

SEQUENCE LISTING

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

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

<130> 27220 WO-HS

<140> Not yet assigned

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<150> US 61/443,128

<151> 2011-02-15

<160> 42

<170> FastSEQ for windows Version 4.0

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<211> 834

<212> PRT

<213> Thermus sp.

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

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Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
35     40     45
Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe
50     55     60
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
65     70     75     80
Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85     90     95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
100    105    110
Glu Val Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys
115    120    125
Lys Ala Glu Arg Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg
130    135    140
Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu
145    150    155    160
Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys
165    170    175
Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp
180    185    190
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu
195    200    205
Leu Lys Glu Trp Gly Ser Leu Glu Asn Ile Leu Lys Asn Leu Asp Arg
210    215    220
Val Lys Pro Glu Ser Val Arg Glu Arg Ile Lys Ala His Leu Glu Asp
225    230    235    240
Leu Lys Leu Ser Leu Glu Leu Ser Arg Val Arg Ser Asp Leu Pro Leu
245    250    255
Glu Val Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Arg
260    265    270
Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
275    280    285
Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro
290    295    300
Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp
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305	Ala	Glu	Leu	Lys	Ala	310	Leu	Ala	Ala	Cys	Lys	315	Glu	Gly	Arg	Val	His	320	Arg
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Leu	Ala	Pro	Ser	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro				
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Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp				
385					390					395					400				
Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ala	Glu	Arg	Leu	Gln	Gln				
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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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465					470					475					480				
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Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Gly	Lys	Thr	Gln	Lys	Thr	Gly				
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Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His				
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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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Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Ile	Arg	Thr	Pro	Leu				
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Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu				
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Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	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	Ser	Pro	Glu	Ala	Val				
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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				
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Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val				
		755					760					765							
Lys	Leu	Phe	Pro	His	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln				
		770				775						780							
Val	His	Asp	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu				
785					790					795					800				
Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala				
				805					810					815					
Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala				
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 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
 35 40 45
 Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val
 50 55 60
 Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly
 65 70 75 80
 Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
 85 90 95
 Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu
 100 105 110
 Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys
 115 120 125
 Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp
 130 135 140
 Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly
 145 150 155 160
 Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
 165 170 175
 Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn
 180 185 190
 Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu
 195 200 205
 Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu
 210 215 220
 Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys
 225 230 235 240
 Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val
 245 250 255
 Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe
 260 265 270
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
 275 280 285
 Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Glu Gly
 290 295 300
 Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp
 305 310 315 320
 Leu Leu Ala Leu Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro
 325 330 335
 Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu
 340 345 350
 Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro
 355 360 365
 Pro Gly Asp Asp Pro Met Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400
 Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu
 405 410 415
 Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu
 420 425 430
 Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala

Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu
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 Asn Leu Ile Arg Val Phe Arg Glu Gly Lys Asp Ile His Thr Glu Thr
 625 630 635 640
 Ala Ala Trp Met Phe Gly Val Pro Pro Glu Gly Val Asp Gly Ala Met
 645 650 655
 Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser
 660 665 670
 Ala His Arg Leu Ser Gln Glu Leu Ser Ile Pro Tyr Glu Glu Ala Ala
 675 680 685
 Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp
 690 695 700
 Ile Ala Lys Thr Leu Glu 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
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 Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln
 740 745 750
 Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro
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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
 Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Val Val Val Val
 50 55 60
 Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala Tyr
 65 70 75 80
 Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
 85 90 95
 Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Val Arg Leu Glu Val
 100 105 110
 Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Arg Ala
 115 120 125
 Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
 130 135 140
 Tyr Gln Leu Leu Ser Glu Arg Ile Ala Ile Leu His Pro Glu Gly Tyr
 145 150 155 160
 Leu Ile Thr Pro Ala Trp Leu Tyr Glu Lys Tyr Gly Leu Arg Pro Glu
 165 170 175
 Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
 180 185 190
 Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Gln Arg Leu Ile Arg
 195 200 205
 Glu Trp Gly Ser Leu Glu Asn Leu Phe Gln His Leu Asp Gln Val Lys
 210 215 220

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Ser	Arg	Lys	Leu	Ser	Gln	Val	His	Thr	Asp	Leu	Pro	Leu	Glu	Val	Asp
				245					250					255	
Phe	Gly	Arg	Arg	Arg	Thr	Pro	Asn	Leu	Gly	Gly	Leu	Arg	Ala	Phe	Leu
			260					265					270		
Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu	Glu
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Gly	Pro	Lys	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala
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Phe	Leu	Gly	Phe	Ser	Phe	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	Leu
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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
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Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	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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Glu	Arg	Leu	Lys	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Glu	Glu	Val
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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
	450					455					460				
Glu	Val	Arg	Gln	Leu	Glu	Glu	Val	Phe	Arg	Arg	Leu	Ala	Gly	His	Pro
465					470				475						480
Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp	Glu
				485					490					495	
Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	Arg	Ser
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Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile	Val
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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
			565						570					575	
Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg
			580					585					590		
Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Gly	Trp	Val	Leu	Val	Val	Leu	
		595					600				605				
Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp
	610				615					620					
Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr	Gln
625					630					635					640
Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Ser	Pro	Glu	Gly	Val	Asp	Pro	Leu
				645					650					655	
Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met
			660					665					670		
Ser	Ala	His	Arg	Leu	Ser	Gly	Glu	Leu	Ser	Ile	Pro	Tyr	Glu	Glu	Ala
		675					680					685			
Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Tyr	Pro	Lys	Val	Arg	Ala
	690					695					700				
Trp	Ile	Glu	Gly	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	Val	Glu
705					710					715					720
Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala	Arg	Val
				725					730					735	
Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val
			740					745					750		
Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Arg	Leu	Phe

