

1
SEQUENCE LISTING

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

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

<130> 26742 WO-HS

<140> Not yet assigned

<141> Not yet assigned

<150> US 61/356,296

<151> 2010-06-18

<160> 49

<170> FastSEQ for windows Version 4.0

<210> 1

<211> 834

<212> PRT

<213> Thermus sp.

<220>

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

<400> 1

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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
      305      310      315      320

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Ala Glu Leu Lys Ala Leu Ala Ala Cys Lys² Glu Gly Arg Val His Arg
 325 330 335
 Ala Lys Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp
 355 360 365
 Leu Ala Pro Ser Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ala Glu Arg Leu Gln Gln
 405 410 415
 Asn Leu Leu Glu Arg Leu Lys Gly Glu Lys Leu Leu Trp Tyr
 420 425 430
 Gln Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445
 Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu
 450 455 460
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
 465 470 475 480
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
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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
 515 520 525
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
 530 535 540
 Asn Thr Tyr Val Asp Pro Leu Pro Gly Leu Val His Pro Arg Thr Gly
 545 550 555 560
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Ile Arg Thr Pro Leu
 580 585 590
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
 595 600 605
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
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 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Ser Pro Glu Ala Val
 645 650 655
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765
 Lys Leu Phe Pro His Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780
 Val His Asp Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
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<211> 832

<212> PRT

<213> *Thermus aquaticus*

<220>

<223> *Thermus aquaticus* DNA polymerase (Taq)

<400> 2

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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
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Glu Ser Pro Lys Ala Leu 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
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Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu
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Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro
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Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
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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
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Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His
 465     470     475     480

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Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
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 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525
 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr
 530 535 540
 Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu
 545 550 555 560
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
 565 570 575
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
 580 585 590
 Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala
 595 600 605
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
 610 615 620
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr
 625 630 635 640
 Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro
 645 650 655
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
 660 665 670
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
 675 680 685
 Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
 690 695 700
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Gly Tyr Val
 705 710 715 720
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg
 725 730 735
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
 740 745 750 755
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
 760 765 770
 Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His
 775 780
 Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala
 785 790 795 800
 Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro
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 Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu
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 <213> *Thermus filiformis*

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

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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
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Thr	Thr	Ser 35	Arg	Gly	Glu	Pro	Val 40	Gln	Ala	Val	Tyr	Gly 45	Phe	Ala	Lys	
Ser	Leu 50	Leu	Lys	Ala	Leu	Lys 55	Glu	Asp	Gly	Asp	Val 60	Val	Val	Val	Val	
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Tyr 145	Gln	Leu	Leu	Ser	Glu 150	Arg	Ile	Ala	Ile	Leu 155	His	Pro	Glu	Gly	Tyr 160	
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Gln	Trp	Val	Asp 180	Tyr	Arg	Ala	Leu	Ala 185	Gly	Asp	Pro	Ser	Asp 190	Asn	Ile	
Pro	Gly	Val 195	Lys	Gly	Ile	Gly	Glu 200	Lys	Thr	Ala	Gln	Arg 205	Leu	Ile	Arg	
Glu	Trp 210	Gly	Ser	Leu	Glu	Asn 215	Leu	Phe	Gln	His	Leu 220	Asp	Gln	Val	Lys	
Pro 225	Ser	Leu	Arg	Glu	Lys 230	Leu	Gln	Ala	Gly	Met 235	Glu	Ala	Leu	Ala	Leu	
Ser	Arg	Lys	Leu	Ser 245	Gln	Val	His	Thr	Asp 250	Leu	Pro	Leu	Glu	Val 255	Asp	
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Leu	Ala	Leu	Ala	Gly	Ala	Trp	Glu	Gly	Arg	Leu	His	Arg	Ala	Gln	Asp
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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	Glu	Val	Phe	Arg	Leu	Ala	Gly	His	Pro
465					470					475					480
Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp	Glu
				485					490					495	
Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	Arg	Ser
			500					505					510		
Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile	Val
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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
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Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser
				565					570					575	
Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg
			580					585					590		
Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Glu	Gly	Trp	Val	Leu	Val	Val	Leu
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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
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Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Ser	Pro	Glu	Gly	Val	Asp	Pro	Leu
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Met	Arg	Arg	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	
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Ser	Ala	His	Arg	Leu	Ser	Gly	Glu	Leu	Ser	Ile	Pro	Tyr	Glu	Glu	Ala
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Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Tyr	Pro	Lys	Val	Arg	Ala
	690					695					700				
Trp	Ile	Glu	Gly	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Gly	Tyr	Val	Glu	
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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
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	770					775					780				
Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Asp	Arg	Ala	Glu	Arg	Val	Ala	Ala
785					790					795					800
Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Trp	Pro	Leu	Gln	Val	Pro	Leu
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Glu Val Glu Val Gly Leu Gly Glu Asp Trp⁸ Leu Ser Ala Lys Glu
820 825 830

