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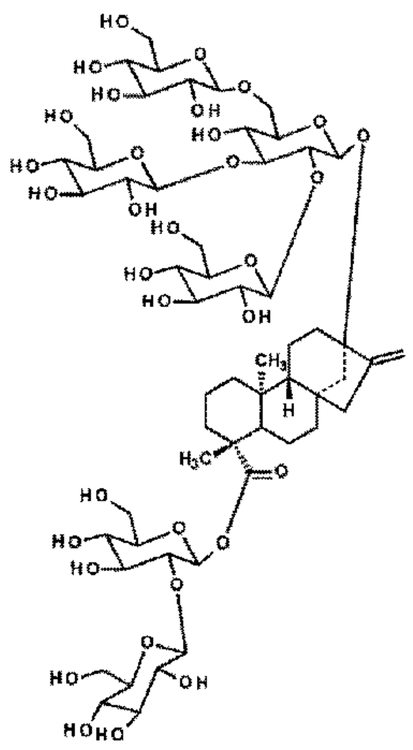
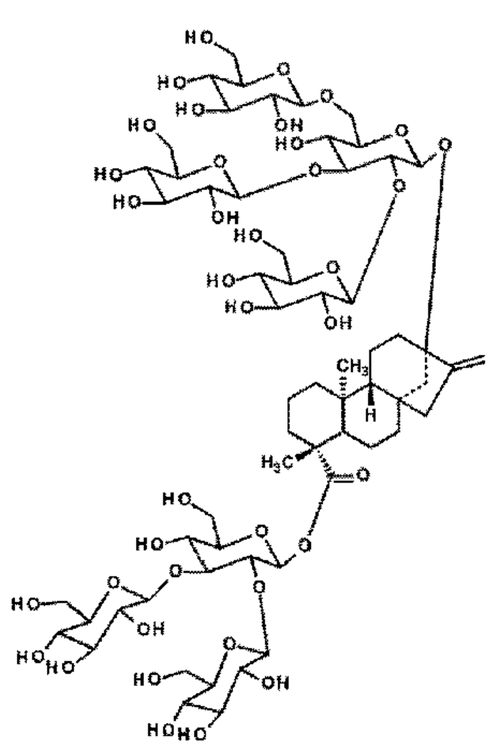
(54) Title: PRODUCTION OF STEVIOL GLYCOSIDES IN RECOMBINANT HOSTS

Figure 3



Steviol+6Glc (isomer 1)
[Compound 6.1]



Steviol+7Glc (isomer 2)
[Compound 7.2]

(57) Abrégé/Abstract:
The invention relates to recombinant microorganisms and methods for producing steviol glycosides, glycosides of steviol precursors, and steviol glycoside precursors.

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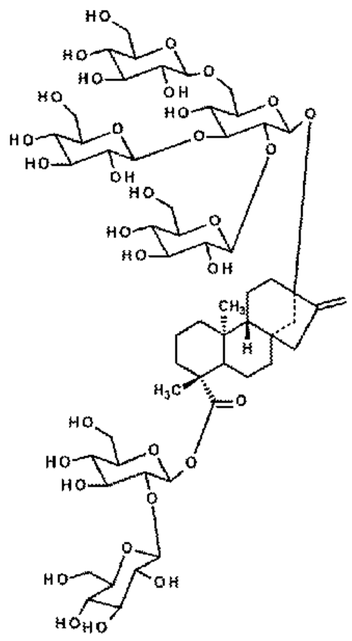
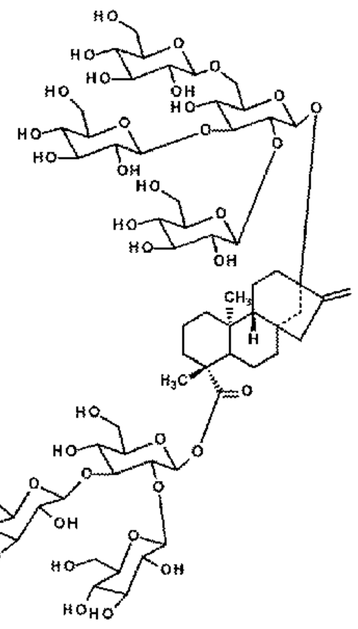
(54) Title: PRODUCTION OF STEVIOL GLYCOSIDES IN RECOMBINANT HOSTS

Figure 3



Steviol+6Glc (isomer 1)
[Compound 6.1]



Steviol+7Glc (isomer 2)
[Compound 7.2]

(57) Abstract: The invention relates to recombinant microorganisms and methods for producing steviol glycosides, glycosides of steviol precursors, and steviol glycoside precursors.

[Continued on next page]

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PRODUCTION OF STEVIOL GLYCOSIDES IN RECOMBINANT HOSTS

BACKGROUND OF THE INVENTION

Field of the Invention

[0001] This disclosure relates to recombinant production of steviol glycosides, glycosides of steviol precursors, and steviol glycoside precursors in recombinant hosts. In particular, this disclosure relates to production of steviol glycosides comprising steviol-13-*O*-glucoside (13-SMG), steviol-19-*O*-glucoside (19-SMG), steviol-1,2-bioside, 1,2-stevioside, rubusoside, rebaudioside A (RebA), rebaudioside B (RebB), rebaudioside D (RebD), rebaudioside M (RebM), mono-glycosylated *ent*-kaurenoic acids, di-glycosylated *ent*-kaurenoic acids, tri-glycosylated *ent*-kaurenoic acids, tri-glycosylated *ent*-kaurenols, tri-glycosylated steviol glycosides, tetra-glycosylated steviol glycosides, penta-glycosylated steviol glycosides, hexa-glycosylated steviol glycosides, hepta-glycosylated steviol glycosides, or isomers thereof in recombinant hosts.

Description of Related Art

[0001] Sweeteners are well known as ingredients used most commonly in the food, beverage, or confectionary industries. The sweetener can either be incorporated into a final food product during production or for stand-alone use, when appropriately diluted, as a tabletop sweetener or an at-home replacement for sugars in baking. Sweeteners include natural sweeteners such as sucrose, high fructose corn syrup, molasses, maple syrup, and honey and artificial sweeteners such as aspartame, saccharine, and sucralose. Stevia extract is a natural sweetener that can be isolated and extracted from a perennial shrub, *Stevia rebaudiana*. Stevia is commonly grown in South America and Asia for commercial production of stevia extract. Stevia extract, purified to various degrees, is used commercially as a high intensity sweetener in foods and in blends or alone as a tabletop sweetener.

[0002] Chemical structures for several steviol glycosides are shown in Figure 1, including the diterpene steviol and various steviol glycosides. Extracts of the Stevia plant generally comprise steviol glycosides that contribute to the sweet flavor, although the amount of each steviol glycoside often varies, *inter alia*, among different production batches.

[0003] As recovery and purification of steviol glycosides from the Stevia plant have proven to be labor intensive and inefficient, there remains a need for a recombinant production system that can accumulate high yields of desired steviol glycosides, such as RebD and RebM. There also remains a need for improved production of steviol glycosides in recombinant hosts for commercial uses.

SUMMARY OF THE INVENTION

[0004] It is against the above background that the present invention provides certain advantages and advancements over the prior art.

[0005] Although this invention as disclosed herein is not limited to specific advantages or functionalities, the invention provides a recombinant host cell capable of producing one or more steviol glycosides and/or glycosylated steviol precursors, or a composition thereof, comprising:

(a) a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position;

(b) a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position;

(c) a gene encoding a polypeptide capable of beta-1,2-glycosylation of the C2' and/or beta-1,3-glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside; and/or

(d) a gene encoding a polypeptide capable of glycosylating a steviol precursor at its C-19 carboxyl or C-19 hydroxyl position;

wherein at least one of the genes is a recombinant gene.

[0006] In one aspect of the recombinant host cell disclosed herein:

(a) the polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position is a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73E1 polypeptide, a UGT75B1 polypeptide, a UGT75L6 polypeptide, a OleI polypeptide, a UGT5 polypeptide, a SA Gtase polypeptide, a UDPG1 polypeptide, a UN1671 polypeptide, a UGT74F1 polypeptide, a UGT84B2 polypeptide, and/or a UGT74F2-like UGT polypeptide;

(b) the polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position is a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73C7 polypeptide, a UGT73E1 polypeptide, and/or a UGT76E12 polypeptide;

(c) the polypeptide capable of beta-1,2-glycosylation of the C2' and/or beta-1,3-glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside is a UGT73C6 polypeptide, a CaUGT3 polypeptide, a UN32491 polypeptide, and/or a UN1671 polypeptide; and/or

(d) the polypeptide capable of glycosylating a steviol precursor at its C-19 carboxyl or C-19 hydroxyl position is a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73E1 polypeptide, a UGT74D1 polypeptide, a UGT75B1 polypeptide, a UGT75L6 polypeptide, a UGT76E12 polypeptide, a OleI polypeptide, a UGT5 polypeptide, a SA Gtase, a UDPG1 polypeptide, a UGT74F1 polypeptide, a UGT75D1 polypeptide, a UGT84B2 polypeptide, a CaUGT2 polypeptide, and/or a UGT74F2-like UGT polypeptide.

[0007] In one aspect of the recombinant host cell disclosed herein: the UGT73C1 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:127, the UGT73C3 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:133, the UGT73C5 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:135, the UGT73C6 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:137, the UGT73E1 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:141, the UGT74D1 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:143, the UGT75B1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:145, the UGT75L6 polypeptide comprises a polypeptide having at least 60% sequence identity to an amino acid sequence set forth in SEQ ID NO:147, the UGT76E12 polypeptide comprises a polypeptide having at least 60% sequence identity to an amino acid sequence set forth in SEQ ID NO:153, the OleI polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:177, the UGT5 polypeptide comprises a polypeptide having at least 65% identity to an amino acid sequence set

forth in SEQ ID NO:181, the SA Gtase polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:183, the UDPG1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:185, the UN1671 polypeptide comprises a polypeptide having at least 45% identity to an amino acid sequence set forth in SEQ ID NO:201, the UGT74F1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:203, the UGT75D1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:205, the UGT84B2 polypeptide comprises a polypeptide having at least 40% sequence identity to an amino acid sequence set forth in SEQ ID NO:207, the UGT74F2-like UGT polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:211, the UGT73C7 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:139, the CaUGT3 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:169, the UN32491 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:199, and/or the CaUGT2 polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:209.

[0008] In one aspect of the recombinant host cell disclosed herein, the recombinant host cell further comprises:

(a) a gene encoding a polypeptide capable of synthesizing geranylgeranyl pyrophosphate (GGPP) from farnesyl diphosphate (FPP) and isopentenyl diphosphate (IPP);

(b) a gene encoding a polypeptide capable of synthesizing ent-copalyl diphosphate from GGPP;

(c) a gene encoding an a polypeptide capable of synthesizing ent-kaurene from ent-copalyl diphosphate;

(d) a gene encoding a polypeptide capable of synthesizing ent-kaurenoic acid from ent-kaurene;

(e) a gene encoding a polypeptide capable of reducing cytochrome P450 complex;

(f) a gene encoding a polypeptide capable of synthesizing steviol from ent-kaurenoic acid;

(g) a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position thereof;

(h) a gene encoding a polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside;

(i) a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position; and/or

(k) a gene encoding a polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside;

wherein at least one of the genes is a recombinant gene.

[0009] In one aspect of the recombinant host cell disclosed herein:

(a) the polypeptide capable of synthesizing GGPP comprises a polypeptide having at least 70% sequence identity to the amino acid sequence set forth in SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, or SEQ ID NO:116;

(b) the polypeptide capable of synthesizing ent-copalyl diphosphate comprises a polypeptide having at least 70% sequence identity to the amino acid sequence set forth in SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, or SEQ ID NO:120;

(c) the polypeptide capable of synthesizing ent-kaurene comprises a polypeptide having at least 70% sequence identity to the amino acid sequence set forth in SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, or SEQ ID NO:52;

(d) the polypeptide capable of synthesizing ent-kaurenoic acid comprises a polypeptide having at least 70% sequence identity to the amino acid sequence set forth in SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:117, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, or SEQ ID NO:76;

(e) the polypeptide capable of reducing cytochrome P450 complex comprises a polypeptide having at least 70% sequence identity to the amino acid sequence

set forth in SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92;

(f) the polypeptide capable of synthesizing steviol comprises a polypeptide having at least 70% sequence identity to the amino acid sequence set forth in SEQ ID NO:94, SEQ ID NO:97, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, or SEQ ID NO:114;

(g) the polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position thereof comprises a polypeptide having at least 55% sequence identity to the amino acid sequence set forth in SEQ ID NO:7;

(h) the polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside comprises a polypeptide having at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:9;

(i) the polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position comprises a polypeptide having at least 55% sequence identity to the amino acid sequence set forth in SEQ ID NO:4; and/or

(k) the polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside comprises a polypeptide having 80% or greater identity to the amino acid sequence set forth in SEQ ID NO:11; a polypeptide having 80% or greater identity to the amino acid sequence set forth in SEQ ID NO:13; or a polypeptide having at least 65% sequence identity to the amino acid sequence set forth in SEQ ID NO:16.

[0010] In one aspect of the recombinant host cell disclosed herein, expression of the one or more recombinant genes increases an amount of the one or more steviol glycosides and/or glycosylated steviol precursors, or a composition thereof accumulated by the cell relative to a corresponding host lacking the one or more recombinant genes.

[0011] In one aspect of the recombinant host cell disclosed herein, expression of the one or more recombinant genes increases the amount of the one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof, accumulated by the cell by at least

about 5%, at least about 10%, at least about 25%, at least about 50%, at least about 75%, or at least about 100% relative to a corresponding host lacking the one or more recombinant genes.

[0012] In one aspect of the recombinant host cell disclosed herein, expression of the one or more recombinant genes increases the amount of *ent*-kaurenoic acid+2Glc (#7), *ent*-kaurenoic acid+3Glc (isomer 1), *ent*-kaurenoic acid+3Glc (isomer 2), steviol-13-*O*-glucoside (13-SMG), Rebaudioside A (RebA), Rebaudioside B (RebB), Steviol+4Glc (#36), Steviol+6Glc (isomer 1), Steviol+7Glc (isomer 2), and/or *ent*-Kaurenol+3Glc (isomer 1 and/or isomer 2) accumulated by the cell relative to a corresponding host lacking the one or more recombinant genes.

[0013] In one aspect of the recombinant host cell disclosed herein, the one or more steviol glycosides and/or glycosylated steviol precursors are, or the composition thereof comprises, 13-SMG, steviol-19-*O*-glucoside (19-SMG), steviol-1,2-bioside, steviol-1,3-bioside, 1,2-stevioside, 1,3-stevioside, rubusoside, RebA, RebB, Rebaudioside C (RebC), Rebaudioside D (RebD), Rebaudioside E (RebE), Rebaudioside F (RebF), Rebaudioside M (RebM), Rebaudioside Q (RebQ), Rebaudioside I (RebI), dulcoside A, a mono-glycosylated *ent*-kaurenoic acid, a di-glycosylated *ent*-kaurenoic acid, a tri-glycosylated *ent*-kaurenoic acid, a mono-glycosylated *ent*-kaurenols, a di-glycosylated *ent*-kaurenol, a tri-glycosylated *ent*-kaurenol, a tri-glycosylated steviol glycoside, a tetra-glycosylated steviol glycoside, a penta-glycosylated steviol glycoside, a hexa-glycosylated steviol glycoside, a hepta-glycosylated steviol glycoside, or an isomer thereof.

[0014] In one aspect of the recombinant host cell disclosed herein, the mono-glycosylated *ent*-kaurenoic acid comprises KA1.58 of Table 1 and/or the penta-glycosylated steviol comprises Compound 5.24 of Table 1.

[0015] In one aspect of the recombinant host cell disclosed herein, the recombinant host cell comprises a plant cell, a mammalian cell, an insect cell, a fungal cell, an algal cell, or a bacterial cell.

[0016] The invention also provides a method of producing in a cell culture one or more steviol glycosides and/or glycosylated steviol precursors, or a composition thereof, comprising growing the recombinant host cell disclosed herein in the cell culture, under conditions in which the genes are expressed, and wherein the one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof is produced by the recombinant host cell.

[0017] In one aspect of the method disclosed herein, the genes are constitutively expressed and/or expression of the genes is induced.

[0018] In one aspect of the method disclosed herein, an amount of *ent*-kaurenoic acid+2Glc (#7), *ent*-kaurenoic acid+3Glc (isomer 1), *ent*-kaurenoic acid+3Glc (isomer 2), 13-SMG, RebA, RebB, Steviol+4Glc (#36), Steviol+6Glc (isomer 1), Steviol+7Glc (isomer 2), and/or *ent*-Kaurenol+3Glc (isomer 1 and/or isomer 2) accumulated by the recombinant host cell is increased by at least about 5% relative to a corresponding host lacking the one or more recombinant genes.

[0019] In one aspect, the method disclosed herein further comprises isolating from the cell cultures the one or more steviol glycosides and/or glycosylated steviol precursors or the composition thereof produced thereby.

[0020] In one aspect of the method disclosed herein, the isolating step comprises:

(a) providing the cell culture comprising the one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof;

(b) separating a liquid phase of the cell culture from a solid phase of the cell culture to obtain a supernatant comprising the produced one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof;

(c) providing one or more adsorbent resins, comprising providing the adsorbent resins in a packed column; and

(d) contacting the supernatant of step (b) with the one or more adsorbent resins in order to obtain at least a portion of the produced one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof, thereby isolating the produced one or more steviol glycosides or the steviol glycoside composition;

or

(a) providing the cell culture comprising the one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof;

(b) separating a liquid phase of the cell culture from a solid phase of the cell culture to obtain a supernatant comprising the produced one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof;

(c) providing one or more ion exchange or ion exchange or reversed-phase chromatography columns; and

(d) contacting the supernatant of step (b) with the one or more ion exchange or ion exchange or reversed-phase chromatography columns in order to obtain at least a portion of the produced one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof, thereby isolating the produced one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof;

or

(a) providing the cell culture comprising the one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof;

(b) separating a liquid phase of the cell culture from a solid phase of the cell culture to obtain a supernatant comprising the produced one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof;

(c) crystallizing or extracting the produced one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof, thereby isolating the produced one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof.

[0021] In one aspect, the method disclosed herein further comprises recovering from the cell culture the one or more steviol glycosides and/or glycosylated steviol precursors or the composition thereof from the cell culture, wherein the cell culture is enriched for the one or more steviol glycosides and/or glycosides of a steviol presursor, or the composition thereof relative to a steviol glycoside composition from a Stevia plant and has a reduced level of Stevia plant-derived components relative to a plant-derived Stevia extract.

[0022] In one aspect of the method disclosed herein, the recovered one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof are present in relative amounts that are different from a steviol glycoside composition recovered from a Stevia plant and have a reduced level of Stevia plant-derived components relative to a plant-derived Stevia extract.

[0023] The invention also provides a method for producing one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof, comprising whole cell bioconversion of plant-derived or synthetic steviol, steviol precursors and/or steviol glycosides in a cell culture medium of a recombinant host using:

(a) a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position;

(b) a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position;

(c) a gene encoding a polypeptide capable of beta-1,2-glycosylation of the C2' and/or beta-1,3-glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside; and/or

(d) a gene encoding a polypeptide capable of glycosylating a steviol precursor at its C-19 carboxyl or C-19 hydroxyl position;

wherein at least one of the polypeptides is a recombinant polypeptide expressed in the recombinant host cell; and producing the one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof, thereby.

[0024] In one aspect of the method disclosed herein:

(a) the polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position is a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73E1 polypeptide, a UGT75B1 polypeptide, a UGT75L6 polypeptide, a OleI polypeptide, a UGT5 polypeptide, a SA Gtase polypeptide, a UDPG1 polypeptide, a UN1671 polypeptide, a UGT74F1 polypeptide, a UGT84B2 polypeptide, and/or a UGT74F2-like UGT polypeptide;

(b) the polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position is a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73C7 polypeptide, a UGT73E1 polypeptide, and/or a UGT76E12 polypeptide;

(c) the polypeptide capable of beta-1,2-glycosylation of the C2' and/or beta-1,3-glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside is a UGT73C6 polypeptide, a CaUGT3 polypeptide, a UN32491 polypeptide, and/or a UN1671 polypeptide; and/or

(d) the polypeptide capable of glycosylating a steviol precursor at its C-19 carboxyl or C-19 hydroxyl position is a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73E1 polypeptide, a

UGT75B1 polypeptide, a UGT75L6 polypeptide, a UGT76E12 polypeptide, a OleI polypeptide, a UGT5 polypeptide, a SA Gtase, a UDPG1 polypeptide, a UGT74F1 polypeptide, a UGT75D1 polypeptide, a UGT84B2 polypeptide, and/or a UGT74F2-like UGT polypeptide.

[0025] In one aspect of the method disclosed herein, the UGT73C1 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:127, the UGT73C3 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:133, the UGT73C5 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:135, the UGT73C6 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:137, the UGT73E1 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:141, a UGT74D1 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:143, the UGT75B1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:145, the UGT75L6 polypeptide comprises a polypeptide having at least 60% sequence identity to an amino acid sequence set forth in SEQ ID NO:147, the UGT76E12 polypeptide comprises a polypeptide having at least 60% sequence identity to an amino acid sequence set forth in SEQ ID NO:153, the OleI polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:177, the UGT5 polypeptide comprises a polypeptide having at least 65% identity to an amino acid sequence set forth in SEQ ID NO:181, the SA Gtase polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:183, the UDPG1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:185, the UN1671 polypeptide comprises a polypeptide having at least 45% identity to an amino acid sequence set forth in SEQ ID NO:201, the UGT74F1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:203, the UGT75D1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:205, the UGT84B2 polypeptide comprises a polypeptide having at least 40% sequence identity to an amino acid sequence set forth in SEQ ID NO:207, the UGT74F2-like UGT polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:211, the UGT73C7 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:139, the CaUGT3 polypeptide comprises a polypeptide having at least 50% identity

to an amino acid sequence set forth in SEQ ID NO:169, the UN32491 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:199, or the CaUGT2 polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:209.

[0026] In one aspect of the method disclosed herein, the recombinant host cell is a plant cell, a mammalian cell, an insect cell, a fungal cell, an algal cell or a bacterial cell.

[0027] The invention also provides an *in vitro* method for producing one or more steviol glycosides and/or glycosylated steviol precursors, or a composition thereof comprising adding:

(a) a UGT85C2 polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:7;

(b) a UGT76G1 polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:9;

(c) a UGT74G1 polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:4;

(d) a UGT91D2 functional homolog polypeptide comprising a UGT91D2e polypeptide having 90% or greater identity to an amino acid sequence set forth in SEQ ID NO:11 or a UGT91D2e-b polypeptide having 90% or greater identity to an amino acid sequence set forth in SEQ ID NO:13;

(e) a EUGT11 polypeptide having at least 65% identity to an amino acid sequence set forth in SEQ ID NO:16; and/or

(f) a UGT73C1 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:127, a UGT73C3 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:133, a UGT73C5 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:135, a UGT73C6 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:137, a UGT73E1 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:141, a UGT74D1 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:143, a UGT75B1 polypeptide comprises a polypeptide having at

least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:145, a UGT75L6 polypeptide comprises a polypeptide having at least 60% sequence identity to an amino acid sequence set forth in SEQ ID NO:147, a UGT76E12 polypeptide comprises a polypeptide having at least 60% sequence identity to an amino acid sequence set forth in SEQ ID NO:153, a Olel polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:177, a UGT5 polypeptide comprises a polypeptide having at least 65% identity to an amino acid sequence set forth in SEQ ID NO:181, a SA Gtase polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:183, a UDPG1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:185, a UN1671 polypeptide comprises a polypeptide having at least 45% identity to an amino acid sequence set forth in SEQ ID NO:201, a UGT74F1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:203, a UGT75D1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:205, a UGT84B2 polypeptide comprises a polypeptide having at least 40% sequence identity to an amino acid sequence set forth in SEQ ID NO:207, a UGT74F2-like UGT polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:211, a UGT73C7 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:139, a CaUGT3 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:169, a UN32491 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:199, or a CaUGT2 polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:209;

and a plant-derived or synthetic steviol glycoside precursor or a plant-derived or synthetic steviol precursor to a reaction mixture;

wherein at least one of the polypeptides is a recombinant polypeptide; and

producing the one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof, thereby.

[0028] In one aspect of the method disclosed herein, the reaction mixture comprises:

(a) glucose, fructose, sucrose, xylose, rhamnose, uridine diphosphate (UDP)-glucose, UDP-rhamnose, UDP-xylose, and/or N-acetyl-glucosamine; and/or

(b) reaction buffer and/or salts.

[0029] In one aspect of the method disclosed herein, the one or more steviol glycosides and/or glycosylated steviol precursors are, or the composition thereof comprises, 13-SMG, 19-SMG, steviol-1,2-bioside, steviol-1,3-bioside, 1,2-stevioside, 1,3-stevioside, rubusoside, RebA, RebB, RebC, RebD, RebE, RebF, RebM, RebQ, RebI, dulcoside A, a mono-glycosylated *ent*-kaurenoic acid, a di-glycosylated *ent*-kaurenoic acid, a tri-glycosylated *ent*-kaurenoic acid, a mono-glycosylated *ent*-kaurenols, a di-glycosylated *ent*-kaurenol, a tri-glycosylated *ent*-kaurenol, a tri-glycosylated steviol glycoside, a tetra-glycosylated steviol glycoside, a penta-glycosylated steviol glycoside, a hexa-glycosylated steviol glycoside, a hepta-glycosylated steviol glycoside, and/or an isomer thereof.

[0030] In one aspect of the method disclosed herein, the mono-glycosylated *ent*-kaurenoic acid comprises KA1.58 of Table 1 and/or the penta-glycosylated steviol comprises Compound 5.24 of Table 1.

[0031] The invention also provides a cell culture, comprising the recombinant host cell disclosed herein, the cell culture further comprising:

(a) one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof produced by the recombinant host cell,

(b) glucose, fructose, sucrose, xylose, rhamnose, UDP-glucose, UDP-rhamnose, UDP-xylose, and/or N-acetyl-glucosamine; and

(c) supplemental nutrients comprising trace metals, vitamins, salts, yeast nitrogen base (YNB), and/or amino acids;

wherein the one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof is present at a concentration of at least 1 mg/liter of the cell culture;

wherein the cell culture is enriched for the one or more steviol glycosides and/or glycosides of a steviol presursor, or the composition thereof relative to a steviol glycoside composition from a Stevia plant and has a reduced level of Stevia plant-derived components relative to a plant-derived Stevia extract.

[0032] The invention also provides a cell lysate from the recombinant host cell disclosed herein grown in the cell culture, comprising:

(a) one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof produced by the recombinant host cell;

(b) glucose, fructose, sucrose, xylose, rhamnose, UDP-glucose, UDP-rhamnose, UDP-xylose, and/or N-acetyl-glucosamine; and/or

(c) supplemental nutrients comprising trace metals, vitamins, salts, yeast nitrogen base, YNB, and/or amino acids;

wherein the one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof produced by the recombinant host cell is present at a concentration of at least 1 mg/liter of the cell culture.

[0033] The invention also provides a reaction mixture, comprising:

(a) a UGT85C2 polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:7;

(b) a UGT76G1 polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:9;

(c) a UGT74G1 polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:4;

(d) a UGT91D2 functional homolog polypeptide comprising a UGT91D2e polypeptide having 90% or greater identity to an amino acid sequence set forth in SEQ ID NO:11 or a UGT91D2e-b polypeptide having 90% or greater identity to an amino acid sequence set forth in SEQ ID NO:13;

(e) a EUGT11 polypeptide having at least 65% identity to an amino acid sequence set forth in SEQ ID NO:16; and/or

(f) a UGT73C1 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:127, a UGT73C3 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:133, a UGT73C5 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:135, a UGT73C6 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:137, a UGT73E1

polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:141, a UGT75B1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:145, a UGT75L6 polypeptide comprises a polypeptide having at least 60% sequence identity to an amino acid sequence set forth in SEQ ID NO:147, a UGT76E12 polypeptide comprises a polypeptide having at least 60% sequence identity to an amino acid sequence set forth in SEQ ID NO:153, a OleI polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:177, a UGT5 polypeptide comprises a polypeptide having at least 65% identity to an amino acid sequence set forth in SEQ ID NO:181, a SA Gtase polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:183, a UDPG1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:185, a UN1671 polypeptide comprises a polypeptide having at least 45% identity to an amino acid sequence set forth in SEQ ID NO:201, a UGT74F1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:203, a UGT75D1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:205, a UGT84B2 polypeptide comprises a polypeptide having at least 40% sequence identity to an amino acid sequence set forth in SEQ ID NO:207, a UGT74F2-like UGT polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:211, a UGT73C7 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:139, a CaUGT3 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:169, or a UN32491 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:199;

and further comprising:

(g) one or more steviol glycosides and/or glycosylated steviol precursors, or a composition thereof;

(h) glucose, fructose, sucrose, xylose, rhamnose, uridine diphosphate (UDP)-glucose, UDP-rhamnose, UDP-xylose, and/or N-acetyl-glucosamine; and/or

(i) reaction buffer and/or salts.

[0034] The invention also provides a composition of one or more steviol glycosides and/or glycosylated steviol precursors produced by the recombinant host cell disclosed herein; wherein the one or more steviol glycosides and/or glycosylated steviol precursors produced by the recombinant host cell are present in relative amounts that are different from a steviol glycoside composition from a Stevia plant and have a reduced level of Stevia plant-derived components relative to a plant-derived Stevia extract.

[0035] The invention also provides a composition of one or more steviol glycosides and/or glycosylated steviol precursors produced by the method disclosed herein; wherein the one or more steviol glycosides and/or glycosylated steviol precursors produced by the recombinant host cell are present in relative amounts that are different from a steviol glycoside composition from a Stevia plant and have a reduced level of Stevia plant-derived components relative to a plant-derived Stevia extract.

[0036] The invention also provides a sweetener composition, comprising one or more steviol glycosides and/or glycosylated steviol precursors produced by the recombinant host cell and/or the method disclosed herein.

[0037] The invention also provides a food product, comprising the sweetener composition disclosed herein.

[0038] The invention also provides a beverage or a beverage concentrate, comprising the sweetener composition disclosed herein.

