(12) STANDARD PATENT (11) Application No. **AU 2017286477 C1**
(19) AUSTRALIAN PATENT OFFICE

(54) Title
Variants of a DNA polymerase of the polX family

(51) International Patent Classification(s)
C12N 9/12 (2006.01) ***C12P 19/34*** (2006.01)

(21) Application No: **2017286477** (22) Date of Filing: **2017.06.13**

(87) WIPO No: **WO17/216472**

(30) Priority Data

(31) Number	(32) Date	(33) Country
1655475	**2016.06.14**	**FR**

(43) Publication Date: **2017.12.21**
(44) Accepted Journal Date: **2023.09.14**
(44) Amended Journal Date: **2023.12.21**

(71) Applicant(s)
DNA Script;Institut Pasteur;Centre national de la recherche scientifique

(72) Inventor(s)
Ybert, Thomas;Delarue, Marc

(74) Agent / Attorney
Davies Collison Cave Pty Ltd, Level 4 7 Macquarie Place, Sydney, NSW, 2000, AU

(56) Related Art
US 6812339 B1

(12) DEMANDE INTERNATIONALE PUBLIÉE EN VERTU DU TRAITÉ DE COOPÉRATION EN MATIÈRE DE BREVETS (PCT)

(19) Organisation Mondiale de la Propriété Intellectuelle
Bureau international

(43) Date de la publication internationale
21 décembre 2017 (21.12.2017)

WIPO | PCT

(10) Numéro de publication internationale
WO 2017/216472 A3

(51) Classification internationale des brevets :
C12N 9/12 (2006.01) *C12P 19/34* (2006.01)

(21) Numéro de la demande internationale :
PCT/FR2017/051519

(22) Date de dépôt international :
13 juin 2017 (13.06.2017)

(25) Langue de dépôt : français

(26) Langue de publication : français

(30) Données relatives à la priorité :
1655475 14 juin 2016 (14.06.2016) FR

(71) Déposants : **DNA SCRIPT** [FR/FR] ; 6 rue Jean Calvin, 75005 PARIS (FR). **INSTITUT PASTEUR** [FR/FR] ; 25-28 rue du Docteur Roux, 75724 Paris Cedex 15 (FR). **CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE** [FR/FR] ; 3 rue Michel Ange, 75016 PARIS (FR).

(72) Inventeurs : **YBERT, Thomas** ; 4 rue de La Vega, 75012 PARIS (FR). **DELARUE, Marc** ; 98 Bd de la Reine, 78000 VERSAILLES (FR).

(74) Mandataire : **LEBRETTE, Camille** et al. ; BECKER & ASSOCIES, 25, rue Louis le Grand, 75002 PARIS (FR).

(81) États désignés *(sauf indication contraire, pour tout titre de protection nationale disponible)* : AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) États désignés *(sauf indication contraire, pour tout titre de protection régionale disponible)* : ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), eurasien (AM, AZ, BY, KG, KZ, RU, TJ, TM), européen (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Publiée:
— *avec rapport de recherche internationale (Art. 21(3))*
— *avant l'expiration du délai prévu pour la modification des revendications, sera republiée si des modifications sont reçues (règle 48.2(h))*
— *avec la partie de la description réservée au listage des séquences (règle 5.2(a))*

(88) Date de publication du rapport de recherche internationale:
15 mars 2018 (15.03.2018)

WO 2017/216472 A3

(54) Title: VARIANTS OF A DNA POLYMERASE OF THE POLX FAMILY

(54) Titre : VARIANTS D'UNE ADN POLYMÉRASE DE LA FAMILLE POLX

(57) Abstract: The invention relates to variants of a DNA polymerase of the polX family capable of synthesising a nucleic acid molecule without a template strand, or of a functional fragment of such a polymerase, comprising at least one mutation of a residue in at least one specific position, and to the uses of said variants, in particular for the synthesis of nucleic acid molecules comprising 3'- OH modified nucleotides.

(57) Abrégé : L'invention concerne des variants d'une ADN polymérase de la famille polX capable de synthétiser une molécule d'acide nucléiquesans brin matrice, ou d'un fragment fonctionnel d'une telle polymérase, comprenant au moins une mutation d'un résidu à au moins une position particulière, et des utilisations de ces variants, notamment pour la synthèse de molécules d'acide nucléiques comprenant des nucléotides modifiés en 3'-OH.

Variants of a DNA Polymerase of the polX Family

Introduction

The present invention relates to the field of enzyme improvement. The present invention relates to an improved variant of a DNA polymerase of the polX family, to a nucleic acid coding for this variant, to the production of this variant in a host cell, to the use thereof for the synthesis of a nucleic acid molecule without a template strand, and to a kit for the synthesis of a nucleic acid molecule without a template strand.

The chemical synthesis of nucleic acid fragments is a widely used laboratory technique (Adams et al., 1983, J. Amer. Chem. Soc. 105:661; Froehler et al., 1983; Tetrahedron Lett. 24:3171). It makes it possible to rapidly obtain nucleic acid molecules comprising the desired nucleotide sequence. In contrast to enzymes which carry out the synthesis in the 5' to 3' direction, the chemical synthesis is carried out in the 3' to 5' direction. However, the chemical synthesis has certain limits. In fact, it requires the use of multiple solvents and reagents. In addition, it only makes it possible to obtain short nucleic acid fragments which then have to be assembled to one another to obtain the desired final nucleic acid strands.

An alternative solution using enzymes for carrying out the coupling reaction between nucleotides from an initial nucleic acid fragment (primer) and in the absence of a template strand has been developed. Several polymerase enzymes appear to be suitable for this type of synthesis methods.

A very large number of DNA polymerases exists, which are capable of catalyzing the synthesis of a nucleic acid strand in the presence or absence of a template strand. Thus, the DNA polymerases of the polX family are involved in a large range of biological processes, in

particular in DNA repair mechanisms or mechanisms for the correction of errors appearing in DNA sequences. These enzymes are capable of inserting nucleotides, which have undergone excisions after the identification of sequence errors, in the nucleic acid strands. The DNA polymerases of the polX family comprise the DNA polymerases β (Pol β), λ (Pol λ), μ (Pol μ), yeast IV (Pol IV), and the terminal deoxyribonucleotidyl transferase (TdT). TdT in particular is used very widely in the methods of enzymatic synthesis of nucleic acid molecules.

However, usually these DNA polymerases allow only the incorporation of natural nucleotides. In all cases, the natural DNA polymerases lose their catalytic activity in the presence of non-natural nucleotides and in particular 3'-OH modified nucleotides which exhibit greater steric hindrance than the natural nucleotides.

However, the use of modified nucleotides can turn out to be useful for certain specific applications. Therefore, enzymes that are capable of catalyzing the synthesis of a nucleic acid strand by incorporating such nucleotides had to be developed. Thus, DNA polymerase variants that can function with nucleotides comprising considerable structural modifications have been developed.

However, the currently available variants are not entirely satisfactory, in particular since they exhibit low activity and since they are only compatible with enzymatic synthesis on the laboratory scale. Thus, a need exists for DNA polymerases capable of synthesizing, if possible on an industrial scale, a nucleic acid in the absence of a template strand and using modified nucleotides.

Summary of the invention

The present invention overcomes certain technological barriers which prevent the use on an industrial scale of DNA polymerases for the enzymatic synthesis of nucleic acids.

The present invention thus proposes DNA polymerases of the polX family capable of synthesizing a nucleic acid in the absence of a template strand and suitable for using modified nucleotides. The variants developed exhibit capabilities of incorporation of modified nucleotides which are much greater than those of the natural DNA polymerases from which they are derived. In particular, the DNA polymerase variants which are the subject matter of the present invention are particularly effective for the incorporation of nucleotides having modifications of the sugar. In fact, the inventors have developed variants having an increased catalytic pocket volume in comparison to that of the DNA polymerases from which they are derived, promoting the incorporation of modified nucleotides exhibiting greater steric hindrance than the natural nucleotides. More particularly, the DNA polymerase variants of the polX family which are the subject matter of the present invention comprise at least one mutation on an amino acid intervening directly at the level of the catalytic cavity of the enzyme, or enabling the deformation of the contours of this cavity in order to accommodate the steric hindrance due to the modifications present at the level of the nucleotides. For example, the mutations introduced enable the enlargement of the catalytic cavity of the enzyme in which the 3'-OH end of the modified nucleotides is accommodated. Alternatively or additionally, the mutations carried out enable the inflation or increase of the volume of the catalytic activity, the increase in the access to the catalytic pocket by the 3'-OH modified nucleotides and/or they confer the necessary flexibility to the structure of the enzyme to enable it to accommodate modifications resulting in great steric hindrance of the 3'-OH modified nucleotides. As a result of such mutations, once the

polymerase is bound to the nucleic acid fragment to be elongated, the modified nucleotide penetrates into the core of the catalytic pocket whose access is widened and it takes on an optimal spatial conformation in said catalytic pocket, a phosphodiester bond forming between the 3'-OH end of the last nucleotide of the nucleic acid strand and the 5'-triphosphate end of the modified nucleotide.

Thus, the subject matter of the invention is a variant of a DNA polymerase of the polX family capable of synthesizing a nucleic acid molecule without a template strand, or a variant of a functional fragment of such a polymerase, said variant comprising at least one mutation of a residue in at least one position selected from the group consisting of T331, G332, G333, F334, R336, K338, H342, D343, V344, *D345,* F346, A397, D399, D434, V436, A446, L447, L448, G449, W450, G452, R454, Q455, F456, E457, R458, R461, N474, E491, D501, Y502, 1503, P505, R508, N509 and A5 10, or a functionally equivalent residue, the positions indicated being determined by alignment with SEQ ID No. 1.

A first aspect of the invention provides a variant of a DNA polymerase of the polX family capable of synthesizing a nucleic acid molecule without a template strand, or of a functional fragment of such a polymerase, said variant comprising a substitution at residue E457, or a functionally equivalent residue, the position indicated being determined by alignment with SEQ ID No. 1, said variant having at least 70% identity with the sequence according to SEQ ID No. 1 and being able to incorporate a modified nucleotide.

In a particular embodiment, the variant is capable of synthesizing a DNA strand or an RNA strand.

The present invention relates in particular to a variant of a DNA polymerase of the polX family and in particular of a Pol IV from yeast, Pol p or wild-type TdT, and comprising the selected mutation(s). In a particular embodiment, the variant according to the present invention is a variant of the TdT of sequence SEQ ID No. 1 or a homologous sequence which

has at least 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% identity with the sequence of the SEQ ID No. 1, and it carries the selected mutation(s).

The invention also relates to a nucleic acid coding for a variant of a DNA polymerase of the polX family according to the present invention, to an expression cassette comprising a

nucleic acid according to the present invention, and to a vector comprising a nucleic acid or an expression cassette according to the present invention. The nucleic acid coding for the variant of the present invention can be the nucleic acid of mature form or of the precursor form of the DNA polymerase according to the invention.

The present invention also relates to the use of a nucleic acid, of an expression cassette or of a vector according to the present invention for transforming or transfecting a host cell. It further relates to a host cell comprising a nucleic acid, an expression cassette or a vector coding for a DNA polymerase of the polX family according to the present invention. It relates to the use of such a nucleic acid, of such an expression cassette, of such a vector or of such a host cell for producing a variant of a DNA polymerase of the polX family according to the present invention.

It also relates to a method for producing a variant of the DNA polymerase of the polX family according to the present invention, comprising the transformation or the transfection of a host cell by a nucleic acid, an expression cassette or a vector according to the present invention, the culturing of the transformed/transfected host cell under culture conditions enabling the expression of the nucleic acid coding for said variant, and optionally, the harvesting of a variant of a DNA polymerase of the polX family produced by the host cell.

The host cell can be prokaryotic or eukaryotic. In particular, the host cell can be a microorganism, preferably a bacterium, a yeast or a mushroom. In an embodiment, the host cell is a bacterium, preferably *E. coli*. In another embodiment, the host cell is a yeast, preferably *P. pastoris* or *K. lactis*. In another embodiment, the host cell is a mammalian cell, preferably a COS7 or CHO cell.

The invention also relates to the use of a variant of a DNA polymerase of the polX family according to the present invention for synthesizing a nucleic acid molecule without a template

strand, from 3'-OH modified nucleotides. Naturally, the variant of a DNA polymerase of the polX family according to the present invention can also be used, in the context of the invention, for synthesizing a nucleic acid molecule without a template strand, from non modified nucleotides or from a mixture of modified and non modified nucleotides.

The invention also proposes a method for the enzymatic synthesis of a nucleic acid molecule without a template strand, according to which a primer strand is brought in contact with at least one nucleotide, preferably a 3'-OH modified nucleotide, in the presence of a variant of a DNA polymerase of the polX family according to the invention. The carrying out of the method can take place in particular by using a purified variant, a culture medium of a host cell which has been transformed to express said variant, and/or a cell extract of such a host cell.

The invention also relates to a kit for the enzymatic synthesis of a nucleic acid molecule without a template strand, comprising at least one variant of a DNA polymerase of the polX family according to the invention, nucleotides, preferably 3'-OH modified nucleotides, and optionally at least one primer strand, or nucleotide primer, and/or a reaction buffer.

Description of the figures

Figure 1: SDS-PAGE gel of fractions of a TdT variant according to an embodiment example of the invention (M: Molecular weight marker; 1: Centrifugate before loading; 2: Centrifugate after loading; 3: Washing buffer after loading; 4: Elution fraction 3 mL; 5: Elution fraction 30 mL; 6: Elution peak compilation; 7: Concentration);

Figure 2: Alignment of the amino acid sequences of the Homo sapiens DNA polymerases Pol μ (UniProtKB Q9NP87), Pan troglodytes Pol μ (UniProtKB H2QUI0), Mus musculus Pol μ (UniProtKB Q924W4), Canis lupus familiaris Pol μ (UniProtKB F1P657), Mus musculus TdT

(UniProtKB Q3UZ80), Gallus gallus TdT (UniProtKB P36195) and Homo sapiens TdT (UniProtKB P04053) obtained by means of the online alignment software (http://multalin.toulouse.infra.fr/multalin/multalin.html);

Figure 3: Comparison of the activity of a truncated wild-type TdT of sequence SEQ ID No. 3 and of several variants of this truncated TdT comprising different substitutions given in table 1, in the presence of a primer which has been radioactively labeled beforehand at the 5' end and of 3'-O-amino-2',3'-dideoxyadenosine-5'-triphosphate modified nucleotides (ONH2 gel) or 3'-biot-EDA-2',3'-dideoxyadenosine-5'-triphosphate modified nucleotides (Biot-EDA gel); on SDS-PAGE gel (No: no enzyme present; wt: truncated wild-type TdT of sequence SEQ ID No. 3; DSi: Variants i defined in table 1);

Figure 4: Study of the activity of the variant DS124 according to the invention (see table 1), in the presence of a primer which has been radioactively labeled beforehand at the 5' end and different 3'-O-amino-2',3'-dideoxyadenosine-5'-triphosphate modified nucleotides on SDS-PAGE gel;

Figure 5: Study of the activity of the variants DS22, DS24, DS124, DS125, DS126, DS127 and DS128 in the presence of a primer which has been radioactively labeled beforehand at the 5' end and different 3'-O-amino-2',3'-dideoxyadenosine-5'-triphosphate modified nucleotides on SDS-PAGE gel;

Figure 6: Synthesis of a DNA strand of sequence: 5'-GTACGCTAGT-3' (SEQ ID No. 15) after the primer of sequence 5'-AAAAAAAAAAGGGG-3' (SEQ ID No. 14) by means of a variant of the TDT according to the invention having the combination of substitutions R336N - R454A - E457G (DS125).

