SEQUENCE LISTING

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

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

<130> 26426 WO-HS

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<150> US 61/356,279
<151> 2010-06-18

<160> 51

<170> FastSEQ for Windows Version 4.0

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<211> 834
<212> PRT
<213> Thermus sp.

<220>
<223> Thermus sp. Z05 DNA polymerase (Z05)

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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 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 Lys 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 Glu Lys Leu Leu Trp Leu 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
                485                 490                 495
Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly
            500                 505                 510
Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
        515                 520                 525
Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
    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
625                 630                 635                 640
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
                805                 810                 815
Val Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala
            820                 825                 830
Lys Gly
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<210> 2

<211> 832
<212> PRT
<213> Thermus aquaticus

<220>
<223> Thermus equaticus DNA polymerase (Taq)

<400> 2

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 1               5                  10                  15
Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His 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 Asp Ala Val Ile Val
    50                  55                  60
Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly
65                  70                  75                  80
Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
                85                  90                  95
Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu
            100                 105                 110
Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys
        115                 120                 125
Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp
    130                 135                 140
Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly
145                 150                 155                 160
Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
                165                 170                 175
Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn
            180                 185                 190
Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu
        195                 200                 205
Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu
    210                 215                 220
Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys
225                 230                 235                 240
Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val
                245                 250                 255
Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe
            260                 265                 270
Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
        275                 280                 285
Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
    290                 295                 300
Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp
305                 310                 315                 320
Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro
                325                 330                 335
Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu
            340                 345                 350
Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro
        355                 360                 365
Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
    370                 375                 380
Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
385                 390                 395                 400
Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu
                405                 410                 415
Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu
            420                 425                 430
Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly
        435                 440                 445
Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala
    450                 455                 460
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
                485                 490                 495
Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg
            500                 505                 510
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 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
Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
        755                 760                 765
Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His
    770                 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
                805                 810                 815
Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu
            820                 825                 830


<210> 3
<211> 830
<212> PRT
<213> Thermus filiformis

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

<400> 3
Met Leu Pro Leu Leu Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly
 1               5                  10                  15
His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu Thr Thr
            20                  25                  30
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
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                100                 105                 110
Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Arg 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 Trp 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 Thr Gly Lys 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 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 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
                485                 490                 495
Gly Leu Pro Pro Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr
            500                 505                 510
Ser Ala Ala Val Leu Glu Leu Leu Arg Glu Ala His Pro Ile Val Gly
        515                 520                 525
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
                565                 570                 575
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
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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 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 Glu
820 825 830

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<211> 831
<212> PRT
<213> Thermus flavus

<220>
<223> Thermus flavus DNA polymerase (Tfl)

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

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Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu
        275                 280                 285
Gly Pro Lys Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala
    290                 295                 300
Phe Leu Gly Phe Ser Phe Ser Arg Pro Glu Pro Met Trp Ala Glu Leu
305                 310                 315                 320
Leu Ala Leu Ala Gly Ala Trp Glu Gly Arg Leu His Arg Ala Gln Asp
                325                 330                 335
Pro Leu Arg Gly Leu Arg Asp Leu Lys Gly Val Arg Gly Ile Leu Ala
            340                 345                 350
Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Phe Pro
        355                 360                 365
Glu Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr
    370                 375                 380
Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp
385                 390                 395                 400
Ala Gly Glu Arg Ala Leu Leu Ala Glu Arg Leu Phe Gln Thr Leu Lys
                405                 410                 415
Glu Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu Val
            420                 425                 430
Glu Lys Pro Leu Ser Arg Val Leu Ala Arg Met Glu Ala Thr Gly Val
        435                 440                 445
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
        515                 520                 525
Asp Arg Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr
    530                 535                 540
Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Gly Arg Leu His
545                 550                 555                 560
Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser
                565                 570                 575
Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg
            580                 585                 590
Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Val Leu Val Val Leu
        595                 600                 605
Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp
    610                 615                 620
Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Gln
625                 630                 635                 640
Thr Ala Ser Trp Met Phe Gly Val Ser Pro Glu Gly Val Asp Pro Leu
                645                 650                 655
Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met
            660                 665                 670
Ser Ala His Arg Leu Ser Gly Glu Leu Ser Ile Pro Tyr Glu Glu Ala
        675                 680                 685
Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg Ala
    690                 695                 700
Trp Ile Glu Gly Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu
705                 710                 715                 720
Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val
                725                 730                 735
Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val
            740                 745                 750
Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Arg Leu Phe
        755                 760                 765
Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His Asp
    770                 775                 780
Glu Leu Val Leu Glu Ala Pro Lys Asp Arg Ala Glu Arg Val Ala Ala
785                 790                 795                 800
Leu Ala Lys Glu Val Met Glu Gly Val Trp Pro Leu Gln Val Pro Leu
                805                 810                 815
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Glu Val Glu Val Gly Leu Gly Glu Asp Trp Leu Ser Ala Lys Glu
820 825 830

<210> 5
<211> 830
<212> PRT
<213> Thermus sp.

