

1
SEQUENCE LISTING

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

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

<130> 26748 WO-HS

<140> Not yet assigned

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<150> US 61/356,219

<151> 2010-06-18

<160> 42

<170> FastSEQ for windows Version 4.0

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<212> PRT

<213> Thermus sp.

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Lys	Ala	Glu	Arg	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg
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 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
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 405 410 415
 Asn Leu Leu Glu Arg Leu Lys Gly Glu Glu Lys Leu Leu Trp Leu Tyr
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 Gln Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
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 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
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 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 Gly Leu Val His Pro Arg 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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4

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785					790					795					800
Arg	Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	Pro
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<220>
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Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Glu	Val	Ala	Ile	Val	Val	Phe	Asp
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Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu	Ala	Tyr	Lys	Ala
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Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala	Leu	Ile
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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
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6

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Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg	Ala	Trp
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Ile	Ala	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Lys	Gly	Tyr	Val	Glu	Thr
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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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785					790					795					800
Ala	Lys	Glu	Thr	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ser	Val	Pro	Leu	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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Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
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Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Val	Arg	Leu	Glu	Val
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Ser	Arg	Lys	Leu	Ser	Gln	Val	His	Thr	Asp	Leu	Pro	Leu	Glu	Val	Asp
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Ala	Gly	Glu	Arg	Ala	Leu	Leu	Ala	Glu	Arg	Leu	Phe	Gln	Thr	Leu	Lys
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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
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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
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Ile	Asp	Pro	Leu	Pro	Ala	Leu	Val	His	Pro	Lys	Thr	Gly	Arg	Leu	His
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Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser
				565					570					575	
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Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr	Gln
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Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Ser	Pro	Glu	Gly	Val	Asp	Pro	Leu
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Trp	Ile	Glu	Gly	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	Val	Glu
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Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala	Arg	Val
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Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val
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Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Arg	Leu	Phe
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Pro	Arg	Leu	Gln	Glu	Leu	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His	Asp
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785					790					795					800
Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Trp	Pro	Leu	Gln	Val	Pro	Leu
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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
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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 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
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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
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Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Lys Glu Asp Ala
385 390 395 400
Ala Ala Arg Ala Leu Ser Glu Arg Leu Trp Gln Ala Leu Tyr Pro
405 410 415
Arg Val Ala Glu Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu
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Arg Pro Leu Ala Gln Val Leu Ala His Met Glu Ala Thr Gly Val Arg

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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
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 Asp Pro Leu Pro Arg Leu Val His Pro Lys Thr Gly Arg Leu His Thr
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 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
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 Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser
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 675 680 685
 Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp
 690 695 700
 Ile Ala Lys Thr Leu Glu Glu Gly Arg Lys Lys Gly Tyr Val Glu Thr
 705 710 715 720
 Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys
 725 730 735
 Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln
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 Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro
 755 760 765
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 770 775 780
 Leu Val Leu Glu Ala Pro Lys Ala Arg Ala Glu Glu Ala Ala Gln Leu
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 35 40 45
 Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe
 50 55 60

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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	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
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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
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Ser	Ser	Ser	Asp 580	Pro	Asn	Leu	Gln	Asn 585	Ile	Pro	Val	Arg	Thr 590	Pro	Leu
Gly	Gln	Arg 595	Ile	Arg	Arg	Ala	Phe 600	Val	Ala	Glu	Ala	Gly 605	Trp	Ala	Leu

