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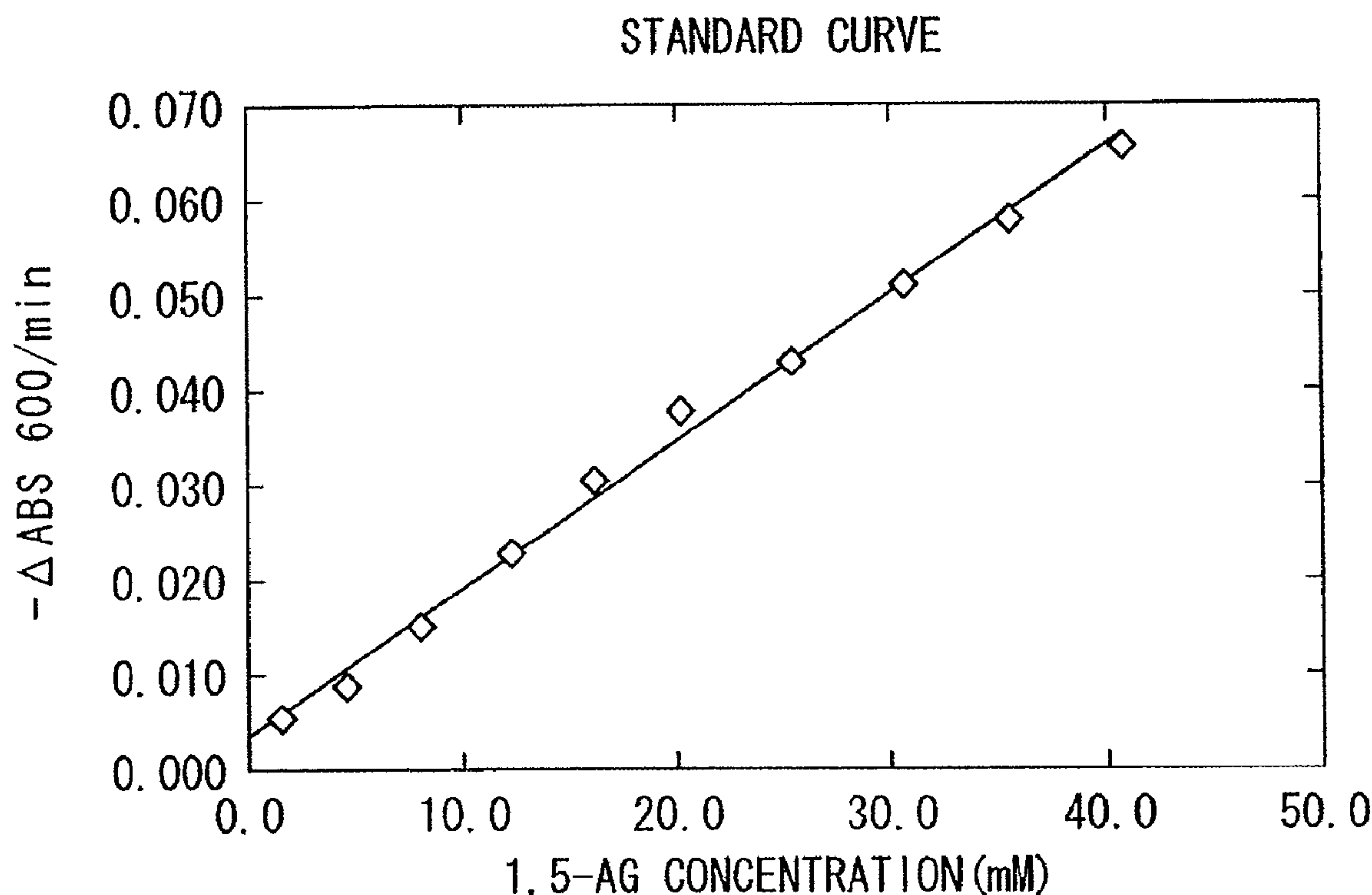
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(54) Titre : PROCEDE DE DOSAGE DU 1,5-ANHYDROGLUCITOL, ET COMPOSITION DE REACTIF POUR LE
DOSAGE DU 1,5-ANHYDROGLUCITOL

(54) Title: METHOD OF DETERMINING 1,5-ANHYDROGLUCITOL, AND REAGENT COMPOSITION FOR
DETERMINING 1,5-ANHYDROGLUCITOL



(57) Abrégé/Abstract:

A method for the determination of 1,5-anhydroglucitol, characterized by using any one of the following proteins (a) to (c): (a) a protein which comprises an amino acid sequence depicted in SEQ ID NO:2; (b) a protein which comprises an amino acid sequence having the deletion, substitution and/or addition of one or several amino acid residues in the amino acid sequence depicted in SEQ ID NO:2 and which has a sorbose dehydrogenase activity; and (c) a protein which comprises an amino acid sequence having at least 60% sequence homology to the amino acid sequence depicted in SEQ ID NO:2 and which has a sorbose dehydrogenase activity.

ABSTRACT

The object of the present invention is to provide a method of determining 1,5-anhydroglucitol, including using (a) a protein which consists of the amino acid sequence of SEQ ID NO: 2; (b) a protein which consists of an amino acid sequence having deletion, substitution and/or addition of one or more amino acid residues in the amino acid sequence of SEQ ID NO: 2 and which has sorbose dehydrogenase activity; or (c) a protein which consists of an amino acid sequence having a homology of at least 60% with the amino acid sequence of SEQ ID NO: 2 and which has sorbose dehydrogenase activity.

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DESCRIPTION

METHOD OF DETERMINING 1,5-ANHYDROGLUCITOL, AND REAGENT
COMPOSITION FOR DETERMINING 1,5-ANHYDROGLUCITOL

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TECHNICAL FIELD

[0001]

The present invention relates to a method of determining 1,5-anhydroglucitol and a reagent composition for determining 1,5-anhydroglucitol.

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This application claims the priority benefit of Japanese Patent Application No. 2006-172619 on June 22nd, 2006, the contents of which are incorporated herein by reference.

BACKGROUND ART

15 [0002]

1,5-Anhydroglucitol (hereinafter, referred to as "1,5-AG") is a reduced form of glucose where the C1 position is reduced, and a small amount of 1,5-AG is present in the living body. It was discovered that 1,5-AG is a useful control marker for diabetes (for example, see Non-patent Document 1 or 2).

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As described in Non-patent Document 1, 1,5-AG may be a marker ranked somewhere between the blood glucose level and hemoglobin A1c (HbA1c). Therefore, it is considered that the 1,5-AG level in blood could be a suitable marker for mild diabetic patients in their self-management of the disease.

[0003]

Table 1

Marker	Characteristics
Blood glucose level	May erratically fluctuate up and down for a short time.
1,5-AG	Indicates the blood glucose level from about five to seven days before the test.
HbA1c	Indicates the mean glucose level from about two months before the test.

[0004]

As disclosed in Non-patent Document 2, the 1,5-AG level in normal healthy people indicates a monosaccharide component that is the second most abundant in the blood after glucose. According to a clinical investigation conducted on a Japanese population, the average level of 1,5-AG is 24.6 ± 7.2 (mean $\pm$ SD) $\mu\text{g/ml}$. The physiologically-fluctuating range among individuals is small, and the 1,5-AG level is hardly influenced by fluctuation during the course of a day or over several days. In general, a male tends to have a level of 1,5-AG slightly higher than a female. The cut-off value is about $14.0 \mu\text{g/ml}$, where 95% of healthy people are diagnosed as “normal”.

[0005]

As a method of determining 1,5-AG, a gas chromatography method or an enzymatic method has been conventionally used, as described in Non-patent document 1. In the enzymatic method, 0.2 ml of a test sample of blood plasma (blood serum) is subjected to a protein removal treatment, and then, the content thereof is subjected to a mini-column to further remove contaminants included therein. Subsequently, the sample is treated with a pyranose oxidase (hereinafter, referred to as “PROD”). Then, hydrogen peroxide produced by the oxidation reaction of the hydroxyl group at the C2 position of 1,5-AG is stained by use of horseradish peroxidase (HRP), and the absorbance is measured at 420 nm. Such a technique can be mentioned as an example of the enzymatic method. A determination kit specific to blood samples using such an enzymatic method has been developed.

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Non-patent Document 1: Atsuo KAWAI and Yasuo AKANUMA, "1,5-anhydroglucitol", "Rinsyo-Kensa", vol. 33, No. 8, 1989 August, pp. 901-907.

Non-patent Document 2: "Medical Technology" (an extra edition), 2002, Vol. 30, No. 13, "All about diabetes testing – Screening to Testing for Complication",
5 pp. 1498-1499 (Ishiyaku Pub, Inc.).

SUMMARY OF THE INVENTION

PROBLEMS TO BE SOLVED BY THE INVENTION

10 [0006]

However, since a PROD, which is used in 1,5-AG determination according to conventional enzymatic methods, has a strong effect on glucose, there is a problem wherein it is required that a large amount of glucose present in blood (e.g. blood glucose) be removed so as to enable highly accurate 1,5-AG determination.

15 If a 1,5-AG-oxidizing enzyme (including oxidase and dehydrogenase), which has a low effect on glucose, is used instead of PROD, 1,5-AG determination could be simpler, the determination accuracy could be improved, or the determination time could be made shorter. Therefore, development of a method of determining 1,5-AG using such an enzyme has been sought.

20 [0007]

The present invention was achieved under the above-described circumstances. That is, an object of the present invention is to provide a method of determining 1,5-AG and a reagent composition for determining 1,5-AG that are less affected by interfering substances and that can achieve 1,5-AG determination with a degree of accuracy higher
25 than the prior-art method.

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MEANS FOR SOLVING THE PROBLEMS

[0008]

In order to achieve the above-mentioned object, the present invention provides the following aspects.

5 [1] A method of determining 1,5-anhydroglucitol, including using (a) a protein which consists of the amino acid sequence of SEQ ID NO: 2; (b) a protein which consists of an amino acid sequence having deletion, substitution and/or addition of one or more amino acid residues in the amino acid sequence of SEQ ID NO: 2 and which has sorbose dehydrogenase activity; or (c) a protein which consists of an amino acid sequence having
10 a homology of at least 60% with the amino acid sequence of SEQ ID NO: 2 and which has sorbose dehydrogenase activity.

[2] The method of determining 1,5-anhydroglucitol according to [1], wherein the protein is derived from a bacterium that belongs to the genus *Sinorhizobium*.

[3] The method of determining 1,5-anhydroglucitol according to [1] or [2],
15 wherein the protein is derived from *Sinorhizobium* sp. 97507 (Accession No. FERM P-19428).

[4] The method of determining 1,5-anhydroglucitol according to any one of [1] to [3], wherein, assuming that the reactivity of the protein to sorbose is 100%, the reactivity of the protein to 1,5-anhydroglucitol is 10% or higher.

20 [0009]

[5] The method of determining 1,5-anhydroglucitol according to any one of [1] to [4], wherein, assuming that the reactivity of the protein to 1,5-anhydroglucitol is 100%, the reactivity of the protein to D-glucose is 10% or less.

[6] The method of determining 1,5-anhydroglucitol according to any one of [1] to [5], wherein 1,5-anhydroglucitol included in a sample is affected by the protein in the
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presence of a chromogenic substrate, and the amount of reacted chromogenic substrate is measured.

[7] The method of determining 1,5-anhydroglucitol according to any one of [1] to [6], wherein D-glucose in a sample is removed before 1,5-anhydroglucitol included in a sample is affected by the protein.

[8] The method of determining 1,5-anhydroglucitol according to any one of [1] to [7], wherein 1,5-anhydroglucitol included in a sample is affected in the presence of a chromogenic substrate and an electron carrier.

[9] The method of determining 1,5-anhydroglucitol according to any one of [1] to [8], wherein 1 to 500 units of the protein is added to 1 mL of a sample where the enzyme activity of the protein measured using 1,5-anhydroglucitol as a substrate is defined as the base unit.

[10] The method of determining 1,5-anhydroglucitol according to any one of [1] to [9], wherein the protein is activated with an electron carrier before 1,5-anhydroglucitol included in a sample is affected by the protein.

[0010]

[11] A reagent composition for determining 1,5-anhydroglucitol, including (a) a protein which consists of the amino acid sequence of SEQ ID NO: 2; (b) a protein which consists of an amino acid sequence having deletion, substitution and/or addition of one or more amino acid residues in the amino acid sequence of SEQ ID NO: 2 and which has sorbose dehydrogenase activity; or (c) a protein which consists of an amino acid sequence having a homology of at least 60% with the amino acid sequence of SEQ ID NO: 2 and which has sorbose dehydrogenase activity.

[12] The reagent composition for determining 1,5-anhydroglucitol according to [11], wherein the protein is derived from a bacterium that belongs to the genus

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Sinorhizobium.

[13] The reagent composition for determining 1,5-anhydroglucitol according to [11] or [12], wherein the protein is derived from *Sinorhizobium* sp. 97507 (Accession No. FERM P-19428).

5 [14] The reagent composition for determining 1,5-anhydroglucitol according to any one of [11] to [13], wherein, assuming that the reactivity of the protein to sorbose is 100%, the reactivity of the protein to 1,5-anhydroglucitol is 10% or higher.

[15] The reagent composition for determining 1,5-anhydroglucitol according to any one of [11] to [14], wherein, assuming that the reactivity of the protein to 1,5-
10 anhydroglucitol is 100%, the reactivity of the protein to D-glucose is 10% or less.

[16] The reagent composition for determining 1,5-anhydroglucitol according to any one of [11] to [15], wherein the protein is activated with an electron carrier.

[0011]

[17] The reagent composition for determining 1,5-anhydroglucitol according to
15 [16], wherein the electron carrier is at least one of phenazine methosulfate and 1-methoxy-5-methylphenazinium methyl sulfate.

[18] The reagent composition for determining 1,5-anhydroglucitol according to any one of [11] to [17], further including a chromogenic substrate.

[19] The reagent composition for determining 1,5-anhydroglucitol according to
20 [18], further including an electron carrier, wherein the chromogenic substrate is a reductive chromogenic substrate.

[0012]

[20] A (a) protein which consists of the amino acid sequence of SEQ ID NO: 2;
(b) a protein which consists of an amino acid sequence having deletion, substitution
25 and/or addition of one or more amino acid residues in the amino acid sequence of SEQ

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ID NO: 2 and which has reactivity of 10% or higher to 1,5-anhydroglucitol, assuming that the reactivity of the protein to sorbose is 100%; or (c) a protein which consists of an amino acid sequence having a homology of at least 85% with the amino acid sequence of SEQ ID NO: 2 and which has activity of 10% or higher to 1,5-anhydroglucitol, assuming
5 that the reactivity of the protein to sorbose is 100%.

[21] A method of diagnosing diabetes, including using the reagent composition for determining 1,5-anhydroglucitol according to any one of [11] to [19].

[22] Use of the reagent composition for determining 1,5-anhydroglucitol according to any one of [11] to [19] for determining 1,5-anhydroglucitol.

10 [23] Use of (a) a protein which consists of the amino acid sequence of SEQ ID NO: 2; (b) a protein which consists of an amino acid sequence having deletion, substitution and/or addition of one or more amino acid residues in the amino acid sequence of SEQ ID NO: 2 and which has sorbose dehydrogenase activity; or (c) a protein which consists of an amino acid sequence having a homology of at least 60%
15 with the amino acid sequence of SEQ ID NO: 2 and which has sorbose dehydrogenase activity, for determining 1,5-anhydroglucitol.

EFFECTS OF THE INVENTION

[0013]

20 The present invention can provide a method of determining 1,5-AG and a reagent composition for determining 1,5-AG that are less affected by interfering substances and that can achieve 1,5-AG determination with a degree of accuracy higher than the prior-art method.

Moreover, the method of determining 1,5-AG and a reagent composition for
25 determining 1,5-AG and the reagent composition for determining 1,5-AG of the present

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invention can be applied to a clinical sample such as blood plasma, serum, cerebrospinal fluid or urine, and 1,5-AG included in such samples can be quickly and simply quantified or detected. Furthermore, small-scale measurement can be achieved in the present invention, and the present invention can achieve highly accurate and sensitive detection
5 or quantification of 1,5-AG in an automatic biochemical-examination analyzing apparatus or the like that is generally used in clinical laboratory tests.

BRIEF DESCRIPTION OF THE DRAWINGS

[0014]

10 FIG. 1 is a schematic diagram that illustrates a first set of procedures for constructing a plasmid “pUCNNT2” used in production of a sorbose dehydrogenase in Example 1.

FIG. 2 is a schematic diagram that illustrates a second set of procedures mentioned in FIG. 1.

15 FIG. 3 is a graph showing measurement results of optimal pH for the sorbose dehydrogenase produced in Example 1.

FIG. 4 a graph showing measurement results of pH stability of the sorbose dehydrogenase produced in Example 1.

20 FIG. 5 is a graph showing measurement results of optimal temperature for the sorbose dehydrogenase produced in Example 1.

FIG. 6 is a graph showing measurement results of temperature stability of the sorbose dehydrogenase produced in Example 1.

FIG. 7 is a graph showing a standard curve formulated in Example 1.

