CLAIMS

1. A genetically-modified or mutated bacterial strain generated using an isolated bacterial strain deposited under number VTT-E-193585, wherein said genetically-modified or mutated bacterial strain has retained the ability to grow using hydrogen gas as energy source and carbon dioxide as the only carbon source.

2. A culture comprising the bacterial strain according to claim 1.

3. A process for the production of biomass, said process comprising culturing the bacterial strain of claim 1, or an isolated bacterial strain deposited under number VTT-E-193585.

4. The process of claim 3, comprising culturing the bacterial strain with hydrogen as energy source and an inorganic carbon source, wherein the inorganic carbon source comprises carbon dioxide.

5. The process according to claim 4, wherein the culture has dissolved oxygen in the culture is maintained between 5% and 10%.

6. The process according to claim 4 or 5, wherein ammonium, urea, nitrate and/or nitrogen gas is used as nitrogen source.

7. The process according to any one of claims 4 to 6, wherein the culture medium comprises minerals wherein said minerals comprises less than 1 g/L of chloride salts.

8. The process according to any one of claims 4 to 7, wherein the medium does not contain vitamins.

9. The processing according to any one of claims 4 to 8, wherein pH in the culture is maintained between 5.5 and 8.0.

10. The process according to any one of claims 4 to 9, wherein said culture is grown at a temperature between 25°C and 40°C.

11. The process according to any one of claims 4 to 10, wherein the bacterial strain has a growth rate of 0.04-0.12 h^{-1}.

12. The process according to any one of claims 4 to 11, wherein the bacterial strain comprises the 16S ribosomal RNA set forth in SEQ ID NO:1 or a 16S ribosomal RNA having up to 20 nucleotide differences with SEQ ID NO:1, e.g. 1 to 10, such as 1 to 5, e.g. one, two, or three nucleotide differences with SEQ ID NO:1.

13. The process according to any one of claims 4 to 12, wherein the bacterial strain comprises:

i) a gene encoding ribulose-1,5-bisphosphate carboxylase/oxygenase (rubisco) large chain having the sequence set forth in SEQ ID NO:3 or a sequence having more than 93% identity to the sequence set forth in SEQ ID NO:3, and/or

ii) a gene encoding a ribulose-1,5-bisphosphate carboxylase/oxygenase (rubisco) small chain having the sequence set forth in SEQ ID NO:5 or a sequence having more than 83% sequence identity to the sequence set forth in SEQ ID NO:5, and/or

iii) a gene encoding a NAD^+-reducing hydrogenase HoxS subunit alpha having the sequence set forth in SEQ ID NO:7 or a sequence having more than 70% sequence identity to the sequence set forth in SEQ ID NO:7, and/or

iv) a gene encoding a NAD^+-reducing hydrogenase HoxS subunit beta having the sequence set forth in SEQ ID NO:9 or a sequence having more than 77% sequence identity, such as more than 80% identity, e.g. more than 90% identity to the sequence set forth in SEQ ID NO:9, and/or

v) a gene encoding a NAD^+-reducing hydrogenase HoxS subunit gamma having the sequence set forth in SEQ ID NO:11 or a sequence having more than 70% sequence identity to the sequence set forth in SEQ ID NO:11, and/or

vi) a gene encoding a NAD^+-reducing hydrogenase HoxS subunit delta having the sequence set forth in SEQ ID NO:13 or a sequence having more than 79% sequence identity to the sequence set forth in SEQ ID NO:13, and/or

vii) a gene encoding a NiFeSe hydrogenase large subunit having the sequence set forth in SEQ ID NO:15 or a sequence having more than 84% sequence identity to the sequence set forth in SEQ ID NO:15, and/or

viii) a gene encoding a NiFeSe hydrogenase small subunit having the sequence set forth in SEQ ID NO:17 or a sequence having more than 90% identity to the sequence set forth in SEQ ID NO:17, and/or

ix) a gene encoding an ATP synthase gamma chain atpG_1 having the sequence set forth in SEQ ID NO:19 or a sequence having more than 70% identity to the sequence set forth in SEQ ID NO:21, and/or

xi) a gene encoding an ATP synthase subunit b atpF_1 having the sequence set forth in SEQ ID NO:23 or a sequence having more than 62% identityto the sequence set forth in SEQ ID NO:23, and/or