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

<400> 5
Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly
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His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu Thr Thr
20 25 30
Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu
35 40 45
Leu Lys Ala Leu Lys Glu Asp Gly Glu Val Ala Ile Val Val Phe Asp
50 55 60
Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala Tyr Lys Ala
65 70 75 80
Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile
85 90 95
Lys Glu Leu Val Asp Leu Leu Gly Leu Val Arg Leu Glu Val Pro Gly
100 105 110
Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala Glu Arg
115 120 125
Glu Gly Tyr Glu Val Arg Ile Leu Ser Ala Asp Arg Asp Leu Tyr Gln
130 135 140
Leu Leu Ser Asp Arg Ile His Leu Leu His Pro Glu Gly Glu Val Leu
145 150 155 160
Thr Pro Gly Trp Leu Gln Glu Arg Tyr Gly Leu Ser Pro Glu Arg Trp
165 170 175
Val Glu Tyr Arg Ala Leu Val Gly Asp Pro Ser Asp Asn Leu Pro Gly
180 185 190
Val Pro Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu Leu Lys Glu Trp
195 200 205
Gly Ser Leu Glu Ala Ile Leu Lys Asn Leu Asp Gln Val Lys Pro Glu
210 215 220
Arg Val Arg Glu Ala Ile Arg Asn Asn Leu Asp Lys Leu Gln Met Ser
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 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 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

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        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
                485                 490                 495
Gly Leu Pro Pro Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr
            500                 505                 510
Ser Ala Ala Val Leu Glu Leu Leu Arg Glu Ala His Pro Ile Val Gly
        515                 520                 525
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
                565                 570                 575
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 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
Met Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
 1               5                  10                  15
Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly
            20                  25                  30
Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
        35                  40                  45
Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe
    50                  55                  60
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                                                    10
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
65                  70                  75                  80
Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
                85                  90                  95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
            100                 105                 110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys
        115                 120                 125
Lys Ala Glu Lys 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 Arg
                165                 170                 175
Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp
            180                 185                 190
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu
        195                 200                 205
Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg
    210                 215                 220
Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp
225                 230                 235                 240
Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu
                245                 250                 255
Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg
            260                 265                 270
Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
        275                 280                 285
Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro
    290                 295                 300
Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp
305                 310                 315                 320
Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val His Arg
                325                 330                 335
Ala Ala 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 Ser Arg Glu Gly Leu Asp
        355                 360                 365
Leu Val Pro Gly 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 Ser Glu Arg Leu His Arg
                405                 410                 415
Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
            420                 425                 430
His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
        435                 440                 445
Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln 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
                485                 490                 495
Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly
            500                 505                 510
Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
        515                 520                 525
Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
    530                 535                 540
Asn Thr Tyr Val Asp Pro Leu Pro Ser 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 Val Arg Thr Pro Leu
            580                 585                 590
Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
        595                 600                 605
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Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
    610                 615                 620
Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
625                 630                 635                 640
His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
                645                 650                 655
Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
            660                 665                 670
Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
        675                 680                 685
Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
    690                 695                 700
Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
705                 710                 715                 720
Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
                725                 730                 735
Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
            740                 745                 750
Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
        755                 760                 765
Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
    770                 775                 780
Val His Asp Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
785                 790                 795                 800
Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
                805                 810                 815
Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
            820                 825                 830
Lys Gly
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<210> 7
<211> 834
<212> PRT
<213> Thermus caldophilus

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

<400> 7

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Met Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
 1               5                  10                  15
Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly
            20                  25                  30
Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
        35                  40                  45
Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe
    50                  55                  60
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
65                  70                  75                  80
Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
                85                  90                  95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
            100                 105                 110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys
        115                 120                 125
Asn Pro Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg
    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 Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp
225                 230                 235                 240
Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu
                245                 250                 255
Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg
            260                 265                 270
Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
        275                 280                 285
Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro
    290                 295                 300
Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp
305                 310                 315                 320
Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val His Arg
                325                 330                 335
Ala Ala 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 Ser Arg Glu Gly Leu Asp
        355                 360                 365
Leu Val Pro Gly 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 Ser Glu Arg Leu His Arg
                405                 410                 415
Asn Leu Leu Lys Arg Leu Gln Gly Glu Glu Lys Leu Leu Trp Leu Tyr
            420                 425                 430
His 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 Gln 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
                485                 490                 495
Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly
            500                 505                 510
Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
        515                 520                 525
Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
    530                 535                 540
Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Asn 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 Val Arg Thr Pro Leu
            580                 585                 590
Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
        595                 600                 605
Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
    610                 615                 620
Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
625                 630                 635                 640
His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
                645                 650                 655
Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
            660                 665                 670
Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
        675                 680                 685
Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
    690                 695                 700
Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
705                 710                 715                 720
Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
                725                 730                 735
Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
            740                 745                 750
Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
        755                 760                 765
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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
820 825 830
Lys Gly

<210> 8
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic DNA polymerase domain motif

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

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

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

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

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

<220>
<223> synthetic DNA polymerase domain motif

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

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

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

<220>

<223> synthetic DNA polymerase domain motif

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

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

<210> 11
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic DNA polymerase domain motif

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

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

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

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

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

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

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

<210> 14
<211> 36
<212> PRT

<213> Artificial Sequence

<220>
<223> synthetic region from polymerase domain of Thermus 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)

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

<210> 16
<211> 36
<212> PRT
<213> Artificial Sequence

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

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

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

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

<400> 17
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
000

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

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

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

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

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

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

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

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

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

<210> 26
<211> 21
<212> PRT

<213> Artificial Sequence

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

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

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

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

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

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

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

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

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

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

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

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

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

<220>
<221> VARIANT

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

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

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

<210> 27
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic polymerase motif corresponding to the D580X mutation of Z05, modified Z05 D580 motif

<220>
<221> VARIANT
<222> (7)...(7)
<223> Xaa = Ser or Thr

<220>
<221> VARIANT
<222> (8)...(8)
<223> Xaa = any amino acid other than Asp or Glu

<400> 27
Thr Gly Arg Leu Ser Ser Xaa Xaa Pro Asn Leu Gln Asn
1 5 10

<210> 28
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic conserved DNA polymerase active site motif A