25 FIG. 8 is a schematic diagram that illustrates procedures for constructing a plasmid “pUCpTrcAGD1” used in production of a sorbose dehydrogenase in Example 2.

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FIG. 9 is a graph showing a standard curve formulated in Example 2.

FIG. 10 is a graph showing results measured in Example 3 using the sorbose dehydrogenase produced in Example 2 with respect to clinical samples.

5 BEST MODE FOR CARRYING OUT THE INVENTION

[0015]

The method of determining 1,5-AG according to the present invention utilizes (a) a protein which consists of the amino acid sequence of SEQ ID NO: 2; (b) a protein which consists of an amino acid sequence having deletion, substitution and/or addition of one or more amino acid residues in the amino acid sequence of SEQ ID NO: 2 and which has sorbose dehydrogenase activity; or (c) a protein which consists of an amino acid sequence having a homology of at least 60% with the amino acid sequence of SEQ ID NO: 2 and which has sorbose dehydrogenase activity.

Hereinafter, the above-described protein is referred to as a sorbose dehydrogenase.

15 [0016]

It is preferable that the sorbose dehydrogenase used in the determination method of the present invention have the following physicochemical properties.

- (1) The optimal pH is about 8.0, whereas the sorbose dehydrogenase exhibits an activity of 50% or higher within a range of 6.3-9.1;
- 20 (2) With regard to the pH stability, the sorbose dehydrogenase is stable within a pH range of 5.9-8.6 after the protein is treated at 40°C for fifteen minutes;
- (3) The optimal temperature is around 60°C in a buffer whose pH is 7.0;
- (4) With regard to the temperature stability, the sorbose dehydrogenase exhibits remaining activity of 77% or higher after the protein is treated in a buffer, whose pH is 25 7.0, at 45°C for ten minutes, and is stable at about 45°C or less;

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(5) With regard to the substrate specificity and the K_m value, the sorbose dehydrogenase has a strong effect on 1,5-AG and L-sorbose as a substrate while the sorbose dehydrogenase has little or a weak effect on sugars such as D-galactose or D-glucose. The K_m value thereof may be about 82.5 mM with respect to 1,5-AG while
5 the K_m value may be about 65.6 mM with respect to L-sorbose.

(6) With regard to the molecular weight and the subunit molecular weight, the total molecular weight is about 150 kDa or about 672 kDa while the subunit molecular weight is about 59.6 kDa.

(7) With regard to the inhibitor specificity, the sorbose dehydrogenase is remarkably
10 inhibited with a heavy metal ion (e.g. Mn^{2+} , Hg^{2+} or Cu^{2+}).

(8) The sorbose dehydrogenase has an effect on L-sorbose, thereby producing L-sorbosone.

(9) The coenzyme thereof is flavin adenine dinucleotide (FAD).

[0017]

15 The sorbose dehydrogenase used in the determination method of the present invention is not particularly limited with regard to its origin, the production method, etc. as long as the sorbose dehydrogenase has features described in the present description. The sorbose dehydrogenase may be a natural protein, a protein expressed from a recombinant DNA by way of genetic engineering techniques, or a chemically-
20 synthesized protein. In particular, the sorbose dehydrogenase may be preferably derived from a bacterium which belongs to the genus *Sinorhizobium*, more preferably derived from *Sinorhizobium* sp. 97507 (Accession No. FERM P-19428) or *Sinorhizobium meliloti* (preferably Strain 1021), and most preferably derived from *Sinorhizobium* sp. 97507 (Accession No. FERM P-19428).

25 The term "derived from", as described above, refers to a protein coded by a

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sorbose dehydrogenase gene of the above-mentioned bacteria. The protein may be those directly extracted from bacteria, those expressed by genetic engineering techniques, those chemically synthesized, etc. and the production method thereof is not particularly limited.

5 [0018]

Hereinafter, an example of the production method using genetic engineering techniques for the sorbose dehydrogenase used in the determination method of the present invention will be described.

(DNA extraction)

10 Bacterial cells of *Sinorhizobium sp.* 97507 (Accession No. FERM P-19428) are subjected to sonication or enzymatic lysis treatment to digest the cell wall. Then, the DNA is extracted with phenol, etc., and the DNA is recovered by way of salt precipitation, ethanol precipitation or the like.

[0019]

15 (PCR)

The above-extracted DNA which is derived from *Sinorhizobium sp.* 97507 (Accession No. FERM P-19428) is used as a template, and a plurality of primers prepared based on the nucleotide sequence of a sorbose dehydrogenase gene is used to conduct a PCR whereby the sorbose dehydrogenase gene is amplified. The produced
20 PCR product is purified by agarose electrophoresis or the like, and DNA of the sorbose dehydrogenase gene is extracted from the agarose gel.

[0020]

(Preparation of recombinant vector)

The expression vector used for preparation of a recombinant vector may be
25 selected optionally from those which produce an intact form of the expressed protein,

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those which produce an N-terminal or C-terminal histidine-tagged form thereof, or those which produce a form in which a maltose-binding protein or a GST peptide is fused to the N-terminal or C-terminal thereof. The expression vector and DNA of the sorbose dehydrogenase gene obtained by the above PCR may be digested with the same
5 restriction enzymes such as Nco I or Hind III, and then, DNA of the enzyme gene is ligated to the expression vector to prepare the recombinant vector.

Additionally, commercially-available products may be used for the expression vector. However, a specific site of commercially-available plasmid vectors may be substituted to stabilize the expression vector, and such substituted plasmid vectors are
10 preferably used.

[0021]

As described above, the method of determining 1,5-AG according to the present invention utilizes (a) a protein which consists of the amino acid sequence of SEQ ID NO: 2; (b) a protein which consists of an amino acid sequence having deletion, substitution
15 and/or addition of one or more amino acid residues in the amino acid sequence of SEQ ID NO: 2 and which has sorbose dehydrogenase activity; or (c) a protein which consists of an amino acid sequence having a homology of at least 60% (60% to 100%) with the amino acid sequence of SEQ ID NO: 2 and which has sorbose dehydrogenase activity. However, the homology is preferably 65% or more (65% to 100%), more preferably 75%
20 or more (75% to 100%), and most preferably 85% or more (85% to 100%).

In terms of the above-described homology of the amino acid sequence, manipulation of substitution, addition, deletion, etc. of an amino acid may be conducted with respect to the sorbose dehydrogenase-coding region inserted into the expression vector by way of site-specific mutagenesis using known base-substitution techniques
25 such as the Kunkel method as long as the produced recombinant sorbose dehydrogenase

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can achieve the object of the present invention. Moreover, manipulation of substitution, addition, deletion, etc. of an amino acid may be conducted by way of random mutagenesis using known base-substitution techniques such as an error-prone PCR. Furthermore, a known technique such as DNA shuffling may be conducted with respect to sorbose dehydrogenase genes isolated from plural species of bacteria to produce a sorbose dehydrogenase having superior properties.

In addition, the term "homology" refers to a degree of identity between sequences of two or more genes. Accordingly, the higher the homology is between two types of genes, the higher the identity or similarity of the sequences. Whether two types of genes possess a homology can be evaluated by direct comparison of the sequences, or by a hybridization technique under stringent conditions for comparison between nucleotide sequences.

[0022]

(Preparation of transformant)

Introduction (e.g. transformation or transfection) of the recombinant vector including the sorbose dehydrogenase gene into a host cell can be achieved by conventional known techniques. For example, a method of Cohen *et al.* (Proc. Natl. Acad. Sci. USA., vol. 69, p. 2110, 1972), a protoplast method (Mol. Gen. Genet., vol. 168, p. 111, 1979) or a competent method (Journal of Molecular Biology, vol. 56, p 209, 1971) may be adopted to transform a bacterial host (*E. coli*, *Bacillus subtilis*, etc.); a method of Hinnen *et al.* (Proc. Natl. Acad. USA., vol. 75, p 1927, 1978) or a lithium method (J. Bacteriol., vol. 153, p. 163, 1983) may be adopted to transform yeasts (*Saccharomyces cerevisiae*, *Pichia pastoris*, etc.); a method of Graham (Virology, vol. 52, p 456, 1973) may be adopted to transform animal cells; and a method of Summers *et al.* (Mol. Cell. Biol., vol. 3, pp. 2156-2165, 1983) may be adopted to transform insect cells.

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Additionally, in the transformation, it is not always required to express the protein from the recombinant vector. For example, the following technique may be adopted. That is, the sorbose dehydrogenase gene used in the present invention may be inserted directly into the chromosome DNA of host cells to express the gene. Bacteria or yeasts are preferably used as hosts in the present invention since these host cells are easily handled and can produce a large amount of recombinant protein in a relatively short time. In particular, a microorganism that belongs to the genus *Escherichia* is more preferably used as the host.

[0023]

10 (Expression and harvest of sorbose dehydrogenase)

Transformant cells harboring the above-prepared expression vector are cultured in a nutrient culture medium and the expressed sorbose dehydrogenase is harvested to obtain the sorbose dehydrogenase used in the determination method of the present invention. The nutrient culture medium preferably contains a carbon source, or an inorganic or organic nitrogen source required for growth of the host cells. Examples of the carbon source include glucose, dextran, soluble starch, sucrose, or methanol. Examples of the inorganic or organic nitrogen source include ammonium salts, nitrates, amino acids, corn steep liquor, peptone, casein, meat extracts, soybean cake, or potato extracts. Additionally, the nutrient culture medium may optionally contain extra nutrients (e.g. inorganic salts such as sodium chloride, calcium chloride, sodium dihydrogen phosphate or magnesium chloride; vitamins; or antibiotics such as tetracycline, neomycin, ampicillin or kanamycin). Culturing can be achieved by methods known in the art. Culturing conditions such as the culturing temperature, pH of the medium or culturing time can be suitably selected so as to produce a large quantity of the sorbose dehydrogenase.

[0024]

Host cells (i.e. transformants) such as microorganisms in which the sorbose dehydrogenase is expressed, as described above, can be recovered from the culture medium by a procedure such as centrifugation. The recovered host cells are suspended
5 in a typical appropriate buffer solution. Then, the suspended host cells are subjected to mechanical treatment such as sonication, or enzymatic treatment such as lysozyme treatment. Furthermore, typical known purification techniques such as affinity chromatography, ion-exchange chromatography or gel filtration chromatography can be combined suitably to purify the sorbose dehydrogenase.

10 [0025]

As described above, the sorbose dehydrogenase used in the present invention requires flavin adenine dinucleotide (FAD) as a coenzyme. However, if the sorbose dehydrogenase is produced under the aforementioned general conditions, a sorbose dehydrogenase which the coenzyme is bound to can be prepared without external
15 addition of FAD.

Accordingly, it is not always required to artificially add FAD in the above-described production process, in the method of determining 1,5-AG or to the reagent composition for determining 1,5-AG of the present invention.

[0026]

20 (Method of activating sorbose dehydrogenase)

The sorbose dehydrogenase of the present invention can be activated if the sorbose dehydrogenase is incubated in the presence of an electron carrier. Therefore, prior to the determination method or production of the reagent composition for determining 1,5-AG of the present invention, the sorbose dehydrogenase may be
25 subjected to such activation treatment. In particular, if the determination method or the

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reagent composition of the present invention is applied to clinical samples such as blood, it is preferable that the sorbose dehydrogenase be subjected to the activation treatment in advance. This is because highly sensitive detection of 1,5-AG can be achieved.

Examples of the electron carriers used for activation include phenazine
5 methosulfate (PMS), 1-methoxy-5-methylphenazinium methyl sulfate (1m-PMS), etc.
When 1m-PMS is used, the compound may be added to the prepared sorbose
dehydrogenase in a final concentration of 0.01 mM to 50 mM, and more preferably in a
final concentration of 0.01 mM to 10 mM, and the sorbose dehydrogenase is incubated
therein at pH 5-9 at 4-45°C for thirty minutes to one day. If an excessive amount of 1m-
10 PMS remains therein after the activation treatment to prepare a measurement reagent, the
excessive 1m-PMS can be removed by way of dialysis, ultrafiltration, etc. to apply the
sorbose dehydrogenase to the determination method or the reagent composition for
determining 1,5-AG of the present invention.

The sorbose dehydrogenase used in the present invention can be activated by the
15 above-mentioned treatment. The enzyme activity after the activation treatment, which
is measured with 1,5-AG as the substrate thereof, as described below, is activated
preferably two times (2-20 folds) higher, and more preferably four times (4-10 folds)
higher than before the activation treatment.

[0027]

20 (Determination method)

According to the method of determining 1,5-AG of the present invention, the
quantity of 1,5-AG in a sample such as blood or cerebrospinal fluid can be precisely
determined. As described above, the 1,5-AG level in blood is useful as a control marker
for diabetes. Accordingly, the determination method of the present invention is useful
25 for diagnosis of diabetes.

[0028]

The method of determining 1,5-AG of the present invention may be conducted, for example, by the following procedures. The sorbose dehydrogenase may be added to 1 mL of a body fluid sample, which is expected to contain 1,5-AG, in a final concentration of 1 to 500 units where the enzyme activity measured using 1,5-AG as a substrate is defined as the base unit. Furthermore, when using a chromogenic substrate which reacts directly due to the sorbose dehydrogenase of the present invention, only the chromogenic substrate may be added thereto. When using a chromogenic substrate which does not react directly due to the sorbose dehydrogenase of the present invention but which develops a color by reduction in the presence of an electron carrier ; or a chromogenic substrate which slightly develops a color due to the sorbose dehydrogenase of the present invention but which remarkably develops a color by reduction in the presence of an electron carrier, an electron carrier may be added thereto besides the chromogenic substrate. While the sample is incubated preferably at 4°C to 50°C (more preferably at 25°C to 40°C) for one minute to three hours (more preferably for one minute to thirty minutes, and most preferably for one minute to ten minutes), changes in the absorbance are measured. Based on a standard curve formulated in advance, the concentration of 1,5-AG in the sample is determined.

In addition, a “chromogenic substrate” includes the chromogenic substrate which reacts directly due to the dehydrogenase; the chromogenic substrate which develops a color by reduction in the presence of an electron carrier; and the chromogenic substrate which remarkably develops a color by reduction in the presence of an electron carrier, as described above. Furthermore, a “reductive chromogenic substrate” include the chromogenic substrate which develops a color by reduction in the presence of an electron carrier; and the chromogenic substrate which remarkably develops a color by reduction

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in the presence of an electron carrier, as described above.

[0029]

The sorbose dehydrogenase used in the method of determining 1,5-AG of the present invention at least needs to react with 1,5-AG to such an extent that the dehydrogenase can stand up to practical use. Sorbose is a sugar which does not exist in a living body. Therefore, the reactivity with sorbose is not particularly a matter. However, with regard to the reactivity of the sorbose dehydrogenase to 1,5-AG, a sorbose dehydrogenase having a reactivity of preferably 10% or higher (10% to 200%), more preferably 50% or higher (50% to 200%) can be used where the reactivity to sorbose is considered as 100% although it depends on a test samples. Furthermore, with regard to the sorbose dehydrogenase used in the method of determining 1,5-AG of the present invention, a sorbose dehydrogenase having little or a weak effect on D-glucose may be used. Since a large amount of D-glucose is present in a test sample, a sorbose dehydrogenase having a reactivity to D-glucose of preferably 10% or less (0.001% to 10%), and more preferably 5% or less (0.001% to 5%) may be selected whereby the requirement and stringency of pretreatment to the sample (in particular, treatment of removing sugars such as D-glucose) can be substantially reduced. Consequently, facilitation of the measurement, reduction in the measurement time, improvements in the measurement accuracy and cost reduction can be achieved.

In addition, the above-mentioned “reactivity” is reactivity evaluated based on the maximum reaction rate of the enzyme that catalyzes the reaction with the substrate, i.e. sorbose, 1,5-AG or D-glucose where the excessive amount of substrate is affected by a certain amount of enzyme used in the reaction. As an example of “reactivity”, the “method of measuring enzyme activity” (where sorbose is used), as described below, can be mentioned.

[0030]

As described above, the sorbose dehydrogenase used in the method of determining 1,5-AG of the present invention has high specificity to 1,5-AG. However, the sorbose dehydrogenase may be slightly influenced by D-glucose. For example, when the sorbose dehydrogenase is applied to samples of diabetics whose concentration of D-glucose reaches thousands of times the concentration of 1,5-AG, the influence of D-glucose may be nonnegligible. When dealing with such samples, a D-glucose-removing agent or D-glucose-eliminating agent may be added to completely prevent the influence of D-glucose. That is, it is required to determine 1,5-AG after the influence of D-glucose is eliminated in advance by addition of such a D-glucose-removing or eliminating agent.

