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(54) Titre : POLYMERASE D'ACIDES NUCLEIQUES THERMOSTABLE

(54) Title: THERMOSTABLE NUCLEIC ACID POLYMERASE

(57) **Abrégé/Abstract:**

The invention relates to purified thermostable DNA polymerases from *Pyrodictium* species, such as *Pyrodictium occultum* or *Pyrodictium abyssi*, which polymerases catalyze the combination of nucleoside triphosphates to form a nucleic acid strand complementary to a nucleic acid template strand. The preferred polymerases are characterized by their ability to function efficiently in a polymerase chain reaction, wherein said reaction includes repeated exposure to a denaturation temperature of about 100°C. Most preferably the polymerases display 5'→3' exonuclease activity, i.e. are proofreading enzymes. The invention also provides DNAs encoding the DNA polymerase activity of the said *Pyrodictium* species, which DNAs can be used to construct recombinant vectors and transformed host cells for production of polypeptides having said activity. The invention also relates to the preparation of said thermostable DNA polymerases, to the use of said polymerases to amplify nucleic acids as well as to kits comprising a polymerase of the present invention.

Abstract

The invention relates to purified thermostable DNA polymerases from *Pyrodictium* species, such as *Pyrodictium occultum* or *Pyrodictium abyssi*, which polymerases catalyze the combination of nucleoside triphosphates to form a nucleic acid strand complementary to a nucleic acid template strand. The preferred polymerases are characterized by their ability to function efficiently in a polymerase chain reaction, wherein said reaction includes repeated exposure to a denaturation temperature of about 100°C. Most preferably the polymerases display 5'→3' exonuclease activity, i.e. are proofreading enzymes. The invention also provides DNAs encoding the DNA polymerase activity of the said *Pyrodictium* species, which DNAs can be used to construct recombinant vectors and transformed host cells for production of polypeptides having said activity. The invention also relates to the preparation of said thermostable DNA polymerases, to the use of said polymerases to amplify nucleic acids as well as to kits comprising a polymerase of the present invention.

The present invention relates to thermostable DNA polymerases from hyperthermophilic archael *Pyrodictium* species and means for isolating and producing the enzymes. Thermostable DNA polymerases are useful in many recombinant DNA techniques, especially nucleic acid amplification by the polymerase chain reaction (PCR).

5 Extensive research has been conducted on the isolation of DNA polymerases from mesophilic microorganisms such as *E. coli*. See, for example, Bessman et al., 1957, *J. Biol. Chem.* 223:171-177, and Buttin and Kornberg, 1966, *J. Biol. Chem.* 241:5419-5427.

Interest in DNA polymerases from thermophilic microbes increased with the invention of nucleic acid amplification processes. The use of thermostable enzymes, such
10 as those described in U.S. Patent No. 4,165,188, to amplify existing nucleic acid sequences in amounts that are large compared to the amount initially present was described in United States Patent Nos. 4,683,195 and 4,683,202, which describe the PCR process. The PCR process involves denaturation of a target nucleic acid, hybridization of primers, and
15 synthesis of complementary strands catalyzed by a DNA polymerase. The extension product of each primer becomes a template for the production of the desired nucleic acid sequence. These patents disclose that, if the polymerase employed is a thermostable enzyme, then polymerase need not be added after every denaturation step, because heat will not destroy the polymerase activity.

The thermostable DNA polymerase from *Thermus aquaticus* (Taq) has been cloned,
20 expressed, and purified from recombinant cells as described in Lawyer et al., 1989, *J. Biol. Chem.* 264:6427-6437, and U.S. Patent Nos. 4,889,818 and 5,079,352. Crude preparations of a DNA polymerase activity isolated from *T. aquaticus* have been described by others (Chien et al., 1976, *J. Bacteriol.* 127:1550-1557, and Kaledin et al., 1980, *Biokhimiya* 45:644-651).

25 U.S. Patent No. 4,889,818, European Patent Application, Publication No. 258,017, and PCT Publication No. WO 89/06691, all describe the isolation and recombinant expression of an ~94 kDa thermostable DNA polymerase from *Thermus aquaticus* and the use of that polymerase in PCR. Although *T. aquaticus* DNA polymerase is especially preferred for use in PCR and other recombinant DNA techniques, a number of other
30 thermophilic DNA polymerases have been purified, cloned, and expressed. (See co-pending, commonly assigned PCT Publication Nos. WO 91/09950, WO 92/03556, WO 92/06200, and WO 92/06202.

Thermostable DNA polymerases are not irreversibly inactivated even when heated to 93-95°C for brief periods of time, as, for example, in the practice of DNA amplification by PCR. In contrast, at this elevated temperature *E. coli* DNA Pol I is inactivated.

Archaeal hyperthermophiles, such as *Pyrodictium* and *Methanopyrus* species, grow at temperatures up to about 110°C and are unable to grow below 80°C (see, Stetter et al., 1990, FEMS Microbiology Reviews 75:117-124. These sulfur reducing, strict anaerobes are isolated from submarine environments.

For example, *P. abyssi* was isolated from a deep sea active "smoker" chimney off Guaymas Mexico at 2,000 meters depth and in 320°C of venting water (Pley et al., 1991, Systematic and Applied Microbiology 14:245). In contrast to the *Pyrodictium* species, other thermophilic microorganisms having an optimum growth temperature at or about 90°C and a maximum growth temperature at or about 100°C are not difficult to culture. For example, a gene encoding DNA polymerase has been cloned and sequenced from *Thermococcus litoralis* (European Patent Application, Publication No. 455,430).

In contrast, culture of the extreme hyperthermophilic microorganisms is made difficult by their inability to grow on agar solidified media. Individual cells of the *Pyrodictium* species are extremely fragile, and the organisms grow as fibrous networks. Standard bacterial fermentation techniques are extremely difficult for culturing *Pyrodictium* species due to the fragility of the cells and tendency of the cells to grow as networks clogging the steel parts of conventional fermentation apparatus. (See Staley, J.T. et al. eds., *Bergey's Manual of Systematic Bacteriology*, 1989, Williams and Wilkins, Baltimore. These difficulties preclude laboratory culture for preparing large amounts of purified nucleic acid polymerase enzymes for characterization and amino acid sequence analysis. Those skilled in the art may be able to culture *Pyrodictium* to a cell density approaching 10^6 - 10^7 cells/ml (see, for example, Phipps et al., 1991, AMBO J. 10(7):1711-1722). In contrast, *E. coli* is routinely grown to $0.3 - 1.0 \times 10^{11}$ cells/ml.

Accordingly, there is a need for further characterizing these hyperthermophile DNA polymerase enzymes, e.g. by determining their amino acid sequence and the DNA sequence encoding it. By cloning and expressing the gene in a suitable host organism the prior difficulties associated with the cultivation of the native host can be avoided. In addition there is a desire in the art to produce thermostable DNA polymerases having enhanced thermostability that may be used to improve the PCR process and to improve the results obtained when using a thermostable DNA polymerase in other recombinant techniques such as DNA sequencing, nick-translation, and reverse transcription.

The present invention meets these needs by providing DNA and amino acid sequence information, recombinant expression vectors and purification protocols for DNA polymerases from *Pyrodictium* species.

The present invention provides thermostable enzymes that catalyze the combination of nucleoside triphosphates to form a nucleic acid strand complementary to a nucleic acid template strand. The enzymes are DNA polymerases from *Pyrodictium* species. In a pre-

ferred embodiment, the enzyme is from *P. occultum* or *P. abyssi*. This material may be used in a temperature-cycling amplification reaction wherein nucleic acid sequences are produced from a given nucleic acid sequence in amounts that are large compared to the amount initially present so that the sequences can be manipulated and/or analyzed easily.

5 The genes encoding the *P. occultum* and *P. abyssi* DNA polymerase enzyme have also been identified and cloned and provide yet another means to prepare the thermostable enzyme of the present invention. In addition, DNA and amino acid sequences of the genes encoding the *P. occultum* and *P. abyssi* enzyme and derivatives of these genes encoding *P. occultum* and *P. abyssi* DNA polymerase activity are also provided. In addition, modified
10 genes encoding and expressing 3'-5' exonuclease-deficient forms of *Pyrodictium occultum* and *P. abyssi* DNA polymerase activity are also provided.

The invention also encompasses stable enzyme compositions comprising a purified, thermostable *P. occultum* and/or *P. abyssi* enzyme as described above in a buffer containing one or more non-ionic polymeric detergents.

15 Finally, the invention provides a method of purification for the thermostable polymerase of the invention.

Thus, the present invention provides DNA sequences and expression vectors that encode *Pyrodictium* DNA polymerase. To facilitate understanding of the invention, a number
20 of terms are defined below.

The terms "cell," "cell line," and "cell culture" can be used interchangeably and all such designations include progeny. Thus, the words "transformants" or "transformed cells" include the primary transformed cell and cultures derived from that cell without regard to the number of transfers. All progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. Mutant progeny that have the same functionality as screened
25 for in the originally transformed cell are included in the definition of transformants.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for procaryotes, for example, include a promoter, optionally an operator sequence, a ribosome binding site, and possibly other sequences. Eucaryotic cells are known
30 to utilize promoters, polyadenylation signals, and enhancers.

The term "expression system" refers to DNA sequences containing a desired coding sequence and control sequences in operable linkage, so that hosts transformed with these sequences are capable of producing the encoded proteins. To effect transformation, the expression system may be included on a vector; however, the relevant DNA may also be integrated into the host chromosome.
35

The term "gene" refers to a DNA sequence that comprises control and coding sequences necessary for the production of a recoverable bioactive polypeptide or precursor. The polypeptide can be encoded by a full length gene sequence or by any portion of the
40 coding sequence so long as the enzymatic activity is retained.

The term "operably linked" refers to the positioning of the coding sequence such that control sequences will function to drive expression of the protein encoded by the coding sequence. Thus, a coding sequence "operably linked" to expression control sequences refers to a configuration wherein the coding sequences can be expressed under the direction of a control sequence.

The term "mixture" as it relates to mixtures containing Pyrodictium polymerase refers to a collection of materials which includes Pyrodictium polymerase but which can also include other proteins. If the Pyrodictium polymerase is derived from recombinant host cells, the other proteins will ordinarily be those associated with the host. Where the host is bacterial, the contaminating proteins will, of course, be bacterial proteins.

The term "non-ionic polymeric detergents" refers to surface-active agents that have no ionic charge and that are characterized for purposes of this invention, by an ability to stabilize the Pyrodictium enzyme at a pH range of from about 3.5 to about 9.5, preferably at a pH range from 4.0 to 9.0.

The term "oligonucleotide" as used herein is defined as a molecule comprised of two or more deoxyribonucleotides or ribonucleotides, preferably more than three, and usually more than ten. The exact size of an oligonucleotide will depend on many factors, including the ultimate function or use of the oligonucleotide.

Oligonucleotides can be prepared by any suitable method, including, for example, cloning and restriction of appropriate sequences and direct chemical synthesis by a method such as the phosphotriester method of Narang et al., 1979, Meth. Enzymol. 68:90-99; the phosphodiester method of Brown et al., 1979, Meth. Enzymol. 68:109-151; the diethyl-phosphoramidite method of Beaucage et al., 1981, Tetrahedron Lett. 22:1859-1862; the tri-ester method of Matteucci et al., 1981, J. Am. Chem. Soc. 103:3185-3191 or automated synthesis methods; and the solid support method of U.S. Patent No. 4,458,066.

The term "primer" as used herein refers to an oligonucleotide, whether natural or synthetic, which is capable of acting as a point of initiation of synthesis when placed under conditions in which primer extension is initiated. Synthesis of a primer extension product which is complementary to a nucleic acid strand is initiated in the presence of nucleoside triphosphates and a DNA polymerase or reverse transcriptase enzyme in an appropriate buffer at a suitable temperature. A "buffer" includes cofactors (such as divalent metal ions) and salt (to provide the appropriate ionic strength), adjusted to the desired pH. For Pyrodictium polymerases, the buffer preferably contains 1 to 3 mM of a magnesium salt, preferably $MgCl_2$, 50 to 200 μM of each nucleotide, and 0.2 to 1 μM of each primer, along with 10-100 mM KCl, 10 mM Tris buffer (pH 7.5-8.5), and 100 $\mu g/ml$ gelatin (although gelatin is not required, and should be avoided in some applications, such as DNA sequencing).

A primer is preferably a single-stranded oligodeoxyribonucleotide. The appropriate length of a primer depends on the intended use of the primer but typically ranges from 15 to 35 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template but must be sufficiently complementary to hybridize with a template.

- 5 -

The term "primer" may refer to more than one primer, particularly in the case where there is some ambiguity in the information regarding one or both ends of the target region to be amplified. For instance, if a nucleic acid sequence is inferred from a protein sequence, a "primer" is actually a collection of primer oligonucleotides containing sequences representing all possible codon variations based on the degeneracy of the genetic code. One of the primers in this collection will be homologous with the end of the target sequence. Likewise, if a "conserved" region shows significant levels of polymorphism in a population, mixtures of primers can be prepared that will amplify adjacent sequences.

A primer may be "substantially" complementary to a strand of specific sequence of the template. A primer must be sufficiently complementary to hybridize with a template strand for primer elongation to occur. A primer sequence need not reflect the exact sequence of the template. For example, a non-complementary nucleotide fragment may be attached to the 5' end of the primer, with the remainder of the primer sequence being substantially complementary to the strand. Non-complementary bases or longer sequences can be interspersed into the primer, provided that the primer sequence has sufficient complementarity with the sequence of the template to hybridize and thereby form a template primer complex for synthesis of the extension product of the primer.

A primer can be labeled, if desired, by incorporating a label detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means. For example, useful labels include ^{32}P , fluorescent dyes, electron-dense reagents, enzymes (as commonly used in ELISAs), biotin, or haptens and proteins for which antisera or monoclonal antibodies are available. A label can also be used to "capture" the primer, so as to facilitate the immobilization of either the primer or a primer extension product, such as amplified DNA, on a solid support.

The terms "restriction endonucleases" and "restriction enzymes" refer to bacterial enzymes which cut double-stranded DNA at or near a specific nucleotide sequence.

The terms "thermostable polymerase" and "thermostable enzyme" refer to an enzyme which is stable to heat and is heat resistant and catalyzes combination of the nucleotides in the proper manner to form primer extension products that are complementary to a template nucleic acid strand. Generally, synthesis of a primer extension product begins at the 3' end of the primer and proceeds in the 5' direction along the template strand, until synthesis terminates.

The Pyrodictium thermostable enzymes of the present invention satisfy the requirements for effective use in the amplification reaction known as the polymerase chain reaction or PCR as described in U.S. Patent No. 4,965,188. The Pyrodictium enzymes do not become irreversibly denatured (inactivated) when subjected to the elevated temperatures for the time necessary to effect denaturation of double-stranded nucleic acids, a key step in the PCR process. Irreversible denaturation for purposes herein refers to permanent and complete loss of enzymatic activity. The heating conditions necessary for nucleic acid denaturation will depend, e.g., on the buffer salt concentration and the composition and length of the nucleic acids being denatured, but typically range from about 90°C

to about 105°C for a time depending mainly on the temperature and the nucleic acid length, typically from a few seconds up to four minutes.

Higher temperatures may be required as the buffer salt concentration and/or GC composition of the nucleic acid is increased. The Pyrodictium enzymes do not become irreversibly denatured from relatively short exposures to temperatures of about 95°C-100°C. The extreme thermostability of the Pyrodictium DNA polymerase enzymes provides additional advantages over previously characterized thermostable enzymes. Prior to the present invention, efficient PCR at denaturation temperatures as high as 100°C had not been demonstrated. No thermostable DNA polymerases have been described up to now for this purpose. However, as the G/C content of a target nucleic acid increases, the temperature necessary to denature (T_{den}), the duplex also increases. For target sequences that require a T_{den} step of over 95°C, previous protocols require that solvents are included in the PCR for partially destabilizing the duplex, thus, lowering the effective T_{den}. Agents such as glycerol, DMSO, or formamide have been used in this manner in PCR (Korge et al., 1992, Proc. Natl. Acad. Sci. USA 89:910-914, and Wong et al., 1991, Nuc. Acids Res. 19:2251-2259. These agents, in addition to destabilizing duplex DNA will affect primer stability, can inhibit enzyme activity, and varying concentrations of DMSO or formamide decrease the thermoresistance (i.e., half-life) of thermophilic DNA polymerases. Accordingly, a significant number of optimization experiments and reaction conditions need to be evaluated when utilizing these cosolvents. In contrast, simply raising the T_{den} to 100°C with Poc or Pab DNA polymerase in an otherwise standard PCR can facilitate complete strand separation of PCR product eliminating the need for DNA helix destabilizing agents.

The extreme hyperthermophilic polymerases disclosed herein are stable at temperatures exceeding 100°C, and even as high as 110°C. However, at these temperatures depending on the pH and ionic strength, the integrity of the target DNA may be adversely affected (Ekert and Kunkel, 1992, In PCR: A Practical Approach, eds. McPherson, Quirke and Taylor, Oxford University Press, pages 225-244.

