

1  
SEQUENCE LISTING

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

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

<130> 26744 WO-HS

<140> Not yet assigned

<141> Not yet assigned

<150> US 61/356,263

<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	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	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 aquaticus* 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 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 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

4

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

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		

7

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	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	Glu	Gly	Trp	Val	Leu	Val	Val	Leu
		595					600					605			
Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	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	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<sup>8</sup> 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 Leu Glu Ala  
275 280 285  
Pro Lys Glu Ala Glu Glu Ala Pro Trp 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 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



Leu	Asp	435	Val	Pro	Tyr	Leu	Glu	440	Ala	Leu	Ser	Gln	Glu	445	Val	Ala	Phe	Glu
450	450						455	455					460	460				
Leu	Glu	Arg	Leu	Glu	Ala	Glu	Val	His	Arg	Leu	Ala	Gly	His	Pro	Phe			
465	465				470	470				475	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	530					535					540							
Asp	Pro	Leu	Pro	Arg	Leu	Val	His	Pro	Lys	Thr	Gly	Arg	Leu	His	Thr			
545	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	610					615					620							
Asn	Leu	Ile	Arg	Val	Phe	Arg	Glu	Gly	Lys	Asp	Ile	His	Thr	Glu	Thr			
625	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	Gly	Arg	Lys	Lys	Gly	Tyr	Val	Glu	Thr				
705	705				710									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	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					

&lt;210&gt; 6

&lt;211&gt; 834

&lt;212&gt; PRT

&lt;213&gt; Thermus thermophilus

&lt;220&gt;

&lt;223&gt; Thermus thermophilus DNA polymerase (Tth)

&lt;400&gt; 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	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				

									10						
Val 65	Val	Phe	Asp	Ala	Lys 70	Ala	Pro	Ser	Phe	Arg 75	His	Glu	Ala	Tyr	Glu 80
Ala	Tyr	Lys	Ala	Gly 85	Arg	Ala	Pro	Thr	Pro 90	Glu	Asp	Phe	Pro	Arg 95	Gln
Leu	Ala	Leu	Ile 100	Lys	Glu	Leu	Val	Asp 105	Leu	Leu	Gly	Phe	Thr 110	Arg	Leu
Glu	Val	Pro 115	Gly	Tyr	Glu	Ala	Asp 120	Asp	Val	Leu	Ala	Thr 125	Leu	Ala	Lys
Lys	Ala 130	Glu	Lys	Glu	Gly	Tyr 135	Glu	Val	Arg	Ile	Leu 140	Thr	Ala	Asp	Arg
Asp 145	Leu	Tyr	Gln	Leu	Val 150	Ser	Asp	Arg	Val	Ala 155	Val	Leu	His	Pro	Glu 160
Gly	His	Leu	Ile	Thr 165	Pro	Glu	Trp	Leu	Trp 170	Glu	Lys	Tyr	Gly	Leu 175	Arg
Pro	Glu	Gln	Trp 180	Val	Asp	Phe	Arg	Ala 185	Leu	Val	Gly	Asp	Pro 190	Ser	Asp
Asn	Leu	Pro 195	Gly	Val	Lys	Gly	Ile 200	Gly	Glu	Lys	Thr	Ala 205	Leu	Lys	Leu
Leu	Lys 210	Glu	Trp	Gly	Ser	Leu 215	Glu	Asn	Leu	Leu	Lys 220	Asn	Leu	Asp	Arg
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	Glu	Gly	Glu 425	Glu	Lys	Leu	Leu	Trp 430	Leu	Tyr
His	Glu	Val 435	Glu	Lys	Pro	Leu	Ser 440	Arg	Val	Leu	Ala	His 445	Met	Glu	Ala
Thr	Gly 450	Val	Arg	Arg	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	Arg	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	G														

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	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				

										12						
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 355	Ala	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	Val	Lys	Leu	Leu	Trp 430	Leu	Tyr	
His	Glu	Val 435	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His 445	Met	Glu	Ala	
Thr	Gly 450	Val	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	Pro	Leu	
Gly	Gln	Arg 595	Ile	Arg	Arg	Ala	Phe 600	Val	Ala	Glu	Ala	Gly 605	Trp	Ala	Leu	
Val	Ala 610	Leu	Asp	Tyr	Ser	Gln 615	Ile	Glu	Leu	Arg	Val	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 690	Ala	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	

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> 11  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> synthetic DNA polymerase domain motif

<220>  
 <221> VARIANT  
 <222> (2)...(2)  
 <223> Xaa = Thr or Ala

<220>  
 <221> VARIANT  
 <222> (3)...(3)  
 <223> Xaa = Ala, Gly or Leu

<220>  
 <221> VARIANT  
 <222> (4)...(4)  
 <223> Xaa = Thr or Val

<220>  
 <221> VARIANT  
 <222> (5)...(5)  
 <223> Xaa = any amino acid other than Ala, Ser or Gln

