

1  
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<110> F. Hoffmann-La Roche AG  
Roche Diagnostics GmbH

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

<130> 26426 WO-HS

<140> Not yet assigned

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<150> US 61/356,279

<151> 2010-06-18

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<170> FastSEQ for windows Version 4.0

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<213> Thermus sp.

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2

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Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ala	Glu	Arg	Leu	Gln	Gln
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 Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro  
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His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser
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Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg
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Arg	Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	Pro
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Glu	Gly	Tyr	115	Glu	Val	Arg	Ile	Leu	120	Ser	Ala	Asp	Arg	125	Asp	Leu	Tyr	Gln
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Ala	Lys	Arg	245	Arg	Glu	Pro	Thr	Gly	250	Lys	Gly	Leu	Lys	255	Ala	Phe	Leu	Glu
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Leu	Gly	Phe	290	Leu	Leu	Ser	Arg	Pro	295	Glu	Pro	Met	Trp	300	Ala	Glu	Leu	Leu
305	Ala	Leu	Ala	Gly	Ala	Lys	Glu	Gly	310	Arg	Val	His	Arg	315	Ala	Glu	Asp	Pro
Val	Gly	Ala	325	Leu	Lys	Asp	Leu	Lys	330	Glu	Ile	Arg	Gly	335	Leu	Leu	Ala	Lys
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Asp	Asp	Pro	355	Met	Leu	Leu	Ala	Tyr	360	Leu	Leu	Asp	Pro	365	Gly	Asn	Thr	Asn
Pro	Glu	Gly	370	Val	Ala	Arg	Arg	Tyr	375	Gly	Gly	Glu	Trp	380	Lys	Glu	Asp	Ala
385	Ala	Ala	Arg	Ala	Leu	Ser	Glu	Arg	390	Leu	Arg	Leu	Trp	395	Gln	Ala	Leu	Tyr
Arg	Val	Ala	405	Glu	Glu	Glu	Arg	Leu	410	Leu	Trp	Leu	Tyr	415	Arg	Glu	Val	Glu
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Ser	Ala	Ala	500	Val	Leu	Glu	Leu	Leu	505	Arg	Glu	Ala	His	510	Pro	Ile	Val	Gly
Arg	Ile	Leu	515	Glu	Tyr	Arg	Glu	Val	520	Leu	Met	Lys	Leu	525	Ser	Thr	Tyr	Ile
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Tyr	Ser	Gln	595	Ile	Glu	Leu	Arg	Val	600	Leu	Ala	His	Leu	605	Ser	Gly	Asp	Glu
Asn	Leu	Ile	610	Arg	Val	Phe	Arg	Glu	615	Gly	Lys	Asp	Ile	620	His	Thr	Glu	Thr
625	Ala	Ala	Trp	Met	Phe	Gly	Val	Pro	630	Pro	Glu	Gly	Val	635	Asp	Gly	Ala	Met

6

Arg	Arg	Ala	Ala	645	Lys	Thr	Val	Asn	Phe	650	Gly	Val	Leu	Tyr	Gly	655	Met	Ser
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Ala	Phe	Ile	Glu	675	Arg	Tyr	Phe	Gln	Ser	680	Phe	Pro	Lys	Val	685	Arg	Ala	Trp
Ile	Ala	Lys	Thr	690	Leu	Glu	Glu	Gly	Arg	695	Lys	Lys	Gly	Tyr	700	Val	Glu	Thr
705	Leu	Phe	Gly	710	Arg	Arg	Tyr	Val	Pro	715	Asp	Leu	Asn	Ala	720	Arg	Val	Lys
725	Ser	Val	Arg	730	Ala	Ala	Glu	Arg	Met	735	Ala	Phe	Asn	Met	740	Pro	Val	Gln
745	Gly	Thr	Ala	750	Asp	Leu	Met	Lys	Leu	755	Ala	Met	Val	Lys	760	Leu	Phe	Pro
765	Arg	Leu	Arg	770	Pro	Leu	Gly	Val	Arg	775	Ile	Leu	Leu	Gln	780	Val	His	Asp
785	Leu	Val	Leu	790	Ala	Pro	Lys	Ala	Arg	795	Ala	Glu	Glu	Ala	800	Ala	Gln	Leu
805	Ala	Lys	Glu	810	Thr	Met	Glu	Gly	Val	815	Tyr	Pro	Leu	Ser	820	Val	Pro	Glu
825	Val	Glu	Val	830	Gly	Met	Gly	Glu	Asp	835	Trp	Leu	Ser	Ala	Lys	Glu		

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Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
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Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu	Ala	Tyr
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Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Val	Arg	Leu	Glu	Val
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Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ala	Ile	Leu	His	Pro	Glu	Gly	Tyr
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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
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Pro	Ser	Leu	Arg	Glu	Lys	Leu	Gln	Ala	Gly	Met	Glu	Ala	Leu	Ala	Leu
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Ser	Arg	Lys	Leu	Ser	Gln	Val	His	Thr	Asp	Leu	Pro	Leu	Glu	Val	Asp
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Phe	Gly	Arg	Arg	Arg	Thr	Pro	Asn	Leu	Glu	Gly	Leu	Arg	Ala	Phe	Leu
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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
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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
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Arg	Leu	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	Val	Glu	Ala
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Glu	Val	Arg	Gln	Leu	Glu	Glu	Glu	Val	Phe	Arg	Leu	Ala	Gly	His	Pro
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Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp	Glu
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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
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Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg
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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
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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	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
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<213> Thermus sp.