The Pyrodictium DNA polymerase has an optimum temperature at which it functions that is higher than about 45°C. Temperatures below 45°C facilitate hybridization of primer to template, but depending on salt composition and concentration and primer composition and length, hybridization of primer to template can occur at higher temperatures (e.g., 45-70°C), which may promote specificity of the primer hybridization reaction. The enzymes of the invention exhibit activity over a broad temperature range up to 85°C. The optimal activity is template dependent and generally in the range of 70-80°C.

The present invention provides DNA sequences encoding the thermostable DNA polymerase activity of Pyrodictium species. The preferred embodiments of the invention provide the nucleic acid and amino acid sequences for P. abyssi and P. occultum DNA polymerase. The entire P. abyssi and P. occultum DNA polymerase coding sequences are depicted below as SEQ ID No. 1 (P. abyssi) and SEQ ID No. 3 (P. occultum). The deduced amino acid sequences are listed as SEQ ID No. 2 (P. abyssi) and SEQ ID No. 4 (P. occultum). For convenience, the nucleotide and amino acid sequences of these polymerases are numbered for reference.

The present invention provides nucleic acid sequences providing means for comparison of *P. occultum* and *P. abyssi* DNA polymerase sequences with other thermostable polymerase enzymes. Such a comparison demonstrates that these novel sequences are unrelated to previously described nucleic acid sequences encoding eubacterial thermostable DNA polymerases. Consequently, methods for identifying *Pyrodictium* DNA polymerase enzymes based on the published sequences of known eubacterial thermostable DNA polymerases are not suitable for isolating nucleic acid sequences encoding *Pyrodictium* DNA polymerase enzymes.

P. abyssi DNA Polymerase

SEQ ID No. 1	ATGCCAGAAGCTATAGAGTTCGTGCTCCTT	
SEQ ID No. 2	MetProGluAlaIleGluPheValLeuLeu	10
31	GATTCAAGCTACGAGATTGTAGGGAAAGAGCCGTAATCATACTATGGGGTGTAACGCTA	
	AspSerSerTyrGluIleValGlyLysGluProValIleIleLeuTrpGlyValThrLeu	30
91	GACGGTAAACGCATAGTCCTACTTGATAGGAGGTTTAGGCCCTACTTCTATGCACTCATA	
	AspGlyLysArgIleValLeuLeuAspArgArgPheArgProTyrPheTyrAlaLeuIle	50
151	TCCCGCGACTACGAAGGTAAGGCCGAGGAGGTAGTAGCTGCTATTAGAAGGCTAAGTATG	
	SerArgAspTyrGluGlyLysAlaGluGluValValAlaAlaIleArgArgLeuSerMet	70
211	GCAAAGAGCCCCATAATAGAAGCAAAGGTGGTTAGTAAGAAGTACTTCGGAAGGCCCCGT	
	AlaLysSerProIleIleGluAlaLysValValSerLysLysTyrPheGlyArgProArg	90
271	AAAGCAGTCAAAGTAACGACAGTTATACCCGAATCTGTCAGAGAATATAGAGAGGCTGTA	
	LysAlaValLysValThrThrValIleProGluSerValArgGluTyrArgGluAlaVal	110
331	AAAAAGCTGGAAGGCGTGGAAGACTCTCTAGAAGCAGACATAAGGTTTCGCGATGAGGTAT	
	LysLysLeuGluGlyValGluAspSerLeuGluAlaAspIleArgPheAlaMetArgTyr	130
391	CTAATCGACAAGAAGCTCTACCCGTTACAGCATAACCGTGTGAGAGCCGAGAACGCTGGA	
	LeuIleAspLysLysLeuTyrProPheThrAlaTyrArgValArgAlaGluAsnAlaGly	150
451	CGCAGCCCTGGTTTCCGTGTAGACTCGGTATACACTATAGTTGAGGACCCAGAGCCTATT	
	ArgSerProGlyPheArgValAspSerValTyrThrIleValGluAspProGluProIle	170
511	GCCGACATAACTAGTATAGATATACCAGAGATGCGTGTGCTCGCGTTCGACATAGAGGTC	
	AlaAspIleThrSerIleAspIleProGluMetArgValLeuAlaPheAspIleGluVal	190
571	TACAGTAAGAGAGGAAGCCCTAACCCGTCCCGCGACCCGGTCATAATAATCTCGATAAAG	
	TyrSerLysArgGlySerProAsnProSerArgAspProValIleIleIleSerIleLys	210
631	GACAGCAAGGGGAACGAGAAGCTACTAGAAGCCAATAACTACGACGACAGAAACGTGCTA	
	AspSerLysGlyAsnGluLysLeuLeuGluAlaAsnAsnTyrAspAspArgAsnValLeu	230
691	CGGGAATTTATAGAGTACATACGCTCCTTTGACCCAGACATAATAGTAGGCTACAATAGC	
	ArgGluPheIleGluTyrIleArgSerPheAspProAspIleIleValGlyTyrAsnSer	250
751	AACAATTTTGAAGTGGCCATACCTTATAGAACGTGCACACAGAATAGGAGTAAAGCTCGAC	
	AsnAsnPheAspTrpProTyrLeuIleGluArgAlaHisArgIleGlyValLysLeuAsp	270
811	GTGACAAGGCGTGTTGGCGCAGAGCCAAGTATGAGCGTCTATGGACATGTCTCAGTGCAG	
	ValThrArgArgValGlyAlaGluProSerMetSerValTyrGlyHisValSerValGln	290
871	GGTAGGCTAAACGTAGACCTCTACAACCTACGTGGAGGAAATGCATGAGATAAAGGTAAAG	
	GlyArgLeuAsnValAspLeuTyrAsnTyrValGluGluMetHisGluIleLysValLys	310

931 ACGCTCGAGGAGGTCGCCGAATACCTAGGCGTTATGCGCAAGAGCGAGCGCGTACTAATA
ThrLeuGluGluValAlaGluTyrLeuGlyValMetArgLysSerGluArgValLeuIle 330

991 GAATGGTGGCGGATCCCAGATTACTGGGACGACGAGAAGAAACGGCCGCTACTGAAGCGT
GluTrpTrpArgIleProAspTyrTrpAspAspGluLysLysArgProLeuLeuLysArg 350

1051 TATGCCCTCGACGATGTGAGAGCCACCTACGGCCTCGCCGAGAAGATACTCCCATTCGCA
TyrAlaLeuAspAspValArgAlaThrTyrGlyLeuAlaGluLysIleLeuProPheAla 370

1111 ATACAGCTTTCGACAGTAACCGGTGTTCTTTAGACCAAGTCGGGGCTATGGGCGTAGGT
IleGlnLeuSerThrValThrGlyValProLeuAspGlnValGlyAlaMetGlyValGly 390

1171 TTCCGTCTAGAATGGTACCTTATGAGAGCAGCGCATGATATGAACGAGCTTGTCCCCAAC
PheArgLeuGluTrpTyrLeuMetArgAlaAlaHisAspMetAsnGluLeuValProAsn 410

1231 CGTGTCAAGCGGCGCGAAGAGAGCTACAAGGGAGCAGTAGTACTAAAGCCCCTAAAGGGT
ArgValLysArgArgGluGluSerTyrLysGlyAlaValValLeuLysProLeuLysGly 430

1291 GTCCATGAGAACGTAGTAGTGCTCGACTTTAGCTCAATGTACCCCAACATAATGATAAAG
ValHisGluAsnValValValLeuAspPheSerSerMetTyrProAsnIleMetIleLys 450

1351 TACAATGTGGGCCCTGACACGATAATTGACGACCCCTCAGAGTGCGAGAAGTACAGTGGA
TyrAsnValGlyProAspThrIleIleAspAspProSerGluCysGluLysTyrSerGly 470

1411 TGCTACGTAGCCCCGAAGTCGGGCACATGTTTAGGCGCTCGCCCTCCGGCTTCTTTAAG
CysTyrValAlaProGluValGlyHisMetPheArgArgSerProSerGlyPhePheLys 490

1471 ACCGTGCTTGAGAACCTCATAGCGCTGCGTAAGCAAGTACGTGAAAAGATGAAGGAGTTC
ThrValLeuGluAsnLeuIleAlaLeuArgLysGlnValArgGluLysMetLysGluPhe 510

1531 CCCCAGATAGCCCAGAATACCGGATATACGATGAACGCCAGAAGGCACTCAAGGTGCTA
ProProAspSerProGluTyrArgIleTyrAspGluArgGlnLysAlaLeuLysValLeu 530

1591 GCCAACGCTAGCTACGGCTACATGGGATGGGTGCACGCTCGCTGGTACTGTAAACGCTGC
AlaAsnAlaSerTyrGlyTyrMetGlyTrpValHisAlaArgTrpTyrCysLysArgCys 550

1651 GCAGAGGCTGTAACAGCCTGGGGCCGTAACCTGATACTCTCAGCAATAGAATATGCTAGG
AlaGluAlaValThrAlaTrpGlyArgAsnLeuIleLeuSerAlaIleGluTyrAlaArg 570

1711 AAGCTCGGCCTCAAAGTAATATACGGAGACACGGACTCCCTATTCGTAACCTATGATATC
LysLeuGlyLeuLysValIleTyrGlyAspThrAspSerLeuPheValThrTyrAspIle 590

1771 GAGAAGGTAAAGAAGCTAATAGAATTCGTCGAGAAACAGCTAGGCTTCGAGATAAAGATA
GluLysValLysLysLeuIleGluPheValGluLysGlnLeuGlyPheGluIleLysIle 610

1831 GACAAGGTATACAAAAGAGTGTTCTTTACCGAGGCAAAGAAGCGCTACGTGGGCCTCCTC
AspLysValTyrLysArgValPhePheThrGluAlaLysLysArgTyrValGlyLeuLeu 630

1891 GAGGACGGGCGTATGGACATAGTAGGCTTTGAGGCTGTTAGAGGCGACTGGTGTGAGCTA
GluAspGlyArgMetAspIleValGlyPheGluAlaValArgGlyAspTrpCysGluLeu 650

1951 GCTAAAGAGGTGCAAGAGAAAGTAGCAGAGATAATACTGAAGACGGGAGACATAAATAGA
AlaLysGluValGlnGluLysValAlaGluIleIleLeuLysThrGlyAspIleAsnArg 670

2011 GCCATAAGCTACATAAGAGAGGTCGTGAGAAAGCTAAGAGAAGGCAAGATACCCATAACA
AlaIleSerTyrIleArgGluValValArgLysLeuArgGluGlyLysIleProIleThr 690

2071 AAGCTCGTAATATGGAAGACCTTGACAAAGAGAATCGAGGAATACGAGCACGAGGCGCCG
LysLeuValIleTrpLysThrLeuThrLysArgIleGluGluTyrGluHisGluAlaPro 710

2131 CACGTTACTGCAGCACGGCGTATGAAAGAAGCAGGCTACGATGTGGCACCGGGAGACAAG
HisValThrAlaAlaArgArgMetLysGluAlaGlyTyrAspValAlaProGlyAspLys 730

2191 ATAGGCTACATCATAGTTAAAGGACATGGCAGTATATCGAGTCGTGCCTACCCGTACTTT
IleGlyTyrIleIleValLysGlyHisGlySerIleSerSerArgAlaTyrProTyrPhe 750

2251 ATGGTAGACTCGTCTAAGGTTGACACAGAGTACTACATAGACCACCAGATAGTACCAGCA
MetValAspSerSerLysValAspThrGluTyrTyrIleAspHisGlnIleValProAla 770

2311 GCAATGAGGATACTCTCATACTTCGGGGTCACAGAGAAGCAGCTTAAGGCAGCATCATCT
AlaMetArgIleLeuSerTyrPheGlyValThrGluLysGlnLeuLysAlaAlaSerSer 790

2371 GGGCATAGGAGTCTCTTCGACTTCTTCGCGGCAAAGAAGTAGccccggctctccaaacta
GlyHisArgSerLeuPheAspPhePheAlaAlaLysLys * 803

P. occultum DNA Polymerase

SEQ ID No. 3
SEQ ID No. 4

ATGACAGAGACTATAGAGTTCGTGCTGCTA
MetThrGluThrIleGluPheValLeuLeu 10

31 GACTCTAGCTACGAGATACTGGGGAAGGAGCCGGTAGTAATCCTCTGGGGGATAACGCTT
AspSerSerTyrGluIleLeuGlyLysGluProValValIleLeuTrpGlyIleThrLeu 30

91 GACGGTAAACGTGTCGTGCTTCTAGACCACCGCTTCCGCCCTACTTCTACGCCCTCATA
AspGlyLysArgValValLeuLeuAspHisArgPheArgProTyrPheTyrAlaLeuIle 50

151 GCCCGGGGCTATGAGGATATGGTGGAGGAGATAGCAGCTTCCATAAGGAGGCTTAGTGTG
AlaArgGlyTyrGluAspMetValGluGluIleAlaAlaSerIleArgArgLeuSerVal 70

211 GTCAAGAGTCCGATAATAGATGCCAAGCCTCTTGATAAGAGGTACTTCGGCAGGCCCCGT
ValLysSerProIleIleAspAlaLysProLeuAspLysArgTyrPheGlyArgProArg 90

271 AAGGCGGTGAAGATTACCACTATGATACCCGAGTCTGTTAGACACTACCGCGAGGCGGTG
LysAlaValLysIleThrThrMetIleProGluSerValArgHisTyrArgGluAlaVal 110

331 AAGAAGATAGAGGGTGTGGAGGACTCCCTCGAGGCAGATATAAGGTTTGCAATGAGATAT
LysLysIleGluGlyValGluAspSerLeuGluAlaAspIleArgPheAlaMetArgTyr 130

391 CTGATAGATAAGAGGCTCTACCCGTTACCGGTTTACCGGATCCCCGTAGAGGATGCGGGC
LeuIleAspLysArgLeuTyrProPheThrValTyrArgIleProValGluAspAlaGly 150

451 CGCAATCCAGGCTTCCGTGTTGACCGTGTCTACAAGGTTGCTGGCGACCCGGAGCCCCTA
ArgAsnProGlyPheArgValAspArgValTyrLysValAlaGlyAspProGluProLeu 170

511 GCGGATATAACGCGGATCGACCTTCCCCCGATGAGGCTGGTAGCTTTTGATATAGAGGTG
AlaAspIleThrArgIleAspLeuProProMetArgLeuValAlaPheAspIleGluVal 190

571 TATAGCAGGAGGGGGAGCCCTAACCTGCAAGGGATCCAGTGATAATAGTGTCGCTGAGG
TyrSerArgArgGlySerProAsnProAlaArgAspProValIleIleValSerLeuArg 210

631 GACAGCGAGGGCAAGGAGAGGCTCATAGAAGCTGAAGGCCATGACGACAGGAGGGTTCTG
AspSerGluGlyLysGluArgLeuIleGluAlaGluGlyHisAspAspArgArgValLeu 230

691 AGGGAGTTCGTAGAGTACGTGAGAGCCTTCGACCCCGACATAATAGTGGGCTATAACAGT
ArgGluPheValGluTyrValArgAlaPheAspProAspIleIleValGlyTyrAsnSer 250

751 AACCACTTCGACTGGCCCTACCTAATGGAGCGCGCCCGTAGGCTCGGGATTAACCTCGAC
AsnHisPheAspTrpProTyrLeuMetGluArgAlaArgArgLeuGlyIleAsnLeuAsp 270

811 GTTACACGCCGTGTGGGGGCAGAGCCCACCACCAGCGTCTACGGCCACGTCTCGGTGCAG
ValThrArgArgValGlyAlaGluProThrThrSerValTyrGlyHisValSerValGln 290

871 GGTAGGCTGAACGTGGACCTCTACGACTATGCCGAGGAGATGCCGGAGATAAAGATGAAG
GlyArgLeuAsnValAspLeuTyrAspTyrAlaGluGluMetProGluIleLysMetLys 310

931 ACGCTTGAGGAGGTAGCGGAGTACCTAGGCGTTATGAAGAAGAGCGAGCGTGTGATAATA
ThrLeuGluGluValAlaGluTyrLeuGlyValMetLysLysSerGluArgValIleIle 330

991 GAGTGGTGGAGGATACCCGAGTACTGGGATGACGAGAAGAAGAGGCAGCTGCTAGAGCGC
GluTrpTrpArgIleProGluTyrTrpAspAspGluLysLysArgGlnLeuLeuGluArg 350

1051 TACGCGCTCGACGATGTGAGGGCTACCTACGGCCTCGCGGAAAAGATGCTACCGTTTCGCC
TyrAlaLeuAspAspValArgAlaThrTyrGlyLeuAlaGluLysMetLeuProPheAla 370

1111 ATACAGCTCTCCACTGTTACGGGTGTGCCTCTCGACCAGGTAGGTGCTATGGGCGTAGGC
IleGlnLeuSerThrValThrGlyValProLeuAspGlnValGlyAlaMetGlyValGly 390