<400> 8  
 Gln Xaa Xaa Xaa Xaa Thr Gly Arg Leu Ser Ser  
 1 5 10

<210> 9  
 <211> 11  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> synthetic DNA polymerase domain motif

<220>  
 <221> VARIANT  
 <222> (3)...(3)  
 <223> Xaa = Ala or Gly

<220>  
 <221> VARIANT  
 <222> (5)...(5)  
 <223> Xaa = any amino acid other than Ala

<400> 9  
 Gln Thr Xaa Thr Xaa Thr Gly Arg Leu Ser Ser  
 1 5 10

<210> 10

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

<220>  
 <223> synthetic DNA polymerase domain motif

<220>  
 <221> VARIANT  
 <222> (5)...(5)  
 <223> Xaa = any amino acid other than Ala

<400> 10  
 Gln Thr Ala Thr Xaa Thr Gly Arg Leu Ser Ser  
 1 5 10

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

<220>  
 <223> synthetic DNA polymerase domain motif

<400> 11  
 Gln Thr Ala Thr Asp Thr Gly Arg Leu Ser Ser  
 1 5 10

<210> 12  
 <211> 36  
 <212> PRT  
 <213> Artificial Sequence

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

<400> 12  
 Pro Gly Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn  
 1 5 10 15  
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu  
 20 25 30  
 Gln Asn Ile Pro  
 35

<210> 13  
 <211> 36  
 <212> PRT  
 <213> Artificial Sequence

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

<400> 13  
 Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn  
 1 5 10 15  
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu  
 20 25 30  
 Gln Asn Ile Pro  
 35

<210> 14  
 <211> 36

<212> PRT  
 <213> Artificial Sequence

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

<400> 14  
 Pro Arg Leu Val His Pro Lys Thr Gly Arg Leu His Thr Arg Phe Asn  
 1 5 10 15  
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu  
 20 25 30  
 Gln Asn Ile Pro  
 35

<210> 15  
 <211> 36  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic region from polymerase domain of Thermus  
 flavus DNA polymerase (Tf1)

<400> 15  
 Pro Ala Leu Val His Pro Lys Thr Gly Arg Leu His Thr Arg Phe Asn  
 1 5 10 15  
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu  
 20 25 30  
 Gln Asn Ile Pro  
 35

<210> 16  
 <211> 36  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic region from polymerase domain of Thermus  
 sp. Sps17 DNA polymerase (Sps17)

<400> 16  
 Pro Arg Leu Val His Pro Lys Thr Gly Arg Leu His Thr Arg Phe Asn  
 1 5 10 15  
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu  
 20 25 30  
 Gln Asn Ile Pro  
 35

<210> 17  
 <211> 36  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic region from polymerase domain of Thermus  
 thermophilus DNA polymerase (Tth)

<400> 17  
 Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn  
 1 5 10 15  
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu  
 20 25 30  
 Gln Asn Ile Pro  
 35

<210> 18  
 <211> 36  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic region from polymerase domain of *Thermus caldophilus* DNA polymerase (Tca)

<400> 18  
 Pro Ser Leu Val His Pro Asn Thr Gly Arg Leu His Thr Arg Phe Asn  
 1 5 10 15  
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu  
 20 25 30  
 Gln Asn Ile Pro  
 35

<210> 19  
 <211> 36  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic region from polymerase domain of *Thermotoga maritima* DNA polymerase (Tma)

<400> 19  
 Pro Lys Met Val Asn Pro Lys Thr Gly Arg Ile His Ala Ser Phe Asn  
 1 5 10 15  
 Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu  
 20 25 30  
 Gln Asn Leu Pro  
 35

<210> 20  
 <211> 36  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic region from polymerase domain of *Thermotoga neopolitana* DNA polymerase (Tne)

<400> 20  
 Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Phe His Ala Ser Phe His  
 1 5 10 15  
 Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu  
 20 25 30  
 Gln Asn Leu Pro  
 35

<210> 21  
 <211> 36  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic region from polymerase domain of *Thermosiphon africanus* DNA polymerase (Taf)

<400> 21  
 Pro Leu Ser Ile Asn Arg Lys Thr Asn Arg Val His Thr Thr Phe His  
 1 5 10 15



Gln Thr Gly Thr Ser Thr Gly Arg Leu Ser Ser Ser Asn Pro Asn Leu  
 Gln Asn Leu Pro  
 20 25 30 35

<210> 22

<400> 22  
000

```
<210> 23
<211> 36
<212> PRT
<213> Artificial Sequence
```

<220>  
<223> synthetic region from polymerase domain of  
Deinococcus radiodurans DNA polymerase (Dra)

<400> 23  
Pro Asn Leu Val Asn Pro His Thr Gly Arg Leu His Thr Thr Phe Ala  
1 5 10 15  
Gln Thr Ala Val Ala Thr Gly Arg Leu Ser Ser Leu Asn Pro Asn Leu  
20 25 30  
Gln Asn Ile Pro  
35

```
<210> 24
<211> 36
<212> PRT
<213> Artificial Sequence
```