<400> 28
Asp Tyr Ser Gln Ile Glu Leu Arg
1 5

<210> 29
<211> 893
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic chimeric CS5 DNA polymerase derived from N-terminal 5'-nuclease domain of Thermus sp. Z05 and C-terminal 3'-5' exonuclease and polymerase domains of Thermotoga maritima DNA polymerases

<400> 29
Met Lys Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
1 5 10 15
Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly

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                                                                  20
                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
    450                 455                 460
Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Thr Leu Ser
465                 470                 475                 480
Leu Lys Leu His Glu Ala Asp Leu Glu Asn Val Phe Tyr Lys Ile Glu
                485                 490                 495
Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr
            500                 505                 510
Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys
        515                 520                 525
Leu Glu Glu Leu Ala Glu Glu Ile Tyr Arg Ile Ala Gly Glu Pro Phe
    530                 535                 540
Asn Ile Asn Ser Pro Lys Gln Val Ser Arg Ile Leu Phe Glu Lys Leu
545                 550                 555                 560
Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Asp Tyr Ser Thr
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                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
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<210> 30
<211> 893
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic chimeric CS6 DNA polymerase derived from
N-terminal 5'-nuclease domain of Thermus sp. Z05
and C-terminal 3'-5' exonuclease and polymerase
domains of Thermotoga maritima DNA polymerases

<400> 30

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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
```

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                100                 105                 110
Glu Val Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys
        115                 120                 125
Lys Ala Glu Arg Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg
    130                 135                 140
Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu
145                 150                 155                 160
Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys
                165                 170                 175
Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp
            180                 185                 190
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu
        195                 200                 205
Leu Lys Glu Trp Gly Ser Leu Glu Asn Ile Leu Lys Asn Leu Asp Arg
    210                 215                 220
Val Lys Pro Glu Ser Val Arg Glu Arg Ile Lys Ala His Leu Glu Asp
225                 230                 235                 240
Leu Lys Leu Ser Leu Glu Leu Ser Arg Val Arg Ser Asp Leu Pro Leu
                245                 250                 255
Glu Val Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Arg
            260                 265                 270
Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
        275                 280                 285
Leu Leu Glu Glu Ser Glu Pro Val Gly Tyr Arg Ile Val Lys Asp Leu
    290                 295                 300
Val Glu Phe Glu Lys Leu Ile Glu Lys Leu Arg Glu Ser Pro Ser Phe
305                 310                 315                 320
Ala Ile Ala Leu Ala Thr Ser Ser Leu Asp Pro Phe Asp Cys Asp Ile
                325                 330                 335
Val Gly Ile Ser Val Ser Phe Lys Pro Lys Glu Ala Tyr Tyr Ile Pro
            340                 345                 350
Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Lys Glu Val Leu Lys
        355                 360                 365
Lys Leu Lys Glu Ile Leu Glu Asp Pro Gly Ala Lys Ile Val Gly Gln
    370                 375                 380
Asn Leu Lys Phe Asp Tyr Lys Val Leu Met Val Lys Gly Val Glu Pro
385                 390                 395                 400
Val Pro Pro Tyr Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro
                405                 410                 415
Asn Glu Lys Lys Phe Asn Leu Asp Asp Leu Ala Leu Lys Phe Leu Gly
            420                 425                 430
Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Phe Pro Leu
        435                 440                 445
Phe Gly Phe Ser Phe Ala Asp Val Pro Val Glu Lys Ala Ala Asn Tyr
    450                 455                 460
Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Thr Leu Ser
465                 470                 475                 480
Leu Lys Leu His Glu Ala Asp Leu Glu Asn Val Phe Tyr Lys Ile Glu
                485                 490                 495
Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr
            500                 505                 510
Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys
        515                 520                 525
Leu Glu Glu Leu Ala Glu Glu Ile Tyr Arg Ile Ala Gly Glu Pro Phe
    530                 535                 540
Asn Ile Asn Ser Pro Lys Gln Val Ser Arg Ile Leu Phe Glu Lys Leu
545                 550                 555                 560
Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Asp Tyr Ser Thr
                565                 570                 575
Arg Ile Glu Val Leu Glu Glu Leu Ala Gly Glu His Glu Ile Ile Pro
            580                 585                 590
Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile
        595                 600                 605
Asp Ala Leu Pro Lys Met Val Asn Pro Lys Thr Gly Arg Ile His Ala
    610                 615                 620
Ser Phe Asn Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp
625                 630                 635                 640
Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile
```

645 650 655
Arg Lys Ala Ile Val Pro Gln Asp Pro Asn Trp Trp Ile Val Ser Ala
660 665 670
Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp
675 680 685
Glu Asn Leu Leu Arg Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu
690 695 700
Thr Ala Ser Arg Ile Phe Asn Val Lys Pro Glu Glu Val Thr Glu Glu
705 710 715 720
Met Arg Arg Ala Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val
725 730 735
Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Val Pro Val Lys Glu Ala
740 745 750
Glu Lys Met Ile Val Asn Tyr Phe Val Leu Tyr Pro Lys Val Arg Asp
755 760 765
Tyr Ile Gln Arg Val Val Ser Glu Ala Lys Glu Lys Gly Tyr Val Arg
770 775 780
Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp
785 790 795 800
Arg Asn Thr Gln Ala Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile
805 810 815
Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Glu Ile Asp
820 825 830
Arg Glu Leu Lys Glu Arg Lys Met Arg Ser Lys Met Ile Ile Gln Val
835 840 845
His Asp Glu Leu Val Phe Glu Val Pro Asn Glu Glu Lys Asp Ala Leu
850 855 860
Val Glu Leu Val Lys Asp Arg Met Thr Asn Val Val Lys Leu Ser Val
865 870 875 880
Pro Leu Glu Val Asp Val Thr Ile Gly Lys Thr Trp Ser
885 890