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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	
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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
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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
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Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
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Asp	Leu	Asp	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	Pro	Glu
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Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Gln	Lys	Tyr	Gly	Leu	Lys
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Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	Ser	Asp
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Glu	Val	Asp	Leu 260	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Arg 270
Ala	Phe	Leu 275	Glu	Arg	Leu	Glu	Phe 280	Gly	Ser	Leu	Leu	His 285	Glu	Phe	Gly
Leu	Leu 290	Glu	Ala	Pro	Ala	Pro 295	Leu	Glu	Glu	Ala	Pro 300	Trp	Pro	Pro	Pro
Glu 305	Gly	Ala	Phe	Val	Gly 310	Phe	Val	Leu	Ser	Arg 315	Pro	Glu	Pro	Met	Trp 320
Ala	Glu	Leu	Lys	Ala 325	Leu	Ala	Ala	Cys	Arg 330	Asp	Gly	Arg	Val	His 335	Arg
Ala	Ala	Asp	Pro 340	Leu	Ala	Gly	Leu	Lys 345	Asp	Leu	Lys	Glu	Val 350	Arg	Gly
Leu	Leu	Ala 355	Lys	Asp	Leu	Ala	Val 360	Leu	Ala	Ser	Arg	Glu 365	Gly	Leu	Asp
Leu	Val 370	Pro	Gly	Asp	Asp	Pro 375	Met	Leu	Leu	Ala	Tyr 380	Leu	Leu	Asp	Pro
Ser 385	Asn	Thr	Thr	Pro	Glu 390	Gly	Val	Ala	Arg	Arg 395	Tyr	Gly	Gly	Glu	Trp 400
Thr	Glu	Asp	Ala	Ala 405	His	Arg	Ala	Leu	Leu 410	Ser	Glu	Arg	Leu	His 415	Arg
Asn	Leu	Leu	Lys 420	Arg	Leu	Gln	Gly	Glu 425	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	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	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	Arg	Leu	Pro	Ala	Leu 505	Gly	Lys	Thr	Gln	Lys	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	Leu 575
Ser	Ser	Ser	Asp 580	Pro	Asn	Leu	Gln	Asn 585	Ile	Pro	Val	Arg	Thr 590	Pro	Leu
Gly	Gln	Arg 595	Ile	Arg	Arg	Ala	Phe 600	Val	Ala	Glu	Ala	Gly 605	Trp	Ala	Leu
Val 610	Ala	Leu	Asp	Tyr	Ser	Gln 615	Ile	Glu	Leu	Arg	Val 620	Leu	Ala	His	Leu
Ser 625	Gly	Asp	Glu	Asn	Leu 630	Ile	Arg	Val	Phe	Gln 635	Glu	Gly	Lys	Asp	Ile 640
His	Thr	Gln	Thr	Ala 645	Ser	Trp	Met	Phe	Gly 650	Val	Pro	Pro	Glu	Ala 655	Val
Asp	Pro	Leu	Met 660	Arg	Arg	Ala	Ala	Lys 665	Thr	Val	Asn	Phe	Gly 670	Val	Leu
Tyr	Gly	Met 675	Ser	Ala	His	Arg	Leu 680	Ser	Gln	Glu	Leu	Ala 685	Ile	Pro	Tyr
Glu	Glu	Ala	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	Glu	Arg	Met	Ala 750	Phe	Asn	
Met	Pro	Val 755	Gln	Gly	Thr	Ala	Ala 760	Asp	Leu	Met	Lys	Leu 765	Ala	Met	Val

Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln
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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	
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 <223> Xaa = any amino acid other than Arg

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 <221> VARIANT
 <222> (12)...(12)
 <223> Xaa = Tyr or Asp

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

<400> 9
 Gly Tyr Val Xaa Thr Leu Phe Gly Arg Xaa Xaa Xaa Xaa Pro
 1 5 10

<210> 10
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic DNA polymerase domain motif

<220>
 <221> VARIANT
 <222> (11)...(11)
 <223> Xaa = any amino acid other than Arg

<400> 10
 Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Xaa Tyr Val Pro
 1 5 10

<210> 11
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic DNA polymerase domain motif

<220>
 <221> VARIANT
 <222> (11)...(11)
 <223> Xaa = Ala, Cys, Asp, Gly or Asn

<400> 11
 Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Xaa Tyr Val Pro
 1 5 10