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

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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  
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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 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  
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Arg Val Ala Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu  
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Arg Pro Leu Ala Gln Val Leu Ala His Met Glu Ala Thr Gly Val Arg



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Leu	Asp	Val	Pro	Tyr	Leu	Glu	Ala	Leu	Ser	Gln	Glu	Val	Ala	Phe	Glu
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Leu	Glu	Arg	Leu	Glu	Ala	Glu	Val	His	Arg	Leu	Ala	Gly	His	Pro	Phe
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Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp	Glu	Leu
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Gly	Leu	Pro	Pro	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	Arg	Ser	Thr
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Ser	Ala	Ala	Val	Leu	Glu	Leu	Leu	Arg	Glu	Ala	His	Pro	Ile	Val	Gly
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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
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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
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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	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
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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		
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&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)

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			20					25					30		
Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala
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Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	Val	Phe
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Ala 70	Tyr 70	Lys 70	Ala 70	Gly 85	Arg 70	Ala 70	Pro 70	Thr 70	Pro 90	Glu 75	Asp 75	Phe 75	Pro 75	Arg 95	Gln 80
Leu 75	Ala 75	Leu 75	Ile 100	Lys 75	Glu 75	Leu 75	Val 75	Asp 105	Leu 75	Leu 75	Gly 75	Phe 75	Thr 110	Arg 75	Leu 75
Glu 80	Val 80	Pro 115	Gly 75	Tyr 75	Glu 75	Ala 75	Asp 120	Asp 75	Val 75	Leu 75	Ala 75	Thr 125	Leu 75	Ala 75	Lys 75
Lys 85	Ala 85	Glu 75	Lys 75	Glu 75	Gly 75	Tyr 75	Glu 75	Val 75	Arg 75	Ile 75	Leu 140	Thr 75	Ala 75	Asp 75	Arg 75
Asp 145	Leu 75	Tyr 75	Gln 75	Leu 75	Val 150	Ser 75	Asp 75	Arg 75	Val 75	Ala 155	Val 75	Leu 75	His 75	Pro 75	Glu 160
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Pro 85	Glu 75	Gln 75	Trp 180	Val 75	Asp 75	Phe 75	Arg 75	Ala 185	Leu 75	Val 75	Gly 75	Asp 75	Pro 190	Ser 75	Asp 75
Asn 85	Leu 75	Pro 195	Gly 75	Val 75	Lys 75	Gly 75	Ile 200	Gly 75	Glu 75	Lys 75	Thr 75	Ala 205	Leu 75	Lys 75	Leu 75
Leu 90	Lys 75	Glu 75	Trp 75	Gly 75	Ser 75	Leu 215	Glu 75	Asn 75	Leu 75	Leu 75	Lys 220	Asn 75	Leu 75	Asp 75	Arg 75
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Glu 100	Val 75	Asp 75	Leu 260	Ala 75	Gln 75	Gly 75	Arg 75	Glu 265	Pro 75	Asp 75	Arg 75	Glu 75	Gly 270	Leu 75	Arg 75
Ala 105	Phe 75	Leu 275	Glu 75	Arg 75	Leu 75	Glu 75	Phe 280	Gly 75	Ser 75	Leu 75	Leu 75	His 285	Glu 75	Phe 75	Gly 75
Leu 110	Leu 290	Glu 75	Ala 75	Pro 75	Ala 75	Pro 295	Phe 75	Val 75	Leu 75	Ser 75	Arg 300	Pro 75	Glu 75	Pro 75	Pro 75
Glu 305	Gly 75	Ala 75	Phe 75	Val 75	Gly 310	Leu 75	Ala 75	Cys 75	Arg 315	Asp 75	Gly 75	Arg 75	Val 75	His 335	Arg 75
Ala 115	Glu 75	Leu 75	Lys 75	Ala 325	Leu 75	Ala 75	Gly 75	Leu 75	Lys 330	Asp 75	Leu 75	Lys 75	Glu 75	Val 350	Gly 75
Ala 120	Ala 75	Asp 75	Pro 340	Leu 75	Ala 75	Gly 75	Leu 75	Lys 345	Asp 75	Leu 75	Lys 75	Glu 75	Val 350	Arg 75	Gly 75
Leu 125	Leu 355	Ala 75	Lys 75	Asp 75	Leu 75	Ala 75	Val 360	Leu 75	Ala 75	Ser 75	Arg 75	Glu 365	Gly 75	Leu 75	Asp 75
Leu 130	Val 370	Pro 75	Gly 75	Asp 75	Asp 75	Pro 375	Met 75	Leu 75	Leu 75	Ala 75	Tyr 380	Leu 75	Leu 75	Asp 75	Pro 75
Ser 385	Asn 75	Thr 75	Thr 75	Pro 75	Glu 390	Gly 75	Val 75	Ala 75	Arg 75	Arg 395	Tyr 75	Gly 75	Gly 75	Glu 75	Trp 400
Thr 135	Glu 75	Asp 75	Ala 75	Ala 405	His 75	Arg 75	Ala 75	Leu 75	Leu 410	Ser 75	Glu 75	Arg 75	Leu 75	His 415	Arg 75
Asn 140	Leu 75	Leu 75	Lys 420	Arg 75	Leu 75	Glu 75	Gly 75	Glu 425	Glu 75	Lys 75	Leu 75	Leu 75	Trp 430	Leu 75	Tyr 75
His 145	Glu 75	Val 435	Glu 75	Lys 75	Pro 75	Leu 75	Ser 440	Arg 75	Val 75	Leu 75	Ala 75	His 445	Met 75	Glu 75	Ala 75
Thr 150	Gly 450	Val 75	Arg 75	Arg 75	Asp 75	Val 455	Ala 75	Tyr 75	Leu 75	Gln 75	Ala 460	Leu 75	Ser 75	Leu 75	Glu 75
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Gly															

11

Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu
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His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val
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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	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	
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<223> Thermus caldophilus DNA polymerase (Tca)

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Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala
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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
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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				

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  
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 325 330 335  
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 340 345 350  
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 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg  
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 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
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 Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu  
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 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
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 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  
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 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Asn Thr Gly  
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 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
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 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu  
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 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  
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 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
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 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr  
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 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 Glu Ala Pro Gln Ala Gly Ala Glu Glu  
 785 790 800  
 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> 21  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic DNA polymerase domain motif

<220>  
 <221> VARIANT  
 <222> (9)...(9)  
 <223> Xaa = Ser, Gly, Ala, Asp, Phe, Lys, Cys, Thr or Tyr

<220>  
 <221> VARIANT  
 <222> (14)...(14)  
 <223> Xaa = any amino acid other than Glu