		755				760				765					
Pro	Arg	Leu	Gln	Glu	Leu	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His	Asp
	770					775					780				
Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Asp	Arg	Ala	Glu	Arg	Val	Ala	Ala
785					790					795					800
Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Trp	Pro	Leu	Gln	Val	Pro	Leu
				805					810					815	
Glu	Val	Glu	Val	Gly	Leu	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Glu	
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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
 145 150 155 160
 Thr Pro Gly Trp Leu Gln Glu Arg Tyr Gly Leu Ser Pro Glu Arg Trp
 165 170 175
 Val Glu Tyr Arg Ala Leu Val Gly Asp Pro Ser Asp Asn Leu Pro Gly
 180 185 190
 Val Pro Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu Leu Lys Glu Trp
 195 200 205
 Gly Ser Leu Glu Ala Ile Leu Lys Asn Leu Asp Gln Val Lys Pro Glu
 210 215 220
 Arg Val Arg Glu Ala Ile Arg Asn Asn Leu Asp Lys Leu Gln Met Ser
 225 230 235 240
 Leu Glu Leu Ser Arg Leu Arg Thr Asp Leu Pro Leu Glu Val Asp Phe
 245 250 255
 Ala Lys Arg Arg Glu Pro Asp Trp Glu Gly Leu Lys Ala Phe Leu Glu
 260 265 270
 Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ala
 275 280 285
 Pro Lys Glu Ala Glu Glu Ala Pro Trp Pro Pro Gly Gly Ala Phe
 290 295 300
 Leu Gly Phe Leu Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Leu
 305 310 315 320
 Ala Leu Ala Gly Ala Lys Glu Gly Arg Val His Arg Ala Glu Asp Pro
 325 330 335
 Val Gly Ala Leu Lys Asp Leu Lys Glu Ile Arg Gly Leu Leu Ala Lys
 340 345 350
 Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Arg Glu Ile Pro Pro Gly
 355 360 365
 Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Gly Asn Thr Asn

370	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Lys	Glu	Asp	Ala
385	Ala	Ala	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	Trp	Gln	Ala	Leu	Tyr	Pro
	Arg	Val	Ala	Glu	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	Glu	Val	Glu
	Arg	Pro	Leu	Ala	Gln	Val	Leu	Ala	His	Met	Glu	Ala	Thr	Gly	Val	Arg
	Leu	Asp	Val	Pro	Tyr	Leu	Glu	Ala	Leu	Ser	Gln	Glu	Val	Ala	Phe	Glu
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	Gly	Leu	Pro	Pro	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	Arg	Ser	Thr
	Ser	Ala	Ala	Val	Leu	Glu	Leu	Leu	Arg	Glu	Ala	His	Pro	Ile	Val	Gly
	Arg	Ile	Leu	Glu	Tyr	Arg	Glu	Leu	Met	Lys	Leu	Lys	Ser	Thr	Tyr	Ile
	Asp	Pro	Leu	Pro	Arg	Leu	Val	His	Pro	Lys	Thr	Gly	Arg	Leu	His	Thr
	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp
	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg	Ile
	Arg	Lys	Ala	Phe	Ile	Ala	Glu	Glu	Gly	His	Leu	Leu	Val	Ala	Leu	Asp
	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp	Glu
	Asn	Leu	Ile	Arg	Val	Phe	Arg	Glu	Gly	Lys	Asp	Ile	His	Thr	Glu	Thr
	Ala	Ala	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Gly	Val	Asp	Gly	Ala	Met
	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser
	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ser	Ile	Pro	Tyr	Glu	Glu	Ala	Ala
	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg	Ala	Trp
	Ile	Ala	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Lys	Gly	Tyr	Val	Glu	Thr
	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala	Arg	Val	Lys
	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val	Gln
	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu	Phe	Pro
	Arg	Leu	Arg	Pro	Leu	Gly	Val	Arg	Ile	Leu	Leu	Gln	Val	His	Asp	Glu
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	Ala	Lys	Glu	Thr	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ser	Val	Pro	Leu	Glu
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<220>
 <223> Thermus thermophilus DNA polymerase (Tth)

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 35 35 Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe
 50 50 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
 65 65 Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 85 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
 100 100 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys
 115 115 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg
 130 130 Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu
 145 145 Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 165 Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp
 180 180 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu
 195 195 Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg
 210 210 Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp
 225 225 Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu
 245 245 Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg
 260 260 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 275 275 Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro
 290 290 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp
 305 305 Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val His Arg
 325 325 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 340 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 355 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 370 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 385 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 405 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 420 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 435 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 450 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
 465 465 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 485 Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly
 500 500 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 515 520 525

