

1  
SEQUENCE LISTING

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

<120> DNA Polymerases with Improved Activity

<130> 27044WO-HS

<140> Not yet assigned

<141> Not yet assigned

<150> US61/474160

<151> April 11, 2011

<160> 48

<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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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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Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
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Glu Val Pro Gly Phe Glu Ala Asp Val Leu Ala Thr Leu Ala Lys
115      120      125
Lys Ala Glu Arg Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg
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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
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Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp
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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
225      230      235      240
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260      265      270
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 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
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Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ser	Ile	Pro	Tyr	Glu	Glu	Ala	Ala
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Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg	Ala	Trp
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Ile	Ala	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Lys	Gly	Tyr	Val	Glu	Thr
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Ala	Lys	Glu	Thr	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ser	Val	Pro	Leu	Glu
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Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	70	His	Glu	Ala	Tyr	Glu	Ala	Tyr	
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Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	115	Ala	Thr	Leu	Ala	Lys	Arg	Ala	
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Pro	Leu	Arg	Gly 340	Leu	Arg	Asp	Leu	Lys 345	Gly	Val	Arg	Gly	Ile 350	Leu	Ala
Lys	Asp	Leu 355	Ala	Val	Leu	Ala	Leu 360	Arg	Glu	Gly	Leu	Asp 365	Leu	Phe	Pro
Glu	Asp 370	Asp	Pro	Met	Leu	Leu 375	Ala	Tyr	Leu	Leu	Asp 380	Pro	Ser	Asn	Thr
Thr 385	Pro	Glu	Gly	Val	Ala 390	Arg	Arg	Tyr	Gly	Gly 395	Glu	Trp	Thr	Glu	Asp 400
Ala	Gly	Glu	Arg	Ala 405	Leu	Leu	Ala	Glu	Arg 410	Leu	Phe	Gln	Thr	Leu 415	Lys
Glu	Arg	Leu	Lys 420	Gly	Glu	Glu	Arg	Leu 425	Leu	Trp	Leu	Tyr	Glu 430	Glu	Val
Glu	Lys	Pro 435	Leu	Ser	Arg	Val	Leu 440	Ala	Arg	Met	Glu	Ala 445	Thr	Gly	Val
Arg	Leu 450	Asp	Val	Ala	Tyr	Leu 455	Gln	Ala	Leu	Ser	Leu 460	Glu	Val	Glu	Ala
Glu 465	Val	Arg	Gln	Leu	Glu 470	Glu	Glu	Val	Phe	Arg 475	Leu	Ala	Gly	His	Pro 480
Phe	Asn	Leu	Asn	Ser 485	Arg	Asp	Gln	Leu	Glu 490	Arg	Val	Leu	Phe	Asp 495	Glu
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Ile 545	Asp	Pro	Leu	Pro	Ala 550	Leu	Val	His	Pro	Lys 555	Thr	Gly	Arg	Leu	His 560
Thr	Arg	Phe	Asn	Gln 565	Thr	Ala	Thr	Ala	Thr 570	Gly	Arg	Leu	Ser	Ser 575	Ser
Asp	Pro	Asn	Leu 580	Gln	Asn	Ile	Pro	Val 585	Arg	Thr	Pro	Leu	Gly 590	Gln	Arg
Ile	Arg	Arg	Ala 595	Phe	Val	Ala	Glu 600	Glu	Gly	Trp	Val	Leu 605	Val	Val	Leu
Asp	Tyr 610	Ser	Gln	Ile	Glu	Leu 615	Arg	Val	Leu	Ala	His 620	Leu	Ser	Gly	Asp
Glu 625	Asn	Leu	Ile	Arg	Val 630	Phe	Gln	Glu	Gly	Arg 635	Asp	Ile	His	Thr	Gln 640
Thr	Ala	Ser	Trp	Met 645	Phe	Gly	Val	Ser	Pro 650	Glu	Gly	Val	Asp	Pro 655	Leu
Met	Arg	Arg	Ala 660	Lys	Thr	Ile	Asn 665	Phe	Gly	Val	Leu	Tyr 670	Gly	Met	
Ser	Ala	His 675	Arg	Leu	Ser	Gly	Glu 680	Leu	Ser	Ile	Pro	Tyr 685	Glu	Glu	Ala
Val	Ala 690	Phe	Ile	Glu	Arg	Tyr 695	Phe	Gln	Ser	Tyr	Pro 700	Lys	Val	Arg	Ala
Trp 705	Ile	Glu	Gly	Thr	Leu 710	Glu	Glu	Gly	Arg	Arg 715	Arg	Gly	Tyr	Val	Glu 720
Thr	Leu	Phe	Gly	Arg 725	Arg	Arg	Tyr	Val	Pro 730	Asp	Leu	Asn	Ala	Arg 735	Val
Lys	Ser	Val	Arg 740	Glu	Ala	Ala	Glu	Arg 745	Met	Ala	Phe	Asn	Met 750	Pro	Val
Gln	Gly	Thr 755	Ala	Ala	Asp	Leu	Met 760	Lys	Leu	Ala	Met	Val 765	Arg	Leu	Phe
Pro	Arg 770	Leu	Gln	Glu	Leu	Gly 775	Ala	Arg	Met	Leu	Leu 780	Gln	Val	His	Asp
Glu 785	Leu	Val	Leu	Glu	Ala 790	Pro	Lys	Asp	Arg	Ala 795	Glu	Arg	Val	Ala	Ala 800
Leu	Ala	Lys	Glu	Val 805	Met	Glu	Gly	Val	Trp 810	Pro	Leu	Gln	Val	Pro 815	Leu
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 Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu  
 35 40 45  
 Leu Lys Ala Leu Lys Glu Asp Gly Glu Val Ala Ile Val Val Phe Asp  
 50 55 60  
 Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala Tyr Lys Ala  
 65 70 75 80  
 Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile  
 85 90 95  
 Lys Glu Leu Val Asp Leu Leu Gly Leu Val Arg Leu Glu Val Pro Gly  
 100 105 110  
 Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala Glu Arg  
 115 120 125  
 Glu Gly Tyr Glu Val Arg Ile Leu Ser Ala Asp Arg Asp Leu Tyr Gln  
 130 135 140  
 Leu Leu Ser Asp Arg Ile His Leu Leu His Pro Glu Gly Glu Val Leu  
 145 150 155 160  
 Thr Pro Gly Trp Leu Gln Glu Arg Tyr Gly Leu Ser Pro Glu Arg Trp  
 165 170 175  
 Val Glu Tyr Arg Ala Leu Val Gly Asp Pro Ser Asp Asn Leu Pro Gly  
 180 185 190  
 Val Pro Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu Lys 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  
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 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  
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 Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Lys Glu Asp Ala  
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 Arg Val Ala Glu Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu  
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 Arg Pro Leu Ala Gln Val Leu Ala His Met Glu Ala Thr Gly Val Arg  
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 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
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Ser Ala Ala Val Leu Glu Leu Leu Arg Glu Ala His Pro Ile Val Gly
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Arg Ile Leu Glu Tyr Arg Glu Leu Met Lys Leu Lys Ser Thr Tyr Ile
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Asp Pro Leu Pro Arg Leu Val His Pro Lys Thr Gly Arg Leu His Thr
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Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp
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Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile
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Arg Lys Ala Phe Ile Ala Glu Glu Gly His Leu Leu Val Ala Leu Asp
      595      600
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
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Ala Ala Trp Met Phe Gly Val Pro Pro Glu Gly Val Asp Gly Ala Met
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Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser
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Ala His Arg Leu Ser Gln Glu Leu Ser Ile Pro Tyr Glu Glu Ala Ala
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Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp
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Ile Ala Lys Thr Leu Glu Glu Gly Arg Lys Lys Gly Tyr Val Glu Thr
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Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys
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Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln
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Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro
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Arg Leu Arg Pro Leu Gly Val Arg Ile Leu Leu Gln Val His Asp Glu
      770      775
Leu Val Leu Glu Ala Pro Lys Ala Arg Ala Glu Glu Ala Ala Gln Leu
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Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
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Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe
      50      55
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
      65      70
Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
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Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
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Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys

