## CLAIMS

1. A method for producing Neu5Ac by fermentation using a non-naturally-occurring microorganism able to produce Neu5Ac, the method comprising the following steps:
   a) providing a non-naturally-occurring microorganism, wherein said non-naturally-occurring microorganism possesses a sialic acid biosynthesis pathway comprising at least one heterologous enzyme, wherein the naturally occurring sialic acid catabolic pathway of the microorganism has been disabled, wherein at least one phosphoenolpyruvate:sugar phosphotransferase system for the import of a saccharide that is not used as a carbon source during fermentative production of Neu5Ac has been disabled, and wherein the microorganism can utilize an exogenous carbon source present in the fermentation broth as a sole carbon source without using a phosphoenolpyruvate:sugar phosphotransferase system for the acquisition of said exogenous carbon source, wherein the sialic acid biosynthesis pathway comprises the enzymes glutamine—fructose-6-phosphate aminotransferase, glucosamine-6-phosphate N-acetyltransferase, *N*-acetylglucosamine 2-epimerase, *N*-acetylneuraminic acid synthase, and a sugar phosphatase of the HAD-like superfamily, and wherein said non-naturally-occurring microorganism is an *E. coli* bacterium;
   b) cultivating the non-naturally-occurring microorganism in a fermentation broth and under conditions permissive for the non-naturally-occurring microorganism to produce Neu5Ac; and
   c) optionally, recovering the Neu5Ac from the fermentation broth.

2. The method according to claim 1, wherein one or more of the genes encoding an enzyme which is involved in the sialic acid catabolic pathway is deleted from the genome of the non-naturally-occurring microorganism, in that the expression of one or more of the genes encoding an enzyme which is involved in the sialic acid catabolic pathway is impaired, or in that the nucleotide sequence of the protein coding region of at least one gene encoding an enzyme which is involved in the sialic acid catabolic pathway is amended such that the polypeptide being

encoded by said altered protein-coding nucleotide sequence does not possess the enzymatic activity of the enzyme being encoded by the non-amended nucleotide sequence.

3. The method according to claim 1 or 2, wherein the non-naturally-occurring microorganism has been genetically engineered to delete one or more of the genes selected from the group of genes encoding N-acetylmannosamine kinase, N-acetylmannosamine-6-phosphate epimerase, N-acetylneuraminic acid aldolase and sialic acid permease, in that the expression of one or more of these genes is impaired, or in that the nucleotide sequence of the protein coding region of at least one of these genes is amended such that the polypeptide encoded by said altered nucleotide sequence does not possess the enzymatic activity of the enzyme encoded by the non-amended nucleotide sequence.

4. The method according to any one of claims 1 to 3, wherein the activities of one or more of the enzymes of the non-naturally-occurring microorganism, the enzymes selected from the group consisting of N-acetylglucosamine-6-phsophate deacetylase and N-acetylglucosamine-6-phosphate deaminase, has been abolished.

5. The method according to any one of claims 1 to 4, wherein the non-naturally-occurring microorganism has been genetically engineered to abolish N-acetylglucosamine-6-phsophate deacetylase and/or N-acetylglucosamine-6-phosphate deaminase activity by deleting one or both genes encoding these enzymes, by impairing expression of one or both of these genes, or by mutating the protein-coding region of one or both genes such that the polypeptide being encoded by each altered nucleotide sequence does not possess the enzymatic activity of the enzyme encoded by the non-amended nucleotide sequence.

6. The method according to any one of claims 1 to 5, wherein at least one phosphoenolpyruvate (PEP)-dependent, sugar transporting phosphotransferase system for the import of a carbohydrate of the non-naturally-occurring microorganism has been disabled.

7. The method according to any one of claims 1 to 6, wherein the non-naturally-occurring microorganism comprises a saccharide/$H^+$ symporter, preferably a saccharide/$H^+$-symporter selected from the group consisting of a sucrose proton symporter, a lactose proton symporter and a glucose proton symporter.

8. The method according to any one of claims 1 to 7, wherein the non-naturally-occurring microorganism possesses an enhanced PEP biosynthesis as compared to the wild-type microorganism.

9. The method according to any one of claims 1 to 8, wherein the non-naturally-occurring microorganism does lacks one or more selected from the group consisting of a functional PEP carboxylase, a functional glutamate synthase, a functional WzxC protein, a functional UDP-glucose:undecaprenylphosphate glucose-1-phosphate transferase, a functional β-galactoside permease, a functional β-galactosidase, a functional YjhC protein, a functional fucose isomerase, a functional fuculokinase, and a functional *N*-acetylglutamine aminoacylase.

10. The method according to any one of claims 1 to 9, wherein the non-naturally-occurring microorganism possesses an enhanced glutamine synthesis as compared to the wild-type microorganism, preferably due to the overexpression of glutamine synthase.

11. The method according to claim 1, wherein the fermentation broth contains a carbon source for growing the non-naturally-occurring microorganism, the carbon source preferably being selected from the group consisting of glucose, xylose, sucrose, fructose, lactose, glycerol, syngas and combinations thereof.

12. Use of Neu5Ac as produced by a method according to any one of claims 1 to 11 for the manufacture of a nutritional composition.