

DESCRIPTION

NOVEL ALCOHOL DEHYDROGENASE, GENE FOR THE ALCOHOL DEHYDROGENASE,
VECTOR, TRANSFORMANT, AND METHOD FOR PRODUCTION OF OPTICALLY
5 ACTIVE ALCOHOL BY USING THEM

FIELD OF THE INVENTION

[0001]

The present invention relates to a novel alcohol
10 dehydrogenase, a gene for the alcohol dehydrogenase, a vector
including the gene, a transformant transformed with the vector,
and a method for producing an optically active alcohol by
utilizing them.

15 BACKGROUND OF THE INVENTION

[0002]

Alcohol dehydrogenases that react with secondary alcohol
compounds, such as 2-butanol, are useful enzymes in syntheses
of optically active alcohol compounds through stereoselective
20 reduction reaction of carbonyl compounds or syntheses of
optically active secondary alcohol compounds through
stereoselective oxidation reaction of racemates of secondary
alcohols.

[0003]

25 Among alcohol dehydrogenases yielded by microorganisms,
there are many reports on alcohol dehydrogenases that require
nicotinamide adenine dinucleotide (hereafter to be abbreviated
as "NAD⁺") as a coenzyme, and oxidize 2-butanol. There are,
however, few reports on alcohol dehydrogenases that
30 preferentially oxidize (S)-2-butanol in comparison with
(R)-2-butanol and whose corresponding structural gene (a DNA
coding for an enzyme) has been acquired.

[0004]

As such an alcohol dehydrogenase, enzymes derived from
35 Gordonia sp. strain TY-5, and Candida parapsilosis IFO 1396

strain have been known.

[0005]

Among the above enzymes, ADH1, which is an enzyme derived from Gordonia sp. strain TY-5, is characterized in that it has a molecular weight of approximately 35,000 as determined by SDS-polyacrylamide electrophoresis, and has an optimum temperature of 30°C and an optimum pH of 10 in oxidation of 2-propanol. ADH3, which is an enzyme derived from the same strain, is characterized in that it has a molecular weight of approximately 58,000 as determined by SDS-polyacrylamide electrophoresis, and has an optimum temperature of 60°C and an optimum pH of 10 in oxidation of 2-propanol (See the Patent Document 1 listed below).

[0006]

An enzyme derived from Candida parapsilosis IFO 1396 strain is characterized in that it has a molecular weight of approximately 40,000 as determined by SDS-polyacrylamide electrophoresis, a stable pH range of 8.0 to 10.0, and an appropriate temperature range for action in oxidation of (S)-2-buthanol is 25°C to 55°C. This enzyme has a character that activity of the enzyme is inhibited by 2-mercaptoethanol or dithiothreitol, whereas it is not inhibited by ethylenediaminetetraacetic acid (See the Patent Document 2 listed below).

[0007]

Thus, there are few alcohol dehydrogenases that preferentially oxidize (S)-2-butanol in comparison with (R)-2-butanol and whose corresponding structural gene (a DNA coding for an enzyme) has been acquired. In view of the state of the art, acquisition of novel enzymes or their corresponding structural gene has been desired. If the structural gene of such enzymes is acquired, the enzyme can be produced through a genetic engineering technique in a large amount, and thereby enables to establish a process that can produce useful compounds, for example, optically active alcohols, with the enzyme in a

remarkably efficient manner.

Patent Document 1:JP-A-2005-102511

Patent Document 2:JP-B-3574682

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DISCLOSURE OF THE INVENTION

PROBLEM WHICH THE INVENTION IS TO SOLVE

[0008]

10 It is an object of the present invention to provide a novel alcohol dehydrogenase, a gene for the alcohol dehydrogenase, a vector including the gene, a transformant transformed with the vector, and a method for producing an optically active alcohol by utilizing them.

15

MEANS FOR SOLVING THE PROBLEM

[0009]

The present invention has one or a plurality of the following technical feature(s):

20 One of the features of the present invention is a polypeptide having the following physicochemical properties:

[0010]

(1) Action:

25 The polypeptide oxidizes an alcohol with NAD^+ as a coenzyme to produce a ketone or an aldehyde. Furthermore, the polypeptide reduces a ketone or an aldehyde with NADH as a coenzyme to produce an alcohol.

[0011]

(2) Substrate specificity:

30 A substrate in oxidation reaction is an aliphatic alcohol which may have an aromatic substituent. The polypeptide preferentially oxidizes (S)-2-butanol in comparison with (R)-2-butanol; a substrate in reduction reaction is a ketone or an aldehyde. The polypeptide reacts with acetophenone to
35 reduce into (S)-1-phenylethanol.

[0012]

(3) Molecular weight:

The molecular weight of the polypeptide is approximately 39,000 as determined by reducing SDS-polyacrylamide electrophoresis.

[0013]

(4) Stability in pH:

Stable pH range of the polypeptide is 5.5 to 7.5.

[0014]

10 (5) Optimum temperature:

Optimum temperature of the polypeptide for oxidation reaction of (S)-2-butanol is 45°C to 70°C.

[0015]

(6) Inhibitor:

15 Enzyme activity of the polypeptide is inhibited by ethylenediaminetetraacetic acid, o-phenanthroline, mercury chloride, copper sulfate or zinc sulfate, whereas it is not inhibited by 2-mercaptoethanol or dithiothreitol.

[0016]

20 Another feature of the present invention is a polypeptide which is any one of the following polypeptides (a), (b), and (c):

[0017]

(a) A polypeptide including the amino acid sequence shown under
25 SEQ ID NO:1 in the sequence listing;

(b) A polypeptide including an amino acid sequence that results from deletion, insertion, substitution and/or addition of one amino acid residue or a plurality of amino acid residues in the amino acid sequence shown under SEQ ID NO:1 in the sequence
30 listing, and having activity to react with acetophenone to reduce into (S)-1-phenylethanol; and

(c) A polypeptide having sequence identity of 85% or higher to the amino acid sequence shown under SEQ ID NO:1 in the sequence listing, and having activity to react with acetophenone to
35 reduce into (S)-1-phenylethanol.

[0018]

Still another feature of the present invention is a DNA coding for the above polypeptide.

[0019]

5 Still another features of the present invention are a DNA which is either one of the following DNAs (A) and (B), a vector including this DNA, and a transformant produced by transformation of a host cell with this vector.

10 (A) a DNA including the base sequence shown under SEQ ID NO:2 in the sequence listing;

(B) a DNA hybridizable under a stringent condition with a DNA that includes the base sequence complementary to the base sequence shown under SEQ ID NO:2 in the sequence listing, and coding for a polypeptide that has activity to react with
15 acetophenone to reduce into (S)-1-phenylethanol;

(C) a DNA having sequence identity of 85% or higher to the base sequence shown under SEQ ID NO:2 in the sequence listing, and coding for a polypeptide that has activity to react with
20 acetophenone to reduce into (S)-1-phenylethanol; and

(D) a DNA including a base sequence that results from deletion, insertion, substitution and/or addition of one base or a plurality of bases in the base sequence shown under SEQ ID NO:2 in the sequence listing, and coding for a polypeptide that has activity to react with acetophenone to reduce into
25 (S)-1-phenylethanol.

[0020]

Still another feature of the present invention is a method for producing an alcohol, particularly an optically-active alcohol, the method including reacting the polypeptide of the
30 present invention, or the transformant of the present invention, in which the DNA is introduced, and a processed product of the transformant with a carbonyl group-containing compound.

EFFECT OF THE INVENTION

35 [0021]

The present invention provides a novel alcohol dehydrogenase, a gene for the alcohol dehydrogenase, a vector including the gene, a transformant transformed with the vector, and a method for producing an optically active alcohol produced by utilizing any of these.

BRIEF DESCRIPTION OF THE DRAWINGS

[0022]

[Fig. 1]

10 Fig. 1 illustrates a method for constructing recombinant vectors pNCM, pNCMG and pNCMFT, and structures of them.

BEST MODE FOR CARRYING OUT THE INVENTION

[0023]

15 The present invention will be described below in detail with reference to specific embodiments. The present invention is, however, not limited to the following embodiments.

[0024]

20 Regarding various physical properties of the polypeptide of the present invention

In the present invention, the polypeptide, which is isolated by a method mentioned below, has the following physicochemical properties (1) to (6):

[0025]

25 (1) Action:

The polypeptide oxidizes an alcohol with NAD^+ as a coenzyme to produce a ketone or an aldehyde. Furthermore, the polypeptide reduces a ketone or an aldehyde with NADH as a coenzyme to produce an alcohol.

30 [0026]

(2) Substrate specificity:

A substrate in oxidation reaction is an aliphatic alcohol which may have an aromatic substituent. The polypeptide preferentially oxidizes (S)-2-butanol in comparison with (R)-2-butanol. A substrate in reduction reaction is a ketone

or an aldehyde. The polypeptide reacts with acetophenone to reduce into (S)-1-phenylethanol.

[0027]

(3) Molecular weight:

5 The molecular weight of the polypeptide is approximately 39,000 as determined by reducing SDS-polyacrylamide electrophoresis.

[0028]

(4) Stability in pH:

10 Stable pH range of the polypeptide is 5.5 to 7.5.

[0029]

(5) Optimum temperature:

 Optimum temperature of the polypeptide for action is 45°C to 70°C.

15 [0030]

(6) Inhibitor:

 Enzyme activity of the polypeptide is inhibited by ethylenediaminetetraacetic acid, o-phenanthroline, mercury chloride, copper sulfate or zinc sulfate.

20 [0031]

 The above physicochemical properties (1) to (6) are explained in the followings.

[0032]

Regarding (1) Action

25 The polypeptide of the present invention has ability to oxidize, under the presence of NAD^+ , a secondary alcohol compound to covert into a ketone compound. Furthermore, the polypeptide of the present invention has ability to oxidize an primary alcohol compound to convert into an aldehyde compound.

30 [0033]

 The ability to oxidize an alcohol compound may be evaluated in the following manner, for example.

[0034]

[Method for evaluating oxidizing ability to an alcohol
35 compound]

Progress of oxidization reaction may be easily evaluated by, at first, preparing a reaction mixture including 2.5 mM NAD⁺, a 50 mM target alcohol compound, oxidation activity of which is to be evaluated, and a polypeptide of the present invention in 50 mM tris-HCl buffer (pH 9.0), then allowing the reaction mixture to react at 30°C and finally observing increase of absorbance at the wavelength of 340 nm, which is accompanied by increase of NADH level. If the absorbance is increased, the polypeptide of the present invention has ability to oxidize a target alcohol compound. Rapid increasing rate of the absorbance reflects high ability of the polypeptide of the present invention to oxidize a target alcohol compound. The oxidizing ability of a polypeptide may be expressed in terms of numerical values. Thus, oxidizing activity 1 U is defined as an enzyme level that catalyzes generation of 1 μ mol of NADH per minute.

[0035]

In addition, the polypeptide of the present invention has another ability to reduce a ketone or aldehyde compound into an alcohol compound in the presence of NADH.

[0036]

The ability to reduce a ketone or aldehyde compound may be evaluated in the following manner, for example.

[0037]

[Method for evaluating reducing ability to a ketone or aldehyde compound]

Progress of reduction reaction may be easily evaluated by, at first, preparing a reaction solution including 0.25 mM NADH, a 50 mM ketone or aldehyde compound, reduction activity of which is to be evaluated, and a polypeptide of the present invention in 100 mM potassium phosphate buffer (pH 6.5) that contains 0.3% (v/v) of dimethyl sulfoxide, and then allowing the reaction solution to react at 30°C with monitoring decrease of absorbance at the wavelength of 340 nm, which is accompanied by decrease of NADH level. If the absorbance is decreased, the

polypeptide of the present invention has ability to reduce a target ketone or aldehyde compound. Rapid decrease of the absorbance reflects high ability of the polypeptide of the present invention to reduce a target ketone or aldehyde compound.