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

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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 Pro Gly Gly Ala Phe
290 295 300
Leu Gly Phe Leu Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Leu
305 310 315 320
Ala Leu Ala Gly Ala Lys Glu Gly Arg Val His Arg Ala Glu Asp Pro
325 330 335
Val Gly Ala Leu Lys Asp Leu Lys Glu Ile Arg Gly Leu Leu Ala Lys
340 345 350
Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Arg Glu Ile Pro Pro Gly
355 360 365
Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Gly Asn Thr Asn
370 375 380
Pro Glu Gly Val Ala Arg Tyr Gly Gly Glu Trp Lys Glu Asp Ala
385 390 395 400
Ala Ala Arg Ala Leu Leu Ser Glu Arg Leu Trp Gln Ala Leu Tyr Pro
405 410 415
Arg Val Ala Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu
420 425 430
Arg Pro Leu Ala Gln Val Leu Ala His Met Glu Ala Thr Gly Val Arg

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

<210> 6

<211> 834

<212> PRT

<213> Thermus thermophilus

<220>

<223> Thermus thermophilus DNA polymerase (Tth)

<400> 6

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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 85	Tyr 85	Lys 85	Ala 85	Gly 85	Arg 85	Ala 85	Pro 85	Thr 85	Pro 90	Glu 90	Asp 90	Phe 90	Pro 90	Arg 95	Gln 95
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Glu 115	Val 115	Pro 115	Gly 115	Tyr 115	Glu 115	Ala 115	Asp 120	Asp 120	Val 120	Leu 120	Ala 120	Thr 125	Leu 125	Ala 125	Lys 125
Lys 130	Ala 130	Glu 130	Lys 130	Glu 130	Gly 130	Tyr 135	Glu 135	Val 135	Arg 135	Ile 135	Leu 140	Thr 140	Ala 140	Asp 140	Arg 140
Asp 145	Leu 145	Tyr 145	Gln 145	Leu 145	Val 150	Ser 150	Asp 150	Arg 150	Val 155	Ala 155	Val 155	Leu 155	His 155	Pro 155	Glu 160
Gly 165	His 165	Leu 165	Ile 165	Thr 165	Pro 165	Glu 165	Trp 165	Leu 165	Trp 170	Glu 170	Lys 170	Tyr 170	Gly 170	Leu 175	Arg 175
Pro 180	Glu 180	Gln 180	Trp 180	Val 180	Asp 180	Phe 180	Arg 180	Ala 185	Leu 185	Val 185	Gly 185	Asp 185	Pro 190	Ser 190	Asp 190
Asn 195	Leu 195	Pro 195	Gly 195	Val 195	Lys 195	Gly 195	Ile 200	Gly 200	Glu 200	Lys 200	Thr 200	Ala 205	Leu 205	Lys 205	Leu 205
Leu 210	Lys 210	Glu 210	Trp 210	Gly 210	Ser 210	Leu 215	Glu 215	Asn 215	Leu 215	Leu 215	Lys 220	Asn 220	Leu 220	Asp 220	Arg 220
Val 225	Lys 225	Pro 225	Glu 225	Asn 225	Val 230	Arg 230	Glu 230	Lys 230	Ile 235	Lys 235	Ala 235	His 235	Leu 235	Glu 240	Asp 240
Leu 245	Arg 245	Leu 245	Ser 245	Leu 245	Glu 245	Leu 245	Ser 245	Arg 245	Val 250	Arg 250	Thr 250	Asp 250	Leu 250	Pro 255	Leu 255
Glu 260	Val 260	Asp 260	Leu 260	Ala 260	Gln 260	Gly 260	Arg 260	Glu 265	Pro 265	Asp 265	Arg 265	Glu 265	Gly 270	Leu 270	Arg 270
Ala 275	Phe 275	Leu 275	Glu 275	Arg 275	Leu 275	Glu 275	Phe 280	Gly 280	Ser 280	Leu 280	Leu 280	His 285	Glu 285	Phe 285	Gly 285
Leu 290	Leu 290	Glu 290	Ala 290	Pro 290	Ala 290	Pro 295	Leu 295	Glu 295	Glu 295	Ala 295	Pro 300	Trp 300	Pro 300	Pro 300	Pro 300
Glu 305	Gly 305	Ala 305	Phe 305	Val 305	Gly 310	Phe 310	Val 310	Leu 310	Ser 315	Arg 315	Pro 315	Glu 315	Pro 315	Met 315	Trp 320
Ala 325	Glu 325	Leu 325	Lys 325	Ala 325	Leu 325	Ala 325	Ala 325	Cys 325	Arg 330	Asp 330	Gly 330	Arg 330	Val 330	His 335	Arg 335
Ala 340	Ala 340	Asp 340	Pro 340	Leu 340	Ala 340	Gly 340	Leu 340	Lys 345	Asp 345	Leu 345	Lys 345	Glu 345	Val 350	Arg 350	Gly 350
Leu 355	Leu 355	Ala 355	Lys 355	Asp 355	Leu 355	Ala 355	Val 360	Leu 360	Ala 360	Ser 360	Arg 360	Glu 365	Gly 365	Leu 365	Asp 365
Leu 370	Val 370	Pro 370	Gly 370	Asp 370	Asp 370	Pro 375	Met 375	Leu 375	Leu 375	Ala 375	Tyr 380	Leu 380	Leu 380	Asp 380	Pro 380
Ser 385	Asn 385	Thr 385	Thr 385	Pro 385	Glu 390	Gly 390	Val 390	Ala 390	Arg 395	Arg 395	Tyr 395	Gly 395	Gly 395	Glu 395	Trp 400
Thr 405	Glu 405	Asp 405	Ala 405	Ala 405	His 405	Arg 405	Ala 405	Leu 410	Leu 410	Ser 410	Glu 410	Arg 410	Leu 410	His 415	Arg 415
Asn 420	Leu 420	Leu 420	Lys 420	Arg 420	Leu 420	Glu 420	Gly 425	Glu 425	Glu 425	Lys 425	Leu 425	Leu 425	Trp 430	Leu 430	Tyr 430
His 435	Glu 435	Val 435	Glu 435	Lys 435	Pro 435	Leu 435	Ser 440	Arg 440	Val 440	Leu 440	Ala 445	His 445	Met 445	Glu 445	Ala 445
Thr 450	Gly 450	Val 450	Arg 450	Arg											