Detailed description of the invention

Definitions

The amino acids are represented in this document by a one-letter or three-letter code according to the following nomenclature: A: Ala (alanine); R: Arg (arginine); N: Asn (asparagine); D: Asp (aspartic acid); C: Cys (cysteine); Q: Gln (glutamine); E: Glu (glutamic acid); G: Gly (glycine); H: His (histidine); I: Ile (isoleucine); L: Leu (leucine); K: Lys (lysine); M: Met (methionine); F: Phe (phenylalanine); P: Pro (proline); S: Ser (serine); T: Thr (threonine); W: Trp (tryptophan); Y: Tyr (tyrosine); V: Val (valine).

"Percentage of identity" between two nucleic acid or amino acid sequences in the sense of the present invention is understood to designate a percentage of nucleotides or of amino acid residues which are identical between the two sequences to be compared, which is obtained after the best alignment, this percentage being purely statistical and the differences between the two sequences being distributed randomly and over their entire length. The best alignment or optimal alignment is the alignment for which the percentage of identity between the two sequences to be compared, as calculated below, is the highest. The comparisons of sequences between two nucleic acid or amino acid sequences are traditionally carried out by comparing these sequences after having aligned them in an optimal manner, said comparison being carried out by segment or by comparison window in order to identify and compare the local regions of sequence similarity. The optimal alignment of the sequences for the comparison can be carried out, besides manually, by means of the local homology algorithm of Smith and Waterman (1981) (Ad. App. Math. 2:482), by means of the local homology algorithm of Neddleman and Wunsch (1970) (J. Mol. Biol. 48:443), by means of the similarity search method of Pearson and Lipman (1988) (Proc. Natl. Acad. Sci. USA 85:2444), by means of computer software using these algorithms (GAP,

BESTFIT, FASTA and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), by means of the online alignment software Mutalin (http://multalin.toulouse.inra.fr/multalin/multalin.html; 1988, Nucl. Acids Res., 16 (22), 10881-10890). The percentage of identity between two nucleic acid or amino acid sequences is determined by comparing these two sequences which are aligned in an optimal manner by comparison window in which the region of the nucleic acid or amino acid sequence to be compared can comprise additions or deletions with respect to the reference sequence for an optimal alignment between these two sequences. The percentage of identity is calculated by determining the number of identical positions for which the nucleotide or the amino acid residue is identical between the two sequences, by dividing this number of identical positions by the total number of positions in the comparison window and by multiplying the result obtained by 100 in order to obtain the percentage of identity between these two sequences.

The variants which are the subject matters of the present invention are described as a function of their mutations on specific residues, the positions of which are determined by alignment with, or reference to, the enzymatic sequence SEQ ID No. 1. In the context of the invention, any variant carrying these same mutations on functionally equivalent residues is also covered. "Functionally equivalent residue" is understood to mean a residue in a sequence of a DNA polymerase of the polX family having a sequence homologous to SEQ ID No. 1 and having an identical functional role. The functionally equivalent residues are identified using sequence alignments which are carried out, for example, by means of the online alignment software Mutalin (http://multalin.toulouse.inra.fr/multalin/multalin.html; 1988, Nucl. Acids Res., 16 (22), 10881-10890). After alignment, the functionally equivalent residues are in homologous positions on the different sequences considered. The alignments of sequences and the

identification of functionally equivalent residues can occur between any DNA polymerases of the polX family and their natural variants, including interspecies variants. For example, the residue L40 of human TdT (UniProtKB P04053) is functionally equivalent to the residue M40 of chicken TdT (UniProtKB P36195) and to the residue V40 of Pan troglodytes Polμ (UniProtKB H2QUI0), said residues being considered after alignment of the sequences (Figure 2).

"Functional fragment" is understood to mean a fragment of a DNA polymerase of the polX family exhibiting the DNA polymerase activity. The fragment can comprise 100, 200, 300, 310, 320, 330, 340, 350, 360, 370, 380 or more consecutive amino acids of a DNA polymerase of the polX family. Preferably, the fragment comprises 380 consecutive amino acids of a DNA polymerase of the polX family consisting of the catalytic fragment of said enzyme.

The terms "mutant" and "variant" can be used interchangeably to refer to polypeptides derived from DNA polymerases of the polX family, or derivatives of functional fragments of such DNA polymerases, and in particular from a TdT such as the murine TdT according to the sequence SEQ ID No. 1, and comprising an alteration, namely a substitution, an insertion and/or a deletion in one or more positions and having a DNA polymerase activity. The variants can be obtained by various techniques well known in the art. In particular, examples of techniques for modifying the DNA sequence coding for the wild-type proteins comprise, without being limited thereto, directed mutagenesis, random mutagenesis, and the construction of synthetic oligonucleotides.

The term "modification" or "mutation" as used here with respect to a position or an amino acid residue means that the amino acid in the position considered has been modified with respect to the amino acid of the reference wild-type protein. Such modifications comprise the substitutions, deletions and/or insertions of one or more amino acids, and in particular 1 to 5, 1 to

4, 1 to 3, 1 to 2 amino acids, in one or more positions, and in particular in 1, 2, 3, 4, 5 or more positions.

The term "substitution," in relation to a position or an amino acid residue, means that the amino acid in the particular position has been replaced by another amino acid than the wild-type or parent DNA polymerase. Preferably, the term "substitution" denotes the replacement of one amino acid residue by another amino acid residue selected from the 20 standard natural amino acid residues, the rare amino acid residues of natural origin (for example, hydroxyproline, hydroxylysine, allohydroxylysine, 6-N-methyllysine, N-ethylglycine, N-methylglycine, N-ethylasparagine, allo-isoleucine, N-methylisoleucine, N-methylvaline, pyroglutamine, aminobutyric acid, ornithine), and the rare non-natural amino acid residues, often produced synthetically (for example, norleucine, norvaline and cyclohexylalanine). Preferably, the term "substitution" denotes the replacement of one amino acid residue by another amino acid residue selected from the 20 standard amino acid residues of natural origin (G, P, A, V, L, I, M, C, F, Y, W, H, K, R, Q, N, E, D, S and T). The substitution can be a conservative or non-conservative substitution. The conservative substitutions occur within the same group of amino acids, among the basic amino acids (arginine, lysine and histidine), the acidic amino acids (glutamic acid and aspartic acid), the polar amino acids (glutamine and asparagine), the hydrophobic amino acids (methionine, leucine, isoleucine and valine), the aromatic amino acids (phenylalanine, tryptophan and tyrosine), and the small amino acids (glycine, alanine, serine and threonine). In the present document, the following terminology is used to designate a substitution: R454F indicates that the amino acid residue in position 454 of the SEQ ID No. 1 (arginine, R) is replaced by a phenylalanine (F). N474S/T/N/Q means that the amino acid in position 474

(asparagine, N) can be replaced by a serine (S), a threonine (T), an asparagine (N) or a glutamine (Q). The "+" indicates a combination of substitutions.

The invention relates to variants of DNA polymerases of the polX family (EC 2.7.7.7; Advances in Protein Chemistry, Vol. 71, 401-440) which are capable of synthesizing a nucleic acid molecule without a template strand, and in particular a DNA or RNA strand. The DNA polymerases of the polX family comprise in particular the DNA polymerase Polβ (UniProt P06746 in humans; Q8K409 in mice), Polσ, Polλ (UniProt Q9UGP5 in humans; Q9QUG2 and Q9QXE2 in mice) and Polμ (UniProt Q9NP87 in humans; Q9JIW4 in mice), Pol4 (UniProt A7TER5 in the yeast *Vanderwaltozyma polyspora*; P25615 in the yeast *Saccharomyces cerevisiae*) and the terminal deoxyribonucleotidyl transferase or TdT (EC 2.7.7.31; UniProt P04053 in humans; P09838 in mice).

The invention relates more particularly to a variant of a DNA polymerase of the polX family capable of synthesizing a nucleic acid molecule without a template strand, or to a variant of a functional fragment of such a polymerase, said variant comprising at least one mutation of a residue in at least one position selected from the group consisting of T331, G332, G333, F334, R336, K338, H342, D343, V344, D345, F346, A397, D399, D434, V436, A446, L447, L448, G449, W450, G452, R454, Q455, F456, E457, R458, R461, N474, E491, D501, Y502, I503, P505, R508, N509 and A510, or a functionally equivalent residue, the positions indicated being determined by alignment with, or reference to, the sequence SEQ ID No. 1.

In an embodiment, the variant is capable of synthesizing a DNA strand and/or an RNA strand.

"Comprise at least one mutation" or "comprising at least one mutation" is understood to mean that the variant has one or more mutations as indicated with respect to the polypeptide

sequence SEQ ID No. 1, but it can have other modifications, in particular substitutions, deletions or additions.

In general, the mutation of one or more residues in the above positions makes it possible to enlarge the catalytic pocket (by targeting, for example, the positions W450, D434, D435, H342, D343, T331, R336, D399, R461, and/or R508) and to increase the accessibility to the catalytic pocket (by targeting, for example, the positions R458, E455, R454, A397, K338, and/or N509) and/or it confers greater flexibility to the structure of the enzyme, enabling it to receive modified nucleotides exhibiting large steric hindrance (by targeting, for example, the positions V436, F346, V344, F334, M330, L448, E491, E457 and/or N474).

The variants which are the subject matters of the present invention can be variants of Pol IV, Pol μ, Polβ, Polλ or of TdT, preferably variants of Pol IV, Pol μ, or TdT. Alternatively, the variants can be variants of chimeric enzymes, combining, for example, portions of different sequences of at least two DNA polymerases of the polX family.

In a particular embodiment, the variant has at least 60% identity with the sequence according to SEQ ID No. 1, preferably at least 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% and less than 100% identity with the sequence according to SEQ ID No. 1.

According to the invention, the mutation can consist of a substitution, a deletion or an addition of one or more amino acid residues. In the deletion case, the annotation X is used, which indicates that the codon coding for the residue considered is replaced by a STOP codon; all the following amino acids as well as the residue in question are thus deleted. Thus, the mutation D501X means that the enzyme ends at the residue preceding the aspartic acid (D) in position 501, that is to say the leucine (L) in position 500, all the residues beyond having been deleted.

The annotation ∅, on the other hand, denotes a single point deletion of the residue considered. Thus, the mutation D501∅ means that the aspartic acid (D) in position 501 has been deleted.

Preferably, the variant according to the invention comprises at least one mutation of a residue in at least one position selected from the group consisting of T331, G332, G333, F334, R336, D343, L447, L448, G449, W450, G452, R454, Q455, E457 and R508, or a functionally equivalent residue, preferably at least one mutation of a residue in at least one position selected from the group consisting of R336, R454, E457, or a functionally equivalent residue, the positions indicated being determined by alignment with SEQ ID No. 1.

In a particular embodiment, said variant comprises at least one mutation of a residue in at least two positions selected from the group consisting of R336, R454 and E457, preferably a mutation of a residue in said three positions R336, R454 and E457, or a functionally equivalent residue, the positions indicated being determined by alignment with SEQ ID No. 1.

In a particular embodiment, the variant moreover comprises at least one mutation of a residue in at least the semi-conserved region of sequence $X_1X_2GGFR_1R_2GKX_3X_4$ (SEQ ID No. 4), in which

X_1 represents a residue selected from M, I, V, L

X_2 represents a residue selected from T, A, M, Q

X_3 represents a residue selected from M, K, E, Q, L, S, P, R, D

X_4 represents a residue selected from T, I, M, F, K, V, Y, E, Q, H, S, R, D.

Preferably, said variant has at least one substitution of a residue in at least one position R_1, R_2 and/or K of the semi-conserved region of sequence SEQ ID No. 4.

In another particular embodiment, the variant moreover comprises at least one mutation of a residue in at least one semi-conserved region of sequence $X_1X_2LGX_3X_4GSR_1X_5X_6ER_2$ (SEQ ID No. 5) in which

X_1 represents a residue selected from A, C, G, S

X_2 represents a residue selected from L, T, R

X_3 represents a residue selected from W, Y

X_4 represents a residue selected from T, S, I

X_5 represents a residue selected from Q, L, H, F, Y, N, E, D or ∅

X_6 represents a residue selected from F, Y

Preferably, said variant has at least one substitution of a residue in at least one position S, R_1 and/or E of the semi-conserved region of sequence SEQ ID No. 5.

In another particular embodiment, the variant moreover comprises at least one mutation of a residue in at least one semi-conserved region of sequence $LX_1YX_2X_3PX_4X_5RNA$ (SEQ ID No. 6) in which

X_1 represents a residue selected from D, E, S, P, A, K

X_2 represents a residue selected from I, L, M, V, A, T

X_3 represents a residue selected from E, Q, P, Y, L, K, G, N

X_4 represents a residue selected from W, S, V, E, R, Q, T, C, K, H

X_5 represents a residue selected from E, Q, D, H, L.

Preferably, said variant has at least one deletion of the residue in position X_1 and/or at least one substitution in positions R and/or N of the semi-conserved region of sequence SEQ ID No. 6.

In a particular embodiment, the variant comprises a substitution of a residue in at least one position selected from the group consisting of R336, K338, H342, A397, S453, R454, E457, N474, D501, Y502, I503, R508 and N509, or a functionally equivalent residue, preferably a substitution of a residue in at least one position selected from the group consisting of R336, A397, R454, E457, N474, D501, Y502 and I503, or a functionally equivalent residue, more preferably at least one substitution of a residue in at least one position selected from the group consisting of R336, R454 and E457, or a functionally equivalent residue, the positions indicated being determined by alignment with SEQ ID No. 1.

The invention preferably relates to a variant of a DNA polymerase of the polX family comprising at least one substitution from the group consisting of R336K/H/G/N/D, K338A/C/G/S/T/N, H342A/C/G/S/T/N, A397R/H/K/D/E, S453A/C/G/S/T, R454F/Y/W/A, E457G/N/S/T, N474S/T/N/Q, D501A/G/X, Y502A/G/X, I503A/G/X, R508A/C/G/S/T, N509A/C/G/S/T. In a particular embodiment, the variant comprises a substitution of a residue in at least two positions selected from the group consisting of R336, R454, E457, or a functionally equivalent residue, preferably a substitution of a residue in said three positions, or a functionally equivalent residue, the positions indicated being determined by alignment with SEQ ID No. 1. In particular, the substitutions are selected from the group consisting of R336K/H/G/N/D, R454F/Y/W/A and E457N/D/G/S/T, preferably from the group consisting of R336N/G, R454A and E457G/N/S/T.

