

CLAIMS

1. A microorganism capable of producing 2-phenylethanol, wherein the microorganism comprises:
 - 5 (a) a heterologous enzyme that converts phenylpyruvate to phenylacetaldehyde; and
 - (b) a heterologous enzyme that converts phenylacetaldehyde to 2-phenylethanol.
2. The microorganism of claim 1, wherein:
 - 10 (a) the heterologous enzyme that converts phenylpyruvate to phenylacetaldehyde is decarboxylase; and
 - (b) the heterologous enzyme that converts phenylacetaldehyde to 2-phenylethanol is phenylacetaldehyde reductase.
- 15 3. The microorganism of claim 2, wherein the decarboxylase is a phenylpyruvate-specific decarboxylase.
4. The microorganism of claim 1, wherein the microorganism is a C1-fixing microorganism.
- 20 5. The microorganism of claim 1, wherein the microorganism is a Wood-Ljungdahl microorganism.
6. The microorganism of claim 1, wherein the microorganism is a bacterium.
- 25 7. The microorganism of claim 1, wherein the microorganism is a member of a genus selected from the group consisting of *Acetobacterium*, *Alkalibaculum*, *Blautia*, *Butyrivacterium*, *Clostridium*, *Eubacterium*, *Moorella*, *Oxobacter*, *Sporomusa*, and *Thermoanaerobacter*.
- 30 8. The microorganism of claim 1, wherein the microorganism is natively capable of producing phenylpyruvate.

9. The microorganism of claim 1, wherein the microorganism comprises a Wood-Ljungdahl pathway that converts CO, CO₂, and/or H₂ to acetyl-CoA.
10. The microorganism of claim 1, wherein the microorganism comprises one or more of:
- 5 (c) a native enzyme that converts acetyl-CoA to pyruvate;
 - (d) a native enzyme that converts pyruvate to phosphoenolpyruvate;
 - (e) a native enzyme that converts phosphoenolpyruvate and erythrose-4-phosphate to 2-dehydro-3-deoxy-D-arabino-heptonate 7-phosphate;
 - (f) a native enzyme that converts 2-dehydro-3-deoxy-D-arabino-heptonate 7-phosphate to 3-dehydroquinate;
 - 10 (g) a native enzyme that converts 3-dehydroquinate to 3-dehydroshikimate;
 - (h) a native enzyme that converts 3-dehydroshikimate to shikimate;
 - (i) a native enzyme that converts shikimate to shikimate 3-phosphate;
 - (j) a native enzyme that converts shikimate 3-phosphate to 5-O-(1-carboxyvinyl)-shikimate 3-phosphate;
 - 15 (k) a native enzyme that converts 5-O-(1-carboxyvinyl)-shikimate 3-phosphate to chorismate; or
 - (l) a native enzyme that converts chorismate to phenylpyruvate.
- 20 11. The microorganism of claim 10, wherein:
- (c) the native enzyme that converts acetyl-CoA to pyruvate is pyruvate:ferredoxin oxidoreductase;
 - (d) the native enzyme that converts pyruvate to phosphoenolpyruvate is pyruvate phosphate dikinase;
 - 25 (e) the native enzyme that converts phosphoenolpyruvate and erythrose-4-phosphate to 2-dehydro-3-deoxy-D-arabino-heptonate 7-phosphate is 2-dehydro-3-deoxy-D-arabino-heptonate 7-phosphate synthase;
 - (f) the native enzyme that converts 2-dehydro-3-deoxy-D-arabino-heptonate 7-phosphate to 3-dehydroquinate is 3-dehydroquinase synthase;
 - 30 (g) the native enzyme that converts 3-dehydroquinase to 3-dehydroshikimate is 3-dehydroquinase dehydratase;
 - (h) the native enzyme that converts 3-dehydroshikimate to shikimate is shikimate dehydrogenase;

- (i) the native enzyme that converts shikimate to shikimate 3-phosphate is shikimate kinase;
- (j) the native enzyme that converts shikimate 3-phosphate to 5-O-(1-carboxyvinyl)-shikimate 3-phosphate is 5-enolpyruvylshikimate 3-phosphate synthase;
- (k) the native enzyme that converts 5-O-(1-carboxyvinyl)-shikimate 3-phosphate to chorismate is chorismate synthase; or
- (l) the native enzyme that converts chorismate to phenylpyruvate is bi-functional chorismate mutase/prephenate dehydratase.