<210> 31
<211> 21
<212> DNA
<213> Artificial Sequence

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

<400> 31
ctacctcctg gacccctcca a 21

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

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

<400> 32
ataaccaact ggtagtggcg tgtaa 25

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

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

<400> 33

ctacctcctg gacccctcca acaccacccc cgaggggtg gcccggcgct acgggggga 60
gtggacggag gacgccgccc accgggccct cctcgctgag cggctccagc aaaacctctt 120
ggaacgcctc aagggagagg aaaagctcct ttggctctac caagaggtgg aaaagcccct 180
ctcccgggtc ctggcccaca tggaggccac cggggtaagg ctggacgtgg cctatctaaa 240
ggccctttcc ctggagcttg cggaggagat tcgccgcctc gaggaggagg tcttccgcct 300
ggcgggccac cccttcaacc tgaactcccg tgaccagcta gagcgggtgc tctttgacga 360
gcttaggctt cccgccctgg gcaagacgca aaagacgggg aagcgctcca ccagcgccgc 420
ggtgctggag gccctcaggg aggcccaccc catcgtggag aagatcctcc agcaccggga 480
gctcaccaag ctcaagaaca cctacgtaga ccccctcccg ggcctcgtcc acccgaggac 540
gggccgcctc cacacccgct tcaaccagac agccacggcc acgggaaggc tctctagctc 600
cgggcccaac ctgcagaaca tccccatccg cacccccttg ggccagagga tccgccgggc 660
cttcgtggcc gaggcgggat gggcgttggt ggccctggac tatagccaga tagagctccg 720
ggtcctcgcc cacctctccg gggacgagaa cctgatcagg gtcttccagg aggggaagga 780
catccacacc cagaccgcaa gctggatgtt cggcgtctcc ccggaggccg tggacccccc 840
gatgcgccgg gcggccaaga cggtgaactt cggcgtcctc tacggcatgt ccgcccatag 900
gctctcccag gagcttgcca tcccctacga ggaggcggtg gcctttatag agcgctactt 960
ccaaagcttc cccaaggtgc gggcctggat agaaaagacc ctggaggagg ggaggaagcg 1020
gggctacgtg gaaaccctct tcggaagaag gcgctacgtg cccgacctca acgcccgggt 1080
gaagagcgtc agggaggccg cggagcgcat ggccttcaac atgcccgtcc agggcaccgc 1140
cgccgacctc atgaagctcg ccatggtgaa gctcttcccc cacctccggg agatgggggc 1200
ccgcatgctc ctccaggtcc acgacgagct cctcctggag gccccccaag cgcgggccga 1260
ggaggtggcg gctttggcca aggaggccat ggagaaggcc tatcccctcg ccgtgccct 1320
ggaggtggag gtggggatcg gggaggactg gctttccgcc aagggctgat atcagatctc 1380
cctgattatg cgtcagtcta tgaagaaaaa tcgtatacag atggacgaag agagaatcct 1440
tgtgaattta acagagggta tagggattac acgccactac cagttggtta t 1491