5 The reducing ability of a polypeptide may be expressed in terms of numerical values. Thus, reduction activity 1 U is defined as an enzyme level that catalyzes consumption of 1 μ mol of NADH per minute.

[0038]

10 (2) Regarding substrate specificity

A substrate in oxidation reaction is an aliphatic alcohol which may have an aromatic substituent. The substrate specificity may be evaluated in accordance with the [Method for evaluating oxidizing ability to an alcohol compound], as

15 described in the above (1) Action.

[0039]

The polypeptide of the present invention preferentially oxidizes (S)-2-butanol in comparison with (R)-2-butanol. This preference means that ability to oxidize (S)-2-butanol is

20 higher than that to oxidize (R)-2-butanol. The fact that the ability to oxidize (S)-2-butanol is higher than that to oxidize (R)-2-butanol may be easily confirmed by evaluating oxidizing ability to each of (R)-2-butanol and (S)-2-butanol in accordance with the [Method for evaluating oxidizing ability

25 to an alcohol compound], as described in the above (1) Action.

[0040]

Furthermore, the polypeptide of the present invention reacts with a ketone and aldehyde substrate in reduction reaction. The substrate specificity may be evaluated in

30 accordance with the [Method for evaluating reducing ability to a ketone or aldehyde compound], as described in the above (1) Action.

[0041]

The polypeptide of the present invention has ability to

35 react with acetophenone to reduce into (S)-1-phenylethanol.

The reducing ability may be tested in the following manner, for example.

[0042]

In a 100 mM phosphate buffer (pH 7), acetophenone, NADH
5 and the polypeptide of the present invention are added, and then
the mixture is allowed to react at 30°C while stirring. After
completion of the reaction, the reaction mixture is extracted
with an organic solvent such as ethyl acetate. The extract was
analyzed by gas chromatography under the following conditions.
10 Thereby, generation of 1-phenylethanol, configuration thereof,
and optical purity thereof may be determined.

[0043]

[Analysis condition (1) for gas chromatography]

Column: CHIRALDEX G-PN (30 m, 0.25 mm ID) (a product of RESTEK),

15 Column temperature: 100°C

Injection temperature: 150°C

Detection temperature: 150°C

Detector: FID

Carrier gas: He, 130 kPa

20 Elution time: acetophenone (9.2 min.)

(S)-1-phenylethanol (14.5 min.)

(R)-1-phenylethanol (15.2 min.)

[0044]

Regarding (3) Molecular weight

25 The molecular weight of the polypeptide of the present
invention is approximately 39,000 as determined by reducing
SDS-polyacrylamide electrophoresis. The molecular weight may
be determined by reducing SDS-polyacrylamide electrophoresis
in accordance with a known method, for example, a method taught
30 in a textbook "Seibutsu-kagaku Jikken no Tebiki 2,
Tanpakushitsu no Bunri-Bunseki hou" (Guide for Biochemical
experiments vol. 2, Method for isolating or separating
proteins) (published by Kagaku-dojin Publishing Company, Inc.,
Tokyo, Japan). The molecular weight of the polypeptide may be
35 calculated from the difference between the polypeptide and a

molecular weight standard protein in their mobility.

[0045]

Regarding (4) Stability in pH

Stable pH range of the polypeptide of the present
5 invention is 5.5 to 7.5. The stable pH range may be determined
in the following manner, for example. A polypeptide was treated
in some Britton-Robinson buffers, each pH of which is varied,
at 30°C for 30 minutes. Then, the oxidizing ability to
(S)-2-butanol is determined in accordance with the [Method for
10 evaluating oxidizing ability to an alcohol compound] as
mentioned above. Stable pH range is defined as a pH range where
remained activity after the treatment is 80% or higher of the
activity of the untreated polypeptide.

[0046]

15 Regarding (5) Optimum temperature:

The polypeptide of the present invention has an optimum
temperature for action of enzyme activity of 45°C to 70°C. The
optimum temperature for action may be measured by the following
manner, for example. In the above [Method for evaluating
20 oxidizing ability to an alcohol compound], oxidizing activities
to (S)-2-butanol are determined at some different temperatures.
The oxidizing activity at the temperature that shows the highest
activity is defined as 100%. Activity at each temperature is
expressed as relative activity to the highest activity. Then,
25 optimum temperature for action is defined as a temperature range
that shows 60% or higher relative activity.

[0047]

Regarding (6) Inhibitors

Enzyme activity of the polypeptide of the present
30 invention is inhibited by ethylenediaminetetraacetic acid,
o-phenanthroline, mercury chloride, copper sulfate or zinc
sulfate, whereas it is not inhibited by 2-mercaptoethanol or
dithiothreitol. Whether or not a compound inhibits enzyme
activity of the polypeptide may be evaluated in the following
35 manner, for example. In 1 mM concentration solution or mixture

of various compounds, a polypeptide is treated at 30°C for 30 minutes. Then, oxidizing activity to (S)-2-butanol is determined in accordance with the above-mentioned [Method for evaluating oxidizing ability to an alcohol compound]. When
5 remained activity after the treatment is 30% or lower of enzyme activity of the untreated polypeptide, the compound used in the treatment may be regarded as an inhibitor of the enzyme activity of the polypeptide. On the contrary, when remained activity after the treatment is 90% or higher of enzyme activity of the
10 untreated polypeptide, the compound used in the treatment may not be regarded as an inhibitor of the enzyme activity of the polypeptide.

[0048]

Regarding isolation of the polypeptide of the present invention

15 The polypeptide of the present invention may be selected from polypeptides that has ability to preferentially oxidize (S)-2-butanol in comparison with (R)-2-butanol. Alternatively, the polypeptide of the present invention may be selected from polypeptides that have activity to reduce a
20 carbonyl group-containing compound to produce an alcohol, preferably polypeptides that have activity to asymmetrically reduce asymmetric ketones to produce an optically active alcohol, and the most preferably polypeptides that has activity to asymmetrically reduce acetophenone to produce
25 (S)-1-phenylethanol.

[0049]

The polypeptides mentioned above may be isolated from organisms such as microorganisms having the above-mentioned activity. The enzyme may be found, for example, in a
30 microorganism according to the following manner. A microorganism in an appropriate medium is cultivated. Cells are collected, and then the cells are reacted with acetophenone in a buffer under the presence of nutriments, such as glucose. After the reaction, the reaction mixture is extracted with a
35 solvent or the like. The resultant extract may be analyzed

under a condition described in the above [Analysis condition (1) for gas chromatography], to monitor generation of 1-phenylethanol.

[0050]

5 The medium for cultivating microorganisms may be a common liquid nutrient medium which contains carbon sources, nitrogen sources, inorganic salts and organic nutriments, provided that the microorganism can proliferate in the medium. Cultivation may be conducted by shaking the medium or aerating the medium
10 at a temperature within the range of 25°C to 37°C, and at a pH within the range of 4 to 8.

[0051]

 The polypeptide of the present invention may be isolated from polypeptide source microorganisms by appropriately
15 combining some known methods for purifying proteins. For example, the isolation may be conducted as follows. First, such a microorganism is cultivated in an appropriate medium, and then cells are collected from the culture fluid by centrifugation or filtration. Thus-collected cells are disrupted by a
20 physical process, such as sonication with an ultrasonic disintegrator or milling with glass beads, and then remove residue of the cells by centrifugation. Cell-free extract is thereby obtained. The polypeptide of the present invention is isolated from the cell-free extract by a single or combined
25 technique(s) selected from thermal treatment, salting out (ammonium sulfate precipitation, sodium phosphate precipitation, etc.), solvent precipitation (method for precipitating protein fraction with acetone or ethanol), dialysis, gel filtration chromatography, ion exchange
30 chromatography, reversed phase chromatography, and ultrafiltration.

[0052]

 The polypeptide of the present invention may be derived from any microorganisms and is not particularly limited.
35 Preferable one is a microorganism that belongs to the genus

Candida. Preferable examples include Candida maltosa, and more preferable one may be Candida maltosa IFO 1977 strain. Candida maltosa IFO 1977 strain is available from the Incorporated Administrative Agency National Institute of Technology and Evaluation, Biotechnology Field, Exploiting the power of Microorganisms for the Development of Bioindustries (NBRC; 2-5-8 Kazusakamatari, Kisarazu-shi, Chiba, 292-0818 JAPAN).

[0053]

10 Regarding the amino acid sequence of the polypeptide of the present invention

The polypeptide of the present invention may be any one of the following polypeptide (a), (b), and (c).

[0054]

15 (a) A polypeptide including the amino acid sequence shown under SEQ ID NO:1 in the sequence listing;

(b) A polypeptide including an amino acid sequence that results from deletion, insertion, substitution and/or addition of one amino acid residue or a plurality of amino acid residues in the amino acid sequence shown under SEQ ID NO:1 in the sequence listing, and having activity to react with acetophenone to reduce into (S)-1-phenylethanol; and

20 (c) A polypeptide having sequence identity of 85% or higher to the amino acid sequence shown under SEQ ID NO:1 in the sequence listing, and having activity to react with acetophenone to reduce into (S)-1-phenylethanol.

[0055]

Three types of polypeptides (a) to (c) are each explained in detail in the followings.

30 [0056]

Regarding the polypeptide (a)

Examples of amino acid sequence of the polypeptide of the present invention include the amino acid sequence shown under SEQ ID NO:1 in the sequence listing, which is encoded by the base sequence shown under SEQ ID NO:2 in the sequence listing.

[0057]

Regarding the polypeptide (b)

The polypeptide (b), which includes an amino acid sequence that results from deletion, insertion, substitution and/or addition of one amino acid residue or a plurality of amino acid residues in the amino acid sequence shown under SEQ ID NO:1 in the sequence listing, may be prepared in accordance with a known method such as a method described in Current Protocols in Molecular Biology (John Wiley and Sons, Inc., 1989). The polypeptide (b) encompasses such a polypeptide having activity to react with acetophenone to reduce into (S)-1-phenylethanol.

[0058]

In the amino acid sequence shown under SEQ ID NO:1 in the sequence listing, sites where amino acids are to be substituted, inserted, deleted, and/or added are not particularly limited, but preferably, highly conserved regions should be avoided. Here, the term "highly conserved region" means a position where, among a plurality of enzymes derived from different sources, amino acids in one sequence coincide with those in other sequences under a condition that amino acid sequences are optimally arranged in line. Highly conserved regions may be determined by comparing, with a tool such as GENETYX, the amino acid sequence shown under SEQ ID NO:1 with an amino acid sequence of alcohol dehydrogenase that derives from a known microorganism.

[0059]

The amino acid sequence modified by substitution, insertion, deletion and/or addition may include a site modified through one type of modification process (for example, substitution), or may include a site or sites modified through two or more modification process (for example, substitution and insertion).

[0060]

When the amino acid sequence is modified by substitution, an amino acid for substituting a part of the amino acid sequence

is preferably an amino acid having a similar characteristic (homologous amino acids) to the amino acid to be substituted. In this application, amino acids belonging to the same group as illustrated below are considered as homologous amino acids.

5 [0061]

(First group: neutral nonpolar amino acids) Gly, Ala, Val, Leu, Ile, Met, Cys, Pro, Phe

(Second group: neutral polar amino acids) Ser, Thr, Gln, Asn, Trp, Tyr

10 (Third group: acidic amino acids) Glu, Asp

(Fourth group: basic amino acids) His, Lys, Arg

[0062]

The term "a plurality of amino acid residues" means, for example, 50 or less, preferably 30 or less, more preferably 15 or less, still more preferably 10 or less, 5 or less, 4 or less, 3 or less, or 2 or less amino acids.

