What is claimed is:

1. A genetically modified microorganism capable of converting a C1 carbon to 2,3-BDO, wherein the microorganism is from the species *Methylococcus capsulatus* and comprises at least one heterologous gene encoding: i) an acetoin reductase; ii) an alpha-acetolactate decarboxylase; and/or iii) an acetolactate synthase.

2. The microorganism of claim 1, wherein the heterologous gene(s) is/are integrated by an integration vector into the genome of said microorganism.

3. The microorganism of claim 1, wherein the heterologous gene(s) is/are expressed on an episomal vector.

4. The microorganism of claim 1 comprising:

(a) a heterologous gene encoding acetolactate synthase that is 5' in relation to any other heterologous gene;

(b) a heterologous gene encoding acetoin reductase that is 3' in relation to any other heterologous gene; and/or

(c) a heterologous gene encoding alpha-acetolactate decarboxylase that is neither 5' or 3' in relation to any other heterologous gene.

5. The microorganism of claim 1, wherein the heterologous gene(s) is/are under the control of a switch.

6. The microorganism of claim 1, wherein: (i) the acetolactate synthase comprises an amino acid sequence at least 90% identical to any one of SEQ ID NOs: 1, 3, or 19; (ii) the alpha-acetolactate decarboxylase comprises an amino acid sequence at least 90% identical to SEQ ID NO: 5 or 7; and/or (iii) the acetoin reductase comprises an amino acid sequence at least 90% identical to any one of SEQ ID NO: 9, 11, or 13.

7. The microorganism of claim 1, comprising: (i) a heterologous acetoin reductase; (ii) a heterologous alpha-acetolactate decarboxylase; and/or (iii) a heterologous acetolactate synthase.

8. The microorganism of claim 7, wherein the acetolactate synthase is non-constitutively expressed.

9. The microorganism of claim 7, wherein: (i) the acetolactate synthase comprises an amino acid sequence that is at least 90% identical to SEQ ID NO: 1 or 19; (ii) the alpha-acetolactate decarboxylase comprises an amino acid sequence that is at least 90% identical to SEQ ID NO: 7; and/or (iii) the acetoin reductase comprises an amino acid sequence that is at least 90% identical to SEQ ID NO: 9.

10. The microorganism of claim 7, wherein the acetoin reductase is NADPH-dependent.

11. A method of making the microorganism of claim 1, the method comprising transforming the microorganism with a heterologous nucleic acid comprising a gene encoding an acetoin reductase, an alpha-acetolactate decarboxylase, and/or an acetolactate synthase.

12. A method of making 2,3-BDO, the method comprising:
a) contacting the microorganism of claim 1 with a C1 carbon; and
b) growing the microorganism to produce 2,3-BDO.

13. The method of claim 12, wherein the C1 carbon is methane.

14. The method of claim 12, wherein the microorganism is grown at a temperature between 32 °C and 49 °C.

15. The method of claim 12, further comprising contacting the microorganism with media containing at least 1 μM lanthanum before growing the microorganism to produce 2,3-BDO.

16. The method of claim 15, further comprising diluting the lanthanum in media before growing the microorganism to produce 2,3-BDO.

17. The method of claim 12, wherein the microorganism comprises a heterologous gene encoding alpha-acetolactate decarboxylase and is grown to produce acetoin.

18. The method of claim 12, further comprising contacting the 2,3-BDO with a catalyst to produce butadiene or methyl ethyl ketone.