

[DESCRIPTION]

[Invention Title]

VARIANT PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE AND METHOD OF PREPARING PURINE NUCLEOTIDE USING THE SAME

[Technical Field]

The present disclosure relates to a variant phosphoribosylpyrophosphate amidotransferase, a microorganism including the same, a method of preparing a purine nucleotide using the same, a composition for producing a purine nucleotide, a method for increasing the production of a purine nucleotide, or use of the variant phosphoribosylpyrophosphate amidotransferase.

[Background Art]

5'-Inosinic acid (5'-inosine monophosphate; hereinafter referred to as IMP), which is a nucleotide-based material, is an intermediate material of the metabolic system of nucleic acid biosynthesis, and is used in a variety of fields, such as medical products and medical applications. IMP is a material that is widely used as a food seasoning additive or for foods, together with 5'-guanylic acid (5'-guanine monophosphate; hereinafter referred to as GMP). IMP itself is known to have a beef flavor, and is known to enhance the flavor of monosodium glutamic acid (MSG), like GMP. Therefore, IMP has received much attention as a nucleotide-based taste seasoning.

Methods of preparing IMP include a method of enzymatically degrading ribonucleic acids which are extracted from yeast cells, a method of chemically phosphorylating inosine which is produced by fermentation (Agri. Biol. Chem., 36, 1511(1972), *etc.*), a method of culturing a microorganism capable of directly producing IMP and then recovering IMP in a culture thereof, *etc.* Among these methods, the most commonly

used method is the method of using a microorganism capable of directly producing IMP.

Further, methods of preparing GMP include a method of converting 5'-xanthylic acid (5'-xanthosine monophosphate; hereinafter referred to as XMP) produced by microbial fermentation into GMP using a coryneform microorganism, and a method of converting XMP produced by microbial fermentation into GMP using *Escherichia coli*. According to the methods, when XMP is produced and then converted into GMP, it is necessary to enhance productivity of XMP, which is a precursor of the conversion reaction during microbial fermentation, and it is required to prevent loss of GMP which has already been produced throughout the conversion reaction as well as produced XMP.

Meanwhile, enzymes in their natural state do not always exhibit optimal properties in terms of activity, stability, substrate specificity for optical isomers, *etc.*, which are required in industrial applications. Therefore, various attempts have been made to improve enzymes through variations of their amino acid sequences, *etc.* such that they become suitable for the intended use. Of these, rational design and site-directed mutagenesis of enzymes have been applied in order to improve enzyme functions. However, in many cases, there is a disadvantage in that information on the structure of a target enzyme is not sufficient, or the structure-function relationship is not clear, and therefore, the methods cannot be effectively applied. In this regard, it is reported that the enzyme improvement is attempted by way of a directed evolution method of screening for an enzyme of a desired trait from a mutant enzyme library which is constructed through random mutagenesis of the enzyme gene, leading to improvement of its activity.

[Disclosure]

[Technical Problem]

The present inventors have conducted extensive studies to produce a purine nucleotide with a high yield by a method of producing the purine nucleotide through microbial fermentation, and they identified a variant of a protein having a higher purine nucleotide productivity, thereby completing the present disclosure.

[Technical Solution]

An object of the present disclosure is to provide a variant phosphoribosylpyrophosphate amidotransferase.

Another object of the present disclosure is to provide a polynucleotide encoding the variant phosphoribosylpyrophosphate amidotransferase.

Still another object of the present disclosure is to provide a vector including the polynucleotide.

Still another object of the present disclosure is to provide a microorganism producing a purine nucleotide, the microorganism including the variant phosphoribosylpyrophosphate amidotransferase or the vector.

Still another object of the present disclosure is to provide a method of preparing a purine nucleotide, the method including the step of culturing a microorganism of the genus *Corynebacterium* in a medium.

Still another object of the present disclosure is to provide a composition for producing a purine nucleotide, comprising the variant phosphoribosylpyrophosphate amidotransferase of the present disclosure.

Still another object of the present disclosure is to provide a method for increasing the production of a purine nucleotide, comprising the variant phosphoribosylpyrophosphate amidotransferase of the present disclosure.

Still another object of the present disclosure is to provide use of the variant phosphoribosylpyrophosphate amidotransferase for the production of a purine nucleotide.

Still another object of the present disclosure is to provide use of the polynucleotide for the production of a purine nucleotide.

Still another object of the present disclosure is to provide use of the microorganism of the genus *Corynebacterium* for the production of a purine nucleotide.

[Advantageous Effects]

When a variant phosphoribosylpyrophosphate amidotransferase of the present disclosure is used to culture a microorganism of the genus *Corynebacterium*, it is possible to produce a purine nucleotide with a high yield. Further, the prepared purine nucleotide may be applied not only to animal feeds or animal feed additives but also to various products such as human food or food additives, seasonings, medicines, *etc.*

[Best Mode]

A detailed description is as follows. Meanwhile, respective descriptions and embodiments disclosed in this application may also be applied to other descriptions and embodiments. That is, all combinations of various elements disclosed in this application fall within the scope of the present application. Further, the scope of the present application is not limited by the specific description described below.

In order to achieve the above objects, an aspect of the present disclosure provides a variant phosphoribosylpyrophosphate amidotransferase having a

polypeptide including substitution of one or more amino acids in an amino acid sequence of SEQ ID NO: 2. Specifically, the present disclosure provides the variant phosphoribosylpyrophosphate amidotransferase having the polypeptide including substitution of one or more amino acids in the amino acid sequence of SEQ ID NO: 2, wherein the amino acid substitution includes substitution of an amino acid at position 2 and/or substitution of an amino acid at position 445 from the N-terminus of SEQ ID NO: 2.

Another aspect of the present disclosure provides a variant phosphoribosylpyrophosphate amidotransferase, wherein i) methionine is substituted for the amino acid at position 2, ii) arginine is substituted for the amino acid at position 455, or iii) methionine is substituted for the amino acid at position 2 and arginine is substituted for the amino acid at position 455 from the N-terminus of the amino acid sequence of SEQ ID NO: 2.

As used herein, the term "phosphoribosylpyrophosphate amidotransferase" refers to an enzyme that has an important role in purine biosynthesis. With respect to the objects of the present disclosure, the enzyme refers to a protein involved in production of purine nucleotides.

In the present disclosure, SEQ ID NO: 2 refers to an amino acid sequence having phosphoribosylpyrophosphate amidotransferase activity. Specifically, SEQ ID NO: 2 is a sequence of a protein having activity of phosphoribosylpyrophosphate amidotransferase, which is encoded by *purF* gene. The amino acid sequence of SEQ ID NO: 2 may be obtained from NCBI GenBank, which is a public database. For example, although not limited thereto, the amino acid sequence of SEQ ID NO: 2 may be derived from the genus *Corynebacterium* (*Corynebacterium* sp.), and may include any sequence having the

same activity as that of the above amino acid sequence without limitation. Further, the scope of the amino acid sequence of SEQ ID NO: 2 may include an amino acid sequence having activity of phosphoribosylpyrophosphate amidotransferase of SEQ ID NO: 2 or an amino acid sequence having 80% or more homology or identity thereto, but is not limited thereto. Specifically, the amino acid sequence may include the amino acid sequence of SEQ ID NO: 2 or an amino acid sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or more homology or identity to the amino acid sequence of SEQ ID NO: 2. The amino acid sequence having homology or identity may be those excluding a sequence having 100% identity from the above range, or may be a sequence having less than 100% identity. Further, it is apparent that a protein having an amino acid sequence having deletion, modification, substitution, or addition of some amino acids also falls within the scope of the present invention, as long as it has the homology or identity and exhibits efficacy corresponding to that of the above protein.

As used herein, the term "variant phosphoribosylpyrophosphate amidotransferase" may be used interchangeably with a variant polypeptide having purine nucleotide productivity, a purine nucleotide-producing variant polypeptide, a variant polypeptide producing a purine nucleotide, a variant polypeptide having phosphoribosylpyrophosphate amidotransferase activity, a phosphoribosylpyrophosphate amidotransferase variant, *etc.*

The variant phosphoribosylpyrophosphate amidotransferase may include variation(s) at position 2 and/or at position 445 from the N-terminus in the amino acid sequence of SEQ ID NO: 2. The variant phosphoribosylpyrophosphate amidotransferase may have substitution of another amino acid(s) for the amino

acid(s) at position 2 and/or at position 445 in the amino acid sequence of SEQ ID NO: 2 and enhanced activity, as compared with those including the amino acid sequence of SEQ ID NO: 2 or a non-modified phosphoribosylpyrophosphate amidotransferase derived from the wild-type microorganism. Such a variant phosphoribosylpyrophosphate amidotransferase means those having variation of the amino acid at position 2 or at position 445 from the N-terminus of the SEQ ID NO: 2 and/or an amino acid sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or more homology or identity to SEQ ID NO: 2, as described above.

