CLAIMS

1. A yeast comprising a nucleotide sequence expression system expressing a synthetic Calvin cycle, comprising

a) a gene encoding an enzyme from the class of the ribulose-bisphosphate carboxylases (EC number: 4.1.1.39) (*RuBisCO* gene); and

b) a gene encoding an enzyme from the class of the ribulose phosphate kinases (EC number: 2.7.1.19) (*PRK* gene);

wherein said *RuBisCO* gene and *PRK* gene are heterologous and wherein each of said *RuBisCO* gene and said *PRK* gene is fused with a nucleotide sequence encoding a peroxisomal targeting signal (PTS);

and wherein the nucleotide sequence expression system further expresses

c) a gene encoding an enzyme from the class of the phosphoglycerate kinases (EC number: 2.7.2.3) (*PGK1* gene);

d) a gene encoding an enzyme from the class of the glyceraldehyde-3-phosphate dehydrogenases (EC number 1.2.1.12) (*TDH3* gene);

e) a gene encoding an enzyme from the class of the triose-phosphate isomerases (EC number 5.3.1.1) (*TPI1* gene), and

f) a gene encoding an enzyme from the class of the transketolases (EC number 2.2.1.1) (*TKL1* gene).

2. The yeast of claim 1, further comprising a heterologous expression construct expressing a gene of interest (GOI).

3. The yeast of claim 1 or 2, wherein the synthetic Calvin cycle comprises one or more further heterologous genes, which are any of:

a) the gene encoding an enzyme from the class of the phosphoglycerate kinases (EC number: 2.7.2.3) (*PGK1* gene), and/or

b) the gene encoding an enzyme from the class of the glyceraldehyde-3-phosphate dehydrogenases (EC number 1.2.1.12) (*TDH3* gene); and/or

c) the gene encoding an enzyme from the class of the triose-phosphate isomerases (EC number 5.3.1.1) (*TPI1* gene); and/or

d) the gene encoding an enzyme from the class of the transketolases (EC number 2.2.1.1) (*TKL1* gene),

optionally wherein one or more, or each of said *PGK1*, *TDH3*, *TPI1*, and *TKL1* genes is/are fused with a nucleotide sequence encoding a PTS.

4. The yeast of claim 3, wherein the synthetic Calvin cycle comprises the following heterologous genes: said *RuBisCO* gene, said *PRK* gene, said *PGK1* gene, said *TDH3* gene, said *TPI1* gene, and said *TKL1* gene.

5. The yeast of any of claims 1 to 4, wherein

a) said *RuBisCO* gene is of *Thiobacillus denitrificans* origin, preferably comprising the nucleotide sequence identified as SEQ ID NO:37, or a functionally active variant thereof with at least 90% sequence identity expressing a ribulose-bisphosphate carboxylase; and/or

b) said *PRK* gene is of *Spinacia oleracea* origin, preferably comprising the nucleotide sequence identified as SEQ ID NO:38, or a functionally active variant thereof with at least 90% sequence identity expressing a ribulose phosphate kinase; and/or

c) said *PGK1* gene is of *Ogataea polymorpha* origin, preferably comprising the nucleotide sequence identified as SEQ ID NO:39, or a functionally active variant thereof with at least 90% sequence identity expressing a phosphoglycerate kinase; and/or

d) said *TDH3* gene is of *Ogataea polymorpha* origin, preferably comprising the nucleotide sequence identified as SEQ ID NO:40, or a functionally active variant thereof with at least 90% sequence identity expressing a glyceraldehyde-3-phosphate dehydrogenase; and/or

e) said *TPI1* gene is of *Ogataea parapolymorpha* origin, preferably comprising the nucleotide sequence identified as SEQ ID NO:41, or a functionally active variant thereof with at least 90% sequence identity expressing a triose-phosphate isomerase; and/or; and/or

f) said *TKL1* gene is of *Ogataea parapolymorpha* origin, preferably comprising the nucleotide sequence identified as SEQ ID NO:42, or a functionally active variant thereof with at least 90% sequence identity expressing a transketolase.

6. The yeast of any of claims 1 to 5, which comprises further heterologous genes expressing one or more molecular chaperones in the cytosol of said yeast, which chaperones assist the covalent folding and/or assembly of at least one of said enzymes.

7. The yeast of claim 6, wherein said chaperones are at least

a) *GroEL* of *Escherichia coli* origin, preferably encoded by a nucleotide sequence identified as SEQ ID NO:43, or a functionally active variant thereof with at least 90% sequence identity expressing a molecular chaperone; and

b) *GroES*, of *Escherichia coli* origin, preferably encoded by a nucleotide sequence identified as SEQ ID NO:8, or a functionally active variant thereof with at least 90% sequence identity expressing a molecular chaperone.

8. The yeast of any of claims 1 to 7, wherein one or more of said heterologous genes of the synthetic Calvin cycle are codon-optimized for expression in said yeast.

9. The yeast of any of claims 1 to 8, which is of the genus selected from the group consisting of *Pichia, Komagataella, Hansenula, Ogataea, Candida,* and *Torulopsis*, preferably selected from the group consisting of *Pichia pastoris Komagataella pastoris*, *K. phaffii*, and *K. pseudopastoris*.

10. A method of culturing the yeast of any of claims 1 to 9 in a cell culture, comprising culturing the yeast in the growing phase using gaseous carbon dioxide and/or dissolved CO_3^{2-} and/or HCO_3^- compounds as a carbon source, thereby obtaining accumulated yeast biomass in the cell culture.

11. The method of claim 10, wherein the yeast incorporates said heterologous genes operably linked to a promoter, which is inducible by methanol, and wherein said growing phase starts upon adding methanol to the culture medium.

12. The method of claim 10 or 11, which further comprises culturing said accumulated yeast biomass in a production phase using a carbon source to produce a protein of interest (POI) and/or metabolite, respectively.

13. Use of a yeast of any of claims 1 to 9 for producing a POI and/or metabolite using a carbon source which is gaseous carbon dioxide and/or dissolved CO_3^{2-} and/or HCO_3^- compounds.