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Lys	Ala	115	Lys	Glu	Gly	Tyr	120	Val	Arg	Ile	Leu	125	Thr	Ala	Asp	Arg
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Pro	Glu	Gln	Trp	180	Val	Asp	Phe	Arg	Ala	185	Gly	Glu	Lys	Thr	Ala	190
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	205	Leu	Lys	Leu
Leu	Lys	Glu	Trp	Gly	Ser	Leu	200	Glu	Asn	Leu	Leu	Lys	220	Asn	Leu	Asp
Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	Glu	Asp	240
225	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	Pro	Leu
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Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	265	Phe	Gly	Ser	Leu	Leu	His	Glu
Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	280	Leu	Glu	Glu	Ala	Pro	Trp	Pro
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Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	320
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Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	345	Asp	Leu	Lys	Glu	Val	Arg	Gly
						340	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly	Leu
Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly	Leu	Asp	365
Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	380
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Asn	Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	425	Val	Leu	Ala	His	Met	Glu	Ala
						420	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	Leu	Ser
His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	440	Ala	Tyr	Leu	Gln	Ala	Leu	Ser
Thr	Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	455	Leu	Glu	Glu	Val	Phe	Arg	Leu
Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	475	Val	Phe	Arg	Leu	Ala
465	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	505	Gly	Lys	Thr	Gln	Lys	Thr	Gly
Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	510
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Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	Leu	Lys	530
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545	Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu
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Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	575
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Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile	625
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Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	660
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11

Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr
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Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys
	690					695					700				
Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly
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Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn
				725					730					735	
Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn
			740					745					750		
Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val
		755					760					765			
Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln
	770					775					780				
Val	His	Asp	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu
	785				790					795					800
Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala
				805					810					815	
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Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Gln	Lys	Tyr	Gly	Leu	Lys
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Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	Ser	Asp
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Glu	Val	Asp	Leu	Ala	Gln	Gly	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	Ala 355	Lys	Asp	Leu	Ala	Val 360	Leu	Ala	Ser	Arg	Glu 365	Gly	Leu	Asp	
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Thr	Glu	Asp	Ala	Ala 405	His	Arg	Ala	Leu	Leu 410	Ser	Glu	Arg	Leu	His 415	Arg	
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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	
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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	
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Ser	Ser	Ser	Asp 580	Pro	Asn	Leu	Gln	Asn 585	Ile	Pro	Val	Arg	Thr 590	Pro	Leu	
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Val	Ala 610	Leu	Asp	Tyr	Ser	Gln 615	Ile	Glu	Leu	Arg	Val 620	Leu	Ala	His	Leu	
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His	Thr	Gln	Thr	Ala 645	Ser	Trp	Met	Phe	Gly 650	Val	Pro	Pro	Glu	Ala 655	Val	
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Tyr	Gly	Met 675	Ser	Ala	His	Arg	Leu 680	Ser	Gln	Glu	Leu	Ala 685	Ile	Pro	Tyr	
Glu	Glu 690	Ala	Val	Ala	Phe	Ile 695	Glu	Arg	Tyr	Phe	Gln 700	Ser	Phe	Pro	Lys	
Val 705	Arg	Ala	Trp	Ile	Glu 710	Lys	Thr	Leu	Glu	Glu 715	Gly	Arg	Lys	Arg	Gly 720	
Tyr	Val	Glu	Thr	Leu 725	Phe	Gly	Arg	Arg	Arg 730	Tyr	Val	Pro	Asp	Leu 735	Asn	
Ala	Arg	Val	Lys 740	Ser	Val	Arg	Glu	Ala 745	Ala	Glu	Arg	Met	Ala 750	Phe	Asn	
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Lys	Leu 770	Phe	Pro	Arg	Leu	Arg 775	Glu	Met	Gly	Ala	Arg 780	Met	Leu	Leu	Gln	
Val 785	His	Asp	Glu	Leu	Leu 790	Leu	Glu	Ala	Pro	Gln 795	Ala	Gly	Ala	Glu	Glu 800	
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Lys	Gly															

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 <223> Xaa = Glu, Arg or Thr

<400> 8  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Tyr Val  
 1 5 10 15  
 Xaa Thr Leu

<210> 9  
 <211> 19  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic DNA polymerase motif

<220>  
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 <222> (1)...(1)  
 <223> Xaa = Ala, Asp or Ser

<220>  
 <221> VARIANT  
 <222> (2)...(2)  
 <223> Xaa = Trp or Tyr

<220>  
 <221> VARIANT  
 <222> (3)...(3)  
 <223> Xaa = any amino acid other than Ile

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

<220>  
 <221> VARIANT  
 <222> (5)...(5)  
 <223> Xaa = Lys, Gly, Arg or Gln

<220>  
 <221> VARIANT  
 <222> (6)...(6)  
 <223> Xaa = Thr or Val

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

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

<220>  
 <221> VARIANT  
 <222> (10)...(10)  
 <223> Xaa = Gly or Ala

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

<220>  
 <221> VARIANT  
 <222> (12)...(12)  
 <223> Xaa = Lys, Arg or Glu

<220>  
 <221> VARIANT  
 <222> (13)...(13)  
 <223> Xaa = Arg or Lys

<220>  
 <221> VARIANT  
 <222> (17)...(17)  
 <223> Xaa = Glu or Arg

<400> 9  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa Xaa Xaa Gly Tyr Val  
 1 5 10 15  
 Xaa Thr Leu

<210> 10  
 <211> 19  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic DNA polymerase motif

<220>  
 <221> VARIANT  
 <222> (3)...(3)  
 <223> Xaa = any amino acid other than Ile

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

<220>  
 <221> VARIANT  
 <222> (5)...(5)  
 <223> Xaa = Lys or Gly

<220>  
 <221> VARIANT  
 <222> (12)...(12)  
 <223> Xaa = Lys or Arg

<220>  
 <221> VARIANT  
 <222> (13)...(13)  
 <223> Xaa = Arg or Lys

<400> 10  
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 1 5 10 15  
 Glu Thr Leu

<210> 11

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

<220>  
 <223> synthetic DNA polymerase motif

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

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

<220>  
 <221> VARIANT  
 <222> (5)...(5)  
 <223> Xaa = Lys or Gly

<220>  
 <221> VARIANT  
 <222> (12)...(12)  
 <223> Xaa = Lys or Arg

<220>  
 <221> VARIANT  
 <222> (13)...(13)  
 <223> Xaa = Arg or Lys

<400> 11  
 Ala Trp Xaa Xaa Xaa Thr Leu Glu Glu Gly Arg Xaa Xaa Gly Tyr Val  
 1 5 10 15  
 Glu Thr Leu

<210> 12  
 <211> 31  
 <212> PRT  
 <213> Artificial Sequence

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

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

<210> 13  
 <211> 31  
 <212> PRT  
 <213> Artificial Sequence

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

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



<210> 14  
 <211> 31  
 <212> PRT  
 <213> Artificial Sequence

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

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

<210> 15  
 <211> 31  
 <212> PRT  
 <213> Artificial Sequence

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

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

<210> 16  
 <211> 31  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic polymerase domain region of Thermus sp.  
 sps17 DNA polymerase (Sps17)

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

<210> 17  
 <211> 31  
 <212> PRT  
 <213> Artificial Sequence

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

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

<210> 18  
 <211> 31  
 <212> PRT

<213> Artificial Sequence

<220>

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

<400> 18

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

<210> 19

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 19

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

<210> 20

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 20

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

<210> 21

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 21

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

<210> 22

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic conserved DNA polymerase active site

## motif A

&lt;400&gt; 22

Asp Tyr Ser Gln Ile Glu Leu Arg  
1 5

&lt;210&gt; 23

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

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

&lt;400&gt; 23

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

&lt;210&gt; 24

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

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

&lt;400&gt; 24

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

&lt;210&gt; 25

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

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

&lt;400&gt; 25

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

&lt;210&gt; 26

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> synthetic polymerase domain region native  
consensus motif