11

Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu
610	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
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Lys	Gly														

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 <212> PRT
 <213> Thermus caldophilus

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

<400> 7

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

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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 275	Leu	Glu	Arg	Leu	Glu	Phe 280	Gly	Ser	Leu	Leu	His 285	Glu	Phe	Gly
Leu 290	Leu	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 450	Val	Arg	Leu	Asp	Val 455	Ala	Tyr	Leu	Gln	Ala 460	Leu	Ser	Leu	Glu
Leu 465	Ala	Glu	Glu	Ile	Arg 470	Arg	Leu	Glu	Glu	Glu 475	Val	Phe	Arg	Leu	Ala 480
Gly	His	Pro	Phe	Asn 485	Leu	Asn	Ser	Arg	Asp 490	Gln	Leu	Glu	Arg	Val 495	Leu
Phe	Asp	Glu	Leu 500	Arg	Leu	Pro	Ala	Leu 505	Gly	Lys	Thr	Gln	Lys 510	Thr	Gly
Lys	Arg	Ser 515	Thr	Ser	Ala	Ala	Val 520	Leu	Glu	Ala	Leu	Arg 525	Glu	Ala	His
Pro	Ile 530	Val	Glu	Lys	Ile	Leu 535	Gln	His	Arg	Glu	Leu 540	Thr	Lys	Leu	Lys
Asn 545	Thr	Tyr	Val	Asp	Pro 550	Leu	Pro	Ser	Leu	Val 555	His	Pro	Asn	Thr	Gly 560
Arg	Leu	His	Thr	Arg 565	Phe	Asn	Gln	Thr	Ala 570	Thr	Ala	Thr	Gly	Arg 575	Leu
Ser	Ser	Ser	Asp 580	Pro	Asn	Leu	Gln	Asn 585	Ile	Pro	Val	Arg	Thr 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 695	Ile	Glu	Arg	Tyr	Phe	Gln 700	Ser	Phe	Pro	Lys
Val 705	Arg	Ala	Trp	Ile	Glu 710	Lys	Thr	Leu	Glu	Glu 715	Gly	Arg	Lys	Arg	Gly 720
Tyr	Val	Glu	Thr	Leu 725	Phe	Gly	Arg	Arg	Arg 730	Tyr	Val	Pro	Asp	Leu 735	Asn
Ala	Arg	Val	Lys 740	Ser	Val	Arg	Glu	Ala 745	Ala	Glu	Arg	Met	Ala 750	Phe	Asn
Met	Pro	Val 755	Gln	Gly	Thr	Ala	Ala 760	Asp	Leu	Met	Lys	Leu 765	Ala	Met	Val

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

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

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

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

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

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

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

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

<220>
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 <223> Xaa = Asp, Lys or Thr

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 <223> Xaa = Leu or Val

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

<220>
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 <223> Xaa = Arg, ASn, Tyr, Thr or Val

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

<220>
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 <222> (18)...(18)
 <223> Xaa = Phe or Tyr

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

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

<400> 8
 Ala Gly xaa xaa Phe xaa xaa xaa xaa xaa xaa Gln xaa xaa xaa xaa
 1 5 10 15
 Leu xaa xaa xaa Leu
 20

<210> 9
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 <213> Artificial Sequence

<220>
 <223> synthetic DNA polymerase domain motif

<220>
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<220>
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 <223> Xaa = Leu or Ile

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 <223> Xaa = any amino acid other than Ser

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 <223> Xaa = Arg or Pro

<220>
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 <223> Xaa = Asp or Lys

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

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 <223> Xaa = Glu or Ser

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 <223> Xaa = Val or Ile

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

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

<400> 9
 Ala Gly Xaa Pro Phe Asn Xaa Asn Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa
 1 5 10 15
 Leu Phe Xaa Xaa Leu
 20

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

<220>
 <223> synthetic DNA polymerase domain motif

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

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

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 <212> PRT
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<220>
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<220>
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 <222> (9)...(9)
 <223> Xaa = Gly, Ala, Asp, Phe, Lys, Cys, Thr or Tyr.