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

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

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

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

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

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

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

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

<400> 36
Met Ala Asp Ala Ser Pro Asp Pro Ser Lys Pro Asp Ala Leu Val Leu
1 5 10 15
Ile Asp Gly His Ala Leu Ala Phe Arg Ser Tyr Phe Ala Leu Pro Pro
20 25 30
Leu Asn Asn Ser Lys Gly Glu Met Thr Asp Ala Ile Val Gly Phe Met
35 40 45
Lys Leu Leu Leu Arg Leu Ala Arg Gln Lys Ser Asn Gln Val Ile Val
50 55 60

```
Val 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
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
            660                 665                 670
Asn Ile Pro Ile Arg Ser Glu Leu Gly Arg Glu Ile Arg Lys Gly Phe
        675                 680                 685
Ile Ala Glu Asp Gly Phe Thr Leu Ile Ala Ala Asp Tyr Ser Gln Ile
    690                 695                 700
Glu Leu Arg Leu Leu Ala His Ile Ala Asp Asp Pro Leu Met Gln Gln
705                 710                 715                 720
Ala Phe Val Glu Gly Ala Asp Ile His Arg Arg Thr Ala Ala Gln Val
                725                 730                 735
Leu Gly Leu Asp Glu Ala Thr Val Asp Ala Asn Gln Arg Arg Ala Ala
            740                 745                 750
Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu
        755                 760                 765
Ser Asn Asp Leu Gly Ile Pro Tyr Ala Glu Ala Ala Thr Phe Ile Glu
    770                 775                 780
Ile Tyr Phe Ala Thr Tyr Pro Gly Ile Arg Arg Tyr Ile Asn His Thr
785                 790                 795                 800
Leu Asp Phe Gly Arg Thr His Gly Tyr Val Glu Thr Leu Tyr Gly Arg
                805                 810                 815
Arg Arg Tyr Val Pro Gly Leu Ser Ser Arg Asn Arg Val Gln Arg Glu
            820                 825                 830
Ala Glu Glu Arg Leu Ala Tyr Asn Met Pro Ile Gln Gly Thr Ala Ala
        835                 840                 845
Asp Ile Met Lys Leu Ala Met Val Gln Leu Asp Pro Gln Leu Asp Ala
    850                 855                 860
Ile Gly Ala Arg Met Leu 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


<210> 37
<211> 892
<212> PRT
<213> Thermosipho africanus

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

<400> 37
Met Gly Lys Met Phe Leu Phe Asp Gly Thr Gly Leu Val Tyr Arg Ala
 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
        195                 200                 205
Leu Lys Lys Tyr Asn Ser Leu Glu Asn Val Leu Lys Asn Ile Asn Leu
    210                 215                 220
Leu Thr Glu Lys Leu Arg Arg Leu Leu Glu Asp Ser Lys Glu Asp Leu
225                 230                 235                 240
Gln Lys Ser Ile Glu Leu Val Glu Leu Ile Tyr Asp Val Pro Met Asp
                245                 250                 255
Val Glu Lys Asp Glu Ile Ile Tyr Arg Gly Tyr Asn Pro Asp Lys Leu
            260                 265                 270
Leu Lys Val Leu Lys Lys Tyr Glu Phe Ser Ser Ile Ile Lys Glu Leu
        275                 280                 285
Asn Leu Gln Glu Lys Leu Glu Lys Glu Tyr Ile Leu Val Asp Asn Glu
    290                 295                 300
Asp Lys Leu Lys Lys Leu Ala Glu Glu Ile Glu Lys Tyr Lys Thr Phe
305                 310                 315                 320
Ser Ile Asp Thr Glu Thr Thr Ser Leu Asp Pro Phe Glu Ala Lys Leu
                325                 330                 335
Val Gly Ile Ser Ile Ser Thr Met Glu Gly Lys Ala Tyr Tyr Ile Pro
            340                 345                 350
Val Ser His Phe Gly Ala Lys Asn Ile Ser Lys Ser Leu Ile Asp Lys
        355                 360                 365
Phe Leu Lys Gln Ile Leu Gln Glu Lys Asp Tyr Asn Ile Val Gly Gln
    370                 375                 380
Asn Leu Lys Phe Asp Tyr Glu Ile Phe Lys Ser Met Gly Phe Ser Pro
385                 390                 395                 400
Asn Val Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Asn Pro
                405                 410                 415
Asp Glu Lys Arg Phe Asn Leu Glu Glu Leu Ser Leu Lys Tyr Leu Gly
            420                 425                 430
Tyr Lys Met Ile Ser Phe Asp Glu Leu Val Asn Glu Asn Val Pro Leu
        435                 440                 445
Phe Gly Asn Asp Phe Ser Tyr Val Pro Leu Glu Arg Ala Val Glu Tyr
    450                 455                 460
Ser Cys Glu Asp Ala Asp Val Thr Tyr Arg Ile Phe Arg Lys Leu Gly
465                 470                 475                 480
Arg Lys Ile Tyr Glu Asn Glu Met Glu Lys Leu Phe Tyr Glu Ile Glu
                485                 490                 495
Met Pro Leu Ile Asp Val Leu Ser Glu Met Glu Leu Asn Gly Val Tyr
            500                 505                 510
Phe Asp Glu Glu Tyr Leu Lys Glu Leu Ser Lys Lys Tyr Gln Glu Lys
        515                 520                 525
Met Asp Gly Ile Lys Glu Lys Val Phe Glu Ile Ala Gly Glu Thr Phe
    530                 535                 540
Asn Leu Asn Ser Ser Thr Gln Val Ala Tyr Ile Leu Phe Glu Lys Leu
545                 550                 555                 560
Asn Ile Ala Pro Tyr Lys Lys Thr Ala Thr Gly Lys Phe Ser Thr Asn
                565                 570                 575
Ala Glu Val Leu Glu Glu Leu Ser Lys Glu His Glu Ile Ala Lys Leu
            580                 585                 590
Leu Leu Glu Tyr Arg Lys Tyr Gln Lys Leu Lys Ser Thr Tyr Ile Asp
        595                 600                 605
Ser Ile Pro Leu Ser Ile Asn Arg Lys Thr Asn Arg Val His Thr Thr
    610                 615                 620
Phe His Gln Thr Gly Thr Ser Thr Gly Arg Leu Ser Ser Ser Asn Pro
625                 630                 635                 640
Asn Leu Gln Asn Leu Pro Thr Arg Ser Glu Glu Gly Lys Glu Ile Arg
                645                 650                 655
Lys Ala Val Arg Pro Gln Arg Gln Asp Trp Trp Ile Leu Gly Ala Asp
            660                 665                 670
Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Val Ser Lys Asp Glu
```