<220>  
<223> synthetic region from polymerase domain of  
Bacillus stearothermophilus DNA polymerase (Bst)

<400> 24  
Leu Lys Val Val His Pro Val Thr Gly Lys Val His Thr Met Phe Asn  
1 5 10 15  
Gln Ala Leu Thr Gln Thr Gly Arg Leu Ser Ser Val Glu Pro Asn Leu  
20 25 30  
Gln Asn Ile Pro  
35

```
<210> 25
<211> 36
<212> PRT
<213> Artificial Sequence
```

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

<400> 25  
Leu Lys Val Val Arg Pro Asp Thr Lys Lys Val His Thr Ile Phe Asn  
1 5 10 15  
Gln Ala Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu  
20 25 30  
Gln Asn Ile Pro  
35

$\langle 210 \rangle$	26
$\langle 211 \rangle$	11

<212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> synthetic native consensus motif for region from  
 polymerase domain of bacterial DNA polymerase  
  
 <220>  
 <221> VARIANT  
 <222> (2)...(2)  
 <223> Xaa = Thr or Ala  
  
 <220>  
 <221> VARIANT  
 <222> (3)...(3)  
 <223> Xaa = Ala, Gly or Leu  
  
 <220>  
 <221> VARIANT  
 <222> (4)...(4)  
 <223> Xaa = Thr or Val  
  
 <220>  
 <221> VARIANT  
 <222> (5)...(5)  
 <223> Xaa = Ala, Ser or Gln  
  
 <400> 26  
 Gln Xaa Xaa Xaa Xaa Thr Gly Arg Leu Ser Ser  
 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

20

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  
 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

21  
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	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
						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		

22

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
			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									
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> 31  
 <211> 21  
 <212> DNA  
 <213> Artificial sequence