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(1)

&lt;223&gt; Xaa = Ala, Asp, Ser, Glu, Arg or Gln

&lt;220&gt;

<221> VARIANT  
 <222> (2)...(2)  
 <223> Xaa = Trp or Tyr

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

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

<220>  
 <221> VARIANT  
 <222> (5)...(5)  
 <223> Xaa = Lys, Gly, Arg, Gln, His or Asn

<220>  
 <221> VARIANT  
 <222> (6)...(6)  
 <223> Xaa = Thr, Val, Met or Ile

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

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

<220>  
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 <222> (9)...(9)  
 <223> Xaa = Glu or Phe

<220>  
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 <222> (10)...(10)  
 <223> Xaa = Gly or Ala

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

<220>  
 <221> VARIANT  
 <222> (12)...(12)  
 <223> Xaa = Lys, Arg, Glu, Thr or Gln

<220>  
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 <222> (13)...(13)  
 <223> Xaa = Arg, Lys or His

<220>  
 <221> VARIANT  
 <222> (17)...(17)  
 <223> Xaa = Glu, Arg or Thr

<400> 26  
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 1 5 10 15  
 Xaa Thr Leu

<210> 27  
 <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> 27  
 Met Lys Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu  
 1 5 10 15  
 Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly  
 20 25 30  
 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala  
 35 40 45  
 Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe  
 50 55 60  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu  
 65 70 75 80  
 Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu  
 100 105 110  
 Glu Val Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Arg Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg  
 130 135 140  
 Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu  
 145 150 155 160  
 Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys  
 165 170 175  
 Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu  
 195 200 205  
 Leu Lys Glu Trp Gly Ser Leu Glu Asn Ile Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Val Lys Pro Glu Ser Val Arg Glu Arg Ile Lys Ala His Leu Glu Asp  
 225 230 235 240  
 Leu Lys Leu Ser Leu Glu Leu Ser Arg Val Arg Ser Asp Leu Pro Leu  
 245 250 255  
 Glu Val Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Arg  
 260 265 270  
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly  
 275 280 285  
 Leu Leu Glu Glu Ser Glu Pro Val Gly Tyr Arg Ile Val Lys Asp Leu  
 290 295 300  
 Val Glu Phe Glu Lys Leu Ile Glu Lys Leu Arg Glu Ser Pro Ser Phe  
 305 310 315 320  
 Ala Ile 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

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      450      455      460
Ser  Cys  Glu  Asp  Ala  Asp  Ile  Thr  Tyr  Arg  Leu  Tyr  Lys  Thr  Leu  Ser
465  Leu  Lys  Leu  His  Glu  Ala  Asp  Leu  Glu  Asn  Val  Phe  Tyr  Lys  Ile  Glu
      485      490      500
Met  Pro  Leu  Val  Asn  Val  Leu  Ala  Arg  Met  Glu  Leu  Asn  Gly  Val  Tyr
      515      520      525
Val  Asp  Thr  Glu  Phe  Leu  Lys  Lys  Leu  Ser  Glu  Glu  Tyr  Gly  Lys  Lys
      530      535      540
Leu  Glu  Glu  Leu  Ala  Glu  Glu  Ile  Tyr  Arg  Ile  Ala  Gly  Glu  Pro  Phe
      545      550      555
Asn  Ile  Asn  Ser  Pro  Lys  Gln  Val  Ser  Arg  Ile  Leu  Phe  Glu  Lys  Leu
      565      570      575
Gly  Ile  Lys  Pro  Arg  Gly  Lys  Thr  Thr  Lys  Thr  Gly  Asp  Tyr  Ser  Thr
      580      585      590
Arg  Ile  Glu  Val  Leu  Glu  Glu  Leu  Ala  Gly  Glu  His  Glu  Ile  Ile  Pro
      595      600      605
Leu  Ile  Leu  Glu  Tyr  Arg  Lys  Ile  Gln  Lys  Leu  Lys  Ser  Thr  Tyr  Ile
      610      615      620
Asp  Ala  Leu  Pro  Lys  Met  Val  Asn  Pro  Lys  Thr  Gly  Arg  Ile  His  Ala
      625      630      635
Ser  Phe  Asn  Gln  Thr  Gly  Thr  Ala  Thr  Gly  Arg  Leu  Ser  Ser  Ser  Asp
      645      650      655
Pro  Asn  Leu  Gln  Asn  Leu  Pro  Thr  Lys  Ser  Glu  Glu  Gly  Lys  Glu  Ile
      660      665      670
Arg  Lys  Ala  Ile  Val  Pro  Gln  Asp  Pro  Asn  Trp  Trp  Ile  Val  Ser  Ala
      675      680      685
Asp  Tyr  Ser  Gln  Ile  Glu  Leu  Arg  Ile  Leu  Ala  His  Leu  Ser  Gly  Asp
      690      695      700
Glu  Asn  Leu  Leu  Arg  Ala  Phe  Glu  Glu  Gly  Ile  Asp  Val  His  Thr  Leu
      705      710      715
Thr  Ala  Ser  Arg  Ile  Phe  Asn  Val  Lys  Pro  Glu  Glu  Val  Thr  Glu  Glu
      725      730      735
Met  Arg  Arg  Ala  Gly  Lys  Met  Val  Asn  Phe  Ser  Ile  Ile  Tyr  Gly  Val
      740      745      750
Thr  Pro  Tyr  Gly  Leu  Ser  Val  Arg  Leu  Gly  Val  Pro  Val  Lys  Glu  Ala
      755      760      765
Glu  Lys  Met  Ile  Val  Asn  Tyr  Phe  Val  Leu  Tyr  Pro  Lys  Val  Arg  Asp
      770      775      780
Tyr  Ile  Gln  Arg  Val  Val  Ser  Glu  Ala  Lys  Glu  Lys  Gly  Tyr  Val  Arg
      785      790      795
Thr  Leu  Phe  Gly  Arg  Lys  Arg  Asp  Ile  Pro  Gln  Leu  Met  Ala  Arg  Asp
      805      810      815
Arg  Asn  Thr  Gln  Ala  Glu  Gly  Glu  Arg  Ile  Ala  Ile  Asn  Thr  Pro  Ile
      820      825      830
Gln  Gly  Thr  Ala  Ala  Asp  Ile  Ile  Lys  Leu  Ala  Met  Ile  Glu  Ile  Asp
      835      840      845
Arg  Glu  Leu  Lys  Glu  Arg  Lys  Met  Arg  Ser  Lys  Met  Ile  Ile  Gln  Val
      850      855      860
His  Asp  Glu  Leu  Val  Phe  Glu  Val  Pro  Asn  Glu  Glu  Lys  Asp  Ala  Leu
      865      870      875
Val  Glu  Leu  Val  Lys  Asp  Arg  Met  Thr  Asn  Val  Val  Lys  Leu  Ser  Val
      885      890
Pro  Leu  Glu  Val  Asp  Val  Thr  Ile  Gly  Lys  Thr  Trp  Ser

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<210> 28  
 <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