[0039] The invention also provides an isolated nucleic acid molecule encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position or a catalytically active portion thereof, wherein the encoded polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position or the catalytically active portion thereof has at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:127, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:133, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:135, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:137, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:141, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID

NO:145, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:147, at least 55% sequence identity to the amino acid sequence set forth in SEQ ID NO:177, at least 65% sequence identity to the amino acid sequence set forth in SEQ ID NO:181, at least 55% sequence identity to the amino acid sequence set forth in SEQ ID NO:183, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:185, at least 45% sequence identity to the amino acid sequence set forth in SEQ ID NO:201, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:203, at least 40% sequence identity to the amino acid sequence set forth in SEQ ID NO:207, or at least 55% sequence identity to the amino acid sequence set forth in SEQ ID NO:211.

[0040] The invention also provides an isolated nucleic acid molecule encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position or a catalytically active portion thereof, wherein the encoded polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position or the catalytically active portion thereof has at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:127, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:133, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:135, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:137, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:139, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:141, or at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:153.

[0041] The invention also provides an isolated nucleic acid molecule encoding a polypeptide capable of beta-1,2-glycosylation of the C2' and/or beta-1,3-glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside or a catalytically active portion thereof, wherein the encoded polypeptide capable of beta-1,2-glycosylation of the C2' and/or beta-1,3-glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside or the catalytically active portion thereof has at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:137, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:169, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:199, or at least 45% sequence identity to the amino acid sequence set forth in SEQ ID NO:201.

[0042] The invention also provides an isolated nucleic acid molecule encoding a polypeptide capable of glycosylating a steviol precursor at its C-19 carboxyl or C-19 hydroxyl position or a catalytically active portion thereof, wherein the encoded polypeptide capable of glycosylating a steviol precursor at its C-19 carboxyl or C-19 hydroxyl position or the catalytically active portion thereof has at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:127, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:133, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:135, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:137, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:141, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:145, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:147, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:153, at least 55% sequence identity to the amino acid sequence set forth in SEQ ID NO:177, at least 65% sequence identity to the amino acid sequence set forth in SEQ ID NO:181, at least 55% sequence identity to the amino acid sequence set forth in SEQ ID NO:183, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:185, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:203, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:205, at least 40% sequence identity to the amino acid sequence set forth in SEQ ID NO:207, or at least 55% sequence identity to the amino acid sequence set forth in SEQ ID NO:211.

[0043] In one aspect of the isolated nucleic acids disclosed herein, the nucleic acid is cDNA.

[0044] These and other features and advantages of the present invention will be more fully understood from the following detailed description taken together with the accompanying claims. It is noted that the scope of the claims is defined by the recitations therein and not by the specific discussion of features and advantages set forth in the present description.

BRIEF DESCRIPTION OF THE DRAWINGS

[0045] The following detailed description of the embodiments of the present invention can be best understood when read in conjunction with the following drawings, where like structure is indicated with like reference numerals and in which:

[0046] Figure 1 shows representative primary steviol glycoside glycosylation reactions catalyzed by suitable uridine 5'-diphospho (UDP) glycosyl transferases (UGT) enzymes and chemical structures for several of the compounds found in Stevia extracts.

[0047] Figure 2 shows the biochemical pathway for producing steviol from geranylgeranyl diphosphate using geranylgeranyl diphosphate synthase (GGPPS), ent-copalyl diphosphate synthase (CDPS), ent-kaurene synthase (KS), ent-kaurene oxidase (KO), and ent-kaurenoic acid hydroxylase (KAH) polypeptides.

[0048] Figure 3 shows the structures of steviol+6Glc (isomer 1) and steviol+7Glc (isomer 2).

[0049] Figure 4 shows the structures of steviol+4Glc (#26) and *ent*-kaurenoic Acid+3Glc (isomer 1).

[0050] Figure 5 shows the structures *ent*-kaurenoic acid+3Glc (isomer 2) and *ent*-kaurenol+3Glc (isomer 1).

[0051] Figures 6A, 6B, and 6C show a ^{1}H NMR spectrum and ^{1}H and ^{13}C NMR chemical shifts (in ppm) for ent-kaurenoic acid+3Glc (isomer 1). Figures 6D, 6E, and 6F show a ^{1}H NMR spectrum and ^{1}H and ^{13}C NMR chemical shifts (in ppm) for ent-kaurenoic acid+3Glc (isomer 2). Figures 6G, 6H, and 6I show a ^{1}H NMR spectrum and ^{1}H and ^{13}C NMR chemical shifts (in ppm) for ent-kaurenol+3Glc (isomer 1). Figures 6J, 6K, 6L, and 6M show a ^{1}H NMR spectrum and ^{1}H and ^{13}C NMR chemical shifts (in ppm) for steviol+6Glc (isomer 1). Figures 6N, 6O, 6P, and 6Q show a ^{1}H NMR spectrum and ^{1}H and ^{13}C NMR chemical shifts (in ppm) for steviol+7Glc (isomer 2). Figures 6R, 6S, 6T, and 6U show a ^{1}H NMR spectrum and ^{1}H and ^{13}C NMR chemical shifts (in ppm) for steviol+4Glc (#26).

[0052] Skilled artisans will appreciate that elements in the Figures are illustrated for simplicity and clarity and have not necessarily been drawn to scale. For example, the dimensions of some of the elements in the Figures can be exaggerated relative to other elements to help improve understanding of the embodiment(s) of the present invention.

DETAILED DESCRIPTION OF THE INVENTION

[0053] All publications, patents and patent applications cited herein are hereby expressly incorporated by reference for all purposes.

[0054] Before describing the present invention in detail, a number of terms will be defined. As used herein, the singular forms “a,” “an,” and “the” include plural referents unless the context clearly dictates otherwise. For example, reference to a “nucleic acid” means one or more nucleic acids.

[0055] It is noted that terms like “preferably,” “commonly,” and “typically” are not utilized herein to limit the scope of the claimed invention or to imply that certain features are critical, essential, or even important to the structure or function of the claimed invention. Rather, these terms are merely intended to highlight alternative or additional features that can or cannot be utilized in a particular embodiment of the present invention.

[0056] For the purposes of describing and defining the present invention it is noted that the term “substantially” is utilized herein to represent the inherent degree of uncertainty that can be attributed to any quantitative comparison, value, measurement, or other representation. The term “substantially” is also utilized herein to represent the degree by which a quantitative representation can vary from a stated reference without resulting in a change in the basic function of the subject matter at issue.

[0057] Methods well known to those skilled in the art can be used to construct genetic expression constructs and recombinant cells according to this invention. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, *in vivo* recombination techniques, and polymerase chain reaction (PCR) techniques. *See*, for example, techniques as described in Green & Sambrook, 2012, MOLECULAR CLONING: A LABORATORY MANUAL, Fourth Edition, Cold Spring Harbor Laboratory, New York; Ausubel *et al*., 1989, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, Greene Publishing Associates and Wiley Interscience, New York, and PCR Protocols: A Guide to Methods and Applications (Innis *et al*., 1990, Academic Press, San Diego, CA).

[0058] As used herein, the terms “polynucleotide,” “nucleotide,” “oligonucleotide,” and “nucleic acid” can be used interchangeably to refer to nucleic acid comprising DNA, RNA, derivatives thereof, or combinations thereof, in either single-stranded or double-stranded embodiments depending on context as understood by the skilled worker.

[0059] As used herein, the terms “microorganism,” “microorganism host,” and “microorganism host cell” can be used interchangeably. As used herein, the terms “recombinant host” and “recombinant host cell” can be used interchangeably. The person of ordinary skill in the art will appreciate that the terms “microorganism,” microorganism host,” and “microorganism host cell,” when used to describe a cell comprising a recombinant gene, may be taken to mean “recombinant host” or “recombinant host cell.” As used herein, the term “recombinant host” is intended to refer to a host, the genome of which has been augmented by at least one DNA sequence. Such DNA sequences include but are not limited to genes that are not naturally present, DNA sequences that are not normally transcribed into RNA or translated into a protein (“expressed”), and other genes or DNA sequences which one desires to introduce into a host. It will be appreciated that typically the genome of a recombinant host described herein is augmented through stable introduction of one or more recombinant genes. Generally, introduced DNA is not originally resident in the host that is the recipient of the DNA, but it is within the scope of this disclosure to isolate a DNA segment from a given host, and to subsequently introduce one or more additional copies of that DNA into the same host, *e.g.*, to enhance production of the product of a gene or alter the expression pattern of a gene. In some instances, the introduced DNA will modify or even replace an endogenous gene or DNA sequence by, *e.g.*, homologous recombination or site-directed mutagenesis. Suitable recombinant hosts include microorganisms.

[0060] As used herein, the term “recombinant gene” refers to a gene or DNA sequence that is introduced into a recipient host, regardless of whether the same or a similar gene or DNA sequence may already be present in such a host. “Introduced,” or “augmented” in this context, is known in the art to mean introduced or augmented by the hand of man. Thus, a recombinant gene can be a DNA sequence from another species or can be a DNA sequence that originated from or is present in the same species but has been incorporated into a host by recombinant methods to form a recombinant host. It will be appreciated that a recombinant gene that is introduced into a host can be identical to a DNA sequence that is normally present in the host being transformed, and is introduced to provide one or more additional copies of the DNA to thereby permit overexpression or modified expression of the gene product of that DNA. In some aspects, said recombinant genes are encoded by cDNA. In other embodiments, recombinant genes are synthetic and/or codon-optimized for expression in *S. cerevisiae*.

[0061] As used herein, the term “engineered biosynthetic pathway” refers to a biosynthetic pathway that occurs in a recombinant host, as described herein. In some aspects, one or more

steps of the biosynthetic pathway do not naturally occur in an unmodified host. In some embodiments, a heterologous version of a gene is introduced into a host that comprises an endogenous version of the gene.

[0062] As used herein, the term “endogenous” gene refers to a gene that originates from and is produced or synthesized within a particular organism, tissue, or cell. In some embodiments, the endogenous gene is a yeast gene. In some embodiments, the gene is endogenous to *S. cerevisiae*, including, but not limited to *S. cerevisiae* strain S288C. In some embodiments, an endogenous yeast gene is overexpressed. As used herein, the term “overexpress” is used to refer to the expression of a gene in an organism at levels higher than the level of gene expression in a wild type organism. *See*, *e.g.*, Prelich, 2012, *Genetics* 190:841-54. In some embodiments, an endogenous yeast gene, for example ADH, is deleted. *See*, *e.g.*, Giaever & Nislow, 2014, *Genetics* 197(2):451-65. As used herein, the terms “deletion,” “deleted,” “knockout,” and “knocked out” can be used interchangabley to refer to an endogenous gene that has been manipulated to no longer be expressed in an organism, including, but not limited to, *S. cerevisiae*.

[0063] As used herein, the terms “heterologous sequence” and “heterologous coding sequence” are used to describe a sequence derived from a species other than the recombinant host. In some embodiments, the recombinant host is an *S. cerevisiae* cell, and a heterologous sequence is derived from an organism other than *S. cerevisiae*. A heterologous coding sequence, for example, can be from a prokaryotic microorganism, a eukaryotic microorganism, a plant, an animal, an insect, or a fungus different than the recombinant host expressing the heterologous sequence. In some embodiments, a coding sequence is a sequence that is native to the host.

[0064] A “selectable marker” can be one of any number of genes that complement host cell auxotrophy, provide antibiotic resistance, or result in a color change. Linearized DNA fragments of the gene replacement vector then are introduced into the cells using methods well known in the art (*see* below). Integration of the linear fragments into the genome and the disruption of the gene can be determined based on the selection marker and can be verified by, for example, PCR or Southern blot analysis. Subsequent to its use in selection, a selectable marker can be removed from the genome of the host cell by, *e.g.*, Cre-LoxP systems (*see*, *e.g.*, Gossen *et al.*, 2002, *Ann. Rev. Genetics* 36:153-173 and U.S. 2006/0014264). Alternatively, a gene replacement vector can be constructed in such a way as to include a portion of the gene to be

disrupted, where the portion is devoid of any endogenous gene promoter sequence and encodes none, or an inactive fragment of, the coding sequence of the gene.

[0065] As used herein, the terms “variant” and “mutant” are used to describe a protein sequence that has been modified at one or more amino acids, compared to the wild-type sequence of a particular protein.

[0066] As used herein, the term “inactive fragment” is a fragment of the gene that encodes a protein having, *e.g.*, less than about 10% (*e.g.*, less than about 9%, less than about 8%, less than about 7%, less than about 6%, less than about 5%, less than about 4%, less than about 3%, less than about 2%, less than about 1%, or 0%) of the activity of the protein produced from the full-length coding sequence of the gene. Such a portion of a gene is inserted in a vector in such a way that no known promoter sequence is operably linked to the gene sequence, but that a stop codon and a transcription termination sequence are operably linked to the portion of the gene sequence. This vector can be subsequently linearized in the portion of the gene sequence and transformed into a cell. By way of single homologous recombination, this linearized vector is then integrated in the endogenous counterpart of the gene with inactivation thereof.

[0067] As used herein, the term “steviol glycoside” refers to rebaudioside A (RebA) (CAS # 58543-16-1), rebaudioside B (RebB) (CAS # 58543-17-2), rebaudioside C (RebC) (CAS # 63550-99-2), rebaudioside D (RebD) (CAS # 63279-13-0), rebaudioside E (RebE) (CAS # 63279-14-1), rebaudioside F (RebF) (CAS # 438045-89-7), rebaudioside M (RebM) (CAS # 1220616-44-3), rubusoside (CAS # 63849-39-4), Dulcoside A (CAS # 64432-06-0), rebaudioside I (RebI) (MassBank Record: FU000332), rebaudioside Q (RebQ), 1,2-stevioside (CAS # 57817-89-7), 1,3-stevioside (RebG), steviol-1,2-bioside (MassBank Record: FU000299), steviol-1,3-bioside, steviol-13-*O*-glucoside (13-SMG), steviol-19-*O*-glucoside (19-SMG), a tri-glucosylated steviol glycoside, a tetra-glycosylated steviol glycoside, a penta-glucosylated steviol glycoside, a hexa-glucosylated steviol glycoside, a hepta-glucosylated steviol glycoside, and isomers thereof. *See* Figure 1; *see also*, Steviol Glycosides Chemical and Technical Assessment 69th JECFA, 2007, prepared by Harriet Wallin, Food Agric. Org. Nuclear magnetic resonance (NMR) spectra for steviol glycoside isomers disclosed herein can be found in Figure 6.

[0068] As used herein, the terms “steviol glycoside precursor” and “steviol glycoside precursor compound” are used to refer to intermediate compounds in the steviol glycoside biosynthetic pathway. Steviol glycoside precursors include, but are not limited to, geranylgeranyl diphosphate (GGPP), *ent*-copalyl-diphosphate, *ent*-kaurene, *ent*-kaurenol, *ent*-

kaurenal, *ent*-kaurenoic acid, and steviol. *See* Figure 2. Also as used herein, the terms "steviol precursor" and "steviol precursor compound" are used to refer to intermediate compounds in the steviol biosynthetic pathway (*i.e.*, compounds from which steviol may ultimately be synthesized). Steviol precursors include, but are not limited to, geranylgeranyl diphosphate (GGPP), ent-copalyl-diphosphate, ent-kaurene, ent-kaurenol, ent-kaurenal, and ent-kaurenoic acid. In some embodiments, steviol precurors can be glycosylated, *e.g.*, tri-glycosylated *ent*-kaurenoic acid (*ent*-kaurenoic acid+3Glc), di-glycosylated *ent*-kaurenoic acid, mono-glycosylated *ent*-kaurenoic acid, tri-glycosylated *ent-kaurenol*, di-glycosylated *ent*-kaurenol (*ent*-kaurenol+2Glc), or mono-glycosylated *ent-kaurenol* (*ent*-kaurenol+1Glc). The person of ordinary skill in the art will appreciate that steviol precursors may be steviol glycoside precursors. In some embodiments, steviol glycoside precursors are themselves steviol glycoside compounds. For example, 19-SMG, rubusoside, stevioside, and RebE are steviol glycoside precursors of RebM. *See* Figure 1.

[0069] As used herein, the term "contact" is used to refer to any physical interaction between two objects. For example, the term "contact" may refer to the interaction between an an enzyme and a susbtrate. In another example, the term "contact" may refer to the interaction between a liquid (*e.g.*, a supernatant) and an adsorbent resin.

[0070] Steviol glycosides, steviol glycoside precursors, and/or glycosides of steviol precursors can be produced *in vivo* (*i.e.*, in a recombinant host), *in vitro* (*i.e.*, enzymatically), or by whole cell bioconversion. As used herein, the terms "produce" and "accumulate" can be used interchangeably to describe synthesis of steviol glycosides, glycosides of steviol precursors, and steviol glycoside precursors *in vivo*, *in vitro*, or by whole cell bioconversion.

[0071] Recombinant steviol glycoside-producing *Saccharomyces cerevisiae* (*S. cerevisiae*) strains are described in WO 2011/153378, WO 2013/022989, WO 2014/122227, and WO 2014/122328. Methods of producing steviol glycosides in recombinant hosts, by whole cell bio-conversion, and *in vitro* are also described in WO 2011/153378, WO 2013/022989, WO 2014/122227, and WO 2014/122328.

[0072] As used herein, the terms "culture broth," "culture medium," and "growth medium" can be used interchangeably to refer to a liquid or solid that supports growth of a cell. A culture broth can comprise glucose, fructose, sucrose, trace metals, vitamins, salts, yeast nitrogen base (YNB), and/or amino acids. The trace metals can be divalent cations, including, but not limited to, Mn^{2+} and/or Mg^{2+}. In some embodiments, Mn^{2+} can be in the form of $MnCl_2$ dihydrate and range from approximately 0.01 g/L to 100 g/L. In some embodiments, Mg^{2+} can be in the form

of $MgSO_4$ heptahydrate and range from approximately 0.01 g/L to 100 g/L. For example, a culture broth can comprise i) approximately 0.02-0.03 g/L $MnCl_2$ dihydrate and approximately 0.5-3.8 g/L $MgSO_4$ heptahydrate, ii) approximately 0.03-0.06 g/L $MnCl_2$ dihydrate and approximately 0.5-3.8 g/L $MgSO_4$ heptahydrate, and/or iii) approximately 0.03-0.17 g/L $MnCl_2$ dihydrate and approximately 0.5-7.3 g/L $MgSO_4$ heptahydrate. Additionally, a culture broth can comprise one or more steviol glycosides produced by a recombinant host, as described herein.

[0073] In some embodiments, a recombinant host comprising a gene encoding a polypeptide capable of synthesizing geranylgeranyl pyrophosphate (GGPP) from farnesyl diphosphate (FPP) and isopentenyl diphosphate (IPP) (*e.g.*, geranylgeranyl diphosphate synthase (GGPPS)); a gene encoding a polypeptide capable of synthesizing *ent*-copalyl diphosphate from GGPP (*e.g.*, ent-copalyl diphosphate synthase (CDPS)); a gene encoding a polypeptide capable of synthesizing *ent*-kaurene from *ent*-copalyl diphosphate (*e.g.*, kaurene synthase (KS)); a gene encoding a polypeptide capable of synthesizing ent-kaurenoic acid, ent-kaurenol, and/or ent-kaurenal from *ent*-kaurene (*e.g.*, kaurene oxidase (KO)); a gene encoding a polypeptide capable of reducing cytochrome P450 complex (*e.g.*, cytochrome P450 reductase (CPR) or P450 oxidoreductase (POR); for example, but not limited to a polypeptide capable of electron transfer from NADPH to cytochrome P450 complex during conversion of NADPH to $NADP^+$, which is utilized as a cofactor for terpenoid biosynthesis); a gene encoding a polypeptide capable of synthesizing steviol from *ent*-kaurenoic acid (*e.g.*, steviol synthase (KAH)); and/or a gene encoding a bifunctional polypeptide capable of synthesizing *ent*-copalyl diphosphate from GGPP and synthesizing *ent*-kaurene from *ent*-copalyl diphosphate (*e.g.*, an ent-copalyl diphosphate synthase (CDPS) – *ent*-kaurene synthase (KS) polypeptide) can produce steviol *in vivo*. *See*, *e.g.*, Figure 1. The skilled worker will appreciate that one or more of these genes can be endogenous to the host provided that at least one (and in some embodiments, all) of these genes is a recombinant gene introduced into the recombinant host.

[0074] In some embodiments, a recombinant host comprising a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position (*e.g.*, a UGT85C2 polypeptide); a gene encoding a polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside (*e.g.*, a UGT76G1 polypeptide); a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position (*e.g.*, a UGT74G1 polypeptide); and/or a gene encoding a polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a

steviol glycoside (*e.g.*, a UGT91D2 or EUGT11 polypeptide) can produce a steviol glycoside *in vivo*. The skilled worker will appreciate that one or more of these genes can be endogenous to the host provided that at least one (and in some embodiments, all) of these genes is a recombinant gene introduced into the recombinant host.

[0075] In some embodiments, steviol glycosides, glycosides of steviol precursors, and/or steviol glycoside precursors are produced *in vivo* through expression of one or more enzymes involved in the steviol glycoside biosynthetic pathway in a recombinant host. For example, a recombinant host comprising a gene encoding a polypeptide capable of synthesizing GGPP from FPP and IPP; a gene encoding a polypeptide capable of synthesizing *ent*-copalyl diphosphate from GGPP; a gene encoding a polypeptide capable of synthesizing *ent*-kaurene from *ent*-copalyl diphosphate; a gene encoding a polypeptide capable of synthesizing ent-kaurenoic acid, ent-kaurenol, and/or ent-kaurenal from *ent*-kaurene; a gene encoding a polypeptide capable of reducing cytochrome P450 complex; a gene encoding a bifunctional polypeptide capable of synthesizing *ent*-copalyl diphosphate from GGPP and synthesizing *ent*-kaurene from *ent*-copalyl diphosphate; a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position; a gene encoding a polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside; a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position; and/or a gene encoding a polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside can produce a steviol glycoside and/or steviol glycoside precursors *in vivo*. *See*, *e.g.*, Figures 1 and 2. The skilled worker will appreciate that one or more of these genes can be endogenous to the host provided that at least one (and in some embodiments, all) of these genes is a recombinant gene introduced into the recombinant host.

[0076] In some aspects, the polypeptide capable of synthesizing GGPP from FPP and IPP comprises a polypeptide having an amino acid sequence set forth in SEQ ID NO:20 (which can be encoded by the nucleotide sequence set forth in SEQ ID NO:19), SEQ ID NO:22 (encoded by the nucleotide sequence set forth in SEQ ID NO:21), SEQ ID NO:24 (encoded by the nucleotide sequence set forth in SEQ ID NO:23), SEQ ID NO:26 (encoded by the nucleotide sequence set forth in SEQ ID NO:25), SEQ ID NO:28 (encoded by the nucleotide sequence set forth in SEQ ID NO:27), SEQ ID NO:30 (encoded by the nucleotide sequence set forth in SEQ

ID NO:29), SEQ ID NO:32 (encoded by the nucleotide sequence set forth in SEQ ID NO:31), or SEQ ID NO:116 (encoded by the nucleotide sequence set forth in SEQ ID NO:115).

[0077] In some aspects, the polypeptide capable of synthesizing ent-copalyl diphosphate from GGPP comprises a polypeptide having an amino acid sequence set forth in SEQ ID NO:34 (which can be encoded by the nucleotide sequence set forth in SEQ ID NO:33), SEQ ID NO:36 (encoded by the nucleotide sequence set forth in SEQ ID NO:35), SEQ ID NO:38 (encoded by the nucleotide sequence set forth in SEQ ID NO:37), SEQ ID NO:40 (encoded by the nucleotide sequence set forth in SEQ ID NO:39), or SEQ ID NO:42 (encoded by the nucleotide sequence set forth in SEQ ID NO:41). In some embodiments, the polypeptide capable of synthesizing *ent*-copalyl diphosphate from GGPP lacks a chloroplast transit peptide.

[0078] In some aspects, the polypeptide capable of synthesizing ent-kaurene from ent-copalyl pyrophosphate comprises a polypeptide having an amino acid sequence set forth in SEQ ID NO:44 (which can be encoded by the nucleotide sequence set forth in SEQ ID NO:43), SEQ ID NO:46 (encoded by the nucleotide sequence set forth in SEQ ID NO:45), SEQ ID NO:48 (encoded by the nucleotide sequence set forth in SEQ ID NO:47), SEQ ID NO:50 (encoded by the nucleotide sequence set forth in SEQ ID NO:49), or SEQ ID NO:52 (encoded by the nucleotide sequence set forth in SEQ ID NO:51).

[0079] In some embodiments, a recombinant host comprises a gene encoding a bifunctional polypeptide capable of synthesizing ent-copalyl diphosphate from GGPP and synthesizing ent-kaurene from ent-copalyl pyrophosphate. In some aspects, the bifunctional polypeptide comprises a polypeptide having an amino acid sequence set forth in SEQ ID NO:54 (which can be encoded by the nucleotide sequence set forth in SEQ ID NO:53), SEQ ID NO:56 (encoded by the nucleotide sequence set forth in SEQ ID NO:55), or SEQ ID NO:58 (encoded by the nucleotide sequence set forth in SEQ ID NO:57).

[0080] In some aspects, the polypeptide capable of synthesizing ent-kaurenoic acid, ent-kaurenol, and/or ent-kaurenal from ent-kaurene comprises a polypeptide having an amino acid sequence set forth in SEQ ID NO:60 (which can be encoded by the nucleotide sequence set forth in SEQ ID NO:59), SEQ ID NO:62 (encoded by the nucleotide sequence set forth in SEQ ID NO:61), SEQ ID NO:117 (encoded by the nucleotide sequence set forth in SEQ ID NO:63 or SEQ ID NO:64), SEQ ID NO:66 (encoded by the nucleotide sequence set forth in SEQ ID NO:65), SEQ ID NO:68 (encoded by the nucleotide sequence set forth in SEQ ID NO:67), SEQ ID NO:70 (encoded by the nucleotide sequence set forth in SEQ ID NO:69), SEQ ID NO:72 (encoded by the nucleotide sequence set forth in SEQ ID NO:71), SEQ ID NO:74 (encoded by

the nucleotide sequence set forth in SEQ ID NO:73), or SEQ ID NO:76 (encoded by the nucleotide sequence set forth in SEQ ID NO:75).

[0081] In some aspects, the polypeptide capable of reducing cytochrome P450 complex comprises a polypeptide having an amino acid sequence set forth in SEQ ID NO:78 (which can be encoded by the nucleotide sequence set forth in SEQ ID NO:77), SEQ ID NO:80 (encoded by the nucleotide sequence set forth in SEQ ID NO:79), SEQ ID NO:82 (encoded by the nucleotide sequence set forth in SEQ ID NO:81), SEQ ID NO:84 (encoded by the nucleotide sequence set forth in SEQ ID NO:83), SEQ ID NO:86 (encoded by the nucleotide sequence set forth in SEQ ID NO:85), SEQ ID NO:88 (encoded by the nucleotide sequence set forth in SEQ ID NO:87), SEQ ID NO:90 (encoded by the nucleotide sequence set forth in SEQ ID NO:89), or SEQ ID NO:92 (encoded by the nucleotide sequence set forth in SEQ ID NO:91).

[0082] In some aspects, the polypeptide capable of synthesizing steviol from ent-kaurenoic acid comprises a polypeptide having an amino acid sequence set forth in SEQ ID NO:94 (which can be encoded by the nucleotide sequence set forth in SEQ ID NO:93), SEQ ID NO:97 (encoded by the nucleotide sequence set forth in SEQ ID NO:95 or SEQ ID NO:96), SEQ ID NO:100 (encoded by the nucleotide sequence set forth in SEQ ID NO:98 or SEQ ID NO:99), SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:106 (encoded by the nucleotide sequence set forth in SEQ ID NO:105), SEQ ID NO:108 (encoded by the nucleotide sequence set forth in SEQ ID NO:107), SEQ ID NO:110 (encoded by the nucleotide sequence set forth in SEQ ID NO:109), SEQ ID NO:112 (encoded by the nucleotide sequence set forth in SEQ ID NO:111), or SEQ ID NO:114 (encoded by the nucleotide sequence set forth in SEQ ID NO:113).

[0083] In some embodiments, a recombinant host comprises a nucleic acid encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position, a nucleic acid encoding a polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside, a nucleic acid encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position, a nucleic acid encoding a polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside. In certain such embodiments, the recombinant host further comprises a gene encoding a polypeptide capable of synthesizing GGPP from FPP and IPP; a gene encoding a polypeptide capable of synthesizing *ent*-copalyl diphosphate from GGPP; a gene encoding a polypeptide capable of synthesizing *ent*-kaurene from *ent*-copalyl diphosphate; a gene encoding

a polypeptide capable of synthesizing ent-kaurenoic acid, ent-kaurenol, and/or ent-kaurenal from *ent*-kaurene; a gene encoding a polypeptide capable of reducing cytochrome P450 complex; and/or a gene encoding a bifunctional polypeptide capable of synthesizing *ent*-copalyl diphosphate from GGPP and synthesizing *ent*-kaurene from *ent*-copalyl diphosphate.

[0084] In some embodiments, a recombinant host comprises a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position, *e.g.*, a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73E1 polypeptide, a UGT75B1 polypeptide, a UGT75L6 polypeptide, a OleI polypeptide, a UGT5 polypeptide, a SA Gtase polypeptide, a UDPG1 polypeptide, a UN1671 polypeptide, a UGT74F1 polypeptide, a UGT84B2 polypeptide, and/or a UGT74F2-like UGT polypeptide. In certain such embodiments, the recombinant host further comprises a gene encoding a polypeptide capable of synthesizing GGPP from FPP and IPP; a gene encoding a polypeptide capable of synthesizing *ent*-copalyl diphosphate from GGPP; a gene encoding a polypeptide capable of synthesizing *ent*-kaurene from *ent*-copalyl diphosphate; a gene encoding a polypeptide capable of synthesizing ent-kaurenoic acid, ent-kaurenol, and/or ent-kaurenal from *ent*-kaurene; a gene encoding a polypeptide capable of reducing cytochrome P450 complex; a gene encoding a bifunctional polypeptide capable of synthesizing *ent*-copalyl diphosphate from GGPP and synthesizing *ent*-kaurene from *ent*-copalyl diphosphate; a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position; a gene encoding a polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside; and/or a gene encoding a polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside.

