bst)

<400> 40

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

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



```
<210> 41
<211> 877
<212> PRT
<213> Bacillus caldotenax
```

<220>  
<223> Bacillus caldotenax DNA polymerase (Bca)

<400> 41

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

Val	Pro	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Val	Lys	Leu	Leu	Arg	Gln	Phe
		195					200				205				
Gly	Thr	Val	Glu	Asn	Val	Leu	Ala	Ser	Ile	Asp	Glu	Ile	Lys	Gly	Glu
	210					215					220				
Lys	Leu	Lys	Glu	Thr	Leu	Arg	Gln	His	Arg	Glu	Met	Ala	Leu	Leu	Ser
225					230					235					240
Lys	Lys	Leu	Ala	Ala	Ile	Arg	Arg	Asp	Ala	Pro	Val	Glu	Leu	Ser	Leu
				245					250					255	
Asp	Asp	Ile	Ala	Tyr	Gln	Gly	Glu	Asp	Arg	Glu	Lys	Val	Val	Ala	Leu
			260					265					270		
Phe	Lys	Glu	Leu	Gly	Phe	Gln	Ser	Phe	Leu	Glu	Lys	Met	Glu	Ser	Pro
		275					280					285			
Ser	Ser	Glu	Glu	Glu	Lys	Pro	Leu	Ala	Lys	Met	Ala	Phe	Thr	Leu	Ala
	290					295					300				
Asp	Arg	Val	Thr	Glu	Glu	Met	Leu	Ala	Asp	Lys	Ala	Ala	Leu	Val	Val
305					310					315					320
Glu	Val	Val	Glu	Glu	Asn	Tyr	His	Asp	Ala	Pro	Ile	Val	Gly	Ile	Ala
				325					330					335	
Val	Val	Asn	Glu	His	Gly	Arg	Phe	Phe	Leu	Arg	Pro	Glu	Thr	Ala	Leu
			340					345					350		
Ala	Asp	Pro	Gln	Phe	Val	Ala	Trp	Leu	Gly	Asp	Glu	Thr	Lys	Lys	Lys
		355					360					365			
Ser	Met	Phe	Asp	Ser	Lys	Arg	Ala	Ala	Val	Ala	Leu	Lys	Trp	Lys	Gly
	370					375					380				
Ile	Glu	Leu	Cys	Gly	Val	Ser	Phe	Asp	Leu	Leu	Ala	Ala	Tyr	Leu	
385					390					395				400	
Leu	Asp	Pro	Ala	Gln	Gly	Val	Asp	Asp	Val	Ala	Ala	Ala	Ala	Lys	Met
				405					410					415	
Lys	Gln	Tyr	Glu	Ala	Val	Arg	Pro	Asp	Glu	Ala	Val	Tyr	Gly	Lys	Gly
			420					425					430		
Ala	Lys	Arg	Ala	Val	Pro	Asp	Glu	Pro	Val	Leu	Ala	Glu	His	Leu	Val
		435					440					445			
Arg	Lys	Ala	Ala	Ala	Ile	Trp	Ala	Leu	Glu	Arg	Pro	Phe	Leu	Asp	Glu
		450				455					460				
Leu	Arg	Arg	Asn	Glu	Gln	Asp	Arg	Leu	Leu	Val	Glu	Leu	Glu	Gln	Pro
465					470					475					480
Leu	Ser	Ser	Ile	Leu	Ala	Glu	Met	Glu	Phe	Ala	Gly	Val	Lys	Val	Asp
			485						490					495	
Thr	Lys	Arg	Leu	Glu	Gln	Met	Gly	Glu	Glu	Leu	Ala	Glu	Gln	Leu	Arg
			500					505					510		
Thr	Val	Glu	Gln	Arg	Ile	Tyr	Glu	Leu	Ala	Gly	Gln	Glu	Phe	Asn	Ile
		515					520					525			
Asn	Ser	Pro	Lys	Gln	Leu	Gly	Val	Ile	Leu	Phe	Glu	Lys	Leu	Gln	Leu
						535					540				
Pro	Val	Leu	Lys	Lys	Ser	Lys	Thr	Gly	Tyr	Ser	Thr	Ser	Ala	Asp	Val
545					550					555					560
Leu	Glu	Lys	Leu	Ala	Pro	Tyr	His	Glu	Ile	Val	Glu	Asn	Ile	Leu	Gln
				565					570					575	
His	Tyr	Arg	Gln	Leu	Gly	Lys	Leu	Gln	Ser	Thr	Tyr	Ile	Glu	Gly	Leu
			580					585					590		
Leu	Lys	Val	Val	Arg	Pro	Asp	Thr	Lys	Lys	Val	His	Thr	Ile	Phe	Asn
		595					600					605			
Gln	Ala	Leu	Thr	Gln	Thr	Gly	Arg	Leu	Ser	Ser	Thr	Glu	Pro	Asn	Leu
						615					620				
Gln	Asn	Ile	Pro	Ile	Arg	Leu	Glu	Glu	Gly	Arg	Lys	Ile	Arg	Gln	Ala
625					630					635					640
Phe	Val	Pro	Ser	Glu	Ser	Asp	Trp	Leu	Ile	Phe	Ala	Ala	Asp	Tyr	Ser
				645					650					655	
Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Ile	Ala	Glu	Asp	Asp	Asn	Leu
			660					665					670		
Met	Glu	Ala	Phe	Arg	Arg	Asp	Leu	Asp	Ile	His	Thr	Lys	Thr	Ala	Met
		675					680					685			
Asp	Ile	Phe	Gln	Val	Ser	Glu	Asp	Glu	Val	Thr	Pro	Asn	Met	Arg	Arg
						695					700				
Gln	Ala	Lys	Ala	Val	Asn	Phe	Gly	Ile	Val	Tyr	Gly	Ile	Ser	Asp	Tyr
705					710					715					720
Gly	Leu	Ala	Gln	Asn	Leu	Asn	Ile	Ser	Arg	Lys	Glu	Ala	Ala	Glu	Phe
				725					730					735	