1171 TTCCGCCTAGAGTGGTATCTCATGCGTGCAGCCTACGATATGAACGAGCTGGTGCCGAAC
PheArgLeuGluTrpTyrLeuMetArgAlaAlaTyrAspMetAsnGluLeuValProAsn 410

1231 CGGGTGGAGAGGAGGGGGGAGAGCTACAAGGGTGCAGTAGTGTTAAAGCCTCTCAAGGGA
ArgValGluArgArgGlyGluSerTyrLysGlyAlaValValLeuLysProLeuLysGly 430

1291 GTCCATGAGAATGTTGTGGTGCTCGATTTTCAGTTCCATGTACCCGAGCATAATGATAAAG
ValHisGluAsnValValValLeuAspPheSerSerMetTyrProSerIleMetIleLys 450

1351 TACAACGTGGGCCCCGACACTATAGTCGACGACCCCTCGGAGTGCCCAAAGTACGGCGGC
TyrAsnValGlyProAspThrIleValAspAspProSerGluCysProLysTyrGlyGly 470

1411 TGCTATGTAGCCCCGAGGTCGGGCACCGGTTCCGTCGCTCCCCGCCAGGCTTCTTCAAG
CysTyrValAlaProGluValGlyHisArgPheArgArgSerProProGlyPhePheLys 490

1471 ACCGTGCTCGAGAACCTACTGAAGCTACGCCGACAGGTAAAGGAGAAGATGAAGGAGTTT
ThrValLeuGluAsnLeuLeuLysLeuArgArgGlnValLysGluLysMetLysGluPhe 510

1531 CCGCCTGACAGCCCCGAGTACAGGCTCTACGATGAGCGCCAGAAGGCGCTCAAGGTTCTT
ProProAspSerProGluTyrArgLeuTyrAspGluArgGlnLysAlaLeuLysValLeu 530

1591 GCGAACGCGAGCTATGGCTACATGGGGTGGAGCCATGCCCGCTGGTACTGCAAACGCTGC
AlaAsnAlaSerTyrGlyTyrMetGlyTrpSerHisAlaArgTrpTyrCysLysArgCys 550

1651 GCCGAGGCTGTCACAGCCTGGGGCCGTAACCTTATACTGACAGCTATCGAGTATGCCAGG
AlaGluAlaValThrAlaTrpGlyArgAsnLeuIleLeuThrAlaIleGluTyrAlaArg 570

1711 AAGCTCGGCCTAAAGGTTATATATGGAGACACCGACTCCCTCTTCGTGGTCTATGACAAG
LysLeuGlyLeuLysValIleTyrGlyAspThrAspSerLeuPheValValTyrAspLys 590

1771 GAGAAGGTTGAGAAGCTGATAGAGTTTGTGCGAGAAGGAGCTGGGCTTTGAGATAAAGATA
GluLysValGluLysLeuIleGluPheValGluLysGluLeuGlyPheGluIleLysIle 610

1831 GACAAGATCTACAAGAAAGTGTTCTTCACGGAGGCTAAGAAGCGCTATGTAGGTCTCCTC
AspLysIleTyrLysLysValPhePheThrGluAlaLysLysArgTyrValGlyLeuLeu 630

1891 GAGGACGGACGTATAGACATCGTGGGCTTTGAAGCAGTCCGCGGCGACTGGTGCGAGCTG
GluAspGlyArgIleAspIleValGlyPheGluAlaValArgGlyAspTrpCysGluLeu 650

1951 GCTAAGGAGGTGCAGGAGAAGGCGGCTGAGATAGTGTGAATACGGGGAACGTGGACAAG
AlaLysGluValGlnGluLysAlaAlaGluIleValLeuAsnThrGlyAsnValAspLys 670

2011 GCTATAAGCTACATAAGGGAGGTAATAAAGCAGCTCCGCGAGGGCAAGGTGCCAATAACA
AlaIleSerTyrIleArgGluValIleLysGlnLeuArgGluGlyLysValProIleThr 690

2071 AAGCTTATCATATGGAAGACGCTGAGCAAGAGGATAGAGGAGTACGAGCATGACGCGCCT
LysLeuIleIleTrpLysThrLeuSerLysArgIleGluGluTyrGluHisAspAlaPro 710

2131 CATGTGATGGCTGCACGGCGTATGAAGGAGGCAGGCTACGAGGTGTCTCCCGGCGATAAG
HisValMetAlaAlaArgArgMetLysGluAlaGlyTyrGluValSerProGlyAspLys 730

2191 GTGGGCTACGTCATAGTTAAGGGTAGCGGGAGTGTGTCCAGCAGGGCCTACCCCTACTTC
ValGlyTyrValIleValLysGlySerGlySerValSerSerArgAlaTyrProTyrPhe 750

2251 ATGGTTGATCCATCGACCATCGACGTCAACTACTATATTGACCACCAGATAGTGCCGGCT
MetValAspProSerThrIleAspValAsnTyrTyrIleAspHisGlnIleValProAla 770

2311 GCTCTGAGGATACTCTCCTACTTCGGAGTCACCGAGAAACAGCTCAAGGCGGCGGCTACG
AlaLeuArgIleLeuSerTyrPheGlyValThrGluLysGlnLeuLysAlaAlaAlaThr 790

2371 GTGCAGAGAAGCCTCTTCGACTTCTTCGCCTCAAAGAAATAGctcctccaccggctagc
ValGlnArgSerLeuPheAspPhePheAlaSerLysLys * 803

As a result of the present invention, Pyrodictium DNA polymerase amino acid sequences can be used to design novel degenerate primers to find new, previously undiscovered hypothermophilic DNA polymerase genes. The generic utility of the degenerate primer process is exemplified in PCT Publication No. WO 92/06202. The publication describes the use of degenerate primers for cloning the gene encoding *Thermosiphon africanus* DNA polymerase. Prior to the present invention, degenerate priming methods were demonstrated to be suitable for isolating genes encoding novel thermostable DNA polymerase enzymes. The success of these methods lies in part in the identification of conserved motifs among the thermostable DNA polymerases of, for example, *Thermus aquaticus* and *Thermus thermophilus*.

Thus, due to the dissimilarity in DNA polymerase amino acid sequences between the extreme hyperthermophiles, for example, Pyrodictium species, and non-hyperthermophiles such as *Thermus* species these degenerate priming methods were not previously suitable for isolating and expressing Pyrodictium polymerase genes. Applicants' invention has enabled the use of degenerate priming methods for isolating genes encoding novel DNA polymerase enzymes from extreme hyperthermophilic microbes. The gene encoding the DNA polymerase of the hyperthermophilic *T. litoralis* (Tli) has been described. While Tli, Pab and Poc DNA polymerases contain the amino acid sequence motifs that reflect eucaryotic DNA polymerases, Pab and Poc DNA polymerases have only limited and spotty amino acid sequence identity with Tli DNA polymerase. Specifically, amino acid sequence alignments indicate only 37% to 39% sequence identity between Poc or Pab with Tli DNA polymerase. Significant regions of non-identity with Tli DNA polymerase occur in the 20 amino acids that precede and the 10 amino acids that follow Region 1 (position 438 through 458 in SEQ ID Nos. 2 and 4). In addition, significant regions of non-identity with Tli DNA polymerase occur in the 10 to 15 amino acids that precede, and the 10 to 15 amino acids that follow Region 4 (position 611 through 634 in SEQ ID Nos. 2 and 4). These regions as well as other portions of the polymerase active site are highly conserved in Poc and Pab DNA polymerases and contribute significantly to the extraordinary thermostability of these DNA polymerase enzymes.

The present invention, by providing DNA and amino acid sequences for two Pyrodictium polymerase enzymes, therefore, enables the isolation of other extremely thermophilic DNA polymerase enzymes and the coding sequences for those enzymes. Further alignment of *P. occultum* and *P. abyssi* sequences with known thermostable enzyme sequences allows

the selective identification of additional novel enzymes suitable for efficient PCR at denaturation temperatures of 100°C.

5 The DNA and amino acid sequences shown above and the DNA compounds that encode those sequences can be used to design and construct recombinant DNA expression vectors to drive expression of Pyrodictium DNA polymerase activity in a wide variety of host cells. A DNA compound encoding all or part of the DNA sequence shown above can also be used as a probe to identify thermostable polymerase-encoding DNA from other archaea, especially Pyrodictium species and the amino acid sequence shown above can be used to design peptides for use as immunogens to prepare antibodies that can be used to identify and
10 purify a thermostable polymerase.

Recombinant vectors that encode an amino acid sequence encoding a Pyrodictium DNA polymerase will typically be purified prior to use in a recombinant DNA technique. The present invention provides such purification methodology.

15 The molecular weight of the DNA polymerase purified from recombinant *E. coli* host which express the *P. occultum* or *P. abyssi* polymerase genes are determined by the above method to be about 90 kDa. The molecular weight of this same DNA polymerase as determined by the predicted amino acid sequence is calculated to be approximately 92.6 kilodaltons.

An important aspect of the present invention is the production of recombinant Pyrodictium DNA polymerase. Thus, the present invention also provides a process for the preparation of thermostable DNA polymerases in accordance with the present invention, which process comprises the steps of:

- 20 (a) culturing a host cell transformed with a DNA vector that comprises a DNA sequence encoding said thermostable DNA polymerase; and
(b) isolating the thermostable DNA polymerase produced in the host cell from the culture.

As noted above, the gene encoding this enzyme has been cloned from two exemplary Pyrodictium species, *P. occultum* and *P. abyssi*, genomic DNA. The complete coding sequence for the *P. occultum* (Poc) DNA polymerase can be easily obtained in an ~2.52 kb
25 NheI restriction fragment of the plasmid pPoc 4. This plasmid was deposited with the American Type Culture Collection (ATCC) in host cell *E. coli* Sure[®] Cells (Stratagene) on May 11, 1993, under Accession No. 69309. The complete coding sequence for *P. abyssi* (Pab) DNA polymerase can be easily obtained in an ~3.74 kb SalI restriction fragment of the plasmid pPab 14. This plasmid was deposited with the ATCC in host cell *E. coli* Sure[®] Cells
30 (Stratagene) on May 11, 1993, and under Accession No. 69310.

The complete coding sequence and deduced amino acid sequence of the thermostable Pab and Poc DNA polymerase enzymes are provided above. The entire coding sequence of the DNA polymerase gene is not required, however, to produce a biologically active gene
35 product with DNA polymerase activity. The availability of DNA encoding the Pyrodictium DNA polymerase sequence provides the opportunity to modify the coding sequence so as to generate mutein (mutant protein) forms also having DNA polymerase activity. Amino(N)-terminal deletions of approximately one-third of the coding sequence can provide a gene pro-

duct that is quite active in polymerase assays. Because certain N-terminal shortened forms of the polymerase are active, the gene constructs used for expression of these polymerases can include the corresponding shortened forms of the coding sequence.

5 In addition to the N-terminal deletions, individual amino acid residues in the peptide chain comprising Pyrodictium polymerase may be modified by oxidation, reduction, or other derivation, and the protein may be cleaved to obtain fragments that retain activity. Such alterations that do not destroy activity do not remove the protein from the definition of a protein with Poc or Pab polymerase activity and so are specifically included within the scope of the present invention. Modifications to the primary structure of the Poc or Pab DNA polymerase gene by deletion, addition, or alteration so as to change the amino acids incorporated into the DNA polymerase during translation can be made without destroying the high temperature DNA polymerase activity of the protein. Such substitutions or other alternations result in the production of proteins having an amino acid sequence encoded by DNA falling within the contemplated scope of the present invention. Likewise, the cloned genomic sequence, or homologous synthetic sequences, of the Poc and Pab DNA polymerase genes can be used to express fusion polypeptides with Pyrodictium DNA polymerase activity or to express a protein with an amino acid sequence identical to that of native Poc or Pab DNA polymerase.

15 Thus, the present invention provides the complete coding sequence for Pab and Poc DNA polymerase enzymes from which expression vectors applicable to a variety of host systems can be constructed and the coding sequence expressed. Portions of the present polymerase-encoding sequence are also useful as probes to retrieve other thermostable polymerase-encoding sequences in a variety of species. Accordingly, portions of the genomic DNA encoding at least four to six amino acids can be synthesized as oligodeoxyribonucleotide probes that encode at least four to six amino acids and used to retrieve additional DNAs encoding a thermostable polymerase. Because there may not be an exact match between the nucleotide sequence of the thermostable DNA polymerase gene of Pab and Poc and the corresponding gene of other species, oligomers containing approximately 12-18 nucleotides (encoding the four to six amino acid sequence) are usually necessary to obtain hybridization under conditions of sufficient stringency to eliminate false positives. Sequences encoding six amino acids supply ample information for such probes.

20 The present invention, by providing the coding and amino acid sequences for Pab and Poc DNA polymerases, therefore enables the isolation of other thermostable polymerase enzymes and the coding sequences for those enzymes. Specifically, the invention provides means for preparing primers and probes for identifying nucleic acids encoding DNA polymerase enzymes contained within DNA isolates from related archaeobacteria such as extreme hyperthermophiles including additional Pyrodictium species, *P. brockii*, and *Methanopyrus* species such as *M. kandleri*.

35 Several such regions of similarity between the Pab and Poc DNA polymerase coding sequences exist. For regions nine codons in length, probes corresponding to these regions can be used to identify and isolate sequences encoding thermostable polymerase enzymes that are identical (and complementary) to the probe for a contiguous sequence of at least five codons. For the region six codons in length, a probe corresponding to this region can be

used to identify and isolate thermostable polymerase-encoding DNA sequences that are identical to the probe for a contiguous sequence of at least four codons.

One property found in the *Pyrodictium* DNA polymerase enzymes, but lacking in native Taq DNA polymerase and native Tth DNA polymerase, is 3'→5' exonuclease activity.

5 This 3'→5' exonuclease activity is generally considered to be desirable, because misincorporated or unmatched bases of the synthesized nucleic acid sequence are eliminated by this activity. Therefore, the fidelity of PCR utilizing a polymerase with 3'→5' exonuclease activity (e.g. *Pyrodictium* DNA polymerase enzymes) is increased. However, the 3'→5' exonuclease activity found in *Pyrodictium* DNA polymerase enzymes can also increase non-specific background amplification in PCR by modifying the 3' end of the primers. The
10 3'→5' exonuclease activity can eliminate single-stranded DNAs, such as primers or single-stranded template. In essence, every 3'-nucleotide of a single-stranded primer or template is treated by the enzyme as unmatched and is therefore degraded. To avoid primer degradation in PCR, one can add phosphorothioate to the 3' ends of the primers. Phosphorothioate modified nucleotides are more resistant to removal by 3'→5' exonucleases.
15

Whether one desires to produce an enzyme identical to native Pab or Poc DNA polymerase or a derivative or homologue of that enzyme, the production of a recombinant form of the polymerase typically involves the construction of an expression vector, the transformation of a host cell with the vector, and culture of the transformed host cell under conditions such that expression will occur. To construct the expression vector, a DNA is obtained
20 that encodes the mature (used here to include all muteins) enzyme or a fusion polypeptide of the polymerase, which fusion polypeptide comprises an amino acid sequence derived from the polymerases of the present invention and an additional amino acid sequence that does not lead to the destruction of the polymerase activity or an additional amino acid sequence cleavable under controlled conditions (such as treatment with peptidase) to give an active protein. The coding sequence is then placed in operable linkage with suitable control sequences
25 in an expression vector. The vector can be designed to replicate autonomously in the host cell or to integrate into the chromosomal DNA of the host cell. The vector is used to transform a suitable host, and the transformed host is cultured under conditions suitable for expression of recombinant *Pyrodictium* polymerase. The *Pyrodictium* polymerase is isolated from the medium or from the cells; recovery and purification of the protein may not be necessary in some instances, where some impurities may be tolerated.
30

Construction of suitable vectors containing the desired coding and control sequences employs standard ligation and restriction techniques that are well understood in the art (see,
35 for example, Molecular Cloning Laboratory Manual 2nd ed., Sambrook et al., 1989, Cold Spring Harbor Press, New York, NY. Isolated plasmids, DNA sequences, or synthesized oligonucleotides are cleaved, modified, and religated in the form desired. Suitable restriction sites can, if not normally available, be added to the ends of the coding sequence as as to facilitate construction of an expression vector by methods well known in the art.

40 For portions of vectors or coding sequences that require sequence modifications, a variety site-specific primer-directed mutagenesis methods are available. For example, the

polymerase chain reaction (PCR) can be used to perform site-specific mutagenesis. PCR Protocols, ed. by Innis et al., 1990, Academic Press, San Diego, CA, and PCR Technology ed. by Henry Erlich, 1989, Stockton Press, New York, NY, describe methods for cloning, modifying, and sequencing DNA using PCR.

5 Control sequences, expression vectors, and transformation methods are dependent on the type of host cell used to express the gene. Generally, procaryotic, yeast, insect, or mammalian cells are used as hosts. Procaryotic hosts are in general the most efficient and convenient for the production of recombinant proteins and are, therefore, preferred for the expression of Pyrodictium DNA polymerase enzymes.