[0031]

As an example of a method of removing sugars such as D-glucose, a method using an ion-exchange resin, as disclosed in Japanese Patent Publication No. H5-41235, can be mentioned. As a method of eliminating D-glucose, a method of converting D-glucose to glucose-6-phosphate using an enzyme phosphorylating glucose at C6 (hexokinase or glucokinase) can be applied to the present invention, as disclosed in Japanese Patent Publication No. H1-320998, Japanese Examined Patent Application, Second Publication No. H7-71514, Japanese Patent Publication No. H6-237795, Japanese Patent Publication No. H3-27299, Japanese Patent Publication No. H6-245796, Japanese Examined Patent Application, Second Publication No. H7-102154, etc. The second method of eliminating D-glucose may be preferably adopted because the samples can be set in a general automatic measurement apparatus for a biochemical examination. In this case, it is preferable that glucokinase, which has high specificity to D-glucose, be used as the enzyme phosphorylating glucose at C6. Although the amount of glucokinase varies

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with the amount of glucose in the sample, the amount of glucokinase may be 1 U/mL to 20U/mL. Moreover, although the amount of adenosine triphosphate (ATP) required for phosphorylation of glucose varies with the amount of glucose in the sample, the amount of ATP may be 0.5 mM to 20 mM. Additionally, 2 mM to 50 mM of magnesium
5 chloride may be added to promote the phosphorylation of D-glucose.

Furthermore, if a higher level of elimination of D-glucose is required, for example, the above-mentioned D-glucose-6-phosphorylation system using glucokinase can be combined with an enzyme-cycling system, e.g. an ATP-cycling system using pyruvate kinase, thereby achieving complete elimination of D-glucose.

10 [0032]

With regard to the chromogenic substrate which reacts directly due to the sorbose dehydrogenase of the present invention, for example, an electron acceptor such as 2,6-dichlorophenol indophenol (DCIP) can be mentioned.

Moreover, a ferricyanide compound such as potassium ferricyanide may be used
15 as an electron acceptor, and changes in the color development of the electron acceptor may be detected after the oxidation-reduction reaction by the sorbose dehydrogenase. Otherwise, a method wherein a ferric sulfate-dupanol reagent is added, and this is color-developed as Prussian blue can be applied. However, in terms of ease and detection sensitivity, chromogenic substrates such as DCIP that react directly due to the sorbose
20 dehydrogenase, thereby enabling highly sensitive measurement, may be preferably used.

[0033]

With regard to the chromogenic substrates which develop a color by reduction in the presence of an electron carrier or which remarkably develop a color by reduction in the presence of an electron carrier, tetrazolium or salts thereof may be used. Typical
25 examples thereof include nitrotetrazolium blue (NTB); 2-(4-iodophenyl)-3-(4-

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nitrophenyl)-5-phenyl-2H-tetrazolium chloride; 3-(4,5-dimethyl-2-thiazolyl)-2,5-diphenyl-2H-tetrazolium bromide; 2-(4-iodophenyl)-3-(4-nitrophenyl)-5-(2,4-disulfophenyl)-2H-tetrazolium, monosodium salt (WST-1); 2-(4-iodophenyl)-3-(2,4-dinitrophenyl)-5-(2,4-disulfophenyl)-2H-tetrazolium, monosodium salt (WST-3); or 2-(2-methoxyl-4-nitrophenyl)-3-(4-nitrophenyl)-5-(2,4-disulfophenyl)-2H-tetrazolium, monosodium salt (WST-8). The concentration thereof may be within a range of 0.05 mM to 4 mM, and preferably within a range of 0.1 mM to 2 mM.

[0034]

With regard to the electron carrier used for the color development of tetrazoliums or salts thereof, phenazine methosulfate (PMS), 1-methoxy-5-methylphenazinium methyl sulfate (1m-PMS), etc. can be mentioned. When using 1m-PMS, the concentration thereof may be within a range of 0.01 mM to 50 mM, and more preferably within a range of 0.01 mM to 10 mM.

[0035]

With regard to a buffer used in the above-described determination method, any generally-used buffer such as a phosphate buffer, Tris-HCl buffer, Good's buffer, or boric acid buffer can be used (pH 6-10).

[0036]

(Reagent composition for determination)

The reagent composition for determining 1,5-AG of the present invention contains the above-described sorbose dehydrogenase as an essential component, and is useful for diagnosis of diabetes. The form of reagent can be modified suitably according to objective samples, a chromogenic agent used therein, a mode of measurement, among others.

25 [0037]

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For example, the reagent composition for determining 1,5-AG of the present invention may be combined with a reagent that eliminates sugars such as D-glucose (sugar-eliminating agent), as described above, when applying the reagent composition to measurement of samples derived from diabetes, containing a high concentration of D-glucose. As such a sugar-eliminating agent, the above-described known techniques can be adopted. Combination of a borate-bound resin, anion-exchange resin and cation-exchange resin, or combination of a strong basic anion-exchange resin and cation-exchange resin is preferable. When a sample is treated with a strong basic anion-exchange resin or boric acid, 1,5-AG is not removed, but sugars are selectively removed, thereby obtaining a sample containing 1,5-AG. Furthermore, an enzyme that does not have effects on 1,5-AG but that has effects on other sugars can be used to remove sugars other than 1,5-AG. Examples of such an enzyme include a hexokinase or glucokinase, as described above. Glucose can be phosphorylated by using such enzymes, thereby removing glucose. Additionally, a method of removing D-glucose in a sample using a glucose oxidase can be mentioned. The reaction product from D-glucose by a glucose oxidase is D-glucono-1,5-lactone.

[0038]

The reagent composition for determining 1,5-AG may be prepared in a form of a single reagent obtained by mixing all components, or may be divided in appropriate combination of components if components interfere with each other. The reagent composition may be prepared into a liquid or powdery reagent. Furthermore, the reagent composition may be included in a support such as filter paper or films whereby the reagent composition can be prepared as a test paper or analytical film. Additionally, a protein-removing agent such as perchloric acid, or a standard reagent containing 1,5-AG may be attached to the reagent composition for determining 1,5-AG. With regard to

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the amount of enzyme (sorbitol dehydrogenase) included in the reagent composition, it is preferable that the reagent composition be prepared such that the final concentration thereof is about 0.1 units/mL to 50 units/mL in a reaction solution with respect to one sample where the enzyme activity measured using 1,5-AG as a substrate is defined as the
5 base unit. As examples of samples for the 1,5-AG quantification, blood plasma, serum, cerebrospinal fluid, or urine can be mentioned.

[0039]

With regard to application of the reagent composition for determining 1,5-AG of the present invention, application to a large-size universal automatic measurement
10 machine for biochemical examination can be considered as the most common use. However, a small-sized specialized machine or a portable machine for general practitioners can be considered.

When a reagent composition for determining 1,5-AG used for such automatic measurement machines is prepared, for example, addition of a reductive color-producing
15 agent (a tetrazolium and an electron carrier when the reductive color-producing agent is a tetrazolium) and a sorbitol dehydrogenase to a sample can be conducted at the same time except that a D-glucose-eliminating agent needs to be added in advance. That is, the components other than the D-glucose-eliminating agent may be prepared into one reagent. Furthermore, if, among a D-glucose-eliminating agent, tetrazolium, electron carrier, and
20 sorbitol dehydrogenase, there are some components that interfere with each other, the components may be prepared, for example, into separate reagents to prevent such interference.

[0040]

Hereinafter, the present invention will be described in detail with respect to
25 Examples. However, the present invention is not limited to Examples below.

EXAMPLES

[0041]

(Example 1)

5 [Identification of a bacterium to use]

The bacterium used in the experiment was isolated from root nodules of alfalfa, and bacteriological properties of the bacterium were as follows.

[0042]

1. Morphological properties

10 The morphological properties of the bacterium grown in a yeast extract-mannitol medium are described below. The morphology of bacterial cells was rod-shaped, and the size was $0.5\text{-}0.9\text{ }\mu\text{m} \times 1.2\text{-}3.0\text{ }\mu\text{m}$. The bacterium did not form a spore, and Gram staining was negative.

15 2. Growth state on a culture medium

The growth state of the bacterium grown in a yeast extract-mannitol medium is described below. The colonies exhibited as cream-white, the morphology thereof was circular and swollen, being gibbous-shaped, and the colonies were viscous. Colonies grown at 30°C for three days had a diameter of 2-4 mm. Additionally, the bacterium
20 had flagella and motility.

3. Physiological properties.

The bacterium was aerobic and the optimal growth temperature was 25-30°C, and the optimal growth pH was 6-8. The consumption of typical sugars is shown in Table 2.
25 The bacterium produced oxidase and catalase.

[0043]

Table 2

D-arabinose	+
Cellobiose	+
Fructose	+
D-galactose	+
Glucose	+
Lactose	+
D-mannose	+
Mannitol	+
D-ribose	+
Xylose	+
Cellulose	—
Sorbose	—
Dulcitol	—
Fucose	—

[0044]

The genus which the bacterium belonged to was determined based on the above-

5 described isolated source and properties in accordance with “Bergey’s Manual of DETERMINATIVE BACTERIOLOGY (9TH edition)”. Consequently, it was discovered that the bacterium was a microorganism that belonged to the genus *Sinorhizobium*. The bacterium was designated as *Sinorhizobium* sp. 97507.

Sinorhizobium sp. 97507 was deposited at the International Patent Organism Depositary,

10 National Institute of Advanced Industrial Science and Technology by the present applicant(s) on July 10th, 2003, and accession No. FERM P-19428 (Japanese national deposit) was obtained on a receipt dated July 11th, 2003 issued by the International Patent Organism Depositary. Hereinafter, *Sinorhizobium* sp. 97507 (FERM P-19428) is referred to as a “deposited strain”.

15 Furthermore, the present applicant(s) filed a request for transferring the above-mentioned *Sinorhizobium* sp. 97507 (original deposit; national accession No. FERM P-19428) to an international deposit at the International Patent Organism Depositary, National Institute of Advanced Industrial Science and Technology (international

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depository authority) on June 22nd, 2007, and the petition was received by the international depository authority on the same day. Receipt No. FERM ABP-10843 was issued on the receipt of the request.

[0045]

5 [Cloning of sorbose dehydrogenase]

A genomic DNA was extracted from the deposited strain, and a sorbose dehydrogenase was cloned by the following procedures.

[0046]

1. Extraction of genomic DNA

10 The bacterial cells of the deposited strain were treated with lysozyme to digest the cell wall. Then, the DNA was extracted with phenol, and the DNA was purified by salt precipitation, and recovered.

[0047]

2. PCR

15 PCR was conducted under the following conditions, and the PCR product including a sorbose dehydrogenase gene of about 1.6 kbp was obtained.

· Template: DNA extracted in 1. (derived from the deposited strain).

· Primers: DNAs represented by SEQ ID NO: 3 and SEQ ID NO: 4.

20 (Primers 1 and 2 were designed based on a nucleotide sequence "SMa1414" (putative L-sorbose dehydrogenase) disclosed by *Sinorhizobium meliloti* strain 1021 Genome Project (web site: <http://sequence.toulouse.inra.fr/meliloti.html>).)

· Polymerase: TaKaRa LA Taq (manufactured by Takara Bio Inc.)

25 ■Reaction conditions:

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- a. Denaturation at 94°C for one minute (one cycle)
- b. Denaturation at 94°C for thirty seconds
- c. Annealing at 57°C for one minute
- d. Extension reaction at 72°C for two minutes
- 5 e. Extension reaction at 72°C for five minutes (one cycle)

30 cycles of the reactions of b to d were conducted.

[0048]

3. Purification of the product from the excised gel.

The PCR product obtained in 2. was subjected to agarose gel electrophoresis to
10 purify the product. The DNA of the sorbose dehydrogenase gene was extracted from
the agarose gel by using “QIAEXII Gel Extraction Kit” (manufactured by Qiagen).

[0049]

4. Treatment with restriction enzyme

The DNA of the sorbose dehydrogenase gene extracted and purified from the
15 agarose gel in 3. and plasmid “pUCNNT2” were treated with restriction enzymes NcoI
and HindIII. The DNA of the sorbose dehydrogenase gene and plasmid pUCNNT2
treated with restriction enzymes were purified by agarose gel electrophoresis, and were
extracted from the agarose gel by using “QIAEXII Gel Extraction Kit” (manufactured by
Qiagen).

20 In addition, the plasmid pUCNNT2 was a plasmid prepared by inserting, to a
commercially-available plasmid pUC19 (manufactured by Takara Bio Inc.), an NcoI
linker and an rrnB ribosomal terminator derived from pKK223-3 (manufactured by
Pharmacia Biotech) that contributes to stabilization of a plasmid, and was particularly
suitable for expression of the sorbose dehydrogenase used in the present invention.

25 FIGs. 1 and 2 are flowcharts that illustrate construction of the plasmid pUCNNT2 used in

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the present Example. As shown in FIGs. 1 and 2, the plasmid pUCNNT2 was constructed by the following steps 1-5.

Step 1: "pUCNde" was prepared by adding an NdeI linker to a commercially-available plasmid pUC19 (manufactured by Takara Bio Inc.).

5 Step 2: the EcoRI-SspI region of pKK223-3 (manufactured by Pharmacia Biotech) was amplified by a PCR. In this case, an NdeI linker was inserted (i.e. NdeI-SspI fragment of a PCR product).

The *rrnBT₁T₂* in the NdeI-SspI fragment of the PCR product shown in FIG. 1 contributes to stability of a plasmid.

10 Step 3: the NdeI-SspI region of pUCNde was substituted with NdeI-SspI fragment of the PCR product to prepare a plasmid pUCNNT.

Step 4: the Cfr10I-BamHI region of pUCNNT was amplified by a PCR. In this case, the NdeI linker was converted to an NcoI linker.

Step 5: the Cfr10I-BamHI region of pUCNNT was substituted with the amplified
15 fragment to prepare plasmid pUCNNT2.

[0050]

5. Ligation

The DNA of sorbose dehydrogenase gene and plasmid pUCNNT2 treated with restriction enzymes in 4. were ligated with DNA Ligation Kit Ver. 2.1 (manufactured by
20 Takara Bio Inc.) to construct plasmid pUCNNT2_AGD1.

[0051]

6. Transformation

E. coli JM109 competent cells (manufactured by Takara Bio Inc.) were transformed with plasmid pUCNNT2_AGD1 constructed in 5. The transformed
25 competent cells were inoculated on an LB plate containing ampicillin sodium, and

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cultured at 37°C overnight. With respect to twenty colonies grown on the LB plate containing ampicillin sodium, it was confirmed by a direct PCR whether the plasmid including the sorbose dehydrogenase gene was introduced thereto. Consequently, seven isolates where amplification of the sorbose dehydrogenase gene was confirmed were inoculated on LB plates containing ampicillin sodium, and purified.

[0052]

7. Confirmation of activity.

(1) the purified seven isolates of gene-manipulated *E. coli* were cultured in liquid media under the following conditions.

10 ■ Culture medium:

LB medium 10 mL

- Bacto Tryptone (manufactured by Becton, Dickinson and Co.) 1.00% (w/v)
- Bacto Yeast Extract (manufactured by Becton, Dickinson and Co.) 0.50% (w/v)
- Sodium chloride (manufactured by Nacalai Tesque Inc.) 1.00% (w/v)
- 15 · Ampicillin sodium (manufactured by Wako Pure Chemical Industries, Ltd.) 0.005% (w/v)

■ Culture container: a test tube (diameter 2.5 cm × length 20 cm)

■ Culture conditions: 37°C, fifteen hours, and 121 rpm

(2) Bacterial cells were harvested from 10 mL of the culture medium (centrifuged at 1000 × g for ten minutes at room temperature).

(3) The supernatant was removed, and the bacterial cells were suspended in 1 mL of a disruption buffer (50 mM KPB, pH 7.5; 0.25% (w/v) “BL-9EX” manufactured by Nikko Chemicals co., Ltd.; and 0.01% (w/v) flavin adenine dinucleotide (FAD)).

(4) The bacterial cells were disrupted with a tip-type sonication disruption apparatus (incubated in an ice bath for five minutes).

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(5) The solution of disrupted bacterial cells was centrifuged at $13000 \times g$ at 4°C for five minutes, and the supernatant (cell-free extract) was recovered. The cell-free extract was used as a sample for the activity measurement.

(6) The expression of activity was confirmed based on the “method of measuring enzyme activity” described below. The strain having the highest sorbose dehydrogenase activity was designated as “*E. coli* JM109/pUCNNT2_AGD1”. In addition, the sorbose dehydrogenase activity / medium was 0.080 U/mL.

Then, the nucleotide sequence of the plasmid pUCNNT2_AGD1, which was extracted from the cultured bacterial cells of *E. coli* JM109/pUCNNT2_AGD1, was determined. It was confirmed that a DNA fragment coding the sorbose dehydrogenase was inserted therein. The nucleotide sequence is shown as SEQ ID NO: 1 while the amino acid sequence is shown as SEQ ID NO: 2.

Furthermore, the nucleotide sequence determined in the present example was compared with a putative sorbose dehydrogenase-coding region (locus tag: SMa1414) disclosed in the above-mentioned genome project of *Sinorhizobium meliloti* strain 1021. Consequently, the 160th nucleotide was adenine (A) in SMa1414 while the corresponding nucleotide was cytosine (C) in the nucleotide sequence of the present example. Resulting from the nucleotide substitution, the 54th amino acid was methionine (Met) in SMa1414 (Accession No.: NP_436019) while the corresponding amino acid was leucine (Leu) in the amino acid sequence of the present example.

[0053]

[Production of sorbose dehydrogenase]

The gene recombinant (*E. coli* JM109/pUCNNT2_AGD1) harboring the sorbose dehydrogenase gene, as prepared above, was cultured, and the sorbose dehydrogenase was extracted and purified from the obtained bacterial cells.