[0063]

Regarding the polypeptide (c)

The polypeptide of the present invention also includes a polypeptide having sequence identity of 85% or higher to the amino acid sequence shown under SEQ ID NO:1 in the sequence listing, and having activity to react with acetophenone to reduce into (S)-1-phenylethanol. Although a polypeptide having sequence identity of 85% or higher to the amino acid sequence shown under SEQ ID NO:1 in the sequence listing may be within the scope of the polypeptide of the present invention, the sequence identity is preferably 90% or higher, more preferably 95% or higher, still more preferably 98% or higher, and the most preferably 99% or higher.

30 [0064]

Sequence identity of an amino acid sequence is expressed as a value determined by, while comparing the amino acid sequence shown under SEQ ID NO:1 in the sequence listing with a target amino acid sequence, dividing the number of positions where amino acids coincide between the two amino acid sequences

by the total number of amino acids in the target amino acid sequence, and further multiplying the result by 100.

[0065]

Additional amino acid sequences may be coupled with the amino acid sequence shown under SEQ ID NO:1 as long as the coupled amino acid sequences have activity to react with acetophenone to reduce into (S)-1-phenylethanol. For example, tag sequences, such as a histidine tag or a HA tag, may be added. The polypeptide of the present invention may be used in a form of fusion protein in combination with another protein. Also, the polypeptide (c) may be a peptide fragment, as long as the fragment has an activity to react with acetophenone to reduce into (S)-1-phenylethanol.

[0066]

The polypeptide of the present invention also includes a polypeptide having sequence identity of 85% or higher to the amino acid sequence shown under SEQ ID NO:1 in the sequence listing, and having activity to react with acetophenone to reduce into (S)-1-phenylethanol.

[0067]

Regarding cloning of DNA coding for the polypeptide of the present invention

A DNA coding for polypeptide of the present invention may be any DNA that can express the enzyme in a host cell into which the DNA is introduced in a manner described below, and may contain any untranslated region. When the enzyme is obtained, a person skilled in the art would produce such a DNA from an organism that produces the enzyme in a known manner. For example, such a DNA may be obtained in a manner mentioned below.

[0068]

Gene manipulations such as DNA cloning, construction of a vector, and transformation, which will be described hereafter in this description, may be conducted in accordance with a manner described in literatures such as Molecular Cloning 2nd Edition (Cold Spring Harbor Laboratory Press, 1989) unless

otherwise indicated. The "%" used herein means "% (w/v)" unless otherwise specified.

[0069]

First, a polypeptide of the present invention, which has
5 been isolated by a method described in the "Regarding isolation
of the polypeptide of the present invention," are digested with
an appropriate endopeptidase, and the resultant peptide
fragments are batched off with reverse phase HPLC. Then, the
amino acid sequence of part of or whole of these peptide
10 fragments are determined with, for example, a type ABI492
protein sequencer (a product of Applied Biosystems).

[0070]

Based on thus-obtained information about amino acid
sequence, PCR (Polymerase Chain Reaction) primers for
15 amplifying a part of a DNA that codes for the polypeptide is
synthesized. Then, a chromosomal DNA of a microorganism that
produces the polypeptide are prepared in accordance with a
common method for isolating DNA, such as a method taught by
Visser et al. (Appl. Microbiol. Biotechnol., 53, 415 (2000)).
20 PCR is carried out from these chromosomal DNA templates with
the above PCR primers, to amplify a part of the DNA that codes
for the polypeptide, and then the base sequence thereof is
determined. The base sequence may be determined with, for
example, Applied Biosystems 3130xl Genetic Analyzer (a product
25 of Applied Biosystems).

[0071]

If part of the base sequence of a DNA coding for
polypeptide is revealed, the whole sequence may be determined
by, for example, Inverse PCR method (Nucl. Acids Res., 16,
30 8186(1988)).

[0072]

Examples of the thus-obtained DNA coding for the
polypeptide of the present invention include a DNA that includes
the base sequence shown under SEQ ID NO:2 in the sequence
35 listing.

[0073]

The base sequence shown under SEQ ID NO:2 will be explained below.

[0074]

5 Regarding the DNA coding for the polypeptide of the present invention

Examples of the DNA coding for the polypeptide of the present invention include:

10 A DNA including the base sequence shown under SEQ ID NO:2 in the sequence listing;

A DNA hybridizable under a stringent condition with a DNA that includes the base sequence complementary to the base sequence shown under SEQ ID NO:2 in the sequence listing, and coding for a polypeptide that has activity to react with acetophenone to
15 reduce into (S)-1-phenylethanol;

A DNA having sequence identity of 85% or higher to the base sequence shown under SEQ ID NO:2 in the sequence listing, and coding for a polypeptide that has activity to react with acetophenone to reduce into (S)-1-phenylethanol; and

20 A DNA including a base sequence that results from deletion, insertion, substitution and/or addition of one base or a plurality of bases in the base sequence shown under SEQ ID NO:2 in the sequence listing, and coding for a polypeptide that has activity to react with acetophenone to reduce into

25 (S)-1-phenylethanol.

[0075]

Here, the "DNA hybridizable under a stringent condition with a DNA that includes the base sequence complementary to the base sequence shown under SEQ ID NO:2 in the sequence listing,
30 and coding for a polypeptide that has activity to react with acetophenone to reduce into (S)-1-phenylethanol" means a DNA obtainable by colony hybridization technique, plaque hybridization technique, Southern hybridization technique, or the like under a stringent condition with a DNA that includes
35 the base sequence complementary to the base sequence shown under

SEQ ID NO:2 in the sequence listing as a probe, and codes for a polypeptide that has activity to react with acetophenone to reduce into (S)-1-phenylethanol.

[0076]

5 Hybridization may be conducted, for example, according to a method described in Molecular Cloning, A laboratory manual, second edition (Cold Spring Harbor Laboratory Press, 1989). Here, examples of "a DNA hybridizable under a stringent condition" include DNAs, which are obtainable through
10 hybridization with a filter, onto which a colony- or plaque-derived DNA is immobilized, in the presence of 0.7 to 1.0 M NaCl, at 65°C, followed by washing the filter with a 2-fold concentration of SSC solution (one-fold concentration of the SSC solution consists of 150 mM NaCl and 15 mM sodium citrate)
15 at 65°C. Preferable examples of the DNA include DNAs obtainable by washing with half-fold concentration of the SSC solution at 65°C. More preferable examples thereof include DNAs obtainable by washing with 0.2-fold concentration of the SSC solution at 65°C. Still more preferable examples thereof
20 include DNAs obtainable by washing with 0.1-fold concentration of the SSC solution at 65°C.

[0077]

Conditions for hybridization are described above, but the condition is not limited to the above described ones.

25 Conceivable factors affecting to stringency in hybridization include a variety of factors, such as temperature conditions, or salt concentrations. A person skilled in the art could attain an optimum stringency by appropriately controlling the above factors.

30 [0078]

Examples of such a DNA hybridizable under the above condition include DNAs having sequence identity of 70% or higher, preferably 85% or higher, more preferably 90% or higher, still more preferably 95% or higher, and most preferably 98% or higher
35 to the base sequence shown under SEQ ID NO:2. As long as a

polypeptide encoded by a DNA has activity to react with acetophenone to reduce into (S)-1-phenylethanol, the DNA coding for the polypeptide is encompassed within the above DNA.

[0079]

5 Here, the "sequence identity (%)" is expressed as a value determined by arranging two DNAs to be compared with one another, dividing the number of positions where nucleobases (for example, A, T, C, G, U, or I) coincide between both sequences by the total number of the bases in the target DNA, and further multiplying
10 the result by 100.

[0080]

 The sequence identity may be calculated by the following sequence analyzers: GCG Wisconsin Package (Program Manual for The Wisconsin Package, Version 8, September 1994, Genetics
15 Computer Group, 575 Science Drive Medison, Wisconsin, USA 53711; Rice, P. (1996) Program Manual for EGCG Package, Peter Rice, The Sanger Centre, Hinxton Hall, Cambridge, CB10 1RQ, England), and the ExPASy World Wide Web molecular biology server (Geneva University Hospital and University of Geneva, Geneva,
20 Switzerland).

[0081]

 Here, if a DNA having sequence identity of 85% or higher to the base sequence shown under SEQ ID NO:2 in the sequence listing codes for a polypeptide that has activity to react with
25 acetophenone to reduce into (S)-1-phenylethanol, the DNA is encompassed within the range of the DNA of the present invention. Although a DNA having sequence identity of 85% or higher to the base sequence shown under SEQ ID NO:2 in the sequence listing is encompassed within the range of the DNA of the present
30 invention, the sequence identity is preferably 90% or higher, more preferably 95% or higher, still more preferably 98% or higher, and the most preferably 99% or higher.

[0082]

 Sequence identity of a base sequence is expressed as a
35 value determined by comparing the base sequence shown under SEQ

ID NO:2 in the sequence listing with a target base sequence, dividing the number of positions where bases coincide between the two base sequences by the total number of bases in the target base sequence, and further multiplying the result by 100.

5 [0083]

Here, "a DNA including a base sequence that results from deletion, insertion, substitution and/or addition of one base or a plurality of bases in the base sequence shown under SEQ ID NO:2 in the sequence listing, and coding for a polypeptide
10 that has activity to react with acetophenone to reduce into (S)-1-phenylethanol" may be prepared in accordance with a known method, such as described in Current Protocols in Molecular Biology (John Wiley and Sons, Inc., 1989). As long as a DNA codes for a polypeptide that has activity to react with
15 acetophenone to reduce into (S)-1-phenylethanol, the DNA is encompassed within the above DNA.

[0084]

In the base sequence shown under SEQ ID NO:2 in the sequence listing, sites where bases are to be substituted,
20 inserted, deleted, and/or added are not particularly limited, but preferably, highly conserved regions should be avoided, and frameshift should also be avoided. Here, the term "highly conserved region" means a position where, among a plurality of enzymes derived from different sources, bases in one sequence
25 coincide with those in other sequences when base sequences are optimally arranged in line and compared with one another. Highly conserved regions may be determined by comparing, with a tool such as GENETYX, the base sequence shown under SEQ ID NO:2 with a base sequence of an alcohol dehydrogenase that
30 derives from a known microorganism.

[0085]

A base sequence modified by substitution, insertion, deletion and/or addition may include a site modified through one type of modification process (for example, substitution),
35 or may be include a site or sites modified through two or more

modification process (for example, substitution and insertion).

[0086]

5 The term "a plurality of bases" as mentioned above means, for example, 150 or less, preferably 100 or less, more preferably 50 or less, still more preferably 20 or less, 10 or less, 5 or less, 4 or less, 3 or less, or 2 or less bases.

[0087]

Regarding host-vector systems and transformants

10 Insertion of a DNA that codes for the polypeptide of the present invention into an expression vector may give a polypeptide-expression vector. Then, the transformant, which is obtainable by transforming a host organism with this polypeptide-expression vector, may be cultivated to express the
15 polypeptide of the present invention. Alternatively, a method including introducing a polynucleotide that codes for the polypeptide of the present invention into a chromosome may be utilized.

[0088]

20 Expression vectors which may be used in the above insertion are not particularly limited as long as the vector can express a polypeptide that is encoded by the DNA. Examples of such expression vectors include plasmid vectors, phage vectors, and cosmid vectors. Shuttle vectors which can
25 exchange a gene with another host strain may also be used.

[0089]

Such a vector generally includes, for example, in the case of Escherichia coli, regulatory factors such as lacUV5 promoter, trp promoter, trc promoter, tac promoter, lpp promoter, tufB
30 promoter, recA promoter, and pL promoter. The vector may be appropriately used as an expression vector that includes expression units operatably connected to the DNA of the present invention. Examples of the vector include pUCN18 (See Example 5), pSTV28 (a product of Takara Bio Inc.), and pUCNT (see WO
35 94/03613).

[0090]

The term "regulatory factor(s)", which is used herein, means a base sequence that has a functional promoter and arbitrary related transcription elements (e.g. enhancer, CCAAT
5 box, TATA box, and SPI site).