[0085] In some embodiments, a recombinant host comprises a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position, *e.g.*, a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73C7 polypeptide, a UGT73E1 polypeptide, and/or a UGT76E12 polypeptide. In certain such embodiments, the recombinant host further comprises a gene encoding a polypeptide capable of synthesizing GGPP from FPP and IPP; a gene encoding a polypeptide capable of synthesizing *ent*-copalyl diphosphate from GGPP; a gene encoding a polypeptide capable of synthesizing *ent*-kaurene from *ent*-copalyl diphosphate; a gene encoding a polypeptide capable of synthesizing ent-kaurenoic acid, ent-kaurenol, and/or ent-kaurenal from *ent*-kaurene; a gene encoding a polypeptide capable of reducing cytochrome P450

complex; a gene encoding a bifunctional polypeptide capable of synthesizing *ent*-copalyl diphosphate from GGPP and synthesizing *ent*-kaurene from *ent*-copalyl diphosphate; a gene encoding a polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside; a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position; and/or a gene encoding a polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside.

[0086] In some embodiments, a recombinant host comprises a gene encoding a polypeptide capable of beta-1,2-glycosylation of the C2' and/or beta-1,3-glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside (that is, examples of glycosyl-position glycosylation), *e.g.*, a UGT73C6 polypeptide, a CaUGT3 polypeptide, a UN32491 polypeptide, and/or a UN1671 polypeptide. In certain such embodiments, the recombinant host further comprises a gene encoding a polypeptide capable of synthesizing GGPP from FPP and IPP; a gene encoding a polypeptide capable of synthesizing *ent*-copalyl diphosphate from GGPP; a gene encoding a polypeptide capable of synthesizing *ent*-kaurene from *ent*-copalyl diphosphate; a gene encoding a polypeptide capable of synthesizing ent-kaurenoic acid, ent-kaurenol, and/or ent-kaurenal from *ent*-kaurene; a gene encoding a polypeptide capable of reducing cytochrome P450 complex; a gene encoding a bifunctional polypeptide capable of synthesizing *ent*-copalyl diphosphate from GGPP and synthesizing *ent*-kaurene from *ent*-copalyl diphosphate; a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position; a gene encoding a polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside; a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position; and/or a gene encoding a polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside.

[0087] In some embodiments, a recombinant host comprises a gene encoding a polypeptide capable of glycosylating a steviol precursor at its C-19 carboxyl or C-19 hydroxyl position, *e.g.*, a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73E1 polypeptide, a UGT75B1 polypeptide, a UGT75L6 polypeptide, a UGT76E12 polypeptide, a OleI polypeptide, a UGT5 polypeptide, a SA Gtase, a UDPG1 polypeptide, a UGT74F1 polypeptide, a UGT75D1 polypeptide, a UGT84B2 polypeptide, and/or a UGT74F2-like UGT polypeptide. In certain such embodiments, the recombinant host further

comprises a gene encoding a polypeptide capable of synthesizing GGPP from FPP and IPP; a gene encoding a polypeptide capable of synthesizing *ent*-copalyl diphosphate from GGPP; a gene encoding a polypeptide capable of synthesizing *ent*-kaurene from *ent*-copalyl diphosphate; a gene encoding a polypeptide capable of synthesizing ent-kaurenoic acid, ent-kaurenol, and/or ent-kaurenal from *ent*-kaurene; a gene encoding a polypeptide capable of reducing cytochrome P450 complex; a gene encoding a bifunctional polypeptide capable of synthesizing *ent*-copalyl diphosphate from GGPP and synthesizing *ent*-kaurene from *ent*-copalyl diphosphate; a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position; a gene encoding a polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside; a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position; and/or a gene encoding a polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside.

[0088] In some embodiments, a recombinant host comprises a nucleic acid encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position (*e.g.*, UGT85C2 polypeptide) (SEQ ID NO:7), a nucleic acid encoding a polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside (*e.g.*, UGT76G1 polypeptide) (SEQ ID NO:9), a nucleic acid encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position (*e.g.*, UGT74G1 polypeptide) (SEQ ID NO:4), a nucleic acid encoding a polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside (*e.g.*, EUGT11 polypeptide) (SEQ ID NO:16). In some aspects, the polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside (*e.g.*, UGT91D2 polypeptide) can be a UGT91D2e polypeptide (SEQ ID NO:11) or a UGT91D2e-b polypeptide (SEQ ID NO:13).

[0089] In some aspects, the polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position is encoded by the nucleotide sequence set forth in SEQ ID NO:5 or SEQ ID NO:6, the polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside is encoded by the nucleotide sequence set forth in SEQ ID NO:8, the polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position is encoded by the

nucleotide sequence set forth in SEQ ID NO:3, the polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside is encoded by the nucleotide sequence set forth in SEQ ID NO:10,12,14 or 15. The skilled worker will appreciate that expression of these genes may be necessary to produce a particular steviol glycoside but that one or more of these genes can be endogenous to the host provided that at least one (and in some embodiments, all) of these genes is a recombinant gene introduced into the recombinant host.

[0090] In a particular embodiment, a steviol-producing recombinant microorganism comprises exogenous nucleic acids encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position, a polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside, and a polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside polypeptides.

[0091] In another particular embodiment, a steviol-producing recombinant microorganism comprises exogenous nucleic acids encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position; a polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside; a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position; and a polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside.

[0092] In some embodiments, polypeptides capable of catalyzing the 19-*O*-glycosylation of *ent*-kaurenoic acid (KA) to *ent*-kaurenoic acid+1Glc (#58), *in vitro*, in a recombinant host, or by whole cell bioconversion include UGT73C1 (SEQ ID NO:127), UGT73C3 (SEQ ID NO:133), UGT73C5 (SEQ ID NO:135), UGT73C6 (SEQ ID NO:137), UGT73E1 (SEQ ID NO:141), UGT74G1 (SEQ ID NO:4), UGT75B1 (SEQ ID NO:145), UGT75L6 (SEQ ID NO:147), UGT76E12 (SEQ ID NO:153), OleI (SEQ ID NO:177), UGT5 (SEQ ID NO:181), SA Gtase (SEQ ID NO:183), UDPG1 (SEQ ID NO:185), UGT74F1 (SEQ ID NO:203), UGT75D1 (SEQ ID NO:205), UGT84B2 (SEQ ID NO:207), CaUGT2 (SEQ ID NO:209), and a UGT74F2-like UGT polypeptide (SEQ ID NO:211). *See*, Example 3.

[0093] In some embodiments, polypeptides capable of catalyzing the 13-*O*-glycosylation of steviol to 13-SMG, *in vitro*, in a recombinant host, or by whole cell bioconversion include UGT73C1 (SEQ ID NO:127), UGT73C3 (SEQ ID NO:133), UGT73C5 (SEQ ID NO:135),

UGT73C6 (SEQ ID NO:137), UGT73C7 (SEQ ID NO:139), UGT73E1 (SEQ ID NO:141), UGT76E12 (SEQ ID NO:153), and UGT85C2 (SEQ ID NO:7). *See*, Example 3.

[0094] In some embodiments, polypeptides capable of catalyzing the 19-*O*-glycosylation of steviol to 19-SMG, in vitro, in a recombinant host, or by whole cell bioconversion include UGT73C1 (SEQ ID NO:127), UGT73C3 (SEQ ID NO:133), UGT73C5 (SEQ ID NO:135), UGT73C6 (SEQ ID NO:137), UGT73E1 (SEQ ID NO:141), UGT74D1 (SEQ ID NO:143), UGT74G1 (SEQ ID NO:4), UGT75B1 (SEQ ID NO:145), UGT75L6 (SEQ ID NO:147), OleI (SEQ ID NO:177), UGT5 (SEQ ID NO:181), SA Gtase (SEQ ID NO:183), and UDPG1 (SEQ ID NO:185). See, Example 3.

[0095] In some embodiments, polypeptides capable of catalyzing the 19-*O*-glycosylation of 13-SMG to rubusoside, *in vitro*, in a recombinant host, or by whole cell bioconversion include UGT73C1 (SEQ ID NO:127), UGT73C6 (SEQ ID NO:137), UGT74G1 (SEQ ID NO:4), UGT85C2 (SEQ ID NO:7), SA Gtase (SEQ ID NO:183), UDPG1 (SEQ ID NO:185), UN1671 (SEQ ID NO:201), UGT74F1 (SEQ ID NO:203), UGT75D1 (SEQ ID NO:205), UGT84B2 (SEQ ID NO:207), CaUGT2 (SEQ ID NO:209), and a UGT74F2-like UGT polypeptide (SEQ ID NO:211). *See*, Example 3.

[0096] In some embodiments, polypeptides capable of catalyzing the glycosylation of 13-SMG (that is, an examples of glycosyl-position glycosylation) to steviol-1,2-bioside, *in vitro*, in a recombinant host, or by whole cell bioconversion include UGT91D2e-b (SEQ ID NO:13), EUGT11 (SEQ ID NO:16), and UN32491 (SEQ ID NO:199).

[0097] In some embodiments, polypeptides capable of catalyzing the glycosyl-position glycosylation of rubusoside to 1,2-stevioside, *in vitro*, in a recombinant host, or by whole cell bioconversion include UGT73C6 (SEQ ID NO:137), UGT91D2e-b (SEQ ID NO:13), CaUGT3 (SEQ ID NO:169), and EUGT11 (SEQ ID NO:16). *See*, Example 3.

[0098] In some embodiments, polypeptides capable of catalyzing the glycosyl-position glycosylation of rubusoside to steviol+3Glc (#55), *in vitro*, in a recombinant host, or by whole cell bioconversion include EUGT11 (SEQ ID NO:16).

[0099] In some embodiments, polypeptides capable of catalyzing the 19-*O*-glycosylation of RebB to RebA, *in vitro*, in a recombinant host, or by whole cell bioconversion include UGT74G1 (SEQ ID NO:4). *See*, Example 3.

[00100] In some embodiments, polypeptides capable of catalyzing the glycosyl-position glycosylation of RebA to RebD, *in vitro*, in a recombinant host, or by whole cell bioconversion include EUGT11 (SEQ ID NO:16).

[00101] In some embodiments, polypeptides capable of catalyzing the glycosyl-position glycosylation of RebA to steviol+5Glc (#24), *in vitro*, in a recombinant host, or by whole cell bioconversion include EUGT11 (SEQ ID NO:16) and UN1671 (SEQ ID NO:201). *See*, Example 3.

[00102] In some aspects, polypeptides capable of 19-*O*-glycosylation activity on steviol, steviol glycosides, and precurors thereof *in vitro*, in a recombinant host, or by whole cell bioconversion include UGT73C1 (SEQ ID NO:127), UGT73C3 (SEQ ID NO:133), UGT73C5 (SEQ ID NO:135), UGT73C6 (SEQ ID NO:137), UGT73E1 (SEQ ID NO:141), UGT74G1 (SEQ ID NO:4), UGT85C2 (SEQ ID NO:7), UGT75B1 (SEQ ID NO:145), UGT75L6 (SEQ ID NO:147), UGT76E12 (SEQ ID NO:153), OleI (SEQ ID NO:177), UGT5 (SEQ ID NO:181), SA Gtase (SEQ ID NO:183), UDPG1 (SEQ ID NO:185), UN1671 (SEQ ID NO:201), UGT74F1 (SEQ ID NO:203), UGT75D1 (SEQ ID NO:205), UGT84B2 (SEQ ID NO:207), and a UGT74F2-like UGT (SEQ ID NO:211). *See*, Example 3. Non-limiting examples of 19-*O*-glycosylation reactions include conversion of *ent*-kaurenoic acid to *ent*-kaurenoic acid+1Glc (#58), conversion of 13-SMG to rubusoside, and/or conversion of steviol to 19-SMG (*see*, *e.g.*, Figure 1).

[00103] In some aspects, polypeptides capable of 13-*O*-glycosylation activity on steviol and steviol glycosides *in vitro*, in a recombinant host, or by whole cell bioconversion include UGT73C1 (SEQ ID NO:127), UGT73C3 (SEQ ID NO:133), UGT73C5 (SEQ ID NO:135), UGT73C6 (SEQ ID NO:137), UGT73C7 (SEQ ID NO:139), UGT73E1 (SEQ ID NO:141), UGT76E12 (SEQ ID NO:153), and UGT85C2 (SEQ ID NO:7). *See*, Example 3. A non-limiting example of a 13-*O*-glycosylation reaction includes conversion of steviol to 13-SMG (*see*, *e.g.*, Figure 1).

[00104] In some aspects, polypeptides capable of glycosylation activity towards the glucose residues of steviol glycosides including, but not limited to, catalyzing the conversion of 13-SMG to steviol-1,2-bioside, catalyzing the conversion of rubusoside to 1,2-stevioside, and/or catalyzing the conversion of RebA to steviol+5Glc (#24) (*see*, *e.g.*, Figure 1), *in vitro*, in a recombinant host, or by whole cell bioconversion include UGT73C6 (SEQ ID NO:137), UGT91D2e-b (SEQ ID NO:13), CaUGT3 (SEQ ID NO:169), EUGT11 (SEQ ID NO:16), UN32491 (SEQ ID NO:199), and UN1671 (SEQ ID NO:201). *See*, Example 3.

[00105] In some embodiments, a recombinant host comprises a nucleic acid encoding a UGT85C2 polypeptide (SEQ ID NO:7), a nucleic acid encoding a UGT76G1 polypeptide (SEQ ID NO:9), a nucleic acid encoding a UGT74G1 polypeptide (SEQ ID NO:4), a nucleic acid encoding a UGT91D2 polypeptide, and/or a nucleic acid encoding a EUGT11 polypeptide (SEQ ID NO:16). In some aspects, the UGT91D2 polypeptide can be a UGT91D2e polypeptide (SEQ ID NO:11) a UGT91D2e-b polypeptide (SEQ ID NO:13). In some embodiments, a recombinant host comprises a nucleic acid encoding a UGT73C1 polypeptide (SEQ ID NO:127), a nucleic acid encoding a UGT73C3 polypeptide (SEQ ID NO:133), a nucleic acid encoding a UGT73C5 polypeptide (SEQ ID NO:135), a nucleic acid encoding a UGT73C6 polypeptide (SEQ ID NO:137), a nucleic acid encoding a UGT73C7 polypeptide (SEQ ID NO:139), a nucleic acid encoding a UGT73E1 polypeptide (SEQ ID NO:141), a nucleic acid encoding a UGT74D1 polypeptide (SEQ ID NO:143), a nucleic acid encoding a UGT75B1 polypeptide (SEQ ID NO:145), a nucleic acid encoding a UGT75L6 polypeptide (SEQ ID NO:147), a nucleic acid encoding a UGT76E12 polypeptide (SEQ ID NO:153), a nucleic acid encoding a CaUGT3 polypeptide (SEQ ID NO:169), a nucleic acid encoding a OleI polypeptide (SEQ ID NO:177), a nucleic acid encoding a UGT5 (SEQ ID NO:181), a nucleic acid encoding a SA Gtase polypeptide (SEQ ID NO:183), a nucleic acid encoding a UDPG1 polypeptide (SEQ ID NO:185), a nucleic acid encoding a UN32491 polypeptide (SEQ ID NO:199), a nucleic acid encoding a UN1671 polypeptide (SEQ ID NO:201), a nucleic acid encoding a UGT74F1 polypeptide (SEQ ID NO:203), a nucleic acid encoding a UGT75D1 polypeptide (SEQ ID NO:205), a nucleic acid encoding a UGT84B2 polypeptide (SEQ ID NO:207), a nucleic acid encoding a CaUGT2 polypeptide (SEQ ID NO:209) or a nucleic acid encoding a UGT74F2-like UGT polypeptide (SEQ ID NO:211).

[00106] In some aspects, the UGT85C2 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:5, SEQ ID NO:6 the UGT76G1 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:8, the UGT74G1 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:3 or SEQ ID NO:213, the UGT91D2e polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:10, the UGT91D2e-b polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:12 or SEQ ID NO:212, the EUGT11 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:14 or SEQ ID NO:15, the UGT73C1 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:126, the UGT73C3 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:132, the UGT73C5 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:134, the UGT73C6 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID

NO:136, the UGT73C7 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:138, the UGT73E1 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:140, the UGT74D1 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:142, the UGT75B1 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:144, the UGT75L6 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:146, the UGT76E12 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:152, the CaUGT3 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:168, the OleI polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:176, the UGT5 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:180, the SA Gtase polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:182, the UDPG1 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:184, the UN32491 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:198, the UN1671 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:200, the UGT74F1 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:202, the UGT75D1 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:204, the UGT84B2 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:206, the CaUGT2 polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:208, and the UGT74F2-like UGT polypeptide is encoded by the nucleotide sequence set forth in SEQ ID NO:210.

[00107] In some embodiments, steviol glycosides, glycosides of steviol precursors, and/or steviol glycoside precursors are produced through contact of a steviol glycoside precursor with one or more enzymes involved in the steviol glycoside pathway *in vitro*. For example, contacting steviol with one or more of a gene encoding a polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside, a polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside, and a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position or a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position can result in production of a steviol glycoside in vitro. In some embodiments, a steviol glycoside precursor is produced through contact of an upstream steviol glycoside precursor with one or more enzymes involved in the steviol glycoside pathway *in vitro*. For example, contacting ent-kaurenoic acid with a polypeptide capable of synthesizing steviol from ent-kaurenoic acid can result in production of steviol *in vitro*.

[00108] In some embodiments, one or more steviol glycosides and/or glycosylated steviol precursors, or a composition thereof are produced *in vitro*. In some embodiments the method comprises adding a UGT85C2 polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:7; a UGT76G1 polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:9; a UGT74G1 polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:4; a UGT91D2 functional homolog polypeptide comprising a UGT91D2e polypeptide having 90% or greater identity to an amino acid sequence set forth in SEQ ID NO:11 or a UGT91D2e-b polypeptide having 90% or greater identity to an amino acid sequence set forth in SEQ ID NO:13; a EUGT11 polypeptide having at least 65% identity to an amino acid sequence set forth in SEQ ID NO:16; a UGT73C1 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:127; a UGT73C3 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:133; a UGT73C5 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:135; a UGT73C6 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:137; a UGT73E1 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:141; a UGT75B1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:145; a UGT75L6 polypeptide comprises a polypeptide having at least 60% sequence identity to an amino acid sequence set forth in SEQ ID NO:147; a UGT76E12 polypeptide comprises a polypeptide having at least 60% sequence identity to an amino acid sequence set forth in SEQ ID NO:153; a OleI polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:177; a UGT5 polypeptide comprises a polypeptide having at least 65% identity to an amino acid sequence set forth in SEQ ID NO:181; a SA Gtase polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:183; a UDPG1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:185; a UN1671 polypeptide comprises a polypeptide having at least 45% identity to an amino acid sequence set forth in SEQ ID NO:201; a UGT74F1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:203; a UGT75D1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:205; a UGT84B2 polypeptide comprises a polypeptide having at least 40% sequence identity to an amino acid sequence set forth in SEQ ID NO:207; a UGT74F2-like UGT polypeptide comprises

a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:211; a UGT73C7 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:139; a CaUGT3 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:169; and/or a UN32491 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:199; and a plant-derived or synthetic steviol glycoside precursor or a plant-derived or synthetic steviol to a reaction mixture; wherein at least one of the polypeptides is a recombinant polypeptide; and producing the one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof, thereby.

[00109] In some embodiments, a steviol glycoside or steviol glycoside precursor is produced by whole cell bioconversion. For whole cell bioconversion to occur, a host cell expressing one or more enzymes involved in the steviol glycoside pathway takes up and modifies the steviol glycoside or steviol glycoside precursor in the cell; following modification *in vivo*, the steviol glycoside or steviol glycoside precursor remains in the cell and/or is excreted into the cell culture medium. For example, a host cell expressing a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position; a gene encoding a polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside; a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position; and/or a gene encoding a polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside can take up steviol and glycosylate steviol in the cell; following glycosylation in vivo, a steviol glycoside can be excreted into the culture medium. In certain such embodiments, the host cell may further express a gene encoding a polypeptide capable of synthesizing GGPP from FPP and IPP; a gene encoding a polypeptide capable of synthesizing ent-copalyl diphosphate from GGPP; a gene encoding a polypeptide capable of synthesizing ent-kaurene from ent-copalyl diphosphate; a gene encoding a polypeptide capable of synthesizing ent-kaurenoic acid, ent-kaurenol, and/or ent-kaurenal from ent-kaurene; a gene encoding a polypeptide capable of reducing cytochrome P450 complex; a gene encoding a polypeptide capable of synthesizing steviol from ent-kaurenoic acid; and/or a gene encoding a bifunctional polypeptide capable of synthesizing ent-copalyl diphosphate from GGPP and synthesizing ent-kaurene from ent-copalyl diphosphate.

[00110] In some embodiments, the method for producing one or more steviol glycosides and/or glycosylated steviol precursors, or a composition thereof as disclosed herein comprises

whole cell bioconversion of a plant-derived or synthetic steviol glycoside precursor or a plant-derived or synthetic steviol precursor in a cell culture medium of a recombinant host cell using (a) a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position; (b) a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position; (c) a polypeptide capable of beta-1,2-glycosylation of the C2' and/or beta-1,3-glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside (that is, examples of glycosyl-position glycosylation) activity on a steviol glycoside; and/or (d) a polypeptide is capable of glycosylating a steviol precursor at its C-19 carboxyl or C-19 hydroxyl position; wherein at least one of the polypeptide is a recombinant polypeptide expressed in the recombinant host cell, and producing the one or more steviol glycosides and/or glycosylated steviol precursors, or a composition thereof, thereby.

[00111] In some embodiments of the method for producing one or more steviol glycosides and/or glycosylated steviol precursors, or a composition thereof as disclosed herein by whole cell bioconversion of a plant-derived or synthetic steviol glycoside precursor or a plant-derived or synthetic steviol precursor in a cell culture medium of a recombinant host cell described herein, the polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position comprises a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73E1 polypeptide, a UGT75B1 polypeptide, a UGT75L6 polypeptide, a OleI polypeptide, a UGT5 polypeptide, a SA Gtase polypeptide, a UDPG1 polypeptide, a UN1671 polypeptide, a UGT74F1 polypeptide, a UGT84B2 polypeptide, and/or a UGT74F2-like UGT polypeptide; the polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position comprises a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73C7 polypeptide, a UGT73E1 polypeptide, and/or a UGT76E12 polypeptide; the polypeptide capable of beta-1,2-glycosylation of the C2' and/or beta-1,3-glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside (that is, examples of glycosyl-position glycosylation) activity on a steviol glycoside comprises a UGT73C6 polypeptide, a CaUGT3 polypeptide, a UN32491 polypeptide, and/or a UN1671 polypeptide; and/or the polypeptide is capable of glycosylating a steviol precursor at its C-19 carboxyl or C-19 hydroxyl position comprises a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73E1 polypeptide, a UGT75B1 polypeptide, a UGT75L6 polypeptide, a UGT76E12 polypeptide, a OleI polypeptide, a UGT5 polypeptide, a SA Gtase, a UDPG1 polypeptide, a UGT74F1 polypeptide, a UGT75D1 polypeptide, a UGT84B2 polypeptide, and/or a UGT74F2-like UGT polypeptide.

[00112] In some embodiments of the method for producing one or more steviol glycosides and/or glycosylated steviol precursors, or a composition thereof as disclosed herein by whole cell bioconversion of a plant-derived or synthetic steviol glycoside precursor or a plant-derived or synthetic steviol precursor in a cell culture medium of a recombinant host cell described herein,, the UGT73C1 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:127, the UGT73C3 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:133, the UGT73C5 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:135, the UGT73C6 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:137, the UGT73E1 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:141, the UGT75B1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:145, the UGT75L6 polypeptide comprises a polypeptide having at least 60% sequence identity to an amino acid sequence set forth in SEQ ID NO:147, the UGT76E12 polypeptide comprises a polypeptide having at least 60% sequence identity to an amino acid sequence set forth in SEQ ID NO:153, the OleI polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:177, the UGT5 polypeptide comprises a polypeptide having at least 65% identity to an amino acid sequence set forth in SEQ ID NO:181, the SA Gtase polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:183, the UDPG1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:185, the UN1671 polypeptide comprises a polypeptide having at least 45% identity to an amino acid sequence set forth in SEQ ID NO:201, the UGT74F1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:203, the UGT75D1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:205, the UGT84B2 polypeptide comprises a polypeptide having at least 40% sequence identity to an amino acid sequence set forth in SEQ ID NO:207, the UGT74F2-like UGT polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:211, the UGT73C7 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:139, the CaUGT3 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:169, or the UN32491 polypeptide comprises

a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:199.

[00113] In some embodiments, a polypeptide, *e.g.*, a UGT polypeptide, can be displayed on the surface of the recombinant host cells disclosed herein by fusing it with anchoring motifs.

[00114] In some embodiments, the cell is permeabilized to take up a substrate to be modified or to excrete a modified product. In some embodiments, a permeabilizing agent can be added to aid the feedstock entering into the host and product getting out. In some embodiments, the cells are permeabilized with a solvent such as toluene, or with a detergent such as Triton-X or Tween. In some embodiments, the cells are permeabilized with a surfactant, for example a cationic surfactant such as cetyltrimethylammonium bromide (CTAB). In some embodiments, the cells are permeabilized with periodic mechanical shock such as electroporation or a slight osmotic shock. For example, a crude lysate of the cultured microorganism can be centrifuged to obtain a supernatant. The resulting supernatant can then be applied to a chromatography column, *e.g.*, a C18 column, and washed with water to remove hydrophilic compounds, followed by elution of the compound(s) of interest with a solvent such as methanol. The compound(s) can then be further purified by preparative HPLC. *See also*, WO 2009/140394.

[00115] In some embodiments, steviol, one or more steviol glycoside precursors, and/or one or more steviol glycosides are produced by co-culturing of two or more hosts. In some embodiments, one or more hosts, each expressing one or more enzymes involved in the steviol glycoside pathway, produce steviol, one or more steviol glycoside precursors, and/or one or more steviol glycosides. For example, a host expressing a gene encoding a polypeptide capable of synthesizing GGPP from FPP and IPP; a gene encoding a polypeptide capable of synthesizing ent-copalyl diphosphate from GGPP; a gene encoding a polypeptide capable of synthesizing ent-kaurene from ent-copalyl diphosphate; a gene encoding a polypeptide capable of synthesizing ent-kaurenoic acid, ent-kaurenol, and/or ent-kaurenal from ent-kaurene; a gene encoding a polypeptide capable of reducing cytochrome P450 complex; a gene encoding a polypeptide capable of synthesizing steviol from ent-kaurenoic acid; and/or a gene encoding a bifunctional polypeptide capable of synthesizing ent-copalyl diphosphate from GGPP and synthesizing ent-kaurene from ent-copalyl diphosphate and a host expressing a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position; a gene encoding a polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside; a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position;

and/or a gene encoding a polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside, produce one or more steviol glycosides.

[00116] In some embodiments, a recombinant host comprising a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position, *e.g.*, a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73E1 polypeptide, a UGT75B1 polypeptide, a UGT75L6 polypeptide, a OleI polypeptide, a UGT5 polypeptide, a SA Gtase polypeptide, a UDPG1 polypeptide, a UN1671 polypeptide, a UGT74F1 polypeptide, a UGT84B2 polypeptide, and/or a UGT74F2-like UGT polypeptide further comprises a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:7); a gene encoding a polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:9); a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:4); and/or a gene encoding a polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:11, SEQ ID NO:13, or SEQ ID NO:16). In certain such embodiments, the recombinant host cell further comprises a gene encoding a polypeptide capable of synthesizing GGPP from FPP and IPP (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:20); a gene encoding a polypeptide capable of synthesizing *ent*-copalyl diphosphate from GGPP (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:40); a gene encoding a polypeptide capable of synthesizing *ent*-kaurene from *ent*-copalyl diphosphate (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:52); a gene encoding a polypeptide capable of synthesizing ent-kaurenoic acid, ent-kaurenol, and/or ent-kaurenal from *ent*-kaurene (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:60 or SEQ ID NO:117); a gene encoding a polypeptide capable of reducing cytochrome P450 complex (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:78, SEQ ID NO:86, or SEQ ID NO:92); and/or a gene encoding a polypeptide capable of synthesizing steviol from *ent*-kaurenoic acid (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:94).

[00117] In some embodiments, a recombinant host comprising a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position, *e.g.*, a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73C7 polypeptide, a UGT73E1 polypeptide, and/or a UGT76E12 polypeptide further comprises a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:7); a gene encoding a polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:9); a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:4); and/or a gene encoding a polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:11, SEQ ID NO:13, or SEQ ID NO:16). In certain such embodiments, the recombinant host cell further comprises a gene encoding a polypeptide capable of synthesizing GGPP from FPP and IPP (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:20); a gene encoding a polypeptide capable of synthesizing *ent*-copalyl diphosphate from GGPP (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:40); a gene encoding a polypeptide capable of synthesizing *ent*-kaurene from *ent*-copalyl diphosphate (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:52); a gene encoding a polypeptide capable of synthesizing ent-kaurenoic acid, ent-kaurenol, and/or ent-kaurenal from *ent*-kaurene (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:60 or SEQ ID NO:117); a gene encoding a polypeptide capable of reducing cytochrome P450 complex (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:78, SEQ ID NO:86, or SEQ ID NO:92); and/or a gene encoding a polypeptide capable of synthesizing steviol from *ent*-kaurenoic acid (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:94).

[00118] In some embodiments, a recombinant host comprising a gene encoding a polypeptide capable of beta-1,2-glycosylation of the C2' and/or beta-1,3-glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside (that is, examples of glycosyl-position glycosylation), *e.g.*, a UGT73C6 polypeptide, a CaUGT3 polypeptide, a UN32491 polypeptide, and/or a UN1671 polypeptide further comprises a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID

NO:7); a gene encoding a polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:9); a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:4); and/or a gene encoding a polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:11, SEQ ID NO:13, or SEQ ID NO:16). In certain such embodiments, the recombinant host cell further comprises a gene encoding a polypeptide capable of synthesizing GGPP from FPP and IPP (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:20); a gene encoding a polypeptide capable of synthesizing *ent*-copalyl diphosphate from GGPP (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:40); a gene encoding a polypeptide capable of synthesizing *ent*-kaurene from *ent*-copalyl diphosphate (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:52); a gene encoding a polypeptide capable of synthesizing ent-kaurenoic acid, ent-kaurenol, and/or ent-kaurenal from *ent*-kaurene (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:60 or SEQ ID NO:117); a gene encoding a polypeptide capable of reducing cytochrome P450 complex (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:78, SEQ ID NO:86, or SEQ ID NO:92); and/or a gene encoding a polypeptide capable of synthesizing steviol from *ent*-kaurenoic acid (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:94).