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In addition, the gene recombinant *E. coli* JM109/pUCNNT2_AGD1 was deposited at the International Patent Organism Depositary, National Institute of Advanced Industrial Science and Technology by the present applicant(s) in March 28th, 2006, and accession No. FERM P-20854 (Japanese national deposit) was obtained on a receipt dated March 28th, 2006 issued by the International Patent Organism Depositary.

[0054]

1. Culturing

Bacterial cell: gene recombinant *E. coli* JM109/pUCNNT2_AGD1

1.1 Seed Culture

One L of LB medium was added to a 2.0 L shake flask, this was autoclaved at 121°C for twenty minutes, and a filter-sterilized ampicillin sodium solution was added in a final concentration of 0.005% (w/v) immediately before use. The gene recombinant *E. coli* JM109/pUCNNT2_AGD1 was inoculated into the LB medium with a platinum loop, and cultured at 37°C with shaking (120 rpm). The culture medium after culturing for thirteen hours was used as an inoculum for main culture.

■ Composition of LB medium:

- Bacto Tryptone (manufactured by Becton, Dickinson and Co.) 1.00% (w/v)
- Bacto Yeast Extract (manufactured by Becton, Dickinson and Co.) 0.50% (w/v)
- Sodium chloride (manufactured by Nacalai Tesque Inc.) 1.00% (w/v)
- Ampicillin sodium (manufactured by Wako Pure Chemical Industries, Ltd.)

0.005% (w/v)

[0055]

1.2 Main culture

Twenty one L of a GYC medium was charged to a 30 L culture apparatus, and autoclaved at 121°C for twenty minutes. A filter-sterilized solution of ampicillin

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sodium (manufactured by Wako Pure Chemical Industries, Ltd.) and a filter-sterilized solution of isopropyl β -D-1-thiogalactopyranoside (manufactured by SIGMA-ALDRICH Japan K.K.) were added in a final concentration of 0.005% (w/v) and 0.024% (w/v), respectively, immediately before use.

5

■ Composition of the GYC medium (adjusted to pH 7.0 with a 15 N NaOH solution):

- glycerol (manufactured by Sakamoto Yakuhin Kogyo Co., Ltd.) 4.0% (w/v)
- Yeast Extract (manufactured by Ajinomoto Co., Inc.) 2.0% (w/v)
- Corn steep liquor (manufactured by San-ei Sucochemical Co., Ltd.) 4.5% (w/v)

10

One L of the seed culture prepared in 1.1 was inoculated into the above medium, and cultured for fifteen hours under the following conditions. In addition, the medium was controlled at pH 7.0 with a 15 N NaOH solution while culturing.

- Culturing temperature: 37°C

15

- Aeration: 1 v/v/m

- Agitation speed: 350 rpm

Fifteen hours after culturing was started, 955.06 g of bacterial cells were harvested with a centrifuge.

[0056]

20 2. Purification

The sorbose dehydrogenase was extracted and purified from bacterial cells obtained by culturing through the purification steps described below. The total activity, specific activity, yield, and specific activity ratio (fold) were measured. The results are shown in Table 3.

25

The sorbose dehydrogenase activity was measured based on the “method of

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measuring enzyme activity”, as described below.

[0057]

Table 3

Purification step	Total activity (U)	Specific activity (U/mg)	Yield (%)	Fold
CFE	3,318	0.24	100	1.00
Ammonium sulfate pre. and dialysis	2,894	0.918	87.2	3.82
Strong anion-exchange chromatography (TOYOPEARL Super Q-650M)	619	0.777	18.7	3.23
Desalting and concentration	798	1.05	24.0	4.35

5 [0058]

2.1 Preparation of cell-free extract (CFE)

With regard to 955.06 g of bacterial cells obtained in the main culture of 1.2, 200 g thereof was used to purify the sorbose dehydrogenase. 1 L of a disruption buffer (50 mM KPB, pH 7.5; 0.25% (w/v) BL-9EX (manufactured by Nikko Chemicals co., Ltd.); and 0.001 mM FAD) was added to 200 g of the bacterial cells to prepare a suspension of bacterial cells. Phenylmethylsulfonyl fluoride (PMSF), i.e. a serine protease inhibitor, was added to the suspension in a final concentration of 1 mM, and the bacterial cells were disrupted with a tip-type sonication disruption apparatus. The solution of the disrupted bacterial cells was centrifuged at $13000 \times g$ at 4°C for fifteen minutes, and the supernatant was recovered. The supernatant was designated as CFE.

[0059]

2.2 Ammonium sulfate fractionation

Ammonium sulfate was added to 1095 mL of CFE recovered in 2.1 in a final concentration of 40% (w/v) in an ice bath. In this case, the CFE was adjusted to pH 7.5 with ammonia. After ammonium sulfate was dissolved, the CFE was allowed to stand

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at 4°C overnight.

[0060]

2.3 Dialysis

The ammonium sulfate precipitate was recovered by centrifugation ($13,000 \times g$,
5 4°C and 15 min.). The recovered ammonium sulfate precipitate was put into a dialysis
tube (seamless cellulose tube, small size 18, manufactured by Wako Pure Chemical
Industries, Ltd.), and this was dialyzed with a dialysis buffer (5 mM KPB, pH 8.0; 0.25%
(w/v) BL-9EX (manufactured by Nikko Chemicals co., Ltd.); and 0.001 mM FAD).

[0061]

10 2.4 Centrifugation

An insoluble matter was present inside the dialysis tube. Therefore, the
insoluble matter was removed by centrifugation ($13000 \times g$, 4°C and 15 min.), and the
supernatant was recovered.

[0062]

15 2.5 Strong anion-exchange chromatography (TOYOPEARL Super Q-650M)

The supernatant recovered in 2.3 was charged to 350 mL (column size: ϕ 6.2 cm $\times$
height 27 cm) of a strong anion-exchange resin “TOYOPEARL Super Q-650M”
(manufactured by Tosoh Corporation) equilibrated with an equilibration buffer (5 mM
KPB, pH 8.0; 0.25% (w/v) BL-9EX (manufactured by Nikko Chemicals co., Ltd.); and
20 0.001 mM FAD). After charging, the resin was washed with five resin-bed volume of
buffer (5 mM KPB, pH 8.0; 0.25% (w/v) BL-9EX (manufactured by Nikko Chemicals
co., Ltd.); and 0.001 mM FAD) for washing. Then, the objective protein was gradient-
eluted with two types of elution buffers (buffer 1: 5 mM KPB, pH 8.0, 0.25% (w/v) BL-
9EX (manufactured by Nikko Chemicals co., Ltd.), and 0.001 mM FAD; and buffer 2: 5
25 mM KPB, pH 8.0, 0.25% (w/v) BL-9EX (manufactured by Nikko Chemicals co., Ltd.),

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0.001 mM FAD, and 1 M NaCl) (each volume was 2.5 times the bed volume of resin) to recover active fractions.

[0063]

2.6 Desalting and concentration

5 The active fractions obtained by the strong anion-exchange chromatography (TOYOPEARL Super Q-650M) of 2.5 were subjected to desalting and concentration treatment using an ultrafiltration equipment "Vivacell 250" (manufactured by Vivascience, molecular cutoff: 10,000). Finally, the buffer solution wherein the sorbose dehydrogenase was dissolved was substituted with a 50 mM KPB buffer, pH 7.5, containing 0.25% (w/v) BL-9EX (manufactured by Nikko Chemicals co., Ltd.), and 0.01 mM FAD, thereby obtaining the sorbose dehydrogenase.

[0064]

[Method of measuring enzyme activity]

One mL of a 0.1 M potassium phosphate buffer, pH 7.0, 1.0 mL of 1.0 M L-sorbose, 0.14 mL of 3 mM 2,6-dichlorophenol indophenol (DCIP), 0.2 mL of 3 mM 1-methoxy-5-methylphenazinium methyl sulfate, and 0.61 mL of water were added to a 3 mL quartz cell, and the quartz cell was set to a spectrophotometer equipped with a thermostat cell holder, and incubated at 37°C for ten minutes. Then, 0.05 mL of the enzyme solution was added to the quartz cell, and changes in absorbance of DCIP at 600 nm ($\Delta\text{ABS}_{600}/\text{min}$) was measured at 37°C. As the molar extinction coefficient of DCIP at pH 7.0 is known as 16.3 mM^{-1} , and the amount of enzyme that reduced 1 μmol of DCIP for one minute is defined as one unit. Following the definition, the concentration of enzyme activity was calculated based on the following equation.

enzyme activity (units/mL) =

25 $(-\Delta\text{ABS}_{600}/\text{min} \times 3.0 \times \text{dilution rate}) / (16.3 \times 1.0 \times 0.05)$

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Optical path length: 1.0 cm

[0065]

[Evaluation of properties of sorbose dehydrogenase]

Measurement conditions in the above “method of measuring enzyme activity”

5 were suitably modified as necessary, and the optimal pH, pH stability, optimal temperature, temperature stability, substrate specificity, K_m value, total molecular weight, subunit molecular weight, inhibitor, and product of the enzyme reaction were identified. The properties of the enzyme were evaluated in accordance with the following tests.

[0066]

10 (1) Optimal pH:

The buffer solution in the above “method of measuring enzyme activity” was substituted with an acetic acid-sodium acetate buffer (pH 3.71-5.36), a citric acid-sodium phosphate buffer (pH 5.55-5.95), a potassium phosphate buffer (pH 6.25-7.35), a Tris-HCl buffer (pH 7.52-8.34), or a glycine-sodium hydroxide buffer (pH 8.68-9.11) (all buffers
15 were adjusted to the final concentration of 33.3 mM) to determine the enzyme activity of the purified enzyme. In addition, the molar extinction coefficient of DCIP at each value of pH obtained in advance was used to calculate the enzyme activity. The results are shown in FIG. 3. As shown in FIG. 3, the optimal pH for the sorbose dehydrogenase was 8.0.

20 [0067]

(2) pH stability:

The sorbose dehydrogenase was dissolved in each 50 mM buffer [i.e. an acetic acid-sodium acetate buffer (pH 4.14-5.91), a citric acid-sodium phosphate buffer (pH 5.91-6.30), a potassium phosphate buffer (pH 6.59-7.47), a Tris-HCl buffer (pH 7.53-
25 8.39), or a glycine-sodium hydroxide buffer (pH 8.61-10.30)]. The enzyme activity

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after the dissolved sorbose dehydrogenase was incubated at 40°C for fifteen minutes was measured based on the above “method of measuring enzyme activity”. The results are shown in FIG. 4. As shown in FIG. 4, the sorbose dehydrogenase was stable within a range of pH 5.9-8.6.

5 [0068]

(3) Optimal temperature:

The sorbose dehydrogenase was dissolved in a 50 mM potassium phosphate buffer, pH 7.0. The enzyme activity was measured while varying the temperature in the above “method of measuring enzyme activity” within a range of 35°C to 70°C. The results are shown in FIG. 5. As shown in FIG. 5, the optimal temperature for the sorbose dehydrogenase was around 60°C.

[0069]

(4) Temperature stability

The sorbose dehydrogenase was dissolved in a 50 mM potassium phosphate buffer, pH 7.0, containing 0.25% (w/v) “BL-9EX” (manufactured by Nikko Chemicals co., Ltd.) and 0.01 mM FAD. After the dissolved sorbose dehydrogenase was incubated at each point of temperature within 30°C to 70°C for ten minutes, the enzyme activity was measured based on the above “method of measuring enzyme activity” to obtain the residual ratio of enzyme activity. The results are shown in FIG. 6. As shown in FIG. 6, the sorbose dehydrogenase retained 77% of the enzyme activity even at 45°C, and was stable at about 45°C or less.

[0070]

(5) Substrate specificity and Km value:

When 1,5-AG, L-sorbose or other substrates shown in Table 4 (the final concentration was 167 mM for lactose, and 333 mM for any other substrate) was used as

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the substrate for the reaction solution for the activity measurement in the above “method of measuring enzyme activity”, the activity thereof was measured by following the above “method of measuring enzyme activity” to obtain a relative reactivity . The results are shown as a relative value of each substrate with reference to the value of activity of L-sorbose as a standard.

[0071]

Table 4

Substrate Specificity

Substrate	Relative activity (%)
L-(-)-sorbose	100
1,5-anhydroglucitol	79.1
Allyl alcohol	3.80
D-(-)-sorbose	2.96
2-methyl-1-propanol	2.06
D-(+)-galactose	1.69
1-butanol	1.29
D-(+)-glucose	1.22
Xylitol	0.89
1-propanol	0.75
Lactose	0.71
2-propanol	0.39
2,3-butanediol	0.26
D-(+)-mannose	0.15
Ethanol	0
Glycerol	0
Maltose	0
D-(-)-fructose	0

10 [0072]

As shown in Table 4, the sorbose dehydrogenase had a strong effect on 1,5-AG and L-sorbose while the sorbose dehydrogenase had a weak effect on an allyl alcohol, D-sorbose, 2-methyl-1-propanol, D-galactose, 1-butanol, or D-glucose. Moreover, the sorbose dehydrogenase had little effect on xylitol, 1-propanol, lactose, 2-propanol, 2,3-butanediol, D-mannose, ethanol, glycerol, maltose, D-fructose, L-rhamnose, D-mannitol, D-sorbitol, D-ribose, D-xylose, L-arabinose, D-cellobiose, sucrose, D- trehalose, D-raffinose, inositol, meso-erythritol, 2-butanol, 2-pentanol, propylene glycol, or methanol.

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Furthermore, the K_m value of the sorbose dehydrogenase was 82.5 mM to 1,5-AG, and 65.6 mM to L-sorbose.

[0073]

(6) Total molecular weight and subunit molecular weight:

5 The total molecular weight of the sorbose dehydrogenase was analyzed with TSKgel BioAssist G4SWXL column (diameter 0.78 cm $\times$ length 30 cm; manufactured by Tosoh Corporation) at a flow rate of 0.5 mL/minute using a 50 mM potassium phosphate buffer, pH 7.5, containing 0.2 M NaCl in the mobile phase. By comparing the sorbose dehydrogenase with a molecular weight marker (manufactured by Oriental Yeast co., Ltd.) and another molecular weight marker (manufactured by Amersham Biosciences) and IgM (manufactured by Sigma), it was assumed that the sorbose dehydrogenase existed in a form having a total molecular weight of about 150 kDa or about 672 kDa.

By use of 10% polyacrylamide gel, the sorbose dehydrogenase was subjected to a SDS-polyacrylamide gel electrophoresis (SDS-PAGE) by following the method according to Laemmli *et al.*. After the electrophoresis, the polyacrylamide gel was stained with Coomassie brilliant blue and the mobility of the sorbose dehydrogenase was compared with mobility of a molecular weight marker (manufactured by Amersham Biosciences). As a result, it was assumed that the subunit molecular weight of the sorbose dehydrogenase was about 59.6 kDa.

20 [0074]

(7) Inhibitor:

Each additive shown in Table 5 was added to the reaction solution for the activity measurement in the above “method of measuring enzyme activity” in a final concentration of 1 mM, and the activity of the sorbose dehydrogenase was measured.

25 The control was measured by following the aforementioned “method of measuring

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enzyme activity” without adding any additives. The activity value obtained when each of additives 1) to 39) was added thereto was calculated as a relative activity (%) where the activity value of the control was considered as 100%. The results are shown in Table 5.

5 [0075]

Table 5

Inhibitor	Final concentration (mM)	Relative activity (%)
Control: inhibitor not added.	0	100
1) NaN_3	1.0	115
2) AlCl_3	1.0	109
3) 8-quinolinol	0.3	106
4) EDTA-2Na	1.0	102
5) Benzoic acid	1.0	101
6) Fumaric acid	1.0	99
7) LiCl	1.0	98
8) H_2O_2	1.0	98
9) ZnCl_2	1.0	98
10) meso-tartaric acid	1.0	94
11) KCN	1.0	94
12) MgCl_2	1.0	93
13) CaCl_2	1.0	92
14) Urea	1.0	92
15) CdCl_2	1.0	91
16) Aminoguanidine sulfate	1.0	91
17) D-cycloserine	1.0	90
18) FeCl_3	1.0	89
19) Tiron	1.0	89
20) N-ethylmaleimide	1.0	88
21) 2,2'-bipyridine	1.0	88
22) SnCl_2	0.5	86
23) CoCl_2	1.0	86
24) Citric acid	1.0	86
25) DL-tartaric acid	1.0	86
26) NaCl	1.0	85
27) DL-malic acid	1.0	85
28) Iodoacetic acid	1.0	83
29) PbCl_2	1.0	83
30) Maleic acid	1.0	82
31) NiCl_2	1.0	80
32) BaCl_2	1.0	80
33) 1,10-phenanthroline	1.0	77
34) 2-(p-)nitrobenzoic acid	1.0	75
35) Acriflavin	1.0	66
36) Triton X-100	1.0	39
37) MnCl_2	1.0	11
38) HgCl_2	1.0	0
39) CuCl_2	1.0	0

[0076]

Based on results shown in Table 5, the sorbose dehydrogenase was remarkably inhibited by heavy metal ions (Mn^{2+} , Hg^{2+} or Cu^{2+}). The relative activity was 66%
5 when acriflavin was added.