<220>  
 <221> VARIANT  
 <222> (18)...(18)  
 <223> Xaa = Phe, Ala, Gly, Ser, Thr, Tyr, Asp or Lys

<400> 8  
 Ala Gly His Pro Phe Asn Leu Asn Xaa Arg Asp Gln Leu Xaa Arg Val  
 1 5 10 15  
 Leu Xaa Asp Glu Leu  
 20

<210> 9  
 <211> 21  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic DNA polymerase domain motif

<220>  
 <221> VARIANT  
 <222> (14)...(14)  
 <223> Xaa = any amino acid other than Glu

<400> 9  
 Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Xaa Arg Val  
 1 5 10 15  
 Leu Phe Asp Glu Leu  
 20

<210> 10  
 <211> 21  
 <212> PRT  
 <213> Artificial Sequence

<220>

14

<223> synthetic DNA polymerase domain motif

<220>

<221> VARIANT

<222> (14)...(14)

<223> Xaa = Ala, Gly, Lys or Arg

<400> 10

Ala	Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Xaa	Arg	Val
1				5					10					15	
Leu	Phe	Asp	Glu	Leu											
			20												

<210> 11

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic DNA polymerase domain motif

<400> 11

Ala	Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Lys	Arg	Val
1				5					10					15	
Leu	Phe	Asp	Glu	Leu											
			20												

<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

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

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

<210> 14

<211> 36

<212> PRT

### <213> Artificial Sequence

**<220>**

<223> synthetic region from polymerase domain of *Thermus filiformis* DNA polymerase (Tfi)

**<400> 14**

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

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

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

100  
1  
Arg  
Leu  
Glu  
Gly  
Lys  
35  
20  
Thr  
5  
Glu  
10  
Asp  
25  
15  
Pro  
30  
Ala  
Ser  
Asn  
Leu  
Arg  
Leu  
Glu  
Phe  
Val  
Leu  
Ala  
Gly  
His  
Pro  
Phe  
Asn  
Leu  
Asn  
Ser

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

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

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

<210> 21  
 <211> 35  
 <212> PRT  
 <213> Artificial Sequence

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

<400> 21  
 Lys Glu Lys Val Phe Glu Ile Ala Gly Glu Thr Phe Asn Leu Asn Ser  
 1 5 10 15  
 Ser Thr Gln Val Ala Tyr Ile Leu Phe Glu Lys Leu Asn Ile Ala Pro



Tyr Lys Lys 20 25 17 30  
 35

<210> 22

<400> 22  
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<210> 23

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 23

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

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

<210> 25

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 25

Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn Ser  
 1 5 10 15  
 Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro Val  
 20 25 30  
 Leu Lys Lys Ser  
 35

<210> 26

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

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

<220>

<221> VARIANT

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

<223> Xaa = His, Glu or Gln

<220>

<221> VARIANT

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

<223> Xaa = Pro, Thr or Glu

<220>

<221> VARIANT

<222> (6)...(6)

<223> Xaa = Asn or His

<220>

<221> VARIANT

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

<223> Xaa = Leu or Ile

<220>

<221> VARIANT

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

<223> Xaa = Asn or Arg

<220>

<221> VARIANT

<222> (10)...(10)

<223> Xaa = Arg, Pro or Ser

<220>

<221> VARIANT

<222> (11)...(11)

<223> Xaa = Asp, Lys or Thr

<220>

<221> VARIANT

<222> (13)...(13)

<223> Xaa = Leu or Val

<220>

<221> VARIANT

<222> (14)...(14)

<223> Xaa = Glu, Ser, Ala or Gly

<220>

<221> VARIANT

<222> (15)...(15)

<223> Xaa = Arg, Asn, Tyr, Thr or Val

<220>

<221> VARIANT

<222> (16)...(16)

<223> Xaa = Val or Ile

<220>

<221> VARIANT

<222> (18)...(18)

<223> Xaa = Phe or Tyr

<220>

<221> VARIANT

<222> (19)...(19)

<223> Xaa = Asp or Glu

<220>

<221> VARIANT

<222> (20)...(20)

<223> Xaa = Glu or Lys

<400> 26

Ala	Gly	Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Ser	Xaa	Xaa	Gln	Xaa	Xaa	Xaa	Xaa
1				5				10						15	
Leu	Xaa	Xaa	Xaa	Leu											
			20												

<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	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly

			20				25		20			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
Val	Val										60				
65		Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu
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
						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
						375					380				
Asn	Leu	Lys	Phe	Asp											

21

Arg	Ile	Glu	Val	565	Leu	Glu	Glu	Leu	Ala	570	Gly	Glu	His	Glu	Ile	575	Ile	Pro
Leu	Ile	Leu	580	Glu	Tyr	Arg	Lys	Ile	585	Gln	Lys	Leu	Lys	Ser	590	Thr	Tyr	Ile
Asp	Ala	Leu	595	Pro	Lys	Met	Val	600	Asn	Pro	Lys	Thr	Gly	605	Arg	Ile	His	Ala
Ser	610	Phe	Asn	Gln	Thr	Gly	615	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp	640
Pro	625	Asn	Leu	Gln	Asn	630	Leu	Pro	Thr	Lys	Ser	635	Glu	Glu	Gly	Lys	Glu	Ile
Arg	Lys	Ala	Ile	645	Val	Pro	Gln	Asp	Pro	650	Asn	Trp	Trp	Ile	Val	655	Ser	Ala
Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Ile	665	Leu	Ala	His	Leu	Ser	Gly	Asp		
Glu	675	Asn	Leu	Leu	Arg	Ala	Phe	680	Glu	Glu	Gly	Ile	Asp	685	Val	His	Thr	Leu
Thr	690	Ala	Ser	Arg	Ile	Phe	Asn	Val	Lys	Pro	Glu	Glu	Val	Thr	Glu	Glu		
Met	705	Arg	Arg	Ala	Gly	Lys	Met	Val	Asn	Phe	715	Ser	Ile	Ile	Tyr	Gly	Val	
Thr	725	Pro	Tyr	Gly	Leu	Ser	Val	Arg	Leu	730	Gly	Val	Pro	Val	Lys	Glu	Ala	
Glu	740	Lys	Met	Ile	Val	Asn	Tyr	Phe	745	Val	Leu	Tyr	Pro	Lys	Val	Arg	Asp	
Tyr	755	Ile	Gln	Arg	Val	Val	Ser	Glu	Ala	Lys	Glu	Lys	Gly	Tyr	Val	Arg		
Thr	770	Leu	Phe	Gly	Arg	Lys	775	Arg	Asp	Ile	Pro	Gln	Leu	Met	Ala	Arg	Asp	
Arg	785	Asn	Thr	Gln	Ala	Glu	Gly	Glu	Arg	Ile	Ala	Ile	Asn	Thr	Pro	Ile		
Gln	805	Gly	Thr	Ala	Ala	Asp	Ile	Ile	Lys	810	Leu	Ala	Met	Ile	Glu	Ile	Asp	
Arg	820	Glu	Leu	Lys	Glu	Arg	Lys	Met	Arg	825	Ser	Lys	Met	Ile	Ile	Gln	Val	
His	835	Asp	Glu	Leu	Val	Phe	Glu	Val	Pro	840	Asn	Glu	Glu	Lys	Asp	Ala	Leu	
Val	850	Glu	Leu	Val	Lys	Asp	Arg	Met	Thr	855	Val	Val	Lys	Leu	Ser	Val		
Pro	865	Leu	Glu	Val	Asp	Val	Thr	Ile	Gly	870	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