[00119] In some embodiments, a recombinant host comprising a gene encoding a polypeptide capable of glycosylating a steviol precursor at its C-19 carboxyl or C-19 hydroxyl position, *e.g.*, a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73E1 polypeptide, a UGT75B1 polypeptide, a UGT75L6 polypeptide, a UGT76E12 polypeptide, a OleI polypeptide, a UGT5 polypeptide, a SA Gtase, a UDPG1 polypeptide, a UGT74F1 polypeptide, a UGT75D1 polypeptide, a UGT84B2 polypeptide, and/or a UGT74F2-like UGT polypeptide further comprises a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:7); a gene encoding a polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:9); a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position (*e.g.*, a

polypeptide having the amino acid sequence set forth in SEQ ID NO:4); and/or a gene encoding a polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:11, SEQ ID NO:13, or SEQ ID NO:16). In certain such embodiments, the recombinant host cell further comprises a gene encoding a polypeptide capable of synthesizing GGPP from FPP and IPP (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:20); a gene encoding a polypeptide capable of synthesizing *ent*-copalyl diphosphate from GGPP (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:40); a gene encoding a polypeptide capable of synthesizing *ent*-kaurene from *ent*-copalyl diphosphate (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:52); a gene encoding a polypeptide capable of synthesizing ent-kaurenoic acid, ent-kaurenol, and/or ent-kaurenal from *ent*-kaurene (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:60 or SEQ ID NO:117); a gene encoding a polypeptide capable of reducing cytochrome P450 complex (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:78, SEQ ID NO:86, or SEQ ID NO:92); and/or a gene encoding a polypeptide capable of synthesizing steviol from *ent*-kaurenoic acid (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:94).

[00120] In some embodiments, a recombinant host comprising a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position, *e.g.*, a SA Gtase (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:183) further comprises a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:7); a gene encoding a polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:9); a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:4); and/or a gene encoding a polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:11, SEQ ID NO:13, or SEQ ID NO:16). In certain such embodiments, the recombinant host cell further comprises a gene encoding a polypeptide capable of synthesizing GGPP from FPP and IPP (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:20); a gene encoding a polypeptide capable of synthesizing *ent*-copalyl diphosphate from GGPP (*e.g.*,

a polypeptide having the amino acid sequence set forth in SEQ ID NO:40); a gene encoding a polypeptide capable of synthesizing *ent*-kaurene from *ent*-copalyl diphosphate (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:52); a gene encoding a polypeptide capable of synthesizing ent-kaurenoic acid, ent-kaurenol, and/or ent-kaurenal from *ent*-kaurene (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:60 or SEQ ID NO:117); a gene encoding a polypeptide capable of reducing cytochrome P450 complex (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:78, SEQ ID NO:86, or SEQ ID NO:92); and/or a gene encoding a polypeptide capable of synthesizing steviol from *ent*-kaurenoic acid (*e.g.*, a polypeptide having the amino acid sequence set forth in SEQ ID NO:94).

[00121] In some aspects, expression of SA Gtase (SEQ ID NO:182, SEQ ID NO:183) in *S. cerevisiae* comprising one or more copies of a recombinant gene encoding a GGPPS polypeptide (*e.g.*, SEQ ID NO:19, SEQ ID NO:20), a recombinant gene encoding a truncated CDPS polypeptide (*e.g.*, SEQ ID NO:39, SEQ ID NO:40), a recombinant gene encoding a KS polypeptide (*e.g.*, SEQ ID NO:51, SEQ ID NO:52), a recombinant gene encoding a KO polypeptide (*e.g.*, SEQ ID NO:59, SEQ ID NO:60), a recombinant gene encoding an ATR2 polypeptide (*e.g.*, SEQ ID NO:91, SEQ ID NO:92), a recombinant gene encoding an EUGT11 polypeptide (*e.g.*, SEQ ID NO:14/SEQ ID NO:15, SEQ ID NO:16), a recombinant gene encoding a KAH polypeptide (*e.g.*, SEQ ID NO:93, SEQ ID NO:94), a recombinant gene encoding a CPR8 polypeptide (*e.g.*, SEQ ID NO:85, SEQ ID NO:86), a recombinant gene encoding a UGT85C2 polypeptide (*e.g.*, SEQ ID NO:5/SEQ ID NO:6/SEQ ID NO:149, SEQ ID NO:7) or a UGT85C2 variant (or functional homolog) of SEQ ID NO:7, a recombinant gene encoding a UGT74G1 polypeptide (*e.g.*, SEQ ID NO:3, SEQ ID NO:4) of a UGT74G1 variant (or functional homolog) of SEQ ID NO:4, a recombinant gene encoding a UGT76G1 polypeptide (*e.g.*, SEQ ID NO:8, SEQ ID NO:9) or a UGT76G1 variant (or functional homolog) of SEQ ID NO:9, and a recombinant gene encoding a UGT91D2e polypeptide (*e.g.*, SEQ ID NO:10, SEQ ID NO:11) and/or a UGT91D2e variant (or functional homolog) of SEQ ID NO:11 such as a UGT91D2e-b (SEQ ID NO:12, SEQ ID NO:13) polypeptide results in increased *ent*-kaurenoic acid+2Glc (#7), *ent*-kaurenoic acid+3Glc (isomer 1), *ent*-kaurenoic acid+3Glc (isomer 2), 13-SMG, RebA, RebB, Steviol+4Glc (#36), Steviol+6Glc (isomer 1), Steviol+7Glc (isomer 2), and/or *ent*-Kaurenol+3Glc (isomer 1 and/or isomer 2). *See*, Example 4.

[00122] In some embodiments, a steviol glycoside and/or glycoside of a steviol precursor, or a composition thereof produced *in vivo, in vitro*, or by whole cell bioconversion comprises fewer

contaminants or less of any particular contaminant than a stevia extract from, *inter alia*, a stevia plant. Contaminants can include plant-derived compounds that contribute to off-flavors. Potential contaminants include pigments, lipids, proteins, phenolics, saccharides, spathulenol and other sesquiterpenes, labdane diterpenes, monoterpenes, decanoic acid, 8,11,14-eicosatrienoic acid, 2-methyloctadecane, pentacosane, octacosane, tetracosane, octadecanol, stigmasterol, β-sitosterol, α-amyrin, β-amyrin, lupeol, β-amryin acetate, pentacyclic triterpenes, centauredin, quercitin, epi-alpha-cadinol, carophyllenes and derivatives, beta-pinene, beta-sitosterol, and gibberellin.

[00123] As used herein, the terms "detectable amount," "detectable concentration," "measurable amount," and "measurable concentration" refer to a level of steviol glycosides measured in AUC, $\mu M/OD_{600}$, mg/L, μM, or mM. Steviol glycoside production (*i.e.*, total, supernatant, and/or intracellular steviol glycoside levels) can be detected and/or analyzed by techniques generally available to one skilled in the art, for example, but not limited to, liquid chromatography-mass spectrometry (LC-MS), thin layer chromatography (TLC), high-performance liquid chromatography (HPLC), ultraviolet-visible spectroscopy/ spectrophotometry (UV-Vis), mass spectrometry (MS), and NMR.

[00124] As used herein, the term "undetectable concentration" refers to a level of a compound that is too low to be measured and/or analyzed by techniques such as TLC, HPLC, UV-Vis, MS, or NMR. In some embodiments, a compound of an "undetectable concentration" is not present in a steviol glycoside or steviol glycoside precursor composition.

[00125] As used herein, the terms "or" and "and/or" is utilized to describe multiple components in combination or exclusive of one another. For example, "x, y, and/or z" can refer to "x" alone, "y" alone, "z" alone, "x, y, and z," "(x and y) or z," "x or (y and z)," or "x or y or z." In some embodiments, "and/or" is used to refer to the exogenous nucleic acids that a recombinant cell comprises, wherein a recombinant cell comprises one or more exogenous nucleic acids selected from a group. In some embodiments, "and/or" is used to refer to production of steviol glycosides and/or steviol glycoside precursors. In some embodiments, "and/or" is used to refer to production of steviol glycosides, wherein one or more steviol glycosides are produced. In some embodiments, "and/or" is used to refer to production of steviol glycosides, wherein one or more steviol glycosides are produced through one or more of the following steps: culturing a recombinant microorganism, synthesizing one or more steviol glycosides in a recombinant microorganism, and/or isolating one or more steviol glycosides.

Functional Homologs

[00126] Functional homologs of the polypeptides described above are also suitable for use in producing steviol glycosides in a recombinant host. A functional homolog is a polypeptide that has sequence similarity to a reference polypeptide, and that carries out one or more of the biochemical or physiological function(s) of the reference polypeptide. A functional homolog and the reference polypeptide can be a natural occurring polypeptide, and the sequence similarity can be due to convergent or divergent evolutionary events. As such, functional homologs are sometimes designated in the literature as homologs, or orthologs, or paralogs. Variants of a naturally occurring functional homolog, such as polypeptides encoded by mutants of a wild type coding sequence, can themselves be functional homologs. Functional homologs can also be created via site-directed mutagenesis of the coding sequence for a polypeptide, or by combining domains from the coding sequences for different naturally-occurring polypeptides ("domain swapping"). Techniques for modifying genes encoding functional polypeptides described herein are known and include, *inter alia*, directed evolution techniques, site-directed mutagenesis techniques and random mutagenesis techniques, and can be useful to increase specific activity of a polypeptide, alter substrate specificity, alter expression levels, alter subcellular location, or modify polypeptide-polypeptide interactions in a desired manner. Such modified polypeptides are considered functional homologs. The term "functional homolog" is sometimes applied to the nucleic acid that encodes a functionally homologous polypeptide.

[00127] Functional homologs can be identified by analysis of nucleotide and polypeptide sequence alignments. For example, performing a query on a database of nucleotide or polypeptide sequences can identify homologs of steviol glycoside biosynthesis polypeptides. Sequence analysis can involve BLAST, Reciprocal BLAST, or PSI-BLAST analysis of non-redundant databases using a UGT amino acid sequence as the reference sequence. Amino acid sequence is, in some instances, deduced from the nucleotide sequence. Those polypeptides in the database that have greater than 40% sequence identity are candidates for further evaluation for suitability as a steviol glycoside biosynthesis polypeptide. Amino acid sequence similarity allows for conservative amino acid substitutions, such as substitution of one hydrophobic residue for another or substitution of one polar residue for another. If desired, manual inspection of such candidates can be carried out in order to narrow the number of candidates to be further evaluated. Manual inspection can be performed by selecting those candidates that appear to have domains present in steviol glycoside biosynthesis polypeptides, *e.g.*, conserved functional domains. In some embodiments, nucleic acids and polypeptides are

identified from transcriptome data based on expression levels rather than by using BLAST analysis.

[00128] Conserved regions can be identified by locating a region within the primary amino acid sequence of a steviol glycoside biosynthesis polypeptide that is a repeated sequence, forms some secondary structure (*e.g.*, helices and beta sheets), establishes positively or negatively charged domains, or represents a protein motif or domain. *See, e.g.*, the Pfam web site describing consensus sequences for a variety of protein motifs and domains on the World Wide Web at sanger.ac.uk/Software/Pfam/ and pfam.janelia.org/. The information included at the Pfam database is described in Sonnhammer *et al.*, *Nucl. Acids Res.*, 26:320-322 (1998); Sonnhammer *et al.*, Proteins, 28:405-420 (1997); and Bateman *et al.*, *Nucl. Acids Res.*, 27:260-262 (1999). Conserved regions also can be determined by aligning sequences of the same or related polypeptides from closely related species. Closely related species preferably are from the same family. In some embodiments, alignment of sequences from two different species is adequate to identify such homologs.

[00129] Typically, polypeptides that exhibit at least about 40% amino acid sequence identity are useful to identify conserved regions. Conserved regions of related polypeptides exhibit at least 45% amino acid sequence identity (*e.g.*, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90% amino acid sequence identity). In some embodiments, a conserved region exhibits at least 92%, 94%, 96%, 98%, or 99% amino acid sequence identity.

[00130] For example, polypeptides suitable for producing steviol in a recombinant host include functional homologs of UGTs.

[00131] Methods to modify the substrate specificity of, for example, a UGT, are known to those skilled in the art, and include without limitation site-directed/rational mutagenesis approaches, random directed evolution approaches and combinations in which random mutagenesis/saturation techniques are performed near the active site of the enzyme. For example see Osmani *et al.*, 2009, *Phytochemistry* 70: 325–347.

[00132] A candidate sequence typically has a length that is from 80% to 200% of the length of the reference sequence, *e.g.*, 82, 85, 87, 89, 90, 93, 95, 97, 99, 100, 105, 110, 115, 120, 130, 140, 150, 160, 170, 180, 190, or 200% of the length of the reference sequence. A functional homolog polypeptide typically has a length that is from 95% to 105% of the length of the reference sequence, *e.g.*, 90, 93, 95, 97, 99, 100, 105, 110, 115, or 120% of the length of the reference sequence, or any range between. A % identity for any candidate nucleic acid or

polypeptide relative to a reference nucleic acid or polypeptide can be determined as follows. A reference sequence (*e.g.*, a nucleic acid sequence or an amino acid sequence described herein) is aligned to one or more candidate sequences using the computer program Clustal Omega (version 1.2.1, default parameters), which allows alignments of nucleic acid or polypeptide sequences to be carried out across their entire length (global alignment). Chenna *et al.*, 2003, *Nucleic Acids Res*. 31(13):3497-500.

[00133] ClustalW calculates the best match between a reference and one or more candidate sequences, and aligns them so that identities, similarities and differences can be determined. Gaps of one or more residues can be inserted into a reference sequence, a candidate sequence, or both, to maximize sequence alignments. For fast pairwise alignment of nucleic acid sequences, the following default parameters are used: word size: 2; window size: 4; scoring method: % age; number of top diagonals: 4; and gap penalty: 5. For multiple alignment of nucleic acid sequences, the following parameters are used: gap opening penalty: 10.0; gap extension penalty: 5.0; and weight transitions: yes. For fast pairwise alignment of protein sequences, the following parameters are used: word size: 1; window size: 5; scoring method:% age; number of top diagonals: 5; gap penalty: 3. For multiple alignment of protein sequences, the following parameters are used: weight matrix: blosum; gap opening penalty: 10.0; gap extension penalty: 0.05; hydrophilic gaps: on; hydrophilic residues: Gly, Pro, Ser, Asn, Asp, Gln, Glu, Arg, and Lys; residue-specific gap penalties: on. The ClustalW output is a sequence alignment that reflects the relationship between sequences. ClustalW can be run, for example, at the Baylor College of Medicine Search Launcher site on the World Wide Web (searchlauncher.bcm.tmc.edu/multi-align/multi-align.html) and at the European Bioinformatics Institute site on the World Wide Web (ebi.ac.uk/clustalw).

[00134] To determine a % identity of a candidate nucleic acid or amino acid sequence to a reference sequence, the sequences are aligned using Clustal Omega, the number of identical matches in the alignment is divided by the length of the reference sequence, and the result is multiplied by 100. It is noted that the% identity value can be rounded to the nearest tenth. For example, 78.11, 78.12, 78.13, and 78.14 are rounded down to 78.1, while 78.15, 78.16, 78.17, 78.18, and 78.19 are rounded up to 78.2.

[00135] It will be appreciated that functional UGT proteins can include additional amino acids that are not involved in the enzymatic activities carried out by the enzymes. In some embodiments, UGT proteins are fusion proteins. The terms “chimera,” “fusion polypeptide,” “fusion protein,” “fusion enzyme,” “fusion construct,” “chimeric protein,” "chimeric polypeptide,"

"chimeric construct," and "chimeric enzyme" can be used interchangeably herein to refer to proteins engineered through the joining of two or more genes that code for different proteins. In some embodiments, a nucleic acid sequence encoding a UGT polypeptide can include a tag sequence that encodes a "tag" designed to facilitate subsequent manipulation (*e.g.*, to facilitate purification or detection), secretion, or localization of the encoded polypeptide. Tag sequences can be inserted in the nucleic acid sequence encoding the polypeptide such that the encoded tag is located at either the carboxyl or amino terminus of the polypeptide. Non-limiting examples of encoded tags include green fluorescent protein (GFP), human influenza hemagglutinin (HA), glutathione S transferase (GST), polyhistidine-tag (HIS tag), and Flag™ tag (Kodak, New Haven, CT). Other examples of tags include a chloroplast transit peptide, a mitochondrial transit peptide, an amyloplast peptide, signal peptide, or a secretion tag.

[00136] In some embodiments, a fusion protein is a protein altered by domain swapping. As used herein, the term "domain swapping" is used to describe the process of replacing a domain of a first protein with a domain of a second protein. In some embodiments, the domain of the first protein and the domain of the second protein are functionally identical or functionally similar. In some embodiments, the structure and/or sequence of the domain of the second protein differs from the structure and/or sequence of the domain of the first protein. In some embodiments, a UGT polypeptide is altered by domain swapping.

[00137] In some embodiments, a fusion protein is a protein altered by circular permutation, which consists in the covalent attachment of the ends of a protein that would be opened elsewhere afterwards. Thus, the order of the sequence is altered without causing changes in the amino acids of the protein. In some embodiments, a targeted circular permutation can be produced, for example but not limited to, by designing a spacer to join the ends of the original protein. Once the spacer has been defined, there are several possibilities to generate permutations through generally accepted molecular biology techniques, for example but not limited to, by producing concatemers by means of PCR and subsequent amplification of specific permutations inside the concatemer or by amplifying discrete fragments of the protein to exchange to join them in a different order. The step of generating permutations can be followed by creating a circular gene by binding the fragment ends and cutting back at random, thus forming collections of permutations from a unique construct.

Steviol and Steviol Glycoside Biosynthesis Nucleic Acids

[00138] A recombinant gene encoding a polypeptide described herein comprises the coding sequence for that polypeptide, operably linked in sense orientation to one or more regulatory regions suitable for expressing the polypeptide. Because many microorganisms are capable of expressing multiple gene products from a polycistronic mRNA, multiple polypeptides can be expressed under the control of a single regulatory region for those microorganisms, if desired. A coding sequence and a regulatory region are considered to be operably linked when the regulatory region and coding sequence are positioned so that the regulatory region is effective for regulating transcription or translation of the sequence. Typically, the translation initiation site of the translational reading frame of the coding sequence is positioned between one and about fifty nucleotides downstream of the regulatory region for a monocistronic gene.

[00139] In many cases, the coding sequence for a polypeptide described herein is identified in a species other than the recombinant host, *i.e.*, is a heterologous nucleic acid. Thus, if the recombinant host is a microorganism, the coding sequence can be from other prokaryotic or eukaryotic microorganisms, from plants or from animals. In some case, however, the coding sequence is a sequence that is native to the host and is being reintroduced into that organism.

[00140] A native sequence can often be distinguished from the naturally occurring sequence by the presence of non-natural sequences linked to the exogenous nucleic acid, *e.g.*, non-native regulatory sequences flanking a native sequence in a recombinant nucleic acid construct. In addition, stably transformed exogenous nucleic acids typically are integrated at positions other than the position where the native sequence is found. “Regulatory region” refers to a nucleic acid having nucleotide sequences that influence transcription or translation initiation and rate, and stability and/or mobility of a transcription or translation product. Regulatory regions include, without limitation, promoter sequences, enhancer sequences, response elements, protein recognition sites, inducible elements, protein binding sequences, 5´ and 3´ untranslated regions (UTRs), transcriptional start sites, termination sequences, polyadenylation sequences, introns, and combinations thereof. A regulatory region typically comprises at least a core (basal) promoter. A regulatory region also may include at least one control element, such as an enhancer sequence, an upstream element or an upstream activation region (UAR). A regulatory region is operably linked to a coding sequence by positioning the regulatory region and the coding sequence so that the regulatory region is effective for regulating transcription or translation of the sequence. For example, to operably link a coding sequence and a promoter sequence, the translation initiation site of the translational reading frame of the coding sequence

is typically positioned between one and about fifty nucleotides downstream of the promoter. A regulatory region can, however, be positioned as much as about 5,000 nucleotides upstream of the translation initiation site, or about 2,000 nucleotides upstream of the transcription start site.

[00141] The choice of regulatory regions to be included depends upon several factors, including, but not limited to, efficiency, selectability, inducibility, desired expression level, and preferential expression during certain culture stages. It is a routine matter for one of skill in the art to modulate the expression of a coding sequence by appropriately selecting and positioning regulatory regions relative to the coding sequence. It will be understood that more than one regulatory region may be present, *e.g.*, introns, enhancers, upstream activation regions, transcription terminators, and inducible elements.

[00142] One or more genes can be combined in a recombinant nucleic acid construct in "modules" useful for a discrete aspect of steviol and/or steviol glycoside production. Combining a plurality of genes in a module, particularly a polycistronic module, facilitates the use of the module in a variety of species. For example, a steviol biosynthesis gene cluster, or a UGT gene cluster, can be combined in a polycistronic module such that, after insertion of a suitable regulatory region, the module can be introduced into a wide variety of species. As another example, a UGT gene cluster can be combined such that each UGT coding sequence is operably linked to a separate regulatory region, to form a UGT module. Such a module can be used in those species for which monocistronic expression is necessary or desirable. In addition to genes useful for steviol or steviol glycoside production, a recombinant construct typically also contains an origin of replication, and one or more selectable markers for maintenance of the construct in appropriate species.

[00143] It will be appreciated that because of the degeneracy of the genetic code, a number of nucleic acids can encode a particular polypeptide; *i.e.*, for many amino acids, there is more than one nucleotide triplet that serves as the codon for the amino acid. Thus, codons in the coding sequence for a given polypeptide can be modified such that optimal expression in a particular host is obtained, using appropriate codon bias tables for that host (*e.g.*, microorganism). As isolated nucleic acids, these modified sequences can exist as purified molecules and can be incorporated into a vector or a virus for use in constructing modules for recombinant nucleic acid constructs.

[00144] In some cases, it is desirable to inhibit one or more functions of an endogenous polypeptide in order to divert metabolic intermediates towards steviol or steviol glycoside biosynthesis. For example, it may be desirable to downregulate synthesis of sterols in a yeast

strain in order to further increase steviol or steviol glycoside production, *e.g.*, by downregulating squalene epoxidase. As another example, it may be desirable to inhibit degradative functions of certain endogenous gene products, *e.g.*, glycohydrolases that remove glucose moieties from secondary metabolites or phosphatases as discussed herein. In such cases, a nucleic acid that overexpresses the polypeptide or gene product may be included in a recombinant construct that is transformed into the strain. Alternatively, mutagenesis can be used to generate mutants in genes for which it is desired to increase or enhance function.

[00145] One aspect of the disclosure is an isolated nucleic acid molecule encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position or a catalytically active portion thereof. The nucleic acid is cDNA. In some embodiments, the encoded polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position or the catalytically active portion thereof comprises a a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73E1 polypeptide, a UGT75B1 polypeptide, a UGT75L6 polypeptide, a OleI polypeptide, a UGT5 polypeptide, a SA Gtase polypeptide, a UDPG1 polypeptide, a UN1671 polypeptide, a UGT74F1 polypeptide, a UGT84B2 polypeptide, or a UGT74F2-like UGT polypeptide. In some embodiments, the encoded polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position or the catalytically active portion thereof comprises a polypeptide having the amino acid sequence set forth in SEQ ID NO:127, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:177, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:207, or SEQ ID NO:211.

[00146] Another aspect of the disclosure is an isolated nucleic acid molecule encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position or a catalytically active portion thereof. In some embodiments, the encoded polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position or the catalytically active portion thereof comprises a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73C7 polypeptide, a UGT73E1 polypeptide, or a UGT76E12 polypeptide. In some embodiments, the encoded polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position or the catalytically active portion thereof comprises a polypeptide having the amino acid sequence set forth in SEQ ID NO:127, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, or SEQ ID NO:153.

[00147] Another aspect of the disclosure is an isolated nucleic acid molecule encoding a polypeptide capable of beta-1,2-glycosylation of the C2' and/or beta-1,3-glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside or a catalytically active portion thereof. The nucleic acid is cDNA. In some embodiments, the encoded polypeptide capable of beta-1,2-glycosylation of the C2' and/or beta-1,3-glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside or the catalytically active portion thereof comprises a UGT73C6 polypeptide, a CaUGT3 polypeptide, a UN32491 polypeptide, or a UN1671 polypeptide. In some embodiments, the encoded polypeptide capable of beta-1,2-glycosylation of the C2' and/or beta-1,3-glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside or the catalytically active portion thereof comprises a polypeptide having the amino acid sequence set forth in SEQ ID NO: 137, SEQ ID NO:169, SEQ ID NO:199, or SEQ ID NO:201.

[00148] Another aspect of the disclosure is an isolated nucleic acid molecule encoding a polypeptide capable of glycosylating a steviol precursor at its C-19 carboxyl or C-19 hydroxyl position or a catalytically active portion thereof. The nucleic acid is cDNA. In some embodiments, the encoded polypeptide capable of glycosylating a steviol precursor at its C-19 carboxyl or C-19 hydroxyl position or the catalytically active portion thereof comprises a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73E1 polypeptide, a UGT75B1 polypeptide, a UGT75L6 polypeptide, a UGT76E12 polypeptide, a OleI polypeptide, a UGT5 polypeptide, a SA Gtase, a UDPG1 polypeptide, a UGT74F1 polypeptide, a UGT75D1 polypeptide, a UGT84B2 polypeptide, or a UGT74F2-like UGT polypeptide. In some embodiments, the encoded polypeptide capable of glycosylating a steviol precursor at its C-19 carboxyl or C-19 hydroxyl position or the catalytically active portion thereof comprises a polypeptide having the amino acid sequence set forth in SEQ ID NO: 127, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:153, SEQ ID NO:177, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, or SEQ ID NO:211.

Host Microorganisms

[00149] Recombinant hosts can be used to express polypeptides for the producing steviol glycosides, including mammalian, insect, plant, and algal cells. A number of prokaryotes and

eukaryotes are also suitable for use in constructing the recombinant microorganisms described herein, *e.g.*, gram-negative bacteria, yeast, and fungi. A species and strain selected for use as a steviol glycoside production strain is first analyzed to determine which production genes are endogenous to the strain and which genes are not present. Genes for which an endogenous counterpart is not present in the strain are advantageously assembled in one or more recombinant constructs, which are then transformed into the strain in order to supply the missing function(s).

[00150] Typically, the recombinant microorganism is grown in a fermenter at a temperature(s) for a period of time, wherein the temperature and period of time facilitate the production of a steviol glycoside. The constructed and genetically engineered microorganisms provided by the invention can be cultivated using conventional fermentation processes, including, *inter alia*, chemostat, batch, fed-batch cultivations, semi-continuous fermentations such as draw and fill, continuous perfusion fermentation, and continuous perfusion cell culture. Depending on the particular microorganism used in the method, other recombinant genes such as isopentenyl biosynthesis genes and terpene synthase and cyclase genes may also be present and expressed. Levels of substrates and intermediates, *e.g.*, isopentenyl diphosphate, dimethylallyl diphosphate, GGPP, *ent*-kaurene and *ent*-kaurenoic acid, can be determined by extracting samples from culture media for analysis according to published methods.

[00151] Carbon sources of use in the instant method include any molecule that can be metabolized by the recombinant host cell to facilitate growth and/or production of the steviol glycosides. Examples of suitable carbon sources include, but are not limited to, sucrose (*e.g.*, as found in molasses), fructose, xylose, ethanol, glycerol, glucose, cellulose, starch, cellobiose or other glucose-comprising polymer. In embodiments employing yeast as a host, for example, carbons sources such as sucrose, fructose, xylose, ethanol, glycerol, and glucose are suitable. The carbon source can be provided to the host organism throughout the cultivation period or alternatively, the organism can be grown for a period of time in the presence of another energy source, *e.g.*, protein, and then provided with a source of carbon only during the fed-batch phase.

[00152] After the recombinant microorganism has been grown in culture for the period of time, wherein the temperature and period of time facilitate the production of a steviol glycoside, steviol and/or one or more steviol glycosides can then be recovered from the culture using various techniques known in the art. In some embodiments, a permeabilizing agent can be added to aid the feedstock entering into the host and product getting out. For example, a crude

lysate of the cultured microorganism can be centrifuged to obtain a supernatant. The resulting supernatant can then be applied to a chromatography column, *e.g.*, a C-18 column, and washed with water to remove hydrophilic compounds, followed by elution of the compound(s) of interest with a solvent such as methanol. The compound(s) can then be further purified by preparative HPLC. *See also*, WO 2009/140394.

[00153] It will be appreciated that the various genes and modules discussed herein can be present in two or more recombinant hosts rather than a single host. When a plurality of recombinant hosts is used, they can be grown in a mixed culture to accumulate steviol and/or steviol glycosides.

[00154] Alternatively, the two or more hosts each can be grown in a separate culture medium and the product of the first culture medium, *e.g.*, steviol, can be introduced into second culture medium to be converted into a subsequent intermediate, or into an end product such as, for example, RebA. The product produced by the second, or final host is then recovered. It will also be appreciated that in some embodiments, a recombinant host is grown using nutrient sources other than a culture medium and utilizing a system other than a fermenter.

[00155] Exemplary prokaryotic and eukaryotic species are described in more detail below. However, it will be appreciated that other species can be suitable. For example, suitable species can be in a genus such as *Agaricus*, *Aspergillus*, *Bacillus*, *Candida*, *Corynebacterium*, *Eremothecium*, *Escherichia*, *Fusarium/Gibberella*, *Kluyveromyces*, *Laetiporus*, *Lentinus*, *Phaffia*, *Phanerochaete*, *Pichia*, *Physcomitrella*, *Rhodoturula*, *Saccharomyces*, *Schizosaccharomyces*, *Sphaceloma*, *Xanthophyllomyces* or *Yarrowia*. Exemplary species from such genera include *Lentinus tigrinus*, *Laetiporus sulphureus*, *Phanerochaete chrysosporium*, *Pichia pastoris*, *Cyberlindnera jadinii*, *Physcomitrella patens*, *Rhodoturula glutinis*, *Rhodoturula mucilaginosa*, *Phaffia rhodozyma*, *Xanthophyllomyces dendrorhous*, *Fusarium fujikuroi/Gibberella fujikuroi*, *Candida utilis*, *Candida glabrata*, *Candida albicans*, and *Yarrowia lipolytica*.