<210> 12
 <211> 34
 <212> PRT

<213> Artificial Sequence

<220>

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

<400> 12

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

<210> 13

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 13

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

<210> 14

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 14

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

<210> 15

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 15

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

<210> 16

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 16

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

Val Lys

<210> 17

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 17

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

Val Lys

<210> 18

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 18

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

Val Lys

<210> 19

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 19

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

Asp Arg

<210> 20

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 20

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

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<210> 21

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 21

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

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<210> 22

<400> 22

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<210> 23

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 23

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

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<210> 24

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 24

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

```

Asn Phe

<210> 25
 <211> 34
 <212> PRT
 <213> Artificial Sequence

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

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

<210> 26
 <211> 14
 <212> PRT
 <213> Artificial Sequence

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

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

<220>
 <221> VARIANT
 <222> (7)...(7)
 <223> Xaa = Phe, Tyr or Leu

<220>
 <221> VARIANT
 <222> (8)...(8)
 <223> Xaa = Gly or His

<220>
 <221> VARIANT
 <222> (10)...(10)
 <223> Xaa = Arg or Lys

<220>
 <221> VARIANT
 <222> (12)...(12)
 <223> Xaa = Tyr or Asp

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

<400> 26
 Gly Tyr Val Xaa Thr Leu Xaa Xaa Arg Xaa Arg Xaa Xaa Pro
 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 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
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Lys	Leu
Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Ile	Leu	Lys	Asn	Leu	Asp	Arg
Val	Lys	Pro	Glu	Ser	Val	Arg	Glu	Arg	Ile	Lys	Ala	His	Leu	Glu	Asp
225					230					235					240
Leu	Lys	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Ser	Asp	Leu	Pro	Leu
				245					250					255	
Glu	Val	Asp	Phe	Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Arg
			260					265					270		
Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly
		275					280					285			
Leu	Leu	Glu	Glu	Ser	Glu	Pro	Val	Gly	Tyr	Arg	Ile	Val	Lys	Asp	Leu
		290				295					300				
Val	Glu	Phe	Glu	Lys	Leu	Ile	Glu	Lys	Leu	Arg	Glu	Ser	Pro	Ser	Phe
305					310					315					320
Ala	Ile	Asp	Leu	Glu	Thr	Ser	Ser	Leu	Asp	Pro	Phe	Asp	Cys	Asp	Ile
			325						330				335		
Val	Gly	Ile	Ser	Val	Ser	Phe	Lys	Pro	Lys	Glu	Ala	Tyr	Tyr	Ile	Pro
			340					345					350		
Leu	His	His	Arg	Asn	Ala	Gln	Asn	Leu	Asp	Glu	Lys	Glu	Val	Leu	Lys
		355					360					365			
Lys	Leu	Lys	Glu	Ile	Leu	Glu	Asp	Pro	Gly	Ala	Lys	Ile	Val	Gly	Gln
		370				375					380				
Asn	Leu	Lys	Phe	Asp	Tyr	Lys	Val	Leu	Met	Val	Lys	Gly	Val	Glu	Pro
385					390					395					400
Val	Pro	Pro	Tyr	Phe	Asp	Thr	Met	Ile	Ala	Ala	Tyr	Leu	Leu	Glu	Pro
			405						410					415	
Asn	Glu	Lys	Lys	Phe	Asn	Leu	Asp	Asp	Leu	Ala	Leu	Lys	Phe	Leu	Gly
			420					425					430		
Tyr	Lys	Met	Thr	Ser	Tyr	Gln	Glu	Leu	Met	Ser	Phe	Ser	Phe	Pro	Leu
		435					440					445			
Phe	Gly	Phe	Ser	Phe	Ala	Asp	Val	Pro	Val	Glu	Lys	Ala	Ala	Asn	Tyr
		450				455					460				
Ser	Cys	Glu	Asp	Ala	Asp	Ile	Thr	Tyr	Arg	Leu	Tyr	Lys	Thr	Leu	Ser
465					470					475					480
Leu	Lys	Leu	His	Glu	Ala	Asp	Leu	Glu	Asn	Val	Phe	Tyr	Lys	Ile	Glu
			485						490					495	
Met	Pro	Leu	Val	Asn	Val	Leu	Ala	Arg	Met	Glu	Leu	Asn	Gly	Val	Tyr
			500					505					510		
Val	Asp	Thr	Glu	Phe	Leu	Lys	Lys	Leu	Ser	Glu	Glu	Tyr	Gly	Lys	Lys
		515					520					525			
Leu	Glu	Glu	Leu	Ala	Glu	Glu	Ile	Tyr	Arg	Ile	Ala	Gly	Glu	Pro	Phe
		530				535					540				
Asn	Ile	Asn	Ser	Pro	Lys	Gln	Val	Ser	Arg	Ile	Leu	Phe	Glu	Lys	Leu
545					550					555					560
Gly	Ile	Lys	Pro	Arg	Gly	Lys	Thr	Thr	Lys	Thr	Gly	Asp	Tyr	Ser	Thr
			565						570					575	
Arg	Ile	Glu	Val	Leu	Glu	Glu	Leu	Ala	Gly	Glu	His	Glu	Ile	Ile	Pro
			580					585					590		
Leu	Ile	Leu	Glu	Tyr	Arg	Lys	Ile	Gln	Lys	Leu	Lys	Ser	Thr	Tyr	Ile
		595					600					605			
Asp	Ala	Leu	Pro	Lys	Met	Val	Asn	Pro	Lys	Thr	Gly	Arg	Ile	His	Ala
		610				615					620				
Ser	Phe	Asn	Gln	Thr	Gly	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp
625					630					635					640
Pro	Asn	Leu	Gln	Asn	Leu	Pro	Thr	Lys	Ser	Glu	Glu	Gly	Lys	Glu	Ile
			645						650					655	
Arg	Lys	Ala	Ile	Val	Pro	Gln	Asp	Pro	Asn	Trp	Trp	Ile	Val	Ser	Ala
			660					665					670		
Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Ile	Leu	Ala	His	Leu	Ser	Gly	Asp
		675					680					685			
Glu	Asn	Leu	Leu	Arg	Ala	Phe	Glu	Glu	Gly	Ile	Asp	Val	His	Thr	Leu
		690				695					700				
Thr	Ala	Ser	Arg	Ile	Phe	Asn	Val	Lys	Pro	Glu	Glu	Val	Thr	Glu	Glu
705					710					715					720

21

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

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 BpI and BglII restriction sites

<400> 33
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 gtggacggag gacgccgccc accgggccct cctcgctgag cggctccagc aaaacctctt 120
 ggaacgcctc aaggagagag aaaagctcct ttggctctac caagaggtgg aaaagccccct 180
 ctcccgggtc ctggcccaaca tggaggccac cggggtaagg ctggacgtgg cctatctaaa 240
 ggccctttcc ctggagcttg cggaggagat tcgccgcctc gaggaggagg tcttccgcct 300
 ggcggggcac cccttcaacc tgaactccc tgaccagcta gagcgggtgc tctttgacga 360