In an embodiment, the variant comprises at least one substitution according to E457G/N/S/T.

Advantageously, the variant comprises a combination of substitutions selected from the group mentioned above. The combination can consist of 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 substitutions selected from this group.

The invention relates more particularly to variants of a DNA polymerase of the polX family which are capable of synthesizing a nucleic acid molecule, such as a DNA or RNA strand without a template strand, or of a functional fragment of such a polymerase, said variants comprising at least one combination of mutations described in table 1, the positions indicated being determined by alignment with SEQ ID No. 1.

In an embodiment, the variant of a DNA polymerase of the polX family comprises a combination of substitutions from R336G - E457N; R336N - E457N; R336N - R454A - E457N; R336N - E454A - E457G; R336N - E457G; and R336G - R454A - E457N.

Table 1: Examples of combinations of mutations of variants of a DNA polymerase of the polX family

	Combinations of mutations
DS1	R454F - E457N - A397D
DS2	R454F - E457N
DS3	R454Y - E457N - A397D
DS4	R454Y - E457N
DS5	R454W - E457N - A397D
DS6	R454W - E457N
DS7	R335A - E457N - A397D
DS8	R335A - E457N
DS9	R335G - E457N - A397D
DS10	R335G - E457N
DS11	R335N - E457N - A397D
DS12	R335N - E457N
DS13	R335D - E457N - A397D
DS14	R335D - E457N
DS15	R336K - E457N - A397D
DS16	R336K - E457N
DS17	R336H - E457N - A397D
DS18	R336H - E457N
DS21	R336G - E457N - A397D
DS22	R336G - E457N
DS23	R336N - E457N - A397D
DS24	R336N - E457N
DS25	R336D - E457N - A397D
DS26	R336D - E457N
DS27	R454A - E457N
DS28	R454A - E457A
DS29	R454A - E457G
DS30	R454A - E457D

DS31	E457N
DS32	E457D
DS33	R454A - E457N - A397D
DS34	R454A - E457N - A397K
DS35	R454A - E457N - N474S
DS36	R454A - E457D - A397D
DS37	D501X
DS38	D501X - E457N
DS39	D501X - E457N - A397D
DS40	R454F - E457S - A397D
DS41	R454F - E457S
DS42	R454Y - E457S - A397D
DS43	R454Y - E457S
DS44	R454W - E457S - A397D
DS45	R454W - E457S
DS46	R335A - E457S - A397D
DS47	R335A - E457S
DS48	R335G - E457S - A397D
DS49	R335G - E457S
DS50	R335N - E457S - A397D
DS51	R335N - E457S
DS52	R335D - E457S - A397D
DS53	R335D - E457S
DS54	R336K - E457S - A397D
DS55	R336K - E457S
DS56	R336H - E457S - A397D
DS57	R336H - E457S
DS60	R336G - E457S - A397D
DS61	R336G - E457S
DS62	R336N - E457S - A397D
DS63	R336N - E457S
DS64	R336D - E457S - A397D

DS65	R336D - E457S
DS66	R454A - E457S
DS70	E457S
DS72	R454A - E457S - A397D
DS73	R454A - E457S - A397K
DS74	R454A - E457S - N474S
DS75	D501X - E457S
DS76	D501X - E457S - A397D
DS77	R454F - E457T - A397D
DS78	R454F - E457T
DS79	R454Y - E457T - A397D
DS80	R454Y - E457T
DS81	R454W - E457T - A397D
DS82	R454W - E457T
DS83	R335A - E457T - A397D
DS84	R335A - E457T
DS85	R335G - E457T - A397D
DS86	R335G - E457T
DS87	R335N - E457T - A397D
DS88	R335N - E457T
DS89	R335D - E457T - A397D
DS90	R335D - E457T
DS91	R336K - E457T - A397D
DS92	R336K - E457T
DS93	R336H - E457T - A397D
DS94	R336H - E457T
DS97	R336G - E457T - A397D
DS98	R336G - E457T
DS99	R336N - E457T - A397D
DS100	R336N - E457T
DS101	R336D - E457T - A397D
DS102	R336D - E457T

DS103	R454A - E457T
DS104	E457T
DS105	R454A - E457T - A397D
DS106	R454A - E457T - A397K
DS107	R454A - E457T - N474S
DS108	D501X - E457T
DS109	D501X - E457T - A397D
DS110	D502X
DS111	D502X - E457N
DS112	D502X - E457TN - A397D
DS113	D502X - E457S
DS114	D502X - E457S - A397D
DS115	D502X - E457T
DS116	D502X - E457T - A397D
DS117	D503X
DS118	D503X - E457N
DS119	D503X - E457TN - A397D
DS120	D503X - E457S
DS121	D503X - E457S - A397D
DS122	D503X - E457T
DS123	D503X - E457T - A397D
DS124	R336N – R454A – E457N
DS125	R336N – R454A – E457G
DS126	R336N – E457G
DS127	R336G – R454A – E457N

In a particular embodiment, the variant is a chimeric construct of DNA polymerases of the polX family. "Chimeric construct" is understood to mean a chimeric enzyme formed by the addition, and in particular the fusion or the conjugation, of one or more predetermined sequences

of an enzyme which is a member of the polX family as a replacement of one or more homologous sequences in the DNA polymerase variant considered.

Thus, the invention proposes a variant of the TdT of sequence SEQ ID No. 1 comprising, in addition to one or more point mutations in one and/or the other of the above positions, a substitution of the residues between the positions C378 to L406, or the functionally equivalent residues, by the residues H363 to C390 of the polymerase Polμ of sequence SEQ ID No. 2, or the functionally equivalent residues.

Alternatively or additionally, variants which are the subject matters of the present invention can have a deletion of one or more successive amino acid residues at the N-terminal end. These deletions can target in particular one or more enzymatic domains involved in the bond with other proteins and/or involved in the cellular localization. For example, the polypeptide sequence of the TdT comprises at the N-terminal end a BRCT domain of interaction with other proteins such as Ku70/80 and a nuclear localization domain (NLS).

In a particular embodiment of the present invention, the variant is a variant of the TdT of sequence SEQ ID No. 1 having, in addition to one or more of the mutations described above, a deletion of the residues 1-129 corresponding to the N-terminal end of the wild-type TdT.

In certain particular cases, the mutagenesis strategies can be guided by known information such as the sequences of natural variants, the sequence comparison with bound proteins, physical properties, the study of a three-dimensional structure or computer simulations involving such entities.

The present invention relates to a nucleic acid coding for a variant of a DNA polymerase of the polX family capable of synthesizing a nucleic acid molecule without a template strand according to the present invention. The present invention also relates to an expression cassette of

a nucleic acid according to the present invention. The invention further relates to a vector comprising a nucleic acid or an expression cassette according to the present invention. The vector can be selected from a plasmid or a viral vector.

The nucleic acid coding for the DNA polymerase variant can be DNA (cDNA or gDNA), RNA, a mixture of the two. It can be in single-strand form or in duplex form or a mixture of the two forms. It can comprise modified nucleotides comprising, for example, a modified bond, a modified purine or pyrimidine base, or a modified sugar. It can be prepared by any of the methods known to the person skilled in the art, including chemical synthesis, recombination, mutagenesis, etc…

The expression cassette comprises all the elements necessary for the expression of the variant of a DNA polymerase of a polX family capable of synthesizing a nucleic acid molecule without a template strand according to the present invention, in particular the elements necessary for transcription and translation in the host cell. The host cell can be prokaryotic or eukaryotic. In particular, the expression cassette comprises a promoter and a terminator, optionally an amplifier. The promoter can be prokaryotic or eukaryotic. The following are examples of preferred prokaryotic promoters: LacI, LacZ, pLacT, ptac, pARA, pBAD, the bacteriophage T3 or T7 RNA polymerase promoters, the polyhydrin promoter, the lambda phage PR or PL promoter. The following are examples of preferred eukaryotic promoters: the early CMV promoter, the HSV thymidine kinase promoter, the early or late SV40 promoter, the murine murine metallothionein-L promoter, and LTR regions of certain retroviruses. In general, for the selection of an appropriate promoter, the person skilled in the art can advantageously refer to the work by Sambrook et al. (1989) or to the techniques described by Fuller et al. (1996; Immunology in Current Protocols in Molecular Biology).

The present invention relates to a vector carrying a nucleic acid or an expression cassette coding for a variant of a DNA polymerase of the polX family capable of synthesizing a nucleic acid molecule without a template strand according to the present invention. The vector is preferably an expression vector, that is to say it comprises the elements necessary for the expression of the variant in the host cell. The host cell can be a prokaryote, for example, *E. coli*, or a eukaryote. The eukaryote can be a lower eukaryote such as a yeast (for example, *P. pastoris* or *K. lactis*) or a fungus (for example, of the *Aspergillus* genus) or a higher eukaryote such as an insect cell (Sf9 or Sf21, for example), a mammalian cell or a plant cell. The cell can be a mammalian cell, for example, COS (green monkey cell line) (for example, COS 1 (ATCC CRL-1650), COS 7 (ATCC CRL-1651), CHO (US 4,889,803; US 5,047,335, CHO-K1 (ATCC CCL-61)), murine cells and human cells. In a particular embodiment, the cell is non-human and non-embryonic. The vector can be a plasmid, a phage, a phagemid, a cosmid, a virus, a YAC, a BAC, an *Agrobacterium* pTi plasmid, etc… The vector can preferably comprise one or more elements selected from a replication origin, a multiple cloning site and a selection gene. In a preferred embodiment, the vector is a plasmid. The following are non-exhaustive examples of prokaryotic vectors: pQE70, pQE60, pQE-9 (Qiagen), pbs, pD10, phagescript, psiX174, pbluescrip SK, pbsks, pNH8A, pNH16A, pNH18A, pNH46A (Stratagene); ptrc99a, pKK223-3, pKK233-3, pDR540, pBR322, and pRIT5 (Pharmacia), pET (Novagen). The following are non-exhaustive examples of eukaryotic vectors: pWLNEO, pSV2CAT, pPICZ, pcDNA3.1 (+) Hyg (Invitrogen), pOG44, pXT1, pSG (Strategene); pSVK3, pBPV, pCI-neo (Stratagene), pMSG, pSVL (Pharmacia); and pQE-30 (QLAexpress). The viral vectors can be in a non-exhaustive manner adenoviruses, AAV, HSV, lentiviruses, etc… Preferably, the expression vector is a plasmid or a viral vector.

The sequence coding for the variant according to the present invention may or may not comprise a signal peptide. In the case in which it does not comprise a signal peptide, a methionine can optionally be added to the N-terminal end. In another alternative, a heterologous signal peptide can be introduced. This heterologous signal peptide can be derived from a prokaryote such as *E. coli* or from a eukaryote, in particular a mammalian cell, an insect cell, or a yeast.

The present invention relates to the use of a polynucleotide, of an expression cassette or of a vector according to the present invention for transforming or transfecting a cell. The present invention relates to a host cell comprising a nucleic acid, an expression cassette or a vector coding for a variant of a polymerase DNA of the polX family capable of synthesizing a nucleic acid molecule without a template strand and to its use for producing a variant of a DNA polymerase of the polX family capable of synthesizing a nucleic acid molecule without a recombinant template strand according to the present invention. The term "host cell" encompasses the daughter cells resulting from the culture or from the growth of this cell. In a particular embodiment, the cell is non-human and non-embryonic. The present invention also relates to a method for producing a variant of a DNA polymerase of the polX family capable of synthesizing a nucleic acid molecule without a recombinant template strand according to the present invention, comprising the transformation or transfection of a cell by a polynucleotide, an expression cassette or a vector according to the present invention; the culturing of the transfected/transformed cell; and the harvesting of the variant of a DNA polymerase of the polX family capable of synthesizing a nucleic acid molecule without a template strand produced by the cell. In an alternative embodiment, a method for producing a variant of a DNA polymerase of the polX family capable of synthesizing a nucleic acid molecule without recombinant template

strand according to the present invention comprises the provision of a cell comprising a polynucleotide, an expression cassette or a vector according to the invention; the culturing of the transfected/transformed cell; and the harvesting of the variant of a DNA polymerase of the polX family capable of synthesizing a nucleic acid molecule without a template strand produced by the cell. In particular, the cell can be transformed/transfected in a transient or stable manner by the nucleic acid coding for the variant. This nucleic acid can be contained in the cell in the form of an episome or in chromosomal form. The methods for producing recombinant proteins are well known to the person skilled in the art. For example, it is possible to cite the specific procedures described in US 5,004,689, EP 446 582, Wang et al. (Sci. Sin. B 24:1076-1084, 1994 and Nature 295, page 503) for production in *E. coli*, and JAMES et al. (Protein Science (1996), 5:331-340) for production in mammalian cells.

The DNA polymerase variants according to the present invention are particularly advantageous for the synthesis of nucleic acids without a template strand. More particularly, the variants according to the invention have an enlarged catalytic pocket which is particularly suitable for the synthesis of nucleic acid by means of modified nucleotides exhibiting greater steric hindrance than the natural nucleotides. The variants according to the invention can in particular make it possible to incorporate modified nucleotides such as those described in the application WO2016/034807 in a nucleic acid strand.

The kinetics of incorporations of DNA polymerase variants and in particular of the variants of the TdT according to the invention, presenting the mutations or the combinations of specific mutations described above, are greatly improved in comparison to the kinetics of incorporation of a wild-type DNA polymerase. These variants can advantageously be used in the context of a high-performance enzymatic DNA synthesis method.

Thus, the invention also relates to a use of a variant of a DNA polymerase of the polX family according to the present invention for synthesizing a nucleic acid molecule without a template strand, from 3'-OH modified nucleotides, and in particular those described in the application WO2016034807.

The invention also relates to a method for the enzymatic synthesis of a nucleic acid molecule without a template strand, according to which a primer strand is brought in contact with at least one nucleotide, preferably a 3'-OH modified nucleotide, in the presence of a variant of a DNA polymerase of the polX family according to the invention.

Advantageously, the variants according to the invention can be used to carry out the synthesis method described in the application WO2015/159023.

The invention also relates to a kit for the enzymatic synthesis of a nucleic acid molecule without a template strand, comprising at least one variant of a DNA polymerase of the polX family according to the invention, nucleotides, preferably 3'-OH modified nucleotides, and optionally at least one nucleotide primer.

All the references cited in this description are incorporated by reference in the present application. Other features and advantages of the invention will become clearer upon reading the following examples which are of course for illustration and non-limiting.

Examples

Example 1– Generation, production and purification of DNA polymerase variants of the polX family according to the invention

Generation of the producer strains

The truncated gene of the murine TdT was generated from the plasmid pET28b, the construction of which is described in [Boulé et al., 1998, *Mol. Biotechnol.*, **10**, 199-208]. The corresponding sequence SEQ ID No. 3 (corresponding to SEQ ID No. 1 truncated by the first 120 amino acids) was amplified using the following primers:

- T7-pro: TAATACGACTCACTATAGGG (SEQ ID No. 7)
- T7-ter: GCTAGTTATTGCTCAGCGG (SEQ ID No. 8)

according to the usual PCR amplification and molecular biology techniques. It was cloned in a plasmid pET32 to yield the vector pET32-SEQ ID No. 3.