&lt;400&gt; 28

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

24  
 Asn Ile Asn Ser Pro Lys Gln Val Ser Arg Ile Leu Phe Glu Lys Leu  
 545 550 555 560  
 Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Asp Tyr Ser Thr  
 565 570 575  
 Arg Ile Glu Val Leu Glu Glu Leu Ala Gly Glu His Glu Ile Ile Pro  
 580 585 590  
 Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile  
 595 600 605  
 Asp Ala Leu Pro Lys Met Val Asn Pro Lys Thr Gly Arg Ile His Ala  
 610 615 620  
 Ser Phe Asn Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp  
 625 630 635 640  
 Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile  
 645 650 655  
 Arg Lys Ala Ile Val Pro Gln Asp Pro Asn Trp Trp Ile Val Ser Ala  
 660 665 670  
 Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp  
 675 680 685  
 Glu Asn Leu Leu Arg Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu  
 690 695 700  
 Thr Ala Ser Arg Ile Phe Asn Val Lys Pro Glu Glu Val Thr Glu Glu  
 705 710 715 720  
 Met Arg Arg Ala Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val  
 725 730 735  
 Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Val Pro Val Lys Glu Ala  
 740 745 750  
 Glu Lys Met Ile Val Asn Tyr Phe Val Leu Tyr Pro Lys Val Arg Asp  
 755 760 765  
 Tyr Ile Gln Arg Val Val Ser Glu Ala Lys Glu Lys Gly Tyr Val Arg  
 770 775 780  
 Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp  
 785 790 795 800  
 Arg Asn Thr Gln Ala Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile  
 805 810 815  
 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Glu Ile Asp  
 820 825 830  
 Arg Glu Leu Lys Glu Arg Lys Met Arg Ser Lys Met Ile Ile Gln Val  
 835 840 845  
 His Asp Glu Leu Val Phe Glu Val Pro Asn Glu Glu Lys Asp Ala Leu  
 850 855 860  
 Val Glu Leu Val Lys Asp Arg Met Thr Asn Val Val Lys Leu Ser Val  
 865 870 875 880  
 Pro Leu Glu Val Asp Val Thr Ile Gly Lys Thr Trp Ser  
 885 890

<210> 29

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic DNA polymerase motif

<220>

<221> VARIANT

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

<223> Xaa = Ile or Leu

<220>

<221> VARIANT

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

<223> Xaa = any amino acid other than Ile or Val

<220>

<221> VARIANT

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

<223> Xaa = Arg or Lys



<220>  
 <221> VARIANT  
 <222> (10)...(10)  
 <223> Xaa = Thr, Ser or Leu

<220>  
 <221> VARIANT  
 <222> (11)...(11)  
 <223> Xaa = Pro or Glu

<220>  
 <221> VARIANT  
 <222> (12)...(12)  
 <223> Xaa = Leu or Glu

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 Pro Asn Leu Gln Asn Xaa Pro Xaa Xaa Xaa Xaa Gly  
 1 5 10

<210> 30  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

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

<400> 30  
 ctacctcctg gacccctcca a 21

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

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

<400> 31  
 ataaccaact ggtagtggcg tgtaa 25

<210> 32  
 <211> 921  
 <212> PRT  
 <213> Deinococcus radiodurans

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

<400> 32  
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 1 5 10 15  
 Ile Asp Gly His Ala Leu Ala Phe Arg Ser Tyr Phe Ala Leu Pro Pro  
 20 25 30  
 Leu Asn Asn Ser Lys Gly Glu Met Thr Asp Ala Ile Val Gly Phe Met  
 35 40 45  
 Lys Leu Leu Leu Arg Leu Ala Arg Gln Lys Ser Asn Gln Val Ile Val  
 50 55 60  
 Val Phe Asp Pro Pro Val Lys Thr Leu Arg His Glu Gln Tyr Glu Gly  
 65 70 75 80  
 Tyr Lys Ser Gly Arg Ala Gln Thr Pro Glu Asp Leu Arg Gly Gln Ile  
 85 90 95  
 Asn Arg Ile Arg Ala Leu Val Asp Ala Leu Gly Phe Pro Arg Leu Glu  
 100 105 110

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Glu	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Ile	Ala	Ser	Leu	Thr	Arg	Met
Ala	Glu	Gly	Lys	Gly	Tyr	Glu	Val	Arg	Ile	Val	Thr	Ser	Asp	Arg	Asp
Ala	Tyr	Gln	Leu	Leu	Asp	Glu	His	Val	Lys	Val	Ile	Ala	Asn	Asp	Phe
145	Ser	Leu	Ile	Gly	Pro	Ala	Gln	Val	Glu	Glu	Lys	Tyr	Gly	Val	Thr
				165	165				170					175	Val
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	Glu	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

Asn	Ile	Pro	Ile	Arg	Ser	Glu	Leu	Gly	Arg	Glu	Ile	Arg	Lys	Gly	Phe
		675					680					685			
Ile	Ala	Glu	Asp	Gly	Phe	Thr	Leu	Ile	Ala	Ala	Asp	Tyr	Ser	Gln	Ile
	690					695					700				
Glu	Leu	Arg	Leu	Leu	Ala	His	Ile	Ala	Asp	Asp	Pro	Leu	Met	Gln	Gln
	705				710					715					720
Ala	Phe	Val	Glu	Gly	Ala	Asp	Ile	His	Arg	Arg	Thr	Ala	Ala	Gln	Val
				725					730					735	
Leu	Gly	Leu	Asp	Glu	Ala	Thr	Val	Asp	Ala	Asn	Gln	Arg	Arg	Ala	Ala
			740					745					750		
Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu
		755					760					765			
Ser	Asn	Asp	Leu	Gly	Ile	Pro	Tyr	Ala	Glu	Ala	Ala	Thr	Phe	Ile	Glu
	770					775					780				
Ile	Tyr	Phe	Ala	Thr	Tyr	Pro	Gly	Ile	Arg	Arg	Tyr	Ile	Asn	His	Thr
	785				790					795					800
Leu	Asp	Phe	Gly	Arg	Thr	His	Gly	Tyr	Val	Glu	Thr	Leu	Tyr	Gly	Arg
				805					810					815	
Arg	Arg	Tyr	Val	Pro	Gly	Leu	Ser	Ser	Arg	Asn	Arg	Val	Gln	Arg	Glu
			820					825					830		
Ala	Glu	Glu	Arg	Leu	Ala	Tyr	Asn	Met	Pro	Ile	Gln	Gly	Thr	Ala	Ala
		835					840					845			
Asp	Ile	Met	Lys	Leu	Ala	Met	Val	Gln	Leu	Asp	Pro	Gln	Leu	Asp	Ala
	850					855					860				
Ile	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His	Asp	Glu	Leu	Leu	Ile	Glu
	865				870					875					880
Ala	Pro	Leu	Asp	Lys	Ala	Glu	Gln	Val	Ala	Ala	Leu	Thr	Lys	Lys	Val
				885					890					895	
Met	Glu	Asn	Val	Val	Gln	Leu	Lys	Val	Pro	Leu	Ala	Val	Glu	Val	Gly
		900						905					910		
Thr	Gly	Pro	Asn	Trp	Phe	Asp	Thr	Lys							
		915					920								

&lt;210&gt; 33

&lt;211&gt; 892

&lt;212&gt; PRT

&lt;213&gt; Thermosipho africanus

&lt;220&gt;

&lt;223&gt; Thermosipho africanus DNA polymerase (Taf)

&lt;400&gt; 33

Met	Gly	Lys	Met	Phe	Leu	Phe	Asp	Gly	Thr	Gly	Leu	Val	Tyr	Arg	Ala
1				5					10					15	
Phe	Tyr	Ala	Ile	Asp	Gln	Ser	Leu	Gln	Thr	Ser	Ser	Gly	Leu	His	Thr
		20						25					30		
Asn	Ala	Val	Tyr	Gly	Leu	Thr	Lys	Met	Leu	Ile	Lys	Phe	Leu	Lys	Glu
		35					40					45			
His	Ile	Ser	Ile	Gly	Lys	Asp	Ala	Cys	Val	Phe	Val	Leu	Asp	Ser	Lys
	50					55					60				
Gly	Gly	Ser	Lys	Lys	Arg	Lys	Asp	Ile	Leu	Glu	Thr	Tyr	Lys	Ala	Asn
	65				70					75				80	
Arg	Pro	Ser	Thr	Pro	Asp	Leu	Leu	Leu	Glu	Gln	Ile	Pro	Tyr	Val	Glu
				85					90					95	
Glu	Leu	Val	Asp	Ala	Leu	Gly	Ile	Lys	Val	Leu	Lys	Ile	Glu	Gly	Phe
			100					105					110		
Glu	Ala	Asp	Asp	Ile	Ile	Ala	Thr	Leu	Ser	Lys	Lys	Phe	Glu	Ser	Asp
		115					120					125			
Phe	Glu	Lys	Val	Asn	Ile	Ile	Thr	Gly	Asp	Lys	Asp	Leu	Leu	Gln	Leu
	130					135					140				
Val	Ser	Asp	Lys	Val	Phe	Val	Trp	Arg	Val	Glu	Arg	Gly	Ile	Thr	Asp
	145				150					155					160
Leu	Val	Leu	Tyr	Asp	Arg	Asn	Lys	Val	Ile	Glu	Lys	Tyr	Gly	Ile	Tyr
				165					170					175	
Pro	Glu	Gln	Phe	Lys	Asp	Tyr	Leu	Ser	Leu	Val	Gly	Asp	Gln	Ile	Asp
			180					185					190		
Asn	Ile	Pro	Gly	Val	Lys	Gly	Ile	Gly	Lys	Lys	Thr	Ala	Val	Ser	Leu

