CLAIMS

1. A method for producing a glycosylated product from glycoside intermediates, comprising:

providing a microbial cell expressing one or more UDP-dependent glycosyl transferase enzymes intracellularly,

incubating the microbial strain with the glycoside intermediates, and

recovering the glycosylated product.

2. The method of claim 1, wherein the glycoside intermediates are provided as a plant extract or fraction thereof.

3. The method of claim 1, wherein the glycoside intermediate is a glycosylated secondary metabolite, optionally selected from a glycosylated terpenoid, a glycosylated flavonoid, a glycosylated cannabinoid, a glycosylated polyketide, a glycosylated stilbenoid, and a glycosylated polyphenol.

4. The method of claim 3, wherein the glycoside intermediate is a glycosylated terpenoid.

5. The method of claim 4, wherein the glycoside intermediate is steviol glycoside or mogroside.

6. The method of any one of claims 1, wherein the glycoside intermediate has one, two, three, four, or five glycosyl groups.

7. The method of claim 6, wherein the glycosyl groups are independently selected from glucosyl, galactosyl, mannosyl, xylosyl, and rhamnosyl groups.

8. The method of claim 6, wherein the glycosylated product has at least five glycosyl groups, or at least six glycosyl groups.

9. The method of claim 8, wherein the glycosylated product has seven, eight, or nine glycosyl groups.

10. The method of claim 8, wherein biosynthesis of the product involves at least two glycosylation reactions of the intermediate in the microbial cell.

11. The method of any one of claims 1, wherein the glycoside intermediates are steviol glycosides from stevia leaf extract.

12. The method of claim 11, wherein the steviol glycoside intermediates comprise one or more of stevioside, steviolbioside, rebaudioside A, dulcoside A, dulcoside B, rebaudioside C, and rebaudioside F.

13. The method of claim 12, wherein the extract comprises stevioside, steviolbioside, and Rebaudioside A as prominent components.

14. The method of claim 13, wherein the glycosylated product comprises RebM.

15. The method of claim 12, wherein the glycosylated product comprises RebK, RebC+1, and/or RebC+2.

16. The method of any one of claims 1 to 15, wherein the microbial cell is a bacterial cell.

17. The method of claim 16, wherein the bacterial cell is *Escherichia* spp., *Bacillus* spp., *Rhodobacter* spp., *Zymomonas* spp., or *Pseudomonas* spp.

18. The method of claim 17, wherein the bacterial cell is *Escherichia coli*, *Bacillus subtilis*, *Rhodobacter capsulatus*, *Rhodobacter sphaeroides*, *Zymomonas mobilis*, or *Pseudomonas putida*.

19. The method of claim 18, wherein the bacterial cell is *E. coli*.

20. The method of claim 19, wherein the bacterial cell comprises the genetic modifications: ushA and galETKM are deleted, inactivated, or reduced in expression; pgi is deleted, inactivated, or reduced in expression; and pgm and galU are overexpressed.

21. The method of any one of claims 1 to 15, wherein the microbial cell is a yeast cell.

22. The method of claim 21, wherein the yeast is *Saccharomyces spp.*, *Schizosaccharomyces spp.*, *Pichia spp.*, *Phaffia spp.*, *Kluyveromyces spp.*, *Candida spp.*, *Talaromyces spp.*, *Brettanomyces spp.*, *Pachysolen spp.*, *Debaryomyces spp.*, or *Yarrowia spp.*

23. The method of claim 22, wherein the yeast is *Saccharomyces cerevisiae, Pichia pastoris,* or *Yarrowia lipolytica.*

24. The method of any one of claims 1 to 23, wherein the microbial cell expresses one or more UGT enzymes comprising the amino acid sequence of any one of SEQ ID NOS:1 to 45, or a derivative thereof.

25. The method of claim 24, wherein the microbial cell expresses a 1-3' glycosylating UGT enzyme.

26. The method of claim 25, wherein the 1-3' glycosylating UGT enzyme is selected from SrUGT76G1, MbUGT1-3, MbUGT1-3_1, MbUGT1-3_1.5, MbUGT1-3_2, and derivatives thereof.