[0091]

The term "operatably connected" as used herein means that a gene, and various regulatory elements such as promoter and enhancer, which regulate expression of a gene, are linked
10 together each in a state operative in a host cell. It would be well known to a person skilled in the art that the type and species of the regulatory factor may vary according to the host.

[0092]

Vectors, promoters, and the like, which is suitably used
15 for each of a variety of organisms, are described in detail in, for example, "Biseibutsugaku Kisokoza 8, Idenshi-Kogaku" (Basic course of microbiology vol. 8, Gene engineering; published by Kyoritsu Shuppan Co., Ltd., Tokyo, Japan).

[0093]

20 Host organisms which may be used for expressing polypeptides are not particularly limited provided that the organisms can be transformed by a polypeptide-expression vector that includes a DNA coding for each polypeptide, and can express a polypeptide which the introduced DNA coded for. Examples of
25 microorganisms which may be used in the present invention include bacteria whose host-vector system has been developed, such as bacteria belonging to the genus Escherichia, the genus Bacillus, the genus Pseudomonas, the genus Serratia, the genus Brevibacterium, the genus Corynebacterium, the genus
30 Streptococcus, and the genus Lactobacillus; actinomycetes whose host-vector system has been developed, such as actinomycetes belonging to the genus Rhodococcus and the genus Streptomyces; yeasts whose host-vector system has been developed, such as yeasts belonging to the genus Saccharomyces,
35 the genus Kluyveromyces, the genus Schizosaccharomyces, the

genus Zygosaccharomyces, the genus Yarrowia, the genus Trichosporon, the genus Rhodospiridium, the genus Pichia, and the genus Candida; and molds whose host-vector system has been developed, such as molds belonging to the genus Neurospora, the
5 genus Aspergillus, the genus Cephalosporium, and the genus Trichoderma. Other than microorganisms, various host-vector systems have been developed in plants or animals. In particular, systems expressing a great amount of heterogeneous proteins in insects such as silkworm (Nature, 315, 592-594 (1985)), or in
10 plants such as coleseed, corn, and potato have been developed, and the system may be preferably utilized. Among these, bacteria are preferable in view of introduction and expression efficacy, and Escherichia coli is particularly preferable.
[0094]

15 The polypeptide-expression vector including a DNA that codes for the polypeptide of the present invention may be introduced into a host microorganism by a known method. For example, explained is a case where the polypeptide-expression vector is plasmid pNCM (See Example 5), which is one of the
20 vectors of the present invention, obtained by introducing the DNA shown under SEQ ID NO:2 into the above expression vector pUCN18, and the host microorganism is Escherichia coli. In this case, by introducing the polypeptide-expression vector and the host microorganism according to the protocol of
25 commercially-available E. coli HB101 competent cell (a product of Takara Bio Inc.), a transformant E. coli HB101(pNCM) (See Example 8) may be obtained.
[0095]

A transformant may be bred, in which both of the
30 polypeptide of the present invention and a polypeptide having ability to reproduce a reduced coenzyme, which will be mentioned below, are expressed in an identical cell. That is, the transformant may be produced by inserting a DNA that codes for the polypeptide of the present invention and a DNA that codes
35 for a polypeptide having ability to reproduce a reduced coenzyme

into one vector, and then introducing the vector into a host cell. Alternatively, such a transformant may be obtained by separately inserting these two types of DNAs into two different vectors, whose incompatible groups are different, and then
 5 introducing the vectors into one host cell. Examples of a transformant which may be produced in such a manner include E. coli HB101(pNCMG) (see Example 8). E. coli HB101(pNCMG) is a transformant produced by introducing a transformed vector pNCMG (see Example 6) into E. coli HB101 competent cell (a product
 10 of Takara Bio Inc.). The transformed vector pNCMG may be produced by introducing both the DNA shown under SEQ ID NO:2 and a DNA coding for glucose dehydrogenase, one of a polypeptide that has ability to reproduce a reduced coenzyme, into the above expression vector pUCN18. Examples of the transformant also
 15 include E. coli HB101(pNCMFT) (see Example 8). E. coli HB101(pNCMFT) is a transformant produced by introducing a transformed vector pNCMFT (see Examples 7) into E. coli HB101 competent cell (a product of Takara Bio Inc.). The transformed vector pNCMFT may be produced by inserting both the DNA shown
 20 under SEQ ID NO:2 and a DNA coding for formate dehydrogenase, one of a polypeptide that has ability to reproduce a reduced coenzyme, into the above expression vector pUCN18.

[0096]

Method for producing an alcohol or an aldehyde with polypeptide
 25 or transformant

[Reaction condition]

A carbonyl group-containing compound may be reduced into an alcohol or an aldehyde in the following manner in the presence of the polypeptide of the present invention or a transformant
 30 in which the polypeptide of the present invention is expressed. The present invention, however, is not limited to the below methods.

[0097]

A carbonyl compound substrate, such as acetophenone, is
 35 added in an appropriate solvent, such as 100 mM phosphate buffer

(pH 6.5). Then, a coenzyme such as NADH and NAD⁺, and culture of the transformant and/or a processed product of the culture are added in the phosphate buffer mixture, and the mixture is stirred to allow reaction while regulating pH of the mixture.

5 [0098]

Here, a processed product means a processed substance having remained enzymatic catalytic activity of the polypeptide. Examples of the processed substance include a crude extract, cultivated cells, freeze-dried organisms, organisms dried over acetone, disrupted cells, or materials on which the above cells or organisms are immobilized.

[0099]

The reaction may be carried out at 5°C to 80°C, preferably 10°C to 60°C, and more preferably 20°C to 40°C. During the reaction, pH of the reaction mixture is 3 to 10, preferably 4 to 9, and more preferably 5 to 8. The reaction may be carried out by batch reaction or sequential reaction. For batch reaction, a reaction substrate may be added at a concentration in total volume of the loaded reaction mixture of 0.01 to 100% (w/v), preferably 0.1 to 70%, and more preferably 0.5 to 50%. For batch reaction, another portion of the reaction substrate may be further added in the course of the reaction.

[0100]

For the reaction, an aqueous solvent may be used, or otherwise, a mixture of an aqueous solvent and an organic solvent may be used. Examples of the organic solvent include toluene, ethyl acetate, n-butyl acetate, hexane, isopropanol, diisopropyl ether, methanol, acetone, and dimethyl sulfoxide.

[0101]

Here, a processed product of the transformant means a crude enzyme extract, cultivated cells, freeze-dried cells, organisms dried over acetone, or a disrupted product of these substances, or a mixture of them. The processed product may be used as an immobilized form of the polypeptide or cells. The immobilized form may be prepared in a known technique. In the

reaction, a transformant producing both the polypeptide of the present invention and a polypeptide that has ability to reproduce a reduced coenzyme may significantly reduce a required amount of the coenzyme. Examples of such a transformant include E. coli HB101(pNCMG) (See Example 8) and E. coli HB101(pNCMFT) (See Example 8). Polypeptides having ability to reproduce a reduced coenzyme will be described below in detail.

[0102]

10 [Polypeptide having ability to reproduce a reduced coenzyme]

NADH is necessary as a coenzyme in a synthesis of an alcohol compound through a reduction of a carbonyl compound with a transformant that can produce the polypeptide of the present invention. As mentioned above, the synthesis may be conducted by adding a required level of NADH in the reaction mixture. The amount of expensive coenzyme to be used may be decreased, however, by utilizing an enzyme with ability to convert an oxidized coenzyme (NAD^+) into reduced NADH (hereafter, the ability is referred to as "ability to reproduce a reduced coenzyme") in combination with its substrate, that is, by conducting the synthesis in the presence of a combination of coenzyme reproduction system and the polypeptide of the present invention. Examples of the enzyme with ability to reproduce the reduced coenzyme, which may be used in the above synthesis, include hydrogenases, formate dehydrogenase, alcohol dehydrogenase, glucose-6-phosphate dehydrogenase, and glucose dehydrogenase. Preferable examples include glucose dehydrogenase and formate dehydrogenase.

[0103]

30 This reaction may be conducted by adding a coenzyme reproduction system to an asymmetric reduction reaction system. This reaction, however, may be efficiently conducted with a transformant catalyst, which is transformed by both a DNA that codes for the enzyme of the present invention and a DNA that codes for a polypeptide having ability to reproduce the reduced

35

coenzyme, without adding another portion of an enzyme having ability to reproduce the reduced coenzyme. Such a transformant may be obtained in accordance with the method as described in the above "Regarding host-vector systems and transformants" section. Examples of such a transformant include E. coli HB101(pNCMG) (See Example 8). E. coli HB101(pNCMG) is a transformant produced by inserting a transformed vector pNCMG (see Example 6) into E. coli HB101 competent cell (a product of Takara Bio Inc.). The transformed vector pNCMG may be produced by inserting both the DNA shown under SEQ ID NO:2 and a DNA coding for glucose dehydrogenase, one of a polypeptide that has ability to reproduce a reduced coenzyme, into the above expression vector pUCN18. Examples of the transformant also include E. coli HB101(pNCMFT) (see Example 8). E. coli HB101(pNCMFT) is a transformant produced by inserting a transformed vector pNCMFT (see Examples 7) into E. coli HB101 competent cell (a product of Takara Bio Inc.). The transformed vector pNCMFT may be produced by inserting both the DNA shown under SEQ ID NO:2 and a DNA coding for formate dehydrogenase, one of a polypeptide that has ability to reproduce a reduced coenzyme, into the above expression vector pUCN18.

[0104]

[Regarding a carbonyl group-containing compound, and a product alcohol]

A substrate carbonyl compound is not limited in a production of an alcohol or an aldehyde by reducing a carbonyl group-containing compound with the polypeptide of the present invention or a transformant in which the polypeptide of the present invention is expressed. The reaction is exceedingly valuable in the case where the carbonyl group-containing compound is an asymmetric ketone because the product of the reaction is a useful optically active alcohol.

[0105]

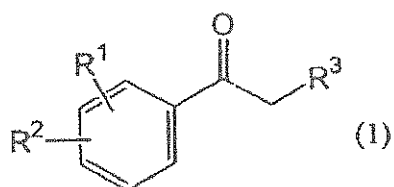
When a carbonyl group-containing compound is 1-phenylethanone derivative, which is one of an asymmetric

ketone, represented by the following formula (1):

[0106]

[Chemical formula 5]

5



10 [0107]

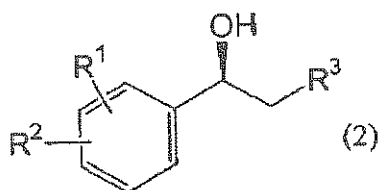
wherein R¹ and R² are each independently a hydrogen atom, a halogen atom, a hydroxy group, a substituted or unsubstituted alkoxy group, a substituted or unsubstituted alkyl group, an amino group or a nitro group, and R¹ and R² may be the same as or different from one another; R³ is a hydrogen atom, a halogen atom, a hydroxy group, or a substituted or unsubstituted alkyl group;

the product is an optically active 1-phenylethanol derivative represented by the following formula (2):

20 [0108]

[Chemical formula 6]

25



[0109]

wherein R¹, R², and R³ is the same as defined above.

30 [0110]

When R¹ and R² is an substituted alkoxy or alkyl group, the substituent may be a halogen atom, a hydroxyl group, an amino group, or a nitro group.

[0111]

35

R³ is a hydrogen atom, a halogen atom, a hydroxyl group,

or a substituted or unsubstituted alkyl group, and preferably a hydrogen atom.

[0112]

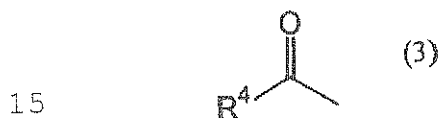
The above "halogen atom" means a fluorine, chlorine, bromine, or iodine atom.