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

<400> 31  
 ctacctcctg gaccctcca a

<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 cctcgctgag cggctccagc aaaacctctt 120
ggaacgcctc aaggagagag aaaagctcct ttggctctac caagagggtg aaaagcccct 180
ctcccgggtc ctggcccaca tggaggccac cggggtaagg ctggacgtgg cctatctaaa 240
ggcccttttc ctggagcttg cggaggagat tcgccgcctc gaggaggagg tcttccgcct 300
ggcggggcac cccttcaacc tgaactcccg tgaccagcta gagcgggtgc tctttgacga 360
gcttaggctt cccgcccttg gcaagacgca aaagacgggg aagcgtcca ccagcgccgc 420
ggtgctggag gccctcaggg agggccaccc catcgtggag aagatcctcc agcaccggga 480
gtcaccaag ctcaagaaca cctacgtaga cccctcccgg ggcctcgtcc acccgaggac 540
gggcccgcct cacacccgct tcaaccagac agccacggcc acgggaaggc tctctagctc 600
cgggcccacac ctgcagaaca tccccatccg caccctcttg ggccagagga tccgccgggc 660
cttcgtggcc gaggcgggat gggcgttggt ggccctggac tatagccaga tagagctccg 720
ggtcctcgcc cacctctccg gggacgagaa cctgatcagg gtcttccagg aggggaagga 780
catccacacc cagaccgcaa gctggatggt cggcgctctc ccggaggccg tggaccccct 840
gatgcgccgg gcggccaaga cggtgaaact cggcgctctc tacggcatgt ccgcccatag 900
gctctccag gagcttgcca tcccctacga ggaggcgggt gcctttatag agcgctactt 960
ccaaagcttc cccaaggtgc gggcctggat agaaaagacc ctggaggagg ggaggaagcg 1020
gggctacgtg gaaaccctct tcggaagaag gcgctacgtg cccgacctca acgcccgggt 1080
gaagagcgtc agggaggccg cggagcgcat ggccttcaac atgcccgtcc agggcaccgc 1140
cgccgacctc atgaagctcg ccatggtgaa gctcttcccc cactccggg agatgggggc 1200
ccgcatgctc ctccaggctc acgacgagct cctcctggag gcccccaag cgcgggccga 1260
ggaggtggcg gctttggcca aggaggccat ggagaaggcc tatccctcg 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 15  
 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  
 225 230 235 240  
 Asn Val Lys Phe Ser His Asp Leu Ser Cys Met Val Thr Asp Leu Pro  
 245 250 255  
 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 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	Val	Ala	Lys	Arg	Tyr	470	Leu	Asp	Arg	Glu	Trp	25	475	Pro	Ala	Asp	Ala	Pro	480	Thr
	Arg	Ala	Ala	Ile	Thr	485	Gly	His	Leu	Val	Arg	490	Glu	Leu	Pro	Pro	Pro	495	Leu	Leu
	Asp	Asp	Ala	Arg	Arg	500	Lys	Met	Tyr	505	Asp	510	Glu	Met	Glu	Lys	Pro	515	Leu	Ser
	Gly	Val	Leu	Gly	Arg	515	Met	Glu	Val	Arg	Gly	520	Val	Gln	Val	Val	Asp	525	Ser	Asp
	Phe	Leu	Gln	Thr	Leu	530	Ser	Ile	Gln	Ala	Gly	535	Val	Arg	Leu	Ala	Asp	540	Leu	Leu
	Glu	Ser	Gln	Ile	His	545	Glu	Tyr	Ala	Gly	Glu	550	Glu	Phe	His	Ile	Arg	555	Ser	Ser
	Pro	Lys	Gln	Leu	Glu	560	Thr	Val	Leu	Tyr	Asp	565	Lys	Leu	Glu	Leu	Ala	570	Ala	Ser
	Ser	Lys	Lys	Thr	Lys	575	Leu	Thr	Gly	Gln	Arg	580	Ser	Thr	Ala	Val	Ser	585	Ala	Ala
	Leu	Glu	Pro	Leu	Arg	590	Asp	Ala	His	Pro	Ile	600	Ile	Ile	Pro	Val	Leu	605	Glu	Glu
	Phe	Arg	Glu	Leu	Asp	610	Lys	Leu	Arg	Gly	Thr	615	Tyr	Leu	Asp	Pro	Ile	620	Pro	Pro
	Asn	Leu	Val	Asn	Pro	625	His	Thr	Gly	Arg	Leu	630	His	Thr	Thr	Phe	Ala	635	Gln	Gln
	Thr	Ala	Val	Ala	Thr	640	Gly	Arg	Leu	Ser	Ser	645	Leu	Asn	Pro	Asn	Leu	650	Gln	Gln
	Asn	Ile	Pro	Ile	Arg	655	Ser	Glu	Leu	Gly	Arg	660	Glu	Ile	Arg	Lys	Gly	665	Phe	Phe
	Ile	Ala	Glu	Asp	Gly	670	Phe	Thr	Leu	Ile	Ala	675	Ala	Ala	Asp	Tyr	Ser	680	Gln	Ile
	Glu	Leu	Arg	Leu	Leu	685	Ala	His	Ile	Ala	Asp	690	Asp	Pro	Leu	Met	Gln	695	Gln	Gln
	Ala	Phe	Val	Glu	Gly	700	Ala	Asp	Ile	His	Arg	705	Arg	Thr	Ala	Ala	Gln	710	Val	Val
	Leu	Gly	Leu	Asp	Glu	715	Ala	Thr	Val	Asp	Ala	720	Asn	Gln	Arg	Arg	Ala	725	Ala	Ala
	Lys	Thr	Val	Asn	Phe	730	Gly	Val	Leu	Tyr	Gly	735	Met	Ser	Ala	His	Arg	740	Leu	Leu
	Ser	Asn	Asp	Leu	Gly	745	Ile	Pro	Tyr	Ala	Glu	750	Ala	Ala	Thr	Phe	Ile	755	Glu	Glu
	Ile	Tyr	Phe	Ala	Thr	760	Tyr	Pro	Gly	Ile	Arg	765	Arg	Tyr	Ile	Asn	His	770	Thr	Thr
	Leu	Asp	Phe	Gly	Arg	775	Thr	His	Gly	Tyr	Val	780	Glu	Thr	Leu	Tyr	Gly	785	Arg	Arg
	Arg	Arg	Tyr	Val	Pro	790	Gly	Leu	Ser	Ser	Arg	795	Asn	Arg	Val	Gln	Arg	800	Glu	Glu
	Ala	Glu	Glu	Arg	Leu	805	Ala	Tyr	Asn	Met	Pro	810	Ile	Gln	Gly	Thr	Ala	815	Ala	Ala
	Asp	Ile	Met	Lys	Leu	820	Ala	Met	Val	Gln	Leu	825	Pro	Gln	Leu	Asp	Ala	830	Ala	Ala
	Ile	Gly	Ala	Arg	Met	835	Leu	Gln	Val	His	Asp	840	Glu	Leu	Leu	Ile	Glu	845	Val	Val
	Ala	Pro	Leu	Asp	Lys	850	Ala	Glu	Gln	Val	Ala	855	Ala	Leu	Thr	Lys	Lys	860	Gly	Gly
	Met	Glu	Asn	Val	Gln	865	Leu	Lys	Val	Pro	Leu	870	Ala	Val	Glu	Val	Gly	875	Gly	Gly
	Thr	Gly	Pro	Asn	Trp	885	Phe	Asp	Thr	Lys		890						895		
						900						905						910		
						915						920								

<210> 37  
 <211> 892  
 <212> PRT  
 <213> Thermosipho africanus

<220>  
 <223> Thermosipho africanus DNA polymerase (Taf)