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

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

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

<400> 38
Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala
1 5 10 15
Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr
20 25 30
Asn Ala Thr Tyr Gly Val Ala Arg Met Leu Val Arg Phe Ile Lys Asp
35 40 45
His Ile Ile Val Gly Lys Asp Tyr Val Ala Val Ala Phe Asp Lys Lys
50 55 60
Ala Ala Thr Phe Arg His Lys Leu Leu Glu Thr Tyr Lys Ala Gln Arg
65 70 75 80
Pro Lys Thr Pro Asp Leu Leu Ile Gln Gln Leu Pro Tyr Ile Lys Lys
85 90 95
Leu Val Glu Ala Leu Gly Met Lys Val Leu Glu Val Glu Gly Tyr Glu
100 105 110
Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Lys Gly Leu Pro Leu Phe
115 120 125
Asp Glu Ile Phe Ile Val Thr Gly Asp Lys Asp Met Leu Gln Leu Val
130 135 140
Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu
145 150 155 160
Glu Leu Tyr Asp Ala Gln Lys Val Lys Glu Lys Tyr Gly Val Glu Pro
165 170 175
Gln Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Glu Ile Asp Asn
180 185 190
Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu
195 200 205
Glu Lys Tyr Lys Asp Leu Glu Asp Ile Leu Asn His Val Arg Glu Leu
210 215 220
Pro Gln Lys Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Asn Ala Ile
225 230 235 240

```
Leu Ser Lys Lys Leu Ala Ile Leu Glu Thr Asn Val Pro Ile Glu Ile
                245                 250                 255
Asn Trp Glu Glu Leu Arg Tyr Gln Gly Tyr Asp Arg Glu Lys Leu Leu
            260                 265                 270
Pro Leu Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln
        275                 280                 285
Leu Tyr Glu Glu Ser Glu Pro Val Gly Tyr Arg Ile Val Lys Asp Leu
    290                 295                 300
Val Glu Phe Glu Lys Leu Ile Glu Lys Leu Arg Glu Ser Pro Ser Phe
305                 310                 315                 320
Ala Ile Asp Leu Glu Thr Ser Ser Leu Asp Pro Phe Asp Cys Asp Ile
                325                 330                 335
Val Gly Ile Ser Val Ser Phe Lys Pro Lys Glu Ala Tyr Tyr Ile Pro
            340                 345                 350
Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Lys Glu Val Leu Lys
        355                 360                 365
Lys Leu Lys Glu Ile Leu Glu Asp Pro Gly Ala Lys Ile Val Gly Gln
    370                 375                 380
Asn Leu Lys Phe Asp Tyr Lys Val Leu Met Val Lys Gly Val Glu Pro
385                 390                 395                 400
Val Pro Pro Tyr Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro
                405                 410                 415
Asn Glu Lys Lys Phe Asn Leu Asp Asp Leu Ala Leu Lys Phe Leu Gly
            420                 425                 430
Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Phe Pro Leu
        435                 440                 445
Phe Gly Phe Ser Phe Ala Asp Val Pro Val Glu Lys Ala Ala Asn Tyr
    450                 455                 460
Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Thr Leu Ser
465                 470                 475                 480
Leu Lys Leu His Glu Ala Asp Leu Glu Asn Val Phe Tyr Lys Ile Glu
                485                 490                 495
Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr
            500                 505                 510
Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys
        515                 520                 525
Leu Glu Glu Leu Ala Glu Glu Ile Tyr Arg Ile Ala Gly Glu Pro Phe
    530                 535                 540
Asn Ile Asn Ser Pro Lys Gln Val Ser Arg Ile Leu Phe Glu Lys Leu
545                 550                 555                 560
Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Asp Tyr Ser Thr
                565                 570                 575
Arg Ile Glu Val Leu Glu Glu Leu Ala Gly Glu His Glu Ile Ile Pro
            580                 585                 590
Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile
        595                 600                 605
Asp Ala Leu Pro Lys Met Val Asn Pro Lys Thr Gly Arg Ile His Ala
    610                 615                 620
Ser Phe Asn Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp
625                 630                 635                 640
Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile
                645                 650                 655
Arg Lys Ala Ile Val Pro Gln Asp Pro Asn Trp Trp Ile Val Ser Ala
            660                 665                 670
Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp
        675                 680                 685
Glu Asn Leu Leu Arg Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu
    690                 695                 700
Thr Ala Ser Arg Ile Phe Asn Val Lys Pro Glu Glu Val Thr Glu Glu
705                 710                 715                 720
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
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30

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

<210> 39
<211> 893
<212> PRT
<213> Thermotoga neopolitana

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

<400> 39
Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala
1 5 10 15
Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr
20 25 30
Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu
35 40 45
His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys
50 55 60
Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg
65 70 75 80
Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg
85 90 95
Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu
100 105 110
Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu
115 120 125
Met Arg Phe Ser Leu Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val
130 135 140
Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu
145 150 155 160
Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro
165 170 175
His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn
180 185 190
Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu
195 200 205
Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu
210 215 220
Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile
225 230 235 240
Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val
245 250 255
Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu
260 265 270
Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln
275 280 285
Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His
290 295 300
Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe
305 310 315 320
Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile
325 330 335
Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro

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            340                 345                 350
Leu His His Arg Asn Ala His Asn Leu Asp Glu Thr Leu Val Leu Ser
        355                 360                 365
Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln
    370                 375                 380
Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro
385                 390                 395                 400
Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro
                405                 410                 415
Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly
            420                 425                 430
Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu
        435                 440                 445
Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Glu Tyr
    450                 455                 460
Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser
465                 470                 475                 480
Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu
                485                 490                 495
Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Phe Asn Trp Val Tyr
            500                 505                 510
Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys
        515                 520                 525
Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe
    530                 535                 540
Asn Ile Asn Ser Pro Lys Gln Val Ser Asn Ile Leu Phe Glu Lys Leu
545                 550                 555                 560
Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Asp Tyr Ser Thr
                565                 570                 575
Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro
            580                 585                 590
Leu Ile Leu Glu Phe Arg Lys Ile Leu Lys Leu Lys Ser Thr Tyr Ile
        595                 600                 605
Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Phe His Ala
    610                 615                 620
Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp
625                 630                 635                 640
Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile
                645                 650                 655
Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala
            660                 665                 670
Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp
        675                 680                 685
Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu
    690                 695                 700
Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu
705                 710                 715                 720
Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val
                725                 730                 735
Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala
            740                 745                 750
Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser
        755                 760                 765
Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg
    770                 775                 780
Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp
785                 790                 795                 800
Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile
                805                 810                 815
Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp
            820                 825                 830
Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val
        835                 840                 845
His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu
    850                 855                 860
Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val
865                 870                 875                 880
Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser
```

