[Best Mode]

To achieve the above objects, an aspect of the present disclosure provides a polypeptide having the activity of exporting *O*-acetylhomoserine, in which at least one amino acid selected from the group consisting of valine at position 1, phenylalanine at position 30, leucine at position 95, and phenylalanine at position 165 in the amino acid sequence of SEQ ID NO: 1 is substituted with another amino acid.

As used herein, the term "*O*-acetylhomoserine", which is a specific intermediate material in the methionine biosynthesis pathway of microorganisms, refers to an acetyl derivative of L-homoserine. *O*-acetylhomoserine is known to be produced by reacting homoserine and acetyl-CoA catalyzed by homoserine acetyltransferase, and it has the formula of $C_6H_{11}NO_4$.

As used herein, the term "peptide having the activity of exporting *O*-acetylhomoserine" refers to a polypeptide having the function of exporting *O*-acetylhomoserine in a cell of a microorganism to the outside of the cell. Specifically, the peptide may refer to a LeuE protein having the activity of exporting *O*-acetylhomoserine and a modified protein thereof, but the peptide is not particularly limited thereto as long as it has the activity of exporting *O*-acetylhomoserine.

As used herein, with regard to amino acid transporters, the term "LeuE", which is a protein belonging to the homoserine/homoserine lactone efflux protein (RhtB) family, refers to a protein present in the inner membrane, but its exact function is not known. In this regard, the inventors of the present disclosure first confirmed that LeuE specifically exports *O*-acetylhomoserine.

The LeuE may be a protein derived from a microorganism of the genus *Escherichia*, and specifically LeuE derived from *E. coli*, but any LeuE having the activity of exporting *O*-acetylhomoserine can be included to the scope of the present disclosure without limitation with regard to the origin of the microorganism.

Specifically, the peptide having the activity of exporting *O*-acetylhomoserine may be a protein having the amino acid sequence of SEQ ID NO: 1. Additionally, the peptide may be a protein which has an amino acid sequence having the activity of exporting *O*-acetylhomoserine substantially the same as or equivalent to that of the amino acid sequence of SEQ ID NO: 1, while having a homology of at least 70%, specifically at least 80%, and more specifically at least

90% to the amino acid sequence of SEQ ID NO: 1. Alternatively, the peptide may be an amino acid sequence having such homology where there is deletion, modification, substitution, or addition in part of the amino acid sequence having the activity of exporting *O*-acetylhomoserine substantially the same as or equivalent to that of the amino acid sequence of SEQ ID NO: 1, and it is obvious that this peptide also belongs to the scope of the present disclosure.

As used herein, the term "modified polypeptide" of the polypeptide having the activity of exporting *O*-acetylhomoserine refers to a polypeptide that has enhanced activity of exporting *O*-acetylhomoserine compared to that of native wild-type polypeptide or unmodified polypeptide. Specifically, the modified polypeptide is a peptide which has enhanced activity of exporting *O*-acetylhomoserine compared to that of the polypeptide which has the amino acid sequence of SEQ ID NO: 1 due to a modification of at least one amino acid in the amino acid sequence of SEQ ID NO: 1.

For example, the modified polypeptide may be a polypeptide in which at least one amino acid selected from the group consisting of valine at position 1, phenylalanine at position 30, leucine at position 95, and phenylalanine at position 165 in the amino acid sequence of SEQ ID NO: 1 is substituted with another amino acid. Specifically, the modified polypeptide may be a polypeptide in which valine at position 1 in the amino acid sequence of SEQ ID NO: 1 is substituted with methionine; phenylalanine at position 30 in the amino acid sequence of SEQ ID NO: 1 is substituted with any one selected from the group consisting of alanine, tryptophan, leucine, valine, glycine, serine, asparagine, aspartic acid, histidine, isoleucine, proline, tyrosine, glutamine, lysine, glutamic acid, cysteine, threonine, and arginine; leucine at position 95 in the amino acid sequence of SEQ ID NO: 1 is substituted with any one selected from the group consisting of valine, phenylalanine, alanine, glycine, threonine, asparagine, aspartic acid, histidine, isoleucine, serine, proline, tyrosine, glutamine, lysine, glutamic acid, cysteine, tryptophan, and arginine; or phenylalanine at position 165 in the amino acid sequence of SEQ ID NO: 1 is substituted with any one selected from the group consisting of alanine, tryptophan, leucine, valine, glycine, serine, asparagine, aspartic acid, histidine, isoleucine, proline, tyrosine, glutamine, lysine, glutamic acid, cysteine, threonine, and arginine. More specifically, the modified polypeptide may be a polypeptide in which valine at position 1 in the amino acid sequence of SEQ ID NO: 1 is substituted with methionine; phenylalanine at position 30 in the amino acid sequence of SEQ ID NO: 1 is substituted with any one selected from the group consisting of alanine, tryptophan, leucine, valine, glycine, serine, asparagine, aspartic acid, and