<400> 37

										26					
Met 1	Gly	Lys	Met	Phe 5	Leu	Phe	Asp	Gly	Thr 10	Gly	Leu	Val	Tyr	Arg 15	Ala
Phe	Tyr	Ala	Ile 20	Asp	Gln	Ser	Leu	Gln 25	Thr	Ser	Ser	Gly	Leu 30	His	Thr
Asn	Ala	Val 35	Tyr	Gly	Leu	Thr	Lys 40	Met	Leu	Ile	Lys	Phe 45	Leu	Lys	Glu
His	Ile 50	Ser	Ile	Gly	Lys	Asp 55	Ala	Cys	Val	Phe	Val 60	Leu	Asp	Ser	Lys
Gly 65	Gly	Ser	Lys	Lys	Arg 70	Lys	Asp	Ile	Leu	Glu 75	Thr	Tyr	Lys	Ala	Asn 80
Arg	Pro	Ser	Thr	Pro 85	Asp	Leu	Leu	Leu	Glu 90	Gln	Ile	Pro	Tyr	Val 95	Glu
Glu	Leu	Val	Asp 100	Ala	Leu	Gly	Ile	Lys 105	Val	Leu	Lys	Ile	Glu 110	Gly	Phe
Glu	Ala	Asp 115	Asp	Ile	Ile	Ala	Thr 120	Leu	Ser	Lys	Lys	Phe 125	Glu	Ser	Asp
Phe	Glu 130	Lys	Val	Asn	Ile	Ile 135	Thr	Gly	Asp	Lys	Asp 140	Leu	Leu	Gln	Leu
Val 145	Ser	Asp	Lys	Val	Phe 150	Val	Trp	Arg	Val	Glu 155	Arg	Gly	Ile	Thr	Asp 160
Leu	Val	Leu	Tyr	Asp 165	Arg	Asn	Lys	Val	Ile 170	Glu	Lys	Tyr	Gly	Ile 175	Tyr
Pro	Glu	Gln	Phe 180	Lys	Asp	Tyr	Leu	Ser 185	Leu	Val	Gly	Asp	Gln 190	Ile	Asp
Asn	Ile	Pro 195	Gly	Val	Lys	Gly	Ile 200	Gly	Lys	Lys	Thr	Ala 205	Val	Ser	Leu
Leu	Lys 210	Lys	Tyr	Asn	Ser	Leu 215	Glu	Asn	Val	Leu	Lys 220	Asn	Ile	Asn	Leu
Leu 225	Thr	Glu	Lys	Leu	Arg 230	Arg	Leu	Leu	Glu	Asp 235	Ser	Lys	Glu	Asp	Leu 240
Gln	Lys	Ser	Ile	Glu 245	Leu	Val	Glu	Leu	Ile 250	Tyr	Asp	Val	Pro	Met 255	Asp
Val	Glu	Lys	Asp 260	Glu	Ile	Ile	Tyr	Arg 265	Gly	Tyr	Asn	Pro	Asp 270	Lys	Leu
Leu	Lys	Val 275	Leu	Lys	Lys	Tyr	Glu 280	Phe	Ser	Ser	Ile	Ile 285	Lys	Glu	Leu
Asn	Leu 290	Gln	Glu	Lys	Leu	Glu 295	Lys	Glu	Tyr	Ile	Leu 300	Val	Asp	Asn	Glu
Asp 305	Lys	Leu	Lys	Lys	Leu 310	Ala	Glu	Glu	Ile	Glu 315	Lys	Tyr	Lys	Thr	Phe 320
Ser	Ile	Asp	Thr	Glu 325	Thr	Thr	Ser	Leu	Asp 330	Pro	Phe	Glu	Ala	Lys 335	Leu
Val	Gly	Ile	Ser 340	Ile	Ser	Thr	Met	Glu 345	Gly	Lys	Ala	Tyr	Tyr 350	Ile	Pro
Val	Ser	His 355	Phe	Gly	Ala	Lys	Asn 360	Ile	Ser	Lys	Ser	Leu 365	Ile	Asp	Lys
Phe	Leu 370	Lys	Gln	Ile	Leu	Gln 375	Glu	Lys	Asp	Tyr	Asn 380	Ile	Val	Gly	Gln
Asn 385	Leu	Lys	Phe	Asp	Tyr 390	Glu	Ile	Phe	Lys	Ser 395	Met	Gly	Phe	Ser	Pro 400
Asn	Val	Pro	His	Phe 405	Asp	Thr	Met	Ile	Ala 410	Ala	Tyr	Leu	Leu	Asn 415	Pro
Asp	Glu	Lys	Arg 420	Phe	Asn	Leu	Glu	Glu 425	Leu	Ser	Leu	Lys	Tyr 430	Leu	Gly
Tyr	Lys	Met 435	Ile	Ser	Phe	Asp	Glu 440	Leu	Val	Asn	Glu	Asn 445	Val	Pro	Leu
Phe	Gly 450	Asn	Asp	Phe	Ser	Tyr 455	Val	Pro	Leu	Glu	Arg 460	Ala	Val	Glu	Tyr
Ser 465	Cys	Glu	Asp	Ala	Asp 470	Val	Thr	Tyr	Arg	Ile 475	Phe	Arg	Lys	Leu	Gly 480
Arg	Lys	Ile	Tyr	Glu 485	Asn	Glu	Met	Glu	Lys 490	Leu	Phe	Tyr	Glu	Ile 495	Glu
Met	Pro	Leu	Ile 500	Asp	Val	Leu	Ser	Glu 505	Met	Glu	Leu	Asn	Gly 510	Val	Tyr
Phe	Asp	Glu 515	Glu	Tyr	Leu	Lys	Glu 520	Leu	Ser	Lys	Lys	Tyr 525	Gln	Glu	Lys
Met	Asp 530	Gly	Ile	Lys	Glu	Lys 535	Val	Phe	Glu	Ile	Ala 540	Gly	Glu	Thr	Phe