23  
 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> 31  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

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

<400> 31  
 ctacctcctg gaccctcca 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 BlnI and BglII restriction sites

<400> 33

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ctacctcctg gacccctcca acaccacccc cgagggggtg gcccggcgct acggggggga 60
gtggacggag gacgccgccc accggggcct cctcgctgag cggctccagc aaaacctctt 120
ggaacgcctc aagggagagg aaaagctcct ttggctctac caagaggttg aaaagcccct 180
ctccccgggtc ctggcccaca tggaggccac cggggtaagg ctggacgttg cctatctaaa 240
ggcccttttc ctggagcttg cggaggagat tcgccgcctc gaggaggagg tcttccgcct 300
ggcggggccac cccttcaacc tgaactcccg tgaccagcta gagcgggtgc tctttgacga 360
gcttaggctt cccgcccttg gcaagacgca aaagacgggg aagcgctcca ccagcgccgc 420
ggtgctggag gccctcaggg agggccaccc catcgtagg aagatcctcc agcaccggga 480
gtcaccaag ctcaagaaca cctacgtaga cccctcccg ggcctcgtcc acccgaggac 540
gggcccctc cacacccgct tcaaccagac agccacggcc acgggaaggc tctctagctc 600
cgggcccac ctgcagaaca tcccctccg cacccttg ggccagagga tccgccgggc 660
cttcgtggcc gaggcgggat gggcgttggt ggccctggac tatagccaga tagagctccg 720
ggtcctcgcc cacctctccg gggacgagaa cctgatcagg gtcttccagg aggggaagga 780
catccacacc cagaccgcaa gctggatgtt cggcgctcct ccggaggccg tggaccccct 840
gatgcgccgg gcggccaaga cggtaactt cggcgctcct tacggcatgt ccgcccatag 900
gtctctcccag gagcttgcca tcccctacga ggaggcgtg gcctttatag agcgctactt 960
ccaaagcttc cccaagggtg gggcctggat agaaaagacc ctggaggagg ggaggaagcg 1020
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gaagagcgtc agggaggccg cggagcgcat ggccttcaac atgcccgctc agggcaccgc 1140
cgccgacctc atgaagctcg ccatggtgaa gctcttcccc cacctccggg agatgggggc 1200
ccgcatgtct ctccaggctc acgacgagct cctcctggag gcccccaag cgcgggccga 1260
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cctgattatg cgtcagtcta tgaagaaaaa tcgtatacag atggacgaag agagaatcct 1440
tgtgaattta acagagggtg tagggattac acgccactac cagttgggta t 1491

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

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

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

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

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

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

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

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

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

26

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	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
		770				775					780				
Ile	Tyr	Phe	Ala	Thr	Tyr	Pro	Gly	Ile	Arg	Arg	Tyr	Ile	Asn	His	Thr
785					790					795					800
Leu	Asp	Phe	Gly	Arg	Thr	His	Gly	Tyr	Val	Glu	Thr	Leu	Tyr	Gly	Arg
				805					810					815	
Arg	Arg	Tyr	Val	Pro	Gly	Leu	Ser	Ser	Arg	Asn	Arg	Val	Gln	Arg	Glu
			820					825					830		
Ala	Glu	Glu	Arg	Leu	Ala	Tyr	Asn	Met	Pro	Ile	Gln	Gly	Thr	Ala	Ala
			835				840					845			
Asp	Ile	Met	Lys	Leu	Ala	Met	Val	Gln	Leu	Asp	Pro	Gln	Leu	Asp	Ala
	850					855				860					
Ile	Gly	Ala	Arg	Met	Leu	Gln	Val	His	Asp	Glu	Leu	Leu	Ile	Glu	
865					870				875					880	
Ala	Pro	Leu	Asp	Lys	Ala	Glu	Gln	Val	Ala	Ala	Leu	Thr	Lys	Lys	Val
				885					890					895	
Met	Glu	Asn	Val	Gln	Leu	Lys	Val	Pro	Leu	Ala	Val	Glu	Val	Gly	
			900				905					910			
Thr	Gly	Pro	Asn	Trp	Phe	Asp	Thr	Lys							
		915					920								

