CLAIMS

~~1. An isolated bacterial strain VTT-E-193585 or genetically modified or mutated strain generated using bacterial strain VTT-E-193585, wherein said genetically modified or mutated 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~~1. A process for the production of biomass, said process comprising culturing an isolated strain ~~the~~ bacterial strain ~~of claim 1~~ VTT-E-193585 or a derivative thereof with hydrogen as energy source and an inorganic carbon source, wherein the inorganic carbon source comprises carbon dioxide, and wherein said derivative has retained the ability to grow using hydrogen gas as energy source and carbon dioxide as the only carbon source.

~~4~~2. The process according to claim ~~3~~ 1, ~~comprising~~ wherein culturing the bacterial strain or derivative thereof is by ~~in~~ continuous culture ~~with hydrogen as energy source and an inorganic carbon source, wherein the inorganic carbon source comprises carbon dioxide~~.

3. A process for the production of biomass, said process comprising culturing a bacterial strain of the genus *Xanthobacter* in continuous culture with hydrogen as energy source and an inorganic carbon source, wherein the inorganic carbon source comprises carbon dioxide.

~~5~~4. The process according to claim ~~4~~ 2, wherein the continuous culture has dissolved oxygen ~~in the culture~~ which is maintained between 5% and 10%.

~~6~~5. The process according to ~~any one of~~ claim~~s 4 or 5~~ 2, wherein ammonium, urea, nitrate and/or nitrogen gas is used as nitrogen source.

~~7~~6. The process according to ~~any of~~ claim~~s 4 to 6~~ 2, wherein the ~~culture~~ medium in the continuous culture comprises minerals wherein said minerals comprises less than 1 g/L of chloride salts~~, such as less than 0.25 g/L of chloride salts, e.g. less than 0.1 g/l of chloride salts, preferably no chloride salts~~.

~~8~~7. The process according to ~~any one of~~ claim~~s 4 to 7~~ 2, wherein the ~~culture~~ medium in the continuous culture does not contain vitamins.

~~9~~8. The processing according to ~~any one of~~ claim~~s 4 to 8~~ 2, wherein pH in the continunous culture is maintained between 5.5 and 8.0~~, e.g. between 6.5 and 7.0, such as at 6.8~~.

~~10~~9. The process according to ~~any one of~~ claim~~s 4 to 9~~ 2, wherein said continuous culture is grown at a temperature between 25°C and 40°C~~, e.g. between 28°C and 32°C, such as at 30°C~~.

~~11~~10. The process according to ~~any one of~~ claim~~s 4 to10~~ 2, wherein the bacterial strain has a growth rate of 0.04-0.12 h^{-1}.

11. The process according to claim 4, wherein the bacterial strain is VTT-E-193585 or *X. tagetidis*.

12. The process according to ~~any one of~~ claim~~s 4 to 11~~ 2, 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~~ claim~~s 4 to12~~ 2, 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~~, e.g. more than 95% identity, such as more than 96% identity, e.g. more than 97% identity, such as more than 98% identity, e.g. more than 99% sequence 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~~, e.g. more than 86%, identity such as more than 90% identity, e.g. more than 95% identity, such as more than 96% identity, e.g. more than 97% identity, such as more than 98% identity, e.g. more than 99% 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~~, such as more than 80% identity, e.g. more than 90% identity, such as more than 95% identity, e.g. more than 96% identity, such as more than 97% identity, e.g. more than 98%, such as more than 99% 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~~, such as more than 95% identity, e.g. more than 96% identity, such as more than 97% identity, e.g. more than 98%, such as more than 99% sequence 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~~, such as more than 80% identity, e.g. more than 90% identity, such as more than 95% identity, e.g. more than 96% identity, such as more than 97% identity, e.g.~~