[00156] In some embodiments, a microorganism can be a prokaryote such as *Escherichia* bacteria cells, for example, *Escherichia coli* cells; *Lactobacillus* bacteria cells; *Lactococcus* bacteria cells; *Comebacterium* bacteria cells; *Acetobacter* bacteria cells; *Acinetobacter* bacteria cells; or *Pseudomonas* bacterial cells.

[00157] In some embodiments, a microorganism can be an Ascomycete such as *Gibberella fujikuroi*, *Kluyveromyces lactis*, *Schizosaccharomyces pombe*, *Aspergillus niger*, *Yarrowia lipolytica*, *Ashbya gossypii*, or *S. cerevisiae*.

[00158] In some embodiments, a microorganism can be an algal cell such as *Blakeslea trispora, Dunaliella salina, Haematococcus pluvialis, Chlorella sp., Undaria pinnatifida, Sargassum, Laminaria japonica, Scenedesmus almeriensis* species.

[00159] In some embodiments, a microorganism can be a cyanobacterial cell such as *Blakeslea trispora, Dunaliella salina, Haematococcus pluvialis, Chlorella sp., Undaria pinnatifida, Sargassum, Laminaria japonica, Scenedesmus almeriensis*.

Saccharomyces spp.

[00160] S*accharomyces* is a widely used chassis organism in synthetic biology, and can be used as the recombinant microorganism platform. For example, there are libraries of mutants, plasmids, detailed computer models of metabolism and other information available for *S. cerevisiae*, allowing for rational design of various modules to enhance product yield. Methods are known for making recombinant microorganisms.

Aspergillus spp.

[00161] *Aspergillus* species such as *A. oryzae*, *A. niger* and *A. sojae* are widely used microorganisms in food production and can also be used as the recombinant microorganism platform. Nucleotide sequences are available for genomes of *A. nidulans*, *A. fumigatus*, *A. oryzae*, *A. clavatus*, *A. flavus*, *A. niger*, and *A. terreus*, allowing rational design and modification of endogenous pathways to enhance flux and increase product yield. Metabolic models have been developed for *Aspergillus*, as well as transcriptomic studies and proteomics studies. *A. niger* is cultured for the industrial production of a number of food ingredients such as citric acid and gluconic acid, and thus species such as *A. niger* are generally suitable for producing steviol glycosides.

E. coli

[00162] *E. coli*, another widely used platform organism in synthetic biology, can also be used as the recombinant microorganism platform. Similar to *Saccharomyces*, there are libraries of mutants, plasmids, detailed computer models of metabolism and other information available for *E. coli*, allowing for rational design of various modules to enhance product yield. Methods similar

to those described above for *Saccharomyces* can be used to make recombinant *E. coli* microorganisms.

Agaricus, Gibberella, and Phanerochaete spp.

[00163] *Agaricus*, *Gibberella*, and *Phanerochaete* spp. can be useful because they are known to produce large amounts of isoprenoids in culture. Thus, the terpene precursors for producing large amounts of steviol glycosides are already produced by endogenous genes. Thus, modules comprising recombinant genes for steviol glycoside biosynthesis polypeptides can be introduced into species from such genera without the necessity of introducing mevalonate or MEP pathway genes.

Arxula adeninivorans (Blastobotrys adeninivorans)

[00164] *Arxula adeninivorans* is dimorphic yeast (it grows as budding yeast like the baker's yeast up to a temperature of 42°C, above this threshold it grows in a filamentous form) with unusual biochemical characteristics. It can grow on a wide range of substrates and can assimilate nitrate. It has successfully been applied to the generation of strains that can produce natural plastics or the development of a biosensor for estrogens in environmental samples.

Yarrowia lipolytica

[00165] *Yarrowia lipolytica* is dimorphic yeast (*see Arxula adeninivorans*) and belongs to the family Hemiascomycetes. The entire genome of *Yarrowia lipolytica* is known. *Yarrowia* species is aerobic and considered to be non-pathogenic. *Yarrowia* is efficient in using hydrophobic substrates (*e.g.* alkanes, fatty acids, oils) and can grow on sugars. It has a high potential for industrial applications and is an oleaginous microorgamism. *Yarrowia lipolyptica* can accumulate lipid content to approximately 40% of its dry cell weight and is a model organism for lipid accumulation and remobilization. *See e.g.,* Nicaud, 2012, *Yeast* 29(10):409-18; Beopoulos *et al.,* 2009, *Biochimie* 91(6):692-6; Bankar *et al.*, 2009, *Appl Microbiol Biotechnol.* 84(5):847-65.

Rhodotorula sp.

[00166] *Rhodotorula* is unicellular, pigmented yeast. The oleaginous red yeast, *Rhodotorula glutinis*, has been shown to produce lipids and carotenoids from crude glycerol (Saenge *et al.*, 2011, *Process Biochemistry* 46(1):210-8). *Rhodotorula toruloides* strains have been shown to be an efficient fed-batch fermentation system for improved biomass and lipid productivity (Li *et al.,* 2007, *Enzyme and Microbial Technology* 41:312-7).

Rhodosporidium toruloides

[00167] *Rhodosporidium toruloides* is oleaginous yeast and useful for engineering lipid-production pathways (*See e.g.* Zhu *et al.*, 2013, *Nature Commun.* 3:1112; Ageitos *et al.*, 2011, *Applied Microbiology and Biotechnology* 90(4):1219-27).

Candida boidinii

[00168] *Candida boidinii* is methylotrophic yeast (it can grow on methanol). Like other methylotrophic species such as *Hansenula polymorpha* and *Pichia pastoris*, it provides an excellent platform for producing heterologous proteins. Yields in a multigram range of a secreted foreign protein have been reported. A computational method, IPRO, recently predicted mutations that experimentally switched the cofactor specificity of *Candida boidinii* xylose reductase from NADPH to NADH. *See*, *e.g.*, Mattanovich *et al.*, 2012, *Methods Mol Biol.* 824:329-58; Khoury *et al.*, 2009, *Protein Sci.* 18(10):2125-38.

Hansenula polymorpha (Pichia angusta)

[00169] *Hansenula polymorpha* is methylotrophic yeast (*see Candida boidinii*). It can furthermore grow on a wide range of other substrates; it is thermo-tolerant and can assimilate nitrate (see also *Kluyveromyces lactis*). It has been applied to producing hepatitis B vaccines, insulin and interferon alpha-2a for the treatment of hepatitis C, furthermore to a range of technical enzymes. *See*, *e.g.*, Xu *et al.*, 2014, *Virol Sin.* 29(6):403-9.

Kluyveromyces lactis

[00170] *Kluyveromyces lactis* is yeast regularly applied to the production of kefir. It can grow on several sugars, most importantly on lactose which is present in milk and whey. It has successfully been applied among others for producing chymosin (an enzyme that is usually present in the stomach of calves) for producing cheese. Production takes place in fermenters on a 40,000 L scale. *See*, *e.g.*, van Ooyen *et al.*, 2006, *FEMS Yeast Res.* 6(3):381-92.

Pichia pastoris

[00171] *Pichia pastoris* is methylotrophic yeast (*see Candida boidinii* and *Hansenula polymorpha*). It provides an efficient platform for producing foreign proteins. Platform elements are available as a kit and it is worldwide used in academia for producing proteins. Strains have been engineered that can produce complex human N-glycan (yeast glycans are similar but not identical to those found in humans). *See*, *e.g.*, Piirainen *et al.*, 2014, *N Biotechnol.* 31(6):532-7.

Physcomitrella spp.

[00172] *Physcomitrella mosses*, when grown in suspension culture, have characteristics similar to yeast or other fungal cultures. This genera can be used for producing plant secondary metabolites, which can be difficult to produce in other types of cells.

[00173] It will be appreciated that the recombinant host cell disclosed herein can comprise a plant cell, comprising a plant cell that is grown in a plant, a mammalian cell, an insect cell, a fungal cell, comprising a yeast cell, wherein the yeast cell is a cell from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Yarrowia lipolytica*, *Candida glabrata*, *Ashbya gossypii*, *Cyberlindnera jadinii*, *Pichia pastoris*, *Kluyveromyces lactis*, *Hansenula polymorpha*, *Candida boidinii*, *Arxula adeninivorans*, *Xanthophyllomyces dendrorhous*, or *Candida albicans species* or is a Saccharomycete or is a Saccharomyces cerevisiae cell, an algal cell or a bacterial cell, comprising *Escherichia* cells, *Lactobacillus* cells, *Lactococcus* cells, *Cornebacterium* cells, *Acetobacter* cells, *Acinetobacter* cells, or *Pseudomonas* cells.

Steviol Glycoside Compositions

[00174] Steviol glycosides do not necessarily have equivalent performance in different food systems. It is therefore desirable to have the ability to direct the synthesis to steviol glycoside compositions of choice. Recombinant hosts described herein can produce compositions that are selectively enriched for specific steviol glycosides (*e.g.*, RebD or RebM) and have a consistent taste profile. As used herein, the term “enriched” is used to describe a steviol glycoside composition with an increased proportion of a particular steviol glycoside, compared to a steviol glycoside composition (extract) from a stevia plant. Thus, the recombinant hosts described herein can facilitate the production of compositions that are tailored to meet the sweetening profile desired for a given food product and that have a proportion of each steviol glycoside that is consistent from batch to batch. In some embodiments, hosts described herein do not produce or produce a reduced amount of undesired plant by-products found in Stevia extracts. Thus, steviol glycoside compositions produced by the recombinant hosts described herein are distinguishable from compositions derived from *Stevia* plants.

[00175] The amount of an individual steviol glycoside (*e.g.*, RebA, RebB, RebD, or RebM) accumulated can be from about 1 to about 7,000 mg/L, *e.g.*, about 1 to about 10 mg/L, about 3 to about 10 mg/L, about 5 to about 20 mg/L, about 10 to about 50 mg/L, about 10 to about 100 mg/L, about 25 to about 500 mg/L, about 100 to about 1,500 mg/L, or about 200 to about 1,000 mg/L, at least about 1,000 mg/L, at least about 1,200 mg/L, at least about at least 1,400 mg/L,

at least about 1,600 mg/L, at least about 1,800 mg/L, at least about 2,800 mg/L, or at least about 7,000 mg/L. In some aspects, the amount of an individual steviol glycoside can exceed 7,000 mg/L. The amount of a combination of steviol glycosides (*e.g.*, RebA, RebB, RebD, or RebM) accumulated can be from about 1 mg/L to about 7,000 mg/L, *e.g.*, about 200 to about 1,500, at least about 2,000 mg/L, at least about 3,000 mg/L, at least about 4,000 mg/L, at least about 5,000 mg/L, at least about 6,000 mg/L, or at least about 7,000 mg/L. In some aspects, the amount of a combination of steviol glycosides can exceed 7,000 mg/L. In general, longer culture times will lead to greater amounts of product. Thus, the recombinant microorganism can be cultured for from 1 day to 7 days, from 1 day to 5 days, from 3 days to 5 days, about 3 days, about 4 days, or about 5 days.

[00176] It will be appreciated that the various genes and modules discussed herein can be present in two or more recombinant microorganisms rather than a single microorganism. When a plurality of recombinant microorganisms is used, they can be grown in a mixed culture to produce steviol and/or steviol glycosides. For example, a first microorganism can comprise one or more biosynthesis genes for producing a steviol glycoside precursor, while a second microorganism comprises steviol glycoside biosynthesis genes. The product produced by the second, or final microorganism is then recovered. It will also be appreciated that in some embodiments, a recombinant microorganism is grown using nutrient sources other than a culture medium and utilizing a system other than a fermenter.

[00177] Alternatively, the two or more microorganisms each can be grown in a separate culture medium and the product of the first culture medium, *e.g.*, steviol, can be introduced into second culture medium to be converted into a subsequent intermediate, or into an end product such as RebA. The product produced by the second, or final microorganism is then recovered. It will also be appreciated that in some embodiments, a recombinant microorganism is grown using nutrient sources other than a culture medium and utilizing a system other than a fermenter.

[00178] Steviol glycosides and compositions obtained by the methods disclosed herein can be used to make food products, dietary supplements and sweetener compositions. *See*, *e.g.*, WO 2011/153378, WO 2013/022989, WO 2014/122227, and WO 2014/122328.

[00179] For example, substantially pure steviol or steviol glycoside such as RebM or RebD can be included in food products such as ice cream, carbonated beverages, fruit juices, yogurts, baked goods, chewing gums, hard and soft candies, and sauces. Substantially pure steviol or steviol glycoside can also be included in non-food products such as pharmaceutical products,

medicinal products, dietary supplements and nutritional supplements. Substantially pure steviol or steviol glycosides may also be included in animal feed products for both the agriculture industry and the companion animal industry. Alternatively, a mixture of steviol and/or steviol glycosides can be made by culturing recombinant microorganisms separately, each producing a specific steviol or steviol glycoside, recovering the steviol or steviol glycoside in substantially pure form from each microorganism and then combining the compounds to obtain a mixture comprising each compound in the desired proportion. The recombinant microorganisms described herein permit more precise and consistent mixtures to be obtained compared to current Stevia products.

[00180] In another alternative, a substantially pure steviol or steviol glycoside can be incorporated into a food product along with other sweeteners, *e.g.* saccharin, dextrose, sucrose, fructose, erythritol, aspartame, sucralose, monatin, or acesulfame potassium. The weight ratio of steviol or steviol glycoside relative to other sweeteners can be varied as desired to achieve a satisfactory taste in the final food product. See, *eg.*, U.S. 2007/0128311. In some embodiments, the steviol or steviol glycoside may be provided with a flavor (*e.g.*, citrus) as a flavor modulator.

[00181] Compositions produced by a recombinant microorganism described herein can be incorporated into food products. For example, a steviol glycoside composition produced by a recombinant microorganism can be incorporated into a food product in an amount ranging from about 20 mg steviol glycoside/kg food product to about 1800 mg steviol glycoside/kg food product on a dry weight basis, depending on the type of steviol glycoside and food product. For example, a steviol glycoside composition produced by a recombinant microorganism can be incorporated into a dessert, cold confectionary (*e.g.*, ice cream), dairy product (*e.g.*, yogurt), or beverage (*e.g.*, a carbonated beverage) such that the food product has a maximum of 500 mg steviol glycoside/kg food on a dry weight basis. A steviol glycoside composition produced by a recombinant microorganism can be incorporated into a baked good (*e.g.*, a biscuit) such that the food product has a maximum of 300 mg steviol glycoside/kg food on a dry weight basis. A steviol glycoside composition produced by a recombinant microorganism can be incorporated into a sauce (*e.g.*, chocolate syrup) or vegetable product (*e.g.*, pickles) such that the food product has a maximum of 1000 mg steviol glycoside/kg food on a dry weight basis. A steviol glycoside composition produced by a recombinant microorganism can be incorporated into bread such that the food product has a maximum of 160 mg steviol glycoside/kg food on a dry weight basis. A steviol glycoside composition produced by a recombinant microorganism, plant, or plant cell can be incorporated into a hard or soft candy such that the food product has a

maximum of 1600 mg steviol glycoside/kg food on a dry weight basis. A steviol glycoside composition produced by a recombinant microorganism, plant, or plant cell can be incorporated into a processed fruit product (*e.g.*, fruit juices, fruit filling, jams, and jellies) such that the food product has a maximum of 1000 mg steviol glycoside/kg food on a dry weight basis. In some embodiments, a steviol glycoside composition produced herein is a component of a pharmaceutical composition. *See*, *e.g.*, Steviol Glycosides Chemical and Technical Assessment 69th JECFA, 2007, prepared by Harriet Wallin, Food Agric. Org.; EFSA Panel on Food Additives and Nutrient Sources added to Food (ANS), "Scientific Opinion on the safety of steviol glycosides for the proposed uses as a food additive," 2010, *EFSA Journal* 8(4):1537; U.S. Food and Drug Administration GRAS Notice 323; U.S Food and Drug Administration GRAS Notice Notice 329; WO 2011/037959; WO 2010/146463; WO 2011/046423; and WO 2011/056834.

[00182] For example, such a steviol glycoside composition can have from 90-99 weight % RebA and an undetectable amount of stevia plant-derived contaminants, and be incorporated into a food product at from 25-1600 mg/kg, *e.g.*, 100-500 mg/kg, 25-100 mg/kg, 250-1000 mg/kg, 50-500 mg/kg or 500-1000 mg/kg on a dry weight basis.

[00183] Such a steviol glycoside composition can be a RebB-enriched composition having greater than 3 weight % RebB and be incorporated into the food product such that the amount of RebB in the product is from 25-1600 mg/kg, *e.g.*, 100-500 mg/kg, 25-100 mg/kg, 250-1000 mg/kg, 50-500 mg/kg or 500-1000 mg/kg on a dry weight basis. Typically, the RebB-enriched composition has an undetectable amount of stevia plant-derived contaminants.

[00184] Such a steviol glycoside composition can be a RebD-enriched composition having greater than 3 weight % RebD and be incorporated into the food product such that the amount of RebD in the product is from 25-1600 mg/kg, *e.g.*, 100-500 mg/kg, 25-100 mg/kg, 250-1000 mg/kg, 50-500 mg/kg or 500-1000 mg/kg on a dry weight basis. Typically, the RebD-enriched composition has an undetectable amount of stevia plant-derived contaminants.

[00185] Such a steviol glycoside composition can be a RebE-enriched composition having greater than 3 weight % RebE and be incorporated into the food product such that the amount of RebE in the product is from 25-1600 mg/kg, *e.g.*, 100-500 mg/kg, 25-100 mg/kg, 250-1000 mg/kg, 50-500 mg/kg or 500-1000 mg/kg on a dry weight basis. Typically, the RebE-enriched composition has an undetectable amount of stevia plant-derived contaminants.

[00186] Such a steviol glycoside composition can be a RebM-enriched composition having greater than 3 weight % RebM and be incorporated into the food product such that the amount

of RebM in the product is from 25-1600 mg/kg, *e.g.*, 100-500 mg/kg, 25-100 mg/kg, 250-1000 mg/kg, 50-500 mg/kg or 500-1000 mg/kg on a dry weight basis. Typically, the RebM-enriched composition has an undetectable amount of stevia plant-derived contaminants.

[00187] In some embodiments, a substantially pure steviol or steviol glycoside is incorporated into a tabletop sweetener or "cup-for-cup" product. Such products typically are diluted to the appropriate sweetness level with one or more bulking agents, *e.g.*, maltodextrins, known to those skilled in the art. Steviol glycoside compositions enriched for RebA, RebB, RebD, RebE, or RebM, can be package in a sachet, for example, at from 10,000 to 30,000 mg steviol glycoside/kg product on a dry weight basis, for tabletop use. In some embodiments, a steviol glycoside produced *in vitro*, *in vivo*, or by whole cell bioconversion

[00188] The invention will be further described in the following examples, which do not limit the scope of the invention described in the claims.

EXAMPLES

[00189] The Examples that follow are illustrative of specific embodiments of the invention, and various uses thereof. They are set forth for explanatory purposes only, and are not to be taken as limiting the invention.

Example 1: LC-MS Analytical Procedures

[00190] LC-MS analyses were performed on Waters ACQUITY UPLC® (Waters Corporation) with a Waters ACQUITY UPLC® BEH C18 column (2.1 x 50 mm, 1.7 µm particles, 130 Å pore size) coupled to a Waters ACQUITY TQD triple quadropole mass spectrometer with electrospray ionization (ESI) in negative mode.

[00191] Compound separation for Method A was achieved by a gradient of the two mobile phases: A (water with 0.1% formic acid) and B (MeCN with 0.1% formic acid) by increasing from 20% to 50 % B between 0.3 to 2.0 min, increasing to 100% B at 2.01 min, holding 100% B for 0.6 min, and re-equilibrating for 0.6 min.

[00192] Compound separation for Method B was achieved by a gradient of the two mobile phases A (water with 0.1% formic acid) and B (MeCN with 0.1% formic acid) by increasing from 60% to 100 % B in 2.5 min, holding 100%B for 0.1 min and re-equilibrating for 0.3 min.

[00193] The flow rate was 0.6 mL/min, and the column temperature was 55°C. Steviol glycosides were monitored using SIM (Single Ion Monitoring) and quantified by comparing with authentic standards. *See* Table 1 for m/z trace and retention time values of steviol glycosides detected.

Table 1: LC-MS Analytical Data for steviol and steviol glycosides.

Compound	MS Trace	RT (min)	Method	Figure	Table
steviol+6Glc (isomer 1) (also referred to as compound 6.1)	1289.53	0.87	A	3	
steviol+7Glc (isomer 2) (also referred to as compound 7.2)	1451.581	0.94	A	3	
RebD	1127.48	1.08	A		
RebM	1289.53	1.15	A		
steviol+4Glc (#26) (also referred to as compound 4.26)	965.42	1.21	A	4	
steviol+5Glc (#24) (also referred to as compound 5.24)	1127.48	1.18	A		7
RebA	965.42	1.43	A		
1,2-stevioside	803.37	1.43	A		6
rubusoside	641.32	1.67	A		5, 8
RebB	803.37	1.76	A		
steviol-1,2-bioside	641.32	1.80	A		5
19-SMG	525.27	1.98	A		4
13-SMG	479.26	2.04	A		4

Compound	MS Trace	RT (min)	Method	Figure	Table
ent-kaurenoic acid+3Glc (isomer 1) (also referred to as compound KA3.1)	787.37	2.16	A	4	
ent-kaurenoic acid+3Glc (isomer 2) (also referred to as compound KA3.2)	787.37	2.28	A	5	
ent-kaurenol+3Glc (isomer 1) co-eluted with *ent*-kaurenol+3Glc (#6) (also referred to as compounds KL3.1 and KL3.6)	773.4	2.36	A	5	
ent-kaurenoic acid+2Glc (#7) (also referred to as compound KA2.7)	625.32	2.35	A		
steviol	317.21	2.39	A		
ent-kaurenoic acid+1Glc (#58) [also referred to as compound KA1.58]	439.27 and 509.61	0.69	B		3, 8

Example 2: Crude Lysate Preparation

[00194] Colonies of *E. coli* strains constructed to express a UGT polypeptide were placed into sterile 96 deep well plates with 1 mL of NZCYM bacterial culture broth comprising ampicillin. The plate was sealed and samples were allowed to grow overnight at 37°C, shaking at 200 rpm. The following day (*i.e.*, Day 2), 50 µL of each culture was transferred to a new sterile 96 deep well plate with 1 mL of NZCYM bacterial culture broth comprising ampicillin and polypeptide expression inducers. The plate was sealed and samples were incubated at 20°C, shaking at 200 rpm for ~20 h. On Day 3, the plate was centrifuged at 4000 rpm for 10 min at 4°C. After decanting the supernatant, 50 µL of a buffer comprising Tris-HCl, $MgCl_2$, $CaCl_2$, and protease inhibitors was added to each well and cells were resuspended by shaking at 200 rpm for 5 min at 4°C. The contents of each well (*i.e.*, cell slurries) were then transferred to a PCR

plate and sealed before freezing at -80°C overnight. Frozen cell slurries were thawed at room temperature for up to 30 min. If the thawing mix was not viscous due to cell lysing, samples were frozen and thawed again. When samples were nearly thawed, 25 µL of binding buffer comprising DNase and $MgCl_2$ was added to each well. The PCR plate was incubated at room temperature for 5 min, shaking at 500 rpm, until samples became less viscous. Finally, samples were centrifuged at 4000 rpm for 5 min, after which the supernatants were used to measure UGT activity, as described in Example 3.

Example 3: UGT Activity Assay

[00195] UGT polypeptide samples prepared according to Example 2 were screened *in vitro* for activity on substrates including RebA, RebB, rubusoside, steviol, *ent*-kaurenoic acid, and 13-SMG by preparing a reaction mixture according to Table 2.

Table 2: UGT Activity Assay Reaction Mixture.

Component	Volume (µL)
H_2O	4.2
Alkaline Phosphatase	0.3
4X Buffer (10 mM Tris-HCl, 5 mM $MgCl_2$, 1 mM $CaCl_2$)	7.5
UDP-Glucose (1 mM)	9
Substrate	3
UGT Sample	6

[00196] The reaction mixture was incubated overnight at 30°C. The reaction was stopped by adding 30 µL of 100% DMSO. The resultant mixture was diluted further with 90 µL 50% DMSO for LC-MS analysis according to Example 1. Both the products formed and the area-under-the-curve (AUC) values of each product are shown in Tables 3-7, organized by substrate.

Table 3: UGT Activity on *ent*-kaurenoic acid.

UGT Polypeptide	SEQ ID NO:	Activity
		ent-kaurenoic acid+1Glc (#58) Production (AUC)
UGT73C1	127	1095
UGT73C3	133	227
UGT73C5	135	2489
UGT73C6	137	699
UGT73E1	141	109
UGT74D1	143	119
UGT74G1	4	38967
UGT75B1	145	1409
UGT75L6	147	1208
UGT76E12	153	161
OleI	177	1086
UGT5	181	5547
SA Gtase	183	11088
UDPG1	185	460
UGT74F1	203	323
UGT75D1	205	2465
UGT84B2	207	31123
CaUGT2	209	446

UGT74F2-like UGT	211	20552

Table 4: UGT Activity on steviol.

UGT Polypeptide	SEQ ID NO:	Activity	
		13-SMG Production (AUC)	19-SMG Production (AUC)
UGT73C1	127	9880	1235
UGT73C3	133	1850	295
UGT73C5	135	7100	2160
UGT73C6	137	2255	4980
UGT73C7	139	1570	N/A
UGT73E1	141	2220	165
UGT74G1	4	N/A	172485
UGT75B1	145	N/A	230
UGT75L6	147	N/A	4615
UGT76E12	153	650	N/A
UGT85C2	7	205575	N/A
OleI	177	N/A	540
UGT5	181	N/A	1375
SA Gtase	183	N/A	10580
UDPG1	185	N/A	4420

Table 5: UGT Activity on 13-SMG.

UGT Polypeptide	SEQ ID NO:	Activity	
		rubusoside Production (AUC)	steviol-1,2-bioside Production (AUC)
UGT73C1	127	550	N/A
UGT73C6	137	1270	N/A
UGT74G1	4	138650	N/A
UGT85C2	7	865	N/A
UGT91D2e-b	13	N/A	1080
EUGT11	16	N/A	10805
SA Gtase	183	4120	N/A
UDPG1	185	2355	N/A
UN32491	199	N/A	1065
UN1671	201	1185	N/A
UGT74F1	203	950	N/A
UGT75D1	205	99885	N/A
UGT84B2	207	1390	N/A
UGT74F2-like UGT	211	31415	N/A

Table 6: UGT Activity on rubusoside.

UGT Polypeptide	SEQ ID NO:	Activity
		1,2-stevioside Production (AUC)
UGT73C6	137	385
UGT91D2e-b	13	4680
CaUGT3	169	610
EUGT11	16	1900

Table 7: UGT Activity on RebA.

UGT Polypeptide	SEQ ID NO:	Activity
		steviol+5Glc (#24) Production (AUC)
EUGT11	16	4950
UN1671	201	52985

[00197] As shown in Tables 3-7, 19-*O*-glycosylation, 13-*O*-glycosylation, and glycosyl-group glycosylation activity by UGT polypeptides on several substrates was observed, resulting in the formation of glycosides of *ent*-kaurenoic acid and steviol.

[00198] **Table 8: UGT Activity on 13-SMG and *ent*-kaurenoic acid.**

UGT Polypeptide	SEQ ID NO:	AUC rubusoside/ AUC KA1.58
UGT73C1	127	0.5
UGT73C6	137	1.8
UGT74G1	4	3.6
SA Gtase	183	0.4
UDPG1	185	5.1
UGT74F1	203	2.9
UGT75D1	205	40.5
UGT74F2-like UGT	211	1.5

[00199] As shown in Table 8, UDPG1 (SEQ ID NO:185) and UGT75D1 (SEQ ID NO:205) produce relatively more rubusoside from 13-SMG than *ent*-kaurenoic acid+1Glc (#58) from *ent*-kaurenoic acid *in vitro*, compared to UGT74G1 (SEQ ID NO:4)

Example 4: Strain Engineering and Fermentation

[00200] SA Gtase (SEQ ID NO:182, SEQ ID NO:183) was expressed with a p416-GPD vector in a steviol glycoside-producing *S. cerevisiae* strain comprising one or more copies of a recombinant gene encoding a GGPPS polypeptide (SEQ ID NO:19, SEQ ID NO:20), a recombinant gene encoding a truncated CDPS polypeptide (SEQ ID NO:39, SEQ ID NO:40), a recombinant gene encoding an KS polypeptide (SEQ ID NO:51, SEQ ID NO:52), a recombinant gene encoding a KO polypeptide (SEQ ID NO:59, SEQ ID NO:60), a recombinant gene encoding an ATR2 polypeptide (SEQ ID NO:91, SEQ ID NO:92), a recombinant gene encoding an EUGT11 polypeptide (SEQ ID NO:14/SEQ ID NO:15, SEQ ID NO:16), a recombinant gene encoding an KAH polypeptide (SEQ ID NO:93, SEQ ID NO:94), a recombinant gene encoding a CPR8 polypeptide (SEQ ID NO:85, SEQ ID NO:86), a recombinant gene encoding an

UGT85C2 polypeptide (SEQ ID NO:5/SEQ ID NO:6/SEQ ID NO:149, SEQ ID NO:7) or a UGT85C2 variant (or functional homolog) of SEQ ID NO:7, a recombinant gene encoding a UGT74G1 polypeptide (SEQ ID NO:3, SEQ ID NO:4) of a UGT74G1 variant (or functional homolog) of SEQ ID NO:4, a recombinant gene encoding a UGT76G1 polypeptide (SEQ ID NO:8, SEQ ID NO:9) or a UGT76G1 variant (or functional homolog) of SEQ ID NO:9, and a recombinant gene encoding a UGT91D2e polypeptide (SEQ ID NO:10, SEQ ID NO:11) and a UGT91D2e variant (or functional homolog) of SEQ ID NO:11 such as a UGT91D2e-b (SEQ ID NO:12, SEQ ID NO:13).