[Claim 6]

The polynucleotide according to claim 5, wherein the start codon of the polynucleotide is additionally substituted with ATG.

[Claim 7]

The polynucleotide according to claim 5, wherein the polynucleotide is selected from the group consisting of nucleic acid sequences of SEQ ID NOS: 4, 135, 136, 139, 140, 143, and 144.

[Claim 8]

A microorganism of the genus *Escherichia* producing *O*-acetylhomoserine, wherein a polypeptide consisting of the amino acid sequence of SEQ ID NO: 1 or a modified polypeptide thereof is comprised or overexpressed.

[Claim 9]

The microorganism according to claim 8, wherein, with regard to the modified polypeptide, at least one amino acid selected from the group consisting of valine at position 1, phenylalanine at position 30, leucine at position 95, and phenylalanine at position 165 in the amino acid sequence of SEQ ID NO: 1 is substituted with another amino acid.

[Claim 10]

The microorganism according to claim 8, wherein, with regard to the modified polypeptide, valine at position 1 in the amino acid sequence of SEQ ID NO: 1 is substituted with methionine; phenylalanine at position 30 in the amino acid sequence of SEQ ID NO: 1 is substituted with any one selected from the group consisting of alanine, tryptophan, leucine, valine, glycine, serine, asparagine, aspartic acid, and histidine; leucine at position 95 in the amino acid sequence of SEQ ID NO: 1 is substituted with any one selected from the group consisting of valine, phenylalanine, alanine, glycine, threonine, asparagine, aspartic acid, and histidine; or phenylalanine at position 165 in the amino acid sequence of SEQ ID NO: 1 is substituted with any one selected from the group consisting of alanine, tryptophan, leucine, valine, glycine, serine, asparagine, aspartic acid, and histidine.

[Claim 11]

The microorganism according to claim 8, wherein, with regard to the modified polypeptide, valine at position 1 in the amino acid sequence of SEQ ID NO: 1 is substituted with methionine; and phenylalanine at position 30, leucine at position 95, or phenylalanine at position 165 in the amino acid sequence of SEQ ID NO: 1 is substituted with another amino acid.

[Claim 12]

The microorganism according to claim 8, wherein the microorganism of the genus *Escherichia* is *Escherichia coli*.

[Claim 13]

The microorganism according to claim 8, wherein, additionally, the activity of cystathionine synthase is inactivated.

[Claim 14]

The microorganism according to claim 8, wherein, additionally, the activity of homoserine kinase is inactivated.

[Claim 15]

The microorganism according to claim 8, wherein, additionally, the activity of homoserine acetyltransferase is enhanced compared to that of an unmodified microorganism.

[Claim 16]

The microorganism according to claim 8, wherein, additionally, the activities of aspartate semialdehyde dehydrogenase, pyridine nucleotide transhydrogenase, or a combination thereof is enhanced compared to that of an unmodified microorganism.

[Claim 17]

A method for producing *O*-acetylhomoserine, comprising:

culturing the microorganism of the genus *Escherichia* producing *O*-acetylhomoserine of any one of claims 8 to 16 in a medium; and

recovering *O*-acetylhomoserine from the cultured microorganism or the cultured medium.