[0077]

(8) Identification of a product of the enzyme reaction:

One and half mL of an enzyme reaction solution of a 50 mM potassium phosphate buffer, pH 7.5, containing 300 mM L-sorbose, 60 mM 1-methoxy-5-methylphenazinium
10 methyl sulfate, 498 U/mL catalase (manufactured by Wako Pure Chemical Industries, Ltd.) and 3.87 U of sorbose dehydrogenase obtained in 2.6 was reacted for two hours at room temperature with stirring. The enzymes were removed with a centrifugal ultrafiltration device "Microcon YM-10" (manufactured by Amicon, molecular cutoff: 10,000), and the enzyme reaction solution was analyzed by high performance liquid
15 chromatography. As a result, by comparison with an authentic sample for a retention time, it was identified that the product of the enzyme reaction was L-sorbosone. The L-sorbosone used as the authentic sample was chemically synthesized.

In addition, the analysis conditions of the high performance liquid chromatography were as follows.

- 20 · Column: "High Performance Carbohydrate column" (manufactured by Waters Corporation).
- Detection: RI.
- Mobile phase: acetonitrile/distilled water = 6:4 (containing 50 mM potassium phosphate buffer, pH 6.0).
- 25 · Flow rate: 1.0 mL/min.

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· Column temperature: 35°C.

· Injection volume: 10 µL.

[0078]

[Formulation of standard curve]

5 The substrate was substituted with 1,5-AG instead of L-sorbose in the
aforementioned “method of measuring enzyme activity”. While varying the final
concentration of 1,5-AG within a range of 1.5-40.6 mM, changes in the absorbance were
measured. By plotting the relationship between the concentration of 1,5-AG and
changes in absorbance ($\Delta \text{ABS}_{600}/\text{min.}$), a standard curve was formulated as shown in
10 FIG. 7. As shown in FIG. 7, it was revealed that 1,5-AG could be quantified with the
sorbose dehydrogenase within a range of the final concentration of 1.5-40.6 mM.

[0079]

[Coenzyme]

 The sorbose dehydrogenase was subjected to acid treatment, and a flavin
15 compound released from the protein of sorbose dehydrogenase by the acid treatment was
analyzed by high performance liquid chromatography. The retention time of the flavin
compound released from the sorbose dehydrogenase agreed with that of a standard of
FAD. Consequently, it was found that the coenzyme for the sorbose dehydrogenase was
FAD.

20 [0080]

(Example 2)

 Next, another example is described of production of the recombinant sorbose
dehydrogenase using a substituted-type high-expression plasmid (hereinafter, referred to
as pUCpTrcAGD1), and high-sensitive detection of 1,5-AG by way of activating the
25 sorbose dehydrogenase.

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Additionally, pUCpTrcAGD1 differs from pUCNNT2_AGD1 in that codons coding for glutamic acid (Glu) and phenylalanine (Phe) were inserted immediately after the start codon in the sorbose dehydrogenase gene, as described below.

Hereinafter, a method of constructing plasmid pTrcAGD1 will be described in detail with reference to procedures briefly summarized in FIG. 8.

[0081]

[1] Construction of plasmid pTrcAGD1

1. PCR (Step 1 in FIG. 8)

PCR was conducted under the following conditions to obtain a PCR product including a substituted-type sorbose dehydrogenase gene of about 1.6 kbp.

- Template: pUCNNT2_AGD1
- Primers: DNAs represented by SEQ ID NO: 7 and SEQ ID NO: 8
- Polymerase: Takara LA Taq (manufactured by Takara Bio Inc.)

In addition, the primer represented by SEQ ID NO: 7 included the restriction recognition site of NcoI and the inserted sequence of glutamic acid (gaa) and phenylalanine (ttc) while the primer represented by SEQ ID NO: 8 included the restriction recognition site of BamHI. The positional relationship of the primers is shown in Step 1 of FIG. 8.

■ Reaction conditions:

- a. Denaturation at 94°C for two minutes (one cycle)
 - b. Denaturation at 94°C for forty seconds
 - c. Annealing at 58°C for thirty seconds
 - d. Extension at 72°C for two minutes
 - e. Extension at 72°C for five minutes (one cycle)
- 35 cycles of the reactions of b to d were conducted.

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[0082]

2. Purification of the PCR product (Step 1 in FIG. 8).

The PCR product obtained in 1. was subjected to agarose gel electrophoresis to confirm the amplification of the product. The DNA of about 1.6 kbp, including the sorbose dehydrogenase gene was purified by using “QIAquick PCR Purification Kit” (manufactured by Qiagen).

[0083]

3. Treatment with restriction enzymes (Step 1 in FIG. 8)

The DNA of about 1.6 kbp, including the sorbose dehydrogenase gene purified in 2. was treated with restriction enzymes NcoI and BamHI. The DNA of about 1.6 kbp, including the sorbose dehydrogenase gene, treated with the restriction enzymes was subjected to agarose gel electrophoresis to purify the DNA, and the DNA of about 1.6 kbp, including the sorbose dehydrogenase gene was extracted from the agarose gel by using “QIAquick Gel Extraction Kit” (manufactured by Qiagen).

A plasmid pTrc99A (manufactured by Amersham Biosciences) was treated with restriction enzymes NcoI and BamHI, and then, was purified by using “QIAquick PCR Purification Kit” (manufactured by Qiagen).

[0084]

4. Ligation (Step 2 in FIG. 8)

The DNA of about 1.6 kbp, including the sorbose dehydrogenase gene and the pTrc99A treated with restriction enzymes in 3. was ligated by using “Ligation High” (manufactured by TOYOBO CO., LTD.) to construct a plasmid pTrcAGD1. The schematic diagram showing the plasmid pTrcAGD1 is shown in Step 2 of FIG. 8.

[0085]

25 5. Transformation

- 45 -

E. coli JM109 competent cells (manufactured by Takara Bio Inc.) were transformed with the plasmid pTrcAGD1 constructed in 4. The transformed cells were inoculated on an LB plate, containing ampicillin sodium, and cultured at 37°C overnight. The grown colonies were further cultured under the following conditions.

- 5 · Culture medium: LB medium 10 mL
- Culture container: a test tube (diameter 2.5 cm × length 20 cm)
- Culture conditions: 30°C, twenty hours and 210 rpm

Plasmids were extracted from the culture by using “QIAprep Spin Miniprep Kit” (manufactured by Qiagen). The plasmids were treated with restriction enzyme NcoI or
 10 BamHI, and the treated plasmids were subjected to agarose gel electrophoresis to confirm whether the sorbose dehydrogenase gene was inserted into the plasmids.
 [0086]

Additionally, the nucleotide sequence of the substituted-type sorbose dehydrogenase gene is shown as SEQ ID NO: 5 while the amino acid sequence thereof is
 15 shown as SEQ ID NO: 6.

[2] Construction of plasmid pUCpTrcAGD1

1. PCR (Step 3 in FIG. 8)

PCR was conducted under the following conditions to obtain a PCR product, including the trc promoter and the sorbose dehydrogenase gene (about 2.2 kbp in total).

- 20 · Template: pTrcAGD1
- Primers: DNAs represented by SEQ ID NO: 9 and SEQ ID NO: 10
- Polymerase: Takara Ex Taq (manufactured by Takara Bio Inc.)

In addition, the primers of SEQ ID NO: 9 and SEQ ID NO: 10 included the BglII-recognition site as an adaptor sequence.

- 25 ■ Reaction conditions:

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- a. Denaturation at 96°C for five minutes (one cycle)
- b. Denaturation at 96°C for forty seconds
- c. Annealing at 58°C for forty seconds
- d. Extension at 72°C for two minutes
- 5 e. Extension at 72°C for five minutes (one cycle)

25 cycles of the reactions of b to d were conducted.

[0087]

2. Purification of the product from the excised gel (Step 3 in FIG. 8)

The PCR product obtained in 1. was subjected to agarose gel electrophoresis to
10 purify the product. The DNA of about 2.2 kbp, including the trc promoter and the
sorbose dehydrogenase gene was extracted from the agarose gel by using "QIAquick Gel
Extraction Kit" (manufactured by Qiagen).

[0088]

3. Treatment with restriction enzymes (Steps 3 and 4 in FIG. 8)

15 The DNA of about 2.2 kbp, including the trc promoter and the sorbose
dehydrogenase gene purified from the agarose gel in 2. was treated with a restriction
enzyme BglII. The DNA of about 2.2 kbp, including the trc promoter and the sorbose
dehydrogenase treated with the restriction enzyme was subjected to agarose gel
electrophoresis to purify the DNA, and the DNA of about 2.2 kbp, including the trc
20 promoter and the sorbose dehydrogenase gene was extracted from the agarose gel by
using "QIAquick Gel Extraction Kit" (manufactured by Qiagen).

A plasmid pUC19 was treated with a restriction enzyme BamHI, and then,
subjected to dephosphorylation treatment.

[0089]

25 4. Ligation (Step 4 in FIG. 8)

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The DNA of about 2.2 kbp, including the *trc* promoter and the sorbose dehydrogenase gene, and the pUC 19 treated with restriction enzymes in 3. were ligated with “Ligation High” (TOYOBO CO., LTD.) to construct a pUCpTrcAGD1. A schematic diagram showing the plasmid pUCpTrcAGD1 is shown in Step 4 of FIG. 8.

5 [0090]

5. Transformation

E. coli JM109 competent cells (manufactured by Takara Bio Inc.) were transformed with the plasmid pUCpTrcAGD1 constructed in 4. The transformed competent cells were inoculated on an LB plate, containing ampicillin sodium, and
10 cultured at 37°C overnight. Grown colonies were cultured under the following conditions.

- Culture medium: LB medium 10 mL
- Culture container: a test tube (2.5 cm in diameter × 20 cm in length)
- Culture conditions: 30°C, twenty hours and 200 rpm

15 Plasmids were extracted from the culture by using “QIAprep Spin Miniprep Kit” (manufactured by Qiagen). The plasmids were treated with restriction enzyme *Eco*RI or *Pst*I, and the treated plasmids were subjected to agarose gel electrophoresis to confirm whether the *trc* promoter and the sorbose dehydrogenase gene were inserted into the plasmids.

20 [0091]

One (hereinafter, referred to as “*E. coli* JM109/pUCpTrcAGD1”) of the *E. coli* clones (it was confirmed that the *trc* promoter and the sorbose dehydrogenase gene were introduced into the clones) was used in “Production of substituted-type sorbose dehydrogenase”, as described below.

25 With respect to the plasmid extracted from the *E. coli* JM109/pUCpTrcAGD1, the

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nucleotide sequence of the sorbose dehydrogenase gene-coding region was determined. The determined nucleotide sequence is shown as SEQ ID NO: 5 while the amino acid sequence thereof is shown as SEQ ID NO: 6.

Based on confirmation of the nucleotide sequence, it was confirmed that gaa (glutamic acid) and ttc (phenylalanine) were inserted immediately after the start codon of the inserted sorbose dehydrogenase in its reading frame in that order.

Furthermore, it was confirmed that the 51st nucleotide of cytosine (C), the 108th nucleotide of guanine (G), and the 168th nucleotide of guanine (G) in the sorbose dehydrogenase-coding region of the pUCNNT2_AGD1 were substituted with thymine (T), adenine (A) and adenine (A), respectively, in pUCpTrcAGD1. However, there were no mutations such as substitution owing to the nucleotide substitutions in the amino acid sequence of the coded sorbose dehydrogenase except that the two amino acids were inserted therein.

[0092]

[3] Production of substituted-type sorbose dehydrogenase

1. Culture

Bacterial cell: genetically-modified *E. coli* JM109/pUCpTrcAGD1

1.1 Seed culture

One hundred mL of an LB medium was charged to a 500 mL Erlenmeyer flask, and this was autoclaved. An ampicillin sodium solution sterilized by filtration was added thereto immediately before use in a final concentration of 0.01% (w/v). The genetically-modified *E. coli* JM109/pUCpTrcAGD1 was inoculated into the LB medium with a platinum loop, and cultured at 25°C with shaking (120 rpm). The culture medium twenty-one hours after culturing was started was used as an inoculum for main culture.

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[0093]

1.2 Main culture

One hundred mL of an LB medium was charged to a 500 mL Erlenmeyer flask, and this was autoclaved. An ampicillin sodium solution sterilized by filtration was added thereto immediately before use in a final concentration of 0.01% (w/v). In this way, forty flasks containing the LB medium were prepared. 2 mL of the seed culture prepared in 1.1 was inoculated into each flask. After these were cultured at 25°C with shaking (120 rpm) for three hours, a filter-sterilized isopropyl β -D-1-thiogalactopyranoside solution was added to culture medium in each flask in a final concentration of 0.0024% (w/v), and these were further cultured at 25°C with shaking for twenty-one hours. After culturing, the bacterial cells were harvested by using a centrifuge.

[0094]

2. Purification

The substituted-type sorbose dehydrogenase was extracted and purified from the bacterial cells obtained by the above culture through the following purification steps. The results are shown in Table 6.

The activity of the sorbose dehydrogenase was measured based on the “method of measuring enzyme activity” described in Example 1.

20 [0095]

Table 6

Purification step	Total activity (U)	Specific activity (U/mg)	Yield (%)	Fold
CFE	883	0.19	100	1.00
Ammonium sulfate precipitation	517	0.24	58.6	1.26
Weak anion-exchange chromatography (DEAE FF)	502	0.91	56.9	4.79
Desalting and Concentration	322	0.94	36.5	4.95

[0096]

2.1 Preparation of Cell-free extract (CFE)

Three hundred and sixty mL of a 50 mM potassium phosphate buffer, pH 7.5 was added to bacterial cells obtained in the main culture of 1.2 to prepare cell suspension. The cell suspension was divided equally into four portions. With respect to the divided portions, the bacterial cells were disrupted with a sonication disruption apparatus ("INSONATOR 201M" manufactured by Kubota Corporation) at the output power of 180 W for thirty minutes. Each of the treated solutions was combined, and the combined solution was centrifuged at $11,000 \times g$ at 4°C for thirty minutes to recover 355 mL of CFE.

[0097]

2.2 Ammonium sulfate fractionation

BL-9EX was added to the CFE recovered in 2.1 in a final concentration of 0.25% (v/v), and this was dissolved while being stirred for thirty minutes. 51.12 g of ammonium sulfate was stepwise added to the CFE in an ice bath, thereby dissolving it, until the saturated concentration reached 25%. The CFE was further stirred for thirty minutes after ammonium sulfate was dissolved. The dissolved solution was centrifuged at $11,000 \times g$ at 4°C for thirty minutes, and 370 mL of the supernatant was recovered.

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Then, 34.41 g of ammonium sulfate was stepwise added to the supernatant in an ice bath, thereby dissolving it, until the saturated concentration reached 40%. The supernatant was further stirred for thirty minutes after ammonium sulfate was dissolved, and the supernatant was allowed to stand at 4°C overnight.

5 [0098]

2.3 Dialysis

The ammonium sulfate precipitate was recovered by centrifugation ($11,000 \times g$, 4°C, thirty minutes). The recovered ammonium sulfate precipitate was dissolved in 10 mL of a 50 mM sodium phosphate buffer, pH 7.5. The dissolved precipitate was put
10 into a dialysis tube, and this was dialyzed with a dialysis buffer (20 mM Tris-HCl, pH 7.5, containing 20% glycerol).

[0099]

2.4 Centrifugation

An insoluble was present inside the dialysis tube. Therefore, the insoluble was
15 removed by centrifugation ($27,000 \times g$, 4°C, and fifteen minutes), and 21 mL of the supernatant was recovered.

[0100]

2.5 Weak anion-exchange chromatography (DEAE Sepharose Fast Flow)

The supernatant recovered in 2.4 was charged to 320 mL (column size: f 2.6 cm $\times$
20 60 cm in length) of a weak anion-exchange resin "DEAE Sepharose Fast Flow"
(manufactured by GE Healthcare Bio-Sciences K.K.) equilibrated with an equilibration buffer (20 mM Tris-HCl, pH 7.5, containing 20% glycerol). After charging, the resin was washed with three resin-bed volume of buffer (20 mM Tris-HCl, pH 7.5, containing 20% glycerol) for washing. Then, the objective protein was gradient-eluted with two
25 types of elution buffers (buffer 1: 20 mM Tris-HCl, pH 7.5, containing 20% glycerol; and

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buffer 2: 20 mM Tris-HCl, pH 7.5, containing 20% glycerol and 1 M NaCl) (their volume was 5 times the bed volume of resin), thereby recovering 262 mL of active fractions.

[0101]

5 2.6 Desalting and concentration

The active fractions obtained in 2.5 were concentrated into 21.5 mL by using a ultrafiltration equipment “model 8200” (manufactured by Amicon, molecular cutoff: 100,000). The concentrated solution was put into a dialysis tube, and dialyzed with a dialysis buffer (50 mM HEPES, pH 7.5) to substitute the buffer. The solution was further concentrated into 2.7 mL by centrifugation ($2,700 \times g$, 4°C, three hours) with an ultrafiltration equipment “Vivaspin 20” (manufactured by Vivascience, molecular cutoff: 100,000). In this way, 322 U of the substituted-type sorbose dehydrogenase was obtained.

