

WHAT IS CLAIMED IS:

1. A recombinant microorganism comprising two or more copies of a nucleic acid sequence encoding xylose isomerase, wherein the nucleic acid encoding xylose isomerase is an exogenous nucleic acid.
2. The recombinant microorganism of claim 1, further comprising at least one nucleic acid sequence encoding a xylulose kinase.
3. The recombinant microorganism of claim 2, wherein the nucleic acid sequence encoding the xylulose kinase is an exogenous nucleic acid sequence.
4. The recombinant microorganism of any one of claims 1-3, further comprising at least one nucleic acid sequence encoding a xylose transporter.
5. The recombinant microorganism of claim 4, wherein the nucleic acid sequence encoding the xylose transporter is an exogenous nucleic acid sequence.
6. The recombinant microorganism of claim 1, wherein the microorganism further comprises at least two or more copies of a nucleic acid sequence encoding a xylulose kinase and at least one nucleic acid sequence encoding a xylose transporter.
7. The recombinant microorganism of any one of claims 1-6, wherein the nucleic acid sequence encoding the xylose isomerase is a heterologous nucleic acid.
8. The recombinant microorganism of any one of claims 1-7, wherein the microorganism comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 copies of the exogenous nucleic acid sequence encoding xylose isomerase.
9. The recombinant microorganism of any one of claims 1-8, wherein the heterologous nucleic acid sequence encoding the xylose isomerase is at least 90% identical to SEQ ID NO:2.
10. The recombinant microorganism of any one of claims 2-9, wherein the microorganism comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 copies of the nucleic acid sequence encoding the xylulose kinase.
11. The recombinant microorganism of any one of claims 4-10, wherein the nucleic acid sequence encoding xylulose kinase is a heterologous nucleic acid.
12. The recombinant microorganism of claim 11, wherein the heterologous nucleic acid sequence encoding the xylulose kinase is at least 90% identical to SEQ ID NO:5.

13. The recombinant microorganism of any one of claims 5-12, wherein the microorganism comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 copies of the nucleic acid sequence encoding the xylose transporter.
14. The recombinant microorganism of any one of claims 5-13, wherein the nucleic acid encoding the xylose transporter is a heterologous nucleic acid.
15. The recombinant microorganism of claim 14, wherein the xylose transporter encoded by the heterologous nucleic acid is GXS1 from *Candida intermedia*.
16. The recombinant microorganism of claim 14, wherein the heterologous nucleic acid sequence encoding the xylose transporter is at least 90% identical to SEQ ID NO:23.
17. The recombinant microorganism of any one of claims 1-16, wherein the recombinant microorganism has increased xylose transport activity as compared to a non-recombinant control microorganism, increased xylose isomerase activity as compared to a non-recombinant control microorganism, increased xylulose kinase activity as compared to a non-recombinant control microorganism, or any combination thereof.
18. The recombinant microorganism of any one of claims 1-17, wherein the recombinant microorganism grows with xylose as the sole carbon source.
19. The recombinant microorganism of any one of claims 1-18, wherein the exogenous nucleic acid sequence encoding the xylose isomerase is operably linked to a promoter.
20. The recombinant microorganism of any one of claims 11-19, wherein the nucleic acid sequence encoding the xylulose kinase is operably linked to a promoter.
21. The recombinant microorganism of any one of claims 14-20, wherein the nucleic acid sequence encoding the xylose transporter is operably linked to a promoter.
22. The recombinant microorganism of any one of claims 19-21, wherein the promoter is a tubulin promoter.
23. The recombinant microorganism of claim 22, wherein the promoter is at least 80% identical to SEQ ID NO:25 or SEQ ID NO:26.
24. The recombinant microorganism of any one of claims 1-23, wherein the exogenous nucleic acid sequence encoding the xylose isomerase comprises a terminator.
25. The recombinant microorganism of any one of claims 11-24, wherein the nucleic acid sequence encoding the xylulose kinase comprises a terminator.

26. The recombinant microorganism of any one of claims 14-25, wherein the nucleic acid sequence encoding the xylose transporter comprises a terminator.
27. The recombinant microorganism of any one of claims 24-26, wherein the terminator is a tubulin terminator.
28. The recombinant microorganism of claim 27, wherein the terminator is at least 80% identical to SEQ ID NO:27, SEQ ID NO:28, or SEQ ID NO:30.
29. The recombinant microorganism of any one of claims 1-28, wherein the microorganism further comprises a selectable marker.
30. The recombinant microorganism of claim 29, wherein the selectable marker is an antibiotic resistance gene.
31. The recombinant microorganism of claim 30, wherein the antibiotic is zeocin, hygromycin B, kanamycin or neomycin.
32. The recombinant microorganism of any one of claims 1-31, wherein the microorganism is either a *Thraustochytrium* or a *Schizochytrium* microorganism.
33. The recombinant microorganism of claim 32, wherein the microorganism is ONC-T18.
34. A method of making a recombinant xylose-metabolizing microorganism comprising:
- providing one or more nucleic acid constructs comprising a nucleic acid sequence encoding a xylose isomerase, a nucleic acid sequence encoding a xylulose kinase and a nucleic acid sequence encoding a xylose transporter;
 - transforming the microorganism with the one or more nucleic acid constructs;
 - and
 - isolating microorganisms comprising at least two or more copies of the nucleic acid sequences encoding the xylose isomerase.
35. The method of claim 34, further comprising isolating microorganisms comprising at least one copy of the nucleic acid sequence encoding the xylulose kinase.
36. The method of claim 35, isolating microorganisms comprising at least one copy of the xylose transporter.
37. The method of any one of claims 34-36, wherein one or more nucleic acid constructs further comprises a selectable marker.
38. The method of any one of claims 34-37, wherein the providing comprises providing a first nucleic acid construct comprising a nucleic acid sequence encoding a xylose isomerase, a second nucleic acid construct comprising a nucleic acid sequence encoding a