10 The procaryote most frequently used to express recombinant proteins is *E. coli*. For cloning and sequencing, and for expression of constructions under control of most bacterial promoters, *E. coli* K12 strain MM294, obtained from the *E. coli* Genetic Stock Center under GCSC #6135, can be used as the host. For expression vectors with the PLNRBS control sequence, *E. coli* K12 strain MC1000 lambda lysogen, N7N53cI857 SusP80, ATCC 39531,
15 may be used. *E. coli* DG116, which was deposited with the ATCC (ATCC 53606) on April 7, 1987, and *E. coli* KB2, which was deposited with the ATCC (ATCC 53075) on March 29, 1985, are also useful host cells. For M13 phage recombinants, *E. coli* strains susceptible to phage infection, such as *E. coli* K12 strain DG98, are employed. The DG98 strain was deposited with the ATCC (ATCC 39768) on July 13, 1984.

20 However, microbial strains other than *E. coli* can also be used, such as bacilli, for example *Bacillus subtilis*, various species of *Pseudomonas*, and other bacterial strains, for recombinant expression of Pyrodictium DNA polymerase enzymes.

 In addition to bacteria, eucaryotic microbes, such as yeast, can also be used as recombinant host cells. See, for example, Stinchcomb et al., 1979, *Nature* 282:39; Tschempe
25 et al., 1980, *Gene* 10:157; and Clarke et al., 1983, *Meth. Enz.* 101:300.

 The Pyrodictium gene can also be expressed in eucaryotic host cell cultures derived from multicellular organisms. See, for example, *Tissue Culture*, Academic Press, Cruz and Patterson, editors (1973). Useful host cell lines include COS-7, COS-A2, CV-1, murine cells such as murine myelomas N51 and VERO, HeLa cells, and Chinese hamster ovary
30 (CHO) cells. Plant cells can also be used as hosts, and control sequences compatible with plant cells, such as the nopaline synthase promoter and polyadenylation signal sequences (Depicker et al., 1982, *J. Mol. Appl. Gen.* 1:561) are available.

 Depending on the host cell used, transformation is done using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described by
35 Cohen, 1972, *Proc. Natl. Acad. Sci. USA* 69:2110 is used for procaryotes or other cells that contain substantial cell wall barriers. For mammalian cells, the calcium phosphate precipitation method of Graham and van der Eb, 1978, *Virology* 52:546 is preferred. Transformations into yeast are carried out according to the method of Van Solingen et al., 1977, *J. Bact.* 130:946 and Hsiao et al., 1979, *Proc. Natl. Acad. Sci. USA* 76:3829.

40 Once the Pyrodictium DNA polymerase has been expressed in a recombinant host cell, purification of the protein may be desired. Although the purification procedures previously described can be used to purify the recombinant thermostable polymerase of the in-

vention, hydrophobic interaction chromatography purification methods are preferred. Hydrophobic interaction chromatography is a separation technique in which substances are separated on the basis of differing strengths of hydrophobic interaction with an uncharged bed material containing hydrophobic groups. Typically, the column is first equilibrated under conditions favorable to hydrophobic binding, e.g., high ionic strength. A descending salt gradient may be used to elute the sample.

Detailed protocols for purifying recombinant thermostable DNA polymerases have been described in, for example, PCT Patent Publication Nos. WO 92/03556, published March 5, 1992, and WO 91/09950, published July 11, 1991. The methods described therein for *Thermotoga maritima* are suitable. Example 9 (see below) provides a preferred protocol for purifying recombinant *Pyrodictium* polymerase enzymes.

For long-term stability, the *Pyrodictium* DNA polymerase enzyme is preferably stored in a buffer that contains one or more non-ionic polymeric detergents. Such detergents are generally those that have a molecular weight in the range of approximately 100 to 250,00 preferably about 4,000 to 200,000 daltons and stabilize the enzyme at a pH of from about 3.5 to about 9.5, preferably from about 4 to 8.5. Examples of such detergents include those specified on pages 295-298 of McCutcheon's *Emulsifiers & Detergents*, North American edition (1983), published by the McCutcheon Division of MC Publishing Co., 175 Rock Road, Glen Rock, NJ (USA). Preferably, the detergents are selected from the group comprising ethoxylated fatty alcohol ethers and lauryl ethers, ethoxylated alkyl phenols, octylphenoxy polyethoxy ethanol compounds, modified oxyethylated and/or oxypropylated straight-chain alcohols, polyethylene glycol monooleate compounds, polysorbate compounds, and phenolic fatty alcohol ethers. More particularly preferred are Tween 20, a polyoxyethylated (20) sorbitan monolaurate from ICI Americas Inc., Wilmington, D.E., and IconolTM NP-40, an ethoxylated alkyl phenol (nonyl) from BASF Wyandotte Corp. Parsippany, N.J.

The thermostable enzyme of this invention may be used for any purpose in which such enzyme activity is necessary or desired. In a particularly preferred embodiment, the enzyme catalyzes the nucleic acid amplification reaction known as PCR.

Although the PCR process is well known in the art (see U.S. Patent Nos. 4,683,195; 4,683,202; and 4,965,188, and although commercial vendors, such as Perkin Elmer, sell PCR reagents and publish PCR protocols, some general PCR information is provided below for purposes of clarity and full understanding of the invention to those unfamiliar with the PCR process.

To amplify a target nucleic acid sequence in a sample by PCR, the sequence must be accessible to the components of the amplification system. In general, this accessibility is ensured by isolating the nucleic acids from the sample. A variety of techniques for extracting nucleic acids from biological samples are known in the art. For example, see those described in Higuchi et al., 1989 in *PCR Technology* (Erlich ed., Stockton Press, New York).

Because the nucleic acid in the sample is first denatured (assuming the sample nucleic acid is double-stranded) to begin the PCR process, and because simply heating some sam-

ples results in the disruption of cells, isolation of nucleic acid from the sample can sometimes be accomplished in conjunction with strand separation. Strand separation can be accomplished by any suitable denaturing method, however, including physical, chemical, or enzymatic means. Typical heat denaturation involves temperatures ranging from about 80-105°C for times ranging from seconds to about 1 to 10 minutes.

As noted above strand separation may be accomplished in conjunction with the isolation of the sample nucleic acid or as a separate step. In the preferred embodiment of the PCR process, strand separation is achieved by heating the reaction to a sufficiently high temperature for an effective time to cause the denaturation of the duplex, but not to cause an irreversible denaturation of the polymerase (see U.S. Patent No. 4,965,188). No matter how strand separation is achieved, however, once the strands are separated, the next step in PCR involves hybridizing the separated strands with primers that flank the target sequence. The primers are then extended to form complementary copies of the target strands, and the cycle of denaturation, hybridization, and extension is repeated as many times as necessary to obtain the desired amount of amplified nucleic acid.

For successful PCR amplification, the primers are designed so that the position at which each primer hybridizes along a duplex sequence is such that an extension product synthesized from one primer, when separated from the template (complement), serves as a template for the extension of the other primer to yield an amplified segment of nucleic acid of defined length.

Template-dependent extension of primers in PCR is catalyzed by a polymerizing agent in the presence of adequate amounts of four deoxyribonucleoside triphosphates (dATP, dGTP, dCTP, and dTTP) in a reaction medium comprised of the appropriate salts, metal cations, and pH buffering system.

The amplification method is useful not only for producing large amounts of a specific nucleic acid sequence of known sequence but also for producing nucleic acid sequences which are known to exist but are not completely specified. One need know only a sufficient number of bases at both ends of the sequence in sufficient detail so that two oligonucleotide primers can be prepared which will hybridize to different strands of the desired sequence at relative positions along the sequence such that an extension product synthesized from one primer, when separated from the template (complement), can serve as a template for extension of the other primer into a nucleic acid sequence of defined length. The greater the knowledge about the bases at both ends of the sequence, the greater can be the specificity of the primers for the target nucleic acid sequence and the efficiency of the process.

Any nucleic acid sequence, in purified or nonpurified form, can be utilized as the starting nucleic acid(s), provided it contains or is suspected to contain the specific nucleic acid sequence desired. Thus, the process may employ, for example, DNA or RNA, including messenger RNA, which DNA or RNA may be single-stranded or double-stranded. For example, if the template is RNA, a suitable polymerizing agent to convert the RNA into a complementary, copy-DNA (cDNA) sequence is reverse transcriptase (RT), such as avian myeloblastosis virus RT and *Thermus thermophilus* DNA polymerase, a thermostable DNA

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polymerase with reverse transcriptase activity developed and manufactured by Hoffmann-La Roche Inc. and marketed by Perkin Elmer (see PCT Patent Publication WO 91/09950).

Whether the nucleic acid is single- or double-stranded, the DNA polymerase from *Pyrodictum* may be added at the denaturation step or when the temperature is being reduced to or is in the range for promoting hybridization. Although the thermostability of *Pyrodictum* polymerase allows one to add the polymerase to the reaction mixture at any time, one can substantially inhibit non-specific amplification by adding the polymerase to the reaction mixture at a point in time when the mixture will not be cooled below the stringent hybridization temperature. After hybridization, the reaction mixture is then heated to or maintained at a temperature at which the activity of the enzyme is promoted or optimized, i.e., a temperature sufficient to increase the activity of the enzyme in facilitating synthesis of the primer extension products from the hybridized primer and template. The temperature must actually be sufficient to synthesize an extension product of each primer which is complementary to each nucleic acid template, but must not be so high as to denature each extension product from its complementary template (i.e., the temperature is generally less than about 80-90°C).

Depending on the nucleic acid(s) employed, the typical temperature effective for this synthesis reaction generally ranges from about 40-80°C, preferably 50-75°C. The temperature more preferably ranges from about 65-75°C for *P. occultum* and *P. abyssi* DNA polymerase enzymes. The period of time required for this synthesis may range from about 0.5 to 40 minutes or more, depending mainly on the temperature, the length of the nucleic acid and the enzyme. The extension time is usually about 30 seconds to three minutes. If the nucleic acid is longer, a longer time period is generally required for complementary strand synthesis.

Those skilled in the art will know that the PCR process is most usually carried out as an automated process with a thermostable enzyme. In this process, the temperature of the reaction mixture is cycled through a denaturing region, a primer annealing region, and a reaction region. A machine specifically adapted for use with a thermostable enzyme is commercially available from Perkin Elmer.

Those skilled in the art will also be aware of the problem of contamination of a PCR by the amplified nucleic acid from previous reactions. Methods to reduce this problem are provided in U.S. Patent 5,310,652.

PCR amplification may yield primer dimers or oligomers, double-stranded side products containing the sequences of several primer molecule joined end-to-end, the yield of which correlates negatively with the yield of amplified target sequence. Non-specific priming and primer dimer and oligomer formation can occur whenever all of the PCR reagents are mixed, even at ambient and sub-ambient temperatures in the absence of thermal cycling and in the presence or absence of target DNA. At 37°C, for example, Taq retains approximate 1-2% activity, although the optimal temperature is about 75-80°C. Methods for overcoming non-specific extension and primer dimer formation include segregation of at least one reagent from the others in a way such that all reagents do not come together before the first amplification cycle. PCT Patent Publication No. WO 91/12342, describes methods and compositions for minimizing non-specific extension and primer dimer.

Because of the extremely high optimum growth temperature of *Pyrodictium* species, the present invention provides compositions that may be useful for minimizing non-specific primer extension. Specifically, the optimal growth temperature for *Pyrodictium occultum* and *P. abyssi* is 100-105°C, approximately 30-35°C higher than, for example, *Thermus aquaticus*. Consequently, the residual activity of *Pyrodictium* DNA polymerases at room temperature is expected to be minimal and may eliminate the need to segregate at least one reagent prior to the first cycle of PCR. Thus, the present invention offers the potential of reduced non-specific extension at non-stringent annealing temperatures in a PCR without the use of wax barriers or other means of reagent segregation.

Those of skill in the art will recognize that the present invention provides novel compositions for the practice of any methods for which a DNA polymerase has utility. In a preferred embodiment, the enzymes are useful for amplifying nucleic acid sequences by PCR. Other amplification methods, particularly those requiring a heat denaturation step such as PLCR (Barany, 1991, PCR Methods and Applications 1(1):5-13) or gap-LCR (see, for example, PCT Patent Publication No. 90/01069, published February 8, 1990) will also benefit from the present invention. Cycle sequencing methods (Caruthers et al., 1989, BioTechniques 7:494-499, and Koop et al., 1992, BioTechniques 14:442-447, will particularly benefit from 3'-5' exonuclease deficient Pab and Poc DNA polymerase enzymes.

The present invention also provides kits comprising a thermostable DNA polymerase of the present invention, preferably a stable enzyme composition comprising said polymerase in a buffer containing one or more non-ionic polymeric detergents, and optionally further reagents useful for performing a PCR reaction, such as a set of primers, probes or nucleoside triphosphate precursors.

Pyrodictium DNA polymerase is very useful in carrying out the diverse processes in which amplification of a nucleic acid sequence by the polymerase chain reaction is useful. Such methods include cloning, DNA sequencing, reverse transcription and asymmetric PCR. Further, the enzymes of the invention are suitable for use in diagnostic, forensic, and research applications. The following examples are offered by way of illustration only and are by no means intended to limit the scope of the claimed invention.

Example 1

Construction of a Genomic *Pyrodictium Abyssi* DNA Library and Identification of the Pab Polymerase Gene by a Colony Blot Thermostable DNA Polymerase Activity Assay

Pyrodictium abyssi cells were received from Dr. Karl O. Stetter, University Regensburg, Regensburg, Germany. The isolate, AVZ (DSM6158) is described in Pley et al., 1991, System Applied Microbiology 14:245-253, DNA was purified by the method described in Lawyer et al., 1989, J. Biological Chemistry 264(11):6427-6437. About 25µg of *Pyrodictium abyssi* DNA was partially digested with the restriction enzyme Sau3AI and size-fractionated by gel electrophoresis. Ten ng of fragments which were larger than 3.5 kb and smaller than

8.5 kb were used for cloning into the BamHI site of pUC19 vector (Clontech, Palo Alto, CA). The pUC19 plasmid vector has the lac promoter upstream from the BamHI cloning site. The promoter can induce heterologous expression of cloned open reading frames lacking promoter sequences. The recombinant plasmids were transformed into E. coli SURE cells (Stratagene). Genotype of SURE[®] cells: mcrA, Δ (mcrBC-hsdRMS-mrr) 171, endA1, supE44, thi-1, λ^- , gyrA96, relA1, lac, recB, recJ, sbcC, umuC::Tn5(kan^R), urvC, (F', proAB, lacI Z Δ M15, Tn10[tet^R]).

A rapid filter assay or the detection of thermoresistant and thermophilic DNA polymerase activity was used to screen the *Pyrodictium abyssi* genomic DNA library (Sagner et al., 1991, Gene 97:119-123). According to the method, recombinant colonies are bound to nitrocellulose membrane and are incubated at elevated temperature in a polymerization buffer containing α [³²P]-labeled dNTPs. By autoradiography of the dried filters, colonies which express thermophilic DNA polymerase activity can be directly identified. The membrane-bound colonies are heated to 95°C to irreversibly inactivate host DNA polymerases and are subsequently incubated at elevated temperatures to reveal the presence of thermophilic DNA polymerase activity.

Approximately 500 colonies were plated per petri dish and grown overnight at 37°C. Subsequently, the colonies were replica-plated onto nitrocellulose membranes and grown for 4 hours. The membranes were placed upside down on agarose plates which were placed for 20 minutes at room temperature on filter papers soaked with a mixture of chloroform/toulene (1:1). The membranes containing the permeabilized colonies were then incubated at 95°C for 5 minutes in a polymerization buffer containing 50 mM Tris-HCl pH 8.8, 7 mM MgCl₂, 3 mM β -mercaptoethanol (β Me) to inactivate any nonthermoresistant (e.g., E. coli) DNA polymerase activity. Immediately after inactivation the membranes were transferred to the polymerization buffer containing 50 mM Tris-HCl pH 8.8, 7 mM MgCl₂, 3 mM β Me, 12 μ M dCTP, 12 μ M dGTP, 12 μ M dATP, 12 μ M dTTP, and 1 μ Ci per ml α [³²P]-dGTP. After incubation for 30 minutes at 65°C the membranes were washed twice for 5 minutes in a solution of 5% (w/v) TCA and 1% (w/v) pyrophosphate to remove unincorporated α [³²P]-dGTP. The membranes were analyzed by autoradiography at -70°C. Seven clones were apparent on X-ray films of duplicated membranes after 3 days.

Plasmid DNAs were isolated from these 7 clones, restriction analysis was performed to determine the size and orientation of insert fragments relative to the pUC19 vector. DNA sequence analysis was performed on the largest clone, pPab14. The "universal" forward and reverse sequencing primers, Nos. 1212 and 1233, respectively, purchased from New England BioLabs, Beverly, MA, were used to obtain preliminary DNA sequences. From the preliminary DNA sequence, further sequencing primers were designed to obtain DNA sequence of more internal regions of the cloned insert. DNA sequence analysis has been performed for both strands.