[00201] The strain was incubated in 1 mL synthetic complete (SC) uracil dropout media at 30°C for five days, shaking at 400 rpm. 50 µL of each culture was transferred into 50 µL DMSO, incubated at 80°C for 10 min, and centrifuged at 3220 g for 5 min. 15 µL of the resulting supernatant was then transferred to 105 µL 50% DMSO for LC-MS analysis, which was carried out according to Example 1. Normalized area-under-the-curve (AUC) values for LC-MS derived peaks corresponding to RebD and RebM were about 0.25 $\mu M/OD_{600}$ and 1.15 $\mu M/OD_{600}$, respectively. *Ent*-kaurenoic acid+2Glc (#7), *ent*-kaurenoic acid+3Glc (isomer 1), and *ent*-kaurenoic acid+3Glc (isomer 2) accumulated at levels of about 200 AUC/OD_{600}, 15 AUC/OD_{600}, and 1000 AUC/OD_{600}, respectively. 13-SMG, RebA, and Reb B accumulated at levels of about 4.8 $\mu M/OD_{600}$, 2.5 $\mu M/OD_{600}$, and 0.25 $\mu M/OD_{600}$, respectively. Steviol+4Glc (#26), steviol+6Glc (isomer 1), steviol+7Glc (isomer 2), and kaurenol+3Glc (isomer 1 and/or 2) accumulated at levels of about 200 AUC/OD_{600}, 15 AUC/OD_{600}, 75 AUC/OD_{600}, and 750 AUC/OD_{600}, respectively.

[00202] Having described the invention in detail and by reference to specific embodiments thereof, it will be apparent that modifications and variations are possible without departing from the scope of the invention defined in the appended claims. More specifically, although some aspects of the present invention are identified herein as particularly advantageous, it is contemplated that the present invention is not necessarily limited to these particular aspects of the invention.

Table 9. Sequences disclosed herein.

SEQ ID NO:3
Artificial Sequence

```
atggcagagc aacaaaagat caaaaagtca cctcacgtct tacttattcc atttcctctg      60
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acaacactgg taaccactat ccacactttg aattctactc tgaaccactc aaatactact     180
actacaagta tagaaattca agctatatca gacggatgcg atgagggtgg ctttatgtct     240
gccggtgaat cttacttgga aacattcaag caagtgggat ccaagtctct ggccgatcta     300
atcaaaaagt tacagagtga aggcaccaca attgacgcca taatctacga ttctatgaca     360
gagtgggttt tagacgttgc tatcgaattt ggtattgatg gaggttcctt tttcacacaa     420
gcatgtgttg tgaattctct atactaccat gtgcataaag ggttaatctc tttaccattg     480
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attgaatgga ctaggaagat ctggaatttg aaagtcattg gtccaacatt gccatcaatg     720
tatttggaca aaagacttga tgatgataaa gataatggtt tcaatttgta caaggctaat     780
catcacgaat gtatgaattg gctggatgac aaaccaaagg aatcagttgt atatgttgct     840
ttcggctctc ttgttaaaca tggtccagaa caagttgagg agattacaag agcacttata     900
gactctgacg taaacttttt gtgggtcatt aagcacaaag aggaggggaa actgccagaa     960
aacctttctg aagtgataaa gaccggaaaa ggtctaatcg ttgcttggtg taaacaattg    1020
gatgttttag ctcatgaatc tgtaggctgt tttgtaacac attgcggatt caactctaca    1080
ctagaagcca tttccttagg cgtacctgtc gttgcaatgc ctcagttctc cgatcagaca    1140
accaacgcta aacttttgga cgaaatacta ggggtgggtg tcagagttaa agcagacgag    1200
aatggtatcg tcagaagagg gaacctagct tcatgtatca aaatgatcat ggaagaggaa    1260
agaggagtta tcataaggaa aaacgcagtt aagtggaagg atcttgcaaa ggttgccgtc    1320
catgaaggcg gctcttcaga taatgatatt gttgaatttg tgtccgaact aatcaaagcc    1380
taa                                                                 1383
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SEQ ID NO:4
S. rebaudiana

```
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EWVLDVAIEF GIDGGSFFTQ ACVVNSLYYH VHKGLISLPL GETVSVPGFP VLQRWETPLI     180
LQNHEQIQSP WSQMLFGQFA NIDQARWVFT NSFYKLEEEV IEWTRKIWNL KVIGPTLPSM     240
YLDKRLDDDK DNGFNLYKAN HHECMNWLDD KPKESVVYVA FGSLVKHGPE QVEEITRALI     300
DSDVNFLWVI KHKEEGKLPE NLSEVIKTGK GLIVAWCKQL DVLAHESVGC FVTHCGFNST     360
LEAISLGVPV VAMPQFSDQT TNAKLLDEIL GVGVRVKADE NGIVRRGNLA SCIKMIMEEE     420
RGVIIRKNAV KWKDLAKVAV HEGGSSDNDI VEFVSELIKA                           460
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SEQ ID NO:5
S. rebaudiana

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cccgaagaga aaaagcaaac tggaattacg agtctccatg gatacagttt agtaaaagaa     840
gaaccagagt gtttccagtg gcttcagtct aaagaaccaa attccgtcgt ttatgtaaat     900
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accaaagtga aacgagatga agtcaagagg cttgtacaag agttgatggg agaaggaggt 1320
cacaaaatga ggaacaaggc taaagattgg aaagaaaagg ctcgcattgc aatagctcct 1380
aacggttcat cttctttgaa catagacaaa atggtcaagg aaatcaccgt gctagcaaga 1440
aactag 1446

SEQ ID NO:6
Artificial Sequence

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ataactttcg tgaataccga cttcatccat aatcaatttc tggaatctag tggccctcat 180
tgtttggacg gagccccagg gtttagattc gaaacaattc ctgacggtgt ttcacattcc 240
ccagaggcct ccatcccaat aagagagagt ttactgaggt caatagaaac caacttttg 300
gatcgtttca ttgacttggt cacaaaactt ccagacccac caacttgcat aatctctgat 360
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attgactggg taccaggtat ggaaggtata agacttaaag attttccttt ggattggtct 600
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gtttcacatc atatctttca caccttgat gaattggaac catcaatcat caaaaccttg 720
tctctaagat acaatcatat ctacactatt ggtccattac aattacttct agatcaaatt 780
cctgaagaga aaaagcaaac tggtattaca tccttacacg gctactcttt agtgaaagag 840
gaaccagaat gttttcaatg gctacaaagt aaagagccta attctgtggt ctacgtcaac 900
ttcggaagta caacagtcat gtccttggaa gatatgactg aatttggttg gggccttgct 960
aattcaaatc attactttct atggattatc aggtccaatt tggtaatagg ggaaaacgcc 1020
gtattacctc cagaattgga ggaacacatc aaaaagagag gtttcattgc ttcctggtgt 1080
tctcaggaaa aggtattgaa acatccttct gttggtggtt tccttactca ttgcggttgg 1140
ggctctacaa tcgaatcact aagtgcagga gttccaatga tttgttggcc atattcatgg 1200
gaccaactta caaattgtag gtatatctgt aaagagtggg aagttggatt agaaatggga 1260
acaaaggtta aacgtgatga agtgaaaaga ttggttcagg agttgatggg ggaaggtggc 1320
cacaagatga gaaacaaggc caaagattgg aaggaaaaag ccagaattgc tattgctcct 1380
aacgggtcat cctctctaaa cattgataag atggtcaaag agattacagt cttagccaga 1440
aactaa 1446

SEQ ID NO:7
S. rebaudiana

MDAMATTEKK PHVIFIPFPA QSHIKAMLKL AQLLHHKGLQ ITFVNTDFIH NQFLESSGPH 60
CLDGAPGFRF ETIPDGVSHS PEASIPIRES LLRSIETNFL DRFIDLVTKL PDPPTCIISD 120
GFLSVFTIDA AKKLGIPVMM YWTLAACGFM GFYHIHSLIE KGFAPLKDAS YLTNGYLDTV 180
IDWVPGMEGI RLKDFPLDWS TDLNDKVLMF TTEAPQRSHK VSHHIFHTFD ELEPSIIKTL 240
SLRYNHIYTI GPLQLLLDQI PEEKKQTGIT SLHGYSLVKE EPECFQWLQS KEPNSVVYVN 300
FGSTTVMSLE DMTEFGWGLA NSNHYFLWII RSNLVIGENA VLPPELEEHI KKRGFIASWC 360
SQEKVLKHPS VGGFLTHCGW GSTIESLSAG VPMICWPYSW DQLTNCRYIC KEWEVGLEMG 420
TKVKRDEVKR LVQELMGEGG HKMRNKAKDW KEKARIAIAP NGSSSLNIDK MVKEITVLAR 480
N 481

SEQ ID NO:8
Artificial Sequence

atggaaaaca agaccgaaac aacagttaga cgtaggcgta gaatcattct gtttccagta 60
ccttttcaag ggcacatcaa tccaatacta caactagcca acgttttgta ctctaaaggt 120
ttttctatta caatctttca caccaatttc aacaaaccaa aaacatccaa ttacccacat 180

ttcacattca gattcatact tgataatgat ccacaagatg aacgtatttc aaacttacct 240
acccacggtc ctttagctgg aatgagaatt ccaatcatca atgaacatgg tgccgatgag 300
cttagaagag aattagagtt acttatgttg gcatccgaag aggacgagga agtctcttgt 360
ctgattactg acgctctatg gtactttgcc caatctgtgg ctgatagttt gaatttgagg 420
agattggtac taatgacatc cagtctgttt aactttcacg ctcatgttag tttaccacaa 480
tttgacgaat tgggatactt ggaccctgat gacaagacta ggttagagga acaggcctct 540
ggttttccta tgttgaaagt caaagatatc aagtctgcct attctaattg gcaaatcttg 600
aaagagatct taggaaagat gatcaaacag acaaaggctt catctggagt gatttggaac 660
agtttcaaag agttagaaga gtctgaattg gagactgtaa tcagagaaat tccagcacct 720
tcattcctga taccattacc aaaacatttg actgcttcct cttcctcttt gttggatcat 780
gacagaacag tttttcaatg gttggaccaa caaccaccta gttctgtttt gtacgtgtca 840
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gatagtaagc agtcattcct ttgggtcgtg cgtccaggtt tcgtgaaagg ctcaacatgg 960
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caacaggaag ttttagctca tggcgctatt ggggcattct ggactcattc cggatggaat 1080
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caaccactga acgcaagata catgtctgat gttttgaaag tgggtgtata tctagaaaat 1200
ggctgggaaa ggggtgaaat agctaatgca ataagacgtg ttatggttga tgaagagggg 1260
gagtatatca gacaaaacgc aagagtgctg aagcaaaagg ccgacgtttc tctaatgaag 1320
ggaggctctt catacgaatc cttagaatct cttgtttcct acatttcatc actgtaa 1377

SEQ ID NO:9

S. rebaudiana

MENKTETTVR RRRRIILFPV PFQGHINPIL QLANVLYSKG FSITIFHTNF NKPKTSNYPH 60
FTFRFILDND PQDERISNLP THGPLAGMRI PIINEHGADE LRRELELLML ASEEDEEVSC 120
LITDALWYFA QSVADSLNLR RLVLMTSSLF NFHAHVSLPQ FDELGYLDPD DKTRLEEQAS 180
GFPMLKVKDI KSAYSNWQIL KEILGKMIKQ TKASSGVIWN SFKELEESEL ETVIREIPAP 240
SFLIPLPKHL TASSSSLLDH DRTVFQWLDQ QPPSSVLYVS FGSTSEVDEK DFLEIARGLV 300
DSKQSFLWVV RPGFVKGSTW VEPLPDGFLG ERGRIVKWVP QQEVLAHGAI GAFWTHSGWN 360
STLESVCEGV PMIFSDFGLD QPLNARYMSD VLKVGVYLEN GWERGEIANA IRRVMVDEEG 420
EYIRQNARVL KQKADVSLMK GGSSYESLES LVSYISSL 458

SEQ ID NO:10

Artificial Sequence

atggctacat ctgattctat tgttgatgac aggaagcagt tgcatgtggc tactttccct 60
tggcttgctt tcggtcatat actgccttac ctacaactat caaaactgat agctgaaaaa 120
ggacataaag tgtcattcct ttcaacaact agaaacattc aaagattatc ttcccacata 180
tcaccattga ttaacgtcgt tcaattgaca cttccaagag tacaggaatt accagaagat 240
gctgaagcta caacagatgt gcatcctgaa gatatccctt acttgaaaaa ggcatccgat 300
ggattacagc ctgaggtcac tagattcctt gagcaacaca gtccagattg gatcatatac 360
gactacactc actattggtt gccttcaatt gcagcatcac taggcatttc tagggcacat 420
ttcagtgtaa ccacaccttg ggccattgct tacatgggtc catccgctga tgctatgatt 480
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tttccaacta aagtctgttg gagaaaacac gacttagcaa gactggttcc atacaaggca 600
ccaggaatct cagacggcta tagaatgggt ttagtcctta aagggtctga ctgcctattg 660
tctaagtgtt accatgagtt tgggacacaa tggctaccac ttttggaaac attacaccaa 720
gttcctgtcg taccagttgg tctattacct ccagaaatcc ctggtgatga gaaggacgag 780
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gcactgggtt ccgaagtttt agtatctcaa acagaagttg tggaacttgc cttaggtttg 900
gaactatctg gattgccatt tgtctgggcc tacagaaaac caaaaggccc tgcaaagtcc 960
gattcagttg aattgccaga cggctttgtc gagagaacta gagatagagg gttggtatgg 1020
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cattgtggtt ctggttctat agttgaagga ctgatgtttg gtcatccact tatcatgttg 1140
ccaatctttg gtgaccagcc tttgaatgca cgtctgttag aagataaaca agttggaatt 1200
gaaatcccac gtaatgagga agatggatgt ttaaccaagg agtctgtggc cagatcatta 1260
cgttccgttg tcgttgaaaa ggaaggcgaa atctacaagg ccaatgcccg tgaactttca 1320

aagatctaca atgacacaaa agtagagaag gaatatgttt ctcaatttgt agattaccta 1380
gagaaaaacg ctagagccgt agctattgat catgaatcct aa 1422

SEQ ID NO:11
S. rebaudiana

MATSDSIVDD RKQLHVATFP WLAFGHILPY LQLSKLIAEK GHKVSFLSTT RNIQRLSSHI 60
SPLINVVQLT LPRVQELPED AEATTDVHPE DIPYLKKASD GLQPEVTRFL EQHSPDWIIY 120
DYTHYWLPSI AASLGISRAH FSVTTPWAIA YMGPSADAMI NGSDGRTTVE DLTTPPKWFP 180
FPTKVCWRKH DLARLVPYKA PGISDGYRMG LVLKGSDCLL SKCYHEFGTQ WLPLLETLHQ 240
VPVVPVGLLP PEIPGDEKDE TWVSIKKWLD GKQKGSVVYV ALGSEVLVSQ TEVVELALGL 300
ELSGLPFVWA YRKPKGPAKS DSVELPDGFV ERTRDRGLVW TSWAPQLRIL SHESVCGFLT 360
HCGSGSIVEG LMFGHPLIML PIFGDQPLNA RLLEDKQVGI EIPRNEEDGC LTKESVARSL 420
RSVVVEKEGE IYKANARELS KIYNDTKVEK EYVSQFVDYL EKNARAVAID HES 473

SEQ ID NO:12
Artificial Sequence

atggctactt ctgattccat cgttgacgat agaaagcaat tgcatgttgc tacttttcca 60
tggttggctt tcggtcatat tttgccatac ttgcaattgt ccaagttgat tgctgaaaag 120
ggtcacaagg tttcattctt gtctaccacc agaaacatcc aaagattgtc ctctcatatc 180
tccccattga tcaacgttgt tcaattgact ttgccaagag tccaagaatt gccagaagat 240
gctgaagcta ctactgatgt tcatccagaa gatatccctt acttgaaaaa ggcttccgat 300
ggtttacaac cagaagttac tagattcttg gaacaacatt ccccagattg gatcatctac 360
gattatactc attactggtt gccatccatt gctgcttcat tgggtatttc tagagcccat 420
ttctctgtta ctactccatg ggctattgct tatatgggtc catctgctga tgctatgatt 480
aacggttctg atggtagaac taccgttgaa gatttgacta ctccaccaaa gtggtttcca 540
tttccaacaa aagtctgttg gagaaaacac gatttggcta gattggttcc atacaaagct 600
ccaggtattt ctgatggtta cagaatgggt atggttttga aaggttccga ttgcttgttg 660
tctaagtgct atcatgaatt cggtactcaa tggttgcctt tgttggaaac attgcatcaa 720
gttccagttg ttccagtagg tttgttgcca ccagaaattc caggtgacga aaaagacgaa 780
acttgggttt ccatcaaaaa gtggttggat ggtaagcaaa agggttctgt tgtttatgtt 840
gctttgggtt ccgaagcttt ggtttctcaa accgaagttg ttgaattggc tttgggtttg 900
gaattgtctg gtttgccatt tgtttgggct tacagaaaac ctaaaggtcc agctaagtct 960
gattctgttg aattgccaga tggtttcgtt gaaagaacta gagatagagg tttggtttgg 1020
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cattgtggtt ctggttctat cgttgaaggt ttgatgtttg gtcacccatt gattatgttg 1140
ccaatctttg gtgaccaacc attgaacgct agattattgg aagataagca agtcggtatc 1200
gaaatcccaa gaaatgaaga agatggttgc ttgaccaaag aatctgttgc tagatctttg 1260
agatccgttg tcgttgaaaa agaaggtgaa atctacaagg ctaacgctag agaattgtcc 1320
aagatctaca acgataccaa ggtcgaaaaa gaatacgttt cccaattcgt tgactacttg 1380
gaaaagaatg ctagagctgt tgccattgat catgaatctt ga 1422

SEQ ID NO:13
Artificial Sequence

MATSDSIVDD RKQLHVATFP WLAFGHILPY LQLSKLIAEK GHKVSFLSTT RNIQRLSSHI 60
SPLINVVQLT LPRVQELPED AEATTDVHPE DIPYLKKASD GLQPEVTRFL EQHSPDWIIY 120
DYTHYWLPSI AASLGISRAH FSVTTPWAIA YMGPSADAMI NGSDGRTTVE DLTTPPKWFP 180
FPTKVCWRKH DLARLVPYKA PGISDGYRMG MVLKGSDCLL SKCYHEFGTQ WLPLLETLHQ 240
VPVVPVGLLP PEIPGDEKDE TWVSIKKWLD GKQKGSVVYV ALGSEALVSQ TEVVELALGL 300
ELSGLPFVWA YRKPKGPAKS DSVELPDGFV ERTRDRGLVW TSWAPQLRIL SHESVCGFLT 360
HCGSGSIVEG LMFGHPLIML PIFGDQPLNA RLLEDKQVGI EIPRNEEDGC LTKESVARSL 420
RSVVVEKEGE IYKANARELS KIYNDTKVEK EYVSQFVDYL EKNARAVAID HES 473

SEQ ID NO:14
Oryza sativa

atggactccg gctactcctc ctcctacgcc gccgccgccg ggatgcacgt cgtgatctgc 60
ccgtggctcg ccttcggcca cctgctcccg tgcctcgacc tcgcccagcg cctcgcgtcg 120

cggggccacc gcgtgtcgtt cgtctccacg ccgcggaaca tatcccgcct cccgccggtg 180
cgccccgcgc tcgcgccgct cgtcgccttc gtggcgctgc cgctcccgcg cgtcgagggg 240
ctccccgacg gcgccgagtc caccaacgac gtcccccacg acaggccgga catggtcgag 300
ctccaccgga gggccttcga cgggctcgcc gcgcccttct cggagttctt gggcaccgcg 360
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cacaaggtgc catgtgcaat gatgttgttg ggctctgcac atatgatcgc ttccatagca 480
gacagacggc tcgagcgcgc ggagacagag tcgcctgcgg ctgccgggca gggacgccca 540
gcggcggcgc caacgttcga ggtggcgagg atgaagttga tacgaaccaa aggctcatcg 600
ggaatgtccc tcgccgagcg cttctccttg acgctctcga ggagcagcct cgtcgtcggg 660
cggagctgcg tggagttcga gccggagacc gtcccgctcc tgtcgacgct ccgcggtaag 720
cctattacct tccttggcct tatgccgccg ttgcatgaag gccgccgcga ggacggcgag 780
gatgccaccg tccgctggct cgacgcgcag ccggccaagt ccgtcgtgta cgtcgcgcta 840
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gccgggacgc gcttcctctg ggctcttagg aagcccactg gcgtctccga cgccgacctc 960
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gaccagggac cgaacgcgcg gctaatcgag gcgaagaacg ccggattgca ggtggcaaga 1200
aacgacggcg atggatcgtt cgaccgagaa ggcgtcgcgg cggcgattcg tgcagtcgcg 1260
gtggaggaag aaagcagcaa agtgtttcaa gccaaagcca agaagctgca ggagatcgtc 1320
gcggacatgg cctgccatga gaggtacatc gacggattca ttcagcaatt gagatcttac 1380
aaggattga 1389

SEQ ID NO:15

Artificial Sequence

atggatagtg gctactcctc atcttatgct gctgccgctg gtatgcacgt tgtgatctgc 60
ccttggttgg cctttggtca cctgttacca tgtctggatt tagcccaaag actggcctca 120
agaggccata gagtatcatt tgtgtctact cctagaaata tctctcgttt accaccagtc 180
agacctgctc tagctcctct agttgcattc gttgctcttc cacttccaag agtagaagga 240
ttgccagacg gcgctgaatc tactaatgac gtaccacatg atagacctga catggtcgaa 300
ttgcatagaa gagcctttga tggattggca gctccatttt ctgagttcct gggcacagca 360
tgtgcagact gggttatagt cgatgtattt catcactggg ctgctgcagc cgcattggaa 420
cataaggtgc cttgtgctat gatgttgtta gggtcagcac acatgatcgc atccatagct 480
gatagaagat tggaaagagc tgaaacagaa tccccagccg cagcaggaca aggtaggcca 540
gctgccgccc caacctttga agtggctaga atgaaattga ttcgtactaa aggtagttca 600
gggatgagtc ttgctgaaag gttttctctg acattatcta gatcatcatt agttgtaggt 660
agatcctgcg tcgagttcga acctgaaaca gtacctttac tatctacttt gagaggcaaa 720
cctattactt tccttggtct aatgcctcca ttacatgaag gaaggagaga agatggtgaa 780
gatgctactg ttaggtggtt agatgcccaa cctgctaagt ctgttgttta cgttgcattg 840
ggttctgagg taccactagg ggtggaaaag gtgcatgaat tagcattagg acttgagctg 900
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ccacaaatga gtattctagc tcatgcagct gtaggggcct ttctaaccca ttgcggttgg 1080
aactcaacaa tagaaggact gatgtttggt catccactta ttatgttacc aatctttggc 1140
gatcagggac ctaacgcaag attgattgag gcaaagaacg caggtctgca ggttgcacgt 1200
aatgatggtg atggttcctt tgatagagaa ggcgttgcag ctgccatcag agcagtcgcc 1260
gttgaggaag agtcatctaa agttttccaa gctaaggcca aaaaattaca agagattgtg 1320
gctgacatgg cttgtcacga aagatacatc gatggtttca tccaacaatt gagaagttat 1380
aaagactaa 1389

SEQ ID NO:16

Oryza sativa

MDSGYSSSYA AAAGMHVVIC PWLAFGHLLP CLDLAQRLAS RGHRVSFVST PRNISRLPPV 60
RPALAPLVAF VALPLPRVEG LPDGAESTND VPHDRPDMVE LHRRAFDGLA APFSEFLGTA 120
CADWVIVDVF HHWAAAAALE HKVPCAMMLL GSAHMIASIA DRRLERAETE SPAAAGQGRP 180
AAAPTFEVAR MKLIRTKGSS GMSLAERFSL TLSRSSLVVG RSCVEFEPET VPLLSTLRGK 240

PITFLGLMPP LHEGRREDGE DATVRWLDAQ PAKSVVYVAL GSEVPLGVEK VHELALGLEL 300
AGTRFLWALR KPTGVSDADL LPAGFEERTR GRGVVATRWV PQMSILAHAA VGAFLTHCGW 360
NSTIEGLMFG HPLIMLPIFG DQGPNARLIE AKNAGLQVAR NDGDGSFDRE GVAAAIRAVA 420
VEEESSKVFQ AKAKKLQEIV ADMACHERYI DGFIQQLRSY KD 462

SEQ ID NO:17
Artificial Sequence
MDSGYSSSYA AAAGMHVVIC PWLAFGHLLP CLDLAQRLAS RGHRVSFVST PRNISRLPPV 60
RPALAPLVAF VALPLPRVEG LPDGAESTND VPHDRPDMVE LHRRAFDGLA APFSEFLGTA 120
CADWVIVDVF HHWAAAAALE HKVPCAMMLL GSAHMIASIA DRRLERAETE SPAAAGQGRP 180
AAAPTFEVAR MKLIRTKGSS GMSLAERFSL TLSRSSLVVG RSCVEFEPET VPLLSTLRGK 240
PITFLGLLPP EIPGDEKDET WVSIKKWLDG KQKGSVVYVA LGSEALVSQT EVVELALGLE 300
LSGLPFVWAY RKPKGPAKSD SVELPDGFVE RTRDRGLVWT SWAPQLRILS HESVCGFLTH 360
CGSGSIVEGL MFGHPLIMLP IFGDQPLNAR LLEDKQVGIE IARNDGDGSF DREGVAAAIR 420
AVAVEEESSK VFQAKAKKLQ EIVADMACHE RYIDGFIQQL RSYKD 465

SEQ ID NO:18
Artificial Sequence
MATSDSIVDD RKQLHVATFP WLAFGHILPY LQLSKLIAEK GHKVSFLSTT RNIQRLSSHI 60
SPLINVVQLT LPRVQELPED AEATTDVHPE DIPYLKKASD GLQPEVTRFL EQHSPDWIIY 120
DYTHYWLPSI AASLGISRAH FSVTTPWAIA YMGPSADAMI NGSDGRTTVE DLTTPPKWFP 180
FPTKVCWRKH DLARLVPYKA PGISDGYRMG MVLKGSDCLL SKCYHEFGTQ WLPLLETLHQ 240
VPVVPVGLMP PLHEGRREDG EDATVRWLDA QPAKSVVYVA LGSEVPLGVE KVHELALGLE 300
LAGTRFLWAL RKPTGVSDAD LLPAGFEERT RGRGVVATRW VPQMSILAHA AVGAFLTHCG 360
WNSTIEGLMF GHPLIMLPIF GDQGPNARLI EAKNAGLQVP RNEEDGCLTK ESVARSLRSV 420
VVEKEGEIYK ANARELSKIY NDTKVEKEYV SQFVDYLEKN ARAVAIDHES 470

SEQ ID NO:19
Stevia rebaudiana
atggctttgg taaacccaac cgctcttttc tatggtacct ctatcagaac aagacctaca 60
aacttactaa atccaactca aaagctaaga ccagtttcat catcttcctt accttctttc 120
tcatcagtta gtgcgattct tactgaaaaa catcaatcta atccttctga gaacaacaat 180
ttgcaaactc atctagaaac tcctttcaac tttgatagtt atatgttgga aaaagtcaac 240
atggttaacg aggcgcttga tgcatctgtc ccactaaaag acccaatcaa aatccatgaa 300
tccatgagat actctttatt ggcaggcggt aagagaatca gaccaatgat gtgtattgca 360
gcctgcgaaa tagtcggagg taatatcctt aacgccatgc cagccgcatg tgccgtggaa 420
atgattcata ctatgtcttt ggtgcatgac gatcttccat gtatggataa tgatgacttc 480
agaagaggta aacctatttc acacaaggtc tacggggagg aaatggcagt attgaccggc 540
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gatagaatcg tcagagctat aggggagttg gcccgttcag ttggctccga aggtttagtg 660
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aaaacagctg gtaaggattt gttgacagat aagacaactt acccaaagtt gttaggtata 960
gaaaagtcca gagaatttgc cgaaaaactt aacaaggaag cacaagagca attaagtggc 1020
tttgatagac gtaaggcagc tcctttgatc gcgttagcca actacaatgc gtaccgtcaa 1080
aattga 1086

SEQ ID NO:20
Stevia rebaudiana
MALVNPTALF YGTSIRTRPT NLLNPTQKLR PVSSSSLPSF SSVSAILTEK HQSNPSENNN 60
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ACEIVGGNIL NAMPAACAVE MIHTMSLVHD DLPCMDNDDF RRGKPISHKV YGEEMAVLTG 180
DALLSLSFEH IATATKGVSK DRIVRAIGEL ARSVGSEGLV AGQVVDILSE GADVGLDHLE 240
YIHIHKTAML LESSVVIGAI MGGGSDQQIE KLRKFARSIG LLFQVVDDIL DVTKSTEELG 300

KTAGKDLLTD KTTYPKLLGI EKSREFAEKL NKEAQEQLSG FDRRKAAPLI ALANYNAYRQ 360
N 361

SEQ ID NO:21
Artificial Sequence
atggctgagc aacaaatatc taacttgctg tctatgtttg atgcttcaca tgctagtcag 60
aaattagaaa ttactgtcca aatgatggac acataccatt acagagaaac gcctccagat 120
tcctcatctt ctgaaggcgg ttcattgtct agatacgacg agagaagagt ctctttgcct 180
ctcagtcata atgctgcctc tccagatatt gtatcacaac tatgtttttc cactgcaatg 240
tcttcagagt tgaatcacag atggaaatct caaagattaa aggtggccga ttctccttac 300
aactatatcc taacattacc atcaaaagga attagaggtg cctttatcga ttccctgaac 360
gtatggttgg aggttccaga ggatgaaaca tcagtcatca aggaagttat tggtatgctc 420
cacaactctt cattaatcat tgatgacttc caagataatt ctccacttag aagaggaaag 480
ccatctaccc atacagtctt cggccctgcc caggctatca atactgctac ttacgttata 540
gttaaagcaa tcgaaaagat acaagacata gtgggacacg atgcattggc agatgttacg 600
ggtactatta caactatttt ccaaggtcag gccatggact tgtggtggac agcaaatgca 660
atcgttccat caatacagga atacttactt atggtaaacg ataaaaccgg tgctctcttt 720
agactgagtt tggagttgtt agctctgaat tccgaagcca gtatttctga ctctgcttta 780
gaaagtttat ctagtgctgt ttccttgcta ggtcaatact tccaaatcag agacgactat 840
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ggcaagtact cactaacact tattcatgcc ctccaaactg attcatccga tctactgacc 960
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tggaaatga 1029