27

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

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

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

<400> 38

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

29

Arg	Lys	Ala	Ile	645	Pro	Gln	Asp	Pro	650	Asn	Trp	Trp	Ile	Val	655	Ser	Ala
Asp	Tyr	Ser	Gln	660	Ile	Glu	Leu	Arg	665	Ile	Leu	Ala	His	Leu	670	Ser	Gly
Glu	Asn	Leu	Leu	675	Arg	Ala	Phe	Glu	680	Glu	Gly	Ile	Asp	Val	685	His	Thr
Thr	Ala	Ser	Arg	690	Ile	Phe	Asn	Val	695	Lys	Pro	Glu	Glu	Val	700	Thr	Glu
705	Met	Arg	Arg	710	Ala	Gly	Lys	Met	715	Val	Asn	Phe	Ser	Ile	720	Ile	Tyr
Met	Arg	Arg	Ala	725	Gly	Lys	Met	Val	730	Asn	Phe	Ser	Ile	Ile	735	Tyr	Gly
Thr	Pro	Tyr	Gly	740	Leu	Ser	Val	Arg	745	Leu	Gly	Val	Pro	Val	750	Lys	Glu
Glu	Lys	Met	Ile	755	Val	Asn	Tyr	Phe	760	Val	Leu	Tyr	Pro	Lys	765	Val	Arg
Tyr	Ile	Gln	Arg	770	Val	Val	Ser	Glu	775	Ala	Lys	Glu	Lys	Gly	780	Tyr	Val
Thr	785	Leu	Phe	Gly	Arg	Lys	790	Arg	Asp	Ile	Pro	Gln	Leu	Met	Ala	Arg	Asp
Arg	Asn	Thr	Gln	805	Ala	Glu	Gly	Glu	810	Arg	Ile	Ala	Ile	Asn	Thr	Pro	Ile
Gln	Gly	Thr	Ala	820	Ala	Asp	Ile	Ile	825	Lys	Leu	Ala	Met	Ile	Glu	830	Ile
Arg	Glu	Leu	Lys	835	Glu	Arg	Lys	Met	840	Arg	Ser	Lys	Met	Ile	845	Ile	Gln
His	Asp	Glu	Leu	850	Val	Phe	Glu	855	Val	Pro	Asn	Glu	Glu	Lys	Asp	Ala	Leu
Val	Glu	Leu	Val	865	Lys	Asp	Arg	Met	870	Thr	Asn	Val	Val	Lys	Leu	Ser	Val
Pro	Leu	Glu	Val	885	Asp	Val	Thr	Ile	890	Gly	Lys	Thr	Trp	Ser			880

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

<220>  
 <223> Thermotoga neopolitana DNA polymerase (Tne)

<400> 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			

30

Gly	Lys	Tyr	Arg	Asn	Leu	Glu	Tyr	Ile	Leu	Glu	His	Ala	Arg	Glu	Leu
210	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		
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		

31

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
				85					90					95	
Ala	Tyr	Arg	Ile	Pro	Ala	Tyr	Glu	Leu	Asp	His	Tyr	Glu	Ala	Asp	Asp
			100					105					110		
Ile	Ile	Gly	Thr	Met	Ala	Ala	Arg	Ala	Glu	Arg	Glu	Gly	Phe	Ala	Val
		115					120					125			
Lys	Val	Ile	Ser	Gly	Asp	Arg	Asp	Leu	Thr	Gln	Leu	Ala	Ser	Pro	Gln
	130					135					140				
Val	Thr	Val	Glu	Ile	Thr	Lys	Lys	Gly	Ile	Thr	Asp	Ile	Glu	Ser	Tyr
145					150					155					160
Thr	Pro	Glu	Thr	Val	Glu	Lys	Tyr	Gly	Leu	Thr	Pro	Glu	Gln	Ile	
				165				170						175	
Val	Asp	Leu	Lys	Gly	Leu	Met	Gly	Asp	Lys	Ser	Asp	Asn	Ile	Pro	Gly
			180					185					190		
Val	Pro	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Val	Lys	Leu	Leu	Lys	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	Asn	Leu	Arg	Gln	Tyr	Arg	Asp	Leu	Ala	Leu	Leu	Ser
225					230					235					240
Lys	Gln	Leu	Ala	Ala	Ile	Cys	Arg	Asp	Ala	Pro	Val	Glu	Leu	Thr	Leu
			245						250					255	
Asp	Asp	Ile	Val	Tyr	Lys	Gly	Glu	Asp	Arg	Glu	Lys	Val	Val	Ala	Leu
			260					265					270		
Phe	Gln	Glu	Leu	Gly	Phe	Gln	Ser	Phe	Leu	Asp	Lys	Met	Ala	Val	Gln
		275					280					285			
Thr	Asp	Glu	Gly	Glu	Lys	Pro	Leu	Ala	Gly	Met	Asp	Phe	Ala	Ile	Ala
	290					295					300				
Asp	Ser	Val	Thr	Asp	Glu	Met	Leu	Ala	Asp	Lys	Ala	Ala	Leu	Val	Val