27. The method of claim 26, wherein the 1-3' glycosylating UGT enzyme is SrUGT76G1 comprising a L200A substitution.

28. The method of claim 26, wherein the 1-3' glycosylating UGT enzyme comprises an amino acid sequence that is at least 70% identical to the amino acid sequence of SEQ ID NO:15, SEQ ID NO:16, or SEQ ID NO:17.

29. The method of any one of claims 1 to 28, wherein the microbial cell expresses a 1-2' glycosylating UGT enzyme.

30. The method of claim 29, wherein the 1-2' glycosylating UGT enzyme is selected from SrUGT91D2, SrUGT91D1, SrUGT91D2e, OsUGT1-2, MbUGT1,2, MbUGT1,2.2, and derivatives thereof.

31. The method of any one of claims 1 to 30, wherein the microbial cell expresses a C13 O-glycosylating UGT enzyme.

32. The method of claim 31, wherein the C13 O-glycosylating UGT enzyme is SrUGT85C2 or a derivative thereof, optionally comprising a P215T substitution.

33. The method of any one of claims 1 to 32, wherein the microbial cell expresses a C19 O-glycosylating UGT enzyme.

34. The method of claim 33, wherein the C19 O-glycosylating UGT enzyme is SrUGT74G1, MbUGTc19, or a derivative thereof.

35. The method of claim 24, wherein the microbial cell expresses a 1-3' glycosylating UGT enzyme and a 1-2' glycosylating UGT enzyme, and optionally a C13 O-glycosylating UGT enzyme and a C19 O-glycosylating enzyme.

36. The method of claim 35, wherein the microbial cell expresses a 1-3' glycosylating UGT enzyme, a 1-2' glycosylating UGT enzyme, a C19 O-glycosylating UGT enzyme, and a C13 O-glycosylating UGT enzyme.

37. The method of claim 36, wherein the microbial cell expresses: a SrUGT85C2 or derivative thereof; MbUGT1,2 or derivative thereof; SrUGT74G1 or derivative thereof; and an enzyme selected from SrUGT76G1 or derivative thereof, MbUGT1-3_1 or derivative thereof, MbUGT1-3_1.5 or derivative thereof, and MbUGT1-3_2 or derivative thereof.

38. The method of any one of claims 1 to 37, wherein the UGT enzymes are integrated into the chromosome of the microbial cell.

39. The method of any one of the claims 1 to 37, wherein the UGT enzymes are expressed extrachromosomally.

40. The method of any one of claims 1 to 39, wherein the microbial cell has one or more genetic modification that increase UDP-glucose availability.

41. The method of claim 40, wherein the microbial cell has a deletion, inactivation, or reduced activity or expression of a gene encoding an enzyme that consumes UDP-glucose.

42. The method of claim 41, wherein the microbial cell has a deletion, inactivation, or reduced activity of ushA or ortholog thereof and/or one or more of galE, galT, galK, and galM, or ortholog.

43. The method of claim 42, wherein galETKM genes are inactivated, deleted, or reduced in expression.

44. The method of claim 40, wherein the microbial cell has a deletion, inactivation, or reduced activity or expression of otsA (trehalose-6-phosphate synthase) or ortholog thereof.

45. The method of claim 40, wherein the microbial cell has a deletion, inactivation, or reduced activity or expression of ugd (UDP-glucose 6-dehydrogenase) or ortholog thereof.

46. The method of claim 40, wherein the microbial cell has a deletion, inactivation, or reduced expression of waaG, waaO, waaJ, yfdG, yfdI, and/or wcaJ, or otholog(s) thereof.

47. The method of claim 40, wherein the microbial cell has a deletion, inactivation, or reduced activity or expression of pgi (glucose-6 phosphate isomerase) or ortholog thereof.

48. The method of claim 40, wherein the microbial cell has an overexpression or increased activity of one or more genes encoding an enzyme involved in converting glucose-6-phosphate to UDP-glucose, which is optionally pgm (phosphoglucomutase) and/or galU (UTP-glucose-1-phosphate uridylyltransferase), or ortholog or derivative thereof.

49. The method of claim 40, wherein the microbial cell has an overexpression or increased activity or expression of ycjU (β-phosphoglucomutase) and *Bifidobacterium bifidum* ugpA, or ortholog or derivative thereof.