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

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

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

<400> 7
 Met Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
 1 5 10 15
 Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly
 20 25 30
 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
 35 40 45
 Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
 65 70 75 80
 Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys
 115 120 125
 Asn Pro Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg

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	Gly	Ala	Glu	Glu	
	785				790				795					800	
Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala
			805						810					815	
Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala
			820					825					830		
Lys	Gly														

<210> 8
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic DNA polymerase domain motif

<220>
 <221> VARIANT
 <222> (2)...(2)
 <223> Xaa = Asp, Thr, Asn or Ser

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

<220>
 <221> VARIANT
 <222> (4)...(4)
 <223> Xaa = Leu, Ala, Glu, Gln or Asn

<220>
 <221> VARIANT
 <222> (5)...(5)
 <223> Xaa = Met or Gln

<220>
 <221> VARIANT
 <222> (8)...(8)
 <223> Xaa = Ala, Val, Gln or Ser

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

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

<220>

<221> VARIANT
<222> (12)...(12)
<223> Xaa = Val or Ile

<400> 8
Val Xaa Xaa Xaa Xaa Arg Arg Xaa Xaa Lys Xaa Xaa Asn Phe
1 5 10

<210> 9
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic DNA polymerase domain motif

<220>
<221> VARIANT
<222> (2)...(2)
<223> Xaa = Asp, Thr or Asn

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

<220>
<221> VARIANT
<222> (4)...(4)
<223> Leu, Ala or Glu

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

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

<220>
<221> VARIANT
<222> (11)...(11)
<223> Xaa = Thr or Met

<220>
<221> VARIANT
<222> (12)...(12)
<223> Xaa = Val or Ile

<400> 9
Val Xaa Xaa Xaa Met Arg Arg Xaa Xaa Lys Xaa Xaa Asn Phe
1 5 10

<210> 10
<211> 14
<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 Ala or Gly
 <400> 10
 Val Asp Pro Leu Met Arg Arg Ala Xaa Lys Thr Val Asn Phe
 1 5 10

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

<220>
 <223> synthetic DNA polymerase domain motif

<220>
 <221> VARIANT
 <222> (9)...(9)
 <223> Xaa = Thr or Val

<400> 11
 Val Asp Pro Leu Met Arg Arg Ala Xaa Lys Thr Val Asn Phe
 1 5 10

<210> 12
 <211> 38
 <212> PRT
 <213> Artificial Sequence

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

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

<210> 13
 <211> 38
 <212> PRT
 <213> Artificial Sequence

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

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

<210> 14
 <211> 38
 <212> PRT
 <213> Artificial Sequence

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

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

<210> 15
 <211> 38
 <212> PRT
 <213> Artificial Sequence

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

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

<210> 16
 <211> 38
 <212> PRT
 <213> Artificial Sequence

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

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

<210> 17
 <211> 38
 <212> PRT
 <213> Artificial Sequence

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

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

<210> 18
 <211> 38
 <212> PRT
 <213> Artificial Sequence

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

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

<210> 19
 <211> 38
 <212> PRT
 <213> Artificial Sequence

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

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

<210> 20
 <211> 38
 <212> PRT
 <213> Artificial Sequence

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

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

<210> 21
 <211> 38
 <212> PRT
 <213> Artificial Sequence

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

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

Gly Leu Ser Lys Arg Ile
 20 25 30
 35

<210> 22
 <211> 38
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic region from polymerase domain of
 Escherichia coli DNA polymerase (E. coli)

<400> 22
 Glu Val Phe Gly Leu Pro Leu Glu Thr Val Thr Ser Glu Gln Arg Arg
 1 5 10 15
 Ser Ala Lys Ala Ile Asn Phe Gly Leu Ile Tyr Gly Met Ser Ala Phe
 20 25 30
 Gly Leu Ala Arg Gln Leu
 35

<210> 23
 <211> 38
 <212> PRT
 <213> Artificial Sequence

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

<400> 23
 Gln Val Leu Gly Leu Asp Glu Ala Thr Val Asp Ala Asn Gln Arg Arg
 1 5 10 15
 Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His
 20 25 30
 Arg Leu Ser Asn Asp Leu
 35

<210> 24
 <211> 38
 <212> PRT
 <213> Artificial Sequence

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

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

<210> 25
 <211> 38
 <212> PRT
 <213> Artificial Sequence

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

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

<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> (2)...(2)
 <223> Xaa = Asp, Thr, Asn or Ser