885 890

<210> 40
<211> 876
<212> PRT
<213> Bacillus stearothermophilus

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

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

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Arg Lys Ala Ala Ala Ile Trp Ala Leu Glu Glu Pro Leu Met Asp Glu
    450                 455                 460
Leu Arg Arg Asn Glu Gln Asp Arg Leu Leu Thr Glu Leu Glu Gln Pro
465                 470                 475                 480
Leu Ala Gly Ile Leu Ala Asn Met Glu Phe Thr Gly Val Lys Val Asp
                485                 490                 495
Thr Lys Arg Leu Glu Gln Met Gly Ala Glu Leu Thr Glu Gln Leu Gln
            500                 505                 510
Ala Val Glu Arg Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile
        515                 520                 525
Asn Ser Pro Lys Gln Leu Gly Thr Val Leu Phe Asp Lys Leu Gln Leu
    530                 535                 540
Pro Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val
545                 550                 555                 560
Leu Glu Lys Leu Ala Pro His His Glu Ile Val Glu His Ile Leu His
                565                 570                 575
Tyr Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu
            580                 585                 590
Lys Val Val His Pro Val Thr Gly Lys Val His Thr Met Phe Asn Gln
        595                 600                 605
Ala Leu Thr Gln Thr Gly Arg Leu Ser Ser Val Glu Pro Asn Leu Gln
    610                 615                 620
Asn Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe
625                 630                 635                 640
Val Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln
                645                 650                 655
Ile Glu Leu Arg Val Leu Ala His Ile Ala Glu Asp Asp Asn Leu Ile
            660                 665                 670
Glu Ala Phe Arg Arg Gly Leu Asp Ile His Thr Lys Thr Ala Met Asp
        675                 680                 685
Ile Phe His Val Ser Glu Glu Asp Val Thr Ala Asn Met Arg Arg Gln
    690                 695                 700
Ala Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly
705                 710                 715                 720
Leu Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile
                725                 730                 735
Glu Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Gln Tyr Met Asp Asn
            740                 745                 750
Ile Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His
        755                 760                 765
Arg Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg
    770                 775                 780
Ser Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala
785                 790                 795                 800
Ala Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ser Val Arg Leu Arg
                805                 810                 815
Glu Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu
            820                 825                 830
Ile Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Arg Leu Val
        835                 840                 845
Pro Glu Val Met Glu Gln Ala Val Ala Leu Arg Val Pro Leu Lys Val
    850                 855                 860
Asp Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
865                 870                 875


<210> 41
<211> 877
<212> PRT
<213> Bacillus caldotenax

<220>
<223> Bacillus caldotenax DNA polymerase (Bca)