[0113]

When a compound having a carbonyl group is an asymmetric methyl ketone compound represented by the following formula (3):

10 [0114]

[Chemical formula 7]



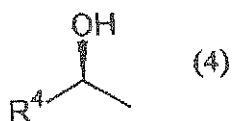
[0115]

wherein R^4 is a substituted or unsubstituted alkyl group, a substituted or unsubstituted alkenyl group, or a substituted or unsubstituted alkynyl group, the product is an optically active 1-substituted-1-ethanol derivative represented by the following formula (4):

[0116]

[Chemical formula 8]

25



30 [0117]

wherein R^4 is the same as defined above.

[0118]

R^4 is a substituted or unsubstituted alkyl group, a substituted or unsubstituted alkenyl group, or a substituted or unsubstituted alkynyl group. R^4 is preferably a C_{1-7} alkyl

35

group which may be substituted by a halogen atom, a hydroxyl group, an alkoxy group, an alkoxycarbonyl group, an amino group, or a nitro group. When the substituent is an alkoxy group, a C₁₋₅ alkoxy group is preferable. When the substituent is an alkoxycarbonyl group, a C₁₋₅ alkoxycarbonyl group is preferable. Examples of such a C₁₋₅ alkoxycarbonyl group include methoxycarbonyl group and ethoxycarbonyl group.

[0119]

Vinyl is also preferable as an example of R⁴.

10 [0120]

[Isolation and purification of an alcohol]

No particular limitation is put on a way for recovering an alcohol or aldehyde compound from a reaction mixture after the reaction. A highly-pure alcohol compound may easily be obtained by directly extracting, or extracting, after removing cells, etc., the alcohol compound from the reaction mixture with a solvent such as ethyl acetate, toluene, t-butyl methyl ether, hexane, or methylene chloride, then dehydrating the extract, and purifying the extract by distillation, recrystallization, silica gel column chromatography, or the like.

EXAMPLES

[0121]

The present invention will be described below in detail with reference to Examples, but the scope of the present invention is not limited to these Examples. Detailed procedures and so on concerning the recombinant DNA technology used in the following Examples are described in the following literatures:

30 Molecular Cloning 2nd Edition (Cold Spring Harbor Laboratory Press, 1989), Current Protocols in Molecular Biology (Greene Publishing Associates and Wiley-Interscience).

[0122]

(Example 1) Purification of a polypeptide

35 A polypeptide having ability to asymmetrically reduce

acetophenone to produce (S)-phenylethanol was separated from Candida maltosa IFO 1977 strain, and purified to isolate the polypeptide in the following protocols. Purification was performed at 4°C unless otherwise noted. Reducing activity to acetophenone was determined in accordance with the procedures described in [Method for evaluating reducing ability to a ketone or aldehyde compound].

[0123]

(Cultivation of a microorganism)

10 A liquid medium (400 mL, pH 7) containing 10 g/L meat extract, 10 g/L peptone, 5 g/L yeast extract, 3 g/L sodium chloride, and 0.1 g/L ADEKA NOL LG-109 (a product of ADEKA CORPORATION) was prepared in a 2-L Sakaguchi flask and steam-sterilized at 120°C for 20 minutes. This medium was
15 inoculated with 4 ml of culture fluid of the strain Candida maltosa IFO 1977, which had been prepared in advance by preculture in the same medium, and the medium was shake-cultivated at 30°C for 60 hours.

[0124]

20 (Preparation of a cell-free extract)

 Cells were collected by centrifugation from the above culture fluid, and washed with 0.8% aqueous sodium chloride. These cells were suspended in 20 mM phosphate buffer (pH 8.0), which contained 5 mM β -mercaptoethanol, and then the cells were
25 ultrasonically disrupted by SONIFIER 250 ultrasonic disintegrator (a product of BRANSON). The cell residues were removed from the resultant extract by centrifugation, whereby a cell-free extract was obtained.

[0125]

30 (Thermal treatment)

 The cell-free extract obtained according to the above manner was treated at 60°C for 30 minutes, and then centrifuged to remove insoluble matters. Thus, a thermally-treated cell-free extract was obtained.

35 [0126]

(DEAE-TOYOPEARL column chromatography)

The cell-free extract obtained according to the above manner was applied to a DEAE-TOYOPEARL 650M column (95 ml; a product of Tosoh Corporation), which had been equilibrated in advance with 20 mM phosphate buffer (pH 6.5) that contained 5 mM β -mercaptoethanol. Unnecessary fractions were thereby adsorbed.

[0127]

(Phenyl-TOYOPEARL column chromatography)

10 In active fractions, which were not adsorbed by the DEAE-TOYOPEARL column chromatography, ammonium sulfate was dissolved so that the final concentration of ammonium sulfate in the solution should be 0.92 M, and then precipitate was removed by centrifugation. Resultant supernatant was applied
15 to a Phenyl-TOYOPEARL 650 M column (60 ml; a product of Tosoh Corporation), which had been equilibrated in advance with 20 mM phosphate buffer (pH 6.5) that contained 0.92 M ammonium sulfate and 5 mM β -mercaptoethanol. Active fractions were thereby adsorbed. The column was washed with 20 mM phosphate
20 buffer (pH 6.5) that contained 0.66 M ammonium sulfate, and active fractions were eluted with a linear gradient of ammonium sulfate (from 0.66 M to 0.26 M). The active fractions were combined and dialyzed overnight with 20 mM phosphate buffer (pH 6.5) that contained 5 mM β -mercaptoethanol.

25 [0128]

(Butyl-TOYOPEARL column chromatography)

In active fractions obtained by Phenyl-TOYOPEARL column chromatography, ammonium sulfate was dissolved so that the final concentration of ammonium sulfate in the solution should
30 be 0.92 M. Thus-obtained solution was applied to a Butyl-TOYOPEARL 650 M column (23 ml; a product of Tosoh Corporation), which had been equilibrated in advance with 20 mM phosphate buffer (pH 6.5) that contained 0.92 M ammonium sulfate and 5 mM β -mercaptoethanol, to adsorb active fractions.
35 The column was washed with the same buffer, and active fractions

were eluted with a linear gradient of ammonium sulfate (from 0.92 M to 0 M). Electrophoretically-pure polypeptide purified sample was thereby obtained.

[0129]

5 Hereafter, this polypeptide is referred to as "RMA".

[0130]

(Example 2) Physicochemical properties of RMA

10 Physicochemical properties of RMA as obtained in the above manner were studied. Each activity was determined in accordance with a method as described in [Method for evaluating oxidizing ability to an alcohol compound].

[0131]

[Substrate specificity]

15 The activity of the RMA to oxidize (S)-2-butanol was defined as 100%. Relative activity of the RMA to each substrate was calculated as a percentage of oxidizing activity to a substrate based on the oxidizing activity to (S)-2-butanol (100%). The results are shown in Table 1. Concentration of each substrate under a condition for measuring oxidizing
20 activity was set as illustrated in Table 1.

[0132]

[Table 1]

Substrates	mM	Relative Activity (%)
(S)-2-butanol	50	100
(R)-2-butanol	50	38
2-Propanol	100	66
2-Pentanol	100	183
3-Pentanol	100	40
2-Octanol	5	134
Cyclohexanol	20	30
(S)-1-Phenylethanol	50	307
(S)-1,3-Butandiol	50	9.5
(R)-1,3-Butandiol	50	1.3
2,4-Pentandiol	100	34
(2R,4R)-2,4-Pentandiol	50	0.5
(S)-1-Amino-2-propanol	50	2.0
2-Hydroxybutyric acid	100	4.9
Methanol	100	0.6
Ethanol	100	5.0
1-Propanol	100	4.3
1-Butanol	100	6.6
(S)-1,2-propandiol	50	0.7
(R)-1,2-Propandiol	50	0.7

[0133]

[Optimum temperature]

Oxidizing activity to (S)-2-butanol was determined under
 5 a standard reaction condition except that the temperature was
 varied. The oxidizing activity at 60°C, which showed the
 highest activity, was defined as 100%. Relative activity of
 the RMA at a temperature was calculated as a percentage of
 oxidizing activity at the temperature based on the oxidizing
 10 activity at 60°C (100%). The results are shown in Table 2. The
 temperature range that showed relative activity of not less than
 60% was 45°C to 70°C.

[0134]

[Table 2]

Temperature (°C)	Relative Activity (%)
25	17
30	24
37	39
40	45
45	68
50	80
55	88
60	100
65	91
70	60
75	29
80	9
85	0

[0135]

[Stable range of temperature]

In 50 mM tris-HCl buffer (pH 8.0), RMA was treated at a temperature of 30°C to 70°C for 10 minutes. Then, oxidizing activity to (S)-2-butanol was measured. The oxidizing activity at 30°C was defined as 100%, and relative activity at each temperature was calculated as a percentage of oxidizing activity at a temperature based on the oxidizing activity at 30°C (100%). The results are shown in Table 3.

[0136]

[Table 3]

Temperature (°C)	Relative Activity (%)
30	100
35	96
40	95
50	75
60	37
70	9.4

[0137]

15 [Optimum pH]

(S)-2-Butanol-oxidizing activity was determined with 50 mM potassium phosphate buffer (pH 7 to pH 9), 50 mM tris-HCl buffer (pH 6 to pH 8) or 50 mM glycine-sodium hydroxide buffer (pH 9 to pH 10.5) while varying pH in the reaction mixture. The

highest oxidizing activity in potassium phosphate buffer at pH 9 was defined as 100%, and relative activity for each buffer and each pH was calculated as a percentage of oxidizing activity of a buffer at a certain pH based on the oxidizing activity in potassium phosphate buffer at pH 9 (100%). The results are shown in Table 4. The pH range that showed relative activity of not less than 60% was pH 7.5 to pH 9.5.

[0138]

[Table 4]

Buffer	pH	Relative activity (%)
Tris-HCl buffer	7	47.5
	7.5	60.2
	8	84.6
	8.5	87.8
	9	100.0
Potassium phosphate buffer	6	41.1
	6.5	44.3
	7	52.9
	7.5	69.8
	8	76.5
Glycine-sodium hydroxide buffer	9	67.7
	9.5	61.9
	10	39.0
	10.5	34.1

10

[0139]

[Stable range of pH]

RMA was treated in 50 mM tris-HCl buffer (pH 8.0 to pH 9.0) and in 50 mM Britton-Robinson buffer (pH 5.0 to pH 12.0) at 30°C for 30 minutes. Then, oxidizing activity to (S)-2-Butanol was determined. Activity of the untreated RMA was defined as 100%, and relative activity for a treated sample was calculated as a percentage of oxidizing activity of the treated sample based on the oxidizing activity of the untreated RMA (100%). The results are shown in Table 5. The pH range that showed relative activity of not less than 80% was pH 5.5 to pH 7.5.

20

[0140]

[Table 5]

Buffer	pH	Relative activity(%)
Britton-Robinson buffer	4	21
	5	56
	5.5	81
	6	87
	6.5	89
	7	83
	7.5	81
	8	42
	8.5	5
	9	1
	9.5	0
Tris-HCl buffer	8	59
	8.5	32
	9	16

[0141]

[Inhibitor]

- 5 RMA was treated at 30°C for 30 minutes in the presence of agents as shown in Table 6. Concentrations of agents at the time of treatment are illustrated in Table 6. Then, oxidizing activity to (S)-2-Butanol was determined in accordance with a method as described in [Method for evaluating oxidizing ability to an alcohol compound]. Activity of the untreated RMA was defined as 100%, and relative activity for each treated sample was calculated as a percentage of oxidizing activity of the treated sample based on the activity of the untreated RMA (100%). The results are shown in Table 6. Ethylenediaminetetraacetic acid, o-phenanthroline, mercury chloride, copper sulfate, or zinc sulfate inhibited RMA, whereas 2-mercaptoethanol, dithiothreitol did not.