 gcttaggctt ccgcccctgg gcaagacgca aaagacgggg aagcgtctca ccagcgccgc 420
 ggtgctggag gccctcaggg aggccacccc catcgtggag aagatcctcc agcaccggga 480
 gctcaccaag ctcaagaaca cctacgtaga cccctctccg ggcctcgtcc acccgaggac 540
 gggccgcctc cacaccgct tcaaccagac agccacggcc acgggaaggc tctctagctc 600
 cgggccaac ctgcagaaca tccccatccg cacccttg ggccagagga tccgcccggc 660
 cttcgtggcc gaggcgggat gggcgttggt ggccctggac tatagccaga tagagctccg 720
 ggtcctcgcc cacctctccg gggacgagaa cctgatcagg gtcttccagg aggggaagga 780
 catccacacc cagaccgcaa gctggatggt cggcgtctcc ccggaggccg tggacccccct 840
 gatgcgccg gcgccaaga cggatgaact cggcgtctcc tacggcatgt ccgcccatag 900
 gctctccag gagcttgaca tcccctacga ggaggcgggt gcctttatag agcgtactt 960
 ccaagcttc cccaagggtc gggcctggat agaaaagacc ctggaggagg ggaggaagcg 1020
 gggctacgtg gaaacctct tcggaagaag gcgctacgtg cccgacctca acgcccgggt 1080
 gaagagcgct agggaggccg cggagcgcat ggccttcaac atgcccgtcc agggcaccgc 1140

24

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cgccgacctc atgaagctcg ccatggtgaa gctcttcccc cacctccggg agatgggggc 1200
ccgcatgctc ctccagggtcc acgacgagct cctcctggag gccccccaag cgcgggccga 1260
ggaggtggcg gctttggcca aggaggccat ggagaaggcc tatccccctc ccgtgcccct 1320
ggaggtggag gtggggatcg gggaggactg gctttccgcc aagggtgat atcagatctc 1380
cctgattatg cgtcagtcta tgaagaaaaa tcgtatacag atggacgaag agagaatcct 1440
tgtgaattta acagagggtg tagggattac acgccactac cagttgggta t 1491
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<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic wild-type BRAF V600K target polynucleotide

<400> 34

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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

<400> 35

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<210> 36

<211> 921

<212> PRT

<213> Deinococcus radiodurans

<220>

<223> Deinococcus radiodurans DNA polymerase (Dra)

<400> 36

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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
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	210					215					220				
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	Leu 270	Val
Thr	Glu	Asp 275	Leu	Leu	Thr	Glu	Leu	Glu 280	Leu	His	Ser	Leu 285	Arg	Pro	Met
Ile 290	Leu	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 500	Ile	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 605	Val	Ser	Ala
Leu	Glu 610	Pro	Leu	Arg	Asp	Ala 615	His	Pro	Ile	Ile	Pro 620	Leu	Val	Leu	Glu
Phe 625	Arg	Glu	Leu	Asp	Lys 630	Leu	Arg	Gly	Thr	Tyr 635	Leu	Asp	Pro	Ile	Pro 640
Asn	Leu	Val	Asn	Pro 645	His	Thr	Gly	Arg	Leu 650	His	Thr	Thr	Phe	Ala 655	Gln
Thr	Ala	Val	Ala 660	Thr	Gly	Arg	Leu	Ser 665	Ser	Leu	Asn	Pro	Asn 670	Leu	Gln
Asn	Ile	Pro 675	Ile	Arg	Ser	Glu	Leu 680	Gly	Arg	Glu	Ile	Arg 685	Lys	Gly	Phe
Ile	Ala	Glu 690	Asp	Gly	Phe	Thr 695	Leu	Ile	Ala	Ala	Asp 700	Tyr	Ser	Gln	Ile
Glu 705	Leu	Arg	Leu	Leu	Ala 710	His	Ile	Ala	Asp	Asp 715	Pro	Leu	Met	Gln	Gln 720
Ala	Phe	Val	Glu 725	Gly	Ala	Asp	Ile	His	Arg 730	Arg	Thr	Ala	Ala	Gln 735	Val
Leu	Gly	Leu	Asp 740	Glu	Ala	Thr	Val	Asp 745	Ala	Asn	Gln	Arg	Arg 750	Ala	Ala
Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu

		755					760		20		765			