The plasmid pET32-SEQ ID No. 3 was first sequenced, and then transformed in the commercial *E. coli* strains BL21 (DE3) (Novagen). The colonies that were capable of growing in kanamycin/chloramphenicol petri dishes were isolated and labeled Ec-SEQ ID No. 3.

Generation of the variants

The vector pET32-SEQ ID No. 3 was used as starting vector. Primers comprising the point mutation (or in some cases the point mutations if they are sufficiently close) were generated from the online tool of Agilent: (http://www.genomics.agilent.com/primerDesignProgram.jsp)

The QuickChange II (Agilent) kit was used to generate the plasmids of the variants comprising the desired mutation(s). The mutagenesis protocol given by the manufacturer was scrupulously respected in order to obtain a plasma pET32-DSi (i is the number of the variant in question given in table 1). At the end of the procedure, the plasmid pET32-DSx was first sequenced, then transformed in the commercial *E. coli* strains BL21 (DE3) (Novagen). The

colonies that were capable of growing in kanamycin/chloramphenicol petri dishes were isolated and labeled Ec-DSx.

Production

The cells Ec- SEQ ID No. 3 and Ec-DSx were precultured in 250 mL Erlenmeyer flasks containing 50 mL of LB medium to which appropriate quantities of kanamycin and chloramphenicol were added. The culture was incubated at 37 °C under stirring overnight. The preculture was then used to inoculate a 5 L Erlenmeyer flask containing 2 L of LB medium with the addition of appropriate quantities of kanamycin and chloramphenicol. The starting optical density (OD) was 0.01. The culture was incubated at 37 °C under stirring. The OD was measured regularly until a value between 0.6 and 0.9 was reached. Once this value was reached, 1 mL of isopropyl β-D-1-thiogalactopyranoside 1 M was added to the culture medium. The culture was incubated again at 37 °C until the next day. The cells were then harvested by centrifugation without exceeding 5,000 rpm. The different pellets obtained were collected to form a single pellet during the washing with the lysis buffer (20 mM Tris-HCl, pH 8.3, 0.5 M NaCl). The cell pellet was frozen at -20 °C. It can be stored in this way for several months.

Extraction

The cell pellet frozen during the preceding step was thawed in a water bath heated at 25 to 37°C. Once the thawing was completed, the cell pellet was resuspended in approximately 100 mL of lysis buffer. Particular attention was paid to the resuspension which must lead to a very homogeneous solution and in particular to complete absence of aggregates. Thus resuspended, the cells were lysed using a French press at a pressure of 14,000 psi. The lysate collected was

centrifuged at high speed, 10,000 g for 1 h to 1 h 30. The centrifugate was filtered through a 0.2 µM filter and collected in a tube of sufficient volume.

Purification

The TdT was purified on an affinity column. 5 mL His-Trap Crude (GE Life Sciences) columns were used with peristaltic pumps (Peristaltic Pump - MINIPULS® Evolution, Gilson). In a first step, the column was equilibrated using 2 to 3 CV (column volume) of lysis buffer. The centrifugate of the preceding step was then loaded onto the column at a rate of approximately 0.5 to 5 mL/min. Once all the centrifugate was loaded, the column was washed using 3 CV of lysis buffer, then 3 CV of washing buffer (20 mM Tris-HCl, pH 8.3, 0.5 M NaCl, 60 mM imidazole). At the end of this step, the elution buffer (20 mM Tris-HCl, pH 8.3, 0.5 M NaCl, 1 M imidazole) was injected in the column at approximately 0.5 to 1 mL/min for a total volume of 3 CV. During the entire elution phase, the outflow of the column was collected in 1 mL fractions. These fractions were analyzed by SDS-PAGE, in order to determine which fractions contain the elution peak. Once the fractions were determined, they were pooled to a form a single fraction and dialyzed against the dialysis buffer (20 mM Tris-HCl, pH 6.8, 200 mM NaCl, 50 mM MgOAc, 100 mM $[NH_4]_2SO_4$. The TdT was then concentrated (Amicon Ultra-30 centrifuge filters, Merk Millipore) to a final concentration of 5 to 15 mg/mL. The concentrated TdT was frozen at -20 °C for long-term storage after the addition of 50% glycerol. Throughout the entire purification phase, aliquots of different samples were collected (approximately 5 µL) for an SDS-PAGE gel analysis, the results of which are presented in figure 1.

Example 2 — Alignment of sequences between different polymerases of the polX family capable of being used for the creation of variants according to the invention

Different DNA polymerases of the polX family were aligned using the online alignment software Mutalin (http://multalin.toulouse.inra.fr/multalin/multalin .html, accessed on April 4, 2016).

Table 2: Aligned sequences

Identifier	DNA polymerase	Species	Length
Q9NP87	Pol μ (SEQ ID No. 2)	*Homo sapiens*	494
H2QUI0	Pol μ (SEQ ID No. 9)	*Pan troglodytes*	494
Q924W4	Pol μ (SEQ ID No. 10)	*Mus musculus*	496
F1P657	TdT (SEQ ID No. 11)	*Canis lupus familiaris*	509
Q3UZ80	TdT (SEQ ID No. 1)	*Mus musculus*	510
P36195	TdT (SEQ ID No. 12)	*Gallus gallus*	506
P04053	TdT (SEQ ID No. 13)	*Homo sapiens*	509

The alignments obtained are presented in figure 2.

Example 3 – Study of the activity of the variants in the presence of non-natural substrates

The activity of different variants according to the invention was determined by the following test. The results were compared to those obtained with the natural enzyme from which each of the variants is derived.

Activity test

Table 3: Reaction mixture

Reagent	Concentration	Volume
H_2O	-	15 µL
Primer	500 nM	2.5 µL
Buffer	10x	2.5 µL
Modified nucleotide	250 µM	2.5 µL
Enzyme	20 µM	2.5 µL

The primer used, of sequence 5'-AAAAAAAAAAGGGG-3' (SEQ ID No. 14), was radioactively labeled at 5' beforehand by means of a standard labeling protocol involving the enzyme PNK (NEB) and the use of radioactive ATP (PerkinElmer).

The buffer 10x consisting of 250 mM Tris-HCl pH 7.2, 80 mM $MgCl_2$, 3.3 mM $ZnSO_4$ was used.

The modified nucleotides used are 3'-O-amino-2',3'-dideoxynucleotides-5'-triphosphate (ONH2, Firebird Biosciences) or 3'-biot-EDA-2',3'-dideoxynucleotides-5'-triphosphate (Biot-EDA, Jena Biosciences), such as 3'-O-amino-2',3'-dideoxyadenosine-5'-triphosphate or 3'-biot-EDA-2',3'-dideoxyadenosine-5'-triphosphate, for example. The 3'-O-amino group is a group of larger volume bound to the 3'-OH end. The 3'-biot-EDA group is an extremely large-volume and inflexible group bound to the 3'-OH end.

The performances of incorporation of a modified nucleotide given by the variants produced by the variants listed in table 1 were evaluated in comparison to the natural TdT (SEQ ID No. 3) by carrying out simultaneous activity tests for which only the enzyme varies.

The reagents were added in the order given in table 3 above and then incubated at 37 °C for 90 min. The reaction was then stopped by the addition of formamide blue (formamide 100%, 1 to 5 mg of bromophenol blue; Simga)

Gel and radiography

A 16% polyacrylamide denaturing gel (Biorad) was used for the analysis of the preceding activity test. The gel was first poured and allowed to polymerize. Then it was mounted on an electrophoresis tank having appropriate dimensions, filled with TBE buffer (Sigma). The different samples were loaded directly on the gel without pretreatment.

The gel was then subjected to a potential difference of 500 to 2000 V for 3 to 6 hours. Once the migration was satisfactory, the gel was dismounted and then transferred to an incubation cassette. The phosphor screen (Amersham) was used for 10 to 60 min for imaging by means of a Typhoon instrument (GE Life Sciences) which was parameterized beforehand with an appropriate detection mode.

Results

The comparative results of the two enzymes used are presented in figure 3.

More precisely, on the first gel (ONH2 incorporation), the natural TdT (wt column) is incapable of incorporating the 3'-O-amino-2',3'-dideoxyadenosine-5'-triphosphate modified nucleotides as shown by the comparison with the negative control (No column).

Among the different variants, 3 different groups can be observed:

A first group of variants (columns DS7 to DS34) is capable of approximately 50% incorporation.

A second group of variants (columns DS46 to DS73) is capable of more than 95%, sometimes more than 98% incorporation.

A third group of variants (columns DS83 to DS106) is capable of 60 to 80% incorporation.

On the second gel (Biot-EDA incorporation), the natural TdT (wt column) is also incapable of incorporating the 3'-biot-EDA-2',3'-dideoxyadenosine-5'-triphosphate modified nucleotides, as shown by the comparison with the negative control (No column).

Among the different variants, 3 different groups can be observed:

A first group of variants (columns DS7 to DS34) is capable of approximately 5 to 10% incorporation.

A second group of variants (columns DS46 to DS73) is capable of more than 30%, sometimes more than 40% incorporation.

A third group of variants (columns DS83 to DS106) is capable of 10 to 25% incorporation.

These results confirm that, in contrast to the wild-type enzyme, the variants of the TdT according to the invention are all capable of using modified nucleotides, in particular 3'-OH modified nucleotides, as a substrate. Particularly advantageously, certain variants have very high incorporation rates and this even in the presence of nucleotides carrying modifications which tend to result in a very large increase in the steric hindrance of said nucleotide.

Example 4 – Study of the kinetics of the variants according to the invention

A mutant having the combination of substitutions R336N - R454A - E457N (DS124) was generated and produced according to the preceding example 1.

Activity test

In the activity test, the enzymes are brought in the presence of ONH2 modified nucleotides and incubated at 37 °C for different times. The reactions are stopped in order to observe the kinetics of incorporation of DS124 and to compare it with the kinetics of the natural WT enzyme (SEQ ID No. 3).

Table 4: Reaction mixture

Reagent	*Concentration*	*Volume*
H_2O	-	15 µL
Buffer	10x	2.5 µL
Nucleotides	2.5 µM	2.5 µL
Enzyme	80 µM	2.5 µL
Primer	1 µM	2.5 µL

The primer and the buffer used are in accordance with example 3.

The modified nucleotides used are 3'-O-amino-2',3'-dideoxynucleotides-5'-triphosphate (ONH2, Firebird Biosciences): 3'-O-amino-2',3'-dideoxyguanosine-5'-triphosphate, 3'-O-amino-

2',3'-dideoxycytidine-5'-triphosphate and 3'-O-amino-2',3'-dideoxythymidine-5'-triphosphate. The 3'-O-amino group is a larger volume group bound to the 3'-OH end.

The performances of incorporation of the mixture of nucleotides by the enzyme DS124 were evaluated by carrying out activity tests for which premixes containing all the reagents (added in the order of table 4) except for the primer were prepared. They are distributed in different reaction wells. At the initial time t = 0, the primer is added to all the wells simultaneously. At the different times t = 2 min, t = 5 min, t = 10 min, t = 15 min, t = 30 min and t = 90 min, the reaction is stopped by the addition of formamide blue (formamide 100%, 1 to 5 mg of bromophenol blue; Simga).

Gel and radiography

The analysis of the activity test is carried out by migration of the different samples in a polyacrylamide gel according to the protocol described in example 3.

Results

The comparative results of the two enzymes (DS124 and WT) are presented in figure 4.

More precisely, on this gel, the negative control (No column) gives the expected size of the primer used when it has not been elongated, that is to say when there has been no incorporation of nucleotides. The natural TdT (WT column) is not capable of incorporating the modified nucleotides (here ONH2-dGTP): a band can be observed at the same level as that of the No column.

For all the nucleotides tested and for all the times from 90 min (used here as a positive control) to 2 min, corresponding to a reduction in the incubation time by a factor of 45, the

variant DS124 is capable of incorporating the modified nucleotides with an apparent effectiveness of 100%.

These results confirm that the variants of the TdT according to the invention are capable of incorporation performances much higher than those of the natural TdT, in terms of both incorporation effectiveness and rapidity of incorporation. The kinetics of the variants of the TdT according to the invention are greatly improved by the mutations or combinations of specific mutations described by the present invention.

Example 5 – Study of the specificity of the variants according to the invention

The mutants having a substitution combination according to table 5 below were generated and produced according to example 1.

Table 5: List of the enzymatic variants used

#	Combinations of mutations
DS124	R336N - R454A - E457N
DS24	R336N - E457N
DS125	R336N - R454A - E457G
DS126	R336N - E457G
DS127	R336G - R454A - E457N
DS22	R336G - E457N
DS128	R336A - R454A - E457G
WT	SEQ ID No. 3

Activity test

In this activity test, the different variants were put in the presence of a mixture of natural nucleotides and of highly concentrated modified nucleotides. The concentration of the enzyme is also increased in order to shorten the incubation time and to achieve a quantitative addition (compare example 4).

The activity of different variants generated was determined by the following test:

Each variant is tested according to two conditions: (1) in the absence of nucleotides (replaced by H_2O) or (2) in the presence of the mixture of nucleotides. The results of the different variants are compared to one another. A control sample was added; it contained neither nucleotide nor enzyme (which were replaced by H_2O).

Table 6: Reaction mixture

Reagent	*Concentration*	*Volume*
H_2O	-	15 µL
Primer	1 µM	2.5 µL
Buffer	10x	2.5 µL
Mixture nucleotides (10:90)	2.5 µM	2.5 µL
Enzyme	80 µM	2.5 µL

The primer and the buffer used are identical to example 3.

When present, the mixture of nucleotides consists of natural 2'-deoxynucleotide 5'-triphosphate nucleotides (Nuc, Sigma-Aldrich) such as 2'-deoxyguanosine 5'-triphosphate (dGTP) and of 3'-O-amino-2',3'-dideoxynucleotides-5'-triphosphate modified nucleotides (ONH2, Firebird Biosciences) such as 3'-O-amino-2',3'-dideoxyguanosine-5'-triphosphate, for example. The 3'-O amino group of larger volume bound to the 3'-OH end. The mixture consists of 90% ONH2-dGTP modified nucleotides and 10% of natural dGTP nucleotides.

The incorporation performances of the mixture of nucleotides by the variants listed in table 5 compared to one another were evaluated by carrying out simultaneous activity tests, for which only the enzyme varies.

The reagents were added in the order given in table 6 above, and then incubated at 37 °C for 15 min. The reaction was then stopped by the addition of formamide blue (formamide 100%, 1 to 5 mg of bromophenol blue; Simga).

Gel and radiography

The analysis of the activity test was carried out by migration of the different samples in a polyacrylamide gel according to the protocol described in example 3.

Results

The comparative results of the enzymes used are presented in figure 5.