[0142]

[Table 6]

Inhibitor	Treatment concentration of inhibitor (mM)	Relative activity(%)
Crotonic acid	50	10.4
Phenylmethanesulfonyl fluoride	1	96.0
N-Ethylmaleimide	1	94.7
Iodoacetic acid	1	78.9
Ethylenediaminetetraacetic acid	1	12.9
o-Phenanthroline	1	0.0
HgCl ₂	1	0.0
CuSO ₄	1	28.5
ZnSO ₄	1	23.1
Dithiothreitol	1	92.2
β-Mercaptoethanol	1	95.4
p-Hydroxybenzoic acid	1	91.5
p-Chloromercuribenzoate	0.05	96.3
NH ₂ OH	0.01	96.1

[0143]

[Molecular weight]

5 Molecular weight of RMA in reducing SDS-polyacrylamide electrophoresis was determined as approximately 39,000 based on the difference between RMA and a molecular weight standard protein in their mobility.

[0144]

10 (Example 3) Substrate specificity of RMA in carbonyl reducing activity

In 100 mM phosphate buffer (pH 6.5), which contained 0.3% (v/v) dimethyl sulfoxide, a substrate carbonyl compound and a coenzyme NADH were dissolved so that final concentration of the carbonyl compound should be 1.5 mM and that of the NADH be 0.25 mM. In the resultant solution, an appropriate amount of purified RMA, which had been prepared in Example 1, was added, and then allowed to react at 30°C for 3 minutes. Reducing activity to each carbonyl compound was determined from reducing rate of absorbance for a reaction mixture at the wavelength of 340 nm. Reducing activity to acetophenone was defined as 100%, and determined reducing activity was converted to a relative

15

20

value to reducing activity to acetophenone. The results are shown in Table 7. As is apparent from Table 7, RMA showed reducing activities to a wide variety of carbonyl compounds.

[0145]

5 [Table 7]

Carbonyl compounds	Relative activity (%)	Carbonyl compounds	Relative activity (%)
Acetone	28	2-Phenylpropionaldehyde	37
2-Butanone	54	3-Phenylpropionaldehyde	112
2-Pentanone	141	Propionaldehyde	39
2-Hexanone	87	n-Butyraldehyde	117
2-Heptanone	82	n-Hexylaldehyde	117
2-Octanone	95	Glutaraldehyde	9
3-Octanone	3	Benzaldehyde	29
Chloroacetone	92	m-Chlorobenzaldehyde	87
4-Methyl-2-pentanone	70	p-Chlorobenzaldehyde	51
Methyl iso-propyl ketone	4	o-Nitrobenzaldehyde	29
Methyl vinyl ketone	94	m-Nitrobenzaldehyde	28
Cyclopentanone	10	p-Nitrobenzaldehyde	27
Acetophenone	100	2-Pyridinecarbaldehyde	11
o-Chloroacetophenone	2	4-Pyridinecarbaldehyde	5
o-Methoxyacetophenone	10		
o-Hydroxyacetophenone	9	Methyl pyruvate	71
m-Chloroacetophenone	130	Ethyl pyruvate	87
m-Methoxyacetophenone	111	Methyl 2-oxodecanate	2
m-Hydroxyacetophenone	12	Ethyl 4-chloroacetoacetate	52
m-Nitroacetophenone	89	Methyl 4-chloroacetoacetate	35
p-Chloroacetophenone	130	Ethyl 3-oxobutanoate	93
p-Fluoroacetophenone	110	Ethyl 3-oxohexanoate	2
p-Methylacetophenone	91	Benzyl acetoacetate	115
Ethyl 4-acetylbenzoate	70	n-Octyl 4-chloroacetoacetate	24
2-Chloro-1-(3'-cholophenyl)ethanone	20	Ethyl 4-azidoacetoacetate	21
Benzylacetone	33	Ethyl 4-benzyloxyacetoacetate	10
		Ethyl 2-chloroacetoacetate	26
2-Acetylpyridine	63	tert-Butylacetoacetate	88
3-Acetylpyridine	19	Methyl acetoacetate	66
4-Acetylpyridine	83		
5-Acetylfuro[2.3-c]pyridine	63	Acetoacetoanilide	1
Acetypyrazine	76	o-Acetoacetanisidide	35
2-Acetyrfuran	8	N-Acetoacetyl-p-toluidine	2
Tetrahydrothiophen-3-one	4	4'-Chloroacetoacetanilide	4
		2',5'-Dichloro acetoacetanilide	34
3-Chloro-2,4-pentadione	43	Acetoacetamide	10
Acethylacetone	19		
diacethyl	24		

[0146]

(Example 4) Acquisition of a DNA coding for RMA

(Construction of PCR primers)

Purified RMA, which had been obtained in Example 1, was denatured in the presence of 8 M urea, and then digested with achromobacter-derived lysyl endopeptidase (available from
5 Wako Pure Chemical Industries, Ltd.). Then, the amino acid sequence of thus-obtained peptide fragment was determined by ABI492-type protein sequencer (a product of PerkinElmer). Based on a DNA sequence which was expected from the amino acid sequence, primer 1: 5'-GGTGATTGGTTYGGTTTRGG-3' (SEQ ID NO:3 in
10 the sequence listing), and primer 2:
5'-SWAGCACCYAAACCAACTGG-3' (SEQ ID NO:4 in sequence listing), which were for amplifying a part of a gene that codes for RMA in PCR, were synthesized.

[0147]

15 (Amplification of a gene through PCR)

Chromosomal DNA was extracted from cells of Candida maltosa IFO 1977 strain, which had been cultivated in a similar manner to Example 1, with GENTorukunTM (a product of Takara Bio Inc.) in accordance with the condition illustrated in an
20 instruction manual. Then, PCR was carried out with the DNA primers 1 and 2, which had been prepared in the above manner, in the presence of the obtained chromosomal DNA as a template. As a result, an about 0.5 kbp DNA fragment assumed to be a part of a target gene was amplified. PCR was carried out with TaKaRa
25 Ex Taq (a product of Takara Bio Inc.) as a DNA polymerase under a reaction condition as illustrated in an instruction manual. This DNA fragment was subjected to direct sequencing with BigDye Terminator Cycle Sequencing Kit (a product of Applied Biosystems) and Applied Biosystems 3130x1 Genetic Analyzer (a
30 product of Applied Biosystems), and thereby the base sequence of the DNA fragment was analyzed. The base sequence acquired is illustrated as SEQ ID NO:5 in the sequence listing.

[0148]

(Determination of complete sequence of a target gene by inverse
35 . PCR method)

Chromosomal DNA of Candida maltosa IFO 1977 strain, which had been prepared in the above manner, was completely digested with a restriction enzyme BglI or MunI or XbaI, and then the thus-obtained mixture of DNA fragments was

5 intramolecularly-cyclized with T4 ligase. With the cyclized product as a template, the complete base sequence of RMA gene, which included the above base sequence shown under SEQ ID NO:5 in the sequence listing, was determined by inverse PCR method (Nucl. Acids Res., 16, 8186 (1988)). The result is shown under

10 SEQ ID NO:2 in the sequence listing. Inverse PCR was carried out with Pyrobest DNA Polymerase (a product of Takara Bio Inc.) as a DNA polymerase, and the reaction condition was followed by the condition illustrated in an instruction manual. In addition, an amino acid sequence coded by the base sequence

15 shown under SEQ ID NO:2 was illustrated in SEQ ID NO:1.

[0149]

(Example 5) Construction of a recombinant vector pNCM

PCR was carried out with primer 3:

5'-GGGAATTCCATATGTCAATCCATCTACTCAATAC-3' (SEQ ID NO:6 in the

20 sequence listing), primer 4:

5'-CCGGAATTCTTATGGATGGAAAACAACTCTACC-3' (SEQ ID NO:7 in the sequence listing) in the presence of the chromosomal DNA of Candida maltosa IFO 1977 strain as a template. As a result, a double-stranded DNA was obtained, in which an NdeI recognition

25 site was inserted in a initiation codon position, and an EcoRI recognition site was inserted at a position immediately downstream of the termination codon, in the gene that consisted of the base sequence shown under SEQ ID NO:2 in the sequence listing. PCR was carried out with Pyrobest DNA Polymerase (a

30 product of Takara Bio Inc.) as DNA polymerase, and the reaction condition was followed by the condition illustrated in an instruction manual.

[0150]

A DNA fragment obtained by the above PCR was digested with

35 NdeI and EcoRI, and then inserted at the site between the NdeI

recognition site and the EcoRI recognition site, downstream of the lac promoter of the plasmid pUCN18 (a plasmid constructed by replacing "T" at the 185th position with "A" of pUC18 (a product of Takara Bio Inc., GenBank Accession No. L09136) by PCR to destroy the NdeI site, and further replacing "GC" at the 471st and 472nd positions with "TG" to introduce a new NdeI site). Thus, a recombinant vector pNCM was constructed. The method for constructing pNCM and the structure thereof are illustrated in Fig. 1.

10 [0151]

(Example 6) Construction of a recombinant vector pNCMG that further contains a glucose dehydrogenase gene

PCR was carried out with primer 5:

5'-CCGGAATTCTAAGGAGGTAAACAATGTATAAAG-3' (SEQ ID NO:8 in the sequence listing) and primer 6:
5'-ACGCGTCGACTTATCCGCGTCCTGCTTGG-3' (SEQ ID NO:9 in the sequence listing) in the presence of the plasmid pGDK1 (a person skilled in the art could acquire or prepare the plasmid in accordance with the way as described in Eur. J. Biochem., 186, 389 (1989)) as a template. As a result, a double-stranded DNA was obtained, in which a ribosome binding site of Escherichia coli was inserted at a position 5-base upstream from the initiation codon of a glucose dehydrogenase (hereafter to be abbreviated as "GDH") gene that was derived from Bacillus megaterium IAM 1030 strain, and an EcoRI recognition site was inserted immediately upstream of the ribosome binding site, and further, SalI recognition site was inserted immediately downstream of the termination codon.

[0152]

30 Thus-obtained DNA fragment was digested with EcoRI and SalI, and then inserted at the site between the EcoRI recognition site and the SalI recognition site, downstream of the RMA gene of the plasmid pNCM as described in Example 5 to construct a recombinant vector pNCMG. The method for
35 constructing pNCMG and the structure thereof are illustrated

in Fig. 1.

[0153]

(Example 7) Construction of a recombinant vector pNCMFT that further contains formate dehydrogenase gene

5 PCR was carried out with primer 7:

5'-ACCACCGAATTCTAAGGAGGTTAACAATGGCGAAA-3' (SEQ ID NO:10 in the sequence listing), primer 8:

5'-CCACCAGAGCTCTCAGCCGGCCTTCTTGAAC-3' (SEQ ID NO:11 in the sequence listing), primer 9:

10 5'-TCGGCGTCGACGAGTTCCTTCTCGAACAC-3' (SEQ ID NO:12 in the sequence listing), primer 10:

5'-GTGTTGAGAAGGAAGTTCGTCGACGCCGA-3' (SEQ ID NO:13 in the sequence listing) in the presence of the plasmid pFT002 (a person skilled in the art could acquire or prepare the plasmid

15 in accordance with the way as described in WO 2003/031626) as a template. An about 0.3 kbp double-stranded DNA was produced by combining the primers 7 and 9, and an about 0.9 kbp

double-stranded DNA was produced by combining the primers 8 and 10. Then, a combination of primers 7 and 8 was subjected to

20 PCR with a mixture of these double-stranded DNAs as templates. As a result, a double-stranded DNA was obtained, in which a ribosome binding site of Escherichia coli was inserted at a position 5-base upstream from the initiation codon of a formate

dehydrogenase (hereafter to be abbreviated as "FDH") gene of Thiobacillus sp., which had been constructed by replacing "G" 25 at the 354th position of the base sequence that is shown under

SEQ ID NO:3 in sequence listing of WO 2003/031626 with "A", and an EcoRI recognition site was inserted immediately upstream of the ribosome binding site, and further an SacI recognition site

30 was added immediately downstream of the termination codon. Thus-obtained DNA fragment was digested with EcoRI and SacI,

and then inserted at the site between the EcoRI recognition site and the SalI recognition site, downstream of the RMA gene of the plasmid pNCM as described in Example 5 to construct a

35 recombinant vector pNCMFT. The method for constructing pNCMFT

and the structure thereof are illustrated in Fig. 1.