For example, the variant phosphoribosylpyrophosphate amidotransferase may have i) substitution of methionine for the amino acid at position 2, ii) substitution of arginine for the amino acid at position 445, or iii) substitution of methionine for the amino acid at position 2 and substitution of arginine for the amino acid at position 445 in the amino acid sequence of SEQ ID NO: 2, and may have enhanced phosphoribosylpyrophosphate amidotransferase activity, as compared with the polypeptide including the amino acid sequence of SEQ ID NO: 2, but is not limited thereto.

With respect to the objects of the present disclosure, a microorganism including the variant phosphoribosylpyrophosphate amidotransferase has higher purine nucleotide productivity than a wild-type microorganism, a microorganism including the wild-type phosphoribosylpyrophosphate amidotransferase, or a microorganism including no variant phosphoribosylpyrophosphate amidotransferase. The present disclosure is of significance in that the purine nucleotide production by microorganisms may be increased by using the variant phosphoribosylpyrophosphate amidotransferase of the present disclosure, whereas the wild-

type strain of the genus *Corynebacterium* is not able to produce purine nucleotides or, even though it produces purine nucleotides, it is able to produce trace amounts thereof.

Specifically, the variant phosphoribosylpyrophosphate amidotransferase may include an amino acid sequence having substitution of another amino acid(s) for the amino acid(s) at position 2 and/or at position 445. Specifically, the variant phosphoribosylpyrophosphate amidotransferase may be composed of a polypeptide including i) substitution of methionine for the amino acid at position 2, ii) substitution of arginine for the amino acid at position 445, or iii) substitution of methionine for the amino acid at position 2 and substitution of arginine for the amino acid at position 445 from the N-terminus in the amino acid sequence of SEQ ID NO: 2. Further, the variant phosphoribosylpyrophosphate amidotransferase may include an amino acid sequence where another amino acid(s) is/are substituted for the amino acid(s) at position 2 and/or at position 445 from the N-terminus in the amino acid sequence of SEQ ID NO: 2, or an amino acid sequence having 80% or more homology or identity thereto, but is not limited thereto. Specifically, the variant phosphoribosylpyrophosphate amidotransferase of the present disclosure may include a polypeptide having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or more homology or identity to the amino acid sequence having substitution of methionine for the amino acid at position 2 or substitution of arginine for the amino acid at position 445 in the amino acid sequence of SEQ ID NO: 2. Further, it is apparent that a protein having an amino acid sequence having deletion, modification, substitution, or addition of other amino acid sequences than the amino acid sequence at positions 2 and/or 445 also falls within the scope of the present invention, as long as it has the homology or

identity and exhibits efficacy corresponding to that of the above protein.

In other words, even though the present disclosure describes a 'protein or polypeptide having an amino acid sequence represented by a particular SEQ ID NO:', it is apparent that a protein having an amino acid sequence having deletion, alteration, substitution, conservative substitution, or addition of some amino acids may also be used in the present disclosure, as long as it has activity identical or corresponding to that of the polypeptide having the amino acid sequence of the corresponding SEQ ID NO:. For example, as long as a protein has the activity identical or corresponding to that of the variant phosphoribosylpyrophosphate amidotransferase, it does not exclude sequence addition, naturally occurring mutation, silent mutation, or conservative substitution thereof which does not alter the function of the protein, before and after the amino acid sequence. It is apparent that a protein having such a sequence addition or mutation also falls within the scope of the present disclosure.

The "conservative substitution" means replacement of an amino acid with another amino acid having similar structural and/or chemical properties. This amino acid substitution may be generally made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or amphipathic nature. For example, positively charged (basic) amino acids include arginine, lysine, and histidine; negatively charged (acidic) amino acids include glutamic acid and aspartic acid; aromatic amino acids include phenylalanine, tryptophan, and tyrosine; and hydrophobic amino acids include alanine, valine, isoleucine, leucine, methionine, phenylalanine, tyrosine, and tryptophan.

Therefore, in the present disclosure, the "variant" may further include conservative substitution and/or modification of one or more amino acids in 'a protein or polypeptide having an amino acid sequence represented by a particular SEQ ID NO:'. For example, certain variants may include variants in which one or more portions, such as a N-terminal leader sequence or transmembrane domain, have been removed. Another variant may include variants in which a portion has been removed from the N- and/or C- terminus of the mature protein. The variant may also include other modifications, including deletion or addition of amino acids, which have minimal effects on properties and a secondary structure of the polypeptide. For example, the polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of a protein that co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to another sequence or a linker for ease of identification, purification, or synthesis of the polypeptide. The term "variant" may be used interchangeably with modification, modified protein, modified polypeptide, mutant, mutein, divergent, *etc.*, and any term may be used without limitation, as long as it is used in a sense of being modified.

Homology and identity mean a degree of relatedness between two given amino acid sequences or nucleotide sequences, and may be expressed as a percentage. The terms homology and identity may often be used interchangeably with each other.

Sequence homology or identity of a conserved polynucleotide or polypeptide may be determined by a standard alignment algorithm used with default gap penalties established by a program to be used. Substantially, homologous or identical sequences may hybridize under moderately or highly stringent conditions along their entire sequence or at

least about 50%, about 60%, about 70%, about 80%, or about 90% of the entire length. With regard to the polynucleotides to be hybridized, polynucleotides including a degenerate codon instead of a codon may also be contemplated.

In general, as codon defines which amino acid to be encoded, a codon is formed by pairing three nucleotide sequences. There are more kinds of codon compared to that of amino acid to be encoded, and the kind of amino acid to be produced differs according to the combination of codons. Translation starts from an initiation codon and the first amino acid to be translated may be fMet. Generally, translation proceeds by transporting fMET for the mRNA codon corresponding to the atg sequence of DNA. However, translation can proceed by transporting fMET when the first DNA of mRNA ORF (open reading frame) is gtg or ttg. That is, the initiation codon may be atg, gtg, or ttg.

Whether any two polynucleotide or polypeptide sequences have homology, similarity, or identity may be determined by, for example, a known computer algorithm such as the "FASTA" program using default parameters as in Pearson *et al.* (1988)[Proc. Natl. Acad. Sci. USA 85]: 2444, and alternatively, determined by using the Needleman-Wunsch algorithm (Needleman and Wunsch, 1970, J. Mol. Biol. 48: 443-453) as implemented in the Needleman program of the EMBOSS package (EMBOSS: The European Molecular Biology Open Software Suite, Rice *et al.*, 2000, Trends Genet. 16: 276-277) (version 5.0.0 or later) (including GCG program package (Devereux, J., *et al.*, Nucleic Acids Research 12: 387 (1984)), BLASTP, BLASTN, FASTA (Atschul, [S.] [F.,] [ET AL, J MOLEC BIOL 215]: 403 (1990); Guide to Huge Computers, Martin J. Bishop, [ED.,] Academic Press, San Diego, 1994, and [CARILLO ETA/.](1988) SIAM J Applied Math 48: 1073). For example, homology, similarity, or identity may be determined using BLAST, or ClustalW of the National Center for

Biotechnology Information.

Homology, similarity, or identity of polynucleotides or polypeptides may be determined by comparing sequence information using a GAP computer program, for example, Needleman *et al.* (1970), J Mol Biol.48: 443, as disclosed in Smith and Waterman, Adv. Appl. Math (1981) 2:482. Briefly, the GAP program defines similarity as the number of aligned symbols (*i.e.*, nucleotides or amino acids) which are similar, divided by the total number of symbols in the shorter of the two sequences. The default parameters for the GAP program may include: (1) a unary comparison matrix (containing a value of 1 for identities and 0 for non-identities) and the weighted comparison matrix (or EDNAFULL (EMBOSS version of NCBI NUC4.4) substitution matrix) of Gribskov *et al.* (1986) Nucl. Acids Res. 14: 6745, as described by Schwartz and Dayhoff, eds., Atlas Of Protein Sequence And Structure, National Biomedical Research Foundation, pp. 353-358 (1979); (2) a penalty of 3.0 for each gap and an additional 0.10 penalty for each symbol in each gap (or gap open penalty 10, gap extension penalty 0.5); and (3) no penalty for end gaps. Therefore, the term "homology" or "identity", as used herein, represents relevance between sequences.