Leu	Lys	195	Tyr	Asn	Ser	Leu	200	Glu	Asn	Val	Leu	Lys	205	Asn	Ile	Asn	Leu
210	Thr	Glu	Lys	Leu	Arg	Arg	215	Leu	Leu	Glu	Asp	Ser	Lys	Glu	Asp	Leu	240
225	Lys	Ser	Ile	Glu	Leu	Val	230	Glu	Leu	Ile	235	Tyr	Asp	Val	Pro	Met	255
245	Glu	Lys	Asp	Glu	Ile	Ile	245	Tyr	Arg	Gly	250	Tyr	Asn	Pro	Asp	Lys	Leu
260	Leu	Lys	Val	Leu	Lys	Lys	265	Glu	Phe	Ser	270	Ser	Ile	Ile	Lys	Glu	Leu
275	Asn	Leu	Gln	Glu	Lys	Leu	280	Lys	Glu	Tyr	285	Ile	Leu	Val	Asp	Asn	Glu
290	Asp	Lys	Leu	Lys	Lys	Leu	295	Glu	Glu	Ile	300	Glu	Lys	Tyr	Lys	Thr	Phe
305	Ser	Ile	Asp	Thr	Glu	Thr	310	Ser	Leu	Asp	315	Pro	Phe	Glu	Ala	Lys	Leu
325	Val	Gly	Ile	Ser	Ile	Ser	330	Met	Glu	Gly	335	Lys	Ala	Tyr	Tyr	Ile	Pro
340	Val	Ser	His	Phe	Gly	Ala	345	Asn	Ile	Ser	350	Lys	Ser	Leu	Ile	Asp	Lys
355	Phe	Leu	Lys	Gln	Ile	Leu	360	Glu	Lys	Asp	365	Tyr	Asn	Ile	Val	Gly	Gln
370	Asn	Leu	Lys	Phe	Asp	Tyr	375	Glu	Ile	Phe	380	Ser	Met	Gly	Phe	Ser	Pro
385	Asn	Val	Pro	His	Phe	Asp	390	Met	Ile	Ala	395	Ala	Tyr	Leu	Leu	Asn	Pro
405	Asp	Glu	Lys	Arg	Phe	Asn	410	Glu	Glu	Leu	415	Ser	Leu	Lys	Tyr	Leu	Gly
420	Tyr	Lys	Met	Ile	Ser	Phe	425	Glu	Leu	Val	430	Asn	Glu	Asn	Val	Pro	Leu
435	Phe	Gly	Asn	Asp	Phe	Ser	440	Val	Pro	Leu	445	Glu	Arg	Ala	Val	Glu	Tyr
450	Ser	Cys	Glu	Asp	Ala	Asp	455	Val	Thr	Tyr	460	Ile	Phe	Arg	Lys	Leu	Gly
465	Arg	Lys	Ile	Tyr	Glu	Asn	470	Met	Glu	Lys	475	Leu	Phe	Tyr	Glu	Ile	Glu
485	Met	Pro	Leu	Ile	Asp	Val	490	Leu	Ser	Glu	495	Met	Glu	Leu	Asn	Gly	Val
500	Phe	Asp	Glu	Glu	Tyr	Leu	505	Glu	Ser	Lys	510	Leu	Leu	Asn	Gly	Val	Tyr
515	Met	Asp	Gly	Ile	Lys	Glu	520	Val	Phe	Glu	525	Lys	Lys	Tyr	Gln	Glu	Lys
530	Asn	Leu	Asn	Ser	Ser	Thr	535	Val	Ala	Tyr	540	Ile	Leu	Phe	Glu	Lys	Leu
545	Asn	Ile	Ala	Pro	Tyr	Lys	550	Thr	Ala	Thr	555	Gly	Lys	Phe	Ser	Thr	Asn
565	Ala	Glu	Val	Leu	Glu	Glu	570	Ser	Lys	Glu	575	His	Glu	Ile	Ala	Lys	Leu
580	Leu	Leu	Glu	Tyr	Arg	Lys	585	Gln	Lys	Leu	590	Lys	Ser	Thr	Tyr	Ile	Asp
595	Ser	Ile	Pro	Leu	Ser	Ile	600	Arg	Lys	Thr	605	Asn	Arg	Val	His	Thr	Thr
610	Phe	His	Gln	Thr	Gly	Thr	615	Ser	Thr	Gly	620	Leu	Ser	Ser	Ser	Asn	Pro
625	Asn	Leu	Gln	Asn	Leu	Pro	630	Thr	Arg	Ser	635	Glu	Gly	Lys	Glu	Ile	Arg
645	Lys	Ala	Val	Arg	Pro	Gln	650	Arg	Gln	Asp	655	Trp	Trp	Ile	Leu	Gly	Ala
660	Tyr	Ser	Gln	Ile	Glu	Leu	665	Val	Leu	Ala	670	Leu	Ala	His	Val	Ser	Lys
675	Asn	Leu	Leu	Lys	Ala	Phe	680	Glu	Asp	Leu	685	Asp	Ile	His	Thr	Ile	Thr
690	Ala	Ala	Lys	Ile	Phe	Gly	695	Val	Ser	Glu	700	Met	Phe	Val	Ser	Glu	Gln
705	Arg	Arg	Val	Gly	Lys	Met	710	Val	Asn	Phe	715	Ala	Ile	Ile	Tyr	Gly	Val
725	Pro	Tyr	Gly	Leu	Ser	Lys	730	Ile	Gly	Leu	735	Ser	Val	Ser	Glu	Thr	Lys
740							745				750						

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

<210> 34  
 <211> 893  
 <212> PRT  
 <213> Thermotoga maritima

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

<400> 34

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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