<400> 11
 Ala Gly His Pro Phe Asn Leu Asn Xaa Arg Asp Gln Leu Glu Arg Val
 1 5 10 15
 Leu Phe Asp Glu Leu
 20

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

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

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

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

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

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

<210> 14
 <211> 36
 <212> PRT
 <213> Artificial Sequence

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

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

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

<220>

<223> synthetic region from polymerase domain of Thermus
flavus DNA polymerase (Tfl)¹⁷

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

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<212> PRT
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<220>
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sp. Sps17 DNA polymerase (Sps17)

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

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

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

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

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

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

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

<210> 19
<211> 36

<212> PRT
 <213> Artificial Sequence

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

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

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

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

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

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

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

<400> 21
 Lys Glu Lys Val Phe Glu Ile Ala Gly Glu Thr Phe Asn Leu Asn Ser
 1 5 10 15
 Ser Thr Gln Val Ala Tyr Ile Leu Phe Glu Lys Leu Asn Ile Ala Pro
 20 25 30
 Tyr Lys Lys
 35

<210> 22

<400> 22
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<210> 23
 <211> 36
 <212> PRT
 <213> Artificial Sequence

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

<400> 23

Glu Ser Gln Ile His Glu Tyr Ala Gly Glu¹⁹ Glu Phe His Ile Arg Ser
 1 5 10 15
 Pro Lys Gln Leu Glu Thr Val Leu Tyr Asp Lys Leu Glu Leu Ala Ser
 20 25 30
 Ser Lys Lys Thr
 35

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

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

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

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

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

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

<210> 26
 <211> 21
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 <213> Artificial Sequence

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

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 <223> Xaa = His, Glu or Gln

<220>
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 <223> Xaa = Pro, Thr or Glu

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 <223> Xaa = Asn or His

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 <223> Xaa = Leu or Ile

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 <223> Xaa = Asn or Arg

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 <223> Xaa = Arg, Pro or Ser

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 <223> Xaa = Asp, Lys or Thr

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 <223> Xaa = Leu or Val

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 <222> (14)...(14)
 <223> Xaa = Glu, Ser, Ala or Gly

<220>
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 <223> Xaa = Arg, Asn, Tyr, Thr or Val

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 <223> Xaa = Val or Ile

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 <223> Xaa = Phe or Tyr

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 <223> Xaa = Asp or Glu

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

<400> 26
 Ala Gly Xaa Xaa Phe Xaa Xaa Xaa Ser Xaa Xaa Gln Xaa Xaa Xaa Xaa
 1 5 10 15
 Leu Xaa Xaa Xaa Leu
 20

<210> 27
 <211> 13
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<220>

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

<220>

<221> VARIANT

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<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

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Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala
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Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu
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Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
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Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	Pro	Glu
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Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	Ser	Asp
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Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Lys	Leu
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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
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Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly
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Ala	Ile	Asp	Leu	Glu	Thr	Ser	Ser	Leu	Asp	Pro	Phe	Asp	Cys	Asp	Ile
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Lys	Leu	Lys	Glu	Ile	Leu	Glu	Asp	Pro	Gly	Ala	Lys	Ile	Val	Gly	Gln
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Asp	Ala	Leu	Pro	Lys	Met	Val	Asn	Pro	Lys	Thr	Gly	Arg	Ile	His	Ala
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Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Ile	Leu	Ala	His	Leu	Ser	Gly	Asp
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Glu	Asn	Leu	Leu	Arg	Ala	Phe	Glu	Glu	Gly	Ile	Asp	Val	His	Thr	Leu
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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
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Tyr	Ile	Gln	Arg	Val	Val	Ser	Glu	Ala	Lys	Glu	Lys	Gly	Tyr	Val	Arg
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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
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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
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His	Asp	Glu	Leu	Val	Phe	Glu	Val	Pro	Asn	Glu	Glu	Lys	Asp	Ala	Leu
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Val	Glu	Leu	Val	Lys	Asp	Arg	Met	Thr	Asn	Val	Val	Lys	Leu	Ser	Val
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<210> 30
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 <212> PRT
 <213> Artificial Sequence

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

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

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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						

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 <212> DNA
 <213> Artificial Sequence

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

<400> 31
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<210> 32
 <211> 25
 <212> DNA
 <213> Artificial Sequence

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

<400> 32
 ataaccaact ggtagtggcg tgtaa 25

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

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

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gaagagcgct	agggaggccg	cggagcgcat	ggccttcaac	atgcccgtcc	agggcaccgc	1140
cgccgacctc	atgaagctcg	ccatggtgaa	gctcttcccc	cacctccggg	agatgggggc	1200
ccgcatgctc	ctccagggtcc	acgacgagct	cctcctggag	gccccccaag	cgcgggccga	1260

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ggaggtggag gtggggatcg gggaggactg gctttccgcc aagggtgat atcagatctc 1380
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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 <212> DNA
 <213> Artificial Sequence

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

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gtttgaacag ttgtctggat ccattttgtg gatggtaaga attgaggcta 110

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

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

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

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				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
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	Pro	Lys	Gln	Leu	Glu	Thr	Val	Leu	Tyr	Asp	Lys	Leu	Glu	Leu	Ala	Ser
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	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
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	Thr	Ala	Val	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Leu	Asn	Pro	Asn	Leu	Gln
			660						665					670		
	Asn	Ile	Pro	Ile	Arg	Ser	Glu	Leu	Gly	Arg	Glu	Ile	Arg	Lys	Gly	Phe
		675					680						685			
	Ile	Ala	Glu	Asp	Gly	Phe	Thr	Leu	Ile	Ala	Ala	Asp	Tyr	Ser	Gln	Ile
		690				695						700				
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	705				710					715						720
	Ala	Phe	Val	Glu	Gly	Ala	Asp	Ile	His	Arg	Arg	Thr	Ala	Ala	Gln	Val
				725						730					735	
	Leu	Gly	Leu	Asp	Glu	Ala	Thr	Val	Asp	Ala	Asn	Gln	Arg	Arg	Ala	Ala
			740						745					750		
	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu
		755						760					765			
	Ser	Asn	Asp	Leu	Gly	Ile	Pro	Tyr	Ala	Glu	Ala	Ala	Thr	Phe	Ile	Glu