305					310					32						320
Glu	Val	Val	Gly	Asp	Asn	Tyr	His	His	Ala	Pro	Ile	Val	Gly	Ile	Ala	
				325					330					335		
Leu	Ala	Asn	Glu	Arg	Gly	Arg	Phe	Phe	Leu	Arg	Pro	Glu	Thr	Ala	Leu	
			340					345					350			
Ala	Asp	Pro	Lys	Phe	Leu	Ala	Trp	Leu	Gly	Asp	Glu	Thr	Lys	Lys	Lys	
			355				360					365				
Thr	Met	Phe	Asp	Ser	Lys	Arg	Ala	Ala	Val	Ala	Leu	Lys	Trp	Lys	Gly	
	370					375					380					
Ile	Glu	Leu	Arg	Gly	Val	Val	Phe	Asp	Leu	Leu	Leu	Ala	Ala	Tyr	Leu	
385					390					395					400	
Leu	Asp	Pro	Ala	Gln	Ala	Ala	Gly	Asp	Val	Ala	Ala	Val	Ala	Lys	Met	
				405					410					415		
His	Gln	Tyr	Glu	Ala	Val	Arg	Ser	Asp	Glu	Ala	Val	Tyr	Gly	Lys	Gly	
			420					425					430			
Ala	Lys	Arg	Thr	Val	Pro	Asp	Glu	Pro	Thr	Leu	Ala	Glu	His	Leu	Ala	
			435				440					445				
Arg	Lys	Ala	Ala	Ala	Ile	Trp	Ala	Leu	Glu	Glu	Pro	Leu	Met	Asp	Glu	
	450					455					460					
Leu	Arg	Arg	Asn	Glu	Gln	Asp	Arg	Leu	Leu	Thr	Glu	Leu	Glu	Gln	Pro	
465					470					475					480	
Leu	Ala	Gly	Ile	Leu	Ala	Asn	Met	Glu	Phe	Thr	Gly	Val	Lys	Val	Asp	
				485					490					495		
Thr	Lys	Arg	Leu	Glu	Gln	Met	Gly	Ala	Glu	Leu	Thr	Glu	Gln	Leu	Gln	
			500					505					510			
Ala	Val	Glu	Arg	Arg	Ile	Tyr	Glu	Leu	Ala	Gly	Gln	Glu	Phe	Asn	Ile	
		515					520					525				
Asn	Ser	Pro	Lys	Gln	Leu	Gly	Thr	Val	Leu	Phe	Asp	Lys	Leu	Gln	Leu	
	530					535					540					
Pro	Val	Leu	Lys	Lys	Thr	Lys	Thr	Gly	Tyr	Ser	Thr	Ser	Ala	Asp	Val	
545					550					555					560	
Leu	Glu	Lys	Leu	Ala	Pro	His	His	Glu	Ile	Val	Glu	His	Ile	Leu	His	
				565					570					575		
Tyr	Arg	Gln	Leu	Gly	Lys	Leu	Gln	Ser	Thr	Tyr	Ile	Glu	Gly	Leu	Leu	
			580					585					590			
Lys	Val	Val	His	Pro	Val	Thr	Gly	Lys	Val	His	Thr	Met	Phe	Asn	Gln	
		595					600					605				
Ala	Leu	Thr	Gln	Thr	Gly	Arg	Leu	Ser	Ser	Val	Glu	Pro	Asn	Leu	Gln	
	610					615					620					
Asn	Ile	Pro	Ile	Arg	Leu	Glu	Glu	Gly	Arg	Lys	Ile	Arg	Gln	Ala	Phe	
625					630					635					640	
Val	Pro	Ser	Glu	Pro	Asp	Trp	Leu	Ile	Phe	Ala	Ala	Asp	Tyr	Ser	Gln	
				645					650					655		
Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Ile	Ala	Glu	Asp	Asp	Asn	Leu	Ile	
			660					665					670			
Glu	Ala	Phe	Arg	Arg	Gly	Leu	Asp	Ile	His	Thr	Lys	Thr	Ala	Met	Asp	
		675					680					685				
Ile	Phe	His	Val	Ser	Glu	Glu	Asp	Val	Thr	Ala	Asn	Met	Arg	Arg	Gln	
	690					695					700					
Ala	Lys	Ala	Val	Asn	Phe	Gly	Ile	Val	Tyr	Gly	Ile	Ser	Asp	Tyr	Gly	
705					710					715					720	
Leu	Ala	Gln	Asn	Leu	Asn	Ile	Thr	Arg	Lys	Glu	Ala	Ala	Glu	Phe	Ile	
				725					730					735		
Glu	Arg	Tyr	Phe	Ala	Ser	Phe	Pro	Gly	Val	Lys	Gln	Tyr	Met	Asp	Asn	
			740					745					750			
Ile	Val	Gln	Glu	Ala	Lys	Gln	Lys	Gly	Tyr	Val	Thr	Thr	Leu	Leu	His	
		755					760					765				
Arg	Arg	Arg	Tyr	Leu	Pro	Asp	Ile	Thr	Ser	Arg	Asn	Phe	Asn	Val	Arg	
	770					775					780					
Ser	Phe	Ala	Glu	Arg	Thr	Ala	Met	Asn	Thr	Pro	Ile	Gln	Gly	Ser	Ala	
785					790					795					800	
Ala	Asp	Ile	Ile	Lys	Lys	Ala	Met	Ile	Asp	Leu	Ser	Val	Arg	Leu	Arg	
				805					810					815		
Glu	Glu	Arg	Leu	Gln	Ala	Arg	Leu	Leu	Leu	Gln	Val	His	Asp	Glu	Leu	
			820					825					830			
Ile	Leu	Glu	Ala	Pro	Lys	Glu	Glu	Ile	Glu	Arg	Leu	Cys	Arg	Leu	Val	
		835					840					845				
Pro	Glu	Val	Met	Glu	Gln	Ala	Val	Ala	Leu	Arg	Val	Pro	Leu	Lys	Val	