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

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

Phe	Gly	Phe	Ser	Phe	Ala	Asp	Val	Pro	Val	Asp	Lys	Ala	Ala	Glu	Tyr	
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Met	Lys	Leu	His	Glu	Ala	Glu	Leu	Glu	Asn	Val	Phe	Tyr	Arg	Ile	Glu	
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Val	Asp	Thr	Glu	Phe	Leu	Lys	Lys	Leu	Ser	Glu	Glu	Tyr	Gly	Lys	Lys	
Leu	Glu	Glu	Leu	Ala	Glu	Lys	Ile	Tyr	Gln	Ile	Ala	Gly	Glu	Pro	Phe	
Asn	Ile	Asn	Ser	Pro	Lys	Gln	Val	Ser	Asn	Ile	Leu	Phe	Glu	Lys	Leu	
Gly	Ile	Lys	Pro	Arg	Gly	Lys	Thr	Thr	Lys	Thr	Gly	Asp	Tyr	Ser	Thr	
Arg	Ile	Glu	Val	Leu	Glu	Glu	Ile	Ala	Asn	Glu	His	Glu	Ile	Val	Pro	
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Asp	Thr	Leu	Pro	Lys	Leu	Val	Asn	Pro	Lys	Thr	Gly	Arg	Phe	His	Ala	
Ser	Phe	His	Gln	Thr	Gly	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp	
Pro	Asn	Leu	Gln	Asn	Leu	Pro	Thr	Lys	Ser	Glu	Glu	Gly	Lys	Glu	Ile	
Arg	Lys	Ala	Ile	Val	Pro	Gln	Asp	Pro	Asp	Trp	Trp	Ile	Val	Ser	Ala	
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Glu	Asn	Leu	Val	Lys	Ala	Phe	Glu	Glu	Gly	Ile	Asp	Val	His	Thr	Leu	
Thr	Ala	Ser	Arg	Ile	Tyr	Asn	Val	Lys	Pro	Glu	Glu	Val	Asn	Glu	Glu	
Met	Arg	Arg	Val	Gly	Lys	Met	Val	Asn	Phe	Ser	Ile	Ile	Tyr	Gly	Val	
Thr	Pro	Tyr	Gly	Leu	Ser	Val	Arg	Leu	Gly	Ile	Pro	Val	Lys	Glu	Ala	
Glu	Lys	Met	Ile	Ile	Ser	Tyr	Phe	Thr	Leu	Tyr	Pro	Lys	Val	Arg	Ser	
Tyr	Ile	Gln	Gln	Val	Val	Ala	Glu	Ala	Lys	Glu	Lys	Gly	Tyr	Val	Arg	
Thr	Leu	Phe	Gly	Arg	Lys	Arg	Asp	Ile	Pro	Gln	Leu	Met	Ala	Arg	Asp	
Lys	Asn	Thr	Gln	Ser	Glu	Gly	Glu	Arg	Ile	Ala	Ile	Asn	Thr	Pro	Ile	
Gln	Gly	Thr	Ala	Ala	Asp	Ile	Ile	Lys	Leu	Ala	Met	Ile	Asp	Ile	Asp	
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His	Asp	Glu	Leu	Val	Phe	Glu	Val	Pro	Asp	Glu	Glu	Lys	Glu	Glu	Leu	
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<211> 876
<212> PRT
<213> Bacillus stearothermophilus
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<220>  
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Asn	Ala	Val	Tyr	Gly	Phe	Thr	Met	Met	Leu	Asn	Lys	Ile	Leu	Ala	Glu			
Glu	Gln	Pro	Thr	His	Ile	Leu	Val	Ala	Phe	Asp	Ala	Gly	Lys	Thr	Thr			
Phe	Arg	His	Glu	Thr	Phe	Gln	Asp	Tyr	Lys	Gly	Gly	Arg	Gln	Gln	Thr			
Pro	Pro	Glu	Leu	Ser	Glu	Gln	Phe	Pro	Leu	Leu	Arg	Glu	Leu	Leu	Lys			
Ala	Tyr	Arg	Ile	Pro	Ala	Tyr	Glu	Leu	Asp	His	Tyr	Glu	Ala	Asp	Asp			
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Lys	Val	Ile	Ser	Gly	Asp	Arg	Asp	Leu	Thr	Gln	Leu	Ala	Ser	Pro	Gln			
Val	Thr	Val	Glu	Ile	Thr	Lys	Lys	Gly	Ile	Thr	Asp	Ile	Glu	Ser	Tyr			
Thr	Pro	Glu	Thr	Val	Val	Glu	Lys	Tyr	Gly	Leu	Thr	Pro	Glu	Gln	Ile			
Val	Asp	Leu	Lys	Gly	Leu	Met	Gly	Asp	Lys	Ser	Asp	Asn	Ile	Pro	Gly			
Val	Pro	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Val	Lys	Leu	Leu	Lys	Gln	Phe			
Gly	Thr	Val	Glu	Asn	Val	Leu	Ala	Ser	Ile	Asp	Glu	Ile	Lys	Gly	Glu			
Lys	Leu	Lys	Glu	Asn	Leu	Arg	Gln	Tyr	Arg	Asp	Leu	Ala	Leu	Leu	Ser			
Lys	Gln	Leu	Ala	Ala	Ile	Cys	Arg	Asp	Ala	Pro	Val	Glu	Leu	Thr	Leu			
Asp	Asp	Ile	Val	Tyr	Lys	Gly	Glu	Asp	Arg	Glu	Lys	Val	Val	Ala	Leu			
Phe	Gln	Glu	Leu	Gly	Phe	Gln	Ser	Phe	Leu	Asp	Lys	Met	Ala	Val	Gln			
Thr	Asp	Glu	Gly	Glu	Lys	Pro	Leu	Ala	Gly	Met	Asp	Phe	Ala	Ile	Ala			
Asp	Ser	Val	Thr	Asp	Glu	Met	Leu	Ala	Asp	Lys	Ala	Ala	Leu	Val	Val			
Glu	Val	Val	Gly	Asp	Asn	Tyr	His	His	Ala	Pro	Ile	Val	Gly	Ile	Ala			
Leu	Ala	Asn	Glu	Arg	Gly	Arg	Phe	Phe	Leu	Arg	Pro	Glu	Thr	Ala	Leu			
Ala	Asp	Pro	Lys	Phe	Leu	Ala	Trp	Leu	Gly	Asp	Glu	Thr	Lys	Lys	Lys			
Thr	Met	Phe	Asp	Ser	Lys	Arg	Ala	Ala	Val	Ala	Leu	Lys	Trp	Lys	Gly			
Ile	Glu	Leu	Arg	Gly	Val	Val	Phe	Asp	Leu	Leu	Leu	Ala	Ala	Tyr	Leu			
Leu	Asp	Pro	Ala	Gln	Ala	Ala	Gly	Asp	Val	Ala	Ala	Val	Ala	Lys	Met			
His	Gln	Tyr	Glu	Ala	Val	Arg	Ser	Asp	Glu	Ala	Val	Tyr	Gly	Lys	Gly			
Ala	Lys	Arg	Thr	Val	Pro	Asp	Glu	Pro	Thr	Leu	Ala	Glu	His	Leu	Ala			
Arg	Lys	Ala	Ala	Ala	Ile	Trp	Ala	Leu	Glu	Glu	Pro	Leu	Met	Asp	Glu			
Leu	Arg	Arg	Asn	Glu	Gln	Asp	Arg	Leu	Leu	Thr	Glu	Leu	Glu	Gln	Pro			
Leu	Ala	Gly	Ile	Leu	Ala	Asn	Met	Glu	Phe	Thr	Gly	Val	Lys	Val	Asp			
Thr	Lys	Arg	Leu	Gln	Met	Gly	Ala	Glu	Leu	Thr	Glu	Gln	Gln	Leu	Gln			
Ala	Val	Glu	Arg	Arg	Ile	Tyr	Glu	Leu	Ala	Gly	Gln	Glu	Phe	Asn	Ile			
Asn	Ser	Pro	Lys	Gln	Leu	Gly	Thr	Val	Leu	Phe	Asp	Lys	Leu	Gln	Leu			
Pro	Val	Leu	Lys	Lys	Thr	Lys	Thr	Gly	Tyr	Ser	Thr	Ser	Ala	Asp	Val			
545					550				555						560			

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			580					585					590		
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	610					615					620				
Asn	Ile	Pro	Ile	Arg	Leu	Glu	Gly	Arg	Lys	Ile	Arg	Gln	Ala	Phe	
625					630				635					640	
Val	Pro	Ser	Glu	Pro	Asp	Trp	Leu	Ile	Phe	Ala	Ala	Asp	Tyr	Ser	Gln
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Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Ile	Ala	Glu	Asp	Asp	Asn	Leu	Ile
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Glu	Ala	Phe	Arg	Arg	Gly	Leu	Asp	Ile	His	Thr	Lys	Thr	Ala	Met	Asp
		675				680						685			
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Leu	Ala	Gln	Asn	Leu	Asn	Ile	Thr	Arg	Lys	Glu	Ala	Ala	Glu	Phe	Ile
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Glu	Arg	Tyr	Phe	Ala	Ser	Phe	Pro	Gly	Val	Lys	Gln	Tyr	Met	Asp	Asn
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Ser	Phe	Ala	Glu	Arg	Thr	Ala	Met	Asn	Thr	Pro	Ile	Gln	Gly	Ser	Ala
785					790					795					800
Ala	Asp	Ile	Ile	Lys	Lys	Ala	Met	Ile	Asp	Leu	Ser	Val	Arg	Leu	Arg
				805					810					815	
Glu	Glu	Arg	Leu	Gln	Ala	Arg	Leu	Leu	Leu	Gln	Val	His	Asp	Glu	Leu
			820					825					830		
Ile	Leu	Glu	Ala	Pro	Lys	Glu	Glu	Ile	Glu	Arg	Leu	Cys	Arg	Leu	Val
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<220>  
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Pro	Pro	Glu	Leu	Ser	Glu	Gln	Phe	Pro	Leu	Leu	Arg	Glu	Leu	Leu	Arg
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	130					135					140				