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

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

Asp	Glu	Leu	Val	Phe	Glu	Val	Pro	Asp	Asn	30	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
 <213> Thermotoga maritima

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 <223> Thermotoga maritima DNA polymerase (Tma)

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		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	
					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	

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Asn	Glu	Lys	Lys	405	Asn	Leu	Asp	Asp	410	Leu	Ala	Leu	Lys	Phe	415	Leu	Gly
Tyr	Lys	Met	Thr	420	Ser	Tyr	Gln	Glu	425	Leu	Met	Ser	Phe	Ser	430	Phe	Leu
Phe	Gly	Phe	Ser	435	Phe	Ala	Asp	Val	440	Pro	Val	Glu	Lys	445	Ala	Ala	Tyr
Ser	Cys	Glu	Asp	450	Ala	Asp	Ile	Thr	455	Tyr	Arg	Leu	Tyr	460	Lys	Thr	Leu
465	Lys	Leu	His	470	Glu	Ala	Asp	Leu	475	Glu	Asn	Val	Phe	480	Tyr	Lys	Ile
Leu	Lys	Leu	His	485	Glu	Ala	Asp	Leu	490	Glu	Asn	Val	Phe	495	Tyr	Lys	Ile
Met	Pro	Leu	Val	500	Asn	Val	Leu	Ala	505	Met	Glu	Leu	Asn	510	Gly	Val	Tyr
Val	Asp	Thr	Glu	515	Phe	Leu	Lys	Lys	520	Leu	Ser	Glu	Glu	525	Tyr	Gly	Lys
Leu	Glu	Glu	Leu	530	Ala	Glu	Glu	Ile	535	Tyr	Arg	Ile	Ala	540	Gly	Glu	Pro
Asn	Ile	Asn	Ser	545	Pro	Lys	Gln	Val	550	Ser	Arg	Ile	Leu	555	Phe	Glu	Lys
Gly	Ile	Lys	Pro	560	Arg	Gly	Lys	Thr	565	Thr	Lys	Thr	Gly	570	Asp	Tyr	Ser
Arg	Ile	Glu	Val	575	Leu	Glu	Glu	Leu	580	Ala	Gly	Glu	His	585	Glu	Ile	Pro
Leu	Ile	Leu	Glu	590	Tyr	Arg	Lys	Ile	595	Gln	Lys	Leu	Lys	600	Ser	Thr	Tyr
Asp	Ala	Leu	Pro	605	Lys	Met	Val	Asn	610	Pro	Lys	Thr	Gly	615	Arg	Ile	His
Ser	Phe	Asn	Gln	620	Thr	Gly	Thr	Ala	625	Thr	Gly	Arg	Leu	630	Ser	Ser	Ser
Pro	Asn	Leu	Gln	635	Asn	Leu	Pro	Thr	640	Lys	Ser	Glu	Glu	645	Gly	Lys	Glu
Arg	Lys	Ala	Ile	650	Val	Pro	Gln	Asp	655	Pro	Asn	Trp	Trp	660	Ile	Val	Ser
Asp	Tyr	Ser	Gln	665	Ile	Glu	Leu	Arg	670	Ile	Leu	Ala	His	675	Leu	Ser	Gly
Glu	Asn	Leu	Leu	680	Arg	Ala	Phe	Glu	685	Glu	Gly	Ile	Asp	690	Val	His	Thr
Thr	Ala	Ser	Arg	695	Ile	Phe	Asn	Val	700	Lys	Pro	Glu	Glu	705	Val	Thr	Glu
Met	Arg	Arg	Ala	710	Gly	Lys	Met	Val	715	Asn	Phe	Ser	Ile	720	Ile	Tyr	Gly
Thr	Pro	Tyr	Gly	725	Leu	Ser	Val	Arg	730	Leu	Gly	Val	Pro	735	Val	Lys	Glu
Glu	Lys	Met	Ile	740	Val	Asn	Tyr	Phe	745	Val	Leu	Tyr	Pro	750	Val	Arg	Asp
Tyr	Ile	Gln	Arg	755	Val	Val	Ser	Glu	760	Ala	Lys	Glu	Lys	765	Gly	Tyr	Val
Thr	Leu	Phe	Gly	770	Arg	Lys	Arg	Asp	775	Ile	Pro	Gln	Leu	780	Met	Ala	Arg
Arg	Asn	Thr	Gln	785	Ala	Glu	Gly	Glu	790	Ile	Ala	Ile	Asn	795	Thr	Pro	Ile
Gln	Gly	Thr	Ala	800	Ala	Asp	Ile	Ile	805	Lys	Leu	Ala	Met	810	Ile	Glu	Ile
Arg	Glu	Leu	Lys	815	Glu	Arg	Lys	Met	820	Arg	Ser	Lys	Met	825	Ile	Ile	Gln
His	Asp	Glu	Leu	830	Val	Phe	Glu	Val	835	Pro	Asn	Glu	Glu	840	Lys	Asp	Ala
Val	Glu	Leu	Val	845	Lys	Asp	Arg	Met	850	Thr	Asn	Val	Val	855	Lys	Leu	Ser
Pro	Leu	Glu	Val	860	Asp	Val	Thr	Ile	865	Gly	Lys	Thr	Trp	870	Ser		Val
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				890													