Due to codon degeneracy, it is apparent that a polynucleotide to be translated into the variant polypeptide having substitution of another amino acid(s) for the amino acid(s) at position 2 and/or at position 445 from the N-terminus of the amino acid sequence of SEQ ID NO: 2, or a variant polypeptide having homology or identity thereto may also be included. Further, by hybridization under stringent conditions with a probe prepared from a known gene sequence, for example, a sequence complementary to all or part of the nucleotide sequence, a polynucleotide sequence encoding the variant phosphoribosylpyrophosphate amidotransferase including

the amino acid sequence wherein i) substitution of methionine for the amino acid at position 2, ii) substitution of arginine for the amino acid at position 445, or iii) substitution of methionine for the amino acid at position 2 and substitution of arginine for the amino acid at position 445 in the amino acid sequence of SEQ ID NO: 2 may be included without limitation.

As used herein, the term "polynucleotide" refers to a DNA or RNA strand having more than a certain length as a nucleotide polymer, which is a long chain of nucleotide monomers connected by covalent bonds, and more specifically, to a polynucleotide fragment encoding a polypeptide.

The polynucleotide encoding the variant phosphoribosylpyrophosphate amidotransferase of the present disclosure may include any polynucleotide sequence without limitation, as long as it encodes the variant polypeptide having phosphoribosylpyrophosphate amidotransferase activity of the present disclosure. In the present disclosure, a gene encoding the amino acid sequence of phosphoribosylpyrophosphate amidotransferase is *purF* gene, and specifically, the gene may be derived from *Corynebacterium stationis*, but is not limited thereto.

Specifically, due to codon degeneracy or by considering codons preferred by a microorganism in which the polypeptide is allowed to express, various modifications may be made in the coding region of the polynucleotide of the present disclosure within the scope that does not change the amino acid sequence of the polypeptide. Any polynucleotide sequence may be included without limitation as long as it encodes the variant phosphoribosylpyrophosphate amidotransferase having substitution of another amino acid for the amino acid at position 2 or at position 445 in the amino acid sequence of

SEQ ID NO: 2. For example, the polynucleotide of the present disclosure may include a sequence having some modified sequence in SEQ ID NO: 1, but is not limited thereto.

Further, by hybridization under stringent conditions with a probe prepared from a known gene sequence, for example, a sequence complementary to all or part of the nucleotide sequence, a sequence encoding a protein having activity of the variant phosphoribosylpyrophosphate amidotransferase having substitution of another amino acid for the amino acid at position 2 or at position 445 in the amino acid sequence of SEQ ID NO: 2 may be included without limitation. The "stringent conditions" mean conditions that permit specific hybridization between polynucleotides. Such conditions are described in detail in a literature (*e.g.*, J. Sambrook *et al.*, *supra*). The stringent conditions may include conditions under which genes having high homology or identity, for instance, genes having 40% or more, specifically 85% or more, 90% or more, more specifically 95% or more, still more specifically 97% or more, particularly specifically 99% or more homology or identity are able to hybridize to each other, and genes having lower homology or identity are not able to hybridize to each other, or conditions which are common washing conditions for Southern hybridization, *e.g.*, a salt concentration and a temperature corresponding to 60°C, 1×SSC, 0.1% SDS, specifically 60°C, 0.1×SSC, 0.1% SDS, more specifically 68°C, 0.1×SSC, 0.1% SDS, once, specifically, twice or three times.

Hybridization requires that two nucleic acids have complementary sequences, although mismatches between bases are possible depending on stringency of hybridization. The term "complementary" is used to describe the relationship between nucleotide bases that are able to hybridize to one another. For example, with respect to DNA, adenosine is complementary to thymine and cytosine is complementary to guanine.

Accordingly, the present disclosure may also include isolated nucleic acid fragments complementary to the complete sequences as well as substantially similar nucleic acid sequences.

Specifically, a polynucleotide having homology or identity may be detected by hybridization conditions including a hybridization step at T_m of 55°C and by utilizing the above-described conditions. Further, the T_m value may be 60°C, 63°C, or 65°C, but is not limited thereto, and may be properly controlled by those skilled in the art according to the purpose.

The appropriate stringency for hybridizing polynucleotides depends on the length of the polynucleotides and the degree of complementation, and variables are well known in the art (see Sambrook *et al.*, *supra*, 9.50-9.51, 11.7-11.8).

In the present disclosure, the gene encoding the amino acid sequence of the variant phosphoribosylpyrophosphate amidotransferase is *purF* gene, and a polynucleotide encoding the same is the same as described above.

In the present disclosure, the polynucleotide encoding the variant phosphoribosylpyrophosphate amidotransferase is also the same as described above.

Still another aspect of the present disclosure provides a polynucleotide encoding the variant phosphoribosylpyrophosphate amidotransferase, or a vector including the polynucleotide.

As used herein, the term "vector" means a DNA construct containing the nucleotide sequence of the polynucleotide encoding the desired polypeptide which is operably linked to a suitable control sequence such that the desired polypeptide is expressed in a suitable host. The control sequences may

include a promoter to direct transcription, a certain operator sequence to control such transcription, a sequence encoding a suitable ribosome-binding site on mRNA, and a sequence to control termination of transcription and translation. Once transformed into a suitable host, the vector may replicate or function independently of the host genome, or may integrate into the genome itself.

The vector used in the present disclosure may not be particularly limited as long as the vector is replicable in the host cell, and any vector known in the art may be used. Examples of the vector commonly used may include natural or recombinant plasmids, cosmids, viruses, and bacteriophages. For example, as a phage vector or a cosmid vector, pWE15, M13, MBL3, MBL4, IXII, ASHII, APII, t10, t11, Charon4A, Charon21A, *etc.* may be used, and as a plasmid vector, those based on pBR, pUC, pBluescriptII, pGEM, pTZ, pCL, pET, *etc.* may be used. Specifically, pDZ, pACYC177, pACYC184, pCL, pECCG117, pUC19, pBR322, pMW118, pCC1BAC vector, *etc.* may be used.

For example, the polynucleotide encoding the desired polypeptide may be inserted into the chromosome through a vector for chromosomal insertion in a cell. The insertion of the polynucleotide into the chromosome may be performed using any method known in the art, *e.g.*, by homologous recombination, but is not limited thereto. A selection marker for confirming the insertion of the vector into the chromosome may be further included. The selection marker is used for selection of cells transformed with the vector, *i.e.*, in order to confirm whether the desired nucleic acid molecule has been inserted, and markers capable of providing selectable phenotypes such as drug resistance, auxotrophy, resistance to cytotoxic agents, and expression of surface proteins may be used. Under the circumstances where selective agents are treated, only the cells capable of expressing the selection markers can survive

or express other phenotypic traits, and thus the transformed cells may be selected.

Still another aspect of the present disclosure provides a microorganism producing a purine nucleotide, the microorganism including the variant phosphoribosylpyrophosphate amidotransferase or the polynucleotide encoding the variant phosphoribosylpyrophosphate amidotransferase. Specifically, the microorganism including the variant phosphoribosylpyrophosphate amidotransferase and/or the polynucleotide encoding the same may be a microorganism prepared by transformation with a vector including the polynucleotide, but is not limited thereto.

As used herein, the term "transformation" refers to a process of introducing a vector which includes a polynucleotide encoding a target protein into a host cell such that the protein encoded by the polynucleotide is able to be expressed in the host cell. It does not matter whether the transformed polynucleotide is inserted into the chromosome of a host cell and located thereon or located outside of the chromosome, as long as the transformed polynucleotide may be expressed in the host cell. Further, the polynucleotide may include DNA and RNA encoding the target protein. The polynucleotide may be introduced in any form, as long as the polynucleotide may be introduced into the host cell and expressed therein. For example, the polynucleotide may be introduced into the host cell in the form of an expression cassette, which is a gene construct including all elements required for its autonomous expression. The expression cassette may include a promoter, a transcription termination signal, a ribosome binding site, and a translation termination signal that may be operably linked to the polynucleotide. The expression cassette may be in the form of an expression vector

performing self-replication. In addition, the polynucleotide may be introduced into the host cell as itself to be operably linked to the sequence required for expression in the host cell, but is not limited thereto.

Further, the term "operably linked" refers to a functional linkage between a gene sequence and a promoter sequence which initiates and mediates transcription of the polynucleotide encoding the desired polypeptide of the present disclosure.