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

<220>
 <221> VARIANT
 <222> (4)...(4)
 <223> Xaa = Leu, Ala, Glu, Gln or Asn

<220>
 <221> VARIANT
 <222> (5)...(5)
 <223> Xaa = Met or Gln

<220>
 <221> VARIANT
 <222> (8)...(8)
 <223> Xaa = Ala, Val, Gln or Ser

<220>
 <221> VARIANT
 <222> (9)...(9)
 <223> Xaa = Ala or Gly

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

<220>
 <221> VARIANT
 <222> (12)...(12)
 <223> Xaa = Val or Ile

<400> 26
 Val Xaa Xaa Xaa Xaa Arg Arg Xaa Xaa Lys Xaa Xaa Asn Phe
 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 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	Val	Asp	Phe	Arg	Ala	170	Leu	Val	Gly	Asp	Pro	Ser
Pro	Glu	Gln	180	Val	Asp	Phe	Arg	Ala	185	Leu	Val	Gly	Asp	Pro	Ser
Asn	Leu	Pro	195	Gly	Val	Lys	Gly	Ile	200	Gly	Lys	Thr	Ala	205	Lys
Leu	Lys	Glu	210	Trp	Gly	Ser	Leu	Glu	215	Asn	Ile	Leu	Lys	220	Asn
Val	Lys	Pro	225	Glu	Ser	Val	Arg	Glu	230	Arg	Ile	Lys	235	Ala	His
Leu	Lys	Leu	245	Ser	Leu	Glu	Leu	Ser	250	Val	Arg	Ser	Asp	Leu	Pro
Glu	Val	Asp	260	Phe	Ala	Arg	Arg	Arg	265	Glu	Pro	Asp	Arg	Glu	Gly
Ala	Phe	Leu	275	Glu	Arg	Leu	Glu	Phe	280	Gly	Ser	Leu	Leu	His	285
Leu	Leu	Glu	290	Glu	Ser	Glu	Pro	Val	295	Gly	Tyr	Arg	Ile	300	Val
Val	Glu	Phe	305	Glu	Lys	Leu	Ile	Glu	310	Lys	Leu	Arg	Glu	Ser	Pro
Ala	Ile	Asp	325	Leu	Glu	Thr	Ser	Ser	330	Leu	Asp	Pro	Phe	Asp	Cys
Val	Gly	Ile	340	Ser	Val	Ser	Phe	Lys	345	Pro	Lys	Glu	Ala	Tyr	Tyr
Leu	His	His	355	Arg	Asn	Ala	Gln	Asn	360	Leu	Asp	Glu	Lys	Glu	Val
Lys	Leu	Lys	370	Glu	Ile	Leu	Glu	Asp	375	Pro	Gly	Ala	Lys	Ile	Val
Asn	Leu	Lys	385	Phe	Asp	Tyr	Lys	Val	390	Leu	Met	Val	Lys	Gly	Val
Val	Pro	Pro	405	Tyr	Phe	Asp	Thr	Met	410	Ile	Ala	Ala	Tyr	Leu	Leu
Asn	Glu	Lys	420	Lys	Phe	Asn	Leu	Asp	425	Asp	Leu	Ala	Leu	Lys	Phe
Tyr	Lys	Met	435	Thr	Ser	Tyr	Gln	Glu	440	Leu	Met	Ser	Phe	Ser	Phe
Phe	Gly	Phe	450	Ser	Phe	Ala	Asp	455	Val	Pro	Val	Glu	Lys	460	Ala
Ser	Cys	Glu	465	Asp	Ala	Asp	Ile	Thr	470	Tyr	Arg	Leu	Tyr	Lys	Thr
Leu	Lys	Leu	485	His	Glu	Ala	Asp	Leu	490	Glu	Asn	Val	Phe	Tyr	Lys
Met	Pro	Leu	500	Val	Asn	Val	Leu	Ala	505	Arg	Met	Glu	Leu	Asn	Gly
Val	Asp	Thr	515	Glu	Phe	Leu	Lys	Lys	520	Leu	Ser	Glu	Glu	Tyr	Gly
Leu	Glu	Glu	530	Leu	Ala	Glu	Glu	Ile	535	Tyr	Arg	Ile	Ala	Gly	Glu
Asn	Ile	Asn	545	Ser	Pro	Lys	Gln	Val	550	Ser	Arg	Ile	Leu	Phe	Glu
Gly	Ile	Lys	565	Pro	Arg	Gly	Lys	Thr	570	Thr	Lys	Thr	Gly	Asp	Tyr
Arg	Ile	Glu	580	Val	Leu	Glu	Glu	Leu	585	Ala	Gly	Glu	His	Glu	Ile
Leu	Ile	Leu	595	Glu	Tyr	Arg	Lys	Ile	600	Gln	Lys	Leu	Lys	Ser	Thr
Asp	Ala	Leu	610	Pro	Lys	Met	Val	Asn	615	Pro	Lys	Thr	Gly	Arg	Ile
Ser	Phe	Asn	625	Gln	Thr	Gly	Thr	Ala	630	Thr	Gly	Arg	Leu	Ser	Ser
Pro	Asn	Leu	645	Gln	Asn	Leu	Pro	Thr	650	Lys	Ser	Glu	Glu	Gly	Lys
Arg	Lys	Ala	660	Ile	Val	Pro	Gln	Asp	665	Pro	Asn	Trp	Trp	Ile	Val
Asp	Tyr	Ser	675	Gln	Ile	Glu	Leu	Arg	680	Ile	Leu	Ala	His	Leu	Ser
Glu	Asn	Leu		Leu	Arg	Ala	Phe	Glu		Glu	Gly	Ile	Asp	Val	His