<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
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Phe	Tyr	Ala	Ile	Asp	Gln	Ser	Leu	Gln	Thr	Ser	Ser	Gly	Leu	His	Thr
			20					25					30		
Asn	Ala	Val	Tyr	Gly	Leu	Thr	Lys	Met	Leu	Ile	Lys	Phe	Leu	Lys	Glu
			35				40					45			
His	Ile	Ser	Ile	Gly	Lys	Asp	Ala	Cys	Val	Phe	Val	Leu	Asp	Ser	Lys
	50					55				60					
Gly	Gly	Ser	Lys	Lys	Arg	Lys	Asp	Ile	Leu	Glu	Thr	Tyr	Lys	Ala	Asn
65					70					75					80
Arg	Pro	Ser	Thr	Pro	Asp	Leu	Leu	Leu	Glu	Gln	Ile	Pro	Tyr	Val	Glu
				85					90					95	
Glu	Leu	Val	Asp	Ala	Leu	Gly	Ile	Lys	Val	Leu	Lys	Ile	Glu	Gly	Phe
			100					105					110		
Glu	Ala	Asp	Asp	Ile	Ile	Ala	Thr	Leu	Ser	Lys	Lys	Phe	Glu	Ser	Asp
		115					120					125			
Phe	Glu	Lys	Val	Asn	Ile	Ile	Thr	Gly	Asp	Lys	Asp	Leu	Leu	Gln	Leu

	130				135				140						
Val	Ser	Asp	Lys	Val	Phe	Val	Trp	Arg	Val	Glu	Arg	Gly	Ile	Thr	Asp
145					150					155					160
Leu	Val	Leu	Tyr	Asp	Arg	Asn	Lys	Val	Ile	Glu	Lys	Tyr	Gly	Ile	Tyr
				165					170					175	
Pro	Glu	Gln	Phe	Lys	Asp	Tyr	Leu	Ser	Leu	Val	Gly	Asp	Gln	Ile	Asp
			180					185					190		
Asn	Ile	Pro	Gly	Val	Lys	Gly	Ile	Gly	Lys	Lys	Thr	Ala	Val	Ser	Leu
		195					200					205			
Leu	Lys	Lys	Tyr	Asn	Ser	Leu	Glu	Asn	Val	Leu	Lys	Asn	Ile	Asn	Leu
		210				215					220				
Leu	Thr	Glu	Lys	Leu	Arg	Arg	Leu	Leu	Glu	Asp	Ser	Lys	Glu	Asp	Leu
225					230					235					240
Gln	Lys	Ser	Ile	Glu	Leu	Val	Glu	Leu	Ile	Tyr	Asp	Val	Pro	Met	Asp
				245					250					255	
Val	Glu	Lys	Asp	Glu	Ile	Ile	Tyr	Arg	Gly	Tyr	Asn	Pro	Asp	Lys	Leu
			260					265					270		
Leu	Lys	Val	Leu	Lys	Lys	Tyr	Glu	Phe	Ser	Ser	Ile	Ile	Lys	Glu	Leu
		275					280					285			
Asn	Leu	Gln	Glu	Lys	Leu	Glu	Lys	Glu	Tyr	Ile	Leu	Val	Asp	Asn	Glu
	290					295					300				
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	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						

&lt;210&gt; 38

&lt;211&gt; 893

&lt;212&gt; PRT

&lt;213&gt; Thermotoga maritima

&lt;220&gt;

&lt;223&gt; Thermotoga maritima DNA polymerase (Tma)

&lt;400&gt; 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
Asn	Trp	Glu	Glu	Leu	Arg	Tyr	Gln	Gly	Tyr	Asp	Arg	Glu	Lys	Leu	Leu
Pro	Leu	Leu	Lys	Glu	Leu	Glu	Phe	Ala	Ser	Ile	Met	Lys	Glu	Leu	Gln
Leu	Tyr	Glu	Glu	Ser	Glu	Pro	Val	Gly	Tyr	Arg	Ile	Val	Lys	Asp	Leu
Val	Glu	Phe	Glu	Lys	Leu	Ile	Glu	Lys	Leu	Arg	Glu	Ser	Pro	Ser	Phe
Ala	Ile	Asp	Leu	Glu	Thr	Ser	Ser	Leu	Asp	Pro	Phe	Asp	Cys	Asp	Ile
Val	Gly	Ile	Ser	Val	Ser	Phe	Lys	Pro	Lys	Glu	Ala	Tyr	Tyr	Ile	Pro
Leu	His	His	Arg	Asn	Ala	Gln	Asn	Leu	Asp	Glu	Lys	Glu	Val	Leu	Lys
Lys	Leu	Lys	Glu	Ile	Leu	Glu	Asp	Pro	Gly	Ala	Lys	Ile	Val	Gly	Gln
Asn	Leu	Lys	Phe	Asp	Tyr	Lys	Val	Leu	Met	Val	Lys	Gly	Val	Glu	Pro
Val	Pro	Pro	Tyr	Phe	Asp	Thr	Met	Ile	Ala	Ala	Tyr	Leu	Leu	Glu	Pro
Asn	Glu	Lys	Lys	Phe	Asn	Leu	Asp	Asp	Leu	Ala	Leu	Lys	Phe	Leu	Gly
Tyr	Lys	Met	Thr	Ser	Tyr	Gln	Glu	Leu	Met	Ser	Phe	Ser	Phe	Pro	Leu
Phe	Gly	Phe	Ser	Phe	Ala	Asp	Val	Pro	Val	Glu	Lys	Ala	Ala	Asn	Tyr
Ser	Cys	Glu	Asp	Ala	Asp	Ile	Thr	Tyr	Arg	Leu	Tyr	Lys	Thr	Leu	Ser
Leu	Lys	Leu	His	Glu	Ala	Asp	Leu	Glu	Asn	Val	Phe	Tyr	Lys	Ile	Glu
Met	Pro	Leu	Val	Asn	Val	Leu	Ala	Arg	Met	Glu	Leu	Asn	Gly	Val	Tyr
Val	Asp	Thr	Glu	Phe	Leu	Lys	Lys	Leu	Ser	Glu	Glu	Tyr	Gly	Lys	Lys
Leu	Glu	Glu	Leu	Ala	Glu	Glu	Ile	Tyr	Arg	Ile	Ala	Gly	Glu	Pro	Phe
Asn	Ile	Asn	Ser	Pro	Lys	Gln	Val	Ser	Arg	Ile	Leu	Phe	Glu	Lys	Leu
Gly	Ile	Lys	Pro	Arg	Gly	Lys	Thr	Thr	Lys	Thr	Gly	Asp	Tyr	Ser	Thr
Arg	Ile	Glu	Val	Leu	Glu	Glu	Leu	Ala	Gly	Glu	His	Glu	Ile	Ile	Pro
Leu	Ile	Leu	Glu	Tyr	Arg	Lys	Ile	Gln	Lys	Leu	Lys	Ser	Thr	Tyr	Ile
Asp	Ala	Leu	Pro	Lys	Met	Val	Asn	Pro	Lys	Thr	Gly	Arg	Ile	His	Ala
Ser	Phe	Asn	Gln	Thr	Gly	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp
Pro	Asn	Leu	Gln	Asn	Leu	Pro	Thr	Lys	Ser	Glu	Glu	Gly	Lys	Glu	Ile
Arg	Lys	Ala	Ile	Val	Pro	Gln	Asp	Pro	Asn	Trp	Trp	Ile	Val	Ser	Ala
Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Ile	Leu	Ala	His	Leu	Ser	Gly	Asp
Glu	Asn	Leu	Leu	Arg	Ala	Phe	Glu	Glu	Gly	Ile	Asp	Val	His	Thr	Leu
Thr	Ala	Ser	Arg	Ile	Phe	Asn	Val	Lys	Pro	Glu	Glu	Val	Thr	Glu	Glu
Met	Arg	Arg	Ala	Gly	Lys	Met	Val	Asn	Phe	Ser	Ile	Ile	Tyr	Gly	Val
Thr	Pro	Tyr	Gly	Leu	Ser	Val	Arg	Leu	Gly	Val	Pro	Val	Lys	Glu	Ala
Glu	Lys	Met	Ile	Val	Asn	Tyr	Phe	Val	Leu	Tyr	Pro	Lys	Val	Arg	Asp
Tyr	Ile	Gln	Arg	Val	Val	Ser	Glu	Ala	Lys	Glu	Lys	Gly	Tyr	Val	Arg