More precisely, on this gel, the negative control (No column) gives the expected size of the primer used when it has not been elongated, that is to say when there has been no incorporation of nucleotides. The following samples are used in pairs, each pair corresponding to

the same enzymatic variant tested under the two conditions: in the absence and in the presence of nucleotides (in the form of a mixture when they are present).

Among the different variants tested, 3 different groups can be observed:

The first group is the variant DS128, which constitutes a negative control. This variant has extremely low rates of incorporation of the nucleotides: 5% to 10% incorporation is observed when the mixture of nucleotides is present; this corresponds to the proportion of natural nucleotides present in the mixture.

The second group consists of the variants DS127 and DS22. These variants have high rates of incorporation of the nucleotides: 50% to 60% of incorporation is observed when the mixture of nucleotides is present. In this case, a band of further addition corresponding to the successive incorporation of two nucleotides is always observed for these two variants. The intensity of this band corresponds to the proportion of natural nucleotides present in the mixture of nucleotides.

The last group consists of the variants DS124, DS24, DS125 and DS126. These variants have extremely high rates of incorporation of the nucleotides: 80% to 100% for DS124 and DS125, when the mixture of nucleotides is present. In this case, no band of further addition is present. In the case of the variants DS24 and DS126, the proportion of non-incorporation is similar to the proportion of natural nucleotides present in the mixture.

These results confirm that the variants of the TdT according to the invention are capable of preferentially using the modified nucleotides among a mixture of modified nucleotides and natural nucleotides. In a particularly advantageous manner, these variants have extremely high rates of incorporation of the modified nucleotides and are capable of discriminating the natural

nucleotides in such a manner as not to incorporate them and thus greatly improve the quality of the DNA to be synthesized by avoiding the further additions.

Example 6 – Example of the synthesis of a DNA strand without a template strand

A variant of TdT having the combination of substitutions R336N - R454A - E457G (DS125) was generated and produced according to example 1.

The variant DS125 is used to synthesize the sequence: 5'-GTACGCTAGT-3' (SEQ ID No. 15) after the primer of sequence 5'-AAAAAAAAAAGGGG-3' (SEQ ID No. 14). The primer was radioactively labeled at 5' beforehand by means of a standard labeling protocol involving the enzyme PNK (NEB) and the use of radioactive ATP (PerkinElmer).

The primer is bound to a solid support by interaction with a capture fragment of complementary sequence: 5'-CCTTTTTTTTTT-3' (SEQ ID No. 16). The capture fragment possesses at its 3' end a group which enables it to react covalently with a reaction group bound to a surface. For example, this group can be NH2, the reaction group N-hydroxysuccinimide, and the surface of a magnetic bead (Dynabeads, Thermofisher). The interaction of the primer with the capture fragment is carried out under standard DNA fragment hybridization conditions.

The modified nucleotides used are 3'-O-amino-2',3'-dideoxynucleotides-5'-triphosphate (ONH2, Firebird Biosciences) such as 3'-O-amino-2',3'-dideoxyguanosine-5'-triphosphate, 3'-O-amino-2',3'-dideoxycytidine-5'-triphosphate, 3'-O-amino-2',3'-dideoxythymidine-5'-triphosphate or 3'-O-amino-2',3'-dideoxyadenosine-5'-triphosphate. The 3'-O-amino group is a larger volume group bound to the 3'-OH end.

Synthesis

Table 7: Reaction mixture

Reagent	*Concentration*	*Volume*
H_2O	-	210 µL
Buffer	10x	70 µL
Nucleotides	2.5 µM	35 µL
Enzyme	80 µM	35 µL
Primer on solid support	1 µM	-

The buffer 10x consisting of 250 mM Tris-HCl pH 7.2, 80 mM MgCl2, 3.3 mM ZnSO4 was used.

The washing buffer L used consists of Tris-HCl 25 mM at pH 7.2.

The deprotection buffer D used consists of sodium acetate 50 mM, pH 5.5 in the presence of 10 mM MgCl2.

Before the start of the synthesis, the beads constituting the solid support on which the primers were hybridized for a total equivalent quantity of primer of 35 pmol were washed several times with the buffer L. After these washings, the beads were held on a magnet, and the supernatant was removed in its entirety.

Several premixes consisting of different reagents added in the order of table 7 were prepared. Each of these premixes contains different nucleotides according to table 8 below.

Table 8: Composition of the premixes

Premix number	Nucleotide of the premix
1	G
2	T
3	A
4	C
5	G
6	C
7	T
8	A
9	G
10	T

The synthesis starts when the premix 1 is added to the beads which have been washed beforehand and freed from their supernatant. The synthesis steps according to table 9 below follow after one another, in order to produce the new sequence 5'-GTACGCTAGT-3'.

Table 9: Step of the method of synthesis of a DNA strand without a template strand

Steps	*Action*	*Volume*	*Duration*
Elongation 1	Addition premix 1	350 µL	15 min
Sampling 1	Sampling	5 µL	< 1 min
1st Washing 1	Addition buffer L	350 µL	5 min

1st Deprotection 1	Additional buffer D	350 μL	15 min
2nd Deprotection 1	Additional buffer D	350 μL	15 min
2nd Washing 1	Addition buffer L	350 μL	5 min
Elongation 2	Addition premix 2	350 μL	15 min
Sampling 2	Sampling	5 μL	< 1 min
1st Washing 2	Addition buffer L	350 μL	5 min
1st Deprotection 2	Addition buffer D	350 μL	15 min
2nd Deprotection 2	Addition buffer D	350 μL	15 min
2nd Washing 2	Addition buffer L	350 μL	5 min
Elongation 3	Addition premix 3	350 μL	15 min
Sampling 3	Sampling	5 μL	< 1 min
1st Washing 3	Addition buffer L	350 μL	5 min
1st Deprotection 3	Addition buffer D	350 μL	15 min
2nd Deprotection 3	Addition buffer D	350 μL	15 min
2nd Washing 3	Addition buffer L	350 μL	5 min
Elongation 4	Addition premix 4	350 μL	15 min
Sampling 4	Sampling	5 μL	< 1 min
1st Washing 4	Addition buffer L	350 μL	5 min
1st Deprotection 4	Addition buffer D	350 μL	15 min
2nd Deprotection 4	Addition buffer D	350 μL	15 min
2nd Washing 4	Addition buffer L	350 μL	5 min
Elongation 5	Addition premix 5	350 μL	15 min
Sampling 5	Sampling	5 μL	< 1 min

1st Washing 5	Addition buffer L	350 µL	5 min
1st Deprotection 5	Addition buffer D	350 µL	15 min
2nd Deprotection 5	Addition buffer D	350 µL	15 min
2nd Washing 5	Addition buffer L	350 µL	5 min
Elongation 6	Addition premix 6	350 µL	15 min
Sampling 6	Sampling	5 µL	< 1 min
1st Washing 6	Addition buffer L	350 µL	5 min
1st Deprotection 6	Addition buffer D	350 µL	15 min
2nd Deprotection 6	Addition buffer D	350 µL	15 min
2nd Washing 6	Addition buffer L	350 µL	5 min
Elongation 7	Addition premix 7	350 µL	15 min
Sampling 7	Sampling	5 µL	< 1 min
1st Washing 7	Addition buffer L	350 µL	5 min
1st Deprotection 7	Addition buffer D	350 µL	15 min
2nd Deprotection 7	Addition buffer D	350 µL	15 min
2nd Washing 7	Addition buffer L	350 µL	5 min
Elongation 8	Addition premix 8	350 µL	15 min
Sampling 8	Sampling	5 µL	< 1 min
1st Washing 8	Addition buffer L	350 µL	5 min
1st Deprotection 8	Addition buffer D	350 µL	15 min
2nd Deprotection 8	Addition buffer D	350 µL	15 min
2nd Washing 8	Addition buffer L	350 µL	5 min
Elongation 9	Addition premix 9	350 µL	15 min

Sampling 9	Sampling	5 µL	< 1 min
1st Washing 9	Addition buffer L	350 µL	5 min
1st Deprotection 9	Addition buffer D	350 µL	15 min
2nd Deprotection 9	Addition buffer D	350 µL	15 min
2nd Washing 9	Addition buffer L	350 µL	5 min
Elongation 10	Addition premix 10	350 µL	15 min
Sampling 10	Sampling	5 µL	< 1 min

Between each step, except for the sampling step, the beads are collected by means of a magnet, and the supernatant is removed in its entirety.

Each sample is added to a solution of 15 µL of formamide blue (formamide 100%, 1 to 5 mg of bromophenol blue; Simga) in order to stop the reaction and prepare the analysis.

Gel and radiography

The analysis of the activity test is carried out by migration of the different samples in a polyacrylamide gel according to the protocol described in example 3.

Results

The results of this synthesis are presented in figure 6.

Column 0 (No, no nucleotides) gives the expected size of the primer used, when it has not been elongated, that is to say when there has been no incorporation of nucleotides.

Columns 1 to 10 correspond to samples 1 to 10 during the synthesis. Each incorporation of nucleotides was carried out by the enzyme with maximum performance. No additional purification step is carried out.

A similar synthesis experiment was carried out with the natural TdT. The latter being incapable of incorporating modified nucleotides, it was not possible to synthesize the desired sequence.

Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integers or steps.

The reference in this specification to any prior publication (or information derived from it), or to any matter which is known, is not, and should not be taken as, an acknowledgement or admission or any form of suggestion that that prior publication (or information derived from it) or known matter forms part of the common general knowledge in the field of endeavour to which this specification relates.

The claims defining the invention are as follows:

1. A variant of a DNA polymerase of the polX family capable of synthesizing a nucleic acid molecule without a template strand, or of a functional fragment of such a polymerase, said variant comprising a substitution at residue E457, or a functionally equivalent residue, the position indicated being determined by alignment with SEQ ID No. 1, said variant having at least 70% identity with the sequence according to SEQ ID No. 1 and being able to incorporate a modified nucleotide.

2. The variant according to claim 1, wherein said substitution at residue E457 is selected from E457G/N/S/T.

3. The variant according to claim 1 or 2, said variant comprising at least one mutation of a residue in at least one position selected from the group consisting of T331, G332, G333, F334, R336, K338, H342, D343, V344, D345, F346, A397, D399, D434, V436, A446, L447, L448, G449, W450, G452, R454, Q455, F456, R458, R461, N474, E491, D501, Y502, I503, P505, R508, N509 and A510, or a functionally equivalent residue, in which at least one mutation consists of a substitution, a deletion or an addition of one or more amino acid residues, the positions indicated being determined by alignment with SEQ ID No. 1.

4. The variant according to any one of the preceding claims, said variant being capable of synthesizing a DNA strand and/or an RNA strand and/or said variant being a variant of Pol IV, Pol μ, or of the terminal deoxyribonucleotidyl transferase (TdT).

5. The variant according to any one of the preceding claims, having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% identity with the sequence according to SEQ ID No. 1.

6. The variant according to any one of the preceding claims, said variant comprising at least one mutation of a residue in at least one position selected from the group consisting of R336 and R454, or a functionally equivalent residue, the positions indicated being determined by alignment with SEQ ID No. 1, and/or said variant comprising a combination of substitutions selected from R336G-E457N; R336N-E457N; R336N-R454A-E457N; R336N-E457N; R336N-R454A-E457G; R336N-E457G; R336G-R454A-E457N; R336G-E457N, the positions indicated being determined by alignment with SEQ ID No. 1.

7. The variant according to claim 6, comprising mutations of residues at each one of positions R336, R454 and E457.

8. The variant according to any one of the preceding claims, said variant having at least one mutation of a residue in at least one semi-conserved sequence region

(i) $X_1X_2GGFR_1R_2GKX_3X_4$ (SEQ ID No. 4), in which

X_1 represents a residue selected from M, I, V, L

X_2 represents a residue selected from T, A, M, Q

X_3 represents a residue selected from M, K, E, Q, L, S, P, R, D

X_4 represents a residue selected from T, I, M, F, K, V, Y, E, Q, H, S, R, D

(ii) $X_1X_2LGX_3X_4GSR_1X_5X_6ER_2$ (SEQ ID No. 5) in which

X_1 represents a residue selected from A, C, G, S

X_2 represents a residue selected from L, T, R

X_3 represents a residue selected from W, Y

X_4 represents a residue selected from T, S, I

X_5 represents a residue selected from Q, L, H, F, Y, N, E, D or ∅

X_6 represents a residue selected from F, Y

(iii) LX1YX2X3PX4X5RNA (SEQ ID No. 6)

X_1 represents a residue selected from D, E, S, P, A, K

X_2 represents a residue selected from I, L, M, V, A, T

X_3 represents a residue selected from E, Q, P, Y, L, K, G, N

X_4 represents a residue selected from W, S, V, E, R, Q, T, C, K, H

X_5 represents a residue selected from E, Q, D, H, L.

9. The variant according to claim 8, said variant having

- at least one substitution of a residue in at least one position R_1, R_2 and/or K of the semi- conserved sequence region SEQ ID No. 4; and/or
- at least one substitution of a residue in at least one position S, R1 and/or E of the semi- conserved sequence region SEQ ID No. 5; and/or
- a deletion of the residue in position X1 and/or at least one substitution in the positions R and/or N of the semi-conserved sequence region SEQ ID No. 6.

10. The variant according to any one of the preceding claims, said variant comprising a substitution of a residue in at least one position selected from the group consisting of R336, K338, H342, A397, S453, R454, R461, N474, D501, Y502, I503, R508 and N509, or a functionally equivalent residue, the positions indicated being determined by alignment with SEQ ID No. 1.

11. The variant according to claim 10, comprising a substitution of a residue in at least one position selected from the group consisting of R336, A397, R454, R461, N474, D501, Y502 and I503, or a functionally equivalent residue.

12. The variant according to claim 10 or 11, wherein the substitutions in positions R336, K338, H342, A397, S453, R454, E457, R461, N474, D501, Y502, I503, R508 and N509 are selected from the group consisting of R336K/H/N/G/D, K338A/C/G/S/T/N, H342A/C/G/S/T.N, A397R/H/K/D/E, S453A/C/G/S/T, R454F/Y/W/A, E457G/N/S/T, N474S/T/N/Q, D501A/G/X, Y502A/G/X, I503A/G/X, R508A/C/G/S/T, N509A/C/G/S/T.

13. The variant according to any one of the preceding claims, in which the variant comprises or has a substitution, deletion, combinations of substitutions and/or of deletions listed in table 1, the positions indicated being determined by alignment with SEQ ID No. 1.

14. The variant according to any one of the preceding claims, said variant being a variant of the TdT of sequence SEQ ID No. 1 and comprising moreover a substitution of the residues between the positions C378 to L406, or the functionally equivalent residues, with the residues H363 to C390 of the polymerase Polμ of sequence SEQ ID No. 2, or the functionally equivalent residues.

15. An isolated nucleic acid coding for a variant of a DNA polymerase of the polX family according to any one of claims 1 to 14.

16. An expression cassette of a nucleic acid according to claim 15.

17. A vector comprising a nucleic acid according to claim 15 or an expression cassette according to claim 16.

18. A host cell comprising a nucleic acid according to claim 15 or an expression cassette according to claim 16 or a vector according to claim 17.