690	695	700													
Thr	Ala	Ser	Arg	Ile	Phe	Asn	Val	Lys	Pro	Glu	Glu	Val	Thr	Glu	Glu
705					710					715					720
Met	Arg	Arg	Ala	Gly	Lys	Met	Val	Asn	Phe	Ser	Ile	Ile	Tyr	Gly	Val
				725					730					735	
Thr	Pro	Tyr	Gly	Leu	Ser	Val	Arg	Leu	Gly	Val	Pro	Val	Lys	Glu	Ala
			740					745					750		
Glu	Lys	Met	Ile	Val	Asn	Tyr	Phe	Val	Leu	Tyr	Pro	Lys	Val	Arg	Asp
		755					760					765			
Tyr	Ile	Gln	Arg	Val	Val	Ser	Glu	Ala	Lys	Glu	Lys	Gly	Tyr	Val	Arg
	770					775					780				
Thr	Leu	Phe	Gly	Arg	Lys	Arg	Asp	Ile	Pro	Gln	Leu	Met	Ala	Arg	Asp
785					790					795					800
Arg	Asn	Thr	Gln	Ala	Glu	Gly	Glu	Arg	Ile	Ala	Ile	Asn	Thr	Pro	Ile
			805						810					815	
Gln	Gly	Thr	Ala	Ala	Asp	Ile	Ile	Lys	Leu	Ala	Met	Ile	Glu	Ile	Asp
			820					825					830		
Arg	Glu	Leu	Lys	Glu	Arg	Lys	Met	Arg	Ser	Lys	Met	Ile	Ile	Gln	Val
		835					840					845			
His	Asp	Glu	Leu	Val	Phe	Glu	Val	Pro	Asn	Glu	Glu	Lys	Asp	Ala	Leu
	850					855					860				
Val	Glu	Leu	Val	Lys	Asp	Arg	Met	Thr	Asn	Val	Val	Lys	Leu	Ser	Val
865					870					875					880
Pro	Leu	Glu	Val	Asp	Val	Thr	Ile	Gly	Lys	Thr	Trp	Ser			
				885					890						

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

<220>
 <223> synthetic chimeric CS6 DNA polymerase derived from
 N-terminal 5'-nuclease domain of Thermus sp. Z05
 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
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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
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Val	Lys	Pro	Glu	Ser	Val	Arg	Glu	Arg	Ile	Lys	Ala	His	Leu	Glu	Asp
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Leu	Lys	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Ser	Asp	Leu	Pro	Leu
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Glu	Val	Asp	Phe	Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Arg
			260					265					270		
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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
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Val	Gly	Ile	Ser	Val	Ser	Phe	Lys	Pro	Lys	Glu	Ala	Tyr	Tyr	Ile	Pro
			340					345					350		
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		355					360					365			
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					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
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Phe	Gly	Phe	Ser	Phe	Ala	Asp	Val	Pro	Val	Glu	Lys	Ala	Ala	Asn	Tyr
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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
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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
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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
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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
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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	Gly	Lys	Glu	Ile	
				645					650				655		
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			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
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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


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gctctcccag gagcttgcca tcccctacga ggaggcggtg gcctttatag agcgctactt 960
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cctgattatg cgtcagtcta tgaagaaaaa tcgtatacag atggacgaag agagaatcct 1440
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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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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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<210> 36
 <211> 921
 <212> PRT
 <213> Deinococcus radiodurans

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

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<400> 36
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Ile Asp Gly His Ala Leu Ala Phe Arg Ser Tyr Phe Ala Leu Pro Pro
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Leu Asn Asn Ser Lys Gly Glu Met Thr Asp Ala Ile Val Gly Phe Met
35     40     45
Lys Leu Leu Leu Arg Leu Ala Arg Gln Lys Ser Asn Gln Val Ile Val
50     55     60
Val Phe Asp Pro Pro Val Lys Thr Leu Arg His Glu Gln Tyr Glu Gly
65     70     75     80
Tyr Lys Ser Gly Arg Ala Gln Thr Pro Glu Asp Leu Arg Gly Gln Ile
85     90     95
Asn Arg Ile Arg Ala Leu Val Asp Ala Leu Gly Phe Pro Arg Leu Glu
100    105    110
Glu Pro Gly Tyr Glu Ala Asp Asp Val Ile Ala Ser Leu Thr Arg Met
115    120    125
Ala Glu Gly Lys Gly Tyr Glu Val Arg Ile Val Thr Ser Asp Arg Asp
130    135    140
Ala Tyr Gln Leu Leu Asp Glu His Val Lys Val Ile Ala Asn Asp Phe
145    150    155    160