The term "microorganism including the variant polypeptide" or "microorganism including the variant phosphoribosylpyrophosphate amidotransferase", as used herein, means a microorganism prepared by providing purine nucleotide productivity for a microorganism having a naturally weak purine nucleotide productivity or a parent strain having no purine nucleotide productivity. The microorganism may be a microorganism expressing the variant phosphoribosylpyrophosphate amidotransferase having the polypeptide including substitution of one or more amino acids in the amino acid sequence of SEQ ID NO: 2, wherein the amino acid substitution may include substitution of methionine for the amino acid at position 2 and/or substitution of arginine for the amino acid at position 445 from the N-terminus of SEQ ID NO: 2. Further, the microorganism may be a microorganism expressing the variant polypeptide, wherein the microorganism has phosphoribosylpyrophosphate amidotransferase activity due to substitution of another amino acid(s) for the amino acid(s) at position 2 and/or at position 445 in the amino acid sequence of SEQ ID NO: 2, but is not limited thereto.

The microorganism may be a cell or a microorganism which may include the polynucleotide encoding the variant phosphoribosylpyrophosphate amidotransferase, or may be

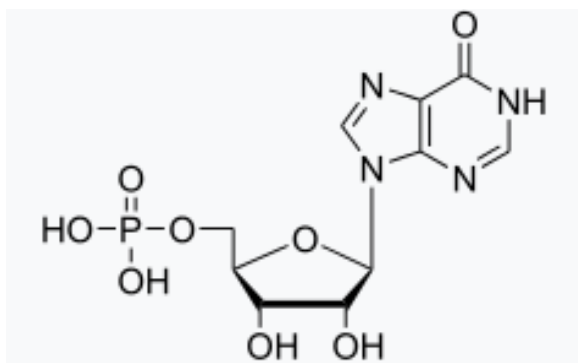
transformed with the vector including the polynucleotide encoding the variant phosphoribosylpyrophosphate amidotransferase to express the same, and with respect to the objects of the present disclosure, the host cell or the microorganism may be any microorganism, as long as it includes the variant phosphoribosylpyrophosphate amidotransferase to produce a purine nucleotide.

In the present disclosure, the microorganism producing a purine nucleotide may be used interchangeably with a purine nucleotide-producing microorganism or a microorganism having purine nucleotide productivity.

With respect to the objects of the present disclosure, the "purine nucleotide" means a nucleotide including a purine structure. Examples thereof may include IMP, XMP, or GMP, but are not limited thereto.

Specifically, the term "IMP (5'-inosine monophosphate)" is a nucleic acid-based material composed of the following Chemical Formula 1:

[Chemical Formula 1]

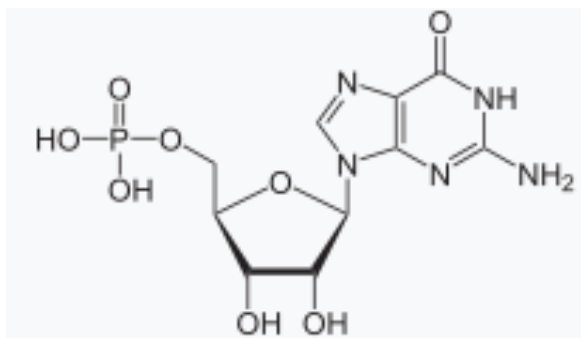


IMP has the IUPAC name of 5'-inosine monophosphate or 5'-inosine acid, and is widely used in foods as a flavor enhancer, together with XMP or GMP.

The term "GMP (5'-guanine monophosphate)" is a nucleic acid-based material composed of the following Chemical Formula

2:

[Chemical Formula 2]



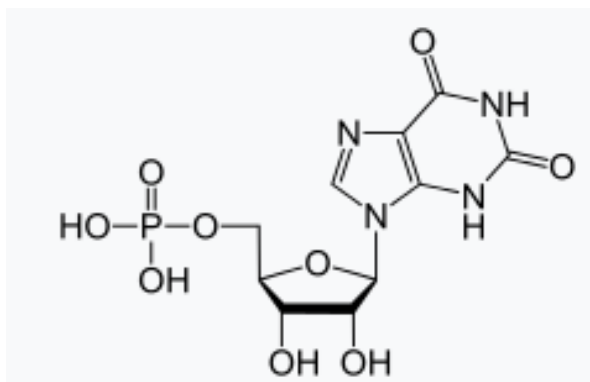
GMP has the IUPAC name of [(2*R*,3*S*,4*R*,5*R*)-5-(2-amino-6-oxo-1,6-dihydro-9*H*-purin-9-yl)-3,4-dihydroxytetrahydro-2-furanyl]methyl dihydrogen phosphate, and is also called 5'-guanidylic acid, 5'-guanylic acid, or guanylic acid.

GMP in the form of its salts, such as sodium guanylate, dipotassium guanylate, and calcium guanylate, is widely used as a food additive. When used as an additive together with IMP, GMP exhibits a synergistic effect to enhance flavor. GMP may be prepared by being converted from XMP, but is not limited thereto. As confirmed in one embodiment of the present disclosure, the variant polypeptide of the present disclosure may increase XMP production, and from the increased XMP production, GMP may be converted and its production may be increased. Accordingly, it is apparent that GMP is also included in the scope of the present disclosure.

The term "XMP (5'-xanthosine monophosphate)" is an intermediate material of purine metabolism and is composed of the following Chemical Formula 3. XMP has the IUPAC name of 5'-inosine monophosphate or 5'-xanthylic acid. XMP may be formed from IMP by action of IMP dehydrogenase, or XMP may be converted into GMP by action of GMP synthetase. Further, XMP may be formed from XTP by deoxyribonucleoside triphosphate pyrophosphohydrolase, which is an enzyme having XTPase

activity.

[Chemical Formula 3]



As used herein, the term "microorganism producing a purine nucleotide" may be a microorganism where a genetic modification occurs or activity is enhanced in order to produce the desired purine nucleotide, including all of a wild-type microorganism or a microorganism where a genetic modification naturally or artificially occurs, and the microorganism may be a microorganism where a particular mechanism is weakened or enhanced by insertion of an exogenous gene or by enhancement or inactivation of activity of an endogenous gene. With respect to the objects of the present disclosure, the microorganism producing a purine nucleotide may be characterized in that the microorganism includes the variant phosphoribosylpyrophosphate amidotransferase to have increased productivity of a desired purine nucleotide, and specifically, the microorganism may be a microorganism of the genus *Corynebacterium*. Specifically, in the present disclosure, the microorganism producing a purine nucleotide or the microorganism having purine nucleotide productivity may be a microorganism where some of the genes involved in the purine nucleotide biosynthesis pathway are enhanced or weakened, or some of the genes involved in the purine nucleotide degradation pathway are enhanced or weakened. For example, the microorganism may be a microorganism where expression of the

purA gene encoding adenylosuccinate synthetase is weakened. Additionally, expression of *guaB*, which is a gene encoding inosine-5'-monophosphate dehydrogenase present in the IMP degradation pathway, may be regulated according to the purine nucleotide. Specifically, when the purine nucleotide is IMP, *guaB* expression may be weakened, or when the purine nucleotide is XMP or GMP, *guaB* expression may be enhanced, but its expression is not limited thereto.

As used herein, the term "microorganism of the genus *Corynebacterium* producing a purine nucleotide" refers to a microorganism of the genus *Corynebacterium* which has purine nucleotide productivity naturally or due to mutation. Specifically, as used herein, the microorganism of the genus *Corynebacterium* having purine nucleotide productivity may be a microorganism of the genus *Corynebacterium* which has improved purine nucleotide productivity due to enhanced activity of the *purF* gene encoding phosphoribosylpyrophosphate amidotransferase. More specifically, as used herein, the microorganism of the genus *Corynebacterium* having purine nucleotide productivity refers to a microorganism of the genus *Corynebacterium* which has improved purine nucleotide productivity due to inclusion of the variant phosphoribosylpyrophosphate amidotransferase or the polynucleotide encoding the same, or due to transformation with the vector including the polynucleotide encoding the variant phosphoribosylpyrophosphate amidotransferase. The 'microorganism of the genus *Corynebacterium* which has improved purine nucleotide productivity' refers to a microorganism having improved purine nucleotide productivity, as compared with a parent strain before transformation or a non-modified microorganism. The 'non-modified microorganism' refers to a wild-type strain itself, or a microorganism that does not include the variant protein producing purine nucleotide, or a

microorganism that is not transformed with the vector including the polynucleotide encoding the variant phosphoribosylpyrophosphate amidotransferase.