[0154]

(Example 8) Construction of a transformant

E. coli HB101(pNCM) was produced by transforming E. coli
5 HB101 competent cell(a product of Takara Bio Inc.) with the
recombinant vector pNCM, which had been constructed in Example
5.

[0155]

E. coli HB101(pNCMG) was produced by transforming E. coli
10 HB101 competent cell(a product of Takara Bio Inc.) with the
recombinant vector pNCMG, which had been constructed in Example
6.

[0156]

E. coli HB101(pNCMFT) was produced by transforming E.
15 coli HB101 competent cell(a product of Takara Bio Inc.) with
the recombinant vector pNCMFT, which had been constructed in
Example 7.

[0157]

(Example 9) Expression of DNA in a transformant

20 Three transformants obtained in Example 8, and E. coli
HB101(pUCN18) (Comparative example), which is a transformant
containing a vector plasmid pUCN18, were each inoculated into
a 5 ml of 2 × YT medium (tryptone 1.6%, yeast extract 1.0%, NaCl
0.5%, and pH 7.0), which contained 200 µg/ml of ampicillin, and
25 then shake-cultivated at 37°C for 24 hours. Cells were
collected by centrifugation, and suspended in 5 ml of 100 mM
phosphate buffer (pH 6.5). Cells in the obtained suspension
were disrupted with UH-50 ultrasonic homogenizer (a product of
SMT Co., Ltd), and then cell residue was removed by
30 centrifugation, to give a cell-free extract. The
acetophenone-reducing activity by RMA, GDH activity, and FDH
activity were tested on this cell-free extract.

[0158]

Reducing activity to acetophenone was determined in
35 accordance with a manner as described in the above [Method for

evaluating reducing ability to a ketone or aldehyde compound]. The GDH activity was determined by, first, adding 0.1 M glucose, 2 mM coenzyme NAD, and crude enzyme liquid in 1 M tris-HCl buffer (pH 8.0), then allowing the mixture to react at 25°C for 1 minute and calculating the GDH activity from increasing rate of absorbance for the reaction mixture at the wavelength of 340 nm. The FDH activity was determined by, first, adding 0.5 M formic acid, 2 mM coenzyme NAD, and crude enzyme liquid in 100 mM phosphate buffer (pH 7.0), then allowing the mixture to react at 30°C for 1 minute and calculating the FDH activity from increasing rate of absorbance for the reaction mixture at the wavelength of 340 nm. Under these reaction conditions, enzyme activity 1 U was defined as enzyme activity that reduced 1 μ m of NAD to NADH per minute.

[0159]

RMA, GDH and FDH were summarized in Table 8 as specific activities. As illustrated in Table 8, acetophenone-reducing activity and RMA expression were observed for three transformants as obtained in Example 8. Also, GDH expression was observed for E. coli HB101 (pNCMG), which contained the GDH gene, and FDH expression was observed for E. coli HB101 (pNCMFT), which contained the FDH gene.

[0160]

[Table 8]

Strain	RMA specific activity (U/mg)	GDH specific activity (U/mg)	FDH specific activity (U/mg)
E. coli HB101	0	0	0
E. coli HB101 (pUCN18)	0	0	0
E. coli HB101 (pNCM)	21.6	0	0
E. coli HB101 (pNCMG)	17.7	42.5	0
E. coli HB101 (pNCMFT)	14.7	0	3.4

[0161]

(Example 10) Production of (S)-phenylethanol with transformant E. coli HB101 (pNCM)

E. coli HB101(pNCM) was cultivated in a similar manner to Example 9, and then cells were disrupted with an ultrasonic homogenizer. Thus, 100 mL of the cell-free extract was produced. In a 100-mL portion of this cell-free extract, 700 U of a glucose dehydrogenase (Trade name: GLUCDH "Amano" II, a product of Amano Enzyme Inc.), 17 g of glucose, 3 mg of NAD^+ , and 10 g of acetophenone were added, and the mixture was stirred at 30°C for 20 hours while controlling the pH of the reaction mixture to 6.5 with 5 N aqueous sodium hydroxide, which was added dropwise to the mixture. After the reaction, the reaction mixture was extracted with toluene, and combined organic layer was dried over anhydrous sodium sulfate. Removal of sodium sulfate, and evaporation of organic solvents from the organic layer yielded 9.8 g of (S)-phenylethanol. The product (S)-phenylethanol was analyzed in accordance with the [Analysis condition (1) for gas chromatography] as described above, and found that the optical purity of the product was 99.9% e.e. or higher.

[0162]

(Example 11) Production of (S)-phenylethanol with transformant E. coli HB101(pNCMG)

Culture fluid was obtained by cultivating E. coli HB101(pNCMG) in a similar manner to Example 9. In a 100-mL portion of the culture fluid, 17 g of glucose, 3 mg of NAD^+ , and 10 g of acetophenone were added and the mixture was stirred at 30°C for 20 hours while controlling the pH of the reaction mixture to 6.5 with 5 N aqueous sodium hydroxide, which was added dropwise to the mixture. After the reaction, the reaction mixture was extracted with toluene, and combined organic layer was dried over anhydrous sodium sulfate. Removal of sodium sulfate, and evaporation of organic solvents from the organic layer under reduced pressure yielded 9.9 g of (S)-phenylethanol. The product (S)-phenylethanol was analyzed in accordance with the [Analysis condition (1) for gas chromatography] as described above, and found that the optical purity of the

product was 99.9% e.e. or higher.

[0163]

(Example 12) Production of (S)-phenylethanol with transformant
E. coli HB101 (pNCMFT)

5 Culture fluid was obtained by cultivating E. coli
HB101 (pNCMFT) in a similar manner to Example 9. In a 100-mL
portion of the culture fluid, 2.8 g of sodium formate, 3 mg of
NAD⁺, and 10 g of acetophenone were added, and the mixture was
10 stirred at 30°C for 20 hours while controlling the pH of the
reaction mixture to 6.0 with 5 N aqueous formic acid, which was
added dropwise to the mixture. After the reaction, the reaction
mixture was extracted with toluene, and combined organic layer
was dried over anhydrous sodium sulfate. Removal of sodium
15 sulfate, and evaporation of organic solvents from the organic
layer under reduced pressure yielded 9.8 g of (S)-phenylethanol.
The product (S)-phenylethanol was analyzed in accordance with
the [Analysis condition (1) for gas chromatography] as
described above, and found that the optical purity of the
product was 99.9% e.e. or higher.

20 [0164]

(Example 13) Production of (S)-3-buten-2-ol with transformant
E. coli HB101 (pNCM)

E. coli HB101 (pNCM) was cultivated in a similar manner
to Example 9, and then cells were disrupted with an ultrasonic
25 homogenizer. Thus, 100 mL of the cell-free extract was produced.
In a 100-mL portion of this cell-free extract, 2000 U of a glucose
dehydrogenase (Trade name: GLUCDH "Amano" II, a product of Amano
Enzyme Inc.), 18.4 g of glucose, and 10 mg of NAD⁺ were added,
and the mixture was stirred at 30°C. In the mixture, 1.05 g
30 of methyl vinyl ketone was added and continued stirring at 30°C
while controlling the pH of the reaction mixture to 5.5 with
5 N aqueous sodium hydroxide, which was added dropwise to the
mixture. Five more portions of 1.05 g of methyl vinyl ketone
were added every 15 minutes (total added amount of methyl vinyl
35 ketone was 6.3 g). After 19-hour reaction, the reaction mixture

was repeatedly extracted with 200 ml of methylene chloride five times, and obtained organic layers were combined, followed by drying over anhydrous sodium sulfate. Sodium sulfate was removed by filtration and organic solvents were eliminated by evaporation under an ordinary pressure. The residue was distilled under an ordinary pressure to yield 4.5 g of (S)-3-buten-2-ol (Boiling point: 96°C). The optical purity of the product was 99.6% e.e. Yield of (S)-3-buten-2-ol was determined from an analysis under the below condition for gas chromatography.

[0165]

[Analysis condition for gas chromatography]

Column: InertCap5 (30 m × 0.25 mm; a product of GL Sciences Inc.)

Detector: FID

Carrier gas: Helium

Column temperature: 35°C

Optical purity of the produced 3-buten-2-ol was determined by first converting the 3-buten-2-ol into a corresponding dinitrobenzoyl compound, and then analyzing the compound by HPLC. Conversion of 3-buten-2-ol into the corresponding dinitrobenzoyl compound was carried out as follows. 3-Buten-2-ol was extracted from the reaction mixture with methylene chloride, then triethylamine and 3,5-dinitrobenzoyl chloride (1.2 equivalents to 3-buten-2-ol) were added to extracted 3-buten-2-ol, and the mixture was stirred at a room temperature for 2 hours. The reaction mixture was washed with 1 N aqueous HCl, and then purified by preparative thin-layer chromatography. Thus-obtained fraction was dissolved in ethanol, and then analyzed under the condition for high performance liquid chromatography as listed below.

[0166]

[Analysis condition of high performance liquid chromatography]

Column: Chiralpak AD-H (250 mm × 4.6 mm, a product of Daicel Chemical Industries)

Eluent: n-hexane/ethanol = 7/3

Flow rate: 1.0 ml/min

Detection: 245 nm

Elution time: S form: 17.2 minutes, R form: 11.0 minutes
[0167]

5 (Example 14) Production of (S)-3-buten-2-ol with transformant
 E. coli HB101(pNCMG)

 Culture fluid was obtained by cultivating E. coli
 HB101(pNCMG) in a similar manner to Example 9. In a 100-mL
 portion of the culture fluid, 7.1 g of glucose, 10 mg of NAD⁺,
10 and 5 g of EMULGEN 810 (a product of Kao Corporation) were added,
 and the mixture was stirred at 30°C for 10 minutes. In this
 mixture, 2.63 g of methyl vinyl ketone was added, and the mixture
 was continued stirring at 30°C while controlling the pH of the
 reaction mixture to 5.5 with 5 N aqueous sodium hydroxide, which
15 was added dropwise to the mixture. After 3-hour reaction, the
 reaction mixture was repeatedly extracted with 200 ml of
 methylene chloride five times, and obtained organic layers were
 combined, followed by drying over anhydrous sodium sulfate.
 Sodium sulfate was removed by filtration and organic solvents
20 were eliminated by evaporation under an ordinary pressure. The
 residue was distilled under an ordinary pressure to yield 2.54
 g of (S)-3-buten-2-ol. The optical purity of the product was
 99.2% e.e. Yield and optical purity of (S)-3-buten-2-ol were
 determined in accordance with the manner as described in Example
25 13.

[0168]

(Example 15) Production of (S)-3-buten-2-ol with transformant
 E. coli HB101(pNCMFT)

 Culture fluid was obtained by cultivating E. coli
30 HB101(pNCMFT) in a similar manner to Example 9. In a 100-mL
 portion of the culture fluid, 1.94 g of sodium formate, and 10
 mg of NAD⁺ were added, and the mixture was stirred at 30°C. In
 this mixture, 0.525 g of methyl vinyl ketone was added, and the
 mixture was continued stirring at 30°C while controlling the
35 pH of the reaction mixture to 5.5 with 5 N aqueous formic acid,

which was added dropwise to the mixture. Seven more portions of 0.525 g of methyl vinyl ketone were added every 30 minutes (total added amount of methyl vinyl ketone was 4.2 g). After 19-hour reaction, the reaction mixture was extracted repeatedly with 200 ml of methylene chloride five times, and obtained organic layers were combined, followed by drying over anhydrous sodium sulfate. Sodium sulfate was removed by filtration and organic solvents were eliminated by evaporation under an ordinary pressure. The residue was distilled under an ordinary pressure to yield 3.94 g of (S)-3-buten-2-ol. The optical purity of the product was 96.3% e.e. Yield and optical purity of (S)-3-buten-2-ol were determined in accordance with the manner as described in Example 13.