										35					
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Thr	Pro	Glu	Ala	Val 165	Arg	Glu	Lys	Tyr	Gly 170	Leu	Thr	Pro	Glu	Gln	Ile
Val	Asp	Leu	Lys 180	Gly	Leu	Met	Gly	Asp 185	Lys	Ser	Asp	Asn	Ile 190	Pro	Gly
Val	Pro	Gly 195	Ile	Gly	Glu	Lys	Thr 200	Ala	Val	Lys	Leu	Leu	Arg	Gln	Phe
Gly	Thr 210	Val	Glu	Asn	Val	Leu 215	Ala	Ser	Ile	Asp	Glu 220	Ile	Lys	Gly	Glu
Lys 225	Leu	Lys	Glu	Thr	Leu 230	Arg	Gln	His	Arg	Glu 235	Met	Ala	Leu	Leu	Ser 240
Lys	Lys	Leu	Ala	Ala 245	Ile	Arg	Arg	Asp	Ala 250	Pro	Val	Glu	Leu	Ser 255	Leu
Asp	Asp	Ile	Ala 260	Tyr	Gln	Gly	Glu	Asp 265	Arg	Glu	Lys	Val	Val 270	Ala	Leu
Phe	Lys	Glu 275	Leu	Gly	Phe	Gln	Ser 280	Phe	Leu	Glu	Lys	Met	Glu	Ser	Pro
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Val	Val	Asn	Glu 340	His	Gly	Arg	Phe	Phe 345	Leu	Arg	Pro	Glu	Thr 350	Ala	Leu
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Ser	Met 370	Phe	Asp	Ser	Lys	Arg 375	Ala	Ala	Val	Ala	Leu 380	Lys	Trp	Lys	Gly
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Arg	Lys 450	Ala	Ala	Ala	Ile	Trp 455	Ala	Leu	Glu	Arg	Pro 460	Phe	Leu	Asp	Glu
Leu 465	Arg	Arg	Asn	Glu	Gln 470	Asp	Arg	Leu	Leu	Val 475	Glu	Leu	Glu	Gln	Pro 480
Leu	Ser	Ser	Ile	Leu 485	Ala	Glu	Met	Glu	Phe 490	Ala	Gly	Val	Lys	Val 495	Asp
Thr	Lys	Arg	Leu 500	Glu	Gln	Met	Gly	Glu 505	Glu	Leu	Ala	Glu	Gln	Leu	Arg
Thr	Val	Glu 515	Gln	Arg	Ile	Tyr	Glu 520	Leu	Ala	Gly	Gln	Glu 525	Phe	Asn	Ile
Asn	Ser 530	Pro	Lys	Gln	Leu	Gly 535	Val	Ile	Leu	Phe	Glu 540	Lys	Leu	Gln	Leu
Pro 545	Val	Leu	Lys	Lys	Ser 550	Lys	Thr	Gly	Tyr	Ser 555	Thr	Ser	Ala	Asp	Val 560
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His	Tyr	Arg	Gln 580	Leu	Gly	Lys	Leu	Gln 585	Ser	Thr	Tyr	Ile	Glu 590	Gly	Leu
Leu	Lys	Val 595	Val	Arg	Pro	Asp	Thr 600	Lys	Lys	Val	His	Thr 605	Ile	Phe	Asn
Gln	Ala 610	Leu	Thr	Gln	Thr	Gly 615	Arg	Leu	Ser	Ser	Thr 620	Glu	Pro	Asn	Leu
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
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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
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	Lys	Glu	Glu	Arg	Leu	Gln	Ala	Arg	Leu	Leu	Gln	Val	His	Asp	Glu	
	Leu	Ile	Leu	Glu	Ala	Pro	Lys	Glu	Glu	Met	Glu	Arg	Leu	Cys	Arg	Leu
	Val	Pro	Glu	Val	Met	Glu	Gln	Ala	Val	Thr	Leu	Arg	Val	Pro	Leu	Lys
	Val	Asp	Tyr	His	Tyr	Gly	Ser	Thr	Trp	Tyr	Asp	Ala	Lys			

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

<220>  
 <223> synthetic polymerase motif corresponding to the D580X mutation of Z05

<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> 38  
 Thr Gly Arg Leu Ser Ser Xaa Xaa Pro Asn Leu Gln Asn  
 1 5 10

<210> 39  
 <211> 1491  
 <212> DNA  
 <213> Artificial Sequence

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

<400> 39  
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 ggaacgcctc aaggagagg aaaagctcct ttggctctac caagaggtgg aaaagcccct 180  
 ctcccgggtc ctggcccaca tggaggccac cggggtaagg ctggacgtgg cctatctaaa 240  
 ggccctttcc ctggagcttg cggaggagat tcgccgcctc gaggaggagg tcttcgcct 300  
 ggcgggccac ccttcaacc tgaactcccg tgaccagcta gagcgggtgc tctttgacga 360  
 gcttaggctt cccgccctgg gcaagacgca aaagacgggg aagcgtcca ccagcgccgc 420  
 ggtgctggag gccctcaggg agggccaccc catcgtggag aagatcctcc agcaccggga 480  
 gctcaccaag ctcaagaaca cctacgtaga ccccctcccg ggcctcgtcc acccgaggac 540

37

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gggccgcctc cacacccgct tcaaccagac agccacggcc acgggaaggc tctctagctc 600
cgggcccacac ctgcagaaca tccccatccg cacccttg ggccagagga tccgccgggc 660
cttcgtggcc gaggcgggat gggcggttgg ggccctggac tatagccaga tagagctccg 720
ggtcctcgcc cacctctccg gggacgagaa cctgatcagg gtcttccagg aggggaagga 780
catccacacc cagaccgcaa gctggatgtt cggcgtctcc ccggaggccg tggacccctc 840
gatgcgccgg gcggccaaga cggtgaactt cggcgtcctc tacggcatgt ccgcccatag 900
gctctcccag gagcttgcca tcccctacga ggaggcgggt gcctttatag agcgctactt 960
ccaaagcttc cccaagggtc gggcctggat agaaaagacc ctggaggagg ggaggaagcg 1020
gggctacgtg gaaacctctc tcggaagaag gcgctacgtg cccgacctca acgcccgggt 1080
gaagagcgct agggaggccg cggagcgcat ggcttcaac atgcccgtcc agggcaccgc 1140
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ccgcatgctc ctccagggtc acgacgagct cctcctggag gccccccaag cgcgggccga 1260
ggaggtggcg gctttggcca aggaggccat ggagaaggcc tatcccctcg ccgtgccctc 1320
ggaggtggag gtgggggatcg gggaggactg gctttccgcc aagggtgat atcagatctc 1380
cctgattatg cgtcagtcta tgaagaaaaa tcgtatacag atggacgaag agagaatcct 1440
tgtgaattta acagagggtg tagggattac acgccactac cagttgggta t 1491

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<210> 40

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic primer extension DG48 primer for Perfect Match template

<400> 40

gggaagggcg atcggtgcgg gcctcttcgc

30

<210> 41

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic primer extension FR743 primer for T:G Mismatch template

<400> 41

gggaagggcg atcggtgcgg gcctcttcgt

30

<210> 42

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic primer extension FR744 primer for A:A Mismatch template