As used herein, the "microorganism of the genus *Corynebacterium*" may be specifically *Corynebacterium glutamicum*, *Corynebacterium ammoniagenes*, *Brevibacterium lactofermentum*, *Brevibacterium flavum*, *Corynebacterium thermoaminogenes*, *Corynebacterium efficiens*, *Corynebacterium stationis*, etc., but is not limited thereto.

Still another aspect of the present disclosure provides a method of preparing a purine nucleotide, the method including the step of culturing the microorganism of the genus *Corynebacterium* producing a purine nucleotide in a medium. For example, the method of the present disclosure may further include the step of recovering the purine nucleotide from the microorganism or the medium after the step of culturing.

In the method, the step of culturing the microorganism may be performed by, but is not particularly limited to, a known batch culture, continuous culture, fed-batch culture, etc. In this regard, the culture conditions are not particularly limited, but an optimal pH (e.g., pH 5 to pH 9, specifically pH 6 to pH 8, and most specifically pH 6.8) may be adjusted by using a basic compound (e.g., sodium hydroxide, potassium hydroxide, or ammonia) or an acidic compound (e.g., phosphoric acid or sulfuric acid). An aerobic condition may be maintained by adding oxygen or an oxygen-containing gas mixture to the culture. The culture temperature may be maintained at 20°C to 45°C, and specifically at 25°C to 40°C, and the culturing may be performed for about 10 hours to about 160 hours, but is not limited thereto. The purine nucleotide produced by the culturing may be secreted into the medium or may remain within the cells.

Moreover, in a culture medium to be used, as a carbon source, sugars and carbohydrates (*e.g.*, glucose, sucrose, lactose, fructose, maltose, molasses, starch, and cellulose), oils and fats (*e.g.*, soybean oil, sunflower seed oil, peanut oil, and coconut oil), fatty acids (*e.g.*, palmitic acid, stearic acid, and linoleic acid), alcohols (*e.g.*, glycerol and ethanol), organic acids (*e.g.*, acetic acid), *etc.* may be used individually or in a mixture, but the carbon source is not limited thereto. As a nitrogen source, a nitrogen-containing organic compound (*e.g.*, peptone, yeast extract, meat extract, malt extract, corn steep liquor, soybean flour, and urea), or an inorganic compound (*e.g.*, ammonium sulfate, ammonium chloride, ammonium phosphate, ammonium carbonate and ammonium nitrate), *etc.* may be used individually or in a mixture, but is not limited thereto. As a phosphorus source, potassium dihydrogen phosphate, dipotassium hydrogen phosphate, sodium-containing salt corresponding thereto, *etc.* may be used individually or in a mixture, but is not limited thereto. The medium may also include essential growth-promoting materials such as other metal salts (*e.g.*, magnesium sulfate or iron sulfate), amino acids, and vitamins.

A method of recovering the purine nucleotide produced in the culturing step of the present disclosure is to collect the desired purine nucleotide from the culture medium by using an appropriate method known in the art according to the culturing method. For example, centrifugation, filtration, anion exchange chromatography, crystallization, HPLC, *etc.* may be used, and the desired purine nucleotide may be recovered from the medium or microorganism by using an appropriate method known in the art.

Further, the recovering step may include a purification process. The purification process may be performed by using an appropriate method known in the art. Therefore, the recovered

purine nucleotide may be a purified form or a microorganism fermentation liquid including the purine nucleotide (Introduction to Biotechnology and Genetic Engineering, A. J. Nair., 2008).

Still another aspect of the present disclosure provides a composition for producing a purine nucleotide, comprising the variant phosphoribosylpyrophosphate amidotransferase.

The composition for producing a purine nucleotide refers to a composition capable of producing a purine nucleotide by the polynucleotide of the present disclosure. For example, the composition comprises the polynucleotide, and further may comprise, without limitation, a constitution capable of operating the polynucleotide. The polynucleotide may be in a form included in a vector so as to express a gene operably linked to the introduced host cell.

Additionally, the composition may further comprise any suitable excipient conventionally used in a composition for producing a purine nucleotide. Such excipient can be, for example, a preservative, a wetting agent, a dispersing agent, a suspending agent, a buffer, a stabilizing agent, or an isotonic agent, but is not limited thereto.

Still another aspect of the present disclosure provides a method for increasing the production of a purine nucleotide, comprising the step of culturing the variant phosphoribosylpyrophosphate amidotransferase in a microorganism of the genus *Corynebacterium*.

The terms "variant phosphoribosylpyrophosphate amidotransferase", "microorganism of the genus *Corynebacterium*", "culture", "homoserine or homoserine-derived L-amino acid" are as described above.

Still another aspect of the present disclosure provides

use of the variant phosphoribosylpyrophosphate amidotransferase for the production of a purine nucleotide, or the preparation of a composition for producing a purine nucleotide.

Still another aspect of the present disclosure provides use of the polynucleotide for the production of a purine nucleotide, or the preparation of a composition for producing a purine nucleotide.

Still another aspect of the present disclosure provides use of the microorganism of the genus *Corynebacterium* for the production of a purine nucleotide, or the preparation of a composition for producing a purine nucleotide.

[Mode for Invention]

Hereinafter, the present disclosure will be described in more detail with reference to Examples. However, it is apparent to those skilled in the art to which the present disclosure pertains that these Examples are for illustrative purposes only, and the scope of the present disclosure is not intended to be limited by these Examples.

Example 1: Preparation of Wild-Type-Based IMP-Producing Strain

The wild-type strains of the genus *Corynebacterium* cannot produce IMP, or can produce IMP in very small amounts. Therefore, an IMP-producing strain was prepared based on wild-type *Corynebacterium stationis* ATCC6872. Specifically, the IMP-producing strain was prepared by weakening activity of *purA*, which encodes adenylosuccinate synthetase, and activity of *guaB*, which encodes 5'-inosinic acid dehydrogenase.

Example 1-1: Preparation of *purA*-Weakened Strain

In order to prepare a strain in which the start codon of *purA* was changed, an insertion vector containing *purA* was first prepared. In order to clone *purA* gene into the insertion vector, PCR was performed using the genomic DNA of *Corynebacterium stationis* ATCC6872 as a template and primers of SEQ ID NOS: 3 and 4 and SEQ ID NOS: 5 and 6 for 30 cycles of denaturation at 94°C for 30 sec, annealing at 55°C for 30 sec, and extension at 72°C for 2 min. PCR was performed using two DNA fragments obtained by the above PCR as a template and primers of SEQ ID NOS: 3 and 6 for 30 cycles of denaturation at 94°C for 30 sec, annealing at 55°C for 30 sec, and extension at 72°C for 2 min to obtain a DNA fragment. The obtained DNA fragment was digested with restriction enzyme XbaI, and cloned into a vector pDZ (Korean Patent No. 10-0924065 and International Patent Publication No. 2008-033001) that had been digested with the same enzyme. The vector prepared by the above method was designated as pDZ-*purA*-alt.

[Table 1]

SEQ ID NO.	Primer name	(Sequence (5'-3'))
3	pDZ- <i>purA</i> (alt)-1	GCTCTAGAGGCCACGATGCCCGGAGCATC
4	pDZ- <i>purA</i> (alt)-2	TAACGATAGCTGCCAAGGTTATTCACTTCCTAGATTT
5	pDZ- <i>purA</i> (alt)-3	AGGAAGTGAATAACCTTGGCAGCTATCGTTATCGTCG
6	pDZ- <i>purA</i> (alt)-4	GCTCTAGAGGTCACGAATGGGTAGGTGCC

The recombinant vector pDZ-*purA*-alt was transformed into *Corynebacterium stationis* ATCC6872 strain by electroporation,

and then strains in which the vector was inserted into the chromosome by homologous recombination were selected on a medium containing 25 mg/L kanamycin. The primary strains thus selected were subjected to secondary crossover, and then selected strains were subjected to sequencing, thereby selecting a final strain into which the mutation was introduced. This strain was designated as ATCC6872-purA(alt).

Example 1-2: Preparation of *guaB*-Weakened Strain

In order to prepare a strain in which the start codon of *guaB* was changed, an insertion vector containing *guaB* was first prepared. In order to clone *guaB* gene into the insertion vector, PCR was performed using the genomic DNA of *Corynebacterium stationis* ATCC6872 as a template and primers of SEQ ID NOS: 7 and 8 and SEQ ID NOS: 9 and 10. PCR was also performed using the above PCR products as a template and primers of SEQ ID NOS: 7 and 10. The obtained DNA fragment was cloned in the same manner as in Example 1-1. The prepared vector was designated as pDZ-guaB-alt.