<400> 41
Met Lys Lys Lys Leu Val Leu Ile Asp Gly Ser Ser Val Ala Tyr Arg
 1               5                  10                  15
Ala Phe Phe Ala Leu Pro Leu Leu His Asn Asp Lys Gly Ile His Thr
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            20                  25                  30
Asn Ala Val Tyr Gly Phe Thr Met Met Leu Asn Lys Ile Leu Ala Glu
        35                  40                  45
Glu Glu Pro Thr His Met Leu Val Ala Phe Asp Ala Gly Lys Thr Thr
    50                  55                  60
Phe Arg His Glu Ala Phe Gln Glu Tyr Lys Gly Gly Arg Gln Gln Thr
65                  70                  75                  80
Pro Pro Glu Leu Ser Glu Gln Phe Pro Leu Leu Arg Glu Leu Leu Arg
                85                  90                  95
Ala Tyr Arg Ile Pro Ala Tyr Glu Leu Glu Asn Tyr Glu Ala Asp Asp
            100                 105                 110
Ile Ile Gly Thr Leu Ala Ala Arg Ala Glu Gln Glu Gly Phe Glu Val
        115                 120                 125
Lys Val Ile Ser Gly Asp Arg Asp Leu Thr Gln Leu Ala Ser Pro His
    130                 135                 140
Val Thr Val Asp Ile Thr Lys Lys Gly Ile Thr Asp Ile Glu Pro Tyr
145                 150                 155                 160
Thr Pro Glu Ala Val Arg Glu Lys Tyr Gly Leu Thr Pro Glu Gln Ile
                165                 170                 175
Val Asp Leu Lys Gly Leu Met Gly Asp Lys Ser Asp Asn Ile Pro Gly
            180                 185                 190
Val Pro Gly Ile Gly Glu Lys Thr Ala Val Lys Leu Leu Arg Gln Phe
        195                 200                 205
Gly Thr Val Glu Asn Val Leu Ala Ser Ile Asp Glu Ile Lys Gly Glu
    210                 215                 220
Lys Leu Lys Glu Thr Leu Arg Gln His Arg Glu Met Ala Leu Leu Ser
225                 230                 235                 240
Lys Lys Leu Ala Ala Ile Arg Arg Asp Ala Pro Val Glu Leu Ser Leu
                245                 250                 255
Asp Asp Ile Ala Tyr Gln Gly Glu Asp Arg Glu Lys Val Val Ala Leu
            260                 265                 270
Phe Lys Glu Leu Gly Phe Gln Ser Phe Leu Glu Lys Met Glu Ser Pro
        275                 280                 285
Ser Ser Glu Glu Glu Lys Pro Leu Ala Lys Met Ala Phe Thr Leu Ala
    290                 295                 300
Asp Arg Val Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val
305                 310                 315                 320
Glu Val Val Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala
                325                 330                 335
Val Val Asn Glu His Gly Arg Phe Phe Leu Arg Pro Glu Thr Ala Leu
            340                 345                 350
Ala Asp Pro Gln Phe Val Ala Trp Leu Gly Asp Glu Thr Lys Lys Lys
        355                 360                 365
Ser Met Phe Asp Ser Lys Arg Ala Ala Val Ala Leu Lys Trp Lys Gly
    370                 375                 380
Ile Glu Leu Cys Gly Val Ser Phe Asp Leu Leu Leu Ala Ala Tyr Leu
385                 390                 395                 400
Leu Asp Pro Ala Gln Gly Val Asp Asp Val Ala Ala Ala Ala Lys Met
                405                 410                 415
Lys Gln Tyr Glu Ala Val Arg Pro Asp Glu Ala Val Tyr Gly Lys Gly
            420                 425                 430
Ala Lys Arg Ala Val Pro Asp Glu Pro Val Leu Ala Glu His Leu Val
        435                 440                 445
Arg Lys Ala Ala Ala Ile Trp Ala Leu Glu Arg Pro Phe Leu Asp Glu
    450                 455                 460
Leu Arg Arg Asn Glu Gln Asp Arg Leu Leu Val Glu Leu Glu Gln Pro
465                 470                 475                 480
Leu Ser Ser Ile Leu Ala Glu Met Glu Phe Ala Gly Val Lys Val Asp
                485                 490                 495
Thr Lys Arg Leu Glu Gln Met Gly Glu Glu Leu Ala Glu Gln Leu Arg
            500                 505                 510
Thr Val Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile
        515                 520                 525
Asn Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu
    530                 535                 540
Pro Val Leu Lys Lys Ser Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val
545                 550                 555                 560
Leu Glu Lys Leu Ala Pro Tyr His Glu Ile Val Glu Asn Ile Leu Gln
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                565                 570                 575
His Tyr Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu
            580                 585                 590
Leu Lys Val Val Arg Pro Asp Thr Lys Lys Val His Thr Ile Phe Asn
        595                 600                 605
Gln Ala Leu Thr Gln Thr Gly Arg Leu Ser Ser Thr Glu Pro Asn Leu
    610                 615                 620
Gln Asn Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala
625                 630                 635                 640
Phe Val Pro Ser Glu Ser Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser
                645                 650                 655
Gln Ile Glu Leu Arg Val Leu Ala His Ile Ala Glu Asp Asp Asn Leu
            660                 665                 670
Met Glu Ala Phe Arg Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met
        675                 680                 685
Asp Ile Phe Gln Val Ser Glu Asp Glu Val Thr Pro Asn Met Arg Arg
    690                 695                 700
Gln Ala Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr
705                 710                 715                 720
Gly Leu Ala Gln Asn Leu Asn Ile Ser Arg Lys Glu Ala Ala Glu Phe
                725                 730                 735
Ile Glu Arg Tyr Phe Glu Ser Phe Pro Gly Val Lys Arg Tyr Met Glu
            740                 745                 750
Asn Ile Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu
        755                 760                 765
His Arg Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val
    770                 775                 780
Arg Ser Phe Ala Glu Arg Met Ala Met Asn Thr Pro Ile Gln Gly Ser
785                 790                 795                 800
Ala Ala Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Asn Ala Arg Leu
                805                 810                 815
Lys Glu Glu Arg Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu
            820                 825                 830
Leu Ile Leu Glu Ala Pro Lys Glu Glu Met Glu Arg Leu Cys Arg Leu
        835                 840                 845
Val Pro Glu Val Met Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys
    850                 855                 860
Val Asp Tyr His Tyr Gly Ser Thr Trp Tyr Asp Ala Lys
865                 870                 875


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

<220>
<223> synthetic DNA polymerase domain motif

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

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

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

<220>
<221> VARIANT
<222> (7)...(7)
<223> Xaa = Leu or Ile
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<220>
<221> VARIANT
<222> (8)...(8)
<223> Xaa = Asn or Arg

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

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

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

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

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

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

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

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

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

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

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

<210> 43
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic DNA polymerase domain motif

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

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

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

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

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

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

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

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

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

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

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

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

<400> 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>
<223> synthetic DNA polymerase domain motif

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

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

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

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

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

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

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

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

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

<400> 44
Ala Gly Xaa Pro Phe Asn Xaa Asn Ser Xaa Xaa Gln Xaa Xaa Arg Xaa
 1   5   10   15
Leu Phe Xaa Xaa Leu
            20

<210> 45
<211> 21
<212> PRT
<213> Artificial Sequence

<220>

<223> synthetic DNA polymerase domain motif

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

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

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

<400> 45
Ala Gly His Pro Phe Asn Leu Asn Xaa Arg Asp Gln Leu Xaa Arg Val
 1   5   10   15
Leu Xaa Asp Glu Leu
            20

<210> 46
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic DNA polymerase domain motif

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

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

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

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

<210> 47
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic DNA polymerase domain motif

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

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

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

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

<210> 48
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic DNA polymerase domain motif

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

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

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

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

<220>
<221> VARIANT
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<223> Xaa = Ser, Gly, Ala, Asp, Phe, Lys, Cys, Thr or
      Tyr

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

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

<400> 49

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

<210> 50
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic DNA polymerase domain motif

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

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

<210> 51
<211> 13
<212> PRT
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<220>
<223> synthetic DNA polymerase domain motif

<220>
<221> VARIANT
<222> (7)...(7)
<223> Xaa = Ser or Thr

<220>
<221> VARIANT
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<223> Xaa = Leu, Gly, Thr, Gln, Ala, Ser, Asn, Arg or
Lys

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