[0102]

15 [4] Activation of substituted-type sorbose dehydrogenase

The sorbose dehydrogenase (hereinafter, referred to as substituted-type enzyme) produced in [3] (“Production of substituted-type sorbose dehydrogenase”) was treated with 1-methoxy-5-methylphenazinium methyl sulfate (1m-PMS) in the manner described below to activate the substitute-type enzyme.

20 A 50 mM HEPES buffer, pH 7.5(1.765 mL) and 0.12 mL of 1m-PMS aqueous solution (20mM) were added to 0.115 mL of the substituted-type enzyme solution (conc. 119 U/mL) produced in [3], and these were mixed. Then, the mixed solution was incubated in a refrigerator overnight to activate the enzyme. After activation, the total portion of the activated enzyme solution was applied to a centrifugal concentrator

25 “Vivaspin 20” (manufactured by Vivascience, molecular cutoff: 50,000), and the solution

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was diluted with 10 mL of a 50 mM HEPES buffer, pH 7.5, therein. Then, the spin column was loaded into a centrifuge, and centrifuged at 4,500 rpm for forty-five minutes to concentrate the solution to the total volume of about 0.3 mL. The concentrated solution was diluted by addition of 10 mL of a 50 mM HEPES buffer, pH 7.5, and then ,
5 the solution was centrifuged again to concentrate the solution, thereby removing 1m-PMS. In addition, the same procedure was repeated two times to completely remove 1m-PMS. Finally, a 50 mM HEPES buffer, pH 7.5 was added to adjust the total volume of the solution to 4 mL, and the concentration of the activated substituted-type enzyme was adjusted to 3.4 U/mL.

10 [0103]

[5] Confirmation of activation effect

R2 reagents described in Example 3 ("clinical method of determining 1,5-AG") were prepared by using the enzyme activated with 1m-PMS and untreated enzyme, respectively. By using R2 reagents, 1,5-AG standard solutions of 0 µg/ mL and 50 µg/
15 mL were measured, and the strength of the color development was compared between samples. The increase in absorbance for the 1,5-AG standard solution of 50 µg/ mL was 0.064 in the non-activated enzyme while the increase was 0.248 (about four folds) in the activated enzyme. It was revealed that the enzyme was activated about four times.

[0104]

20 (Example 3)

[1] Clinical method of determining 1,5-AG

Considering the application to an automatic biochemistry analyzer used widely in clinical laboratory tests, a determination method on the minimum scale was constructed.

In advance, determination reagents having the following compositions, i.e. R1-1
25 reagent (glucose-eliminating agent), R1-2 reagent (1m-PMS aqueous solution) and R2

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reagent (1,5-AG detection reagent) were prepared.

Nine μL of a 1,5-AG standard solution or a clinical sample (i.e. test sample) and 200 μL of R1-1 reagent were added to a test tube, and these were stirred. The mixture was reacted in a water bath at 37°C for five minutes. After the reaction, 10 μL of R1-2 reagent and 100 μL of R2 reagent were added thereto. The mixture was stirred, and the reaction solution was immediately transferred to a cell for a spectrophotometer. The cell was set in a cell holder heated to 37°C, and changes in the absorbance at 450 nm were measured for five minutes.

The clinical samples used in the present example were serums collected from a healthy person and a diabetic.

[0105]

■ Reagent composition

	· R1-1 reagent (glucose-eliminating agent)	
	Potassium chloride	49.6 mM
15	Sodium chloride	100 mM
	EDTA·2Na	0.1 mM
	Phosphoenolpyruvic acid	8.01 mM
	ATP	0.99 mM
	Magnesium chloride	7.38 mM
20	Pyruvate kinase (TOYOBO CO., LTD.)	5 U/mL
	Glucokinase (UNITIKA, LTD.)	4 U/mL
	WST-1	0.95 mM
	HEPES buffer	50 mM (pH 7.5)
25	· R1-2 reagent (1m-PMS aqueous solution)	
	1m-PMS	0.4 mM
	· R2 reagent (1,5-AG detection agent)	
	Substituted-type enzyme	3.4 U/mL

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HEPES buffer

50 mM (pH 7.5)

[0106]

[2] Formulation of standard curve

By using a serum-based matrix, 1,5-AG standard solutions of 0, 5, 12.5, 25 and 50 $\mu\text{g/mL}$ were prepared. The 1,5-AG standard solutions were measured by the above-described clinical method of determining 1,5-AG, and a standard curve was formulated as shown in FIG. 9. The increment in absorbance is shown in Table 7 with respect to each standard solution.

[0107]

10 Table 7

1,5-AG ($\mu\text{g/mL}$)	0	5	12.5	25	50
Increment in absorbance	0.128	0.146	0.175	0.224	0.320

[0108]

[3] Measurement in clinical sample

Twenty serum samples collected from healthy volunteer and diabetic patients were subjected to the measurement according to the above-described clinical method of determining 1,5-AG (present method), and the clinical method was compared with results obtained by measuring the samples with a previously-established 1,5-AG measurement kit "Lana 1,5AG Auto Liquid",. The results are shown in Table 8 and FIG. 10.

20 [0109]

Table 8

Sample No.	AUTO LIQUID ($\mu\text{g/mL}$)	Present method ($\mu\text{g/mL}$)
No. 73	1.1	3.1
No. 1	4.5	6.5
No. 5	6.5	9.1
No. 9	7.8	14.3
S-5	9.7	13.5
No. 42	10.4	11.2
S-4	12.4	16.1
No. 11	14.7	16.1
S-1	15.1	18.5
S-3	16.5	20.8
No. 14	17.1	23.7
No. 15	20.8	19.5
No. 23	21.7	30.7
No. 25	23.6	26.6
S-2	26.4	35.7
S-6	29.4	36.2
No. 29	30.1	34.1
S-7	31.8	30.7
S-8	33.6	35.2
No. 33	36.2	38.5

[0110]

As shown in the graph of FIG. 10, a good correlation was found between the measurement values of both methods where the correlation formula was y (present method) = $1.0124x$ (Lana 1,5AG Auto Liquid) + 3.3199, and the correlation coefficient (r) was 0.964.

INDUSTRIAL APPLICABILITY

10 [0111]

According to the method of determining 1,5-AG and the reagent composition for determining 1,5-AG of the present invention, 1,5-AG, which is a control marker for diabetes, can be quantified with high accuracy. By applying the present invention to clinical samples such as blood plasma, serum, cerebrospinal fluid or urine, diagnosis of diabetes can be quickly and simply achieved.

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Therefore, the present invention has high industrial applicability.

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PC-10768

PCT

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0-1	Form – PCT/RO/134 (SAFE) Indications Relating to Deposited Microorganism(s) or Other Biological Material (PCT Rule 13bis) Prepared using	
0-1-1		JPO-PAS 0341
0-2	International Application No.	
0-3	Applicant's or agent's file reference	PC-10768

1	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
1-1	Paragraph No.	0044
1-3	Identification of Deposit	
1-3-1	Name of depositary institution	IPOD International Patent Organism Depositary National Institute of Advanced Industrial Science and Technology
1-3-2	Address of depositary institution	Central 6, 1-1, Higashi 1-chome Tsukuba-shi, Ibaraki-ken 305-8566 Japan
1-3-3	Date of deposit	10 July 2003 (10. 07. 2003)
1-3-4	Accession Number	IPOD FERM P-19428
1-4	Additional Indications	Sinorhizobium sp. 97507
1-5	Designated States for Which Indications are Made	All designated States
2	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
2-1	Paragraph No.	0053
2-3	Identification of Deposit	
2-3-1	Name of depositary Institution	IPOD International Patent Organism Depositary National Institute of Advanced Industrial Science and Technology
2-3-2	Address of depositary institution	Central 6, 1-1, Higashi 1-chome Tsukuba-shi, Ibaraki-ken 305-8566 Japan
2-3-3	Date of deposit	28 March 2006 (28. 03. 2006)
2-3-4	Accession Number	IPOD FERM P-20854
2-4	Additional Indications	Escherichia coli/transformant, harboring a sorbose dehydrogenase of Sinorhizobium sp. 97507
2-5	Designated States for Which Indications are Made	All designated States

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0-4-1	Authorized officer	

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CECI EST LE TOME 1 DE 2
CONTENANT LES PAGES 1 À 59

NOTE : Pour les tomes additionels, veuillez contacter le Bureau canadien des brevets

JUMBO APPLICATIONS/PATENTS

THIS SECTION OF THE APPLICATION/PATENT CONTAINS MORE THAN ONE VOLUME

THIS IS VOLUME 1 OF 2
CONTAINING PAGES 1 TO 59

NOTE: For additional volumes, please contact the Canadian Patent Office

NOM DU FICHER / FILE NAME :

NOTE POUR LE TOME / VOLUME NOTE:

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CLAIMS

1. A method of determining 1,5-anhydroglucitol, comprising using
 - (a) a protein which consists of the amino acid sequence of SEQ ID NO: 2;
 - (b) a protein which consists of an amino acid sequence having deletion, substitution and/or addition of one or more amino acid residues in the amino acid sequence of SEQ ID NO: 2 and which has sorbose dehydrogenase activity; or
 - (c) a protein which consists of an amino acid sequence having a homology of at least 60% with the amino acid sequence of SEQ ID NO: 2 and which has sorbose dehydrogenase activity.
2. The method of determining 1,5-anhydroglucitol according to Claim 1, wherein the protein is derived from a bacterium that belongs to the genus *Sinorhizobium*.
3. The method of determining 1,5-anhydroglucitol according to Claim 1, wherein the protein is derived from *Sinorhizobium* sp. 97507 FERM P-19428.
4. The method of determining 1,5-anhydroglucitol according to Claim 1, wherein, assuming that the reactivity of the protein to sorbose is 100%, the reactivity of the protein to 1,5-anhydroglucitol is 10% or higher.
5. The method of determining 1,5-anhydroglucitol according to Claim 4, wherein, assuming that the reactivity of the protein to 1,5-anhydroglucitol is 100%, the reactivity of the protein to D-glucose is 10% or less.

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6. The method of determining 1,5-anhydroglucitol according to Claim 1, wherein 1,5-anhydroglucitol included in a sample is affected by the protein in the presence of a chromogenic substrate, and the amount of the reacted chromogenic substrate is measured.
7. The method of determining 1,5-anhydroglucitol according to Claim 6, wherein D-glucose in the sample is removed before 1,5-anhydroglucitol included in the sample is affected by the protein.
8. The method of determining 1,5-anhydroglucitol according to Claim 7, wherein 1,5-anhydroglucitol included in the sample is affected in the presence of the chromogenic substrate and an electron carrier.
9. The method of determining 1,5-anhydroglucitol according to Claim 8, wherein 1 to 500 units of the protein is added to 1 mL of the sample where the enzyme activity of the protein measured using 1,5-anhydroglucitol as a substrate is defined as the base unit.
10. The method of determining 1,5-anhydroglucitol according to Claim 8, wherein the protein is activated with the electron carrier before 1,5-anhydroglucitol included in the sample is affected by the protein.
11. A reagent composition for determining 1,5-anhydroglucitol, comprising
 - (a) a protein which consists of the amino acid sequence of SEQ ID NO: 2;
 - (b) a protein which consists of an amino acid sequence having deletion, substitution and/or addition of one or more amino acid residues in the amino acid sequence of SEQ ID NO: 2 and which has sorbose dehydrogenase activity; or

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(c) a protein which consists of an amino acid sequence having a homology of at least 60% with the amino acid sequence of SEQ ID NO: 2 and which has sorbose dehydrogenase activity.

12. The reagent composition for determining 1,5-anhydroglucitol according to Claim 11, wherein the protein is derived from a bacterium that belongs to the genus *Sinorhizobium*.

13. The reagent composition for determining 1,5-anhydroglucitol according to Claim 11, wherein the protein is derived from *Sinorhizobium* sp. 97507 FERM P-19428.

14. The reagent composition for determining 1,5-anhydroglucitol according to Claim 11, wherein, assuming that the reactivity of the protein to sorbose is 100%, the reactivity of the protein to 1,5-anhydroglucitol is 10% or higher.

15. The reagent composition for determining 1,5-anhydroglucitol according to Claim 14, wherein, assuming that the reactivity of the protein to 1,5-anhydroglucitol is 100%, the reactivity of the protein to D-glucose is 10% or less.

16. The reagent composition for determining 1,5-anhydroglucitol according to Claim 11, wherein the protein is activated with an electron carrier.

17. The reagent composition for determining 1,5-anhydroglucitol according to Claim 16, wherein the electron carrier is at least one of phenazine methosulfate and 1-methoxy-5-methylphenazinium methyl sulfate.

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18. The reagent composition for determining 1,5-anhydroglucitol according to Claim 11, further comprising a chromogenic substrate.
19. The reagent composition for determining 1,5-anhydroglucitol according to Claim 18, further comprising an electron carrier, wherein the chromogenic substrate is a reductive chromogenic substrate.
20. A (a) protein which consists of the amino acid sequence of SEQ ID NO: 2; (b) a protein which consists of an amino acid sequence having deletion, substitution and/or addition of one or more amino acid residues in the amino acid sequence of SEQ ID NO: 2 and which has reactivity of 10% or higher to 1,5-anhydroglucitol, assuming that the reactivity of the protein to sorbose is 100%; or (c) a protein which consists of an amino acid sequence having a homology of at least 85% with the amino acid sequence of SEQ ID NO: 2 and which has activity of 10% or higher to 1,5-anhydroglucitol, assuming that the reactivity of the protein to sorbose is 100%.
21. A method of diagnosing diabetes, comprising using the reagent composition for determining 1,5-anhydroglucitol according to Claim 11.
22. Use of the reagent composition for determining 1,5-anhydroglucitol according to Claim 11 for determining 1,5-anhydroglucitol.
23. Use of (a) a protein which consists of the amino acid sequence of SEQ ID NO: 2; (b) a protein which consists of an amino acid sequence having deletion, substitution

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and/or addition of one or more amino acid residues in the amino acid sequence of SEQ ID NO: 2 and which has sorbose dehydrogenase activity; or (c) a protein which consists of an amino acid sequence having a homology of at least 60% with the amino acid sequence of SEQ ID NO: 2 and which has sorbose dehydrogenase activity, for determining 1,5-anhydroglucitol.