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Arg	Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Ala	Ser	Asp	Asn
			180					185					190		
Ile	Pro	Gly	Ala	Lys	Gly	Ile	Gly	Pro	Lys	Thr	Ala	Ala	Lys	Leu	Leu
		195					200					205			
Gln	Glu	Tyr	Gly	Thr	Leu	Glu	Lys	Val	Tyr	Glu	Ala	Ala	His	Ala	Gly
	210					215					220				
Thr	Leu	Lys	Pro	Asp	Gly	Thr	Arg	Lys	Lys	Leu	Leu	Asp	Ser	Glu	Glu
	225				230					235					240
Asn	Val	Lys	Phe	Ser	His	Asp	Leu	Ser	Cys	Met	Val	Thr	Asp	Leu	Pro
				245					250					255	
Leu	Asp	Ile	Glu	Phe	Gly	Val	Arg	Arg	Leu	Pro	Asp	Asn	Pro	Leu	Val
			260					265					270		
Thr	Glu	Asp	Leu	Leu	Thr	Glu	Leu	Glu	Leu	His	Ser	Leu	Arg	Pro	Met
		275					280					285			
Ile	Leu	Gly	Leu	Asn	Gly	Pro	Glu	Gln	Asp	Gly	His	Ala	Pro	Asp	Asp
	290					295					300				
Leu	Leu	Glu	Arg	Glu	His	Ala	Gln	Thr	Pro	Glu	Glu	Asp	Glu	Ala	Ala
	305				310					315					320
Ala	Leu	Pro	Ala	Phe	Ser	Ala	Pro	Glu	Leu	Ala	Glu	Trp	Gln	Thr	Pro
				325					330					335	
Ala	Glu	Gly	Ala	Val	Trp	Gly	Tyr	Val	Leu	Ser	Arg	Glu	Asp	Asp	Leu
			340					345					350		
Thr	Ala	Ala	Leu	Leu	Ala	Ala	Ala	Thr	Phe	Glu	Asp	Gly	Val	Ala	Arg
		355					360					365			
Pro	Ala	Arg	Val	Ser	Glu	Pro	Asp	Glu	Trp	Ala	Gln	Ala	Glu	Ala	Pro
	370					375					380				
Glu	Asn	Leu	Phe	Gly	Glu	Leu	Leu	Pro	Ser	Asp	Lys	Pro	Leu	Thr	Lys
	385				390					395					400
Lys	Glu	Gln	Lys	Ala	Leu	Glu	Lys	Ala	Gln	Lys	Asp	Ala	Glu	Lys	Ala
				405					410					415	
Arg	Ala	Lys	Leu	Arg	Glu	Gln	Phe	Pro	Ala	Thr	Val	Asp	Glu	Ala	Glu
			420					425					430		
Phe	Val	Gly	Gln	Arg	Thr	Val	Thr	Ala	Ala	Ala	Ala	Lys	Ala	Leu	Ala
		435					440					445			
Ala	His	Leu	Ser	Val	Arg	Gly	Thr	Val	Val	Glu	Pro	Gly	Asp	Asp	Pro
	450					455					460				
Leu	Leu	Tyr	Ala	Tyr	Leu	Leu	Asp	Pro	Ala	Asn	Thr	Asn	Met	Pro	Val
	465				470					475					480
Val	Ala	Lys	Arg	Tyr	Leu	Asp	Arg	Glu	Trp	Pro	Ala	Asp	Ala	Pro	Thr
			485						490					495	
Arg	Ala	Ala	Ile	Thr	Gly	His	Leu	Val	Arg	Glu	Leu	Pro	Pro	Leu	Leu
			500					505					510		
Asp	Asp	Ala	Arg	Arg	Lys	Met	Tyr	Asp	Glu	Met	Glu	Lys	Pro	Leu	Ser
		515					520					525			
Gly	Val	Leu	Gly	Arg	Met	Glu	Val	Arg	Gly	Val	Gln	Val	Asp	Ser	Asp
	530					535					540				
Phe	Leu	Gln	Thr	Leu	Ser	Ile	Gln	Ala	Gly	Val	Arg	Leu	Ala	Asp	Leu
	545				550					555					560
Glu	Ser	Gln	Ile	His	Glu	Tyr	Ala	Gly	Glu	Glu	Phe	His	Ile	Arg	Ser
			565						570					575	
Pro	Lys	Gln	Leu	Thr	Val	Leu	Tyr	Asp	Lys	Leu	Glu	Leu	Ala	Ser	
			580				585					590			
Ser	Lys	Lys	Thr	Lys	Leu	Thr	Gly	Gln	Arg	Ser	Thr	Ala	Val	Ser	Ala
		595					600					605			
Leu	Glu	Pro	Leu	Arg	Asp	Ala	His	Pro	Ile	Ile	Pro	Leu	Val	Leu	Glu
	610					615					620				
Phe	Arg	Glu	Leu	Asp	Lys	Leu	Arg	Gly	Thr	Tyr	Leu	Asp	Pro	Ile	Pro
	625				630					635					640
Asn	Leu	Val	Asn	Pro	His	Thr	Gly	Arg	Leu	His	Thr	Thr	Phe	Ala	Gln
				645					650					655	
Thr	Ala	Val	Ala	Thr	Gly	Arg	Leu	Ser	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	Glu	Leu	Arg	Leu	Leu	Ala	His	Ile	Ala	Asp	Asp	Pro	Leu	Met	Gln	Gln
705	Ala	Phe	Val	Glu	Gly	Ala	Asp	Ile	His	Arg	Arg	Thr	Ala	Ala	Gln	Val
	Leu	Gly	Leu	Asp	Glu	Ala	Thr	Val	Asp	Ala	Asn	Gln	Arg	Arg	Ala	Ala
	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu
	Ser	Asn	Asp	Leu	Gly	Ile	Pro	Tyr	Ala	Glu	Ala	Ala	Thr	Phe	Ile	Glu
	Ile	Tyr	Phe	Ala	Thr	Tyr	Pro	Gly	Ile	Arg	Arg	Tyr	Ile	Asn	His	Thr
785	Leu	Asp	Phe	Gly	Arg	Thr	His	Gly	Tyr	Val	Glu	Thr	Leu	Tyr	Gly	Arg
	Arg	Arg	Tyr	Val	Pro	Gly	Leu	Ser	Ser	Arg	Asn	Arg	Val	Gln	Arg	Glu
	Ala	Glu	Glu	Arg	Leu	Ala	Tyr	Asn	Met	Pro	Ile	Gln	Gly	Thr	Ala	Ala
	Asp	Ile	Met	Lys	Leu	Ala	Met	Val	Gln	Leu	Asp	Pro	Gln	Leu	Asp	Ala
	Ile	Gly	Ala	Arg	Met	Leu	Gln	Val	His	Asp	Glu	Leu	Leu	Ile	Glu	
865	Ala	Pro	Leu	Asp	Lys	Ala	Glu	Gln	Val	Ala	Ala	Leu	Thr	Lys	Lys	Val
	Met	Glu	Asn	Val	Gln	Leu	Lys	Val	Pro	Leu	Ala	Val	Glu	Val	Gly	
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<210> 37