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<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
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Leu	Ser	Lys	Lys	Leu	Ala	Thr	Leu	Val	Thr	Asn	Ala	Pro	Val	Glu	Val
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	370					375					380				
Asn	Leu	Lys	Tyr	Asp	Tyr	Lys	Val	Leu	Met	Val	Lys	Gly	Ile	Ser	Pro
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Asn	Glu	Lys	Lys	Phe	Asn	Leu	Glu	Asp	Leu	Ser	Leu	Lys	Phe	Leu	Gly
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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
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Ser	Cys	Glu	Asp	Ala	Asp	Ile	Thr	Tyr	Arg	Leu	Tyr	Lys	Ile	Leu	Ser
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Met	Lys	Leu	His	Glu	Ala	Glu	Leu	Glu	Asn	Val	Phe	Tyr	Arg	Ile	Glu
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33

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

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	Lys	Val	Ile	Ser	Gly	Asp	Arg	Asp	Leu	Thr	Gln	Leu	Ala	Ser	Pro	Gln	Pro	Gln	Gln	
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	Thr	Pro	Glu	Thr	Val	Val	Glu	Lys	Tyr	Gly	Leu	Thr	Pro	Glu	Gln	Ile	Thr	Ile	Ile	
	Val	Asp	Leu	Lys	Gly	Leu	Met	Gly	Asp	Lys	Ser	Asp	Asn	Ile	Pro	Gly	Thr	Gly	Gly	
	Val	Pro	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Val	Lys	Leu	Leu	Lys	Gln	Phe	Thr	Phe	Phe	
	Gly	Thr	Val	Glu	Asn	Val	Leu	Ala	Ser	Ile	Asp	Glu	Ile	Lys	Gly	Glu	Thr	Gly	Glu	
	Lys	Leu	Lys	Glu	Asn	Leu	Arg	Gln	Tyr	Arg	Asp	Leu	Ala	Leu	Leu	Ser	Thr	Leu	Ser	
	Lys	Gln	Leu	Ala	Ala	Ile	Cys	Arg	Asp	Ala	Pro	Val	Glu	Leu	Thr	Leu	Thr	Leu	Leu	
	Asp	Asp	Ile	Val	Tyr	Lys	Gly	Glu	Asp	Arg	Glu	Lys	Val	Val	Ala	Leu	Thr	Ala	Leu	
	Phe	Gln	Glu	Leu	Gly	Phe	Gln	Ser	Phe	Leu	Asp	Lys	Met	Ala	Val	Gln	Thr	Val	Gln	
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	Glu	Val	Val	Gly	Asp	Asn	Tyr	His	His	Ala	Pro	Ile	Val	Gly	Ile	Ala	Thr	Ile	Ala	
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	Ala	Asp	Pro	Lys	Phe	Leu	Ala	Trp	Leu	Gly	Asp	Glu	Thr	Lys	Lys	Lys	Thr	Lys	Lys	
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	His	Gln	Tyr	Glu	Ala	Val	Arg	Ser	Asp	Glu	Ala	Val	Tyr	Gly	Lys	Gly	Thr	Lys	Gly	
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	Asn	Ser	Pro	Lys	Gln	Leu	Gly	Thr	Val	Leu	Phe	Asp	Lys	Leu	Gln	Leu	Thr	Ala	Leu	
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Asn 625	Ile 610	Pro	Ile	Arg	Leu 630	Glu 615	Glu	Gly	Arg	Lys 635	Ile 620	Arg	Gln	Ala	Phe 640
Val	Pro	Ser	Glu	Pro 645	Asp	Trp	Leu	Ile	Phe 650	Ala	Ala	Asp	Tyr	Ser 655	Gln
Ile	Glu	Leu	Arg 660	Val	Leu	Ala	His	Ile 665	Ala	Glu	Asp	Asp	Asn 670	Leu	Ile
Glu	Ala	Phe 675	Arg	Arg	Gly	Leu	Asp 680	Ile	His	Thr	Lys	Thr 685	Ala	Met	Asp
Ile	Phe 690	His	Val	Ser	Glu	Glu 695	Asp	Val	Thr	Ala	Asn 700	Met	Arg	Arg	Gln
Ala 705	Lys	Ala	Val	Asn	Phe 710	Gly	Ile	Val	Tyr	Gly 715	Ile	Ser	Asp	Tyr	Gly 720
Leu	Ala	Gln	Asn	Leu 725	Asn	Ile	Thr	Arg	Lys 730	Glu	Ala	Ala	Glu	Phe 735	Ile
Glu	Arg	Tyr	Phe 740	Ala	Ser	Phe	Pro	Gly 745	Val	Lys	Gln	Tyr	Met 750	Asp	Asn
Ile	Val	Gln	Glu	Ala	Lys	Gln	Lys 760	Gly	Tyr	Val	Thr	Thr 765	Leu	Leu	His
Arg	Arg 770	Arg	Tyr	Leu	Pro	Asp 775	Ile	Thr	Ser	Arg	Asn 780	Phe	Asn	Val	Arg
Ser 785	Phe	Ala	Glu	Arg	Thr 790	Ala	Met	Asn	Thr	Pro 795	Ile	Gln	Gly	Ser	Ala 800