30  
 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 Asp Ile Ile Lys Leu Ala Met Ile Glu Ile Asp  
 820 825 830  
 Arg Glu Leu Lys Glu Arg Lys Met 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  
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 Pro Leu Glu Val Asp Val Thr Ile Gly Lys Thr Trp Ser  
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<220>  
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 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		
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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				
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	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		
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Pro	Leu	Glu	Val	Asp	Ile	Ser	Ile	Gly	Lys	Ser	Trp	Ser					

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 <211> 876  
 <212> PRT  
 <213> Bacillus stearothermophilus

<220>  
 <223> Bacillus stearothermophilus DNA polymerase (Bst)

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 Ala Phe Phe Ala Leu Pro Leu Leu His Asn Asp Lys Gly Ile His Thr  
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 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  
 305 310 315 320  
 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



33

Arg	Lys	Ala	Ala	Ala	Ile	Trp	Ala	Leu	Glu	Glu	Pro	Leu	Met	Asp	Glu
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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	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
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 <220>  
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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	Leu 95	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 195	Ile	Gly	Glu	Lys	Thr 200	Ala	Val	Lys	Leu	Leu 205	Arg	Gln	Phe
Gly	Thr 210	Val	Glu	Asn	Val	Leu 215	Ala	Ser	Ile	Asp	Glu 220	Ile	Lys	Gly	Glu
Lys 225	Leu	Lys	Glu	Thr	Leu 230	Arg	Gln	His	Arg	Glu 235	Met	Ala	Leu	Leu	Ser 240
Lys	Lys	Leu	Ala	Ala 245	Ile	Arg	Arg	Asp	Ala 250	Pro	Val	Glu	Leu	Ser 255	Leu
Asp	Asp	Ile	Ala 260	Tyr	Gln	Gly	Glu	Asp 265	Arg	Glu	Lys	Val	Val 270	Ala	Leu
Phe	Lys	Glu 275	Leu	Gly	Phe	Gln	Ser 280	Phe	Leu	Glu	Lys	Met 285	Glu	Ser	Pro
Ser	Ser 290	Glu	Glu	Glu	Lys	Pro 295	Leu	Ala	Lys	Met	Ala 300	Phe	Thr	Leu	Ala
Asp 305	Arg	Val	Thr	Glu	Glu 310	Met	Leu	Ala	Asp	Lys 315	Ala	Ala	Leu	Val	Val 320
Glu	Val	Val	Glu	Glu 325	Asn	Tyr	His	Asp	Ala 330	Pro	Ile	Val	Gly	Ile 335	Ala
Val	Val	Asn	Glu 340	His	Gly	Arg	Phe	Phe 345	Leu	Arg	Pro	Glu	Thr 350	Ala	Leu
Ala	Asp	Pro 355	Gln	Phe	Val	Ala	Trp 360	Leu	Gly	Asp	Glu	Thr 365	Lys	Lys	Lys
Ser	Met 370	Phe	Asp	Ser	Lys	Arg 375	Ala	Ala	Val	Ala	Leu 380	Lys	Trp	Lys	Gly
Ile 385	Glu	Leu	Cys	Gly	Val 390	Ser	Phe	Asp	Leu	Leu 395	Leu	Ala	Ala	Tyr	Leu 400
Leu	Asp	Pro	Ala	Gln 405	Gly	Val	Asp	Asp	Val 410	Ala	Ala	Ala	Ala	Lys 415	Met
Lys	Gln	Tyr	Glu 420	Ala	Val	Arg	Pro	Asp 425	Glu	Ala	Val	Tyr	Gly 430	Lys	Gly
Ala	Lys	Arg 435	Ala	Val	Pro	Asp	Glu 440	Pro	Val	Leu	Ala	Glu 445	His	Leu	Val
Arg	Lys 450	Ala	Ala	Ala	Ile	Trp 455	Ala	Leu	Glu	Arg	Pro 460	Phe	Leu	Asp	Glu
Leu 465	Arg	Arg	Asn	Glu	Gln 470	Asp	Arg	Leu	Leu	Val 475	Glu	Leu	Glu	Gln	Pro 480
Leu	Ser	Ser	Ile 485	Leu	Ala	Glu	Met	Glu	Phe 490	Ala	Gly	Val	Lys	Val 495	Asp
Thr	Lys	Arg	Leu 500	Glu	Gln	Met	Gly	Glu 505	Glu	Leu	Ala	Glu	Gln 510	Leu	Arg
Thr	Val	Glu 515	Gln	Arg	Ile	Tyr	Glu 520	Leu	Ala	Gly	Gln	Glu 525	Phe	Asn	Ile
Asn	Ser 530	Pro	Lys	Gln	Leu	Gly 535	Val	Ile	Leu	Phe	Glu 540	Lys	Leu	Gln	Leu
Pro 545	Val	Leu	Lys	Lys	Ser 550	Lys	Thr	Gly	Tyr	Ser 555	Thr	Ser	Ala	Asp	Val 560
Leu	Glu	Lys	Leu	Ala											