<211> 892

<212> PRT

<213> Thermosipho africanus

<220>

<223> Thermosipho africanus DNA polymerase (Taf)

<400> 37

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

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
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Leu	Lys	Val	Asp	Val	Tyr	Tyr	Gly	Lys	Glu	Trp	Glu				
			885				890								

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

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

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

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

		835					840					845					
His	Asp	Glu	Leu	Val	Phe	Glu	Val	Pro	Asn	Glu	Glu	Lys	Asp	Ala	Leu		
	850					855					860						
Val	Glu	Leu	Val	Lys	Asp	Arg	Met	Thr	Asn	Val	Val	Lys	Leu	Ser	Val		
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Pro	Leu	Glu	Val	Asp	Val	Thr	Ile	Gly	Lys	Thr	Trp	Ser					
				885					890								

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

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

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			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	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	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	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	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			
Arg	Lys	Ala	Ala	Ala	Ile	Trp	Ala	Leu	Glu	Glu	Pro	Leu	Met	Asp	Glu
	450					455					460				
Leu	Arg	Arg	Asn	Glu	Gln	Asp	Arg	Leu	Leu	Thr	Glu	Leu	Glu	Gln	Pro
465					470					475					480

Leu Ala Gly Ile Leu Ala Asn Met Glu Phe Thr Gly Val Lys Val Asp
 Thr Lys Arg Leu 485 Glu Gln Met Gly Ala 490 Glu Leu Thr Glu Gln Leu Gln
 Ala Val Glu 500 Arg Arg Ile Tyr Glu 505 Leu Ala Gly Gln Glu 510 Phe Asn Ile
 Asn Ser Pro Lys Gln Leu Gly 520 Thr Val Leu Phe Asp 525 Lys Leu Gln Leu
 Pro Val Leu Lys Lys Thr 535 Lys Thr Gly Tyr Ser 540 Thr Ser Ala Asp Val
 545 Leu Glu Lys Leu 550 Pro His His Glu 555 Val Glu His Ile Leu 560 His
 Tyr Arg Gln Leu 565 Gly Lys Leu Gln Ser 570 Thr Tyr Ile Glu Gly 575 Leu Leu
 Lys Val Val 580 His Pro Val Thr Gly 585 Lys Val His Thr Met 590 Phe Asn Gln
 Ala Leu Thr Gln Thr Gly Arg 600 Leu Ser Ser Val Glu 605 Pro Asn Leu Gln
 610 Asn Ile Pro Ile Arg Leu 615 Glu Glu Gly Arg Lys 620 Ile Arg Gln Ala Phe
 625 Val Pro Ser Glu Pro 630 Asp Trp Leu Ile Phe 635 Ala Ala Asp Tyr Ser 640 Gln
 Ile Glu Leu Arg Val Leu Ala His Ile 645 Ala Glu Asp Asp Asn Leu Ile
 650 Glu Ala Phe 655 Arg Arg Gly Leu Asp 660 Ile His Thr Lys Thr 665 Ala Met Asp
 Ile Phe 670 His Val Ser Glu Glu 675 Asp Val Thr Ala Asn 680 Met Arg Arg Gln
 685 Ala Lys Ala Val Asn Phe 690 Gly Ile Val Tyr Gly 695 Ile Ser Asp Tyr Gly
 700 Leu Ala Gln Asn Leu 705 Phe 710 Asn Ile Thr Arg Lys 715 Glu Ala Ala Glu Phe 720 Ile
 Glu Arg Tyr Phe 725 Ala Ser Phe Pro Gly 730 Val Lys Gln Tyr Met 735 Asp Asn
 Ile Val Gln Glu Ala Lys Gln Lys 740 Gly Tyr Val Thr Thr 745 Leu Leu His
 750 Arg Arg Arg Tyr Leu Pro Asp 755 Ile Thr Ser Arg Asn 760 Phe Asn Val Arg
 765 Ser Phe Ala Glu Arg Thr Ala Met Asn Thr Pro 770 Ile Gln Gly Ser Ala
 775 Ala Asp Ile Ile Lys 780 Lys Ala Met Ile Asp 785 Leu Ser Val Arg Leu Arg
 790 Glu Glu Arg Leu 800 Gln Ala Arg Leu Leu 805 Gln Val His Asp 810 Glu Leu
 Ile Leu Glu Ala Pro Lys Glu Glu 815 Ile Glu Arg Leu Cys 820 Arg Leu Val
 825 Pro Glu Val Met Glu Gln Ala Val 830 Ala Leu Arg Val 835 Pro Leu Lys Val
 840 Asp Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala 845 Lys
 850 855 860 865 870 875