50. The method of claim 40, wherein the microbial cell has one or more genetic modifications that increase flux to the pentose phosphate pathway (PPP), and which is optionally an overexpression or activity of *E. coli* zwf or homologue or engineered derivative thereof.

51. The method of claim 40, wherein the microbial cell has one or more genetic modifications that increase glucose transport, and which optionally includes increased expression or activity of *E. coli* galP and *E. coli* glk (glucokinase), or alternatively *Zymomonas mobilis* glf and *E. coli* glk, or homologs, orthologs, or engineered derivatives of thereof.

52. The method of claim 40, wherein the microbial cell has one or more genetic modifications that increase UTP production and recycling, and which optionally include increased expression or activity of *E. coli* pyrH (UMP kinase), *E. coli* cmk (cytidylate kinase), *E. coli* adk (adenylate kinase), or *E. coli* ndk (nucleoside diphosphate kinase), or homologs, orthologs, or engineered derivatives of these enzymes.

53. The method of claim 40, wherein the microbial cell has one or more genetic modifications that increase UDP production, and which optionally include: overexpression or increased activity of upp (uracil phosphoribosyltransferase), pyrH (UMP kinase), and cmk (cytidylate kinase), or homolog or engineered derivatives thereof; or overexpression or increased activity of dctA (C4 dicarboxylate/orotate:H+ symporter), pyrE (orotate phosphoribosyltransferase), pyrH (UMP kinase) and cmk (cytidylate kinase), or homolog or engineered derivatives thereof.

54. The method of claim 40, wherein the microbial cell has one or more genetic modifications to remove or reduce regulation of glucose uptake, which optionally include deletion, inactivation, or reduced expression of sgrS small regulatory RNA.

55. The method of claim 40, wherein the microbial cell has one or more genetic modifications that reduce dephosphorylation of glucose-1-phosphate, which optionally include deletion, inactivation, or reduced expression or activity of one or more of *E. coli* agp (glucose-1-phosphatase), *E. coli* yihX (α-D-glucose-1-phosphate phosphatase), *E. coli* ybiV

(sugar phosphatase), *E. coli* yidA (sugar phosphatase), *E. coli* yigL (phosphosugar phosphatase), and *E. coli* phoA (alkaline phosphatase), or an ortholog thereof.

56. The method of claim 40, wherein the microbial cell has one or more genetic modifications that reduce conversion of glucose-1-phosphate to TDP-glucose, which optionally include a deletion, inactivation, or reduced expression or activity of one or more of *E. coli* rffH (dTDP-glucose pyrophosphorylase) and *E. coli* rfbA (dTDP glucose pyrophosphorylase), or an ortholog thereof.

57. The method of claim 40, wherein the microbial cell has one or more genetic modifications that reduce conversion of glucose-1-phosphate to ADP-glucose, and which optionally include deletion, inactivation, or reduced expression or activity of *E. coli* gigC (glucose-1-phosphate adenylyltransferase), or an ortholog thereof.

58. The method of claim 40, wherein the microbial cell is a bacterial cell comprising the genetic modifications: ushA and galETKM are deleted, inactivated, or reduced in expression; pgi is deleted, inactivated, or reduced in expression; and pgm and galU are overexpressed.

59. The method of any one of claims 1 to 58, wherein the microbial cell expresses an endogenous transport protein that transports the glycoside intermediate(s) into the cell.

60. The method of any one of claims 1 to 58, wherein the microbial cell overexpresses a recombinant transport protein that transports the glycoside intermediate(s) into the cell.

61. The method of any one of claims 59 or 60, wherein the microbial strain expresses a transport protein selected from *E. coli* acrAD, xylE, ascF, bglF, chbA, ptsG/crr, wzxE, rfbX, or an ortholog or derivative thereof.

62. The method of any one of claims 1 to 61, wherein the microbial cell expresses an endogenous or recombinant transporter that transports glycosylated product outside the cell.

63. The method of any one of claims 1 to 62, wherein the method results in at least 40% conversion of glycoside intermediate to glycosylated product by weight.

64. The method of claim 63, wherein the method results in a least 50% conversion of glycoside intermediate to glycosylated product by weight.