<400> 42

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31

<210> 43

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic primer extension FR745 primer for A:C Mismatch template

<400> 43

gggaagggcg atcggtgcgg gcctcttca

29

<210> 44

<211> 32

<212> DNA

<213> Artificial Sequence

<220>  
 <223> synthetic primer extension FR750 primer for T:T  
 Mismatch template

<400> 44  
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<210> 45  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 Mismatch template

<400> 45  
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<210> 46  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 Mismatch template

<400> 46  
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<210> 47  
 <211> 29  
 <212> DNA  
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<220>  
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 Mismatch template

<400> 47  
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<210> 48  
 <211> 831  
 <212> PRT  
 <213> Carboxydotherrnus hydrogenoformans

<220>  
 <223> Carboxydotherrnus hydrogenoformans DNA polymerase (Chy)

<400> 48  
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 Phe Phe Ala Leu Pro Pro Leu Lys Thr Thr Lys Gly Glu Pro Thr Gly  
 20 25 30  
 Ala Val Tyr Glu Phe Leu Thr Met Leu Phe Arg Val Ile Lys Asp Glu  
 35 40 45  
 Lys Pro Glu Tyr Leu Ala Val Ala Phe Asp Ile Ser Arg Lys Thr Phe  
 50 55 60  
 Arg Thr Glu Gln Phe Thr Ala Tyr Lys Gly His Arg Lys Glu Ala Pro  
 65 70 75 80  
 Asp Glu Leu Val Pro Gln Phe Ala Leu Val Arg Glu Val Leu Lys Val  
 85 90 95  
 Leu Asn Val Pro Tyr Ile Glu Leu Asp Gly Tyr Glu Ala Asp Asp Ile  
 100 105 110  
 Ile Gly His Leu Ser Arg Ala Phe Ala Gly Gln Gly His Glu Val Val

Ile	Tyr	115	Ala	Asp	Arg	Asp	120	Met	Leu	Gln	Leu	Val	125	Asp	Glu	Lys	Thr
Val	Val	130	Tyr	Leu	Thr	Lys	135	Gly	Ile	Thr	Glu	Leu	140	Val	Lys	Met	Asp
145	Ala	Ala	Ile	Leu	Glu	Asn	Tyr	Gly	Leu	Lys	Pro	Lys	Gln	Leu	160	Val	
Leu	Val	Lys	Gly	Leu	Met	Gly	Asp	Pro	Ser	Asp	Asn	Ile	Pro	Gly	175	Val	
Asp	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Asp	Leu	Ile	Lys	Thr	Tyr	Gly		
Pro	Val	Glu	Glu	Val	Leu	Ala	Arg	Lys	Asp	Glu	Leu	Lys	Pro	Lys	Leu		
Ser	Glu	Lys	Leu	Ala	Glu	His	Glu	Asn	Leu	Ala	Lys	Ile	Ser	Lys	Gln		
Arg	Ala	Thr	Ile	Leu	Arg	Glu	Ile	Pro	Leu	Glu	Ile	Ser	Leu	Glu	Asp		
Leu	Lys	Val	Lys	Glu	Pro	Asn	Tyr	Glu	Val	Ala	Lys	Leu	Phe	Leu			
His	Leu	Glu	Phe	Lys	Ser	Phe	Leu	Lys	Glu	Ile	Glu	Pro	Lys	Ile	Lys		
Lys	Glu	Tyr	Gln	Glu	Gly	Lys	Asp	Leu	Val	Gln	Val	Glu	Thr	Val	Glu		
Thr	Glu	Gly	Gln	Ile	Ala	Val	Val	Phe	Ser	Asp	Gly	Phe	Tyr	Val	Asp		
305	Asp	Gly	Glu	Lys	Thr	Lys	Phe	Tyr	Ser	Leu	Asp	Arg	Leu	Asn	Glu	Ile	
Asp	Glu	Ile	Phe	Arg	Asn	Lys	Lys	Ile	Thr	Asp	Asp	Ala	Lys	Gly			
Glu	Glu	Ile	Val	Cys	Leu	Glu	Lys	Gly	Leu	Thr	Phe	Pro	Glu	Val	Cys		
Ile	Tyr	His	Ala	Arg	Ile	Ala	Ala	Tyr	Val	Leu	Asn	Pro	Ala	Asp	Gln	Asn	
Phe	Asp	Ala	Arg	Ile	Ala	Ala	Tyr	Val	Leu	Asn	Pro	Ala	Asp	Gln	Asn		
Pro	Gly	Leu	Lys	Gly	Leu	Tyr	Leu	Lys	Tyr	Asp	Leu	Pro	Val	Tyr	Glu		
385	Asp	Val	Ser	Leu	Asn	Ile	Arg	Gly	Leu	Phe	Tyr	Leu	Lys	Lys	Glu	Met	
Asp	Val	Ser	Leu	Asn	Ile	Arg	Gly	Leu	Phe	Tyr	Leu	Lys	Lys	Glu	Met		
Met	Arg	Lys	Ile	Phe	Glu	Gln	Glu	Gln	Arg	Leu	Phe	Tyr	Glu	Ile			
Glu	Leu	Pro	Leu	Thr	Pro	Val	Leu	Ala	Gln	Met	Glu	His	Thr	Gly	Ile		
Gln	Val	Asp	Arg	Glu	Ala	Leu	Lys	Glu	Met	Ser	Leu	Glu	Leu	Gly	Glu		
Gln	Ile	Glu	Glu	Leu	Ile	Arg	Glu	Ile	Tyr	Val	Leu	Ala	Gly	Glu	Glu		
465	Phe	Asn	Leu	Asn	Ser	Pro	Arg	Gln	Leu	Gly	Val	Ile	Leu	Phe	Glu	Lys	
Phe	Asn	Leu	Asn	Ser	Pro	Arg	Gln	Leu	Gly	Val	Ile	Leu	Phe	Glu	Lys		
Leu	Gly	Leu	Pro	Val	Ile	Lys	Lys	Thr	Lys	Thr	Gly	Tyr	Ser	Thr	Asp		
Ala	Glu	Val	Leu	Glu	Glu	Leu	Leu	Pro	Phe	His	Glu	Ile	Ile	Gly	Lys		
Ile	Leu	Asn	Tyr	Arg	Gln	Leu	Met	Lys	Leu	Lys	Ser	Thr	Tyr	Thr	Asp		
Gly	Leu	Met	Pro	Leu	Ile	Asn	Glu	Arg	Thr	Gly	Lys	Leu	His	Thr	Thr		
545	Phe	Asn	Gln	Thr	Gly	Thr	Leu	Thr	Gly	Arg	Leu	Ala	Ser	Ser	Glu	Pro	
Phe	Asn	Gln	Thr	Gly	Thr	Leu	Thr	Gly	Arg	Leu	Ala	Ser	Ser	Glu	Pro		
Asn	Leu	Gln	Asn	Ile	Pro	Ile	Arg	Leu	Glu	Leu	Gly	Arg	Lys	Leu	Arg		
Lys	Met	Phe	Ile	Pro	Ser	Pro	Gly	Tyr	Asp	Tyr	Ile	Val	Ser	Ala	Asp		
Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Leu	Leu	Ala	His	Phe	Ser	Glu	Glu	Pro		
Lys	Leu	Ile	Glu	Ala	Tyr	Gln	Lys	Gly	Glu	Asp	Ile	His	Arg	Lys	Thr		
625	Ala	Ser	Glu	Val	Phe	Gly	Val	Ser	Leu	Glu	Val	Thr	Pro	Glu	Met		
Ala	Ser	Glu	Val	Phe	Gly	Val	Ser	Leu	Glu	Val	Thr	Pro	Glu	Met			
Arg	Ala	His	Ala	Lys	Ser	Val	Asn	Phe	Gly	Ile	Val	Tyr	Gly	Ile	Ser		
Arg	Ala	His	Ala	Lys	Ser	Val	Asn	Phe	Gly	Ile	Val	Tyr	Gly	Ile	Ser		

40

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