SEQ ID NO:22
Gibberella fujikuroi
MAEQQISNLL SMFDASHASQ KLEITVQMMD TYHYRETPPD SSSSEGGSLS RYDERRVSLP 60
LSHNAASPDI VSQLCFSTAM SSELNHRWKS QRLKVADSPY NYILTLPSKG IRGAFIDSLN 120
VWLEVPEDET SVIKEVIGML HNSSLIIDDF QDNSPLRRGK PSTHTVFGPA QAINTATYVI 180
VKAIEKIQDI VGHDALADVT GTITTIFQGQ AMDLWWTANA IVPSIQEYLL MVNDKTGALF 240
RLSLELLALN SEASISDSAL ESLSSAVSLL GQYFQIRDDY MNLIDNKYTD QKGFCEDLDE 300
GKYSLTLIHA LQTDSSDLLT NILSMRRVQG KLTAQKRCWF WK 342

SEQ ID NO:23
Artificial Sequence
atggaaaaga ctaaggagaa agcagaacgt atcttgctgg agccatacag atacttatta 60
caactaccag gaaagcaagt ccgttctaaa ctatcacaag cgttcaatca ctggttaaaa 120
gttcctgaag ataagttaca aatcattatt gaagtcacag aaatgctaca caatgcttct 180
ttactgatcg atgatataga ggattcttcc aaactgagaa gaggttttcc tgtcgctcat 240
tccatatacg gggtaccaag tgtaatcaac tcagctaatt acgtctactt cttgggattg 300
gaaaaagtat tgacattaga tcatccagac gctgtaaagc tattcaccag acaacttctt 360
gaattgcatc aaggtcaagg tttggatatc tattggagag acacttatac ttgcccaaca 420
gaagaggagt acaaagcaat ggttctacaa aagactggcg gtttgttcgg acttgccgtt 480
ggtctgatgc aacttttctc tgattacaag gaggacttaa agcctctgtt ggataccttg 540
ggcttgtttt tccagattag agatgactac gctaacttac attcaaagga atattcagaa 600
aacaaatcat tctgtgaaga tttgactgaa gggaagttta gttttccaac aatccacgcc 660
atttggtcaa gaccagaatc tactcaagtg caaaacattc tgcgtcagag aacagagaat 720
attgacatca aaaagtattg tgttcagtac ttggaagatg ttggttcttt tgcttacaca 780
agacatacac ttagagaatt agaggcaaaa gcatacaagc aaatagaagc ctgtggaggc 840
aatccttctc tagtggcatt ggttaaacat ttgtccaaaa tgttcaccga ggaaaacaag 900
taa 903

SEQ ID NO:24
Mus musculus
MEKTKEKAER ILLEPYRYLL QLPGKQVRSK LSQAFNHWLK VPEDKLQIII EVTEMLHNAS 60
LLIDDIEDSS KLRRGFPVAH SIYGVPSVIN SANYVYFLGL EKVLTLDHPD AVKLFTRQLL 120

ELHQGQGLDI YWRDTYTCPT EEEYKAMVLQ KTGGLFGLAV GLMQLFSDYK EDLKPLLDTL 180
GLFFQIRDDY ANLHSKEYSE NKSFCEDLTE GKFSFPTIHA IWSRPESTQV QNILRQRTEN 240
IDIKKYCVQY LEDVGSFAYT RHTLRELEAK AYKQIEACGG NPSLVALVKH LSKMFTEENK 300

SEQ ID NO:25
Artificial Sequence

atggcaagat tctattttct taacgcacta ttgatggtta tctcattaca atcaactaca 60
gccttcactc cagctaaact tgcttatcca acaacaacaa cagctctaaa tgtcgcctcc 120
gccgaaactt ctttcagtct agatgaatac ttggcctcta agataggacc tatagagtct 180
gccttggaag catcagtcaa atccagaatt ccacagaccg ataagatctg cgaatctatg 240
gcctactctt tgatggcagg aggcaagaga attagaccag tgttgtgtat cgctgcatgt 300
gagatgttcg gtggatccca agatgtcgct atgcctactg ctgtggcatt agaaatgata 360
cacacaatgt ctttgattca tgatgatttg ccatccatgg ataacgatga cttgagaaga 420
ggtaaaccaa caaaccatgt cgttttcggc gaagatgtag ctattcttgc aggtgactct 480
ttattgtcaa cttccttcga gcacgtcgct agagaaacaa aaggagtgtc agcagaaaag 540
atcgtggatg ttatcgctag attaggcaaa tctgttggtg ccgagggcct tgctggcggt 600
caagttatgg acttagaatg tgaagctaaa ccaggtacca cattagacga cttgaaatgg 660
attcatatcc ataaaaccgc tacattgtta caagttgctg tagcttctgg tgcagttcta 720
ggtggtgcaa ctcctgaaga ggttgctgca tgcgagttgt ttgctatgaa tataggtctt 780
gcctttcaag ttgccgacga tatccttgat gtaaccgctt catcagaaga tttgggtaaa 840
actgcaggca aagatgaagc tactgataag acaacttacc caaagttatt aggattagaa 900
gagagtaagg catacgcaag acaactaatc gatgaagcca aggaaagttt ggctcctttt 960
ggagatagag ctgccccttt attggccatt gcagatttca ttattgatag aaagaattga 1020

SEQ ID NO:26
Thalassiosira pseudonana

MARFYFLNAL LMVISLQSTT AFTPAKLAYP TTTTALNVAS AETSFSLDEY LASKIGPIES 60
ALEASVKSRI PQTDKICESM AYSLMAGGKR IRPVLCIAAC EMFGGSQDVA MPTAVALEMI 120
HTMSLIHDDL PSMDNDDLRR GKPTNHVVFG EDVAILAGDS LLSTSFEHVA RETKGVSAEK 180
IVDVIARLGK SVGAEGLAGG QVMDLECEAK PGTTLDDLKW IHIHKTATLL QVAVASGAVL 240
GGATPEEVAA CELFAMNIGL AFQVADDILD VTASSEDLGK TAGKDEATDK TTYPKLLGLE 300
ESKAYARQLI DEAKESLAPF GDRAAPLLAI ADFIIDRKN 339

SEQ ID NO:27
Artificial Sequence

atgcacttag caccacgtag agtccctaga ggtagaagat caccacctga cagagttcct 60
gaaagacaag gtgccttggg tagaagacgt ggagctggct ctactggctg tgcccgtgct 120
gctgctggtg ttcaccgtag aagaggagga ggcgaggctg atccatcagc tgctgtgcat 180
agaggctggc aagccggtgg tggcaccggt ttgcctgatg aggtggtgtc taccgcagcc 240
gccttagaaa tgtttcatgc ttttgcttta atccatgatg atatcatgga tgatagtgca 300
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gacccagatc aggccggtca actaggagtt tctactgcta tcttggttgg agatctggct 420
ttgacatggt ccgatgaatt gttatacgct ccattgactc cacatagact ggcagcagta 480
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agtgctagaa gacctgggac cgatacttct cttgcattga gaatagccag atataagaca 600
gcagcttaca caatggaacg tccactgcac attggtgcag ccctggctgg ggcaagacca 660
gaactattag cagggctttc agcatacgcc ttgccagctg gagaagcctt ccaattggca 720
gatgacctgc taggcgtctt cggtgatcca agacgtacag ggaaacctga cctagatgat 780
cttagaggtg gaaagcatac tgtcttagtc gccttggcaa gagaacatgc cactccagaa 840
cagagacaca cattggatac attattgggt acaccaggtc ttgatagaca aggcgcttca 900
agactaagat gcgtattggt agcaactggt gcaagagccg aagccgaaag acttattaca 960
gagagaagag atcaagcatt aactgcattg aacgcattaa cactgccacc tcctttagct 1020
gaggcattag caagattgac attagggtct acagctcatc ctgcctaa 1068

SEQ ID NO:28
Streptomyces clavuligerus

MHLAPRRVPR GRRSPPDRVP ERQGALGRRR GAGSTGCARA AAGVHRRRGG GEADPSAAVH 60
RGWQAGGGTG LPDEVVSTAA ALEMFHAFAL IHDDIMDDSA TRRGSPTVHR ALADRLGAAL 120
DPDQAGQLGV STAILVGDLA LTWSDELLYA PLTPHRLAAV LPLVTAMRAE TVHGQYLDIT 180
SARRPGTDTS LALRIARYKT AAYTMERPLH IGAALAGARP ELLAGLSAYA LPAGEAFQLA 240
DDLLGVFGDP RRTGKPDLDD LRGGKHTVLV ALAREHATPE QRHTLDTLLG TPGLDRQGAS 300
RLRCVLVATG ARAEAERLIT ERRDQALTAL NALTLPPPLA EALARLTLGS TAHPA 355

SEQ ID NO:29
Artificial Sequence

atgtcatatt tcgataacta cttcaatgag atagttaatt ccgtgaacga catcattaag 60
tcttacatct ctggcgacgt accaaaacta tacgaagcct cctaccattt gtttacatca 120
ggaggaaaga gactaagacc attgatcctt acaatttctt ctgatctttt cggtggacag 180
agagaaagag catactatgc tggcgcagca atcgaagttt tgcacacatt cactttggtt 240
cacgatgata tcatggatca agataacatt cgtagaggtc ttcctactgt acatgtcaag 300
tatggcctac ctttggccat tttagctggt gacttattgc atgcaaaagc ctttcaattg 360
ttgactcagg cattgagagg tctaccatct gaaactatca tcaaggcgtt tgatatcttt 420
acaagatcta tcattatcat atcagaaggt caagctgtcg atatggaatt cgaagataga 480
attgatatca aggaacaaga gtatttggat atgatatctc gtaaaaccgc tgccttattc 540
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atgtccgatt tcggtacaaa tcttgggatc gcatttcaaa ttgtagatga tatacttggt 660
ttaacagctg atgaaaaaga gctaggaaaa cctgttttca gtgatatcag agaaggtaaa 720
aagaccatat tagtcattaa gactttagaa ttgtgtaagg aagacgagaa aaagattgtg 780
ttaaaagcgc taggcaacaa gtcagcatca aaggaagagt tgatgagttc tgctgacata 840
atcaaaaagt actcattgga ttacgcctac aacttagctg agaaatacta caaaaacgcc 900
atcgattctc taaatcaagt ttcaagtaaa agtgatattc cagggaaggc attgaaatat 960
cttgctgaat tcaccatcag aagacgtaag taa 993

SEQ ID NO:30
Sulfolobus acidocaldarius

MSYFDNYFNE IVNSVNDIIK SYISGDVPKL YEASYHLFTS GGKRLRPLIL TISSDLFGGQ 60
RERAYYAGAA IEVLHTFTLV HDDIMDQDNI RRGLPTVHVK YGLPLAILAG DLLHAKAFQL 120
LTQALRGLPS ETIIKAFDIF TRSIIIISEG QAVDMEFEDR IDIKEQEYLD MISRKTAALF 180
SASSSIGALI AGANDNDVRL MSDFGTNLGI AFQIVDDILG LTADEKELGK PVFSDIREGK 240
KTILVIKTLE LCKEDEKKIV LKALGNKSAS KEELMSSADI IKKYSLDYAY NLAEKYYKNA 300
IDSLNQVSSK SDIPGKALKY LAEFTIRRRK 330

SEQ ID NO:31
Artificial Sequence

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ttggcaggtg gttctgttga acaagccatg ccaactgcgt gtgcacttga aatgatccat 240
acaatgtcac taattcatga tgacctgcca gccatggata acgatgattt cagaagagga 300
aagccaacta atcacaaggt gttcggggaa gatatagcca tcttagcggg tgatgcgctt 360
ttagcttacg cttttgaaca tattgcttct caaacaagag gagtaccacc tcaattggtg 420
ctacaagtta ttgctagaat cggacacgcc gttgctgcaa caggcctcgt tggaggccaa 480
gtcgtagacc ttgaatctga aggtaaagct atttccttag aaacattgga gtatattcac 540
tcacataaga ctggagcctt gctggaagca tcagttgtct caggcggtat tctcgcaggg 600
gcagatgaag agcttttggc cagattgtct cattacgcta gagatatagg cttggctttt 660
caaatcgtcg atgatatcct ggatgttact gctacatctg aacagttggg gaaaaccgct 720
ggtaaagacc aggcagccgc aaaggcaact tatccaagtc tattgggttt agaagcctct 780
agacagaaag cggaagagtt gattcaatct gctaaggaag ccttaagacc ttacggttca 840
caagcagagc cactcctagc gctggcagac ttcatcacac gtcgtcagca ttaa 894

SEQ ID NO:32
Synechococcus sp.

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MVAQTFNLDT YLSQRQQQVE EALSAALVPA YPERIYEAMR YSLLAGGKRL RPILCLAACE        60
LAGGSVEQAM PTACALEMIH TMSLIHDDLP AMDNDDFRRG KPTNHKVFGE DIAILAGDAL       120
LAYAFEHIAS QTRGVPPQLV LQVIARIGHA VAATGLVGGQ VVDLESEGKA ISLETLEYIH       180
SHKTGALLEA SVVSGGILAG ADEELLARLS HYARDIGLAF QIVDDILDVT ATSEQLGKTA       240
GKDQAAAKAT YPSLLGLEAS RQKAEELIQS AKEALRPYGS QAEPLLALAD FITRRQH          297
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SEQ ID NO:33

Artificial Sequence

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atgaaaaccg ggtttatctc accagcaaca gtatttcatc acagaatctc accagcgacc         60
actttcagac atcacttatc acctgctact acaaactcta caggcattgt cgccttaaga        120
gacatcaact tcagatgtaa agcagtttct aaagagtact ctgatctgtt gcagaaagat        180
gaggcttctt tcacaaaatg ggacgatgac aaggtgaaag atcatcttga taccaacaaa        240
aacttatacc caaatgatga gattaaggaa tttgttgaat cagtaaaggc tatgttcggt        300
agtatgaatg acggggagat aaacgtctct gcatacgata ctgcatgggt tgctttggtt        360
caagatgtcg atggatcagg tagtcctcag ttcccttctt ctttagaatg gattgccaac        420
aatcaattgt cagatggatc atggggagat catttgctgt tctcagctca cgatagaatc        480
atcaacacat tagcatgcgt tattgcactt acaagttgga atgttcatcc ttctaagtgt        540
gaaaaaggtt tgaattttct gagagaaaac atttgcaaat tagaagatga aaacgcagaa        600
catatgccaa ttggttttga agtaacattc ccatcactaa ttgatatcgc gaaaaagttg        660
aacattgaag tacctgagga tactccagca cttaaagaga tctacgcacg tagagatatc        720
aagttaacta agatcccaat ggaagttctt cacaaggtac ctactacttt gttacattct        780
ttggaaggaa tgcctgattt ggagtgggaa aaactgttaa agctacaatg taaagatggt        840
agtttcttgt tttccccatc tagtaccgca ttcgccctaa tgcaaacaaa agatgagaaa        900
tgcttacagt atctaacaaa tatcgtcact aagttcaacg gtggcgtgcc taatgtgtac        960
ccagtcgatt tgtttgaaca tatttgggtt gttgatagac tgcagagatt ggggattgcc       1020
agatacttca aatcagagat aaaagattgt gtagagtata tcaataagta ctggaccaaa       1080
aatggaattt gttgggctag aaatactcac gttcaagata tcgatgatac agccatggga       1140
ttcagagtgt tgagagcgca cggttatgac gtcactccag atgttttag acaatttgaa         1200
aaagatggta aattcgtttg ctttgcaggg caatcaacac aagccgtgac aggaatgttt        1260
aacgtttaca gagcctctca aatgttgttc ccaggggaga gaattttgga agatgccaaa        1320
aagttctctt acaattactt aaaggaaaag caaagtacca acgaattgct ggataaatgg        1380
ataatcgcta aagatctacc tggtgaagtt ggttatgctc tggatatccc atggtatgct        1440
tccttaccaa gattggaaac tcgttattac cttgaacaat acggcggtga agatgatgtc        1500
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gcaaagctgg attacaataa ctatgttgca gtccttcaat tagaatggta cacaatacaa        1620
caatggtacg tcgatattgg tatagagaag ttcgaatctg acaacatcaa gtcagtcctg        1680
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SEQ ID NO:34

