Claims

1. A method for production of N-Acetyl-D-Glucosamine and/or D-Glucosamine by microbial fermentation, including:

A) Cultivation of microorganism in the fermentation medium, where the said microorganism contains at least one genetic modification that may express vitreoscilla hemoglobin (Vhb); and

B) Collection of N-Acetyl-D-Glucosamine produced in the cultivation step A).

2. The method of Claim 1, wherein the microorganism is transformed by nucleic acid molecules with at least one nucleotide sequence encoding vitreoscilla hemoglobin (Vhb);

the nucleotide sequence encoding vitreoscilla hemoglobin (Vhb) contains at least one genetic modification that may increase the activities of vitreoscilla hemoglobin (Vhb).

3. The method of Claim 2, wherein said genetic modification contains one or more substitutions at the following corresponding sites of the amino acid sequence SEQ ID NO:61: Methionine at Site 45 is substituted by leucine, cysteine at Site 86 is substituted by glycine, and tyrosine at Site 95 is substituted by serine.

4. the method of Claim 2, wherein the nucleic acid sequence encoding the said vitreoscilla hemoglobin (Vhb) is SEQ ID NO: 64.

5. The method of Claim 2, wherein at least approximately 30% (more preferably at least approximately 50%, further more preferably at least approximately 70%, further more preferably at least approximately 80%, and further more at least approximately 90%, and most preferably at least approximately 95%) of the amino acid sequence of the said vitreoscilla hemoglobin (Vhb) is the same as that of SEQ ID NO:61, where the said vitreoscilla hemoglobin (Vhb) is active; Further preferably,

the said vitreoscilla hemoglobin (Vhb) has the amino acid sequence of SEQ ID NO:61.

6. The method of Claim 2, wherein the gene copies in the recombinant nucleic acid molecules, encoding vitreoscilla hemoglobin (Vhb), are more then or equal to 1; the recombinant nucleic acid molecules contain an endogenous promoter, or a promoter with a higher expression level than that of tge natural endogenous promoter; preferably, the promoter with higher level than the natural endogenous promoter is selected from HCE promoter, gap promoter, trc promoter, andT7 promoter; most preferably, the promoter with higher level than the natural endogenous promoter is trc promoter.

7. The method of any one of Claims 1-6, wherein the said microorganism contains one or more of the following genetic modifications:

(1) Contain at least one genetic modification that may increase the effects of N-Acetyl-D-Mannosamine Kinase (NanK) in microorganism;

(2) Contain at least one genetic modification that may increase the effects of N-Acetyl-D-Mannosamine-6-Phosphate Epimerase in microorganism;

(3) Contain at least one genetic modification that may increase the effects of D-Glucosamine-6-Phosphate Deaminase in microorganism, and preferably contain at least one genetic modification that may decrease the effects of Glucosamine- 6-Phosphate Synthase;

(4) Contain at least one genetic modification that may increase the effects of D-Glucosamine-6-Phosphate Synthase in microorganism, and preferably contain at least one genetic modification that may decrease the effects of D-Glucosamine- 6-Phosphate Deaminase;

(5) Contain at least one genetic modification that may increase the effects of UDP-N-Acetyl-D-Glucosamine-2-Epimerase (WecB) in microorganism.

8. The method of Claim 7, wherein the genetic modification to increase the effects of N-Acetyl-D-Mannosamine Kinase in microorganism are selected from: a) increased effects of N-Acetyl-D-Mannosamine Kinase in microorganism; and/or b) overexpression of N-Acetyl-D-Mannosamine Kinase in microorganism.

9. The method of Claim 8, wherein the microorganism is transformed by molecules of at least one recombinant nucleic acid, containing one nucleotide sequence encoding N-Acetyl-D-Mannosamine Kinase; the amino acid sequence encoding N-Acetyl-D-Mannosamine Kinase is SEQ ID NO: 26.

10. The method of Claim 7, wherein the genetic modification to increase the effects of N-Acetyl-D-Mannosamine-6-Phosphate Epimerase in microorganism are selected from: a) increased effects of N-Acetyl-D-Mannosamine-6-Phosphate Epimerase in microorganism; and/or b) overexpression of N-Acetyl-D-Mannosamine- 6-Phosphate Epimerase in microorganism.

11. The method of Claim 10, wherein the microorganism is transformed by molecules of at least one recombinant nucleic acid, containing one nucleotide sequence encoding N-Acetyl-D-Mannosamine-6-Phosphate Epimerase;

the amino acid sequence encoding the said N-Acetyl-D- Mannosamine-6-Phosphate Epimerase (NanE) is SEQ ID NO: 56.

12. The method of Claim 7, wherein the genetic modification increasing the effects of UDP-N-Acetyl-D-Glucosamine-2-Epimerase in microorganism is selected from a) increasing the effects of UDP-N-Acetyl-D-Glucosamine-2-Epimerase in microorganism; and/or b) overexpression of UDP-N-Acetyl-D- Glucosamine- 2-Epimerase in microorganism.

13. The method of Claim 12, wherein the microorganism is transformed by

molecules of at least one recombinant nucleic acid, containing one nucleotide sequence encoding UDP-N-Acetyl-D-Glucosamine-2-Epimerase; the amino acid sequence encoding UDP-N-Acetyl-D-Glucosamine-2-Epimerase (WecB) is SEQ ID NO: 58.

14. The method of any one of Claims 1-13, where the said microorganism contains one or more of the following genetic modifications:

(1) Contain at least genetic modification that may decrease the effects of Mannose transporter EIIM, P/III^{man}(ManXYZ) in microorganism;

(2) Contain at least one genetic modification that may decrease the effects of N-Acetylneuraminate Lyase (NanA) in microorganism;

(3) Contain at least one genetic modification that may decrease the effects of N-Acetyl-D-Glucosamine-6-Phosphate Deactylase (NagA) in microorganism;

(4) Contain at least one genetic modification that may decrease the effects of N-Acetyl-D-Glucosamine Specific Enzyme II^{Nag} (NagE) in microorganism;

(5) Contain at least one genetic modification that may increase the effects of PhosphoGlucosamine Mutase (GlmM) in microorganism;

(6) Contain at least one genetic modification that may increase the effects of bifunctional N-acetyl Glucosamine-1-Phosphate Uridyltransferase (GlmU) in microorganism.

15. A microorganism which contains at least one genetic modification that may express vitreoscilla hemoglobin (Vhb).

16. The microorganism of Claim 15, wherein the microorganism is transformed by nucleic acid molecules with at least one nucleotide sequence encoding vitreoscilla hemoglobin (Vhb), the nucleic acid sequence encoding the said vitreoscilla hemoglobin (Vhb) is SEQ ID NO: 64.

17. One vitreoscilla hemoglobin (Vhb) with higher activities, which has the amino acid sequence as shown in SEQ ID NO:65.

18. A nucleic acid molecule encoding vitreoscilla hemoglobin (Vhb) with higher activities according to Claim 17, where the said nucleic acid molecules have the nucleotide sequence as shown in SEQ ID NO: 64.

19. A carrier containing said nucleic acid molecules according to Claim 18.

20. A microorganism with genomes containing said nucleic acid molecule according to Claim 18.