Example 2Expression of the Pab Polymerase Gene

Plasmid pDG168 is a λ P_L cloning and expression vector that comprises the λ P_L promoter and gene N ribosome-binding site (see, U.S. Patent No. 4,711,845), a restriction site polylinker positioned so that the sequences cloned in to the polylinker can be expressed under control of the λ P_L-N_{RBS}, and a transcription terminator from the *Bacillus thuringiensis* delta-toxin gene (see, U.S. Patent No. 4,666,848). Plasmid pDG168 also carries a mutated RNA II gene which renders the plasmid temperature sensitive for copy number (see, U.S. Patent No. 4,631,257), and an ampicillin resistance gene in *E. coli* K12 strain DG116. The construction of pDG168 is described in PCT Patent Publication No. WO 91/09950, published July 11, 1991, at Example 6.

These elements act in concert to provide a useful and powerful expression vector. At 30-32°C, the copy number of the plasmid is low, and in a host cell that carries a temperature sensitive λ repressor gene, such as cI857 the P_L promoter does not function. At 37-41°C, however, the copy number of the plasmid is 25-50 fold higher than at 30-32°C, and the cI857 repressor is inactivated allowing the promoter to function. Thus, pDG168 was selected for constructing expression vectors for Pab DNA polymerase.

The DNA sequence analysis of pPab14 revealed an open reading frame of 803 amino acids having an ATG start codon at nucleotide position 869 and a TGA stop codon at nucleotide position 3280. The 5' end of the Pab gene was mutagenized with oligonucleotide primers AW397 (SEQ ID No. 5) and AW398 (SEQ ID No. 6) by PCR amplification (as described below). AW397 (SEQ ID No. 5) is forward primer which was designed to alter the Pab DNA sequence at the ATG start to introduce an NdeI restriction site. Primer AW397 (SEQ ID No. 5) also introduced mutations in the fifth and sixth codons of the Pab polymerase gene sequence to be more compatible with the codon usage of *E. coli*, without changing the amino acid sequence of the encoded protein. The reverse primer, AW398 (SEQ ID No. 6), was chosen to include a SpeI site corresponding to amino acid position 174. In addition, a KpnI site was introduced after the SpeI site.

The PCR reaction mixture contained 10 ng of SalI linearized pPab14 DNA as the template; 10 pmol of primers AW397 (SEQ ID No. 5) and AW398 (SEQ ID No. 6); 50 μ M of each dATP, dCTP, dTTP, and dGTP; 2 mM MgCl₂; 10 mM Tris-HCl, pH 8.3; 50 mM KCl and 1 unit Taq polymerase in 50 μ l reaction volume. The reaction thermo-profile was 95°C for 30 seconds; 65°C for 30 seconds and 72°C for 30 seconds and amplified for 12 cycles. The 500 bp amplified product was digested with NdeI and KpnI and loaded on an 1% (w/v) Seakem agarose gel. The PCR product fragment was purified with Geneclean kit (Bio 101, San Diego, CA) and subcloned into expression vector pDG168, which had been digested with NdeI and KpnI. The resulting clone was named pAW111. The desired mutations were confirmed via restriction enzyme analysis and DNA sequence analysis.

The 3' end of the Pab polymerase gene was modified via restriction enzyme digestion and use of a synthetic oligonucleotide duplex. AW399 (SEQ ID No. 7) was designed

according to the 3' end of the Pab polymerase (pol) gene from the AflII site at amino acid position 785-786. It changes the TGA stop codon to TAA as well. AW400 (SEQ ID No. 8) is the complementary strand of AW399 (SEQ ID No. 7) except that it has XmaI cohesive end at its 5' end. When AW399 (SEQ ID No. 7) anneals to AW400 (SEQ ID No. 8), it produces a 60 bp synthetic duplex with 5' cohesive AflII/XmaI ends. The duplex was then cloned into plasmid pPab2 that have been digested with AflII and XmaI. The resulting plasmid was designated pAW113. Plasmid Pab2 was one of the 7 clones isolated from the genomic library as described in Example 1. Plasmid Pab2 contains the entire Pab pol gene but is ~250 bp shorter than Pab14 at the 5' end. Thus, it lacks a flanking 5'-end AflII site which facilitated the cloning strategy of replacing the 3' end AflII - XmaI fragment with the synthetic duplex AW399 (SEQ ID No. 7)/AW400 (SEQ ID No. 8) as described above. The DNA sequence of the replaced fragment was confirmed by DNA sequence analysis.

Finally, the 1.89 kb fragment of the Pab polymerase gene region, SpeI through the stop codon was isolated from pAW113 by digestion with SpeI and XmaI, and purified via gel electrophoresis. The resulting fragment was ligated with plasmid pAW111 that had been digested with SpeI and XmaI.

The ligation condition was 20 µg/ml DNA, 20 mM Tris-HCl, pH 7.4, 50 mM NaCl, 10 mM MgCl₂, 40 µM ATP and 0.2 Weiss unit T4 DNA ligase per 20 µl reaction at 16°C overnight. Ligations were transformed into DG116 host cells. Candidates were screened for appropriate restriction enzyme sites. The desired plasmid was designated pAW115.

The oligonucleotides used in this example are shown below.

AW397	SEQ ID No. 5	5'-GGACCCATATGCCAGAAGCTATTGAATTCGTGCTCC
AW398	SEQ ID No. 6	5'-GGCAGGTACCACTAGTTATGTCCGGCAATAGGCTC
AW399	SEQ ID No. 7	5'-TTAAGGCAGCATCATCTGGGCATAGGAGTCT- CTTCGACTTCTTCGCGGCAAAGAAGTAAC
AW400	SEQ ID No. 8	5'-CCGGGTTACTTCTTTGCCGCGAAGAAGTCGAAGAGACT- CCTATGCCCAGATGATGCTGCC

Example 3

Cloning the Pyrodictium Occultum (Poc) DNA Polymerase Gene

Pab and Poc genomic DNA (0.5 µg each) were digested with HindIII, and were separated by gel electrophoresis through an 0.8% (w/v) agarose gel. Pyrodictium occultum cells were received from Dr. Karl O. Stetter, University Regensburg, Regensburg, Germany. DNA was purified by the method described in Lawyer et al., 1989, J. Biological Chemistry 264(11):6427-6437. The DNA fragments in the gel were denatured in 1.5 M NaCl and 0.5 M NaOH solution for 30 minutes and were neutralized in a solution of 1 M Tris-HCl, pH 8.0 and 1.5 M NaCl for 30 minutes, and then were transferred to a Biodyne nylon membrane (Pall Biosupport, East Hills, NY) using 20 x SSPE (3.6 M NaCl, 200 mM NaPO₄/pH 7.4, 20 mM EDTA/pH 7.4). The DNA attached to the membrane was then hybridized to a ³²P-labelled 240 bp PCR product which encoded amino acids 515-614 of the Pab polymerase gene. The prehybridization solution

was 6 x SSPE, 5X Denhardt's reagent, 0.5% (w/v) SDS, 100 µg/ml denatured, sheared, salmon sperm DNA. Hybridization solution was the same except that Denhardt's reagent was used at 2X, and contained 10⁶ cpm ³²P-labeled PCR-amplified probe. Prehybridization and hybridization were both at 55°C. The blot was washed sequentially as follows: 2 x
5 SSPE, 0.5% (w/v) SDS, 10 minutes at room temperature; 2 x SSPE, 0.1% (w/v) SDS, 15 minutes at room temperature; 0.1% (w/v) SSPE, 0.1% (w/v) SDS, 5 minutes at room temperature.

A strong signal was apparent at approximately 3.8 kb in the HindIII digest. This suggested that the Poc polymerase gene has homology with the Pab polymerase gene. Consequently, several PCR primers, designed from the Pab polymerase gene sequence, were
10 evaluated for amplification of portions of the Poc polymerase gene. A specific PCR product, 295 bp in size resulted from a PCR using primer pair LS417 (SEQ ID No. 34) and LS396 (SEQ ID No. 35).

LS417 SEQ ID No. 34 5'-GATAAAGATAGACAAGGTATAC
15 LS396 SEQ ID No. 35 5'-CGTATTCCTCGATTCTCTTT
AW394 SEQ ID No. 9 5'-GCTTATAGCCTTGTCCACGTTC

The PCR was performed at final concentration of 1 X PCR buffer, 50 µM dNTPs, 0.1 µM each primers, 1.25 units Taq in a total volume of 50 µl. 1 X PCR buffer contains 20 mM Tris pH 8.4, 50 mM KCl, 2 mM MgCl₂. The reaction was amplified for 35 cycles.

20 The 295 bp PCR product was then subjected to DNA sequence analysis. The DNA sequence result showed that the Poc polymerase gene has 78% identity with the Pab polymerase gene in this region. A Poc polymerase specific oligonucleotide probe AW394 (SEQ ID No. 9) was designed using this DNA sequence data. The ³²P-labeled AW394 (SEQ ID No. 9) was then used to screen a genomic Poc DNA bank to obtain Poc polymerase clones. The
25 constriction of the genomic Poc DNA bank was as described in Example 1 for the genomic Pab DNA bank.

About 5,500 ampicillin-resistant colonies were selected on nitrocellulose filters and hybridized with ³²P-labeled AW394 (SEQ ID No. 9). Plasmid DNA was isolated from 6 colonies that hybridized with the probe. Prehybridization and hybridization conditions were
30 as described above. Wash conditions were 6 x SSPE, 0.1% (w/v) SDS for 5 minutes at room temperature and followed by 2 x SSPE, 0.1% (w/v) SDS for 15 minutes at 55°C. Restriction enzyme analysis and PCR analysis were performed to determine the size and orientation of insert fragment relative to the pUC19 vector. The results revealed that pPoc3 and pPoc5 are identical clones. The sizes of the coding region, 5' end non-translated region and 3' end non-translated region of all identified Poc polymerase clones are listed below.
35

	<u>Coding Region</u>	<u>5'-end</u>	<u>3'-end</u>
	pPoc1 1.9 kb	0	3.6 kb
	pPoc2 1.9 kb	0	4.2 kb
	pPoc4 2.4 kb	0.4 kb	0.7 kb
40	pPoc5 0.35 kb	0	4.5 kb
	pPoc6 0.35 kb	0	3.2 kb
	pPoc8 0.7 kb	3 kb	0

DNA sequence analysis was performed on pPoc4. Universal and reverse sequencing primers were used to obtain preliminary DNA sequence information. From this DNA sequence additional sequencing primers were designed to obtain the DNA sequence of more internal regions of the insert. DNA sequence analysis has been performed for both strands.

5

Example 4

Expression of the Poc Polymerase Gene

The 5' end of the Poc polymerase gene in plasmid pPoc4 was mutagenized with oligonucleotide primers AW408 (SEQ ID No. 10) and AW409A (SEQ ID No. 11) via PCR amplification. AW408 (SEQ ID No. 10) is a forward primer designed to alter the DNA sequence of the Poc gene at the ATG start codon to introduce an NsiI restriction site. AW408 (SEQ ID No. 10) also was designed to introduce alterations in the second, third, fifth, and sixth codons of the Poc gene to provide a sequence more compatible with the codon usage of E. coli without changing the amino acid sequence of the encoded protein. The reverse primer AW409A (SEQ ID No. 11) was chosen to include an XbaI site at amino acid position 38. In addition, a KpnI site was introduced after the XbaI site for subsequent subcloning.

Plasmid pPoc4, linearized with KpnI, was used as the PCR template for amplification using the AW408 (SEQ ID No. 10)/AW409A (SEQ ID No. 11) primer pair, yielding a 138 bp PCR product. The PCR amplification procedure was as described above at Example 2. The amplified fragment was digested with NsiI, then treated with Klenow to create a blunt end at the NsiI-cleaved end, and finally digested with KpnI. The resulting fragment was ligated with expression vector pDG164 (which is described in detail in PCT Patent Publication No. WO 91/09950, at Example 6b, that has been digested with NdeI, repaired with Klenow, to fill in the overhang and provide a blunt end for ligation, and then digested with KpnI. The ligation yielded an in-frame coding sequence of the 5' end of the Poc polymerase gene under control of the λP_L promoter and bacteriophage T₇ gene 10 ribosome binding site. The resulting construct was designated pAW118.

To effect subcloning of the 3' end of the Poc polymerase gene, a KpnI site was introduced after the stop codon. This was done by a PCR process as follows. The forward primer was chosen to include an EspI site at amino acid position 698-699, and the reverse primer was designed to incorporate a KpnI site immediately following an altered stop codon (TAA). The amplified 335 bp fragment was digested with EspI and KpnI, and cloned into plasmid pPoc4 digested with EspI and KpnI. The resulting construct was designated pAW120.

Finally, the Poc pol gene region XbaI through the stop codon was isolated from pAW120 by digestion with XbaI and KpnI. The resulting 2.3 kb fragment was ligated with pAW118 that had been digested with Xba and KpnI. The ligation product was transformed into DG116 host cells for expression and designated pAW121.

The oligonucleotides used in this example are given below.

AW408	SEQ ID No. 10	GGACCATGCATGACTGAACTATTGAATTCGTGCTG
AW409A	SEQ ID No. 11	GGAAGGTACCTGATCATCTAGAAGCACGACACGTT
AW410	SEQ ID No. 12	GGAAGCTGAGCAAGAGGATAGAGG

40

- 25 -

AW411A SEQ ID No. 13 GGAAGGTACCTTATTTCTTTGAGGCGAAGAAG

Example 5Expression of Pab pol Gene and Poc pol Gene in Tryptophan Promoter Vector

Both the Pab pol gene and the Poc pol gene can be over-expressed under the control of the E. coli Trp promoter. Construction of the expression clones was performed as follows: The λ PL promoter in expression clone, pAW115, was replaced by a Trp promoter sequences which was generated by PCR amplification using plasmid pLSG10 (plasmid pLSG10 is described in U.S. Patent No. 5,079,352,) as template and AW500 (SEQ ID No. 14) and AW501 (SEQ ID No. 15) as primers. primers.

The resulting PCR product was digested with NspV and NdeI and cloned into NspV and NdeI digested pAW115 to give rise to a Pab pol expression clone, pAW118, under control of the E. coli Trp promoter.

An internal NdeI site in the Poc pol gene of pAW121, complicates of the exchange NspV - NdeI λ PL promoter fragment and the Trp promoter fragment. Therefore, primers AW500 (SEQ ID No. 14) and AW502 (SEQ ID No. 16) were designed to amplify the Trp promoter sequence fragment from pLSG10 and primers AW503 (SEQ ID No. 17) and AW504 (SEQ ID No. 18) were designed to amplify the 5' end 110 bp NdeI - XbaI fragment from pAW121. AW502 (SEQ ID No. 16) and AW503 (SEQ ID No. 17) overlap by 9 nucleotides. Using overlap extension PCR, the Trp promoter fragment and the 5' end 110 bp fragments were fused. The resulting PCR product was digested with NspV and XbaI and cloned into pAW121 which had been was digested with NspV and XbaI. The resulting Poc pol expression clone was named pAW123.

AW500	SEQ ID No. 14	TTTTTCGAAAGAAGAAAAAACC
AW501	SEQ ID No. 15	TCTCATATGCTTATCGATACCC
25 AW502	SEQ ID No. 16	CATAAGCTTATCGATACCCTT
AW503	SEQ ID No. 17	AAGCTTATGACAGAGACTATAGAGTT
AW504	SEQ ID No. 18	GTGGTCTAGAAGCACGACACGT

Example 6Assessment of 3'-5' Exonuclease Activity: A Fidelity Assay

Because of the dramatic levels of amplification provided by the PCR process (up to 10^{11} to 6×10^{12} -fold), for certain applications the accuracy of replication (fidelity) is important. PCR fidelity is based on a two step process: misinsertion and misextension. If the DNA polymerase inserts an incorrect base and the resulting 3'-mismatched terminus is not extended, this truncated extension product cannot be amplified since the binding site for the downstream primer is not present. DNA polymerases extend a mismatched 3'-terminus more slowly than a matched 3'-terminus. In addition, different mismatches extend at disparate rates. See Kwok et al., 1990, Nuc. Acids Res. 18:999-1005, and Huang et al., 1992, Nuc. Acids Res. 20:4567-4573.