19. Use of a nucleic acid according to claim 15, of an expression cassette according to claim 16, of a vector according to claim 17 or of a cell according to claim 18, for producing a variant of a DNA polymerase of the polX family according to any one of claims 1-14.

20. A method for producing a variant of a DNA polymerase of the polX family according to any one of claims 1-14, according to which a host cell according to claim 18 is cultured under culture conditions enabling the expression of the nucleic acid coding for said variant.

21. Use of a variant of a DNA polymerase of the polX family according to any one of claims 1-14, for synthesizing a nucleic acid molecule without a template strand, from 3'-OH modified nucleotides.

22. A method for the enzymatic synthesis of a nucleic acid molecule without a template strand, according to which a primer strand is brought in contact with at least one nucleotide in the presence of a variant of a DNA polymerase of the polX family according to any one of claims 1-14.

23. The method according to claim 22, wherein the at least one nucleotide is a 3'-OH modified nucleotide.

24. A kit for the enzymatic synthesis of a nucleic acid molecule without a template strand, comprising at least one variant of a DNA polymerase of the polX family according to any one of claims 1-14, and nucleotides.

25. The kit according to claim 24, wherein the nucleotides comprise 3'-OH nucleotides.

26. The kit according to claim 24 or 25, further comprising at least one nucleotide primer.

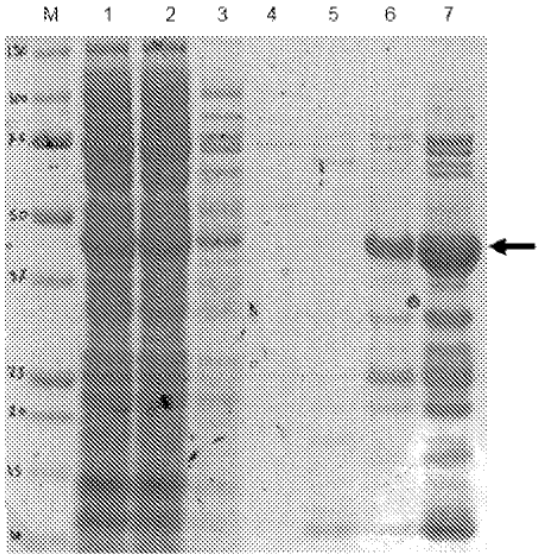

FIGURE 1

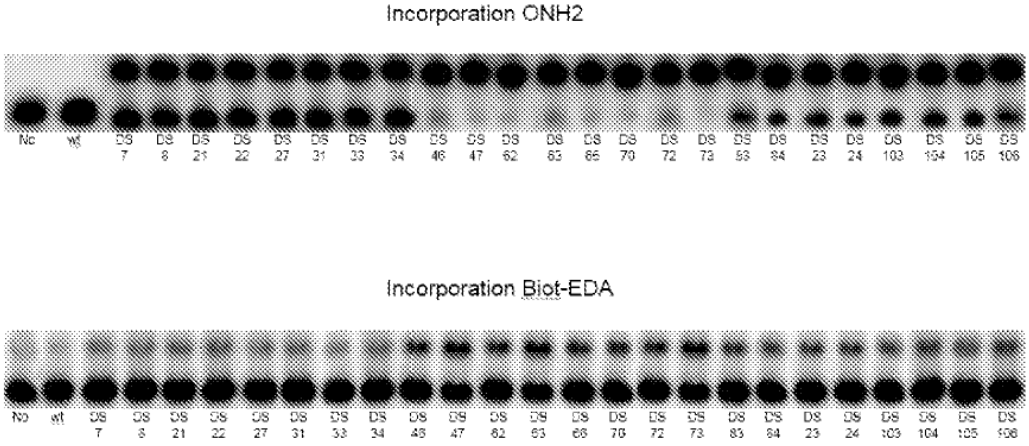

FIGURE 3

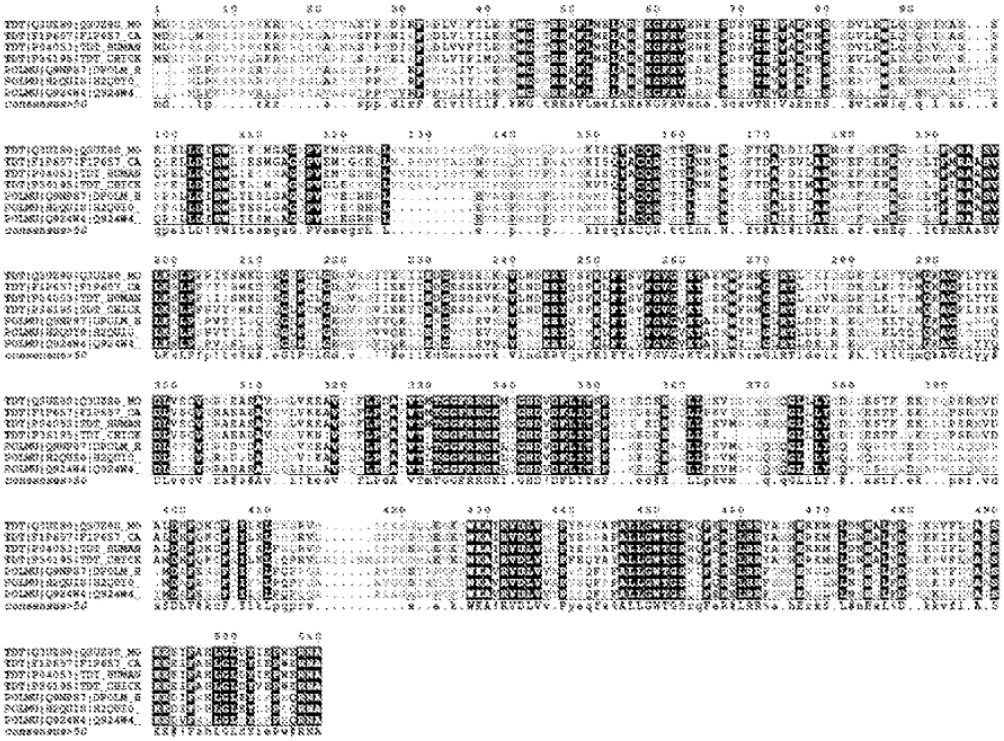

FIGURE 2

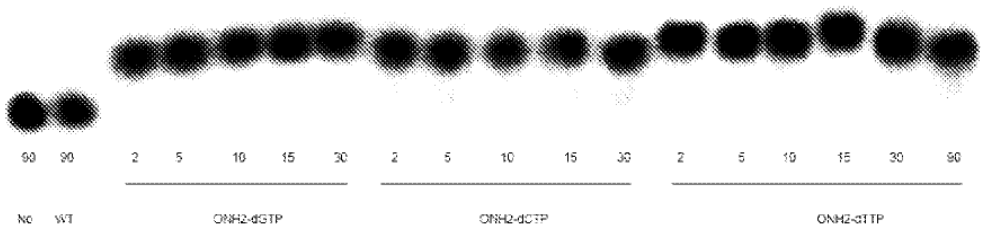

FIGURE 4

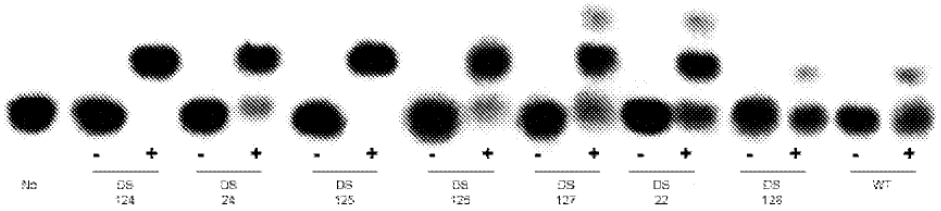

FIGURE 5

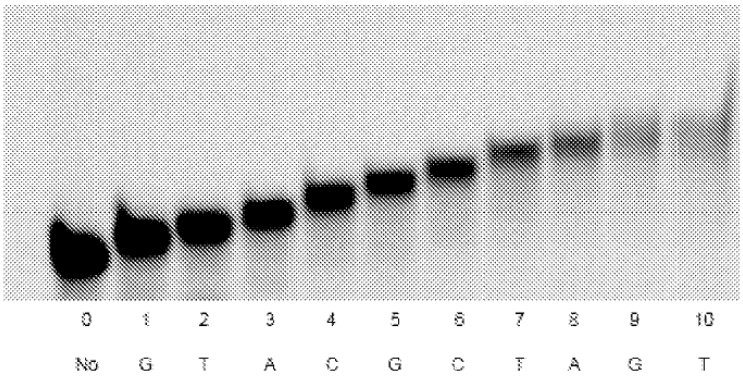

FIGURE 6

SEQUENCE LISTING

<110> DNA Script
Institut Pasteur

<120> Variants d'une ADN polymérase de la famille X

<130> PR1898

<160> 16

<170> PatentIn version 3.5

<210> 1
<211> 510
<212> PRT
<213> artificial sequence

<220>
<223> TdT de souris

<400> 1

Met Asp Pro Leu Gln Ala Val His Leu Gly Pro Arg Lys Lys Arg Pro
1 5 10 15

Arg Gln Leu Gly Thr Pro Val Ala Ser Thr Pro Tyr Asp Ile Arg Phe
20 25 30

Arg Asp Leu Val Leu Phe Ile Leu Glu Lys Lys Met Gly Thr Thr Arg
35 40 45

Arg Ala Phe Leu Met Glu Leu Ala Arg Arg Lys Gly Phe Arg Val Glu
50 55 60

Asn Glu Leu Ser Asp Ser Val Thr His Ile Val Ala Glu Asn Asn Ser
65 70 75 80

Gly Ser Asp Val Leu Glu Trp Leu Gln Leu Gln Asn Ile Lys Ala Ser
85 90 95

Ser Glu Leu Glu Leu Leu Asp Ile Ser Trp Leu Ile Glu Cys Met Gly
100 105 110

Ala Gly Lys Pro Val Glu Met Met Gly Arg His Gln Leu Val Val Asn

```
        115                 120                 125

Arg Asn Ser Ser Pro Ser Pro Val Pro Gly Ser Gln Asn Val Pro Ala
    130                 135                 140

Pro Ala Val Lys Lys Ile Ser Gln Tyr Ala Cys Gln Arg Arg Thr Thr
145                 150                 155                 160

Leu Asn Asn Tyr Asn Gln Leu Phe Thr Asp Ala Leu Asp Ile Leu Ala
                165                 170                 175

Glu Asn Asp Glu Leu Arg Glu Asn Glu Gly Ser Cys Leu Ala Phe Met
            180                 185                 190

Arg Ala Ser Ser Val Leu Lys Ser Leu Pro Phe Pro Ile Thr Ser Met
        195                 200                 205

Lys Asp Thr Glu Gly Ile Pro Cys Leu Gly Asp Lys Val Lys Ser Ile
    210                 215                 220

Ile Glu Gly Ile Ile Glu Asp Gly Glu Ser Ser Glu Ala Lys Ala Val
225                 230                 235                 240

Leu Asn Asp Glu Arg Tyr Lys Ser Phe Lys Leu Phe Thr Ser Val Phe
                245                 250                 255

Gly Val Gly Leu Lys Thr Ala Glu Lys Trp Phe Arg Met Gly Phe Arg
            260                 265                 270

Thr Leu Ser Lys Ile Gln Ser Asp Lys Ser Leu Arg Phe Thr Gln Met
        275                 280                 285

Gln Lys Ala Gly Phe Leu Tyr Tyr Glu Asp Leu Val Ser Cys Val Asn
    290                 295                 300

Arg Pro Glu Ala Glu Ala Val Ser Met Leu Val Lys Glu Ala Val Val
305                 310                 315                 320

Thr Phe Leu Pro Asp Ala Leu Val Thr Met Thr Gly Gly Phe Arg Arg
```