850 855 860  
 Asp Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys  
 865 870 875

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

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

<400> 41  
 Met Lys Lys Lys Leu Val Leu Ile Asp Gly Ser 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 Glu Pro Thr His Met Leu Val Ala Phe Asp Ala Gly Lys Thr Thr  
 50 55 60  
 Phe Arg His Glu Ala Phe Glu 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 Arg  
 85 90 95  
 Ala Tyr Arg Ile Pro Ala Tyr Glu Leu Glu Asn Tyr Glu Ala Asp Asp  
 100 105 110  
 Ile Ile Gly Thr Leu Ala Ala Arg Ala Glu Gln Glu Gly Phe Glu Val  
 115 120 125  
 Lys Val Ile Ser Gly Asp Arg Asp Leu Thr Gln Leu Ala Ser Pro His  
 130 135 140  
 Val Thr Val Asp Ile Thr Lys Lys Gly Ile Thr Asp Ile Glu Pro Tyr  
 145 150 155 160  
 Thr Pro Glu Ala Val Arg Glu Lys Tyr Gly Leu Thr Pro Glu Gln Ile  
 165 170 175  
 Val Asp Leu Lys Gly Leu Met Gly Asp Lys Ser Asp Asn Ile Pro Gly  
 180 185 190  
 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 Leu Ala Ala Tyr Leu  
 385 390 395 400  
 Leu Asp Pro Ala Gln Gly Val Asp Asp Val 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

34

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
	530					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
	610					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
	690					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
			740					745					750		
Asn	Ile	Val	Gln	Glu	Ala	Lys	Gln	Lys	Gly	Tyr	Val	Thr	Thr	Leu	Leu
		755					760					765			
His	Arg	Arg	Arg	Tyr	Leu	Pro	Asp	Ile	Thr	Ser	Arg	Asn	Phe	Asn	Val
	770					775					780				
Arg	Ser	Phe	Ala	Glu	Arg	Met	Ala	Met	Asn	Thr	Pro	Ile	Gln	Gly	Ser
	785				790					795					800
Ala	Ala	Asp	Ile	Ile	Lys	Lys	Ala	Met	Ile	Asp	Leu	Asn	Ala	Arg	Leu
			805						810					815	
Lys	Glu	Glu	Arg	Leu	Gln	Ala	Arg	Leu	Leu	Gln	Val	His	Asp	Glu	
			820					825				830			
Leu	Ile	Leu	Glu	Ala	Pro	Lys	Glu	Glu	Met	Glu	Arg	Leu	Cys	Arg	Leu
		835					840					845			
Val	Pro	Glu	Val	Met	Glu	Gln	Ala	Val	Thr	Leu	Arg	Val	Pro	Leu	Lys
	850					855					860				
Val	Asp	Tyr	His	Tyr	Gly	Ser	Thr	Trp	Tyr	Asp	Ala	Lys			
865					870					875					

<210> 42

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic DNA polymerase domain motif

<220>

<221> VARIANT

<222> (2)...(2)

<223> Xaa = Thr or Ala

<220>

<221> VARIANT

<222> (3)...(3)

<223> Xaa = Ala, Gly or Leu

<220>

<221> VARIANT

<222> (4)...(4)

<223> Xaa = Thr or Val

<220>

<221> VARIANT

<222> (5)...(5)

<223> Xaa = Gly, Leu, Met, Trp, Pro, Thr, Phe, Tyr, Cys,  
Asn, Asp, Glu, Val, Ile, Arg, Lys or His

<400> 42

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