Ser	Asn 770	Leu	Gly	Ile	Pro 775	Tyr	Ala	Glu	Ala	Ala 780	Thr	Phe	Ile	Glu
Ile	Tyr	Phe	Ala	Thr	Tyr 790	Pro	Gly	Ile	Arg	Arg 795	Tyr	Ile	Asn	His
785														Thr 800
Leu	Asp	Phe	Gly	Arg 805	Thr	His	Gly	Tyr	Val 810	Glu	Thr	Leu	Tyr	Gly 815
														Arg
Arg	Arg	Tyr	Val 820	Pro	Gly	Leu	Ser	Ser 825	Arg	Asn	Arg	Val	Gln 830	Arg
														Glu
Ala	Glu	Glu 835	Arg	Leu	Ala	Tyr	Asn 840	Met	Pro	Ile	Gln	Gly 845	Thr	Ala
														Ala
Asp	Ile 850	Met	Lys	Leu	Ala	Met 855	Val	Gln	Leu	Asp	Pro 860	Gln	Leu	Asp
														Ala
Ile	Gly	Ala	Arg	Met	Leu 870	Leu	Gln	Val	His	Asp 875	Glu	Leu	Leu	Ile
865														Glu 880
Ala	Pro	Leu	Asp	Lys 885	Ala	Glu	Gln	Val	Ala 890	Ala	Leu	Thr	Lys	Lys 895
														Val
Met	Glu	Asn	Val 900	Val	Gln	Leu	Lys	Val 905	Pro	Leu	Ala	Val	Glu 910	Val
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Thr	Gly	Pro 915	Asn	Trp	Phe	Asp	Thr 920	Lys						

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

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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	Glu	Leu		

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
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Phe	Leu	Lys	Gln	Ile	Leu	Gln	Glu	Lys	Asp	Tyr	Asn	Ile	Val	Gly	Gln
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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
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<210> 38
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 <212> PRT
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<220>
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 His Ile Ile Val Gly Lys Asp Tyr Val Ala Val Ala Phe Asp Lys Lys
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 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
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 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
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 Lys Leu Lys Glu Ile Leu Glu Asp Pro Gly Ala Lys Ile Val Gly Gln
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 Asn Leu Lys Phe Asp Tyr Lys Val Leu Met Val Lys Gly Val Glu Pro

385	Val	Pro	Pro	Tyr	Phe	Asp	Thr	Met	Ile	Ala	Ala	Tyr	Leu	Leu	Glu	Pro
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Asn	Glu	Lys	Lys	Phe	Asn	Leu	Asp	Asp	Leu	Ala	Leu	Lys	Phe	Leu	Gly	
			420					425					430			
Tyr	Lys	Met	Thr	Ser	Tyr	Gln	Glu	Leu	Met	Ser	Phe	Ser	Phe	Pro	Leu	
		435					440					445				
Phe	Gly	Phe	Ser	Phe	Ala	Asp	Val	Pro	Val	Glu	Lys	Ala	Ala	Asn	Tyr	
	450					455					460					
Ser	Cys	Glu	Asp	Ala	Asp	Ile	Thr	Tyr	Arg	Leu	Tyr	Lys	Thr	Leu	Ser	
465					470					475					480	
Leu	Lys	Leu	His	Glu	Ala	Asp	Leu	Glu	Asn	Val	Phe	Tyr	Lys	Ile	Glu	
				485					490					495		
Met	Pro	Leu	Val	Asn	Val	Leu	Ala	Arg	Met	Glu	Leu	Asn	Gly	Val	Tyr	
			500					505					510			
Val	Asp	Thr	Glu	Phe	Leu	Lys	Lys	Leu	Ser	Glu	Glu	Tyr	Gly	Lys	Lys	
		515					520					525				
Leu	Glu	Glu	Leu	Ala	Glu	Glu	Ile	Tyr	Arg	Ile	Ala	Gly	Glu	Pro	Phe	
	530					535					540					
Asn	Ile	Asn	Ser	Pro	Lys	Gln	Val	Ser	Arg	Ile	Leu	Phe	Glu	Lys	Leu	
545					550					555					560	
Gly	Ile	Lys	Pro	Arg	Gly	Lys	Thr	Thr	Lys	Thr	Gly	Asp	Tyr	Ser	Thr	