5

more than 98%, such as more than 99% 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, such as more than 80% identity, e.g. more than 90% identity, such as more than 95% identity, e.g. more than 96% identity, such as more than 97% identity, e.g. more than 98%, such as more than 99% 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, e.g. more than 90% identity, such as more than 95% identity, e.g. more than 96% identity, such as more than 97% identity, e.g. more than 98%, such as more than 99% 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, such as more than 95% identity, e.g. more than 96% identity, such as more than 97% identity, e.g. more than 98%, such as more than 99% sequence 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, such as more than 80% identity, e.g. more than 90% identity, such as more than 95% identity, e.g. more than 96% identity, such as more than 97% identity, e.g. more than 98%, such as more than 99% sequence identity to the sequence set forth in SEQ ID NO:19, and/or

x) a gene encoding an ATP synthase subunit alpha atpA_1 having the sequence set forth in SEQ ID NO:21 or a sequence having more than 78% identity, such as more than 80% identity, e.g. more than 90% identity, such as more than 95% identity, e.g. more than 96% identity, such as more than 97% identity, e.g. more than 98%, such as more than 99% sequence 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% identity, e.g. more than 70% identity, such as more than 80% identity, e.g. more than 90% identity, such as more than 95% identity, e.g. more than 96% identity, such as more than 97% identity, e.g. more than 98%, such as more than 99% sequence identity to 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, such as more than 95% identity, e.g. more than 96% identity, such as more than 97%

identity, e.g. more than 98%, such as more than 99% sequence 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, e.g. more than 90% identity, such as more than 95% identity, e.g. more than 96% identity, such as more than 97% identity, e.g. more than 98%, such as more than 99% sequence 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, such as more than 80% identity, e.g. more than 90% identity, such as more than 95% identity, e.g. more than 96% identity, such as more than 97% identity, e.g. more than 98%, such as more than 99% sequence identity to the sequence set forth in SEQ ID NO:29, and/or

xv) a gene encoding an ATP synthase subunit beta atpD_1 having the sequence set forth in SEQ ID NO:31 or a sequence having more than 84% identity, e.g. more than 90% identity, such as more than 95% identity, e.g. more than 96% identity, such as more than 97% identity, e.g. more than 98%, such as more than 99% sequence 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, e.g. more than 98%, such as more than 99% sequence 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, e.g. more than 90% identity, such as more than 95% identity, e.g. more than 96% identity, such as more than 97% identity, e.g. more than 98%, such as more than 99% sequence 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%, such as more than 99% sequence identity 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, e.g. more than 90% identity, such as more than 95% identity, e.g. more than 96% identity, such as more than 97% identity, e.g. more than 98%, such as more than 99% sequence 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, e.g. more than 90% identity, such as more than 95% identity, e.g. more than 96% identity, such as more

~~than 97% identity, e.g. more than 98%, such as more than 99% sequence 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~~, e.g. more than 90% identity, such as more than 95% identity, e.g. more than 96% identity, such as more than 97% identity, e.g. more than 98%, such as more than 99% sequence 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%~~, such as more than 99% sequence identity~~ 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~~, such as more than 95% identity, e.g. more than 96% identity, such as more than 97% identity, e.g. more than 98%, such as more than 99% sequence 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~~, e.g. more than 70% identity, such as more than 80% identity, e.g. more than 90% identity, such as more than 95% identity, e.g. more than 96% identity, such as more than 97% identity, e.g. more than 98%, such as more than 99% sequence 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~~, e.g. more than 70% identity, such as more than 92% identity, such as more than 95% identity, e.g. more than 96% identity, such as more than 97% identity, e.g. more than 98%, such as more than 99% sequence 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~~, e.g. more than 98%, such as more than 99% sequence 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~~, e.g. more than 90% identity, such as more than 95% identity, e.g. more than 96% identity, such as more than 97% identity, e.g. more than 98%, such as more than 99% sequence 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~~, e.g. more than 96% identity, such as more than 97% identity, e.g. more than 98%, such as more than 99% sequence 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~~ claim~~s 4 to 13~~ 2, comprising the further step of harvesting biomass produced during the continuous 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.

17. A product, such as biomass, protein, or non-protein components obtained or ~~product containing cellular material, wherein said biomass is~~ obtainable by the process according to ~~any one of~~ claim~~s 4 to 16~~ 2.

18. A food or feed product obtained or obtainable by the process according to claim 16.