DNA polymerases with inherent 3' to 5' exonuclease or proofreading activity are able to improve fidelity by removing misinserted bases before extension. A convenient PCR and restriction endonuclease digestion assay has been developed to assess the ability of DNA polymerases with 3' to 5' exonuclease activity to remove 3'-terminal mismatched nucleotides prior to misextension. Several primers were designed which were either perfectly matched or 3'-mismatched (with every possible combination) to the first nucleotide of the BamHI restriction enzyme recognition sequence in the *Thermus aquaticus* DNA polymerase gene (Lawyer et al., 1989, J. Biol. Chem. 264:6427-6437 and U.S. Patent No. 5,079,352). The perfect match primers, FR434 (SEQ ID No. 29) and FR438 (SEQ ID No. 33), amplify a 151 bp product that is completely digested with BamHI restriction enzyme to generate 132 bp and 19 bp DNA fragments. The 3'-terminal nucleotide of forward primer FR434 (SEQ ID No. 29) corresponds to nucleotide 1778 of the Taq DNA pol gene. Forward primers FR435 (SEQ ID No. 30), FR436 (SEQ ID No. 31), and FR437 (SEQ ID No. 32) contain a single 3'-terminal mismatch with respect to the wild-type Taq DNA pol gene and wild-type primer FR438 (SEQ ID No. 33) extension products, corresponding to A:C, T:C, and C:C mismatches, respectively. Any incorrect or misextension from primers FR435 (SEQ ID No. 30), FR436 (SEQ ID No. 31), or FR437 (SEQ ID No. 32) eliminates the BamHI recognition site corresponding to nucleotides 1778 - 1783 of the Taq DNA pol gene. Alternatively, exonucleolytic proofreading removes the 3'-terminal mismatched nucleotides and permits incorporation of the correct dG residue, resulting in the accumulation of PCR products that now contain the diagnostic BamHI restriction enzyme site. Since all of the FR435 (SEQ ID No. 30), FR436 (SEQ ID No. 31), or FR437 (SEQ ID No. 32) primers are mismatched to the original target, this PCR/endonuclease digestion assay requires exonucleolytic proofreading in every cycle to correct the "mutant" primers and generate a PCR product that contains the diagnostic BamHI cleavage site. Misextension at any cycle will generate an efficiently copied (now mutant) template in the succeeding cycle (from primer FR438 [SEQ ID No. 33] extension) that is perfectly matched to all of the primers in the assay.

*

FR434	SEQ ID No. 29	5'-GCACCCCGCTTGGGCAGAG
FR435	SEQ ID No. 30	5'-GCACCCCGCTTGGGCAGAA
FR436	SEQ ID No. 31	5'-GCACCCCGCTTGGGCAGAT
FR437	SEQ ID No. 32	5'-GCACCCCGCTTGGGCAGAC
FR438	SEQ ID No. 33	5'-TCCCGCCCCTCCTGGAAGAC

Primer FR434 (SEQ ID No. 29) corresponds identically to nucleotides 1760 through 1778 of the Taq DNA polymerase gene, and primer FR438 (SEQ ID No. 33) is complementary to nucleotides 1891 through 1910 of the Taq DNA polymerase gene. Primers FR435 (SEQ ID No. 30), FR436 (SEQ ID No. 31), and FR437 (SEQ ID No. 32) correspond identically to nucleotides 1760 through 1777 of the Taq DNA polymerase gene and contain the indicated (by *, underlined) 3'-terminal mismatched nucleotide at position 1778.

Recombinant Pab and Poc DNA polymerases were purified from E. coli K12 strain DG116 harboring plasmids pAW115 or pAW121, respectively. The purification involved cell lysis, heat treatment at 75-85°C, polymyxin P precipitation of bulk nucleic acids, Phenyl Sepharose chromatography and Heparin Sepharose chromatography, according to Example 9.

Using this fidelity assay, wild-type recombinant Pab and Poc DNA polymerases are able to correct mismatch primers FR435 (SEQ ID No. 30), FR436 (SEQ ID No. 31) and FR437 (SEQ ID No. 32) to generate PCR product that contains the requisite BamHI cleavage site, demonstrating the presence of 3' to 5' exonucleolytic proofreading activity.

Example 7

Production of 3'-5' exonuclease mutants of Pab pol and Poc pol

Pab and Poc pol genes lacking 3'-5' exonuclease activity were constructed using site-directed mutagenesis by overlap extension PCR to alter the codons for Asp187 and Glu189 to code for alanine. Briefly, mutagenesis by overlap extension PCR involves the generation of DNA fragments that, by virtue of having incorporated complementary oligo primers in independent PCR reactions (see, Higuchi et al., 1988, Nuc. Acids Res. 16:7351-7367, and Ho et al., 1989, Gene 77:51-59, for a detailed description of this method). According to the method, these fragments are combined in a subsequent "fusion" reaction in which the overlapping ends anneal, allowing the 3' overlap of each strand to serve as a primer for the 3' extension of the complementary strand. The resulting fusion product is amplified further by PCR. Specific alterations in the nucleotide sequence can be introduced by incorporating nucleotide changes into the overlapping oligo primers.

The construction of a 3'-5' exonuclease minus mutant of Pab was accomplished as follows. The two overlapped primers AW493 (SEQ ID No. 20) and AW494 (SEQ ID No. 21) were designed to span Asp187 and Glu189, in which both Asp187 and Glu189 are replaced by alanine. The two external primers, AW492 (SEQ ID No. 19) and AW495 (SEQ ID No. 22), were chosen to locate at the unique SpeI and NsiI restriction sites at amino acid position 174-175 and amino acid position 304-305, respectively, thus making it possible to ligate the fusion product back into the expression vector. The products from the PCR using primer sets AW492 (SEQ ID No. 19)/AW493 (SEQ ID No. 20) and AW494 (SEQ ID No. 21)/AW495 (SEQ ID No. 22) were 70 bp and 373 bp fragments, respectively. The resulting two fragments (27 nucleotide 3' overlap) were fused by denaturing and annealing them in a subsequent primer extension reaction. The 416 bp fusion product was amplified further by PCR using the two external primers AW492 (SEQ ID No. 19) and AW495 (SEQ ID No. 22). The mutagenized 416 bp fragment was then cut with SpeI and NsiI and ligated back into the parent clone pAW115 which had also been digested with SpeI and NsiI. The resulting mutant clone was named pexo-Pab, and the desired mutations were confirmed by sequence analysis.

Similarly, the 3'-5' exonuclease minus mutant of Poc was constructed using the same approach. The overlapping primer pair used to introduce the mutation are AW489 (SEQ ID No. 24) and AW490 (SEQ ID No. 25). The two external primers, AW488 (SEQ ID No. 23) and AW491 (SEQ ID No. 26) are located at the unique XbaI and BssHII restriction sites at amino acid positions 37-39 and 260-262, respectively. The products from PCR using primer sets AW488 (SEQ ID No. 23)/AW489 (SEQ ID No. 24) and AW490 (SEQ ID No. 25)/AW491 (SEQ ID No. 26) were 476 bp and 243 bp fragments, respectively. These two fragments were fused and subjected to PCR amplification using the external primers AW488 (SEQ ID No. 23) and AW491 (SEQ ID No. 26). The mutagenized fragment was then cut with XbaI and BssHII and ligated back into the parent clone pAW121. The resulting mutant clone was named pexo-Poc.

The exonuclease activities of the exo-Pab DNA polymerase and exo-Poc DNA polymerase were determined using the mismatch incorporation proofreading assay. The results showed that both the exo-Pab pol and exo-Poc pol lacked the 3'-5' exonuclease activity.

AW492	SEQ ID No. 19	5'-TATTGCCGACATAACTAGTATAGA
AW493	SEQ ID No. 20	5'-ACTGTAGACCGCGATCGCGAACGCGAGC
AW494	SEQ ID No. 21	5'-CTCGCGTTCGCGATCGCGGTCTACAGTAAGAGAG
AW495	SEQ ID No. 22	5'-TTATCTCATGCATTTCTCTCC
AW488	SEQ ID No. 23	5'-GTGTCGTGCTTCTAGACCA
AW489	SEQ ID No. 24	5'-GCTATACACCGCGATCGCAAAAGCTACCAGC
AW490	SEQ ID No. 25	5'-GGTAGCTTTTGCGATCGCGGTGTATAGCAGGA
AW491	SEQ ID No. 26	5'-TACGGGCGCGCTCCATTAG

Example 8

Thermostability comparison of Pab pol, Poc pol and Taq pol in PCR

The upper growth temperature of hyperthermophilic genus Pyrodictium is 110°C. To test the thermostability of purified recombinant Pab pol, Poc pol and Taq pol in the PCR process, the following experiment was performed: 0.1 pg, 1 pg, and 10 pg of M13 DNA (New England Biolabs, Beverly, MA) were used as templates for PCR analysis by Pab, Poc and Taq. The reactions were subjected to 25, 30, 35 and 40 cycles at denaturing temperatures of 95°C or 100°C. A PCR product of 350 bp was generated by using BW36 (SEQ ID No. 27) and BW42 (SEQ ID No. 28) as primers.

BW36 SEQ ID No. 27 5'-CCGATAGTTTGAGTTCTTCTACTCAGGC
 BW42 SEQ ID No. 28 5'-GAAGAAAGCGAAAGGAGCGGGCGCTAGGGC
 PCR was performed at a final concentration of 1 x PCR buffer, 50 µM dNTPs, 0.1 µM each primers, 0.25 units Pab or 0.1 units Poc or 1.25 units Taq in a total reaction volume of 50 µl.

A unit of Pab DNA polymerase and a unit of Poc DNA polymerase is defined, like for Taq DNA polymerase, as the amount of enzyme that will incorporate 10 nmoles total

dNTPs into acid insoluble material per 30 minutes at 74°C. Poc and Pab DNA polymerases are assayed as described in U.S. Patent No. 4,889,818, for Taq DNA polymerase with the following changes in reaction components. Pab DNA polymerase: Tris-HCl pH 8.3 (25°C), 100 mM KCl, 5 mM MgCl₂. Poc DNA polymerase: Tris-HCl pH 8.0 (25°C), 10 mM KCl, 5 mM MgCl₂. 1 x PCR buffer for Pab contains: 20 mM Tris-HCl, pH 8.4, 100 mM KCl, 1.5 mM MgCl₂. 1 x PCR buffer for Poc contains: 20 mM Tris-HCl, pH 8.4, 10 mM KCl, 1.0 mM MgCl₂. 1 x PCR buffer for Taq contains: 20 mM Tris, pH 8.4, 50 mM KCl, 1.5 mM MgCl₂. The amplification profile involved denaturation at 95°C or 100°C for 30 seconds, primer annealing and extension at 55°C for 30 seconds. The results showed that both Pab pol and Poc pol were extremely thermostable, functioning effectively in the PCR with denaturing temperature up to 100°C. In contrast, Taq pol produced no product under these conditions at 100°C.

Example 9

Purification of Recombinant Pyrodictum DNA Polymerase

Recombinant Pyrodictum DNA polymerase is purified as follows. Briefly, cells are thawed in 1 volume of TE buffer (50 mM Tris-HCl, pH 7.5, and 1.0 mM EDTA with 1 mM DTT), and protease inhibitors are added (PMSF [phenylmethylsulfonyl fluoride] to 2.4 mM, leupeptin to 1 µg/ml, and TLCK [(*-*)-1-chloro-3-tosylamido-7-amino-2-heptanone hydrochloride] to 0.2 mM). The cells are lysed in an Aminco french pressure cell at 20,000 psi and sonicated to reduce viscosity. The sonicate is diluted with TE buffer and protease inhibitors to 5.5 X wet weight cell mass (Fraction I), adjusted to 0.2 M ammonium sulfate, and brought rapidly to 85°C and maintained at 85°C for 15 minutes. The heat-treated supernatant is chilled rapidly to 0°C, and the E. coli cell membranes and denatured proteins are removed following centrifugation at 20,000 X G for 30 minutes. The supernatant containing Pyrodictum DNA polymerase (Fraction II) is saved. The level of Polymyxin P^{*} necessary to precipitate >95% of the nucleic acids is determined by trial precipitation (usually in the range of 0.6 to 1% w/v). The desired amount of Polymyxin P is added slowly with rapid stirring at 0°C for 30 minutes and the suspension centrifuged at 20,000 X G for 30 min. to remove the precipitated nucleic acids. The supernatant (Fraction III) containing the Pyrodictum DNA polymerase is saved.

Fraction III is adjusted to 0.3 M ammonium sulfate and applied to a Phenyl Sepharose column that has been equilibrated in 50 mM Tris-HCl, pH 7.5, 0.3 M ammonium sulfate, 10 mM EDTA, and 1 mM DTT. The column is washed with 2 to 4 column volumes of the same buffer (A₂₈₀ to baseline), and then 1 to 2 column volumes of TE buffer containing 50 mM KCl to remove most contaminating E. coli proteins. Pyrodictum DNA polymerase is then eluted from the column with buffer containing 50 mM Tris-HCl, pH 7.5, 2 M urea, 20% (w/v) ethylene glycol, 10 mM EDTA, and 1 mM DTT, and fractions containing DNA polymerase activity are pooled (Fraction IV).

* Trade Mark

Final purification of recombinant *Pyrodictium* DNA polymerase is achieved using Heparin Sepharose chromatography, anion exchange chromatography, or Affigel^{*} blue chromatography. Recombinant *Pyrodictium* DNA polymerase may be diafiltered into 2.5X storage buffer (50 mM Tris-HCl pH 8.0, 250 mM KCl, 2.5 mM DTT, 0.25 mM EDTA, 0.5% [w/v] Tween20), combined with 1.5 volumes of sterile 80% (w/v) glycerol, and stored at -20°C.

Example 10

Thermostability of *Pyrodictium occultum* DNA polymerase

The thermal stability of the *Pyrodictium occultum* DNA polymerase was assessed by measuring the activity after incubations at 100°C for varying lengths of time. The DNA polymerase was incubated in a mixture intended to mimic PCR amplification conditions, but chosen such that no DNA synthesis occurred. The enzyme mixture contained the following reagents:

10 mM Tris-HCl pH 8.0
50 mM KCl
200 µM dATP
1 mM MgCl₂
0.1 µg single-stranded DNA
20 pmoles primer (30 base oligomer)

To measure activity, 5 µl of incubated enzyme mixture was added to 45 µl of reaction mixture consisting of the following reagents:

10 mM Tris pH 8.0
6 mM MgCl₂
75 mM KCl
1 mM beta-mercaptoethanol
200 µM each dATP, dTTP, and dGTP
200 µM [α -³³P]dCTP
2.5 µg activated salmon sperm DNA

Activity was measured as the amount of dNMP incorporated in 10 minutes at 75°C.

In one experiment, incubations were carried out for 0, 1, 2, and 4 hours. Reactions incubated for less than 4 hours were held on ice until all incubations were completed so that all activity assays were carried out together. The measured activities are provided below represented as the fraction of the initial activity remaining after each high temperature incubation.

<u>Hours</u>	<u>Relative Activity (%)</u>
1	93
2	116
4	104

* Trade Mark

A similar experiment was carried out using incubations of 0, 1, 2, 3, 4, 6, 7, and 8 hours at 100°C; the results are provided below.

	<u>Hours</u>	<u>Relative Activity (%)</u>
5	1	86
	2	82
	3	86
	4	67
	6	82
	7	104
10	8	104

No detectable loss in activity was observed even after an 8 hour incubation at 100°C. The thermal stability of the DNA polymerase from *Pyrodictium abyssi* is expected to be similar.

15

Example 11

Exo-minus Deletion Mutants

Amino(N)-terminal deletion mutant DNA polymerases were created which lack exonuclease activity while retaining polymerase activity. Three "mini" Pab DNA polymerases were produced in which 366, 386, and 403 amino acids were deleted, producing 48, 46, and 44 kilodalton (kDa) proteins, respectively. The mutant polymerase genes were created and expressed as described below.

Subsequences of the full length sequences that encodes the Pab DNA polymerase were amplified from expression plasmid pAW115 using the primers shown below. Each of the upstream primers, AW594, AW593, and AW576, introduces an ATG start codon, introduces an Nde I restriction site before the ATG start codon, and introduces some alterations in the first six codons to provide a sequence more compatible with the codon usage of *E. coli* without changing the amino acid sequence of the encoded protein. Primer AW594 introduces the ATG start codon between amino acid positions 367 and 368, resulting in a 366 amino acid deletion mutant. Similarly, primer AW593 introduces the ATG start codon between amino acid positions 387 and 388, resulting in a 386 amino acid deletion mutant, and primer AW576 introduces the ATG start codon between amino acid positions 404 and 405, resulting in a 403 amino acid deletion mutant. A single downstream primer, AW577, was used for each amplification that includes an Apa I site corresponding to amino acid position 454. The sequences of the primers are provided below, shown 5' to 3'.

35

<u>Primer</u>	<u>Seq ID No.</u>	<u>Sequence</u>
AW594	36	TTCGCATATGCCATTTGCAATACAACCTTTCGACAGTAACC
AW593	37	TTCGCATATGGGTGTAGGTTTTTCGTCTAGAATGGTAC
AW576	38	CGCATATGAACGAACTGGTTCCCAACCGTGTCAAG
AW577	39	GTCAGGGCCCACATTGTACTT

Each amplification was carried out in a 50 µl reaction volume using 100 pg of linearized pAW115 as template under the following conditions: 10 pmol each primer; 50 µM each dNTP, 1.5 mM MgCl₂; 10 mM Tris-HCl, pH 8.8; 10 mM KCl; and 1 U UITma DNA
5 polymerase (Perkin Elmer, Norwalk, CT). The temperature profile for the amplification was 20 cycles each consisting of 95°C for 30 seconds and 55°C for 30 seconds.