xii) a gene encoding an ATP synthase subunit c, sodium ion specific atpE_1 having the sequence set forth in SEQ ID NO:25 or a sequence having more than 90% identity to the sequence set forth in SEQ ID NO:25, and/or

xiii) a gene encoding an ATP synthase subunit a atpB_1 having the sequence set forth in SEQ ID NO:27 or a sequence having more than 80% identity to the sequence set forth in SEQ ID NO:27, and/or

xiv) a gene encoding an ATP synthase epsilon chain atpC_1 having the sequence set forth in SEQ ID NO:29 or a sequence having more than 71% identity to the sequence set forth in SEQ ID NO:31, and/or

xvi) a gene encoding an ATP synthase subunit beta atpD_2 having the sequence set forth in SEQ ID NO:33 or a sequence having more than 97% identity to the sequence set forth in SEQ ID NO:33, and/or

xvii) a gene encoding an ATP synthase gamma chain atpG_2 having the sequence set forth in SEQ ID NO:35 or a sequence having more than 86% identity to the sequence set forth in SEQ ID NO:35, and/or

xviii) a gene encoding an ATP synthase subunit alpha atpA_2 having the sequence set forth in SEQ ID NO:37 or a sequence having more than 98%, to the sequence set forth in SEQ ID NO:37, and/or

xix) a gene encoding an ATP synthase subunit delta atpH having the sequence set forth in SEQ ID NO:39 or a sequence having more than 85% identity to the sequence set forth in SEQ ID NO:39, and/or

xx) a gene encoding an ATP synthase subunit b atpF_2 having the sequence set forth in SEQ ID NO:41 or a sequence having more than 87% identity to the sequence set forth in SEQ ID NO:41, and/or

xxi) a gene encoding an ATP synthase subunit b' atpG_3 having the sequence set forth in SEQ ID NO:43 or a sequence having more than 81% identity to the sequence set forth in SEQ ID NO:43, and/or

xxii) a gene encoding ATP synthase subunit c atpE_2 having the sequence set forth in SEQ ID NO:45 or a sequence having more than 98%to the sequence set forth in SEQ ID NO:45, and/or

xxiii) a gene encoding an ATP synthase subunit a atpB_2 having the sequence set forth in SEQ ID NO:47 or a sequence having more than 92% identity to the sequence set forth in SEQ ID NO:47, and/or

xiv) a gene encoding an ATP synthase protein I atpI having the sequence set forth in SEQ ID NO:49 or a sequence having more than 60% identity to the sequence set forth in SEQ ID NO:49, and/or

xv) a gene encoding a nitrogenase molybdenum-iron protein alpha chain nifD_1 having the sequence set forth in SEQ ID NO:51 or a sequence having more than 60% identity to the sequence set forth in SEQ ID NO:51, and/or

xvi) a gene encoding nitrogenase molybdenum-iron protein alpha chain nifD_2 having the sequence set forth in SEQ ID NO:53 or a sequence having more than 60% identity to the sequence set forth in SEQ ID NO:53, and/or

xvii) a gene encoding a nitrogenase molybdenum-iron protein beta chain nifK_1 having the sequence set forth in SEQ ID NO:55 or a sequence having more than 87% identity to the sequence set forth in SEQ ID NO:55, and/or

xviii) a gene encoding a nitrogenase molybdenum-iron protein beta chain nifK_2 having the sequence set forth in SEQ ID NO:57 or a sequence having more than 95% identity to the sequence set forth in SEQ ID NO:57, and/or

xxix) a gene encoding a nitrogenase iron protein nifH having the sequence set forth in SEQ ID NO:59 or a sequence having more than 98.5% sequence identity to the sequence set forth in SEQ ID NO:59, wherein the strain preferably comprises:

- the genes described in iii), iv), v) and vi),
- the genes described in vii) and viii), or
- the genes described in iii), iv), v), vi), vii) and viii).

14. The process according to any one of claims 4 to 13, comprising the further step of harvesting biomass produced during the culture, optionally comprising a further step of drying the biomass.

15. A process for the production of protein, comprising performing the process according to claim 14 and a further step of isolating protein from said biomass, wherein the process results in a protein fraction and a fraction comprising non-protein components.

16. The process according to claim 14 or 15, comprising the further step of producing a food or feed product from said biomass, from said protein fraction or from said fraction comprising non-protein components.