35

His	Tyr	Arg	Gln	565	Leu	Gly	Lys	Leu	Gln	570	Ser	Thr	Tyr	Ile	Glu	575	Gly	Leu
			580						585						590			
Leu	Lys	Val	Val	Arg	Pro	Asp	Thr	600	Lys	Lys	Val	His	Thr	605	Ile	Phe	Asn	
Gln	Ala	Leu	Thr	Gln	Thr	Gly	Arg	610	Leu	Ser	Ser	Thr	Glu	620	Pro	Asn	Leu	
						615												
Gln	Asn	Ile	Pro	Ile	Arg	630	Leu	Glu	Glu	Gly	Arg	Lys	Ile	635	Arg	Gln	Ala	640
Phe	Val	Pro	Ser	Glu	Ser	Asp	Trp	Leu	Ile	650	Phe	Ala	Ala	655	Asp	Tyr	Ser	
Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Ile	665	Ala	Glu	Asp	670	Asp	Asn	Leu	
Met	Glu	Ala	Phe	Arg	Arg	Asp	Leu	Asp	Ile	680	His	Thr	Lys	685	Thr	Ala	Met	
Asp	Ile	Phe	Gln	Val	Ser	Glu	Asp	Glu	Val	695	Thr	Pro	Asn	700	Met	Arg	Arg	
Gln	Ala	Lys	Ala	Val	Asn	Phe	Gly	Ile	Val	710	Tyr	Gly	Ile	715	Ser	Asp	Tyr	
Gly	Leu	Ala	Gln	Asn	Leu	Asn	Ile	Ser	Arg	725	Lys	Glu	Ala	730	Ala	Glu	Phe	
Ile	Glu	Arg	Tyr	Phe	Glu	Ser	Phe	Pro	Gly	740	Val	Lys	Arg	745	Tyr	Met	Glu	
Asn	Ile	Val	Gln	Glu	Ala	Lys	Gln	Lys	Gly	755	Tyr	Val	Thr	760	Thr	Leu	Leu	
His	Arg	Arg	Arg	Tyr	Leu	Pro	Asp	Ile	Thr	765	Ser	Arg	Asn	770	Phe	Asn	Val	
Arg	Ser	Phe	Ala	Glu	Arg	Met	Ala	Met	Asn	775	Thr	Pro	Ile	780	Gln	Gly	Ser	
Ala	Ala	Asp	Ile	Ile	Lys	Lys	Ala	Met	Ile	785	Asp	Leu	Asn	790	Ala	Arg	Leu	
Lys	Glu	Glu	Arg	Leu	Gln	Ala	Arg	Leu	Leu	805	Gln	Val	His	810	Asp	Glu		
Leu	Ile	Leu	Glu	Ala	Pro	Lys	Glu	Glu	Met	820	Glu	Arg	Leu	825	Cys	Arg	Leu	
Val	Pro	Glu	Val	Met	Glu	Gln	Ala	Val	Thr	835	Leu	Arg	Val	840	Pro	Leu	Lys	
Val	Asp	Tyr	His	Tyr	Gly	Ser	Thr	Trp	Tyr	850	Asp	Ala	Lys	855				
865					870					875								

<210> 42  
 <211> 21  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic DNA polymerase domain motif

<220>  
 <221> VARIANT  
 <222> (3)...(3)  
 <223> Xaa = His, Glu or Gln

<220>  
 <221> VARIANT  
 <222> (4)...(4)  
 <223> Xaa = Pro, Thr or Glu

<220>  
 <221> VARIANT  
 <222> (6)...(6)  
 <223> Xaa = Asn or His

<220>  
 <221> VARIANT  
 <222> (7)...(7)  
 <223> Xaa = Leu or Ile

<220>  
 <221> VARIANT  
 <222> (8)...(8)  
 <223> Xaa = Asn or Arg

<220>  
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 <222> (9)...(9)  
 <223> Xaa = any amino acid

<220>  
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 <222> (10)...(10)  
 <223> Xaa = Arg, Pro or Ser

<220>  
 <221> VARIANT  
 <222> (11)...(11)  
 <223> Xaa = Asp, Lys or Thr

<220>  
 <221> VARIANT  
 <222> (13)...(13)  
 <223> Xaa = Leu or Val

<220>  
 <221> VARIANT  
 <222> (14)...(14)  
 <223> Xaa = any amino acid other than Glu, Ser, Ala or Gly

<220>  
 <221> VARIANT  
 <222> (15)...(15)  
 <223> Xaa = Arg, Asn, Tyr, Thr or Val

<220>  
 <221> VARIANT  
 <222> (16)...(16)  
 <223> Xaa = Val or Ile

<220>  
 <221> VARIANT  
 <222> (18)...(18)  
 <223> Xaa = any amino acid

<220>  
 <221> VARIANT  
 <222> (19)...(19)  
 <223> Xaa = Asp or Glu

<220>  
 <221> VARIANT  
 <222> (20)...(20)  
 <223> Xaa = Glu or Lys

<400> 42  
 Ala Gly Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa  
 1 5 10 15  
 Leu Xaa Xaa Xaa Leu  
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<210> 43  
 <211> 21  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<220>  
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 <223> Xaa = His or Glu