The amplified products were digested with Nde I and Apa I and purified using agarose gel electrophoresis. The purified products were subcloned into pAW115 which had been digested with Nde I and Apa I, thereby replacing the original 1364 base fragment with either
10 the 266, 206, or 155 base amplified inserts. The resulting clones were named pAW126 (403 amino acid deletion mutant), pAW129 (386 amino acid deletion mutant), and pAW130 (366 amino acid deletion mutant). The DNA sequences of the replaced fragments were confirmed by DNA sequence analysis.

Each of the resulting expression vectors were expressed in E. coli essentially as
15 described in the previous examples. The expression of the 48 and 46 kDa proteins was moderate, whereas the expression of the 44 kDa protein was very high. Crude, heat-treated extracts of each protein showed polymerase activity using the activity assay described in Example 10.

20

ATCC Deposits

The following bacteriophage and bacterial strains were deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, Maryland, U.S.A. (ATCC). These deposits were made under the provisions of the Budapest Treaty on the International
25 Recognition of the Deposit of Microorganisms for purposes of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture for 30 years from the date of deposit. The organisms will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Applicants and ATCC that assures unrestricted availability upon issuance of the pertinent U.S. patent and/or publication of foreign patents or patent applications. Availability of the deposited strains is not to
30 be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

<u>Deposit Designation</u>	<u>ATCC No.</u>	<u>Date of Deposit</u>
pPab14	69310	05/11/93
pPoc4	69309	05/11/93

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The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the cell lines deposited, since the deposited embodiment is intended as a single illustration of one aspect of the invention and any cell lines that are functionally equivalent are within the scope of this invention. The deposit of materials therein does not constitute an admission that the
40 written description herein contained is inadequate to enable the practice of any aspect of the

invention, including the best mode thereof, nor are the deposits to be construed as limiting the scope of the claims to the specific illustrations that they represent. Indeed, various modifications of the invention in addition to those shown are described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the
5 appended claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: F.Hoffmann-La Roche AG
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(I) TELEX: 962292/965542 hlr ch

(ii) TITLE OF INVENTION: Thermostable Nucleic Acid Polymerase

(iii) NUMBER OF SEQUENCES: 39

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/062,368
(B) FILING DATE: 14-MAY-1993

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2430 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGCCAGAAG CTATAGAGTT CGTGCTCCTT GATTCAAGCT ACGAGATTGT AGGGAAAGAG	60
CCGGTAATCA TACTATGGGG TGTAACGCTA GACGGTAAAC GCATAGTCCT ACTTGATAGG	120
AGGTTTAGGC CCTACTTCTA TGCACTCATA TCCCGCGACT ACGAAGGTAA GGCCGAGGAG	180
GTAGTAGCTG CTATTAGAAG GCTAAGTATG GCAAAGAGCC CCATAATAGA AGCAAAGGTG	240
GTTAGTAAGA AGTACTTCGG AAGGCCCCGT AAAGCAGTCA AAGTAACGAC AGTTATACCC	300
GAATCTGTCA GAGAATATAG AGAGGCTGTA AAAAAGCTGG AAGGCGTGGA AGACTCTCTA	360
GAAGCAGACA TAAGGTTTCGC GATGAGGTAT CTAATCGACA AGAAGCTCTA CCCGTTTACA	420

GCATACCGTG	TCAGAGCCGA	GAACGCTGGA	CGCAGCCCTG	GTTTCCGTGT	AGACTCGGTA	480
TACACTATAG	TTGAGGACCC	AGAGCCTATT	GCCGACATAA	CTAGTATAGA	TATACCAGAG	540
ATGCGTGTGC	TCGCGTTCGA	CATAGAGGTC	TACAGTAAGA	GAGGAAGCCC	TAACCCGTCC	600
CGCGACCCGG	TCATAATAAT	CTCGATAAAG	GACAGCAAGG	GGAACGAGAA	GCTACTAGAA	660
GCCAATAACT	ACGACGACAG	AAACGTGCTA	CGGGAATTTA	TAGAGTACAT	ACGCTCCTTT	720
GACCCAGACA	TAATAGTAGG	CTACAATAGC	AACAATTTTG	ACTGGCCATA	CCTTATAGAA	780
CGTGACACACA	GAATAGGAGT	AAAGCTCGAC	GTGACAAGGC	GTGTTGGCGC	AGAGCCAAGT	840
ATGAGCGTCT	ATGGACATGT	CTCAGTGCAG	GGTAGGCTAA	ACGTAGACCT	CTACAACTAC	900
GTGGAGGAAA	TGCATGAGAT	AAAGGTAAAG	ACGCTCGAGG	AGGTCGCCGA	ATACCTAGGC	960
GTTATGCGCA	AGAGCGAGCG	CGTACTAATA	GAATGGTGGC	GGATCCCAGA	TTACTGGGAC	1020
GACGAGAAGA	AACGGCCGCT	ACTGAAGCGT	TATGCCCTCG	ACGATGTGAG	AGCCACCTAC	1080
GGCCTCGCCG	AGAAGATACT	CCCATTCGCA	ATACAGCTTT	CGACAGTAAC	CGGTGTTCCCT	1140
TTAGACCAAG	TCGGGGCTAT	GGGCGTAGGT	TTCCGTCTAG	AATGGTACCT	TATGAGAGCA	1200
GCGCATGATA	TGAACGAGCT	TGTCCCCAAC	CGTGTCAAGC	GGCGCGAAGA	GAGCTACAAG	1260
GGAGCAGTAG	TACTAAAGCC	CCTAAAGGGT	GTCCATGAGA	ACGTAGTAGT	GCTCGACTTT	1320
AGCTCAATGT	ACCCCAACAT	AATGATAAAG	TACAATGTGG	GCCCTGACAC	GATAATTGAC	1380
GACCCCTCAG	AGTGCGAGAA	GTACAGTGGA	TGCTACGTAG	CCCCCGAAGT	CGGGCACATG	1440
TTTAGGCGCT	CGCCCTCCGG	CTTCTTTAAG	ACCGTGCTTG	AGAACCTCAT	AGCGCTGCGT	1500
AAGCAAGTAC	GTGAAAAGAT	GAAGGAGTTC	CCCCCAGATA	GCCCAGAATA	CCGGATATAC	1560
GATGAACGCC	AGAAGGCACT	CAAGGTGCTA	GCCAACGCTA	GCTACGGCTA	CATGGGATGG	1620
GTGCACGCTC	GCTGGTACTG	TAAACGCTGC	GCAGAGGCTG	TAACAGCCTG	GGGCCGTAAC	1680
CTGATACTCT	CAGCAATAGA	ATATGCTAGG	AAGCTCGGCC	TCAAAGTAAT	ATACGGAGAC	1740
ACGGACTCCC	TATTCGTAAC	CTATGATATC	GAGAAGGTAA	AGAAGCTAAT	AGAATTCGTC	1800
GAGAAACAGC	TAGGCTTCGA	GATAAAGATA	GACAAGGTAT	ACAAAAGAGT	GTTCTTTACC	1860
GAGGCAAAGA	AGCGCTACGT	GGGCCTCCTC	GAGGACGGGC	GTATGGACAT	AGTAGGCTTT	1920
GAGGCTGTTA	GAGGCGACTG	GTGTGAGCTA	GCTAAAGAGG	TGCAAGAGAA	AGTAGCAGAG	1980
ATAATACTGA	AGACGGGAGA	CATAAATAGA	GCCATAAGCT	ACATAAGAGA	GGTCGTGAGA	2040
AAGCTAAGAG	AAGGCAAGAT	ACCCATAACA	AAGCTCGTAA	TATGGAAGAC	CTTGACAAAG	2100

AGAATCGAGG AATACGAGCA CGAGGCGCCG CACGTTACTG CAGCACGGCG TATGAAAGAA	2160
GCAGGCTACG ATGTGGCACC GGGAGACAAG ATAGGCTACA TCATAGTTAA AGGACATGGC	2220
AGTATATCGA GTCGTGCCTA CCCGTACTTT ATGGTAGACT CGTCTAAGGT TGACACAGAG	2280
TACTACATAG ACCACCAGAT AGTACCAGCA GCAATGAGGA TACTCTCATA CTTCGGGGTC	2340
ACAGAGAAGC AGCTTAAGGC AGCATCATCT GGGCATAGGA GTCTCTTCGA CTTCTTCGCG	2400
GCAAAGAAGT AGCCCCGGCT CTCCAAACTA	2430

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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

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Asp	Ile	Pro	Glu	Met	Arg	Val	Leu	Ala	Phe	Asp	Ile	Glu	Val	Tyr	Ser	180	185	190	
Lys	Arg	Gly	Ser	Pro	Asn	Pro	Ser	Arg	Asp	Pro	Val	Ile	Ile	Ile	Ser	195	200	205	
Ile	Lys	Asp	Ser	Lys	Gly	Asn	Glu	Lys	Leu	Leu	Glu	Ala	Asn	Asn	Tyr	210	215	220	
Asp	Asp	Arg	Asn	Val	Leu	Arg	Glu	Phe	Ile	Glu	Tyr	Ile	Arg	Ser	Phe	225	230	235	240
Asp	Pro	Asp	Ile	Ile	Val	Gly	Tyr	Asn	Ser	Asn	Asn	Phe	Asp	Trp	Pro	245	250	255	
Tyr	Leu	Ile	Glu	Arg	Ala	His	Arg	Ile	Gly	Val	Lys	Leu	Asp	Val	Thr	260	265	270	
Arg	Arg	Val	Gly	Ala	Glu	Pro	Ser	Met	Ser	Val	Tyr	Gly	His	Val	Ser	275	280	285	
Val	Gln	Gly	Arg	Leu	Asn	Val	Asp	Leu	Tyr	Asn	Tyr	Val	Glu	Glu	Met	290	295	300	
His	Glu	Ile	Lys	Val	Lys	Thr	Leu	Glu	Glu	Val	Ala	Glu	Tyr	Leu	Gly	305	310	315	320
Val	Met	Arg	Lys	Ser	Glu	Arg	Val	Leu	Ile	Glu	Trp	Trp	Arg	Ile	Pro	325	330	335	
Asp	Tyr	Trp	Asp	Asp	Glu	Lys	Lys	Arg	Pro	Leu	Leu	Lys	Arg	Tyr	Ala	340	345	350	
Leu	Asp	Asp	Val	Arg	Ala	Thr	Tyr	Gly	Leu	Ala	Glu	Lys	Ile	Leu	Pro	355	360	365	
Phe	Ala	Ile	Gln	Leu	Ser	Thr	Val	Thr	Gly	Val	Pro	Leu	Asp	Gln	Val	370	375	380	
Gly	Ala	Met	Gly	Val	Gly	Phe	Arg	Leu	Glu	Trp	Tyr	Leu	Met	Arg	Ala	385	390	395	400
Ala	His	Asp	Met	Asn	Glu	Leu	Val	Pro	Asn	Arg	Val	Lys	Arg	Arg	Glu	405	410	415	
Glu	Ser	Tyr	Lys	Gly	Ala	Val	Val	Leu	Lys	Pro	Leu	Lys	Gly	Val	His	420	425	430	
Glu	Asn	Val	Val	Val	Leu	Asp	Phe	Ser	Ser	Met	Tyr	Pro	Asn	Ile	Met	435	440	445	
Ile	Lys	Tyr	Asn	Val	Gly	Pro	Asp	Thr	Ile	Ile	Asp	Asp	Pro	Ser	Glu	450	455	460	
Cys	Glu	Lys	Tyr	Ser	Gly	Cys	Tyr	Val	Ala	Pro	Glu	Val	Gly	His	Met	465	470	475	480

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Phe	Arg	Arg	Ser	Pro	Ser	Gly	Phe	Phe	Lys	Thr	Val	Leu	Glu	Asn	Leu			
				485					490					495				
Ile	Ala	Leu	Arg	Lys	Gln	Val	Arg	Glu	Lys	Met	Lys	Glu	Phe	Pro	Pro			
			500					505					510					
Asp	Ser	Pro	Glu	Tyr	Arg	Ile	Tyr	Asp	Glu	Arg	Gln	Lys	Ala	Leu	Lys			
		515					520					525						
Val	Leu	Ala	Asn	Ala	Ser	Tyr	Gly	Tyr	Met	Gly	Trp	Val	His	Ala	Arg			
	530					535					540							
Trp	Tyr	Cys	Lys	Arg	Cys	Ala	Glu	Ala	Val	Thr	Ala	Trp	Gly	Arg	Asn			
545					550					555					560			
Leu	Ile	Leu	Ser	Ala	Ile	Glu	Tyr	Ala	Arg	Lys	Leu	Gly	Leu	Lys	Val			
				565					570					575				
Ile	Tyr	Gly	Asp	Thr	Asp	Ser	Leu	Phe	Val	Thr	Tyr	Asp	Ile	Glu	Lys			
			580					585					590					
Val	Lys	Lys	Leu	Ile	Glu	Phe	Val	Glu	Lys	Gln	Leu	Gly	Phe	Glu	Ile			
		595					600					605						
Lys	Ile	Asp	Lys	Val	Tyr	Lys	Arg	Val	Phe	Phe	Thr	Glu	Ala	Lys	Lys			
	610					615					620							
Arg	Tyr	Val	Gly	Leu	Leu	Glu	Asp	Gly	Arg	Met	Asp	Ile	Val	Gly	Phe			
625					630					635					640			
Glu	Ala	Val	Arg	Gly	Asp	Trp	Cys	Glu	Leu	Ala	Lys	Glu	Val	Gln	Glu			
				645					650					655				
Lys	Val	Ala	Glu	Ile	Ile	Leu	Lys	Thr	Gly	Asp	Ile	Asn	Arg	Ala	Ile			
			660					665				670						
Ser	Tyr	Ile	Arg	Glu	Val	Val	Arg	Lys	Leu	Arg	Glu	Gly	Lys	Ile	Pro			
		675					680					685						
Ile	Thr	Lys	Leu	Val	Ile	Trp	Lys	Thr	Leu	Thr	Lys	Arg	Ile	Glu	Glu			
	690					695					700							
Tyr	Glu	His	Glu	Ala	Pro	His	Val	Thr	Ala	Ala	Arg	Arg	Met	Lys	Glu			
705					710					715					720			
Ala	Gly	Tyr	Asp	Val	Ala	Pro	Gly	Asp	Lys	Ile	Gly	Tyr	Ile	Ile	Val			
				725					730					735				
Lys	Gly	His	Gly	Ser	Ile	Ser	Ser	Arg	Ala	Tyr	Pro	Tyr	Phe	Met	Val			
			740					745					750					
Asp	Ser	Ser	Lys	Val	Asp	Thr	Glu	Tyr	Tyr	Ile	Asp	His	Gln	Ile	Val			
		755					760					765						
Pro	Ala	Ala	Met	Arg	Ile	Leu	Ser	Tyr	Phe	Gly	Val	Thr	Glu	Lys	Gln			
	770					775					780							

Leu Lys Ala Ala Ser Ser Gly His Arg Ser Leu Phe Asp Phe Phe Ala
 785 790 795 800

Ala Lys Lys

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGACAGAGA CTATAGAGTT CGTGCTGCTA GACTCTAGCT ACGAGATACT GGGGAAGGAG	60
CCGGTAGTAA TCCTCTGGGG GATAACGCTT GACGGTAAAC GTGTCGTGCT TCTAGACCAC	120
CGCTTCCGCC CCTACTTCTA CGCCCTCATA GCCCGGGGCT ATGAGGATAT GGTGGAGGAG	180
ATAGCAGCTT CCATAAGGAG GCTTAGTGTG GTCAAGAGTC CGATAATAGA TGCCAAGCCT	240
CTTGATAAGA GGTACTTCGG CAGGCCCCGT AAGGCGGTGA AGATTACCAC TATGATACCC	300
GAGTCTGTTA GACACTACCG CGAGGCGGTG AAGAAGATAG AGGGTGTGGA GGACTCCCTC	360
GAGGCAGATA TAAGGTTTGC AATGAGATAT CTGATAGATA AGAGGCTCTA CCCGTTACAG	420
GTTTACCGGA TCCCCGTAGA GGATGCGGGC CGCAATCCAG GCTTCCGTGT TGACCGTGTC	480
TACAAGGTTG CTGGCGACCC GGAGCCCCTA GCGGATATAA CGCGGATCGA CCTTCCCCCG	540
ATGAGGCTGG TAGCTTTTGA TATAGAGGTG TATAGCAGGA GGGGGAGCCC TAACCCTGCA	600
AGGGATCCAG TGATAATAGT GTCGCTGAGG GACAGCGAGG GCAAGGAGAG GCTCATAGAA	660
GCTGAAGGCC ATGACGACAG GAGGGTTCTG AGGGAGTTCG TAGAGTACGT GAGAGCCTTC	720
GACCCCGACA TAATAGTGGG CTATAACAGT AACCACTTCG ACTGGCCCTA CCTAATGGAG	780
CGCGCCCGTA GGCTCGGGAT TAACCTCGAC GTTACACGCC GTGTGGGGGC AGAGCCCACC	840
ACCAGCGTCT ACGGCCACGT CTCGGTGCAG GGTAGGCTGA ACGTGGACCT CTACGACTAT	900
GCCGAGGAGA TGCCGGAGAT AAAGATGAAG ACGCTTGAGG AGGTAGCGGA GTACCTAGGC	960
GTTATGAAGA AGAGCGAGCG TGTGATAATA GAGTGGTGGA GGATACCCGA GTACTGGGAT	1020
GACGAGAAGA AGAGGCAGCT GCTAGAGCGC TACGCGCTCG ACGATGTGAG GGCTACCTAC	1080
GGCCTCGCGG AAAAGATGCT ACCGTTGCGC ATACAGCTCT CCACTGTTAC GGGTGTGCCT	1140