				565					570					575		
Arg	Ile	Glu	Val	Leu	Glu	Glu	Leu	Ala	Gly	Glu	His	Glu	Ile	Ile	Pro	
			580					585					590			
Leu	Ile	Leu	Glu	Tyr	Arg	Lys	Ile	Gln	Lys	Leu	Lys	Ser	Thr	Tyr	Ile	
	595						600					605				
Asp	Ala	Leu	Pro	Lys	Met	Val	Asn	Pro	Lys	Thr	Gly	Arg	Ile	His	Ala	
	610					615					620					
Ser	Phe	Asn	Gln	Thr	Gly	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp	
625					630					635					640	
Pro	Asn	Leu	Gln	Asn	Leu	Pro	Thr	Lys	Ser	Glu	Glu	Gly	Lys	Glu	Ile	
				645					650					655		
Arg	Lys	Ala	Ile	Val	Pro	Gln	Asp	Pro	Asn	Trp	Trp	Ile	Val	Ser	Ala	
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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> 39
 <211> 893
 <212> PRT

<213> Thermotoga neopolitana

<220>

<223> Thermotoga neopolitana DNA polymerase (Tne)

<400> 39

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

31

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	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

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

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			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	Gln	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	Ala	Ala	Ala	Tyr	Leu
385					390					395					400
Leu	Asp	Pro	Ala	Gln	Gly	Val	Asp	Asp	Val	Ala	Ala	Ala	Ala	Lys	Met
			405						410					415	
Lys	Gln	Tyr	Glu	Ala	Val	Arg	Pro	Asp	Glu	Ala	Val	Tyr	Gly	Lys	Gly
			420					425					430		
Ala	Lys	Arg	Ala	Val	Pro	Asp	Glu	Pro	Val	Leu	Ala	Glu	His	Leu	Val
		435					440					445			
Arg	Lys	Ala	Ala	Ala	Ile	Trp	Ala	Leu	Glu	Arg	Pro	Phe	Leu	Asp	Glu
	450					455					460				
Leu	Arg	Arg	Asn	Glu	Gln	Asp	Arg	Leu	Leu	Val	Glu	Leu	Glu	Gln	Pro
465					470					475					480
Leu	Ser	Ser	Ile	Leu	Ala	Glu	Met	Glu	Phe	Ala	Gly	Val	Lys	Val	Asp
			485						490				495		
Thr	Lys	Arg	Leu	Glu	Gln	Met	Gly	Glu	Glu	Leu	Ala	Glu	Gln	Leu	Arg
			500					505					510		
Thr	Val	Glu	Gln	Arg	Ile	Tyr	Glu	Leu	Ala	Gly	Gln	Glu	Phe	Asn	Ile
		515					520					525			
Asn	Ser	Pro	Lys	Gln	Leu	Gly	Val	Ile	Leu	Phe	Glu	Lys	Leu	Gln	Leu
	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	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
 Ile Glu Arg Tyr Phe Glu Ser Phe Pro Gly Val Lys Arg Tyr Met Glu
 Asn Ile Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu
 His Arg Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val
 Arg Ser Phe Ala Glu Arg Met Ala Met Asn Thr Pro Ile Gln Gly Ser
 Ala Ala Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Asn Ala Arg Leu
 Lys Glu Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu
 Leu Ile Leu Glu Ala Pro Lys Glu Glu Met Glu Arg Leu Cys Arg Leu
 Val Pro Glu Val Met Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys
 Val Asp Tyr His Tyr Gly Ser Thr Trp Tyr Asp Ala Lys
 865 870 875

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 Tyr, Cys, Asn, Gln, Asp, Glu, Lys, Val, Ile or His

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 <223> Xaa = Val, Ile or Leu

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 Gly Tyr Val Xaa Thr Leu Xaa Xaa Arg Xaa Xaa Xaa Xaa Pro

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