<220>  
 <221> VARIANT  
 <222> (7)...(7)  
 <223> Xaa = Leu or Ile

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

<220>  
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 <222> (10)...(10)  
 <223> Xaa = Arg or Pro

<220>  
 <221> VARIANT  
 <222> (11)...(11)  
 <223> Xaa = Asp or Lys

<220>  
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<220>  
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 <223> Xaa = any amino acid other than Glu or Ser

<220>  
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 <223> Xaa = Arg or Asn

<220>  
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 <223> Xaa = Val or Ile

<220>  
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 <223> Xaa = any amino acid

<220>  
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 <223> Xaa = Asp or Glu

<220>  
 <221> VARIANT  
 <222> (20)...(20)  
 <223> Xaa = Glu or Lys

<400> 43  
 Ala Gly Xaa Pro Phe Asn Xaa Asn Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa  
 1 5 10 15  
 Leu Xaa Xaa Xaa Leu  
 20

<210> 44  
 <211> 21  
 <212> PRT  
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<220>  
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 <223> Xaa = His or Glu

<220>  
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 <222> (7)...(7)  
 <223> Xaa = Leu or Ile

<220>  
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 <222> (10)...(10)  
 <223> Xaa = Arg or Pro

<220>  
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 <222> (11)...(11)  
 <223> Xaa = Asp or Lys

<220>  
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 <222> (13)...(13)  
 <223> Xaa = Leu or Val

<220>  
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 <222> (14)...(14)  
 <223> Xaa = any amino acid other than Glu or Ser

<220>  
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 <223> Xaa = Val or Ile

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 <222> (19)...(19)  
 <223> Xaa = Asp or Glu

<220>  
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 <222> (20)...(20)  
 <223> Xaa = Glu or Lys

<400> 44  
 Ala Gly Xaa Pro Phe Asn Xaa Asn Ser Xaa Xaa Gln Xaa Xaa Arg Xaa  
 1 5 10 15  
 Leu Phe Xaa Xaa Leu  
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<210> 45  
 <211> 21  
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<220>

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<222> (9)...(9)

<223> Xaa = any amino acid

<220>

<221> VARIANT

<222> (14)...(14)

<223> Xaa = any amino acid other than Glu

<220>

<221> VARIANT

<222> (18)...(18)

<223> Xaa = any amino acid

<400> 45

Ala	Gly	His	Pro	Phe	Asn	Leu	Asn	Xaa	Arg	Asp	Gln	Leu	Xaa	Arg	Val
1					5				10					15	
Leu	Xaa	Asp	Glu	Leu											
			20												

<210> 46

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic DNA polymerase domain motif

<220>

<221> VARIANT

<222> (9)...(9)

<223> Xaa = any amino acid other than Ser

<220>

<221> VARIANT

<222> (14)...(14)

<223> Xaa = any amino acid other than Glu

<220>

<221> VARIANT

<222> (18)...(18)

<223> Xaa = any amino acid other than Phe

<400> 46

Ala	Gly	His	Pro	Phe	Asn	Leu	Asn	Xaa	Arg	Asp	Gln	Leu	Xaa	Arg	Val
1					5				10					15	
Leu	Xaa	Asp	Glu	Leu											
			20												

<210> 47

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic DNA polymerase domain motif

<220>

<221> VARIANT

<222> (9)...(9)

<223> Xaa = Ser, Gly, Ala, Asp, Phe, Lys, Cys, Thr or Tyr

<220>  
 <221> VARIANT  
 <222> (14)...(14)  
 <223> Xaa = Ser, Gln, Ala, Gly, Lys or Arg

<220>  
 <221> VARIANT  
 <222> (18)...(18)  
 <223> Xaa = Phe, Ala, Gly, Ser, Thr, Tyr, Asp or Lys

<400> 47  
 Ala Gly His Pro Phe Asn Leu Asn Xaa Arg Asp Gln Leu Xaa Arg Val  
 1 5 10 15  
 Leu Xaa Asp Glu Leu  
 20

<210> 48  
 <211> 21  
 <212> PRT  
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<220>  
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<220>  
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 <223> Xaa = Ser, Gly, Ala, Asp, Phe, Lys, Cys, Thr or Tyr

<220>  
 <221> VARIANT  
 <222> (18)...(18)  
 <223> Xaa = Phe, Ala, Gly, Ser, Thr, Tyr, Asp or Lys

<400> 48  
 Ala Gly His Pro Phe Asn Leu Asn Xaa Arg Asp Gln Leu Lys Arg Val  
 1 5 10 15  
 Leu Xaa Asp Glu Leu  
 20

<210> 49  
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<220>  
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 <223> Xaa = Ser, Gly, Ala, Asp, Phe, Lys, Cys, Thr or Tyr

<220>  
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 <222> (14)...(14)  
 <223> Xaa = Arg, Lys, Ala or Gly

<220>  
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 <222> (18)...(18)  
 <223> Xaa = Phe, Ala, Gly, Ser, Thr, Tyr, Asp or Lys

<400> 49



Ala Gly His Pro Phe Asn Leu Asn Xaa Arg Asp Gln Leu Xaa Arg Val  
 1 5 10 15  
 Leu Xaa Asp Glu Leu  
 20

<210> 50  
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<220>  
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<220>  
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 <223> Xaa = Arg, Lys, Ala or Gly

<400> 50  
 Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Xaa Arg Val  
 1 5 10 15  
 Leu Phe Asp Glu Leu  
 20

<210> 51  
 <211> 13  
 <212> PRT  
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<220>  
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<220>  
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 <223> Xaa = Ser or Thr

<220>  
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 <222> (8)...(8)  
 <223> Xaa = Leu, Gly, Thr, Gln, Ala, Ser, Asn, Arg or  
 Lys

<400> 51  
 Thr Gly Arg Leu Ser Ser Xaa Xaa Pro Asn Leu Gln Asn  
 1 5 10