CTCGACCAGG TAGGTGCTAT GGGCGTAGGC TTCCGCCTAG AGTGGTATCT CATGCGTGCA	1200
GCCTACGATA TGAACGAGCT GGTGCCGAAC CGGGTGGAGA GGAGGGGGGA GAGCTACAAG	1260
GGTGCAGTAG TGTTAAAGCC TCTCAAGGGA GTCCATGAGA ATGTTGTGGT GCTCGATTTC	1320
AGTTCCATGT ACCCGAGCAT AATGATAAAG TACAACGTGG GCCCCGACAC TATAGTCGAC	1380
GACCCCTCGG AGTGCCCAA GTACGGCGGC TGCTATGTAG CCCCCGAGGT CGGGCACCGG	1440
TTCCGTCGCT CCCC GCCAGG CTTCTTCAAG ACCGTGCTCG AGAACCTACT GAAGCTACGC	1500
CGACAGGTAA AGGAGAAGAT GAAGGAGTTT CCGCCTGACA GCCCCGAGTA CAGGCTCTAC	1560
GATGAGCGCC AGAAGGCGCT CAAGGTTCTT GCGAACGCGA GCTATGGCTA CATGGGGTGG	1620
AGCCATGCCC GCTGGTACTG CAAACGCTGC GCCGAGGCTG TCACAGCCTG GGGCCGTAAC	1680
CTTATACTGA CAGCTATCGA GTATGCCAGG AAGCTCGGCC TAAAGGTTAT ATATGGAGAC	1740
ACCGACTCCC TCTTCGTGGT CTATGACAAG GAGAAGGTTG AGAAGCTGAT AGAGTTTGTC	1800
GAGAAGGAGC TGGGCTTTGA GATAAAGATA GACAAGATCT ACAAGAAAGT GTTCTTCACG	1860
GAGGCTAAGA AGCGCTATGT AGGTCTCCTC GAGGACGGAC GTATAGACAT CGTGGGCTTT	1920
GAAGCAGTCC GCGGCGACTG GTGCGAGCTG GCTAAGGAGG TGCAGGAGAA GGCGGCTGAG	1980
ATAGTGTTGA ATACGGGGAA CGTGGACAAG GCTATAAGCT ACATAAGGGA GGTAATAAAG	2040
CAGCTCCGCG AGGGCAAGGT GCCAATAACA AAGCTTATCA TATGGAAGAC GCTGAGCAAG	2100
AGGATAGAGG AGTACGAGCA TGACGCGCCT CATGTGATGG CTGCACGGCG TATGAAGGAG	2160
GCAGGCTACG AGGTGTCTCC CGGCGATAAG GTGGGCTACG TCATAGTTAA GGGTAGCGGG	2220
AGTGTGTCCA GCAGGGCCTA CCCCTACTTC ATGGTTGATC CATCGACCAT CGACGTCAAC	2280
TACTATATTG ACCACCAGAT AGTGCCGGCT GCTCTGAGGA TACTCTCCTA CTTCGGAGTC	2340
ACCGAGAAAC AGCTCAAGGC GGCGGCTACG GTGCAGAGAA GCCTCTTCGA CTTCTTCGCC	2400
TCAAAGAAAT AGCTCCTCCA CCCGGCTAGC	2430

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 803 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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

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Pro 305	Glu	Ile	Lys	Met	Lys 310	Thr	Leu	Glu	Glu	Val 315	Ala	Glu	Tyr	Leu	Gly 320
Val	Met	Lys	Lys	Ser 325	Glu	Arg	Val	Ile	Ile 330	Glu	Trp	Trp	Arg	Ile 335	Pro
Glu	Tyr	Trp	Asp 340	Asp	Glu	Lys	Lys	Arg 345	Gln	Leu	Leu	Glu	Arg 350	Tyr	Ala
Leu	Asp	Asp 355	Val	Arg	Ala	Thr	Tyr 360	Gly	Leu	Ala	Glu	Lys 365	Met	Leu	Pro
Phe 370	Ala	Ile	Gln	Leu	Ser	Thr 375	Val	Thr	Gly	Val	Pro 380	Leu	Asp	Gln	Val
Gly 385	Ala	Met	Gly	Val	Gly 390	Phe	Arg	Leu	Glu	Trp 395	Tyr	Leu	Met	Arg	Ala 400
Ala	Tyr	Asp	Met	Asn 405	Glu	Leu	Val	Pro	Asn 410	Arg	Val	Glu	Arg	Arg 415	Gly
Glu	Ser	Tyr	Lys 420	Gly	Ala	Val	Val	Leu	Lys 425	Pro	Leu	Lys	Gly 430	Val	His
Glu	Asn	Val 435	Val	Val	Leu	Asp	Phe 440	Ser	Ser	Met	Tyr	Pro 445	Ser	Ile	Met
Ile 450	Lys	Tyr	Asn	Val	Gly	Pro 455	Asp	Thr	Ile	Val	Asp 460	Asp	Pro	Ser	Glu
Cys 465	Pro	Lys	Tyr	Gly	Gly 470	Cys	Tyr	Val	Ala	Pro 475	Glu	Val	Gly	His	Arg 480
Phe	Arg	Arg	Ser	Pro 485	Pro	Gly	Phe	Phe	Lys 490	Thr	Val	Leu	Glu	Asn 495	Leu
Leu	Lys	Leu	Arg 500	Arg	Gln	Val	Lys	Glu 505	Lys	Met	Lys	Glu	Phe 510	Pro	Pro
Asp	Ser	Pro 515	Glu	Tyr	Arg	Leu	Tyr 520	Asp	Glu	Arg	Gln	Lys 525	Ala	Leu	Lys
Val 530	Leu	Ala	Asn	Ala	Ser	Tyr 535	Gly	Tyr	Met	Gly	Trp 540	Ser	His	Ala	Arg
Trp 545	Tyr	Cys	Lys	Arg	Cys 550	Ala	Glu	Ala	Val	Thr 555	Ala	Trp	Gly	Arg	Asn 560
Leu	Ile	Leu	Thr 565	Ala	Ile	Glu	Tyr	Ala	Arg 570	Lys	Leu	Gly	Leu	Lys 575	Val
Ile	Tyr	Gly	Asp 580	Thr	Asp	Ser	Leu	Phe 585	Val	Val	Tyr	Asp	Lys 590	Glu	Lys
Val	Glu	Lys 595	Leu	Ile	Glu	Phe	Val 600	Glu	Lys	Glu	Leu	Gly 605	Phe	Glu	Ile

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Lys 610	Ile	Asp	Lys	Ile	Tyr	Lys 615	Lys	Val	Phe	Phe	Thr 620	Glu	Ala	Lys	Lys
Arg 625	Tyr	Val	Gly	Leu	Leu 630	Glu	Asp	Gly	Arg	Ile 635	Asp	Ile	Val	Gly	Phe 640
Glu	Ala	Val	Arg	Gly 645	Asp	Trp	Cys	Glu	Leu 650	Ala	Lys	Glu	Val	Gln 655	Glu
Lys	Ala	Ala	Glu 660	Ile	Val	Leu	Asn 665	Thr	Gly	Asn	Val	Asp	Lys 670	Ala	Ile
Ser	Tyr	Ile 675	Arg	Glu	Val	Ile	Lys 680	Gln	Leu	Arg	Glu	Gly 685	Lys	Val	Pro
Ile 690	Thr	Lys	Leu	Ile	Ile	Trp 695	Lys	Thr	Leu	Ser	Lys 700	Arg	Ile	Glu	Glu
Tyr 705	Glu	His	Asp	Ala	Pro 710	His	Val	Met	Ala	Ala 715	Arg	Arg	Met	Lys	Glu 720
Ala	Gly	Tyr	Glu	Val 725	Ser	Pro	Gly	Asp	Lys 730	Val	Gly	Tyr	Val	Ile 735	Val
Lys	Gly	Ser	Gly 740	Ser	Val	Ser	Ser	Arg 745	Ala	Tyr	Pro	Tyr	Phe 750	Met	Val
Asp	Pro	Ser 755	Thr	Ile	Asp	Val	Asn 760	Tyr	Tyr	Ile	Asp	His 765	Gln	Ile	Val
Pro 770	Ala	Ala	Leu	Arg	Ile	Leu 775	Ser	Tyr	Phe	Gly	Val 780	Thr	Glu	Lys	Gln
Leu 785	Lys	Ala	Ala	Ala	Thr 790	Val	Gln	Arg	Ser	Leu 795	Phe	Asp	Phe	Phe	Ala 800
Ser Lys Lys															

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGACCCATAT GCCAGAAGCT ATTGAATTCG TGCTCC

36

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGCAGGTACC ACTAGTTATG TCGGCAATAG GCTC

34

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTAAGGCAGC ATCATCTGGG CATAGGAGTC TCTTCGACTT CTTCGCGGCA AAGAAGTAAC

60

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCGGGTTACT TCTTTGCCGC GAAGAAGTCG AAGAGACTCC TATGCCCAGA TGATGCTGCC

60

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCTTATAGCC TTGTCCACGT TC

22

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGACCATGCA TGACTGAAAC TATTGAATTC GTGCTG

36

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGAAGGTACC TGATCATCTA GAAGCACGAC ACGTT

35

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGAAGCTGAG CAAGAGGATA GAGG

24

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGAAGGTACC TTATTTCTTT GAGGCGAAGA AG

32

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTTTCGAAA GAAGAAAAAA CC

22

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCTCATATGC TTATCGATAC CC

22

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CATAAGCTTA TCGATACCCT T

21

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AAGCTTATGA CAGAGACTAT AGAGTT

26

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTGGTCTAGA AGCACGACAC GT

22

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TATTGCCGAC ATAAC TAGTA TAGA

24

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ACTGTAGACC GCGATCGCGA ACGCGAGC

28

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTCGCGTTTCG CGATCGCGGT CTACAGTAAG AGAG

34

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTATCTCATG CATTCCTCC

20

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGTCGTGCT TCTAGACCA

19

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCTATACACC GCGATCGCAA AAGCTACCAG C

31

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGTAGCTTTT GCGATCGCGG TGTATAGCAG GA

32

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TACGGGCGCG CTCCATTAG

19

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCGATAGTTT GAGTTCTTCT ACTCAGGC

28

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAAGAAAGCG AAAGGAGCGG GCGCTAGGGC

30

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GCACCCCGCT TGGGCAGAG

19

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCACCCCGCT TGGGCAGAA

19

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCACCCCGCT TGGGCAGAT

19

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCACCCCGCT TGGGCAGAC

19

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TCCCGCCCCT CCTGGAAGAC

20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATAAAGATA GACAAGGTAT AC

22

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CGTATTCCTC GATTCTCTTT

20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTCGCATATG CCATTGCAA TACAACTTTC GACAGTAACC

40

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TTCGCATATG GGTGTAGGTT TTCGTCTAGA ATGGTAC

37

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGCATATGAA CGAACTGGTT CCCAACCGTG TCAAG

35

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GTCAGGGCCC ACATTGTACT T

21

CLAIMS:

1. A purified thermostable DNA polymerase that catalyzes the combination of nucleoside triphosphates to form a nucleic acid strand complementary to a nucleic acid template strand, wherein said polymerase is a Pyrodictium DNA polymerase, having an amino sequence from amino terminus to carboxy terminus of SEQ ID NO: 2 or SEQ ID NO: 4.
2. A purified thermostable DNA polymerase that catalyzes the combination of nucleoside triphosphates to form a nucleic acid strand complementary to a nucleic acid template strand, wherein said polymerase comprises an N-terminal shortened fragment of a thermostable DNA polymerase having an amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 4 wherein said fragment lacks up to one third of the amino terminal sequence of the amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 4.
3. An N-terminal shortened fragment of a purified thermostable DNA polymerase that catalyzes the combination of nucleoside triphosphates to form a nucleic acid strand complementary to a nucleic acid template strand and is lacking exonuclease activity, selected from the group of:
 - (a) the 366 amino acid deletion mutant having the amino acid sequence from position 1, which is methionine, immediately followed by amino acids 368 through 803 of SEQ ID NO: 2;
 - (b) the 386 amino acid deletion mutant having the amino acid sequence from position 1, which is methionine, immediately followed by amino acids 388 through 803 of SEQ ID NO: 2; or
 - (c) the 403 amino acid deletion mutant having the amino acid sequence from position 1, which is methionine, immediately followed by amino acids 405 through 803 of SEQ ID NO: 2.
4. The polymerase of any one of claims 1 to 3, wherein said polymerase is further characterized by the ability to function efficiently in a polymerase chain reaction, wherein said reaction includes repeated exposure to a denaturation temperature of about 100 °C.

5. The thermostable DNA polymerase as claimed in any one of claims 1 to 3, having optimal activity between 70 and 80°C.
6. The thermostable DNA polymerase as claimed in any one of claims 1 to 5, which is modified by oxidation or reduction, whereby this modification does not destroy the DNA polymerase activity of the resulting thermostable DNA polymerase.
7. The polymerase of claim 1 or 2, wherein said polymerase is characterized as comprising a 3' to 5' exonuclease activity.
8. A recombinant DNA encoding a thermostable DNA polymerase as claimed in any one of claims 1 to 7.
9. The recombinant DNA of claim 8 that encodes the DNA polymerase of *Pyrodictium abyssi*.
10. The recombinant DNA of claim 1 or claim 2 that encodes the DNA polymerase of *Pyrodictium occultum*.
11. A recombinant DNA encoding a thermostable DNA polymerase obtainable from *Pyrodictium abyssi* that encodes the amino acid sequence from amino to carboxy terminus of the SEQ ID NO: 2.
12. A recombinant DNA encoding a thermostable DNA polymerase obtainable from *Pyrodictium abyssi* that has the nucleotide sequence of SEQ ID NO: 1.
13. A recombinant DNA encoding a thermostable DNA polymerase obtainable from *Pyrodictium occultum* that encodes the amino acid sequence from amino to carboxy terminus of the SEQ ID NO: 4.

14. A recombinant DNA encoding a thermostable DNA polymerase obtainable from *Pyrodictium occultum* that has the nucleotide sequence of SEQ ID NO: 3.
15. A recombinant DNA vector that comprises a DNA sequence encoding a thermostable DNA polymerase as claimed in any one of claims 1 to 7.
16. A recombinant DNA vector as claimed in claim 15, which is selected from the group of vectors consisting of pAW121, pPoc4, pAW114, pPab14, pAW123, pAW118, pexo-Pab, and pexo-Poc.
17. A recombinant host cell transformed with a DNA vector that comprises a DNA sequence encoding a thermostable DNA polymerase as claimed in any one of claims 1 to 7.
18. A polypeptide displaying *Pyrodictium* DNA polymerase activity produced in a recombinant host cell as claimed in claim 17.
19. A stable enzyme composition comprising a thermostable DNA polymerase as claimed in any one of claims 1 to 7 and 18 in a buffer containing one or more non-ionic polymeric detergents.
20. A process for the preparation of a thermostable DNA polymerase as claimed in claim 1, which process comprises the steps of:
 - (a) culturing a host cell transformed with a recombinant DNA vector that comprises a DNA sequence encoding said thermostable DNA polymerase wherein said DNA sequence has the nucleotide sequence of SEQ ID NO: 1 or SEQ ID NO: 3; and
 - (b) isolating the thermostable DNA polymerase produced in the host cell from the culture.

21. A process for amplifying a nucleic acid, which process comprises subjecting said nucleic acid to polymerase chain reaction thermal cycling in the presence of a DNA polymerase as defined in any one of claims 1 to 7 and 18 and a set of primers and nucleoside triphosphate precursors to yield amplified said nucleic acid.
22. Use of a thermostable DNA polymerase as claimed in any one of claims 1 to 7 and 18 for amplifying a nucleic acid.
23. A kit comprising a thermostable DNA polymerase as claimed in any one of claims 1 to 7 and 18 or a stable enzyme composition comprising said polymerase in a buffer containing one or more non-ionic polymeric detergents, and a further reagent useful for performing a polymerase chain reaction selected from the group consisting of a set of primers and nucleoside triphosphate precursors.