[Table 2]

SEQ ID NO.	Primer name	(Sequence (5'-3'))
7	pDZ-guaB(alt)-1	GCTCTAGACTACGACAACACGGTGCCTAA
8	pDZ-guaB(alt)-2	CACGATTTTCGGTCAATACGGGTCTTCTCCTTCGCAC
9	pDZ-guaB(alt)-3	AGGAGAAGACCCGTATTGACCGAAAATCGTGTTTCT
10	pDZ-guaB(alt)-4	GCTCTAGAATCGACAAGCAAGCCTGCACG

The recombinant vector pDZ-guaB-alt was transformed into

the ATCC6872-purA(alt) strain prepared in Example 1-1 by electroporation, and then strains in which the vector was inserted into the chromosome by homologous recombination were selected on a medium containing 25 mg/L kanamycin. The primary strains thus selected were subjected to secondary crossover, and then selected strains were subjected to sequencing, thereby selecting a final strain into which the mutation was introduced.

The finally selected IMP-producing strain based on wild-type *Corynebacterium stationis* ATCC6872 was designated as CJI9088.

Example 1-3: Fermentation Titer Test of CJI9088

2 mL of a seed culture medium was dispensed into test tubes with a diameter of 18 mm and autoclaved under pressure. Each of ATCC6872 and CJI9088 was inoculated and incubated at 30°C for 24 h with shaking to be used as seed cultures. 29 mL of a fermentation medium was dispensed into 250 mL shaking Erlenmeyer flasks and autoclaved under pressure at 121°C for 15 min, and 2 mL of the seed culture was inoculated and incubated for 3 days. Culture conditions were adjusted to a rotation speed of 170 rpm, a temperature of 30°C, and pH 7.5.

After completion of the culturing, IMP production was measured by HPLC (SHIMAZDU LC20A), and the culturing results are as in the following Table 3. The following results suggest that the *purA*- and *guaB*-weakened strains have IMP productivity.

[Table 3]

Strain	IMP (g/L)
ATCC6872	0
CJI9088	0.52

- Seed culture medium: 1% glucose, 1% peptone, 1% meat extract, 1% yeast extract, 0.25% sodium chloride, 100 mg/L

adenine, 100 mg/L guanine, pH 7.5

- Fermentation medium: 0.1% sodium glutamate, 1% ammonium chloride, 1.2% magnesium sulfate, 0.01% calcium chloride, 20 mg/L iron sulfate, 20 mg/L manganese sulfate, 20 mg/L zinc sulfate, 5 mg/L copper sulfate, 23 mg/L L-cysteine, 24 mg/L alanine, 8 mg/L nicotinic acid, 45 µg/L biotin, 5 mg/L thiamine hydrochloric acid, 30 mg/L adenine, 1.9% phosphoric acid (85%), 2.55% glucose, 1.45% fructose

Example 2: Identification of Phosphoribosylpyrophosphate Amidotransferase-Enhanced Variant

In order to enhance activity of phosphoribosylpyrophosphate amidotransferase, which is the first enzyme in the IMP biosynthetic pathway, for the improvement of IMP productivity, a mutant library of *purF*, which is a gene encoding phosphoribosylpyrophosphate amidotransferase, was prepared, and an IMP productivity-enhancing mutation was identified.

Example 2-1: Preparation of *purF*-Containing Vector

In order to prepare a *purF* mutant library, a *purF*-containing recombinant vector was first prepared. PCR was performed using the genomic DNA of *Corynebacterium stationis* ATCC6872 as a template and primers of SEQ ID NO: 11 and SEQ ID NO: 12, and a PCR product was cloned into *E. coli* vector pCR2.1 by using a TOPO Cloning Kit (Invitrogen) to obtain pCR-*purF*.

[Table 4]

SEQ ID NO.	Primer name	(Sequence (5'-3'))
11	<i>purF</i> tempF	AAGTTGATGCTTCAGGCACA
12	<i>purF</i> tempR	TGCAAGGATTGGCTCTTTGT

Example 2-2: Preparation of *purF* Mutant Library

A *purF* mutant library was prepared based on the vector prepared in Example 2-1. The library was prepared by using an error-prone PCR kit (clontech Diversify® PCR Random Mutagenesis Kit). Under conditions where mutations may occur, PCR was performed using primers of SEQ ID NO: 13 and SEQ ID NO: 14. Specifically, under conditions where 0 to 3 mutations per 1000 bp may occur, pre-heating was performed at 94°C for 30 sec, followed by 25 cycles of 94°C for 30 sec and 68°C for 1 min 30 sec. A PCR product thus obtained was subjected to PCR using a megaprimer (500 ng to 125 ng) for 25 cycles of 95°C for 50 sec, 60°C for 50 sec, and 68°C for 12 min, and then treated with DpnI, and transformed into *E. coli* DH5α and spread on an LB solid medium containing kanamycin (25 mg/L). 20 kinds of transformed colonies were selected and then plasmids were obtained, followed by sequencing analysis. As a result, it was confirmed that mutations were introduced at different sites at a frequency of 2 mutations/kb. About 20,000 transformed *E. coli* colonies were taken and plasmids were extracted therefrom, and designated as a pTOPO-*purF*-library. [Table 5]

SEQ ID NO.	Primer name	(Sequence (5'-3'))
13	purF lib F	ACACGAGATAGCCCAGTGG
14	purF lib R	TCGTAGTTGCCATCAAAGCA

Example 2-3: Evaluation of Prepared Library and Selection of Strain

The pTOPO-*purF*-library prepared in Example 2-2 was transformed into the CJI9088 strain prepared in Example 1 by electroporation, and then spread on a nutrient medium containing 25 mg/L kanamycin to obtain 10,000 colonies into

which the mutant gene was inserted. The colonies were designated as CJI9088_pTOPO_purF(mt)1 to CJI9088_pTOPO_purF(mt)10000.

- Nutrient medium: 1% peptone, 1% meat extract, 0.25% sodium chloride, 1% yeast extract, 2% agar, pH 7.2

Each of the obtained 10,000 colonies was inoculated in 200 μ L of a seed culture medium autoclaved under pressure, and cultured in a 96-deep-well plate with shaking at 30°C and 1200 rpm for 24 h by using a microplate shaker (TAITEC), and then used as a seed culture. 290 μ L of fermentation medium autoclaved under pressure was dispensed into a 96-deep-well plate, and 20 μ L each of the seed cultures was inoculated thereto, followed by culturing with shaking under the same conditions as above for 72 h.

In order to analyze production of 5'-inosinic acid in the culture medium, after completion of the culturing, 3 μ L of culture supernatant was transferred to a 96-well UV-plate, each well containing 197 μ L of distilled water. Next, a microplate reader was used to perform shaking for 30 sec, and a spectrophotometer was used to measure optical density at 25°C and 270 nm and compared with the optical density of the CJI9088 strain to select 50 mutant strain colonies showing an increase of 10% or more in the optical density. Other colonies showed similar or decreased optical density compared to the control.

Optical densities of the 50 selected strains were measured in the same manner as above to repeatedly examine production amounts of 5'-inosinic acid. Two strains of CJI9088_pTOPO_purF(mt)201 and CJI9088_pTOPO_purF (mt)5674, which showed remarkable improvement in 5'-inosinic acid productivity compared to the CJI9088 strain, were selected.

Example 2-4: Identification of Mutation by Sequencing

In order to identify gene mutations of the mutant strains, each of CJI9088_pTOPO_purF(mt)201 and CJI9088_pTOPO_guaB(mt)5674 strains was subjected to PCR using primers of SEQ ID NOS: 15 and 16, followed by sequencing. Their *purF* genes were compared with those of the ATCC6872 and CJI9088 strains containing wild-type *purF* gene.

As a result, both of the strains were found to include *purF* gene mutation at different sites.

Specifically, it was confirmed that the CJI9088_pTOPO_purF(mt)201 strain has a substitution mutation of methionine for valine at position 2 in the *purF* amino acid sequence represented by SEQ ID NO: 2, and the CJI9088_pTOPO_purF(mt)5674 strain has a substitution mutation of arginine for glycine at position 445 in the *purF* amino acid sequence represented by SEQ ID NO: 2.

[Table 6]

SEQ ID NO.	Primer name	(Sequence (5'-3'))
15	purF-seq-F	ACACGAGATAGCCCAGTGG
16	purF-seq-R	ACCAAGTCATCGACGCACATT

In the following Examples 3 and 4, it was examined whether the above mutations affected IMP production of the microorganism of the genus *Corynebacterium*.