Ala	Asp	Ile	Ile	Lys 805	Lys	Ala	Met	Ile	Asp 810	Leu	Ser	Val	Arg	Leu 815	Arg
Glu	Glu	Arg	Leu 820	Gln	Ala	Arg	Leu	Leu 825	Leu	Gln	Val	His	Asp 830	Glu	Leu
Ile	Leu	Glu 835	Ala	Pro	Lys	Glu	Glu 840	Ile	Glu	Arg	Leu	Cys 845	Arg	Leu	Val
Pro	Glu 850	Val	Met	Glu	Gln	Ala 855	Val	Ala	Leu	Arg	Val 860	Pro	Leu	Lys	Val
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Asn	Ala	Val	Tyr	Gly	Phe	Thr	Met	Met	Leu	Asn	Lys	Ile	Leu	Ala	Glu	
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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	
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Pro	Pro	Glu	Leu	Ser	Glu	Gln	Phe	Pro	Leu	Leu	Arg	Glu	Leu	Leu	Arg	
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Ala	Tyr	Arg	Ile	Pro	Ala	Tyr	Glu	Leu	Glu	Asn	Tyr	Glu	Ala	Asp	Asp	
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Thr	Pro	Glu	Ala	Val	Arg	Glu	Lys	Tyr	Gly	Leu	Thr	Pro	Glu	Gln	Ile	
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Val	Asp	Leu	Lys	Gly	Leu	Met	Gly	Asp	Lys	Ser	Asp	Asn	Ile	Pro	Gly	
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Gly	Thr ₂₁₀	Val	Glu	Asn	Val	Leu ₂₁₅	Ala	Ser	Ile	Asp	Glu ₂₂₀	Ile	Lys	Gly	Glu
Lys ₂₂₅	Leu	Lys	Glu	Thr	Leu ₂₃₀	Arg	Gln	His	Arg	Glu ₂₃₅	Met	Ala	Leu	Leu	Ser ₂₄₀
Lys	Lys	Leu	Ala	Ala ₂₄₅	Ile	Arg	Arg	Asp	Ala ₂₅₀	Pro	Val	Glu	Leu	Ser ₂₅₅	Leu
Asp	Asp	Ile	Ala ₂₆₀	Tyr	Gln	Gly	Glu	Asp ₂₆₅	Arg	Glu	Lys	Val	Val ₂₇₀	Ala	Leu
Phe	Lys	Glu ₂₇₅	Leu	Gly	Phe	Gln	Ser ₂₈₀	Phe	Leu	Glu	Lys	Met ₂₈₅	Glu	Ser	Pro
Ser	Ser ₂₉₀	Glu	Glu	Glu	Lys	Pro ₂₉₅	Leu	Ala	Lys	Met	Ala ₃₀₀	Phe	Thr	Leu	Ala
Asp ₃₀₅	Arg	Val	Thr	Glu	Glu ₃₁₀	Met	Leu	Ala	Asp	Lys ₃₁₅	Ala	Ala	Leu	Val	Val ₃₂₀
Glu	Val	Val	Glu	Glu ₃₂₅	Asn	Tyr	His	Asp	Ala ₃₃₀	Pro	Ile	Val	Gly	Ile ₃₃₅	Ala
Val	Val	Asn	Glu ₃₄₀	His	Gly	Arg	Phe	Phe ₃₄₅	Leu	Arg	Pro	Glu	Thr ₃₅₀	Ala	Leu
Ala	Asp	Pro ₃₅₅	Gln	Phe	Val	Ala	Trp ₃₆₀	Leu	Gly	Asp	Glu	Thr ₃₆₅	Lys	Lys	Lys
Ser	Met ₃₇₀	Phe	Asp	Ser	Lys	Arg ₃₇₅	Ala	Ala	Val	Ala	Leu ₃₈₀	Lys	Trp	Lys	Gly
Ile ₃₈₅	Glu	Leu	Cys	Gly	Val ₃₉₀	Ser	Phe	Asp	Leu	Leu ₃₉₅	Leu	Ala	Ala	Tyr	Leu ₄₀₀
Leu	Asp	Pro	Ala	Gln ₄₀₅	Gly	Val	Asp	Asp	Val ₄₁₀	Ala	Ala	Ala	Ala	Lys ₄₁₅	Met
Lys	Gln	Tyr	Glu ₄₂₀	Ala	Val	Arg	Pro	Asp ₄₂₅	Glu	Ala	Val	Tyr	Gly ₄₃₀	Lys	Gly
Ala	Lys	Arg ₄₃₅	Ala	Val	Pro	Asp	Glu ₄₄₀	Pro	Val	Leu	Ala	Glu ₄₄₅	His	Leu	Val
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Leu ₄₆₅	Arg	Arg	Asn	Glu	Gln ₄₇₀	Asp	Arg	Leu	Leu	Val ₄₇₅	Glu	Leu	Glu	Gln	Pro ₄₈₀
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Thr	Lys	Arg	Leu ₅₀₀	Glu	Gln	Met	Gly	Glu ₅₀₅	Leu	Ala	Gly	Gln	Glu ₅₁₀	Leu	Arg
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His	Tyr	Arg	Gln ₅₈₀	Leu	Gly	Lys	Leu	Gln ₅₈₅	Ser	Thr	Tyr	Ile	Glu ₅₉₀	Gly	Leu
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Gln ₆₂₅	Asn	Ile	Pro	Ile	Arg ₆₃₀	Leu	Glu	Glu	Gly	Arg ₆₃₅	Lys	Ile	Arg	Gln	Ala ₆₄₀
Phe	Val	Pro	Ser	Glu ₆₄₅	Ser	Asp	Trp	Leu	Ile ₆₅₀	Phe	Ala	Ala	Asp	Tyr ₆₅₅	Ser
Gln	Ile	Glu	Leu ₆₆₀	Arg	Val	Leu	Ala	His ₆₆₅	Ile	Ala	Glu	Asp	Asp ₆₇₀	Asn	Leu
Met	Glu	Ala ₆₇₅	Phe	Arg	Arg	Asp	Leu ₆₈₀	Asp	Ile	His	Thr	Lys ₆₈₅	Thr	Ala	Met
Asp	Ile ₆₉₀	Phe	Gln	Val	Ser	Glu ₆₉₅	Asp	Glu	Val	Thr	Pro ₇₀₀	Asn	Met	Arg	Arg
Gln ₇₀₅	Ala	Lys	Ala	Val	Asn ₇₁₀	Phe	Gly	Ile	Val	Tyr ₇₁₅	Gly	Ile	Ser	Asp	Tyr ₇₂₀
Gly	Leu	Ala	Gln	Asn ₇₂₅	Leu	Asn	Ile	Ser	Arg ₇₃₀	Lys	Glu	Ala	Ala	Glu ₇₃₅	Phe