[0169]

15 (Example 16) Production of (S)-2-hydroxy-5-pentanol with transformant E. coli HB101(pNCMG)

Culture fluid was obtained by cultivating E. coli HB101(pNCMG) in a similar manner to Example 9. In a 50-mL portion of the culture fluid, 21.2 g of glucose, 2.5 mg of NAD^+ , and 10.0 g of 2-oxo-5-pentanol were added, and the mixture was continued stirring at 30°C while controlling the pH of the reaction mixture to 6.5 with 5 N aqueous sodium hydroxide, which was added dropwise to the mixture. After 45-hour reaction, cells were removed from the reaction mixture by centrifugation. The resultant solution was repeatedly extracted with 200 ml of ethyl acetate 3 times, and obtained organic layers were combined, followed by drying over anhydrous sodium sulfate. Sodium sulfate was removed by filtration and organic solvents were eliminated by evaporation under an ordinary pressure. Then, solvents were evaporated, to yield 8.68 g of (S)-2-hydroxy-5-pentanol. Optical purity of the produced (S)-2-hydroxy-5-pentanol was 99.2% e.e. Yield of (S)-2-hydroxy-5-pentanol was determined under the following condition (a) for gas chromatography, and optical purity thereof was determined under the following condition (b) for

gas chromatography.

[0170]

[Analysis condition (a) for gas chromatography]

Column: InertCap5 (30 m × 0.25 mm; a product of GL Sciences Inc.)

5 Detector: FID

Carrier gas: Helium

Column temperature: 80°C

[0171]

[Analysis condition (b) for gas chromatography]

10 Column: InertCap CHIRAMIX (30 m × 0.25 mm; a product of GL Sciences Inc.)

Detector: FID

Carrier gas: Helium

Column temperature: 90°C

15 Elution time: S-form: 17.2 minutes, R-form: 18.3 minutes

[0172]

(Example 17) Production of methyl (S)-3-hydroxybutyrate with transformant E. coli HB101(pNCMFT)

Culture fluid was obtained by cultivating E. coli
20 HB101(pNCMFT) in a similar manner to Example 9. In a 100-mL portion of the culture fluid, 2.8 g of sodium formate, 3 mg of NAD⁺, and 10 g of methyl acetoacetate were added, and the mixture was stirred at 30°C for 20 hours while controlling the pH of the reaction mixture to 6.0 with 5 N aqueous formic acid, which
25 was added dropwise to the mixture. After the reaction, the reaction mixture was extracted with toluene, and combined organic layer was dried over anhydrous sodium sulfate. Removal of sodium sulfate, and evaporation of organic solvents from the organic layer under reduced pressure yielded 9.7 g of methyl
30 (S)-3-hydroxybutyrate. The optical purity of the product was 99% e.e. or higher. Yield of ethyl (S)-3-hydroxybutyrate was calculated based on the analysis under the following condition for gas chromatography.

[0173]

35 [Analysis condition of gas chromatography]

Column: TC-WAX (15 m × 0.25 mm; a product of GL Sciences Inc.)

Detector: FID

Column temperature: 85°C

Injector temperature: 200°C

5 Detector temperature: 200°C

Carrier gas: Helium (70kPa)

Split ratio: 100/1

Elution time: methyl acetoacetate: 2.9 minutes, methyl

3-hydroxybutyrate: 3.8 minutes

10 [0174]

Optical purity of the produced methyl

(S)-3-hydroxybutyrate was determined by first converting the

methyl (S)-3-hydroxybutyrate into a corresponding

dinitrobenzoyl compound, and then analyzing the compound in

15 accordance with the following condition for high performance

liquid chromatography. Conversion of methyl

3-hydroxybutanoate into the corresponding dinitrobenzoyl

compound was carried out as follows. Methyl

3-hydroxybutanoate was extracted from the reaction mixture with

20 ethyl acetate, then pyridine and 3,5-dinitrobenzoyl chloride

(1.2 equivalents to methyl 3-hydroxybutanoate) was added to

extracted methyl 3-hydroxybutanoate, and the mixture was

stirred at a room temperature for 2 hours. The reaction mixture

was washed with 1 N aqueous HCl, and then purified by preparative

25 thin-layer chromatography. Thus-obtained fraction was

dissolved in ethanol, and then analyzed under the following HPLC

condition.

[0175]

[Analysis condition for high performance liquid

30 chromatography]

Column: Chiralpak AD-H (a product of Daicel Chemical Industries,
Ltd.)

Detection wavelength: 230 nm

Column temperature: 20°C

35 Eluent: n-hexane/ethanol = 3/7

Flow rate: 0.7 ml/min

Elution time: (S)-form: 21.7 minutes, (R)-form: 29.8 minutes

CLAIMS

1. A DNA which is any one of the following DNAs (A), (B), (C), and (D):

5 (A) a DNA comprising the base sequence shown under SEQ ID NO:2 in the sequence listing;

(B) a DNA hybridizable under a stringent condition with a DNA that comprises the base sequence complementary to the base sequence shown under SEQ ID NO:2 in the sequence listing, and coding for a polypeptide
10 that has activity to react with acetophenone to reduce into (S)-1-phenylethanol,

wherein said DNA hybridizable under a stringent condition is obtainable by hybridization with a filter in the presence of 0.7 to 1.0 M NaCl at 65 °C, followed by washing the filter with a 0.5-fold
15 concentration of SSC solution at 65 °C;

(C) a DNA having sequence identity of 85% or higher to the base sequence shown under SEQ ID NO:2 in the sequence listing, and coding for a polypeptide that has activity to react with acetophenone to reduce into (S)-1-phenylethanol; and

20 (D) a DNA comprising a base sequence that results from deletion, insertion, substitution and/or addition of one base or 150 or less bases in the base sequence shown under SEQ ID NO:2 in the sequence listing, and coding for a polypeptide that has activity to react with acetophenone to reduce into (S)-1-phenylethanol.

25

2. A polypeptide having the following physicochemical properties (1) to (6):

(1) Action:

The polypeptide oxidizes an alcohol with NAD^+ as a coenzyme
30 to produce a ketone or an aldehyde, or reduces a ketone or an aldehyde with NADH as coenzyme to produce an alcohol;

(2) Substrate specificity:

A substrate in oxidation reaction is an aliphatic alcohol which may have an aromatic substituent, and the polypeptide preferentially
35 oxidizes (S)-2-butanol in comparison with (R)-2-butanol; and a substrate in reduction reaction is a ketone or an aldehyde, and the polypeptide reacts with acetophenone to reduce into (S)-1-phenylethanol;

(3) Molecular weight:

The molecular weight of the polypeptide is approximately 39,000 as determined by reducing SDS-polyacrylamide gel electrophoresis;

5 (4) Stability in pH:

Stable pH range of the polypeptide is 5.5 to 7.5;

(5) Optimum temperature:

Optimum temperature of the polypeptide for action is 45°C to 70°C;

10 (6) Inhibitor:

Enzyme activity of the polypeptide is inhibited by ethylenediaminetetraacetic acid, o-phenanthroline, mercury chloride, copper sulfate or zinc sulfate, whereas is not inhibited by 2-mercaptoethanol or dithiothreitol.

15

3. The polypeptide according to claim 2,
which is derived from a microorganism that belongs to the
genus Candida.

20

4. The polypeptide according to claim 3,
wherein the microorganism is Candida maltosa.

5. A polypeptide which is any one of the following
polypeptides (a), (b), (c), and (d):

25 (a) A polypeptide comprising the amino acid sequence shown under
SEQ ID NO:1 in the sequence listing;

(b) A polypeptide comprising an amino acid sequence that results
from deletion, insertion, substitution and/or addition of one
amino acid residue or 50 or less amino acid residues in the amino
30 acid sequence shown under SEQ ID NO:1 in the sequence listing,
and having activity to react with acetophenone to reduce into
(S)-1-phenylethanol;

(c) A polypeptide having sequence identity of 85% or higher to
the amino acid sequence shown under SEQ ID NO:1 in the sequence
35 listing, and having activity to react with acetophenone to

reduce into (S)-1-phenylethanol; and

(d) A polypeptide encoded by the DNA according to claim 1.

5 6. A DNA coding for the polypeptide according to any one of claim 2 to 5.

7. A vector comprising the DNA according to claim 1 or 6.

10 8. The vector according to claim 7, further comprising a DNA that codes for a polypeptide with ability to reproduce a reduced coenzyme.

15 9. The vector according to claim 8, wherein the polypeptide with ability to reproduce a reduced coenzyme is glucose dehydrogenase or formate dehydrogenase.

20 10. A transformant which is producible by transformation of a host cell with the vector according to any one of claims 7 to 9.

25 11. The transformant according to claim 10, wherein the host cell is Escherichia coli.

30 12. A method for producing an alcohol comprising reacting the polypeptide according to any one of claims 2 to 5, or the transformant according to claim 10 or 11, and/or a processed product of the transformant with a carbonyl group-containing compound.

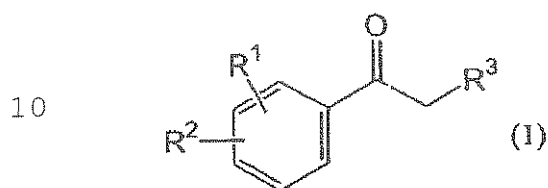
13. The method for producing an alcohol according to claim 12, wherein the carbonyl group-containing compound is an asymmetric ketone, and a product therefrom is an optically

35

active alcohol.

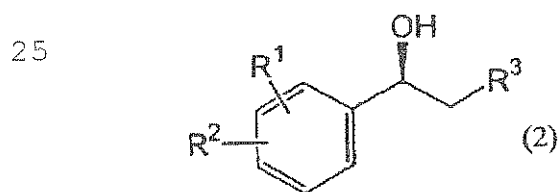
14. The method for producing an alcohol according to claim 13,

wherein the asymmetric ketone is a 1-phenylethanone derivative represented by the following formula (1):
[Chemical formula 1]



wherein R^1 and R^2 are each independently a hydrogen atom, a halogen atom, a hydroxy group, a substituted or unsubstituted alkoxy group, a substituted or unsubstituted alkyl group, an amino group or a nitro group, and R^1 and R^2 may be the same as or different from one another; R^3 is a hydrogen atom, a halogen atom, a hydroxy group or a substituted or unsubstituted alkyl group; and

the product optically active alcohol therefrom is an optically active 1-phenylethanol derivative represented by the following formula (2):
[Chemical formula 2]



wherein R^1 , R^2 and R^3 are the same as defined above.

15. The method for producing an alcohol according to claim 14,

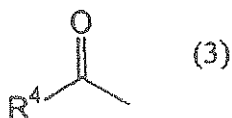
wherein R^3 is a hydrogen atom.

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16. The method for producing an alcohol according to claim
13,

wherein the asymmetric ketone is a methyl ketone compound
represented by the following formula (3):

5 [Chemical formula 3]

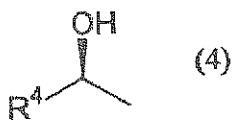


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wherein R^4 is a substituted or unsubstituted alkyl group, a
substituted or unsubstituted alkenyl group or a substituted or
unsubstituted alkynyl group, and

the product optically active alcohol therefrom is an
15 optically active 1-substituted-1-ethanol derivative
represented by the formula (4):

[Chemical formula 4]



20

wherein R^4 is the same as defined above.

17. The method for producing an alcohol according to claim
25 16,

wherein R^4 is a C_{1-7} alkyl group which may be substituted
by a halogen atom, a hydroxy group, an alkoxy group, an
alkoxycarbonyl group, an amino group or a nitro group.

18. The method for producing an alcohol according to claim
30 16,

wherein R^4 is a vinyl group.