Ile Glu Arg Tyr Phe Glu Ser Phe Pro Gly Val Lys Arg Tyr Met Glu  
 Asn Ile Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu  
 His Arg Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val  
 Arg Ser Phe Ala Glu Arg Met Ala Met Asn Thr Pro Ile Gln Gly Ser  
 Ala Ala Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Asn Ala Arg Leu  
 Lys Glu Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu  
 Leu Ile Leu Glu Ala Pro Lys Glu Glu Met Glu Arg Leu Cys Arg Leu  
 Val Pro Glu Val Met Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys  
 Val Asp Tyr His Tyr Gly Ser Thr Trp Tyr Asp Ala Lys  
 865 870 875

<210> 42  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic DNA polymerase domain motif

<220>  
 <221> VARIANT  
 <222> (6)...(6)  
 <223> Xaa = Ile or Leu

<220>  
 <221> VARIANT  
 <222> (8)...(8)  
 <223> Xaa = Ile, Val or Thr

<220>  
 <221> VARIANT  
 <222> (9)...(9)  
 <223> Xaa = Gly, Ala, Leu, Met, Trp, Pro, Ser, Thr, Phe,  
 Tyr, Cys, Asn, Gln, Asp, Glu, Val, Ile or His

<220>  
 <221> VARIANT  
 <222> (10)...(10)  
 <223> Xaa = Thr, Ser or Leu

<220>  
 <221> VARIANT  
 <222> (11)...(11)  
 <223> Xaa = Pro or Glu

<220>  
 <221> VARIANT  
 <222> (12)...(12)  
 <223> Xaa = Leu or Glu

<400> 42  
 Pro Asn Leu Gln Asn Xaa Pro Xaa Xaa Xaa Xaa Xaa Gly  
 1 5 10