xylulose kinase and a third nucleic acid construct comprising a nucleic acid sequence encoding a xylose transporter;

39. The method of claim 38, wherein the first, second and third nucleic acid constructs comprise the same selectable marker.

40. The method of claim 38 or 39, wherein the first nucleic acid construct comprises a promoter, a selectable marker, a nucleic acid sequence encoding a 2A peptide, the nucleic acid sequence encoding the xylose isomerase, and a terminator.

41. The method of any one of claims 38-40, wherein the second nucleic acid construct comprises a promoter, selectable marker, a nucleic acid sequence encoding a 2A peptide, the nucleic acid sequence encoding the xylulose kinase, and a terminator.

42. The method of any one of claims 38-41, wherein the third nucleic acid construct comprises a promoter, the nucleic acid sequence encoding the xylose transporter, a nucleic acid sequence encoding a 2A peptide, a selectable marker, and a terminator.

43. The method of any one of claims 37-42, wherein the selectable marker is an antibiotic resistance gene.

44. The method of claim 43, wherein the antibiotic is zeocin, hygromycin B, kanamycin or neomycin.

45. The method of any one of claims 40-44, wherein the promoter is a tubulin promoter.

46. The method of claim 45, wherein the promoter is at least 80% identical to SEQ ID NO:25 or SEQ ID NO:26.

47. The method of any one of claims 40-46, wherein the terminator is a tubulin terminator.

48. The method of claim 47, wherein the terminator is at least 80% identical to SEQ ID NO:27, SEQ ID NO:28, or SEQ ID NO:30.

49. The method of any one of claims 34-48, wherein the isolated recombinant microorganism comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 copies of the exogenous nucleic acid sequence encoding xylose isomerase.

50. The method of any one of claims 34-49, wherein the xylose isomerase is a heterologous xylose isomerase.

51. The method of any one of claims 34-49, wherein the nucleic acid sequence encoding the xylose isomerase is at least 90% identical to SEQ ID NO:2.

52. The method of any one of claims 34-51, wherein the isolated recombinant microorganism comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 copies of the nucleic acid sequence encoding the xylulose kinase.

53. The method of any one of claims 34-52, wherein the xylulose kinase is a heterologous xylulose kinase.

54. The method of any one of claims 34-52, wherein the nucleic acid sequence encoding the xylulose kinase is at least 90% identical to SEQ ID NO:5.

55. The method of any one of claims 34-54, wherein the isolated recombinant microorganism comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 copies of the nucleic acid sequence encoding the xylose transporter.

56. The method of any one of claims 34-55, wherein the xylose transporter is a heterologous xylose transporter.

57. The method of any one of claims 34-56, wherein the xylose transporter is GXS1 from *Candida intermedia*.

58. The method of any one of claims 34-56, wherein the nucleic acid sequence encoding the xylose transporter is at least 90% identical to SEQ ID NO:23.

59. The method of any one of claims 34-58, wherein the isolated recombinant microorganism has increased xylose transport activity as compared to a control non-recombinant microorganism, increased xylose isomerase activity as compared to a control non-recombinant microorganism, increased xylulose kinase activity as compared to a control non-recombinant microorganism, or a combination thereof.

60. The method of any one of claims 34-59, wherein the isolated recombinant microorganism grows with xylose as the sole carbon source.

61. The method of any one of claims 34-60, wherein the microorganism is either a *Thraustochytrium* or a *Schizochytrium* microorganism.

62. The method of any one of claims 34-60, wherein the microorganism is ONC-T18.

63. A method of producing oil comprising
providing the recombinant microorganism of any one of claims 1-33, wherein the microorganism grows on xylose as the sole carbon source, and
culturing the microorganism in a culture medium under suitable conditions to produce the oil.

64. The method of claim 63, wherein the oil comprises triglycerides.
65. The method of claim 63, wherein the oil comprises alpha linolenic acid, arachidonic acid, docosahexanoic acid, docosapentaenoic acid, eicosapentaenoic acid, gamma-linolenic acid, linoleic acid, linolenic acid, or a combination thereof.
66. The method of claim 63, further comprising isolating the oil.