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 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
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 <223> Xaa = Arg, Pro or Ser

 <220>
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 <223> Xaa = Asp, Lys or Thr

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

<220>
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 <222> (14)...(14)
 <223> Xaa = any amino acid

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

<220>
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 <223> Xaa = Val or Ile

<220>
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 <223> Xaa = any amino acid

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

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

<400> 42
 Ala Gly Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa
 1 5 10 15
 Leu Xaa Xaa Xaa Leu
 20

<210> 43
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 <212> PRT
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<220>
 <223> synthetic DNA polymerase domain motif

<220>
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 <223> Xaa = His or Glu

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

<220>
 <221> VARIANT
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 <223> Xaa = any amino acid other than Ser

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<223> Xaa = Arg or Pro

<220>

<221> VARIANT

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

<223> Xaa = Asp or Lys

<220>

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<223> Xaa = any amino acid

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<223> Xaa = Arg or Asn

<220>

<221> VARIANT

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

<223> Xaa = Val or Ile

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<221> VARIANT

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

<223> Xaa = any amino acid

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<221> VARIANT

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<223> Xaa = Asp or Glu

<220>

<221> VARIANT

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

<223> Xaa = Glu or Lys

<400> 43

Ala	Gly	Xaa	Pro	Phe	Asn	Xaa	Asn	Xaa	Xaa	Xaa	Gln	Xaa	Xaa	Xaa	Xaa
1				5				10						15	
Leu	Xaa	Xaa	Xaa	Leu											
			20												

<210> 44

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

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<220>

<221> VARIANT

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<223> Xaa = any amino acid other than Ser

<220>

<221> VARIANT

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

<223> Xaa = any amino acid

<220>

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

<400> 44
 Ala Gly His Pro Phe Asn Leu Asn Xaa Arg Asp Gln Leu Xaa Arg Val
 1 5 10 15
 Leu Xaa Asp Glu Leu
 20

<210> 45
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<220>
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<220>
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<400> 45
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 1 5 10 15
 Leu Phe Asp Glu Leu
 20

<210> 46
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<220>
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<220>
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 <222> (14)...(14)
 <223> Xaa = any amino acid other than Glu

<220>
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 <223> Xaa = any amino acid other than Phe

<400> 46
 Ala Gly His Pro Phe Asn Leu Asn Xaa Arg Asp Gln Leu Xaa Arg Val
 1 5 10 15
 Leu Xaa Asp Glu Leu
 20

<210> 47
 <211> 21
 <212> PRT
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<220>
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 <220>
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 <223> Xaa = Glu, Ser, Ala, Gln, Gly, Lys or Arg

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

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

<210> 48
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<220>
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<220>
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 <223> Xaa = Glu, Ser, Ala, Gln, Gly, Lys or Arg

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

<210> 49
 <211> 21
 <212> PRT
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<220>
 <223> synthetic DNA polymerase domain motif

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

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

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

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

<220>
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 <223> Xaa = Gly, Ala, Val, Leu, Ile, Met, Phe, Trp, Pro, Thr, Cys, Tyr, Asn, Gln, Asp, Glu, Lys, Arg or His

<220>
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 <223> Xaa = Arg, Pro or Ser

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

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

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

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

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

<220>
 <221> VARIANT
 <222> (18)...(18)
 <223> Xaa = Phe or Tyr

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

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

<400> 49
 Ala Gly Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa
 1 5 10 15
 Leu Xaa Xaa Xaa Leu