325 330 335

Gly Lys Met Thr Gly His Asp Val Asp Phe Leu Ile Thr Ser Pro Glu
340 345 350

Ala Thr Glu Asp Glu Glu Gln Gln Leu Leu His Lys Val Thr Asp Phe
355 360 365

Trp Lys Gln Gln Gly Leu Leu Leu Tyr Cys Asp Ile Leu Glu Ser Thr
370 375 380

Phe Glu Lys Phe Lys Gln Pro Ser Arg Lys Val Asp Ala Leu Asp His
385 390 395 400

Phe Gln Lys Cys Phe Leu Ile Leu Lys Leu Asp His Gly Arg Val His
405 410 415

Ser Glu Lys Ser Gly Gln Gln Glu Gly Lys Gly Trp Lys Ala Ile Arg
420 425 430

Val Asp Leu Val Met Cys Pro Tyr Asp Arg Arg Ala Phe Ala Leu Leu
435 440 445

Gly Trp Thr Gly Ser Arg Gln Phe Glu Arg Asp Leu Arg Arg Tyr Ala
450 455 460

Thr His Glu Arg Lys Met Met Leu Asp Asn His Ala Leu Tyr Asp Arg
465 470 475 480

Thr Lys Arg Val Phe Leu Glu Ala Glu Ser Glu Glu Glu Ile Phe Ala
485 490 495

His Leu Gly Leu Asp Tyr Ile Glu Pro Trp Glu Arg Asn Ala
500 505 510

<210> 2
<211> 494
<212> PRT
<213> artificial sequence

<220>
<223> Pol µ humaine

<400> 2

```
Met Leu Pro Lys Arg Arg Arg Ala Arg Val Gly Ser Pro Ser Gly Asp
1               5                  10                  15

Ala Ala Ser Ser Thr Pro Pro Ser Thr Arg Phe Pro Gly Val Ala Ile
            20                  25                  30

Tyr Leu Val Glu Pro Arg Met Gly Arg Ser Arg Arg Ala Phe Leu Thr
        35                  40                  45

Gly Leu Ala Arg Ser Lys Gly Phe Arg Val Leu Asp Ala Cys Ser Ser
    50                  55                  60

Glu Ala Thr His Val Val Met Glu Glu Thr Ser Ala Glu Glu Ala Val
65                  70                  75                  80

Ser Trp Gln Glu Arg Arg Met Ala Ala Ala Pro Pro Gly Cys Thr Pro
                85                  90                  95

Pro Ala Leu Leu Asp Ile Ser Trp Leu Thr Glu Ser Leu Gly Ala Gly
            100                 105                 110

Gln Pro Val Pro Val Glu Cys Arg His Arg Leu Glu Val Ala Gly Pro
        115                 120                 125

Arg Lys Gly Pro Leu Ser Pro Ala Trp Met Pro Ala Tyr Ala Cys Gln
    130                 135                 140

Arg Pro Thr Pro Leu Thr His His Asn Thr Gly Leu Ser Glu Ala Leu
145                 150                 155                 160

Glu Ile Leu Ala Glu Ala Ala Gly Phe Glu Gly Ser Glu Gly Arg Leu
                165                 170                 175

Leu Thr Phe Cys Arg Ala Ala Ser Val Leu Lys Ala Leu Pro Ser Pro
            180                 185                 190
```

```
Val Thr Thr Leu Ser Gln Leu Gln Gly Leu Pro His Phe Gly Glu His
        195                 200                 205

Ser Ser Arg Val Val Gln Glu Leu Leu Glu His Gly Val Cys Glu Glu
    210                 215                 220

Val Glu Arg Val Arg Arg Ser Glu Arg Tyr Gln Thr Met Lys Leu Phe
225                 230                 235                 240

Thr Gln Ile Phe Gly Val Gly Val Lys Thr Ala Asp Arg Trp Tyr Arg
                245                 250                 255

Glu Gly Leu Arg Thr Leu Asp Asp Leu Arg Glu Gln Pro Gln Lys Leu
            260                 265                 270

Thr Gln Gln Gln Lys Ala Gly Leu Gln His His Gln Asp Leu Ser Thr
        275                 280                 285

Pro Val Leu Arg Ser Asp Val Asp Ala Leu Gln Gln Val Val Glu Glu
    290                 295                 300

Ala Val Gly Gln Ala Leu Pro Gly Ala Thr Val Thr Leu Thr Gly Gly
305                 310                 315                 320

Phe Arg Arg Gly Lys Leu Gln Gly His Asp Val Asp Phe Leu Ile Thr
                325                 330                 335

His Pro Lys Glu Gly Gln Glu Ala Gly Leu Leu Pro Arg Val Met Cys
            340                 345                 350

Arg Leu Gln Asp Gln Gly Leu Ile Leu Tyr His Gln His Gln His Ser
        355                 360                 365

Cys Cys Glu Ser Pro Thr Arg Leu Ala Gln Gln Ser His Met Asp Ala
    370                 375                 380

Phe Glu Arg Ser Phe Cys Ile Phe Arg Leu Pro Gln Pro Pro Gly Ala
385                 390                 395                 400
```

```
Ala Val Gly Gly Ser Thr Arg Pro Cys Pro Ser Trp Lys Ala Val Arg
                405                 410                 415


Val Asp Leu Val Val Ala Pro Val Ser Gln Phe Pro Phe Ala Leu Leu
            420                 425                 430


Gly Trp Thr Gly Ser Lys Leu Phe Gln Arg Glu Leu Arg Arg Phe Ser
        435                 440                 445


Arg Lys Glu Lys Gly Leu Trp Leu Asn Ser His Gly Leu Phe Asp Pro
    450                 455                 460


Glu Gln Lys Thr Phe Phe Gln Ala Ala Ser Glu Glu Asp Ile Phe Arg
465                 470                 475                 480


His Leu Gly Leu Glu Tyr Leu Pro Pro Glu Gln Arg Asn Ala
                485                 490


<210>  3
<211>  401
<212>  PRT
<213>  artificial sequence

<220>
<223>  TdT de souris tronquée

<400>  3

Thr Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val
1               5                   10                  15


Pro Arg Gly Ser His Met Ser Pro Ser Pro Val Pro Gly Ser Gln Asn
            20                  25                  30


Val Pro Ala Pro Ala Val Lys Lys Ile Ser Gln Tyr Ala Cys Gln Arg
        35                  40                  45


Arg Thr Thr Leu Asn Asn Tyr Asn Gln Leu Phe Thr Asp Ala Leu Asp
    50                  55                  60


Ile Leu Ala Glu Asn Asp Glu Leu Arg Glu Asn Glu Gly Ser Cys Leu
```

65 70 75 80

Ala Phe Met Arg Ala Ser Ser Val Leu Lys Ser Leu Pro Phe Pro Ile
85 90 95

Thr Ser Met Lys Asp Thr Glu Gly Ile Pro Cys Leu Gly Asp Lys Val
100 105 110

Lys Ser Ile Ile Glu Gly Ile Ile Glu Asp Gly Glu Ser Ser Glu Ala
115 120 125

Lys Ala Val Leu Asn Asp Glu Arg Tyr Lys Ser Phe Lys Leu Phe Thr
130 135 140

Ser Val Phe Gly Val Gly Leu Lys Thr Ala Glu Lys Trp Phe Arg Met
145 150 155 160

Gly Phe Arg Thr Leu Ser Lys Ile Gln Ser Asp Lys Ser Leu Arg Phe
165 170 175

Thr Gln Met Gln Lys Ala Gly Phe Leu Tyr Tyr Glu Asp Leu Val Ser
180 185 190

Cys Val Asn Arg Pro Glu Ala Glu Ala Val Ser Met Leu Val Lys Glu
195 200 205

Ala Val Val Thr Phe Leu Pro Asp Ala Leu Val Thr Met Thr Gly Gly
210 215 220

Phe Arg Arg Gly Lys Met Thr Gly His Asp Val Asp Phe Leu Ile Thr
225 230 235 240

Ser Pro Glu Ala Thr Glu Asp Glu Glu Gln Gln Leu Leu His Lys Val
245 250 255

Thr Asp Phe Trp Lys Gln Gln Gly Leu Leu Leu Tyr Cys Asp Ile Leu
260 265 270

Glu Ser Thr Phe Glu Lys Phe Lys Gln Pro Ser Arg Lys Val Asp Ala

275 280 285

Leu Asp His Phe Gln Lys Cys Phe Leu Ile Leu Lys Leu Asp His Gly
290 295 300

Arg Val His Ser Glu Lys Ser Gly Gln Gln Glu Gly Lys Gly Trp Lys
305 310 315 320

Ala Ile Arg Val Asp Leu Val Met Cys Pro Tyr Asp Arg Arg Ala Phe
325 330 335

Ala Leu Leu Gly Trp Thr Gly Ser Arg Gln Phe Glu Arg Asp Leu Arg
340 345 350

Arg Tyr Ala Thr His Glu Arg Lys Met Met Leu Asp Asn His Ala Leu
355 360 365

Tyr Asp Arg Thr Lys Arg Val Phe Leu Glu Ala Glu Ser Glu Glu Glu
370 375 380

Ile Phe Ala His Leu Gly Leu Asp Tyr Ile Glu Pro Trp Glu Arg Asn
385 390 395 400

Ala

<210> 4
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> séquence semi-conservée

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> X=M, I, V, L

<220>
<221> MISC_FEATURE
<222> (2)..(2)

<223> X=T, A, M, Q

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> X=M, K, E, Q, L, S, P, R, D

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> X=T, I, M, F, K, V, Y, E, Q, H, S, R, D

<400> 4

Xaa Xaa Gly Gly Phe Arg Arg Gly Lys Xaa Xaa
1 5 10

<210> 5
<211> 13
<212> PRT
<213> artificial sequence

<220>
<223> région semi-conservée

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> X=A, C, G, S

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> X=L, T, R

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> X=W, Y

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> X=T, S, I

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> X=Q, L, H, F, Y, N, E, D,

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> X=F, Y

<400> 5

Xaa Xaa Leu Gly Xaa Xaa Gly Ser Arg Xaa Xaa Glu Arg
1 5 10

<210> 6
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> région semi-conservée

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> X=D, E, S, P, A, K

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> X=I, L, M, V, A, T

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> X=E, Q, P, Y, L, K, G, N

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> X=W, S, V, E, R, Q, T, C, K, H

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> X=E, Q, D, H, L

<400> 6

Leu Xaa Tyr Xaa Xaa Pro Xaa Xaa Arg Asn Ala
1 5 10

<210> 7

<211> 20
<212> DNA
<213> artificial sequence

<220>
<223> amorce

<400> 7
taatacgact cactataggg 20

<210> 8
<211> 19
<212> DNA
<213> artificial sequence

<220>
<223> amorce

<400> 8
gctagttatt gctcagcgg 19

<210> 9
<211> 494
<212> PRT
<213> Pan troglodytes

<400> 9

Met Leu Pro Lys Arg Arg Arg Ala Arg Val Gly Ser Pro Ser Gly Asp
1 5 10 15

Ala Ala Ser Ser Thr Pro Pro Ser Thr Arg Phe Pro Gly Val Ala Ile
20 25 30

Tyr Leu Val Glu Pro Arg Met Gly Arg Ser Arg Arg Ala Phe Leu Thr
35 40 45

Arg Leu Thr Arg Ser Lys Gly Phe Arg Val Leu Asp Ala Cys Ser Ser
50 55 60

Glu Ala Thr His Val Val Met Glu Glu Thr Ser Ala Glu Glu Ala Val
65 70 75 80

Ser Trp Gln Glu Arg Arg Met Ala Ala Ala Pro Pro Gly Cys Thr Pro
85 90 95

```
Pro Ala Leu Leu Asp Ile Ser Trp Leu Thr Glu Ser Leu Gly Ala Gly
            100                 105                 110

Gln Pro Val Pro Val Glu Cys Arg His Arg Leu Glu Val Ala Gly Pro
        115                 120                 125

Arg Lys Gly Pro Leu Ser Pro Ala Trp Met Pro Ala Tyr Val Cys Gln
    130                 135                 140

Arg Pro Thr Pro Leu Thr His His Asn Thr Gly Leu Ser Glu Ala Leu
145                 150                 155                 160

Glu Thr Leu Ala Glu Ala Ala Gly Phe Glu Gly Ser Glu Gly Arg Leu
                165                 170                 175

Leu Thr Phe Cys Arg Ala Ala Ser Val Leu Lys Ala Leu Pro Ser Pro
            180                 185                 190

Val Thr Thr Leu Ser Gln Leu Gln Gly Leu Pro His Phe Gly Glu His
        195                 200                 205

Ser Ser Arg Val Val Gln Glu Leu Leu Glu His Gly Val Cys Glu Glu
    210                 215                 220

Val Glu Arg Val Gln Arg Ser Glu Arg Tyr Gln Thr Met Lys Leu Phe
225                 230                 235                 240

Thr Gln Ile Phe Gly Val Gly Val Lys Thr Ala Asp Arg Trp Tyr Arg
                245                 250                 255

Glu Gly Leu Arg Thr Leu Asp Asp Leu Arg Glu Gln Pro Gln Lys Leu
            260                 265                 270

Thr Gln Gln Gln Lys Ala Gly Leu Gln His His Gln Asp Leu Ser Thr
        275                 280                 285

Pro Val Leu Arg Ser Asp Val Asp Ala Leu Gln Gln Val Val Glu Glu
    290                 295                 300
```

```
Ala Val Gly Gln Ala Leu Pro Gly Ala Thr Val Thr Leu Thr Gly Gly
305                 310                 315                 320

Phe Arg Arg Gly Lys Leu Gln Gly His Asp Val Asp Phe Leu Ile Thr
                325                 330                 335

His Pro Lys Glu Gly Gln Glu Ala Gly Leu Leu Pro Arg Val Met Cys
            340                 345                 350

Arg Leu Gln Asp Gln Gly Leu Ile Leu Tyr His Gln His Gln His Ser
        355                 360                 365

Cys Trp Glu Ser Pro Thr Arg Leu Ala Gln Gln Ser His Met Asp Ala
    370                 375                 380

Phe Glu Arg Ser Phe Cys Ile Phe Arg Leu Pro Gln Pro Pro Gly Ala
385                 390                 395                 400

Ala Val Gly Gly Ser Thr Arg Pro Cys Pro Ser Trp Lys Ala Val Arg
                405                 410                 415

Val Asp Leu Val Val Ala Pro Val Ser Gln Phe Pro Phe Ala Leu Leu
            420                 425                 430

Gly Trp Thr Gly Ser Lys Leu Phe Gln Arg Glu Leu Arg Arg Phe Ser
        435                 440                 445

Arg Lys Glu Lys Gly Leu Trp Leu Asn Ser His Gly Leu Phe Asp Pro
    450                 455                 460

Glu Gln Lys Thr Phe Phe Gln Ala Ala Ser Glu Glu Asp Ile Phe Arg
465                 470                 475                 480

His Leu Gly Leu Glu Tyr Leu Pro Pro Glu Gln Arg Asn Ala
                485                 490
```