Example 3: Examination of IMP Productivity in CJI9088

The mutations identified in Example 2 were introduced into CJI9088, which is an ATCC6872-derived IMP-producing strain, and IMP productivity was examined.

Example 3-1: Preparation of Insertion Vector Containing *purF* Mutation

In order to introduce strains with the mutation selected in Example 2, an insertion vector was prepared. A vector for introduction of *purF* mutation is prepared as follows.

PCR was performed using the genomic DNA of ATCC6872 as a template and primers of SEQ ID NOS: 17 and 18 and SEQ ID NOS: 19 and 20. PCR was performed by denaturation at 94°C for 5 min, and then, for 20 cycles of at 94°C for 30 sec, at 55°C for 30 sec, at 72°C for 1 min, followed by polymerization at 72°C for 5 min. PCR was performed using each of the resulting DNA fragments as a template and primers of SEQ ID NO: 17 and SEQ ID NO: 20. The resulting DNA fragment was digested with XbaI. By using T4 ligase, the DNA fragment was cloned into a linear pDZ vector which had been digested with restriction enzyme XbaI, and thus pDZ-purF(V2M) was prepared. PCR was performed using primers of SEQ ID NOS: 21 and 22, and SEQ ID NOS: 23 and 24 in the same manner as above. PCR was performed using each of the resulting DNA fragments as a template and primers of SEQ ID NO: 21 and SEQ ID NO: 24. The resulting DNA fragment was digested with XbaI. By using T4 ligase, the DNA fragment was cloned into a linear pDZ vector which had been digested with restriction enzyme XbaI, and thus pDZ-purF(G445R) was prepared.

[Table 7]

SEQ ID NO.	Primer name	(Sequence (5'-3'))
17	purF V2M 1F	GGGTCTAGAAGTACTGACCCGACCACTGCA
18	purF V2M 1R	TGGGGAAAGTAGTGTTTCATCACGACGC
19	purF V2M 2F	TAGTAGAATCAGCGTCGTGATGAACAC
20	purF V2M 2R	GGGTCTAGATGGATTCCCTGCCTCATTGACA

21	purF G445R 1F	GGGTCTAGACCGATGGCAAGACCTTGTACG
22	purF G445R 1R	CAAACCCTAAAGAGTCTGCTCTGATAGCTTC
23	purF G445R 2F	CAGTGTGCGAAGCTATCAGAGCAGACTCTT
24	purF G445R 2R	GGGTCTAGACAAGGTCATCGATGTAGCCATCG

Example 3-2: Introduction of Mutant into CJI9088 Strain and Evaluation

CJI9088 was transformed with each of the pDZ-purF(V2M) and pDZ-purF(G445R) vectors prepared in Example 3-1, and strains in which the vector was inserted into the chromosome by homologous recombination were selected on a medium containing 25 mg/L kanamycin. The primary strains thus selected were subjected to secondary crossover to select strains into which the target gene mutation was introduced. Introduction of the gene mutation into the final transformed strains was examined by PCR using primers of SEQ ID NO: 15 and SEQ ID NO: 16, and then sequencing was performed to confirm introduction of the mutation into the strains. Specifically, the strain introduced with V2M mutation of purF gene was designated as CJI9088_purF_m1, and the strain introduced with G445R mutation of *purF* gene was designated as CJI9088_purF_m2. Further, in order to prepare a mutant strain having both of V2M and G445R mutations, CJI9088_purF_m1 strain was transformed with the pDZ-purF(G445R) vector, and colonies were obtained in the same manner as above. Through sequencing analysis of the obtained colonies, a strain introduced with both of V2M and G445R mutations of *purF* gene was selected and designated as CJI9088_purF_m1m2.

As shown in the results below, the CJI9088_purF_m1 or CJI9088_purF_m2 strain having V2M mutation or G445R mutation in the *purF* gene showed IMP concentration of 0.15 g/L (128%) or 0.09 g/L (117%), respectively, indicating improvement compared to the control CJI9088 strain. Further, the

CJI9088_purF_m1m2 strain having both of V2M and G445R mutations showed IMP concentration improvement of 0.31 g/L (159%), indicating that when both of the two mutations are included, most effective improvement may be obtained in IMP concentration.

[Table 8]

Strain	IMP (g/L)
CJI9088	0.52
CJI9088_purF_m1	0.67
CJI9088_purF_m2	0.61
CJI9088_purF_m1m2	0.83

Example 4: Examination of IMP Productivity in ATCC6872-Derived IMP-Producing Strain

To examine the effect of the *purF* mutant which was identified in Example 2, based on a strain producing a high concentration of IMP, the mutant was introduced into CJI0323 (Accession No. KCCM12151P, Korean Patent No. 10-1904675), which is a strain producing a high concentration of IMP, and IMP productivity was examined.

Example 4-1: Introduction of Mutant into CJI0323 Strain and Evaluation

CJI0323 was transformed with each of the pDZ-purF(V2M) and pDZ-purF(G445R) vectors prepared in Example 3-1, and strains in which the vector was inserted into the chromosome by homologous recombination were selected on a medium containing 25 mg/L kanamycin. The primary strains thus selected were subjected to secondary crossover to select strains into which the target gene mutation was introduced. Introduction of the gene mutation into the final transformed strains was examined by PCR using primers of SEQ ID NO: 15 and

SEQ ID NO: 16, and then sequencing was performed to confirm introduction of the mutation into the strains. Specifically, the strain introduced with V2M mutation of *purF* gene was designated as CJI0323_purF_m1, and the strain introduced with G445R mutation of *purF* gene was designated as CJI0323_purF_m2. Further, in order to prepare a mutant strain having both of V2M and G445R mutations, CJI0323_purF_m1 strain was transformed with the pDZ-purF(G445R) vector, and colonies were obtained in the same manner as above. Through sequencing analysis of the obtained colonies, a strain introduced with both of V2M and G445R mutations of *purF* gene was selected and designated as CJI0323_purF_m1m2.

The CJI0323_purF_m1 was called CJI2353, deposited at the Korean Culture Center of Microorganisms on September 10, 2018, under the provisions of the Budapest Treaty, and assigned accession number KCCM12316P. Further, the prepared CJI0323_purF_m2 was called CJI2354, deposited at the Korean Culture Center of Microorganisms on September 10, 2018, under the provisions of the Budapest Treaty, and assigned accession number KCCM12317P.

As shown in the results below, the CJI0323_purF_m1 or CJI0323_purF_m2 strain having V2M mutation or G445R mutation in the *purF* gene showed IMP concentration of 1.9 g/L (119%) or 0.95 g/L (109%), respectively, indicating improvement compared to the control CJI0323 strain. Further, the CJI0323_purF_m1m2 strain having both of V2M and G445R mutations showed IMP concentration improvement of 3.33 g/L (134%), indicating that when both of the two mutations are included, most effective improvement may be obtained in IMP concentration.

[Table 9]

Strain	IMP (g/L)
CJI0323	9.52

CJI0323_purF_m1	11.42
CJI0323_purF_m2	10.47
CJI0323_purF_m1m2	12.85

Example 5: Examination of 5'-Xanthylic Acid Productivity of *purF* Mutant

To examine the effect of the *purF* mutant which was identified in Example 2, based on a XMP-producing strain, the mutant was introduced into KCCM10530 (Korean Patent Publication No. 10-2005-0056670), which is a strain producing a high concentration of XMP, and XMP productivity was examined.

Example 5-1: Introduction of Mutant into KCCM10530 Strain and Evaluation

KCCM10530 was transformed with each of the pDZ-purF(V2M) and pDZ-purF(G445R) vectors prepared in Example 3-1, and strains in which the vector was inserted into the chromosome by homologous recombination were selected on a medium containing 25 mg/L kanamycin. The primary strains thus selected were subjected to secondary crossover to select strains into which the target gene mutation was introduced. Introduction of the gene mutation into the final transformed strains was examined by PCR using primers of SEQ ID NO: 15 and SEQ ID NO: 16, and then sequencing was performed to confirm introduction of the mutation into the strains. Specifically, the strain introduced with V2M mutation of *purF* gene was designated as KCCM10530_purF_m1, and the strain introduced with G445R mutation of *purF* gene was designated as KCCM10530_purF_m2. Further, in order to prepare a mutant strain having both of V2M and G445R mutations, KCCM10530_purF_m1 strain was transformed with the pDZ-purF(G445R) vector, and colonies were obtained in the same

manner as above. Through sequencing analysis of the obtained colonies, a strain introduced with both of the V2M and G445R mutations of *purF* gene was selected and designated as KCCM10530_purF_m1m2.