65. The method of claim 64, wherein the method results in at least 75% conversion of glycoside intermediate to glycosylated product by weight.

66. The method of any one of claims 1 to 65, wherein a ratio of RebM to RebD of at least 5:1 is recovered as the glycosylated product.

67. The method of any one of claim 1 to 66, wherein the method is performed by batch fermentation, continuous fermentation, or semi-continuous fermentation.

68. The method of claim 67, wherein the method is performed by fed batch fermentation.

69. The method of claim 68, wherein the glycoside intermediates are incubated with the cell for about 72 hours or less.

70. A microbial cell comprising:

one or more recombinant genes encoding UDP-dependent glycosyl transferase (UGT) enzyme(s) for intracellular expression; and

one or more genetic modifications that increase UDP-glucose availability.

71. The microbial cell of claim 70, wherein the microbial cell converts fed glycoside intermediates into a glycosylated product.

72. The microbial cell of claim 71, wherein the microbial cell is a bacterial cell.

73. The microbial cell of claim 72, wherein the bacterial cell is *Escherichia* spp., *Bacillus* spp., *Rhodobacter* spp., *Zymomonas* spp., or *Pseudomonas* spp.

74. The microbial cell of claim 73, wherein the bacterial cell is selected from *Escherichia coli*, *Bacillus subtilis*, *Rhodobacter capsulatus*, *Rhodobacter sphaeroides*, *Zymomonas mobilis*, or *Pseudomonas putida*.

75. The microbial cell of claim 74, wherein the bacterial cell is *E. coli*.

76. The microbial cell of claim 75, wherein the bacterial cell comprises the genetic modifications: ushA and galETKM are deleted, inactivated, or reduced in expression; pgi is deleted, inactivated, or reduced in expression; and pgm and galU are overexpressed.

77. The microbial cell of claim 70, wherein the microbial cell is a yeast cell.

78. The microbial cell of claim 77, wherein the yeast is *Saccharomyces spp.*, *Schizosaccharomyces spp.*, *Pichia spp.*, *Phaffia spp.*, *Kluyveromyces spp.*, *Candida spp.*, *Talaromyces spp.*, *Brettanomyces spp.*, *Pachysolen spp.*, *Debaryomyces spp.*, or *Yarrowia spp.*

79. The microbial cell of claim 78, wherein the yeast cell is selected from *Saccharomyces cerevisiae, Pichia pastoris,* and *Yarrowia lipolytica.*

80. The microbial cell of any one of claims 70 to 79, wherein the microbial cell does not express a plant biosynthetic pathway producing a glycoside intermediate.

81. The microbial cell of any one of claims 70 to 80, wherein the microbial cell expresses an endogenous or recombinant transport protein that transports glycoside intermediate into the cell.

82. The microbial cell of any one of claims 70 to 81, wherein the microbial cell expresses a 1-3' glycosylating UGT enzyme, which is optionally selected from SrUGT76G1, MbUGT1-3, MbUGT1-3_1, MbUGT1-3_1.5, MbUGT1-3_2, or a derivative thereof.

83. The microbial cell of claim 82, wherein the microbial cell expresses a 1-2' glycosylating UGT enzyme, which is optionally selected from SrUGT91D2, SrUGT91D1, SrUGT91D2e, OsUGT1-2, MbUGT1,2, MbUGT1,2.2, and derivatives thereof.

84. The microbial cell of any one of claims 83, wherein the microbial cell expresses a C13 O-glycosylating UGT enzyme, which is optionally selected from SrUGT85C2 and derivatives thereof.

85. The microbial cell of claim 84, wherein the microbial cell expresses a C19 O-glycosylating UGT enzyme, which is optionally selected from SrUGT74G1, MbUGTc19, and derivatives thereof.

86. The microbial cell of claim 82, wherein the microbial cell expresses a 1-3' glycosylating UGT enzyme, a 1-2' glycosylating UGT enzyme, a C19 O-glycosylating UGT enzyme, and a C13 O-glycosylating UGT enzyme.

87. The microbial cell of claim 86, wherein the microbial cell expresses a SrUGT85C2 or derivative thereof, MbUGT1,2 or derivative thereof, SrUGT74G1 or derivative thereof, and SrUGT76G1 or derivative thereof.