FIG. 1

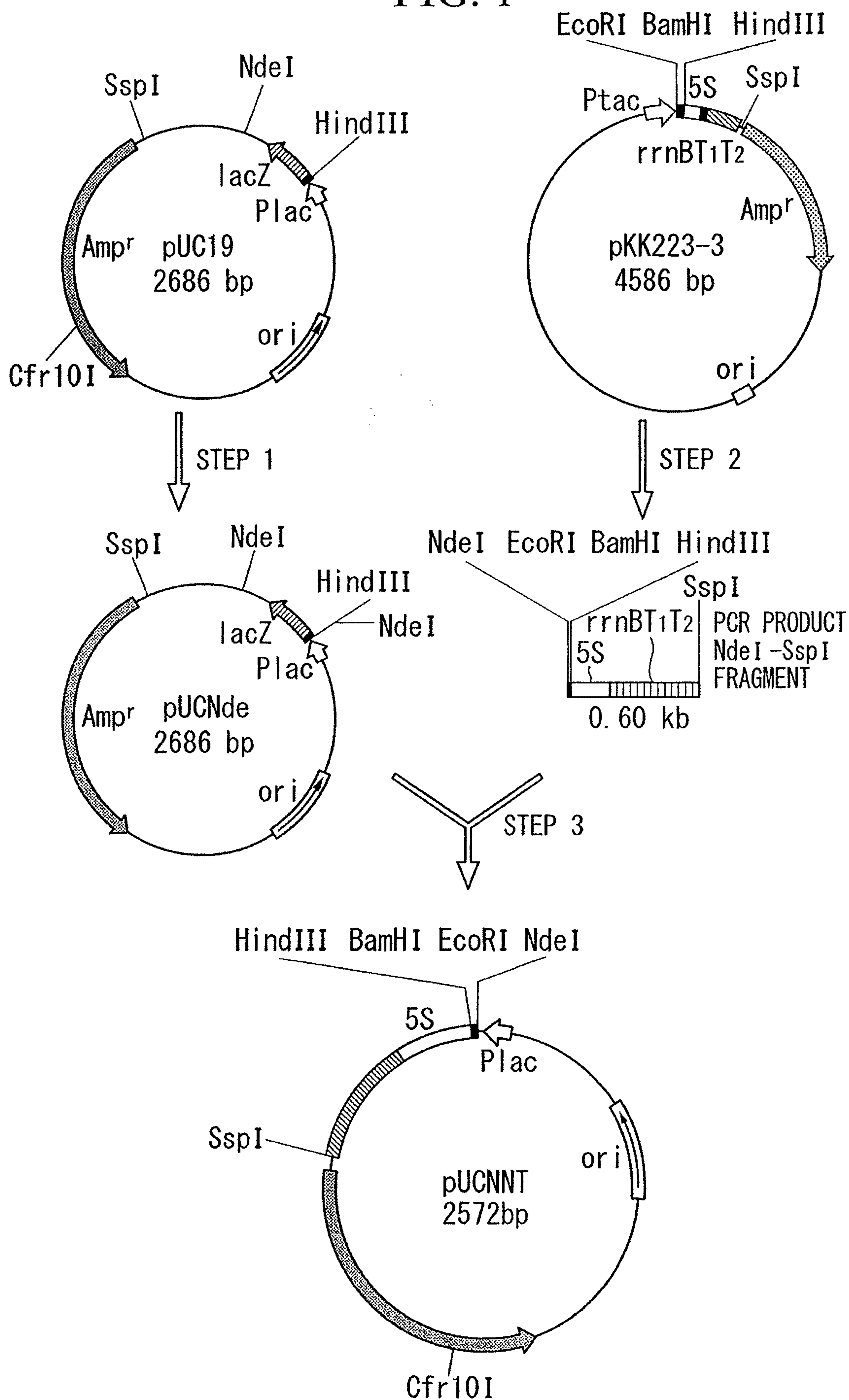
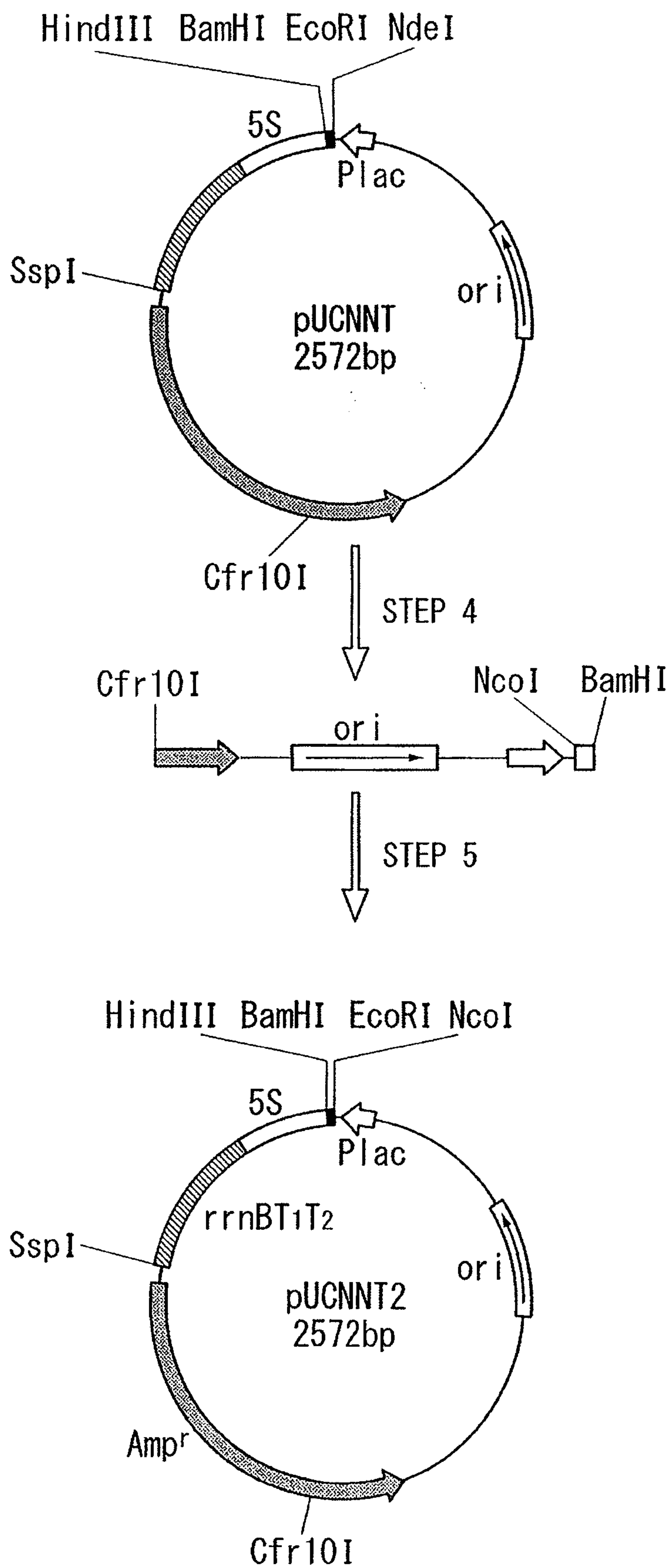