<210> 41

<211> 877

<212> PRT

<213> Bacillus caldotenax

<220>

<223> Bacillus caldotenax DNA polymerase (Bca)

<400> 41

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 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
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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
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Gly	Thr	Val	Glu	Asn	Val	Leu	Ala	Ser	Ile	Asp	Glu	Ile	Lys	Gly	Glu
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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
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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
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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
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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
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Ser	Met	Phe	Asp	Ser	Lys	Arg	Ala	Ala	Val	Ala	Leu	Lys	Trp	Lys	Gly
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Ile	Glu	Leu	Cys	Gly	Val	Ser	Phe	Asp	Leu	Leu	Leu	Ala	Ala	Tyr	Leu
385					390					395					400
Leu	Asp	Pro	Ala	Gln	Gly	Val	Asp	Asp	Val	Ala	Ala	Ala	Ala	Lys	Met
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Lys	Gln	Tyr	Glu	Ala	Val	Arg	Pro	Asp	Glu	Ala	Val	Tyr	Gly	Lys	Gly
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Ala	Lys	Arg	Ala	Val	Pro	Asp	Glu	Pro	Val	Leu	Ala	Glu	His	Leu	Val
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Arg	Lys	Ala	Ala	Ala	Ile	Trp	Ala	Leu	Glu	Arg	Pro	Phe	Leu	Asp	Glu
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Leu	Ser	Ser	Ile	Leu	Ala	Glu	Met	Glu	Phe	Ala	Gly	Val	Lys	Val	Asp
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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
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Asn	Ser	Pro	Lys	Gln	Leu	Gly	Val	Ile	Leu	Phe	Glu	Lys	Leu	Gln	Leu
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Pro	Val	Leu	Lys	Lys	Ser	Lys	Thr	Gly	Tyr	Ser	Thr	Ser	Ala	Asp	Val
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Leu	Glu	Lys	Leu	Ala	Pro	Tyr	His	Glu	Ile	Val	Glu	Asn	Ile	Leu	Gln
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Leu	Lys	Val	Val	Arg	Pro	Asp	Thr	Lys	Lys	Val	His	Thr	Ile	Phe	Asn
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Gln	Ala	Leu	Thr	Gln	Thr	Gly	Arg	Leu	Ser	Ser	Thr	Glu	Pro	Asn	Leu
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Phe	Val	Pro	Ser	Glu	Ser	Asp	Trp	Leu	Ile	Phe	Ala	Ala	Asp	Tyr	Ser
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Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Ile	Ala	Glu	Asp	Asp	Asn	Leu
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Gln	Ala	Lys	Ala	Val	Asn	Phe	Gly	Ile	Val	Tyr	Gly	Ile	Ser	Asp	Tyr
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Gly	Leu	Ala	Gln	Asn	Leu	Asn	Ile	Ser	Arg	Lys	Glu	Ala	Ala	Glu	Phe
			725						730					735	
Ile	Glu	Arg	Tyr	Phe	Glu	Ser	Phe	Pro	Gly	Val	Lys	Arg	Tyr	Met	Glu
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Asn	Ile	Val	Gln	Glu	Ala	Lys	Gln	Lys	Gly	Tyr	Val	Thr	Thr	Leu	Leu
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His	Arg	Arg	Arg	Tyr	Leu	Pro	Asp	Ile	Thr	Ser	Arg	Asn	Phe	Asn	Val
	770					775					780				
Arg	Ser	Phe	Ala	Glu	Arg	Met	Ala	Met	Asn	Thr	Pro	Ile	Gln	Gly	Ser
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Ala	Ala	Asp	Ile	Ile	Lys	Lys	Ala	Met	Ile	Asp	Leu	Asn	Ala	Arg	Leu
			805						810					815	
Lys	Glu	Glu	Arg	Leu	Gln	Ala	Arg	Leu	Leu	Leu	Gln	Val	His	Asp	Glu
			820					825					830		
Leu	Ile	Leu	Glu	Ala	Pro	Lys	Glu	Glu	Met	Glu	Arg	Leu	Cys	Arg	Leu
	835						840					845			
Val	Pro	Glu	Val	Met	Glu	Gln	Ala	Val	Thr	Leu	Arg	Val	Pro	Leu	Lys
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