88. The microbial cell of claim 86 or 87, wherein the UGT enzymes are integrated into the chromosome of the microbial cell.

89. The microbial cell of claim 86 or 87, wherein the UGT enzymes are expressed extrachromosomally.

90. The microbial cell of claim 70, wherein the microbial cell has a deletion, inactivation, or reduced activity or expression of a gene encoding an enzyme that consumes UDP-glucose.

91. The method of claim 90, wherein the microbial cell has a deletion, inactivation, or reduced activity of ushA or ortholog thereof and/or one or more of galE, galT, galK, and galM, or ortholog.

92. The method of claim 91, wherein galETKM genes are inactivated, deleted, or reduced in expression.

93. The method of claim 70, wherein the microbial cell has a deletion, inactivation, or reduced activity or expression of otsA (trehalose-6-phosphate synthase) or ortholog thereof.

94. The method of claim 70, wherein the microbial cell has a deletion, inactivation, or reduced activity or expression of ugd (UDP-glucose 6-dehydrogenase) or ortholog thereof.

95. The method of claim 70, wherein the microbial cell has a deletion, inactivation, or reduced expression of waaG, waaO, waaJ, yfdG, yfdI, and/or wcaJ, or otholog(s) thereof.

96. The method of claim 70, wherein the microbial cell has a deletion, inactivation, or reduced activity or expression of pgi (glucose-6 phosphate isomerase) or ortholog thereof.

97. The method of claim 70, wherein the microbial cell has an overexpression or increased activity of one or more genes encoding an enzyme involved in converting glucose-6-phosphate to UDP-glucose, which is optionally pgm (phosphoglucomutase) and/or galU (UTP-glucose-1-phosphate uridylyltransferase), or ortholog or derivative thereof.

98. The method of claim 70, wherein the microbial cell has an overexpression or increased activity or expression of ycjU (β-phosphoglucomutase) and *Bifidobacterium bifidum* ugpA, or ortholog or derivative thereof.

99. The method of claim 70, wherein the microbial cell has one or more genetic modifications that increase flux to the pentose phosphate pathway (PPP), and which is optionally an overexpression or increased activity of *E. coli* zwf or homologue or engineered derivative thereof.

100. The method of claim 70, wherein the microbial cell has one or more genetic modifications that increase glucose transport, and which optionally includes increased expression or activity of *E. coli* galP and *E. coli* glk (glucokinase), or alternatively *Zymomonas mobilis* glf and *E. coli* glk, or homologs, orthologs, or engineered derivatives of these genes.

101. The method of claim 70, wherein the microbial cell has one or more genetic modifications that increase UTP production and recycling, and which optionally include increased expression or activity of *E. coli* pyrH (UMP kinase), *E. coli* cmk (cytidylate kinase), *E. coli* adk (adenylate kinase), or *E. coli* ndk (nucleoside diphosphate kinase), or homologs, orthologs, or engineered derivatives of these enzymes.

102. The method of claim 70, wherein the microbial cell has one or more genetic modifications that increase UDP production, and which optionally include: overexpression

or increased activity of upp (uracil phosphoribosyltransferase), pyrH (UMP kinase), and cmk (cytidylate kinase), or homolog or engineered derivatives thereof; or overexpression or increased activity of dctA (C4 dicarboxylate/orotate:H+ symporter), pyrE (orotate phosphoribosyltransferase), pyrH (UMP kinase) and cmk (cytidylate kinase), or homolog or engineered derivatives thereof.

103. The method of claim 70, wherein the microbial cell has one or more genetic modifications to remove or reduce regulation of glucose uptake, which optionally include deletion, inactivation, or reduced expression of sgrS small regulatory RNA.

104. The method of claim 70, wherein the microbial cell has one or more genetic modifications that reduce dephosphorylation of glucose-1-phosphate, which optionally include deletion, inactivation, or reduced expression or activity of one or more of *E. coli* agp (glucose-1-phosphatase), *E. coli* yihX (α-D-glucose-1-phosphate phosphatase), *E. coli* ybiV (sugar phosphatase), *E. coli* yidA (sugar phosphatase), *E. coli* yigL (phosphosugar phosphatase), and *E. coli* phoA (alkaline phosphatase), or an ortholog thereof in the microbial cell.