FIG. 2



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FIG. 3

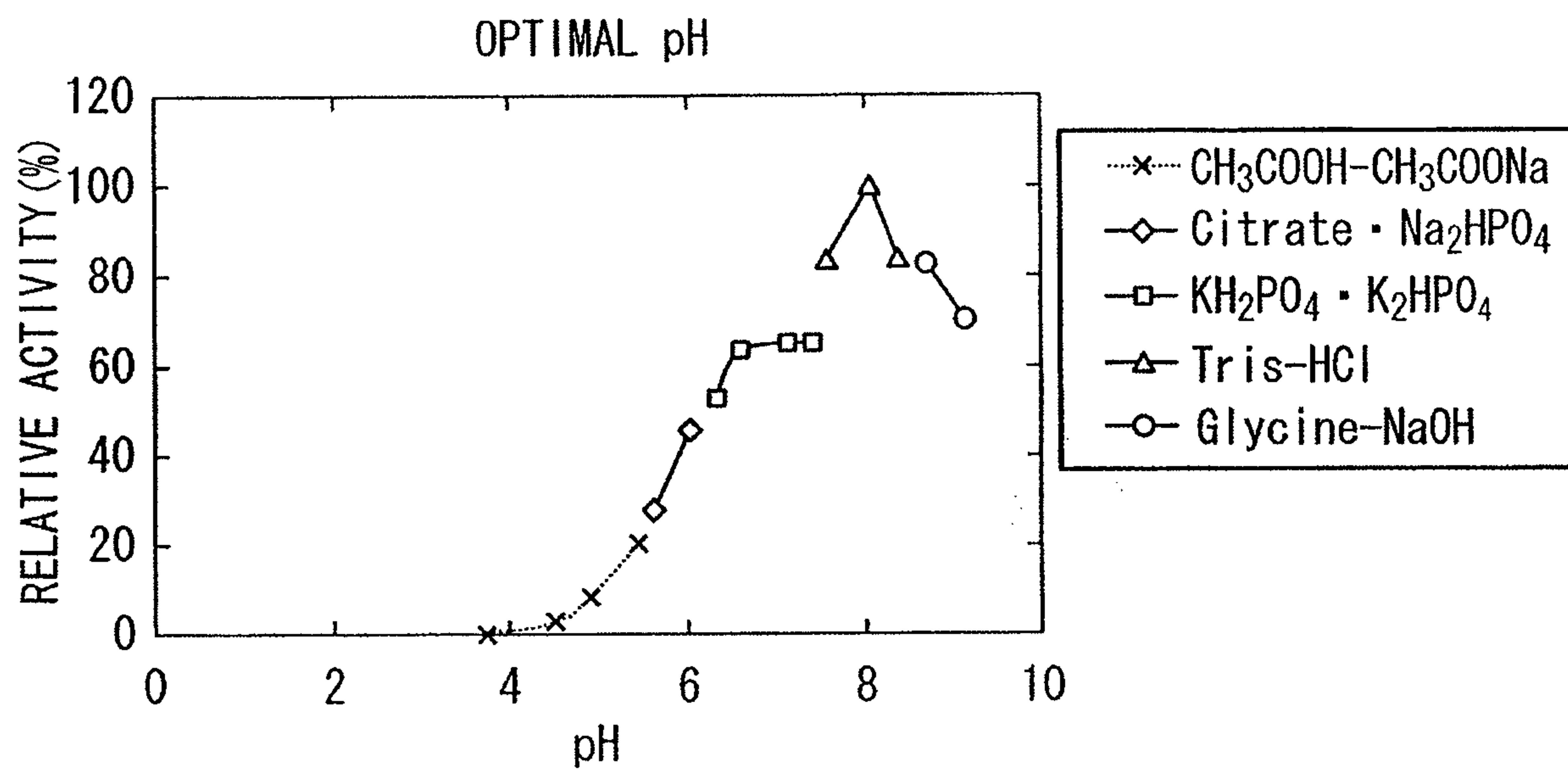


FIG. 4

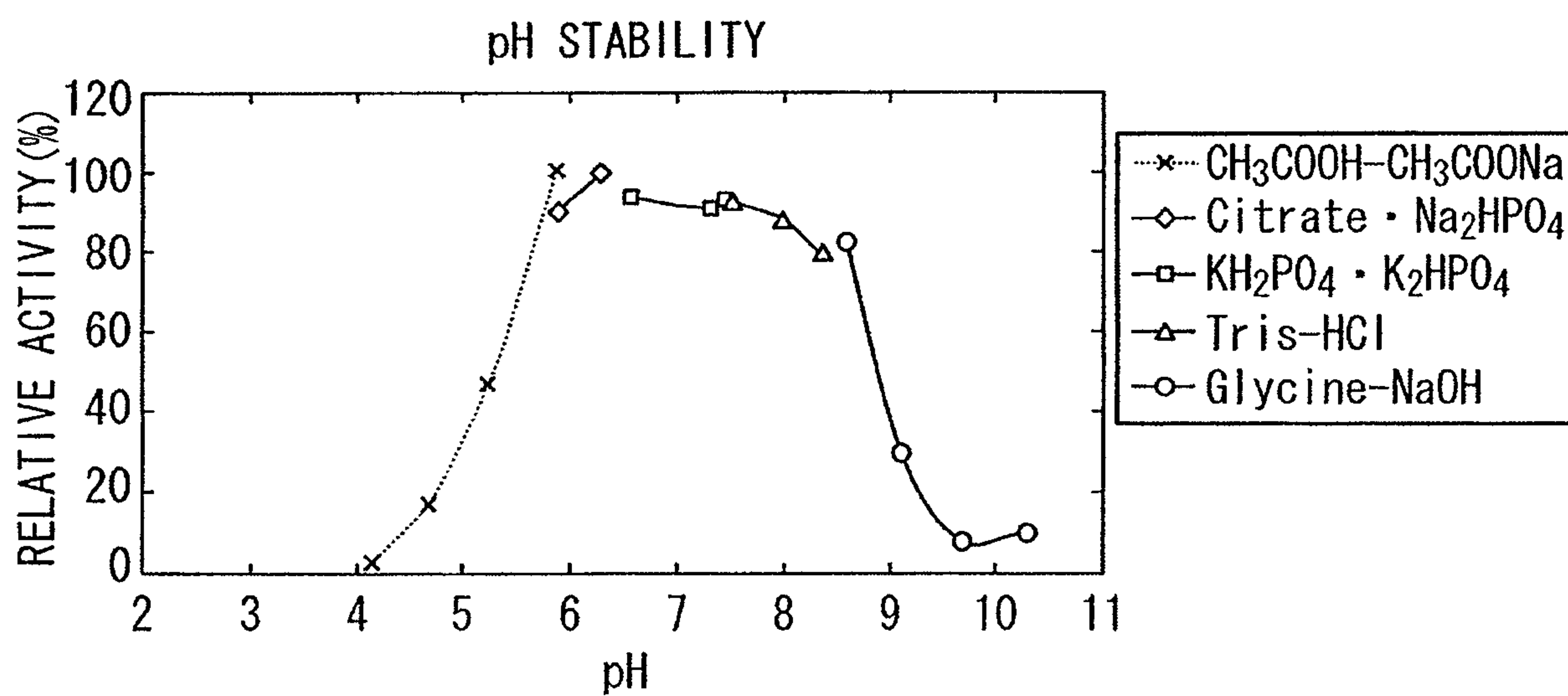


FIG. 5

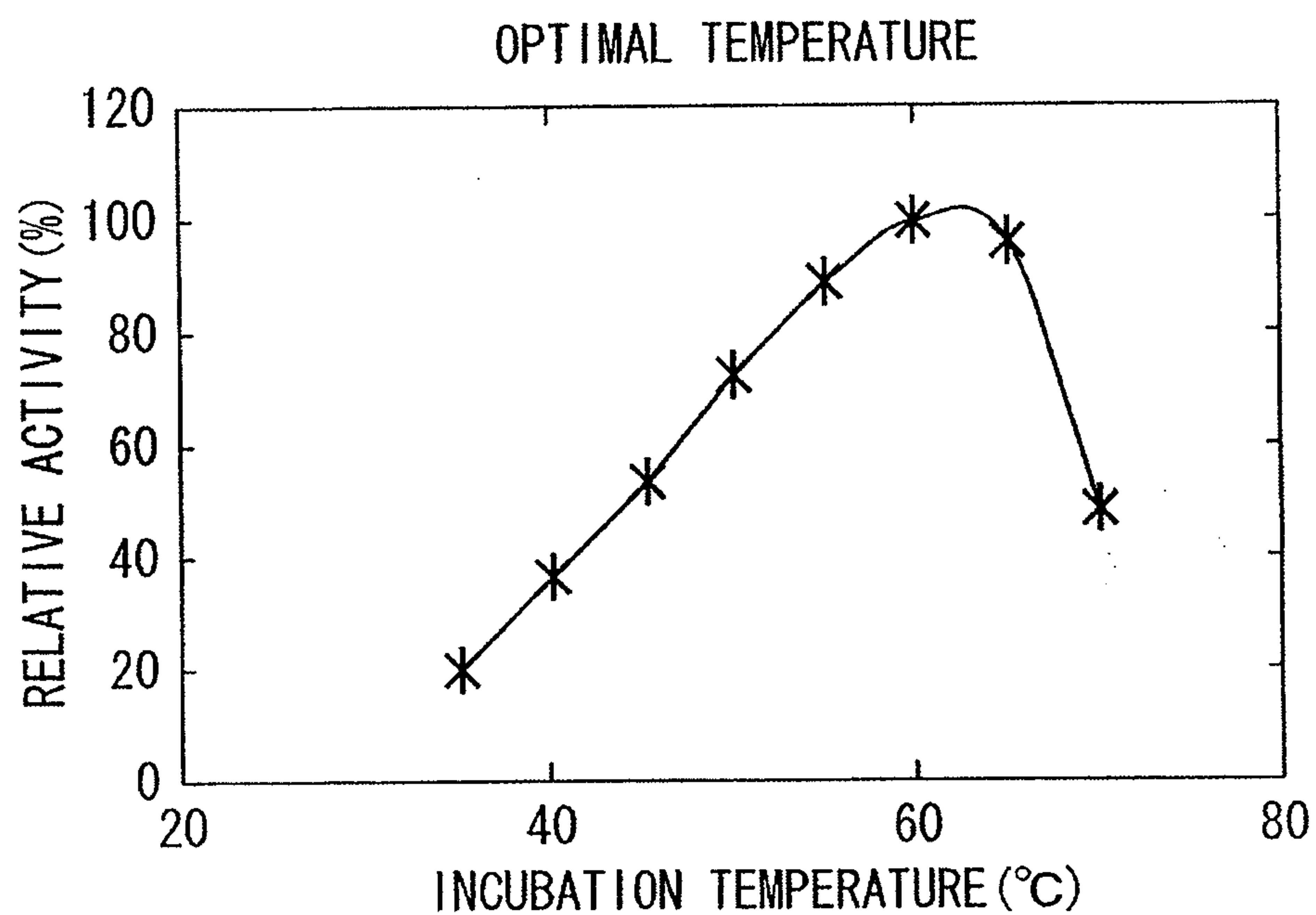


FIG. 6

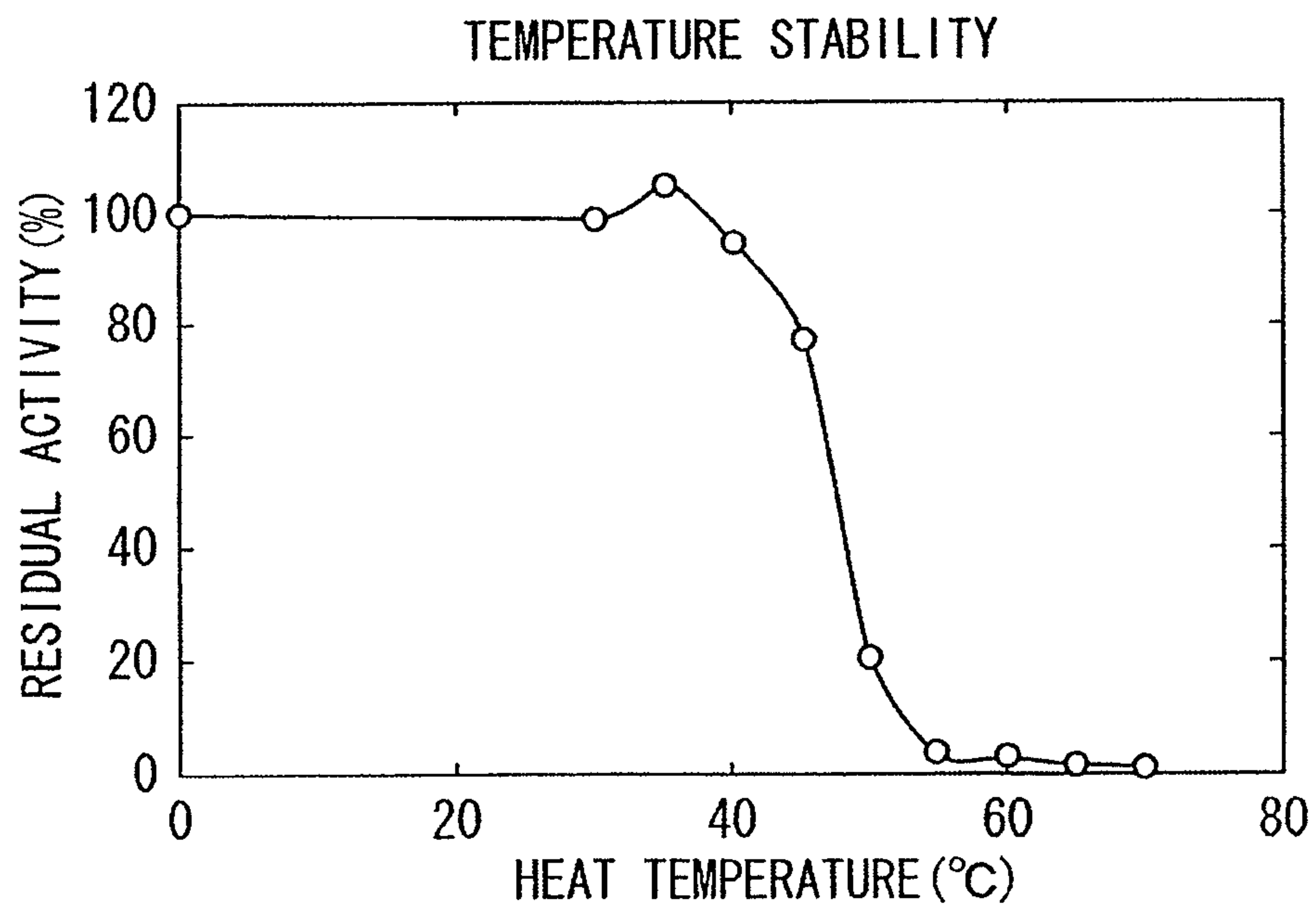


FIG. 7

STANDARD CURVE

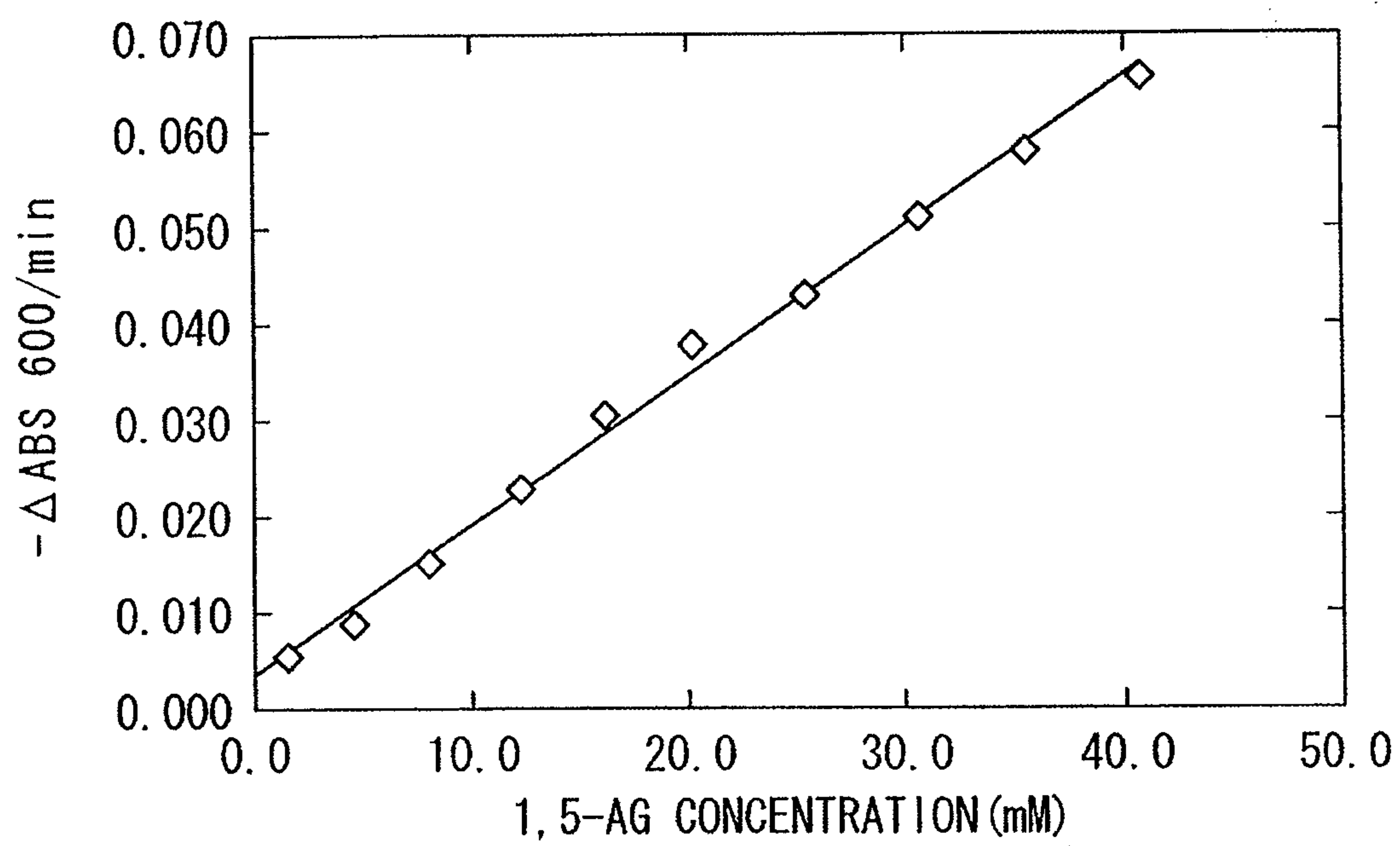


FIG. 8

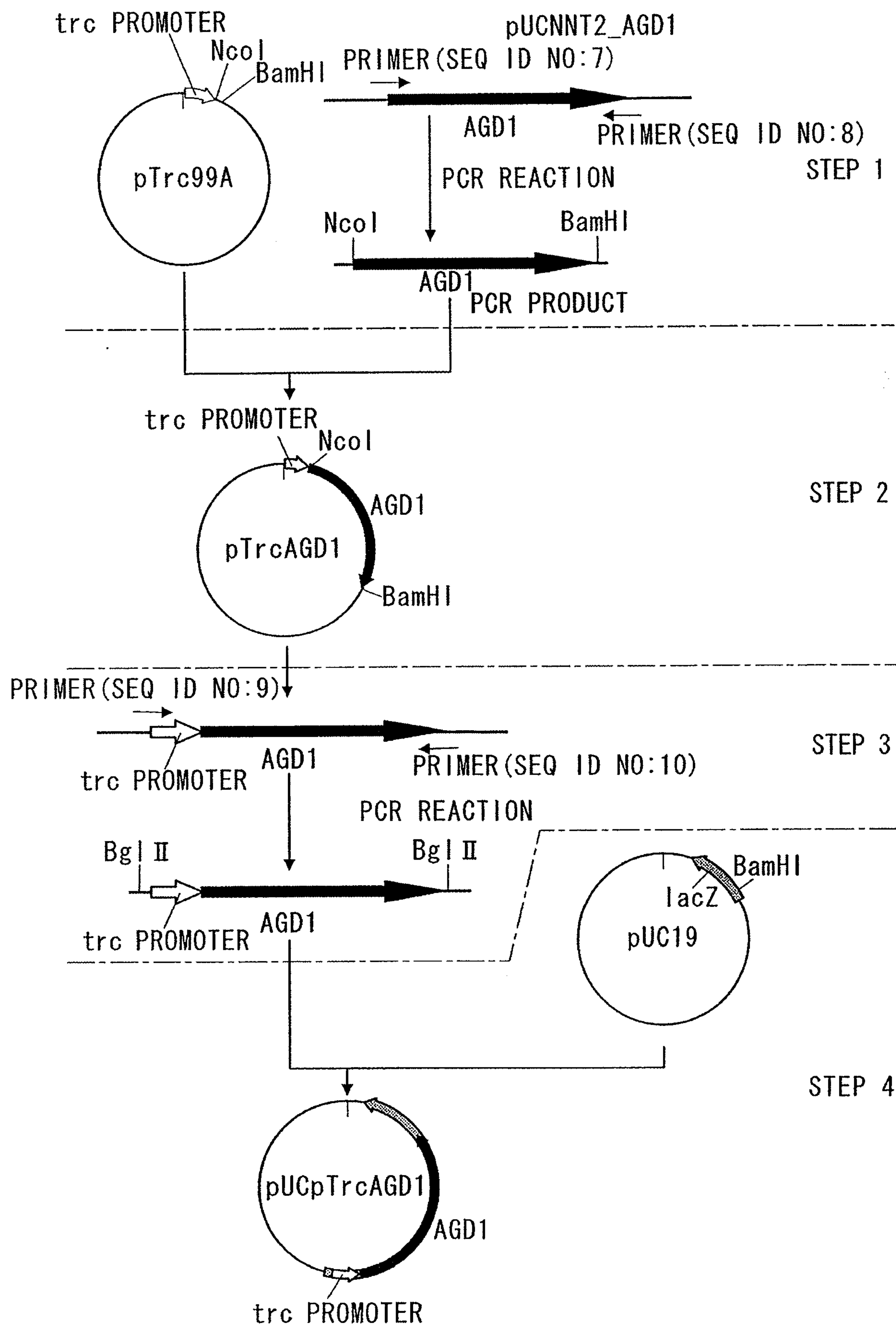


FIG. 9

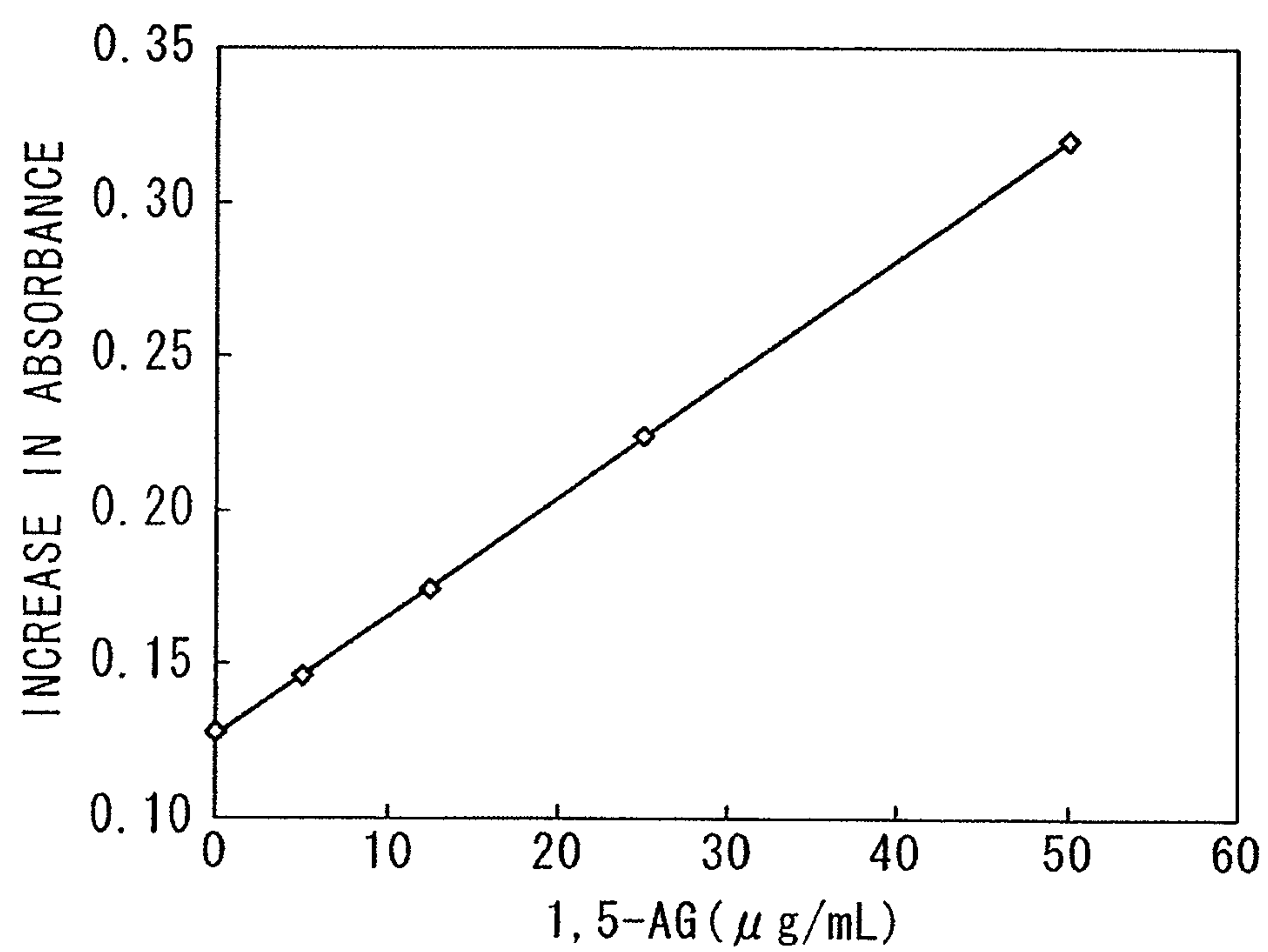
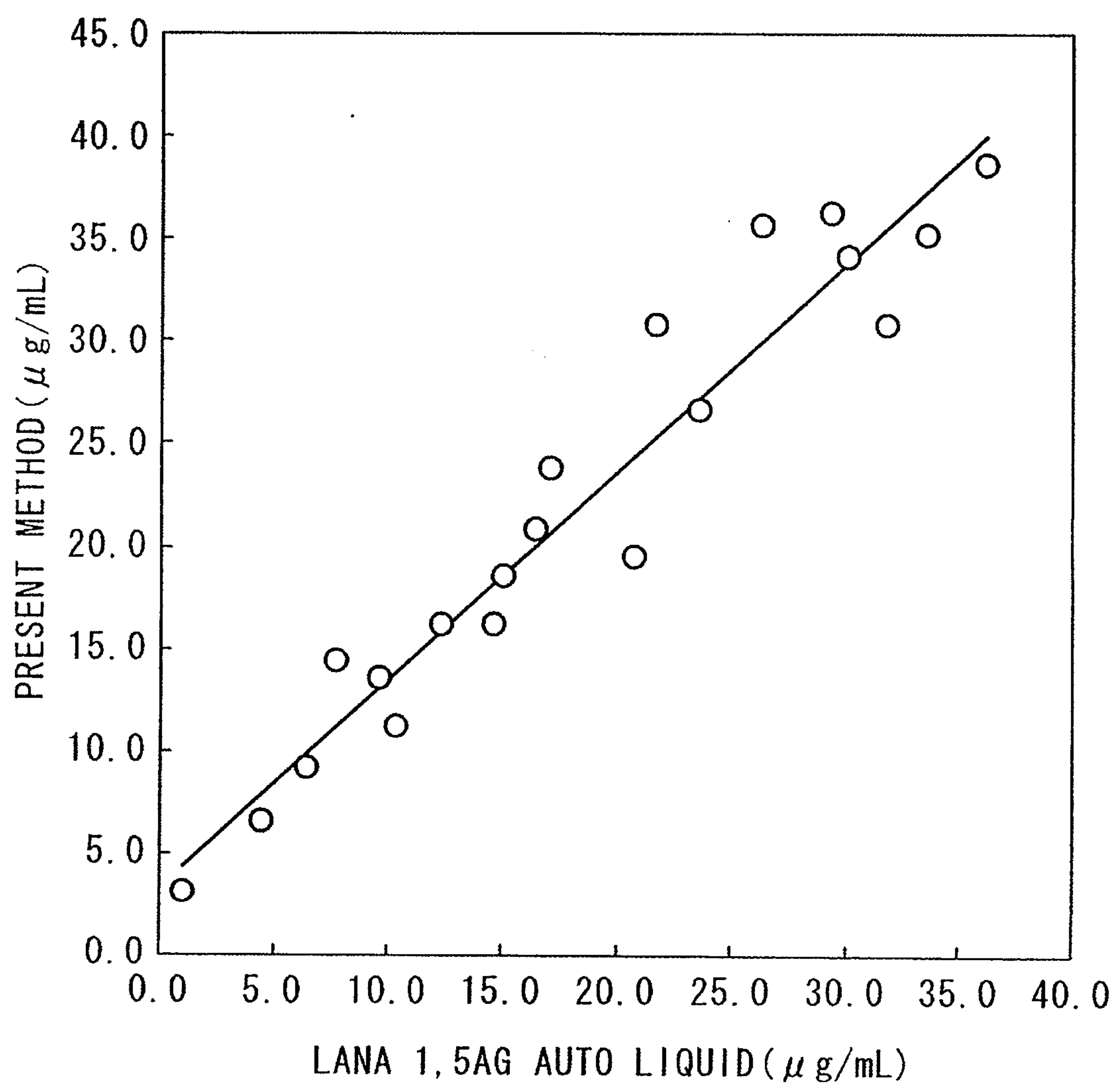


FIG. 10



STANDARD CURVE