KCCM10530_purF_m1 was called CJX1681, deposited at the Korean Culture Center of Microorganisms on September 10, 2018, under the provisions of the Budapest Treaty, and assigned accession number KCCM12312P. Further, the prepared KCCM10530_purF_m2 was called CJX1682, deposited at the Korean Culture Center of Microorganisms on September 10, 2018, under the provisions of the Budapest Treaty, and assigned accession number KCCM12313P.

As shown in the results below, the KCCM10530_purF_m1 or KCCM10530_purF_m2 strain having V2M mutation or G445R mutation in the *purF* gene showed XMP concentration of 1.77 g/L (115%) or 0.8 g/L (107%), respectively, indicating improvement, as compared with the control KCCM10530 strain. Further, the KCCM10530_purF_m1m2 strain having both of V2M and G445R mutations showed XMP concentration improvement of 2.36 g/L (120%), indicating that when both of the two mutations are included, the most effective improvement may be obtained in XMP concentration.

[Table 10]

Strain	IMP (g/L)
KCCM10530	11.8
KCCM10530_purF_m1	13.57
KCCM10530_purF_m2	12.68
KCCM10530_purF_m1m2	14.16

Based on the above description, it will be understood by those skilled in the art that the present disclosure may be implemented in a different specific form without changing the

technical spirit or essential characteristics thereof. Therefore, it should be understood that the above embodiments are not limitative, but illustrative in all aspects. The scope of the present disclosure is defined by the appended claims rather than by the description preceding them, and therefore all changes and modifications that fall within the metes and bounds of the claims, or equivalents of such metes and bounds are therefore intended to be embraced by the claims.



BUDAPEST TREATY ON THE INTERNATIONAL
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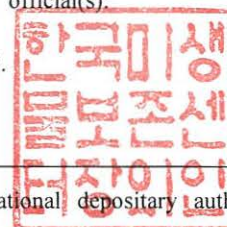
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CJ CHEILJEDANG CENTER,
330, DONGHO-RO,
JUNG-GU, SEOUL 100-400
REPUBLIC OF KOREA

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT
issued pursuant to Rule 7.1 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

I. IDENTIFICATION OF THE MICROORGANISM	
Identification reference given by the DEPOSITOR: <i>Corynebacterium stationis</i> CJX1681	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: KCCM12312P
II. SCIENTIFIC DESCRIPTION AND/OR PROPOSED TAXONOMIC DESIGNATION	
The microorganism identified under I above was accompanied by: ☐ a scientific description ☐ a proposed taxonomic designation (Mark with a cross where applicable)	
III. RECEIPT AND ACCEPTANCE	
This International Depositary Authority accepts the microorganism identified under I above, which was received by it on September. 10. 2018 (date of the original deposit). ¹	
IV. RECEIPT OF REQUEST FOR CONVERSION	
The microorganism identified under I above was received by this International Depositary Authority on (date of the original deposit) and a request to convert the original deposit to a deposit under the Budapest Treaty was received by it on (date of receipt of request for conversion).	
V. INTERNATIONAL DEPOSITARY AUTHORITY	
Name : Korean Culture Center of Microorganisms Address : Yurim B/D 45, Hongjenae-2ga-gil Seodaemun-gu SEOUL 03641 Republic of Korea	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): Date: September. 10. 2018.

¹ Where Rule 6.4(d) applies, such date is the date on which the status of international depositary authority was acquired.





BUDAPEST TREATY ON THE INTERNATIONAL
RECOGNITION OF THE DEPOSIT OF MICROORGANISMS
FOR THE PURPOSES OF PATENT PROCEDURE

INTERNATIONAL FORM

To. CJ CheilJedang Corporation
CJ CHEILJEDANG CENTER,
330, DONGHO-RO,
JUNG-GU, SEOUL 100-400
REPUBLIC OF KOREA

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT
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INTERNATIONAL DEPOSITARY AUTHORITY
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I. IDENTIFICATION OF THE MICROORGANISM	
Identification reference given by the DEPOSITOR: <i>Corynebacterium stationis</i> CJX1682	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: KCCM12313P
II. SCIENTIFIC DESCRIPTION AND/OR PROPOSED TAXONOMIC DESIGNATION	
The microorganism identified under I above was accompanied by: ☐ a scientific description ☐ a proposed taxonomic designation (Mark with a cross where applicable)	
III. RECEIPT AND ACCEPTANCE	
This International Depositary Authority accepts the microorganism identified under I above, which was received by it on September. 10. 2018 (date of the original deposit). ¹	
IV. RECEIPT OF REQUEST FOR CONVERSION	
The microorganism identified under I above was received by this International Depositary Authority on (date of the original deposit) and a request to convert the original deposit to a deposit under the Budapest Treaty was received by it on (date of receipt of request for conversion).	
V. INTERNATIONAL DEPOSITARY AUTHORITY	
Name : Korean Culture Center of Microorganisms Address : Yurim B/D 45, Hongjenae-2ga-gil Seodaemun-gu SEOUL 03641 Republic of Korea	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): Date: September. 10. 2018.

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I. IDENTIFICATION OF THE MICROORGANISM	
Identification reference given by the DEPOSITOR: <i>Corynebacterium stationis</i> CJI2353	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: KCCM12316P
II. SCIENTIFIC DESCRIPTION AND/OR PROPOSED TAXONOMIC DESIGNATION	
The microorganism identified under I above was accompanied by: ☐ a scientific description ☐ a proposed taxonomic designation (Mark with a cross where applicable)	
III. RECEIPT AND ACCEPTANCE	
This International Depositary Authority accepts the microorganism identified under I above, which was received by it on September. 10. 2018 (date of the original deposit). ¹	
IV. RECEIPT OF REQUEST FOR CONVERSION	
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V. INTERNATIONAL DEPOSITARY AUTHORITY	
Name : Korean Culture Center of Microorganisms Address : Yurim B/D 45, Hongjennale-2ga-gil Seodaemun-gu SEOUL 03641 Republic of Korea	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): Date: September. 10. 2018.

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BUDAPEST TREATY ON THE INTERNATIONAL
RECOGNITION OF THE DEPOSIT OF MICROORGANISMS
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I. IDENTIFICATION OF THE MICROORGANISM	
Identification reference given by the DEPOSITOR: <i>Corynebacterium stationis</i> CJI2354	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: KCCM12317P
II. SCIENTIFIC DESCRIPTION AND/OR PROPOSED TAXONOMIC DESIGNATION	
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[CLAIMS]

[Claim 1]

A variant phosphoribosylpyrophosphate amidotransferase, wherein i) methionine is substituted for an amino acid at position 2, ii) arginine is substituted for an amino acid at position 455, or iii) methionine is substituted for the amino acid at position 2 and arginine is substituted for the amino acid at position 455 from the N-terminus of an amino acid sequence of SEQ ID NO: 2.

[Claim 2]

A polynucleotide encoding the variant phosphoribosylpyrophosphate amidotransferase of claim 1.

[Claim 3]

A vector comprising the polynucleotide of claim 2.

[Claim 4]

A microorganism of the genus *Corynebacterium* producing a purine nucleotide, the microorganism comprising the variant phosphoribosylpyrophosphate amidotransferase of claim 1.

[Claim 5]

The microorganism of the genus *Corynebacterium* producing a purine nucleotide of claim 4, wherein the microorganism of the genus *Corynebacterium* is *Corynebacterium stationis*.

[Claim 6]

A method of preparing a purine nucleotide, comprising the step of culturing the microorganism of the genus *Corynebacterium* of claim 4 in a medium.

[Claim 7]

The method of preparing a purine nucleotide of claim 6, further comprising the step of recovering the purine nucleotide from the microorganism or the medium after the step of culturing.

[Claim 8]

The method of preparing a purine nucleotide of claim 6, wherein the microorganism of the genus *Corynebacterium* is *Corynebacterium stationis*.

[Claim 9]

A composition for producing a purine nucleotide, comprising the variant phosphoribosylpyrophosphate amidotransferase of claim 1 or the microorganism of claim 4.

[Claim 10]

A method for increasing the production of a purine nucleotide, comprising the variant phosphoribosylpyrophosphate amidotransferase of claim 1 or the microorganism of claim 4.

[Claim 11]

Use of the variant phosphoribosylpyrophosphate amidotransferase of claim 1 for the production of a purine nucleotide.

[Claim 12]

Use of the polynucleotide of claim 2 for the production of a purine nucleotide.

[Claim 13]

Use of the microorganism of the genus *Corynebacterium* of claim 4 for the production of a purine nucleotide.