105. The method of claim 70, wherein the microbial cell has one or more genetic modifications that reduce conversion of glucose-1-phosphate to TDP-glucose, which optionally include a deletion, inactivation, or reduced expression or activity of one or more of *E. coli* rffH (dTDP-glucose pyrophosphorylase) and *E. coli* rfbA (dTDP glucose pyrophosphorylase), or an ortholog thereof.

106. The method of claim 70, wherein the microbial cell has one or more genetic modifications that reduce conversion of glucose-1-phosphate to ADP-glucose, and which optionally include deletion, inactivation, or reduced expression or activity of *E. coli* gigC (glucose-1-phosphate adenylyltransferase), or an ortholog thereof.

Claims

1. A method for producing a steviol glycoside product from steviol glycoside intermediates, comprising:

providing a bacterial cell expressing one or more UDP-dependent glycosyl transferase enzymes (UGT enzymes) intracellularly, wherein the UGT enzymes glycosylate steviol and steviol glycoside substrates, and wherein the bacterial cell comprises the following genetic modifications:

deletion, inactivation, or reduced activity or expression of UDP-sugar hydrolase and one or more UDP-galactose biosynthesis enzymes;

deletion, inactivation, or reduced activity or expression of glucose-6-phosphate isomerase; and

overexpression of phosphoglucomutase and UTP-glucose-1-phosphate uridylyltransferase;

incubating the bacterial cell with a *stevia* leaf extract or fraction thereof comprising the steviol glycoside intermediates thereby glycosylating the steviol glycoside intermediates to the steviol glycoside product by enzymatic transfer of one or more glucosyl groups from UDP-glucose cofactor, and

recovering the steviol glycoside product.

2. The method of claim 1, wherein the steviol glycoside intermediates comprise one or more of stevioside, steviolbioside, rebaudioside A, dulcoside A, dulcoside B, rebaudioside C, and rebaudioside F.

3. The method of claim 2, wherein the extract comprises stevioside, steviolbioside, and Rebaudioside A as prominent components.

4. The method of claim 3, wherein the steviol glycoside product comprises RebM.

5. The method of claim 2, wherein the steviol glycoside product comprises RebK, RebC+1, and/or RebC+2.

6. The method of claim 1, wherein the bacterial cell is *Escherichia* spp., *Bacillus* spp., *Rhodobacter* spp., *Zymomonas* spp., or *Pseudomonas* spp.

7. The method of claim 6, wherein the bacterial cell is *Escherichia coli, Bacillus subtilis, Rhodobacter capsulatus, Rhodobacter sphaeroides, Zymomonas mobilis*, or *Pseudomonas putida.*

8. The method of claim 7, wherein the bacterial cell is *E. coli.*

9. The method of claim 8, wherein the bacterial cell comprises the genetic modifications: ushA and galETKM are deleted; pgi is deleted; and pgm and galU are overexpressed.

10. The method of claim 1, wherein the bacterial cell expresses a 1-3′ glycosylating UGT enzyme.

11. The method of claim 10, wherein the 1-3′ glycosylating UGT enzyme comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:15, SEQ ID NO:16, or SEQ ID NO:17.

12. The method of claim 1, wherein the bacterial cell expresses a 1-2′ glycosylating UGT enzyme.

13. The method of claim 1, wherein the bacterial cell expresses a UGT enzyme that glycosylates the C13 hydroxyl of steviol or steviol glycoside substrate.

14. The method of claim 1, wherein the bacterial cell expresses a UGT enzyme that glycosylates the C19 hydroxyl of steviol or steviol glycoside substrate.

15. The method of claim 1, wherein the bacterial cell expresses a 1-3′ glycosylating UGT enzyme and a 1-2′ glycosylating UGT enzyme.

16. The method of claim 15, wherein the bacterial cell expresses a 1-3′ glycosylating UGT enzyme, a 1-2′ glycosylating UGT enzyme, a C19 O-glycosylating UGT enzyme, and a C13 O-glycosylating UGT enzyme.