<210> 10
<211> 496

<212> PRT
<213> Mus musculus

<400> 10

```
Met Leu Pro Lys Arg Arg Arg Val Arg Ala Gly Ser Pro His Ser Ala
1               5                  10                  15

Val Ala Ser Ser Thr Pro Pro Ser Val Val Arg Phe Pro Asp Val Ala
            20                  25                  30

Ile Tyr Leu Ala Glu Pro Arg Met Gly Arg Ser Arg Arg Ala Phe Leu
        35                  40                  45

Thr Arg Leu Ala Arg Ser Lys Gly Phe Arg Val Leu Asp Ala Tyr Ser
    50                  55                  60

Ser Lys Val Thr His Val Val Met Glu Gly Thr Ser Ala Lys Glu Ala
65                  70                  75                  80

Ile Cys Trp Gln Lys Asn Met Asp Ala Leu Pro Thr Gly Cys Pro Gln
                85                  90                  95

Pro Ala Leu Leu Asp Ile Ser Trp Phe Thr Glu Ser Met Ala Ala Gly
            100                 105                 110

Gln Pro Val Arg Glu Glu Gly Arg His His Leu Glu Val Ala Glu Pro
        115                 120                 125

Arg Lys Glu Pro Pro Val Ser Ala Ser Met Pro Ala Tyr Ala Cys Gln
    130                 135                 140

Arg Pro Ser Pro Leu Thr His His Asn Thr Leu Leu Ser Glu Ala Leu
145                 150                 155                 160

Glu Thr Leu Ala Glu Ala Ala Gly Phe Glu Ala Asn Glu Gly Arg Leu
                165                 170                 175

Leu Ser Phe Ser Arg Ala Asp Ser Val Leu Lys Ser Leu Pro Cys Pro
            180                 185                 190
```

```
Val Ala Ser Leu Ser Gln Leu His Gly Leu Pro Tyr Phe Gly Glu His
        195                 200                 205

Ser Thr Arg Val Ile Gln Glu Leu Leu Glu His Gly Thr Cys Glu Glu
    210                 215                 220

Val Lys Gln Val Arg Cys Ser Glu Arg Tyr Gln Thr Met Lys Leu Phe
225                 230                 235                 240

Thr Gln Val Phe Gly Val Gly Val Lys Thr Ala Asn Arg Trp Tyr Gln
                245                 250                 255

Glu Gly Leu Arg Thr Leu Asp Glu Leu Arg Glu Gln Pro Gln Arg Leu
            260                 265                 270

Thr Gln Gln Gln Lys Ala Gly Leu Gln Tyr Tyr Gln Asp Leu Ser Thr
        275                 280                 285

Pro Val Arg Arg Ala Asp Ala Glu Ala Leu Gln Gln Leu Ile Glu Ala
    290                 295                 300

Ala Val Arg Gln Thr Leu Pro Gly Ala Thr Val Thr Leu Thr Gly Gly
305                 310                 315                 320

Phe Arg Arg Gly Lys Leu Gln Gly His Asp Val Asp Phe Leu Ile Thr
                325                 330                 335

His Pro Glu Glu Gly Gln Glu Val Gly Leu Leu Pro Lys Val Met Ser
            340                 345                 350

Cys Leu Gln Ser Gln Gly Leu Val Leu Tyr His Gln Tyr His Arg Ser
        355                 360                 365

His Leu Ala Asp Ser Ala His Asn Leu Arg Gln Arg Ser Ser Thr Met
    370                 375                 380

Asp Ala Phe Glu Arg Ser Phe Cys Ile Leu Gly Leu Pro Gln Pro Gln
385                 390                 395                 400
```

```
Gln Ala Ala Leu Ala Gly Ala Leu Pro Pro Cys Pro Thr Trp Lys Ala
                405                 410                 415


Val Arg Val Asp Leu Val Val Thr Pro Ser Ser Gln Phe Pro Phe Ala
            420                 425                 430


Leu Leu Gly Trp Thr Gly Ser Gln Phe Phe Glu Arg Glu Leu Arg Arg
        435                 440                 445


Phe Ser Arg Gln Glu Lys Gly Leu Trp Leu Asn Ser His Gly Leu Phe
    450                 455                 460


Asp Pro Glu Gln Lys Arg Val Phe His Ala Thr Ser Glu Glu Asp Val
465                 470                 475                 480


Phe Arg Leu Leu Gly Leu Lys Tyr Leu Pro Pro Glu Gln Arg Asn Ala
                485                 490                 495


<210>  11
<211>  509
<212>  PRT
<213>  Canis lupus

<400>  11

Met Asp Pro Leu Gln Met Ala His Ser Gly Pro Arg Lys Lys Arg Pro
1               5                   10                  15


Arg Gln Met Gly Ala Pro Met Val Ser Pro Pro His Asn Ile Lys Phe
            20                  25                  30


Gln Asp Leu Val Leu Tyr Ile Leu Glu Lys Lys Met Gly Thr Thr Arg
        35                  40                  45


Arg Ala Phe Leu Met Glu Leu Ala Arg Arg Lys Gly Phe Arg Val Asp
    50                  55                  60


Asn Glu Phe Ser Asp Ser Ile Thr His Ile Val Ala Glu Asn Asn Ser
65                  70                  75                  80
```

```
Gly Ser Asp Val Leu Glu Trp Leu Gln Val Gln Asn Ile Lys Ala Ser
                85                  90                  95

Ser Gln Leu Glu Leu Leu Asp Ile Ser Trp Leu Ile Glu Ser Met Gly
            100                 105                 110

Ala Gly Lys Pro Val Glu Met Thr Gly Lys His Gln Leu Met Arg Arg
        115                 120                 125

Asp Tyr Thr Ala Ser Pro Asn Pro Glu Leu Gln Lys Thr Leu Pro Val
    130                 135                 140

Ala Val Lys Lys Ile Ser Gln Tyr Ala Cys Gln Arg Arg Thr Thr Leu
145                 150                 155                 160

Asn Asn Tyr Asn Asn Val Phe Thr Asp Ala Phe Glu Val Leu Ala Glu
                165                 170                 175

Asn Tyr Glu Phe Arg Glu Asn Glu Val Phe Ser Leu Thr Phe Met Arg
            180                 185                 190

Ala Ala Ser Val Leu Lys Ser Leu Pro Phe Thr Ile Ile Ser Met Lys
        195                 200                 205

Asp Thr Glu Gly Ile Pro Cys Leu Gly Asp Gln Val Lys Cys Ile Ile
    210                 215                 220

Glu Glu Ile Ile Glu Asp Gly Glu Ser Ser Glu Val Lys Ala Val Leu
225                 230                 235                 240

Asn Asp Glu Arg Tyr Gln Ser Phe Lys Leu Phe Thr Ser Val Phe Gly
                245                 250                 255

Val Gly Leu Lys Thr Ser Glu Lys Trp Phe Arg Met Gly Phe Arg Thr
            260                 265                 270

Leu Ser Lys Ile Lys Ser Asp Lys Ser Leu Lys Phe Thr Pro Met Gln
        275                 280                 285
```

```
Lys Ala Gly Phe Leu Tyr Tyr Glu Asp Leu Val Ser Cys Val Thr Arg
    290                 295                 300

Ala Glu Ala Glu Ala Val Gly Val Leu Val Lys Glu Ala Val Gly Ala
305                 310                 315                 320

Phe Leu Pro Asp Ala Phe Val Thr Met Thr Gly Gly Phe Arg Arg Gly
                325                 330                 335

Lys Lys Met Gly His Asp Val Asp Phe Leu Ile Thr Ser Pro Gly Ser
            340                 345                 350

Thr Asp Glu Asp Glu Glu Gln Leu Leu Pro Lys Val Ile Asn Leu Trp
        355                 360                 365

Glu Arg Lys Gly Leu Leu Leu Tyr Cys Asp Leu Val Glu Ser Thr Phe
    370                 375                 380

Glu Lys Leu Lys Leu Pro Ser Arg Lys Val Asp Ala Leu Asp His Phe
385                 390                 395                 400

Gln Lys Cys Phe Leu Ile Leu Lys Leu His His Gln Arg Val Asp Gly
                405                 410                 415

Gly Lys Cys Ser Gln Gln Glu Gly Lys Thr Trp Lys Ala Ile Arg Val
            420                 425                 430

Asp Leu Val Met Cys Pro Tyr Glu Arg Arg Ala Phe Ala Leu Leu Gly
        435                 440                 445

Trp Thr Gly Ser Arg Gln Phe Glu Arg Asp Leu Arg Arg Tyr Ala Ser
    450                 455                 460

His Glu Arg Lys Met Ile Leu Asp Asn His Ala Leu Tyr Asp Lys Thr
465                 470                 475                 480

Lys Lys Ile Phe Leu Lys Ala Glu Ser Glu Glu Glu Ile Phe Ala His
                485                 490                 495
```

Leu Gly Leu Asp Tyr Ile Glu Pro Trp Glu Arg Asn Ala
500 505

<210> 12
<211> 506
<212> PRT
<213> Gallus gallus

<400> 12

Met Glu Arg Ile Arg Pro Pro Thr Val Val Ser Gln Arg Lys Arg Gln
1 5 10 15

Lys Gly Met Tyr Ser Pro Lys Leu Ser Cys Gly Tyr Glu Ile Lys Phe
20 25 30

Asn Lys Leu Val Ile Phe Ile Met Gln Arg Lys Met Gly Met Thr Arg
35 40 45

Arg Thr Phe Leu Met Glu Leu Ala Arg Ser Lys Gly Phe Arg Val Glu
50 55 60

Ser Glu Leu Ser Asp Ser Val Thr His Ile Val Ala Glu Asn Asn Ser
65 70 75 80

Tyr Pro Glu Val Leu Asp Trp Leu Lys Gly Gln Ala Val Gly Asp Ser
85 90 95

Ser Arg Phe Glu Ile Leu Asp Ile Ser Trp Leu Thr Ala Cys Met Glu
100 105 110

Met Gly Arg Pro Val Asp Leu Glu Lys Lys Tyr His Leu Val Glu Gln
115 120 125

Ala Gly Gln Tyr Pro Thr Leu Lys Thr Pro Glu Ser Glu Val Ser Ser
130 135 140

Phe Thr Ala Ser Lys Val Ser Gln Tyr Ser Cys Gln Arg Lys Thr Thr
145 150 155 160

Leu Asn Asn Cys Asn Lys Lys Phe Thr Asp Ala Phe Glu Ile Met Ala

```
                165                 170                 175

Glu Asn Tyr Glu Phe Lys Glu Asn Glu Ile Phe Cys Leu Glu Phe Leu
            180                 185                 190

Arg Ala Ala Ser Val Leu Lys Ser Leu Pro Phe Pro Val Thr Arg Met
        195                 200                 205

Lys Asp Ile Gln Gly Leu Pro Cys Met Gly Asp Arg Val Arg Asp Val
    210                 215                 220

Ile Glu Glu Ile Ile Glu Glu Gly Glu Ser Ser Arg Ala Lys Asp Val
225                 230                 235                 240

Leu Asn Asp Glu Arg Tyr Lys Ser Phe Lys Glu Phe Thr Ser Val Phe
                245                 250                 255

Gly Val Gly Val Lys Thr Ser Glu Lys Trp Phe Arg Met Gly Leu Arg
            260                 265                 270

Thr Val Glu Glu Val Lys Ala Asp Lys Thr Leu Lys Leu Ser Lys Met
        275                 280                 285

Gln Arg Ala Gly Phe Leu Tyr Tyr Glu Asp Leu Val Ser Cys Val Ser
    290                 295                 300

Lys Ala Glu Ala Asp Ala Val Ser Ser Ile Val Lys Asn Thr Val Cys
305                 310                 315                 320

Thr Phe Leu Pro Asp Ala Leu Val Thr Ile Thr Gly Gly Phe Arg Arg
                325                 330                 335

Gly Lys Lys Ile Gly His Asp Ile Asp Phe Leu Ile Thr Ser Pro Gly
            340                 345                 350

Gln Arg Glu Asp Asp Glu Leu Leu His Lys Gly Leu Leu Leu Tyr Cys
        355                 360                 365

Asp Ile Ile Glu Ser Thr Phe Val Lys Glu Gln Ile Pro Ser Arg His
```

370 375 380

Val Asp Ala Met Asp His Phe Gln Lys Cys Phe Ala Ile Leu Lys Leu
385 390 395 400

Tyr Gln Pro Arg Val Asp Asn Ser Ser Tyr Asn Met Ser Lys Lys Cys
405 410 415

Asp Met Ala Glu Val Lys Asp Trp Lys Ala Ile Arg Val Asp Leu Val
420 425 430

Ile Thr Pro Phe Glu Gln Tyr Ala Tyr Ala Leu Leu Gly Trp Thr Gly
435 440 445

Ser Arg Gln Phe Gly Arg Asp Leu Arg Arg Tyr Ala Thr His Glu Arg
450 455 460

Lys Met Met Leu Asp Asn His Ala Leu Tyr Asp Lys Arg Lys Arg Val
465 470 475 480

Phe Leu Lys Ala Gly Ser Glu Glu Glu Ile Phe Ala His Leu Gly Leu
485 490 495

Asp Tyr Val Glu Pro Trp Glu Arg Asn Ala
500 505

<210> 13
<211> 509
<212> PRT
<213> Homo sapiens

<400> 13

Met Asp Pro Pro Arg Ala Ser His Leu Ser Pro Arg Lys Lys Arg Pro
1 5 10 15

Arg Gln Thr Gly Ala Leu Met Ala Ser Ser Pro Gln Asp Ile Lys Phe
20 25 30

Gln Asp Leu Val Val Phe Ile Leu Glu Lys Lys Met Gly Thr Thr Arg
35 40 45

```
Arg Ala Phe Leu Met Glu Leu Ala Arg Arg Lys Gly Phe Arg Val Glu
    50                  55                  60

Asn Glu Leu Ser Asp Ser Val Thr His Ile Val Ala Glu Asn Asn Ser
65                  70                  75                  80

Gly Ser Asp Val Leu Glu Trp Leu Gln Ala Gln Lys Val Gln Val Ser
                85                  90                  95

Ser Gln Pro Glu Leu Leu Asp Val Ser Trp Leu Ile Glu Cys Ile Arg
            100                 105                 110

Ala Gly Lys Pro Val Glu Met Thr Gly Lys His Gln Leu Val Val Arg
        115                 120                 125

Arg Asp Tyr Ser Asp Ser Thr Asn Pro Gly Pro Pro Lys Thr Pro Pro
    130                 135                 140

Ile Ala Val Gln Lys Ile Ser Gln Tyr Ala Cys Gln Arg Arg Thr Thr
145                 150                 155                 160

Leu Asn Asn Cys Asn Gln Ile Phe Thr Asp Ala Phe Asp Ile Leu Ala
                165                 170                 175

Glu Asn Cys Glu Phe Arg Glu Asn Glu Asp Ser Cys Val Thr Phe Met
            180                 185                 190

Arg Ala Ala Ser Val Leu Lys Ser Leu Pro Phe Thr Ile Ile Ser Met
        195                 200                 205

Lys Asp Thr Glu Gly Ile Pro Cys Leu Gly Ser Lys Val Lys Gly Ile
    210                 215                 220

Ile Glu Glu Ile Ile Glu Asp Gly Glu Ser Ser Glu Val Lys Ala Val
225                 230                 235                 240

Leu Asn Asp Glu Arg Tyr Gln Ser Phe Lys Leu Phe Thr Ser Val Phe
                245                 250                 255
```

```
Gly Val Gly Leu Lys Thr Ser Glu Lys Trp Phe Arg Met Gly Phe Arg
            260                 265                 270

Thr Leu Ser Lys Val Arg Ser Asp Lys Ser Leu Lys Phe Thr Arg Met
        275                 280                 285

Gln Lys Ala Gly Phe Leu Tyr Tyr Glu Asp Leu Val Ser Cys Val Thr
    290                 295                 300

Arg Ala Glu Ala Glu Ala Val Ser Val Leu Val Lys Glu Ala Val Trp
305                 310                 315                 320

Ala Phe Leu Pro Asp Ala Phe Val Thr Met Thr Gly Gly Phe Arg Arg
                325                 330                 335

Gly Lys Lys Met Gly His Asp Val Asp Phe Leu Ile Thr Ser Pro Gly
            340                 345                 350

Ser Thr Glu Asp Glu Glu Gln Leu Leu Gln Lys Val Met Asn Leu Trp
        355                 360                 365

Glu Lys Lys Gly Leu Leu Leu Tyr Tyr Asp Leu Val Glu Ser Thr Phe
    370                 375                 380

Glu Lys Leu Arg Leu Pro Ser Arg Lys Val Asp Ala Leu Asp His Phe
385                 390                 395                 400

Gln Lys Cys Phe Leu Ile Phe Lys Leu Pro Arg Gln Arg Val Asp Ser
                405                 410                 415

Asp Gln Ser Ser Trp Gln Glu Gly Lys Thr Trp Lys Ala Ile Arg Val
            420                 425                 430

Asp Leu Val Leu Cys Pro Tyr Glu Arg Arg Ala Phe Ala Leu Leu Gly
        435                 440                 445

Trp Thr Gly Ser Arg Gln Phe Glu Arg Asp Leu Arg Arg Tyr Ala Thr
    450                 455                 460
```

His Glu Arg Lys Met Ile Leu Asp Asn His Ala Leu Tyr Asp Lys Thr
465 470 475 480

Lys Arg Ile Phe Leu Lys Ala Glu Ser Glu Glu Glu Ile Phe Ala His
485 490 495

Leu Gly Leu Asp Tyr Ile Glu Pro Trp Glu Arg Asn Ala
500 505

<210> 14
<211> 14
<212> DNA
<213> artificial sequence

<220>
<223> amorce

<400> 14
aaaaaaaaaa gggg 14

<210> 15
<211> 10
<212> DNA
<213> artificial sequence

<220>
<223> séquence synthètisée

<400> 15
gtacgctagt 10

<210> 16
<211> 12
<212> DNA
<213> artificial sequence

<220>
<223> fragment de capture

<400> 16
ccttttttt tt 12