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12. The microorganism of claim 1, wherein the microorganism further comprises one or more of:

- (e) a heterologous enzyme that converts phosphoenolpyruvate and erythrose-4-phosphate to 2-dehydro-3-deoxy-D-arabino-heptonate 7-phosphate;
- (h) a heterologous enzyme that converts 3-dehydroshikimate to shikimate; or
- (l) a heterologous enzyme that converts chorismate to phenylpyruvate.

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13. The microorganism of claim 12, wherein:

- (e) the heterologous enzyme that converts phosphoenolpyruvate and erythrose-4-phosphate to 2-dehydro-3-deoxy-D-arabino-heptonate 7-phosphate is 2-dehydro-3-deoxy-D-arabino-heptonate 7-phosphate synthase;
- (h) the heterologous enzyme that converts 3-dehydroshikimate to shikimate is shikimate dehydrogenase; or
- (l) the heterologous enzyme that converts chorismate to phenylpyruvate is bi-functional chorismate mutase/prephenate dehydratase.

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14. The microorganism of any one of claims 1-13, wherein the microorganism comprises:

- (1) ecAroE, kivD, lePAR, pheA2, and aroG;
- (2) ecAroE, abPPDC, ecPAR, pheA1, and aroG;
- (3) cgAroE, abPPDC, lePAR, pheA2, and aroG;
- (4) ecAroE, abPPDC, lePAR, pheA2, and aroG;
- (5) cgAroE, kivD, rrPAR, pheA2, and aroG;
- (6) ecAroE, abPPDC, lePAR, pheA2, and aroG;
- (7) pheA1, aroG, abPPDC, and ecPAR;

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- 5 (8) egAroE, abPPDC, lePAR, pheA1, and aroG;
 (9) ecAroE, abPPDC, ecPAR, pheA2, and aroG;
 (10) cgAroE, aro10, ecPAR, pheA2, and aroG;
 (11) cgAroE, abPPDC, lePAR, pheA1, and aroG;
 (12) cgAroE, aro10, lePAR, pheA2, and aroG;
 (13) ecAroE, abPPDC, lePAR, pheA1, and aroG;
 (14) ecAroE, aro10, ecPAR, pheA2, and aroG;
 (15) ecAroE, aro10, lePAR, pheA2, and aroG;
 (16) cgAroE, abPPDC, lePAR, pheA1, and aroG;
 10 (17) cgAroE, aro10, rsPAR, pheA2, and aroG;
 (18) cgAroE, abPPDC, blPAR, pheA2, and aroG;
 (19) ecAroE, kivD, blPAR, pheA2, and aroG;
 (20) cgAroE, aro10, blPAR, pheA2, and aroG;
 (21) ecAroE, abPPDC, blPAR, pheA2, and aroG;
 15 (22) ecAroE, abPPDC, adh6, pheA1, and aroG;
 (23) cgAroE, abPPDC, adh6, pheA2, and aroG;
 (24) cgAroE, abPPDC, ecPAR, pheA2, and aroG;
 (25) ecAroE, aro10, rsPAR, pheA2, and aroG;
 (26) ecAroE, aro10, adh6, pheA2, and aroG; or
 20 (27) ecAroE, abPPDC, ecPAR, pheA2, and aroG.

15. The microorganism of any one of claims 1-14, wherein the microorganism comprises the heterologous genes and promoters of combinatorial strain 2C03, 1C10, 2C54, 2C09, 2C47, 2C55, 2C53, H57, 1C47, 2C10, 2A18, 1C54, 2C01, 1C31, 2B17, 2C52, 1C09, H18,
 25 H58, 2C27, 2D22, 2D07, 2D24, 2D03, 1C29, 2B26, 2C38, 2A27, 2C12, or 2B27.

16. The microorganism of any one of claims 1-15, wherein the microorganism ferments a gaseous substrate comprising CO, CO₂, and/or H₂ to produce 2-phenylethanol.

30 17. The microorganism of claim 16, wherein the gaseous substrate comprises syngas or industrial waste gas.

18. The microorganism of claim 16, wherein the microorganism does not produce any other C₃+ alcohols.

19. The microorganism of claim 18, wherein the microorganism does not produce any other C3, C4, C5, C6, C7, C8, C9, or C10 alcohols.
20. A method of producing 2-phenylethanol comprising culturing the microorganism of
5 any one of claims 1-17 in the presence of a gaseous substrate.
21. The method of claim 20, wherein the gaseous substrate comprises a C1-carbon source comprising CO, CO₂, and/or H₂.
- 10 22. The method of any one of claims 20-22, wherein the gaseous substrate comprises syngas or industrial waste gas.