17. The method of claim 16, wherein the bacterial cell expresses: a SrUGT85C2 (SEQ ID NO: 1) or derivative thereof having at least 90% sequence identity thereto; MbUGT1,2 (SEQ ID NO: 9) or derivative thereof having at least 90% sequence identity thereto; SrUGT74G1 (SEQ ID NO: 2) or derivative thereof having at least 90% sequence identity thereto; and an enzyme selected from SrUGT76G1 (SEQ ID NO: 3) or derivative thereof having at least 90% sequence identity thereto, MbUGT1-3_1 (SEQ ID NO: 15) or derivative thereof having at least 90% sequence identity thereto, MbUGT1-3_1.5 (SEQ ID NO: 16) or derivative thereof having at least 90% sequence identity thereto, and MbUGT1-3_2 (SEQ ID NO: 17) or derivative thereof having at least 90% sequence identity thereto.

18. The method of claim 1, wherein the UGT enzymes are integrated into the chromosome of the bacterial cell or are expressed extrachromosomally.

19. The method of claim 1, wherein galETKM genes are inactivated, deleted, or reduced in expression.

20. The method of claim 1, wherein the bacterial cell has a deletion, inactivation, or reduced activity or expression of trehalose-6-phosphate synthase.

21. The method of claim 1, wherein the bacterial cell has a deletion, inactivation, or reduced activity or expression of UDP-glucose 6-dehydrogenase.

22. The method of claim 1, wherein the bacterial cell has an overexpression or increased activity or expression of ycjU (βphosphoglucomutase) and *Bifidobacterium* bifidum ugpA.

23. The method of claim 1, wherein the bacterial cell has one or more genetic modifications that increase flux to the pentose phosphate pathway (PPP), and which is an overexpression of *E. coli* zwf.

24. The method of claim 1, wherein the bacterial cell has one or more genetic modifications that increase UTP production and recycling, and which are selected from increased expression or activity of *E. coli* pyrH (UMP kinase), *E. coli* cmk (cytidylate kinase), *E. coli* adk (adenylate kinase), and *E. coli* ndk (nucleoside diphosphate kinase).

25. The method of claim 1, wherein the bacterial cell has one or more genetic modifications that increase UDP production, and which are selected from overexpression or increased activity of: upp (uracil phosphoribosyltransferase), pyrH (UMP kinase), cmk (cytidylate kinase); dctA (C4 dicarboxylate/orotate:H+symporter), pyrE (orotate phosphoribosyltransferase), pyrH (UMP kinase) and cmk (cytidylate kinase).

26. The method of claim 1, wherein the bacterial cell has one or more genetic modifications to remove or reduce regulation of glucose uptake, which include deletion, inactivation, or reduced expression of sgrS small regulatory RNA.

27. The method of claim 1, wherein the bacterial cell has one or more genetic modifications that reduce conversion of glucose-1-phosphate to TDP-glucose, which include a deletion, inactivation, or reduced expression or activity of one or more dTDP-glucose pyrophosphorylase genes.

28. The method of claim 1, wherein the bacterial cell has one or more genetic modifications that reduce conversion of glucose-1-phosphate to ADP-glucose, and which include deletion, inactivation, or reduced expression or activity of glucose-1-phosphate adenylyltransferase.

29. The method of claim 1, wherein the method results in at least 40% conversion of steviol glycoside intermediate to steviol glycoside product by weight.

30. The method of claim 29, wherein the method results in a least 50% conversion of steviol glycoside intermediate to steviol glycoside product by weight.

31. The method of claim 30, wherein the method results in at least 75% conversion of steviol glycoside intermediate to steviol glycoside product by weight.

32. The method of claim 1, wherein a ratio of RebM to RebD of at least 5:1 is recovered as the steviol glycoside product.

33. The method of claim 1, wherein the method is performed by batch fermentation, continuous fermentation, or semi-continuous fermentation.

34. The method of claim 33, wherein the method is performed by fed batch fermentation.

35. The method of claim 34, wherein the steviol glycoside intermediates are incubated with the bacterial cell for about 72 hours or less.

36. The method of claim 2, wherein the steviol glycosideglycosylated product comprises RebD, RebE, RebI, or RebB.