Stevia rebaudiana

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MKTGFISPAT VFHHRISPAT TFRHHLSPAT TNSTGIVALR DINFRCKAVS KEYSDLLQKD         60
EASFTKWDDD KVKDHLDTNK NLYPNDEIKE FVESVKAMFG SMNDGEINVS AYDTAWVALV        120
QDVDGSGSPQ FPSSLEWIAN NQLSDGSWGD HLLFSAHDRI INTLACVIAL TSWNVHPSKC        180
EKGLNFLREN ICKLEDENAE HMPIGFEVTF PSLIDIAKKL NIEVPEDTPA LKEIYARRDI        240
KLTKIPMEVL HKVPTTLLHS LEGMPDLEWE KLLKLQCKDG SFLFSPSSTA FALMQTKDEK        300
CLQYLTNIVT KFNGGVPNVY PVDLFEHIWV VDRLQRLGIA RYFKSEIKDC VEYINKYWTK        360
NGICWARNTH VQDIDDTAMG FRVLRAHGYD VTPDVFRQFE KDGKFVCFAG QSTQAVTGMF        420
NVYRASQMLF PGERILEDAK KFSYNYLKEK QSTNELLDKW IIAKDLPGEV GYALDIPWYA        480
SLPRLETRYY LEQYGGEDDV WIGKTLYRMG YVSNNTYLEM AKLDYNNYVA VLQLEWYTIQ        540
QWYVDIGIEK FESDNIKSVL VSYYLAAASI FEPERSKERI AWAKTTILVD KITSIFDSSQ        600
SSKEDITAFI DKFRNKSSSK KHSINGEPWH EVMVALKKTL HGFALDALMT HSQDIHPQLH        660
QAWEMWLTKL QDGVDVTAEL MVQMINMTAG RWVSKELLTH PQYQRLSTVT NSVCHDITKL        720
HNFKENSTTV DSKVQELVQL VFSDTPDDLD QDMKQTFLTV MKTFYYKAWC DPNTINDHIS        780
KVFEIVI                                                                  787
```

SEQ ID NO:35

Artificial Sequence

atgcctgatg cacacgatgc tccacctcca caaataagac agagaacact agtagatgag 60
gctacccaac tgctaactga gtccgcagaa gatgcatggg gtgaagtcag tgtgtcagaa 120
tacgaaacag caaggctagt tgcccatgct acatggttag gtggacacgc cacaagagtg 180
gccttccttc tggagagaca acacgaagac gggtcatggg gtccaccagg tggatatagg 240
ttagtcccta cattatctgc tgttcacgca ttattgacat gtcttgcctc tcctgctcag 300
gatcatggcg ttccacatga tagactttta agagctgttg acgcaggctt gactgccttg 360
agaagattgg ggacatctga ctccccacct gatactatag cagttgagct ggttatccca 420
tctttgctag agggcattca acacttactg gaccctgctc atcctcatag tagaccagcc 480
ttctctcaac atagaggctc tcttgtttgt cctggtggac tagatgggag aactctagga 540
gctttgagat cacacgccgc agcaggtaca ccagtaccag gaaaagtctg gcacgcttcc 600
gagactttgg gcttgagtac cgaagctgct tctcacttgc aaccagccca aggtataatc 660
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gattctgcca gaagatacct tgaggaatta caacacagat actctggccc agttccttcc 780
attaccccta tcacatactt cgaaagagca tggttattga acaattttgc agcagccggt 840
gttccttgtg aggctccagc tgctttgttg gattccttag aagcagcact tacaccacaa 900
ggtgctcctg ctggagcagg attgcctcca gatgctgatg atacagccgc tgtgttgctt 960
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ttacagatct tggccccacc ttctggtggt ggcaatatcc cagtccaaca agcacttact 1440
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ttgtatactc cagtaagagt agtcagagct gccagagctg ctgctctgta cactaccaga 1560
gatctattgt taccaccatt gtaa 1584

SEQ ID NO:36

Streptomyces clavuligerus

MPDAHDAPPP QIRQRTLVDE ATQLLTESAE DAWGEVSVSE YETARLVAHA TWLGGHATRV 60
AFLLERQHED GSWGPPGGYR LVPTLSAVHA LLTCLASPAQ DHGVPHDRLL RAVDAGLTAL 120
RRLGTSDSPP DTIAVELVIP SLLEGIQHLL DPAHPHSRPA FSQHRGSLVC PGGLDGRTLG 180
ALRSHAAAGT PVPGKVWHAS ETLGLSTEAA SHLQPAQGII GGSAAATATW LTRVAPSQQS 240
DSARRYLEEL QHRYSGPVPS ITPITYFERA WLLNNFAAAG VPCEAPAALL DSLEAALTPQ 300
GAPAGAGLPP DADDTAAVLL ALATHGRGRR PEVLMDYRTD GYFQCFIGER TPSISTNAHV 360
LETLGHHVAQ HPQDRARYGS AMDTASAWLL AAQKQDGSWL DKWHASPYYA TVCCTQALAA 420
HASPATAPAR QRAVRWVLAT QRSDGGWGLW HSTVEETAYA LQILAPPSGG GNIPVQQALT 480
RGRARLCGAL PLTPLWHDKD LYTPVRVVRA ARAAALYTTR DLLLPPL 527

SEQ ID NO:37

Artificial Sequence

atgaacgccc tatccgaaca cattttgtct gaattgagaa gattattgtc tgaaatgagt 60
gatggcggat ctgttggtcc atctgtgtat gatacggccc aggccctaag attccacggt 120
aacgtaacag gtagacaaga tgcatatgct tggttgatcg cccagcaaca agcagatgga 180
ggttggggct ctgccgactt tccactcttt agacatgctc caacatgggc tgcacttctc 240
gcattacaaa gagctgatcc acttcctggc gcagcagacg cagttcagac cgcaacaaga 300
ttcttgcaaa gacaaccaga tccatacgct catgccgttc ctgaggatgc ccctattggt 360
gctgaactga tcttgcctca gttttgtgga gaggctgctt ggttgttggg aggtgtggcc 420
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ccaacaacag cctgtccaga cgatgatggt tctataggta tctcaccagc agctacagcc 600
gcctggagag cccaggctgt gaccagaggc tcaactcctc aagtgggcag agctgacgca 660
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tggcctataa acgtattcga accatgctgg tcactgtaca ctctccatct tgccggtctg 780
ttcgcccatc cagcactggc tgaggctgta agagttatcg ttgctcaact tgaagcaaga 840

ttgggagtgc atggcctcgg accagcttta cattttgctg ccgacgctga tgatactgca 900
gttgccttat gcgttctgca tttggctggc agagatcctg cagttgacgc attgagacat 960
tttgaaattg gtgagctctt tgttacattc ccaggagaga gaaatgctag tgtctctacg 1020
aacattcacg ctcttcatgc tttgagattg ttaggtaaac cagctgccgg agcaagtgca 1080
tacgtcgaag caaatagaaa tccacatggt ttgtgggaca acgaaaaatg gcacgtttca 1140
tggctttatc caactgcaca cgccgttgca gctctagctc aaggcaagcc tcaatggaga 1200
gatgaaagag cactagccgc tctactacaa gctcaaagag atgatggtgg ttggggagct 1260
ggtagaggat ccactttcga ggaaaccgcc tacgctcttt tcgctttaca cgttatggac 1320
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tggatgctag ctagacatgc cgcacatgga ttaccacaaa caccactctg gattggtaag 1440
gaattgtact gtcctactag agtcgtaaga gtagctgagc tagctggcct gtggttagca 1500
ttaagatggg gtagaagagt attagctgaa ggtgctggtg ctgcacctta a 1551

SEQ ID NO:38

Bradyrhizobium japonicum

MNALSEHILS ELRRLLSEMS DGGSVGPSVY DTAQALRFHG NVTGRQDAYA WLIAQQQADG 60
GWGSADFPLF RHAPTWAALL ALQRADPLPG AADAVQTATR FLQRQPDPYA HAVPEDAPIG 120
AELILPQFCG EAAWLLGGVA FPRHPALLPL RQACLVKLGA VAMLPSGHPL LHSWEAWGTS 180
PTTACPDDDG SIGISPAATA AWRAQAVTRG STPQVGRADA YLQMASRATR SGIEGVFPNV 240
WPINVFEPCW SLYTLHLAGL FAHPALAEAV RVIVAQLEAR LGVHGLGPAL HFAADADDTA 300
VALCVLHLAG RDPAVDALRH FEIGELFVTF PGERNASVST NIHALHALRL LGKPAAGASA 360
YVEANRNPHG LWDNEKWHVS WLYPTAHAVA ALAQGKPQWR DERALAALLQ AQRDDGGWGA 420
GRGSTFEETA YALFALHVMD GSEEATGRRR IAQVVARALE WMLARHAAHG LPQTPLWIGK 480
ELYCPTRVVR VAELAGLWLA LRWGRRVLAE GAGAAP 516

SEQ ID NO:39

Artificial Sequence

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SEQ ID NO:40

Zea mays

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PRLDGGEGPQ FPAAVRWIRN NQLPDGSWGD AALFSAYDRL INTLACVVTL TRWSLEPEMR 180
GRGLSFLGRN MWKLATEDEE SMPIGFELAF PSLIELAKSL GVHDFPYDHQ ALQGIYSSRE 240
IKMKRIPKEV MHTVPTSILH SLEGMPGLDW AKLLKLQSSD GSFLFSPAAT AYALMNTGDD 300
RCFSYIDRTV KKFNGGVPNV YPVDLFEHIW AVDRLERLGI SRYFQKEIEQ CMDYVNRHWT 360
EDGICWARNS DVKEVDDTAM AFRLLRLHGY SVSPDVFKNF EKDGEFFAFV GQSNQAVTGM 420
YNLNRASQIS FPGEDVLHRA GAFSYEFLRR KEAEGALRDK WIISKDLPGE VVYTLDFPWY 480
GNLPRVEARD YLEQYGGGDD VWIGKTLYRM PLVNNDVYLE LARMDFNHCQ ALHQLEWQGL 540
KRWYTENRLM DFGVAQEDAL RAYFLAAASV YEPCRAAERL AWARAAILAN AVSTHLRNSP 600
SFRERLEHSL RCRPSEETDG SWFNSSSGSD AVLVKAVLRL TDSLAREAQP IHGGDPEDII 660
HKLLRSAWAE WVREKADAAD SVCNGSSAVE QEGSRMVHDK QTCLLLARMI EISAGRAAGE 720
AASEDGDRRI IQLTGSICDS LKQKMLVSQD PEKNEEMMSH VDDELKLRIR EFVQYLLRLG 780
EKKTGSSETR QTFLSIVKSC YYAAHCPPHV VDRHISRVIF EPVSAAK 827

SEQ ID NO:41

Artificial Sequence

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SEQ ID NO:42

Arabidopsis thaliana

MSLQYHVLNS IPSTTFLSST KTTISSSFLT ISGSPLNVAR DKSRSGSIHC SKLRTQEYIN 60
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AWVALIDAGD KTPAFPSAVK WIAENQLSDG SWGDAYLFSY HDRLINTLAC VVALRSWNLF 180
PHQCNKGITF FRENIGKLED ENDEHMPIGF EVAFPSLLEI ARGINIDVPY DSPVLKDIYA 240
KKELKLTRIP KEIMHKIPTT LLHSLEGMRD LDWEKLLKLQ SQDGSFLFSP SSTAFAFMQT 300
RDSNCLEYLR NAVKRFNGGV PNVFPVDLFE HIWIVDRLQR LGISRYFEEE IKECLDYVHR 360
YWTDNGICWA RCSHVQDIDD TAMAFRLLRQ HGYQVSADVF KNFEKEGEFF CFVGQSNQAV 420
TGMFNLYRAS QLAFPREEIL KNAKEFSYNY LLEKREREEL IDKWIIMKDL PGEIGFALEI 480
PWYASLPRVE TRFYIDQYGG ENDVWIGKTL YRMPYVNNNG YLELAKQDYN NCQAQHQLEW 540
DIFQKWYEEN RLSEWGVRRS ELLECYYLAA ATIFESERSH ERMVWAKSSV LVKAISSSFG 600
ESSDSRRSFS DQFHEYIANA RRSDHHFNDR NMRLDRPGSV QASRLAGVLI GTLNQMSFDL 660
FMSHGRDVNN LLYLSWGDWM EKWKLYGDEG EGELMVKMII LMKNNDLTNF FTHTHFVRLA 720
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SEQ ID NO:43

Artificial Sequence

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SEQ ID NO:44
Stevia rebaudiana

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SATAAAFINH QNPGCLNYLN SLLDKFGNAV PTVYPHDLFI RLSMVDTIER LGISHHFRVE 300
IKNVLDETYR CWVERDEQIF MDVVTCALAF RLLRINGYEV SPDPLAEITN ELALKDEYAA 360
LETYHASHIL YQEDLSSGKQ ILKSADFLKE IISTDSNRLS KLIHKEVENA LKFPINTGLE 420
RINTRRNIQL YNVDNTRILK TTYHSSNISN TDYLRLAVED FYTCQSIYRE ELKGLERWVV 480
ENKLDQLKFA RQKTAYCYFS VAATLSSPEL SDARISWAKN GILTTVVDDF FDIGGTIDEL 540
TNLIQCVEKW NVDVDKDCCS EHVRILFLAL KDAICWIGDE AFKWQARDVT SHVIQTWLEL 600
MNSMLREAIW TRDAYVPTLN EYMENAYVSF ALGPIVKPAI YFVGPKLSEE IVESSEYHNL 660
FKLMSTQGRL LNDIHSFKRE FKEGKLNAVA LHLSNGESGK VEEEVVEEMM MMIKNKRKEL 720
MKLIFEENGS IVPRACKDAF WNMCHVLNFF YANDDGFTGN TILDTVKDII YNPLVLVNEN 780
EEQR 784

SEQ ID NO:45
Artificial Sequence

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SEQ ID NO:46

Stevia rebaudiana

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IKNVLDETYR CWVERDEQIF MDVVTCALAF RLLRIHGYKV SPDQLAEITN ELAFKDEYAA 360
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TNLIQCVEKW NVDVDKDCCS EHVRILFLAL KDAICWIGDE AFKWQARDVT SHVIQTWLEL 600
MNSMLREAIW TRDAYVPTLN EYMENAYVSF ALGPIVKPAI YFVGPKLSEE IVESSEYHNL 660
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EEQR 784

SEQ ID NO:47

Artificial Sequence

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caaggttctc atacactggt atctgatgtt taa 1773

SEQ ID NO:48

Zea mays

MAMPVKLTPA SLSLKAVCCR FSSGGHALRF GSSLPCWRRT PTQRSTSSST TRPAAEVSSG 60
KSKQHDQEAS EATIRQQLQL VDVLENMGIS RHFAAEIKCI LDRTYRSWLQ RHEEIMLDTM 120
TCAMAFRILR LNGYNVSSDE LYHVVEASGL HNSLGGYLND TRTLLELHKA STVSISEDES 180
ILDSIGSRSR TLLREQLESG GALRKPSLFK EVEHALDGPF YTTLDRLHHR WNIENFNIIE 240
QHMLETPYLS NQHTSRDILA LSIRDFSSSQ FTYQQELQHL ESWVKECRLD QLQFARQKLA 300
YFYLSAAGTM FSPELSDART LWAKNGVLTT IVDDFFDVAG SKEELENLVM LVEMWDEHHK 360
VEFYSEQVEI IFSSIYDSVN QLGEKASLVQ DRSITKHLVE IWLDLLKSMM TEVEWRLSKY 420
VPTEKEYMIN ASLIFGLGPI VLPALYFVGP KISESIVKDP EYDELFKLMS TCGRLLNDVQ 480
TFEREYNEGK LNSVSLLVLH GGPMSISDAK RKLQKPIDTC RRDLLSLVLR EESVVPRPCK 540
ELFWKMCKVC YFFYSTTDGF SSQVERAKEV DAVINEPLKL QGSHTLVSDV 590

SEQ ID NO:49

Artificial Sequence

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gacattatct ttccaggtat gattgaatac gctatagact tagacctgaa tctaccacta 420
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gatgaattat ga 2232

SEQ ID NO:50

Populus trichocarpa

MSCIRPWFCP SSISATLTDP ASKLVTGEFK TTSLNFHGTK ERIKKMFDKI ELSVSSYDTA 60
WVAMVPSPDC PETPCFPECT KWILENQLGD GSWSLPHGNP LLVKDALSST LACILALKRW 120
GIGEEQINKG LRFIELNSAS VTDNEQHKPI GFDIIFPGMI EYAKDLDLNL PLKPTDINSM 180
LHRRALELTS GGGKNLEGRR AYLAYVSEGI GKLQDWEMAM KYQRKNGSLF NSPSTTAAAF 240
IHIQDAECLH YIRSLLQKFG NAVPTIYPLD IYARLSMVDA LERLGIDRHF RKERKFVLDE 300
TYRFWLQGEE EIFSDNATCA LAFRILRLNG YDVSLEDHFS NSLGGYLKDS GAALELYRAL 360
QLSYPDESLL EKQNSRTSYF LKQGLSNVSL CGDRLRKNII GEVHDALNFP DHANLQRLAI 420
RRRIKHYATD DTRILKTSYR CSTIGNQDFL KLAVEDFNIC QSIQREEFKH IERWVVERRL 480
DKLKFARQKE AYCYFSAAAT LFAPELSDAR MSWAKNGVLT TVVDDFFDVG GSEEELVNLI 540
ELIERWDVNG SADFCSEEVE IIYSAIHSTI SEIGDKSFGW QGRDVKSHVI KIWLDLLKSM 600
LTEAQWSSNK SVPTLDEYMT TAHVSFALGP IVLPALYFVG PKLSEEVAGH PELLNLYKVM 660
STCGRLLNDW RSFKRESEEG KLNAISLYMI HSGGASTEEE TIEHFKGLID SQRRQLLQLV 720
LQEKDSIIPR PCKDLFWNMI KLLHTFYMKD DGFTSNEMRN VVKAIINEPI SLDEL 775

SEQ ID NO:51

Artificial Sequence

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aaagaatctt taacttga 2358

SEQ ID NO:52
Arabidopsis thaliana

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VAMVPSPSSQ NAPLFPQCVK WLLDNQHEDG SWGLDNHDHQ SLKKDVLSST LASILALKKW 120
GIGERQINKG LQFIELNSAL VTDETIQKPT GFDIIFPGMI KYARDLNLTI PLGSEVVDDM 180
IRKRDLDLKC DSEKFSKGRE AYLAYVLEGT RNLKDWDLIV KYQRKNGSLF DSPATTAAAF 240
TQFGNDGCLR YLCSLLQKFE AAVPSVYPFD QYARLSIIVT LESLGIDRDF KTEIKSILDE 300
TYRYWLRGDE EICLDLATCA LAFRLLLAHG YDVSYDPLKP FAEESGFSDT LEGYVKNTFS 360
VLELFKAAQS YPHESALKKQ CCWTKQYLEM ELSSWVKTSV RDKYLKKEVE DALAFPSYAS 420
LERSDHRRKI LNGSAVENTR VTKTSYRLHN ICTSDILKLA VDDFNFCQSI HREEMERLDR 480
WIVENRLQEL KFARQKLAYC YFSGAATLFS PELSDARISW AKGGVLTTVV DDFFDVGGSK 540
EELENLIHLV EKWDLNGVPE YSSEHVEIIF SVLRDTILET GDKAFTYQGR NVTHHIVKIW 600
LDLLKSMLRE AEWSSDKSTP SLEDYMENAY ISFALGPIVL PATYLIGPPL PEKTVDSHQY 660
NQLYKLVSTM GRLLNDIQGF KRESAEGKLN AVSLHMKHER DNRSKEVIIE SMKGLAERKR 720
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KESLT 785

SEQ ID NO:53
Artificial Sequence

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SEQ ID NO:54

Phomopsis amygdali

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AASLRAQLAA LDVSTTEHVG FEIIVPAMLD PLEAEDPSLV FDFPARKPLM KIHDAKMSRF 180
RPEYLYGKQP MTALHSLEAF IGKIDFDKVR HHRTHGSMMG SPSSTAAYLM HASQWDGDSE 240
AYLRHVIKHA AGQGTGAVPS AFPSTHFESS WILTTLFRAG FSASHLACDE LNKLVEILEG 300
SFEKEGGAIG YAPGFQADVD DTAKTISTLA VLGRDATPRQ MIKVFEANTH FRTYPGERDP 360
SLTANCNALS ALLHQPDAAM YGSQIQKITK FVCDYWWKSD GKIKDKWNTC YLYPSVLLVE 420
VLVDLVSLLE QGKLPDVLDQ ELQYRVAITL FQACLRPLLD QDAEGSWNKS IEATAYGILI 480
LTEARRVCFF DRLSEPLNEA IRRGIAFADS MSGTEAQLNY IWIEKVSYAP ALLTKSYLLA 540
ARWAAKSPLG ASVGSSLWTP PREGLDKHVR LFHQAELFRS LPEWELRASM IEAALFTPLL 600
RAHRLDVFPR QDVGEDKYLD VVPFFWTAAN NRDRTYASTL FLYDMCFIAM LNFQLDEFME 660
ATAGILFRDH MDDLRQLIHD LLAEKTSPKS SGRSSQGTKD ADSGIEEDVS MSDSASDSQD 720
RSPEYDLVFS ALSTFTKHVL QHPSIQSASV WDRKLLAREM KAYLLAHIQQ AEDSTPLSEL 780
KDVPQKTDVT RVSTSTTTFF NWVRTTSADH ISCPYSFHFV ACHLGAALSP KGSNGDCYPS 840
AGEKFLAAAV CRHLATMCRM YNDLGSAERD SDEGNLNSLD FPEFADSAGN GGIEIQKAAL 900
LRLAEFERDS YLEAFRRLQD ESNRVHGPAG GDEARLSRRR MAILEFFAQQ VDLYGQVYVI 960
RDISARIPKN EVEKKRKLDD AFN 983

SEQ ID NO:55

Artificial Sequence

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SEQ ID NO:56

Physcomitrella patens

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IIDNQLPDGD WGEPSLFLGY DRVCNTLACV IALKTWGVGA QNVERGIQFL QSNIYKMEED 240
DANHMPIGFE IVFPAMMEDA KALGLDLPYD ATILQQISAE REKKMKKIPM AMVYKYPTTL 300

LHSLEGLHRE VDWNKLLQLQ SENGSFLYSP ASTACALMYT KDVKCFDYLN QLLIKFDHAC 360
PNVYPVDLFE RLWMVDRLQR LGISRYFERE IRDCLQYVYR YWKDCGIGWA SNSSVQDVDD 420
TAMAFRLLRT HGFDVKEDCF RQFFKDGEFF CFAGQSSQAV TGMFNLSRAS QTLFPGESLL 480
KKARTFSRNF LRTKHENNEC FDKWIITKDL AGEVEYNLTF PWYASLPRLE HRTYLDQYGI 540
DDIWIGKSLY KMPAVTNEVF LKLAKADFNM CQALHKKELE QVIKWNASCQ FRDLEFARQK 600
SVECYFAGAA TMFEPEMVQA RLVWARCCVL TTVLDDYFDH GTPVEELRVF VQAVRTWNPE 660
LINGLPEQAK ILFMGLYKTV NTIAEEAFMA QKRDVHHHLK HYWDKLITSA LKEAEWAESG 720
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QGMKREASQG KISSVQIYME EHPSVPSEAM AIAHLQELVD NSMQQLTYEV LRFTAVPKSC 840
KRIHLNMAKI MHAFYKDTDG FSSLTAMTGF VKKVLFEPVP E 881

SEQ ID NO:57

Artificial Sequence

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SEQ ID NO:58
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LERMHGEKLG HFDLEQVYGK PSSLLHSLEA FLGKLDFDRL SHHLYHGSMM ASPSSTAAYL 240
IGATKWDDEA EDYLRHVMRN GAGHGNGGIS GTFPTTHFEC SWIIATLLKV GFTLKQIDGD 300
GLRGLSTILL EALRDENGVI GFAPRTADVD DTAKALLALS LVNQPVSPDI MIKVFEGKDH 360
FTTFGSERDP SLTSNLHVLL SLLKQSNLSQ YHPQILKTTL FTCRWWWGSD HCVKDKWNLS 420
HLYPTMLLVE AFTEVLHLID GGELSSLFDE SFKCKIGLSI FQAVLRIILT QDNDGSWRGY 480
REQTCYAILA LVQARHVCFF THMVDRLQSC VDRGFSWLKS CSFHSQDLTW TSKTAYEVGF 540
VAEAYKLAAL QSASLEVPAA TIGHSVTSAV PSSDLEKYMR LVRKTALFSP LDEWGLMASI 600
IESSFFVPLL QAQRVEIYPR DNIKVDEDKY LSIIPFTWVG CNNRSRTFAS NRWLYDMMYL 660
SLLGYQTDEY MEAVAGPVFG DVSLLHQTID KVIDNTMGNL ARANGTVHSG NGHQHESPNI 720
GQVEDTLTRF TNSVLNHKDV LNSSSSDQDT LRREFRTFMH AHITQIEDNS RFSKQASSDA 780
FSSPEQSYFQ WVNSTGGSHV ACAYSFAFSN CLMSANLLQG KDAFPSGTQK YLISSVMRHA 840
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SEQ ID NO:59
Artificial Sequence
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SEQ ID NO:60
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VKNNPEQEEV DLRKIFQSEL FGLAMRQALG KDVESLYVED LKITMNRDEI FQVLVVDPMM 240
GAIDVDWRDF FPYLKWVPNK KFENTIQQMY IRREAVMKSL IKEHKKRIAS GEKLNSYIDY 300
LLSEAQTLTD QQLLMSLWEP IIESSDTTMV TTEWAMYELA KNPKLQDRLY RDIKSVCGSE 360
KITEEHLSQL PYITAIFHET LRRHSPVPII PLRHVHEDTV LGGYHVPAGT ELAVNIYGCN 420
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EWKLKDMTQE EVNTIGLTTQ MLRPLRAIIK PRI 513

SEQ ID NO:61
Artificial Sequence

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ccgcgg 1566

SEQ ID NO:62
Lactuca sativa

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FEKNPNQEVN LRKIFQSQLF GLAMKQALGK DVESIYVKDL ETTMKREEIF EVLVVDPMMG 240
AIEVDWRDFF PYLKWVPNKS FENIIHRMYT RREAVMKALI QEHKKRIASG ENLNSYIDYL 300
LSEAQTLTDK QLLMSLWEPI IESSDTTMVT TEWAMYELAK NPNMQDRLYE EIQSVCGSEK 360
ITEENLSQLP YLYAVFQETL RKHCPVPIMP LRYVHENTVL GGYHVPAGTE VAINIYGCNM 420
DKKVWENPEE WNPERFLSEK ESMDLYKTMA FGGGKRVCAG SLQAMVISCI GIGRLVQDFE 480
WKLKDDAEED VNTLGLTTQK LHPLLALINP RK 512

SEQ ID NO:63
Rubus suavissimus

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SEQ ID NO:64

Artificial Sequence

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aagttgagag atggtgaaga agaaaacgtt gatactgttg gtttgaccac ccataagaga 1500
tatccaatgc atgctatttt gaagccaaga tcttaa 1536

SEQ ID NO:65

Artificial Sequence

aagcttacta gtaaaatggc ctccatcacc catttcttac aagattttca agctactcca 60

ttcgctactg cttttgctgt tggtggtgtt tctttgttga tattcttctt cttcatccgt 120
ggtttccact ctactaagaa aaacgaatat tacaagttgc caccagttcc agttgttcca 180
ggtttgccag ttgttggtaa tttgttgcaa ttgaaagaaa agaagccata caagactttc 240
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gttgttgtta actctactca tgttgccaaa gaagctatgg ttaccagatt ctcttcaatc 360
tctaccagaa agttgtccaa ggctttggaa ttattgacct ccaacaaatc tatggttgcc 420
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tgttacttga attacttgtt gtccgaagct aagactttga ccgaaaagca aatttccatt 960
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gtctgcggta ctgataagat taccgaagaa catttgtcca agttgcctta cttgtctgct 1140
gtttttcacg aaaccttgag aaagtattct ccatctccat tggttccatt gagatacgct 1200
catgaagata ctcaattggg tggttattat gttccagccg gtactgaaat tgctgttaat 1260
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agatttttgg acgaaaagta cgatccaatg gacatgtaca agactatgtc ttttggttcc 1380
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ttgggtttga ctacccataa gttgtatcca atgcaagcta tcttgcaacc tagaaactga 1560
ctcgagccgc gg 1572

SEQ ID NO:66

Castanea mollissima

MASITHFLQD FQATPFATAF AVGGVSLLIF FFFIRGFHST KKNEYYKLPP VPVVPGLPVV 60
GNLLQLKEKK PYKTFLRWAE IHGPIYSIRT GASTMVVVNS THVAKEAMVT RFSSISTRKL 120
SKALELLTSN KSMVATSDYN EFHKMVKKYI LAELLGANAQ KRHRIHRDTL IENVLNKLHA 180
HTKNSPLQAV NFRKIFESEL FGLAMKQALG YDVDSLFVEE LGTTLSREEI YNVLVSDMLK 240
GAIEVDWRDF FPYLKWIPNK SFEMKIQRLA SRRQAVMNSI VKEQKKSIAS GKGENCYLNY 300
LLSEAKTLTE KQISILAWET IIETADTTVV TTEWAMYELA KNPKQQDRLY NEIQNVCGTD 360
KITEEHLSKL PYLSAVFHET LRKYSPSPLV PLRYAHEDTQ LGGYYVPAGT EIAVNIYGCN 420
MDKNQWETPE EWKPERFLDE KYDPMDMYKT MSFGSGKRVC AGSLQASLIA CTSIGRLVQE 480
FEWRLKDGEV ENVDTLGLTT HKLYPMQAIL QPRN 514

SEQ ID NO:67

Artificial Sequence

atgatttcct tgttgttggg ttttgttgtc tcctccttct tgtttatctt cttcttgaaa 60
aaattgttgt tcttcttcag tcgtcacaaa atgtccgaag tttctagatt gccatctgtt 120
ccagttccag gttttccatt gattggtaac ttgttgcaat tgaaagaaaa gaagccacac 180
aagactttca ccaagtggtc tgaattatat ggtccaatct actctatcaa gatgggttcc 240
tcttctttga tcgtcttgaa ctctattgaa accgccaaag aagctatggt cagtagattc 300
tcttcaatct ctaccagaaa gttgtctaac gctttgactg ttttgacctg caacaaatct 360
atggttgcta cctctgatta cgatgacttt cataagttcg tcaagagatg cttgttgaac 420
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aacgttacct ctaaattgca tgcccatacc agaaatcatc cacaagaacc agttaacttc 540
agagccattt tcgaacacga attattcggt gttgctttga aacaagcctt cggtaaagat 600
gtcgaatcca tctatgtaaa agaattgggt gtcaccttgt ccagagatga aattttcaag 660
gttttggtcc acgacatgat ggaaggtgct attgatgttg attggagaga tttcttccca 720
tacttgaaat ggatcccaaa caactctttc gaagccagaa ttcaacaaaa gcacaagaga 780
agattggctg ttatgaacgc cttgatccaa gacagattga atcaaaacga ttccgaatcc 840
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attgctattt tggtttggga aaccattatc gaaactgctg ataccacttt ggttactact 960
gaatgggcta tgtacgaatt ggccaaacat caatctgttc aagatagatt attcaaagaa 1020
atccaatccg tctgcggtgg tgaaaagatc aaagaagaac aattgccaag attgccttac 1080
gtcaatggtg tttttcacga aaccttgaga aagtattctc cagctccatt ggttccaatt 1140
agatacgctc atgaagatac ccaaattggt ggttatcata ttccagccgg ttctgaaatt 1200
gccattaaca tctacggttg caacatggat aagaagagat gggaaagacc tgaagaatgg 1260
tggccagaaa gatttttgga agatagatac gaatcctccg acttgcataa gactatggct 1320
tttggtgctg gtaaaagagt ttgtgctggt gctttacaag ctagtttgat ggctggtatt 1380
gctatcggta gattggttca agaattcgaa tggaagttga gagatggtga agaagaaaac 1440
gttgatactt acggtttgac ctcccaaaag ttgtatccat tgatggccat tatcaaccca 1500
agaagatctt aa 1512

SEQ ID NO:68
Thellungiella halophila

MASMISLLLG FVVSSFLFIF FLKKLLFFFS RHKMSEVSRL PSVPVPGFPL IGNLLQLKEK 60
KPHKTFTKWS ELYGPIYSIK MGSSSLIVLN SIETAKEAMV SRFSSISTRK LSNALTVLTC 120
NKSMVATSDY DDFHKFVKRC LLNGLLGANA QERKRHYRDA LIENVTSKLH AHTRNHPQEP 180
VNFRAIFEHE LFGVALKQAF GKDVESIYVK ELGVTLSRDE IFKVLVHDMM EGAIDVDWRD 240
FFPYLKWIPN NSFEARIQQK HKRRLAVMNA LIQDRLNQND SESDDDCYLN FLMSEAKTLT 300
MEQIAILVWE TIIETADTTL VTTEWAMYEL AKHQSVQDRL FKEIQSVCGG EKIKEEQLPR 360
LPYVNGVFHE TLRKYSPAPL VPIRYAHEDT QIGGYHIPAG SEIAINIYGC NMDKKRWERP 420
EEWWPERFLE DRYESSDLHK TMAFGAGKRV CAGALQASLM AGIAIGRLVQ EFEWKLRDGE 480
EENVDTYGLT SQKLYPLMAI INPRRS 506

SEQ ID NO:69
Artificial Sequence

aagcttacta gtaaaatgga catgatgggt attgaagctg ttccatttgc tactgctgtt 60
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aagagatccg ttgaaggttt gccaccagtt ccagatattc caggtttacc attgattggt 180
aacttgttgc aattgaaaga aaagaagcca cataagacct ttgctagatg ggctgaaact 240
tacggtccaa ttttctctat tagaactggt gcttctacca tgatcgtctt gaattcttct 300
gaagttgcca aagaagctat ggtcactaga ttctcttcaa tctctaccag aaagttgtcc 360
aacgccttga agattttgac cttcgataag tgtatggttg ccacctctga ttacaacgat 420
tttcacaaaa tggtcaaggg tttcatcttg agaaacgttt taggtgctcc agcccaaaaa 480
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gttaagactt ctccattgga accagttgtc ttgaagaaga ttttcgaatc cgaaattttc 600
ggtttggctt tgaaacaagc cttgggtaag gatatcgaat ccatctatgt tgaagaattg 660
ggtactacct tgtccagaga agaaattttt gccgttttgg ttgttgatcc aatggctggt 720
gctattgaag ttgattggag agatttttc ccatacttgt cctggattcc aaacaagtct 780
atggaaatga agatccaaag aatggatttt agaagaggtg ctttgatgaa ggccttgatt 840
ggtgaacaaa agaaaagaat cggttccggt gaagaaaaga actcctacat tgatttcttg 900
ttgtctgaag ctaccacttt gaccgaaaag caaattgcta tgttgatctg ggaaaccatc 960
atcgaaattt ccgatacaac tttggttacc tctgaatggg ctatgtacga attggctaaa 1020
gacccaaata gacaagaaat cttgtacaga gaaatccaca aggtttgcgg ttctaacaag 1080
ttgactgaag aaaacttgtc caagttgcca tacttgaact ctgttttcca cgaaaccttg 1140
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ggtggttacc atattccagc tggttctcaa attgccatta acatctacgg ttgcaacatg 1260
aacaaaaagc aatgggaaaa tcctgaagaa tggaagccag aaagattctt ggacgaaaag 1320
tatgacttga tggacttgca taagactatg gcttttggtg gtggtaaaag agtttgtgct 1380
ggtgctttac aagcaatgtt gattgcttgc acttccatcg gtagattcgt tcaagaattt 1440
gaatggaagt tgatgggtgg tgaagaagaa aacgttgata ctgttgcttt gacctcccaa 1500
aaattgcatc caatgcaagc cattattaag gccagagaat gactcgagcc gcgg 1554

SEQ ID NO:70
Vitis vinifera

MDMMGIEAVP FATAVVLGGI SLVVLIFIRR FVSNRKRSVE GLPPVPDIPG LPLIGNLLQL 60

KEKKPHKTFA RWAETYGPIF SIRTGASTMI VLNSSEVAKE AMVTRFSSIS TRKLSNALKI 120
LTFDKCMVAT SDYNDFHKMV KGFILRNVLG APAQKRHRCH RDTLIENISK YLHAHVKTSP 180
LEPVVLKKIF ESEIFGLALK QALGKDIESI YVEELGTTLS REEIFAVLVV DPMAGAIEVD 240
WRDFFPYLSW IPNKSMEMKI QRMDFRRGAL MKALIGEQKK RIGSGEEKNS YIDFLLSEAT 300
TLTEKQIAML IWETIIEISD TTLVTSEWAM YELAKDPNRQ EILYREIHKV CGSNKLTEEN 360
LSKLPYLNSV FHETLRKYSP APMVPVRYAH EDTQLGGYHI PAGSQIAINI YGCNMNKKQW 420
ENPEEWKPER FLDEKYDLMD LHKTMAFGGG KRVCAGALQA MLIACTSIGR FVQEFEWKLM 480
GGEEENVDTV ALTSQKLHPM QAIIKARE 508

SEQ ID NO:71
Artificial Sequence

aagcttaaaa tgagtaagtc taatagtatg aattctacat cacacgaaac ccttttcaa 60
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gctttcggcg catggttatg ttcttatgtg atacatgttt tatcatcttc ctctacagta 180
aaagtgccag ttgttggata caggtctgta ttcgaaccta catggttgct tagacttaga 240
ttcgtctggg aaggtggctc tatcataggt caagggtaca ataagtttaa agactctatt 300
ttccaagtta ggaaattggg aactgatatt gtcattatac cacctaacta tattgatgaa 360
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gctttaacaa aagagatgcc tgatatgaaa aatgacgaat gggtagaagt agatatcagt 600
agtataatgg tgagattgat ttccaggatc tccgccagag tctttctagg gcctgaacac 660
tgtcgtaacc aggaatggtt gactactaca gcagaatatt cagaatcact tttcattaca 720
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tcatacagga ctctacttag aaacgtttca agtggtagaa gagtcatcgg tgacatcata 840
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cgttctgata gtaactacgc acaaaagtac ctattctcca tgaccgattc ttcaaacatg 1380
gctttcggat acggcaagta tgcttgtcca ggtagatttt acgcgtctaa tgagatgaaa 1440
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cctagaaata tcactatcga ttctgatatg attccagacc caagagctag actttgcgtc 1560
agaaaaagat cacttagaga tgaatgaccg cgg 1593

SEQ ID NO:72
Gibberella fujikuroi

MSKSNSMNST SHETLFQQLV LGLDRMPLMD VHWLIYVAFG AWLCSYVIHV LSSSSTVKVP 60
VVGYRSVFEP TWLLRLRFVW EGGSIIGQGY NKFKDSIFQV RKLGTDIVII PPNYIDEVRK 120
LSQDKTRSVE PFINDFAGQY TRGMVFLQSD LQNRVIQQRL TPKLVSLTKV MKEELDYALT 180
KEMPDMKNDE WVEVDISSIM VRLISRISAR VFLGPEHCRN QEWLTTTAEY SESLFITGFI 240
LRVVPHILRP FIAPLLPSYR TLLRNVSSGR RVIGDIIRSQ QGDGNEDILS WMRDAATGEE 300
KQIDNIAQRM LILSLASIHT TAMTMTHAMY DLCACPEYIE PLRDEVKSVV GASGWDKTAL 360
NRFHKLDSFL KESQRFNPVF LLTFNRIYHQ SMTLSDGTNI PSGTRIAVPS HAMLQDSAHV 420
PGPTPPTEFD GFRYSKIRSD SNYAQKYLFS MTDSSNMAFG YGKYACPGRF YASNEMKLTL 480
AILLLQFEFK LPDGKGRPRN ITIDSDMIPD PRARLCVRKR SLRDE 525

SEQ ID NO:73
Artificial Sequence

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caagagggat atgatggcta cagaggatct acattcaaaa tcgcgatgtt agaccgttgg 240
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gccgtgcttc ctgatgtcat tgaagagttg acacttgcgg ttagacagta cattccaaca 480
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gcttctaata gagtctttgt aggtttgcct gcttgcagaa accaaggtta cttagatttg 600
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aacatcgtat ctttaactag aatggctgac aaagatatta cattgagtga tggcacattt 1140
ttgccaaaag gtactctagt ggccgttcca gcgtattcta ctcatagaga tgatgctgtc 1200
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tggggtccaa cagttttgcc tgcaccagca ggccaagtat tgttcagaaa gagacaagtt 1500
agtctataac cgcgg 1515

SEQ ID NO:74

Trametes versicolor

MEDPTVLYAC LAIAVATFVV RWYRDPLRSI PTVGGSDLPI LSYIGALRWT RRGREILQEG 60
YDGYRGSTFK IAMLDRWIVI ANGPKLADEV RRRPDEELNF MDGLGAFVQT KYTLGEAIHN 120
DPYHVDIIRE KLTRGLPAVL PDVIEELTLA VRQYIPTEGD EWVSVNCSKA ARDIVARASN 180
RVFVGLPACR NQGYLDLAID FTLSVVKDRA IINMFPELLK PIVGRVVGNA TRNVRRAVPF 240
VAPLVEERRR LMEEYGEDWS EKPNDMLQWI MDEAASRDSS VKAIAERLLM VNFAAIHTSS 300
NTITHALYHL AEMPETLQPL REEIEPLVKE EGWTKAAMGK MWWLDSFLRE SQRYNGINIV 360
SLTRMADKDI TLSDGTFLPK GTLVAVPAYS THRDDAVYAD ALVFDPFRFS RMRAREGEGT 420
KHQFVNTSVE YVPFGHGKHA CPGRFFAANE LKAMLAYIVL NYDVKLPGDG KRPLNMYWGP 480
TVLPAPAGQV LFRKRQVSL 499

SEQ ID NO:75

Artificial Sequence

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ataaagatgg gttcttcatc tcttattgta ttgaacagta cagaaactgc taaggaagca 300
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aggttgtgta aggagatcca gaacgtgtgt ggtggagaga aattcaagga agagcagttg 1080

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gctgggtccg aaattgctat aaacatctac gggtgcaaca tggacaaaaa gagatgggaa 1260
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tccctaatgg ctggtatcgc tattggtaga ttggtccaag agttcgaatg gaaacttaga 1440
gatggtgaag aggaaaatgt cgatacttat gggttaacat ctcaaaagtt atacccacta 1500
atggcaatca tcaatcctag aagatcctaa 1530

SEQ ID NO:76
Arabidopsis thaliana
MAFFSMISIL LGFVISSFIF IFFFKKLLSF SRKNMSEVST LPSVPVVPGF PVIGNLLQLK 60
EKKPHKTFTR WSEIYGPIYS IKMGSSSLIV LNSTETAKEA MVTRFSSIST RKLSNALTVL 120
TCDKSMVATS DYDDFHKLVK RCLLNGLLGA NAQKRKRHYR DALIENVSSK LHAHARDHPQ 180
EPVNFRAIFE HELFGVALKQ AFGKDVESIY VKELGVTLSK DEIFKVLVHD MMEGAIDVDW 240
RDFFPYLKWI PNKSFEARIQ QKHKRRLAVM NALIQDRLKQ NGSESDDDCY LNFLMSEAKT 300
LTKEQIAILV WETIIETADT TLVTTEWAIY ELAKHPSVQD RLCKEIQNVC GGEKFKEEQL 360
SQVPYLNGVF HETLRKYSPA PLVPIRYAHE DTQIGGYHVP AGSEIAINIY GCNMDKKRWE 420
RPEDWWPERF LDDGKYETSD LHKTMAFGAG KRVCAGALQA SLMAGIAIGR LVQEFEWKLR 480
DGEEENVDTY GLTSQKLYPL MAIINPRRS 509

SEQ ID NO:77
Artificial Sequence
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aagatgctag ttgaaaatag agaattgttg acactgttca caacttcctt cgcagttctt 180
attgggtgtc ttgtatttct aatgtggaga cgttcatcct ctaaaaagct ggtacaagat 240
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tgtatagaag atgacttcac cgcctggaag gaattggtat ggccagaatt ggatcaactt 780
ttaagggacg aagatgatac ttctgtgact accccataca ctgcagccgt attggagtac 840
agagtggttt accatgataa accagcagac tcatatgctg aagatcaaac ccatacaaac 900
ggtcatgttg ttcatgatgc acagcatcct tcaagatcta atgtggcttt caaaaaggaa 960
ctacacacct ctcaatcaga taggtcttgt actcacttag aattcgatat ttctcacaca 1020
ggactgtctt acgaaactgg cgatcacgtt ggcgtttatt ccgagaactt gtccgaagtt 1080
gtcgatgaag cactaaaact gttagggtta tcaccagaca catacttctc agtccatgct 1140
gataaggagg atgggacacc tatcggtggt gcttcactac caccaccttt tcctccttgc 1200
acattgagag acgctctaac cagatacgca gatgtcttat cctcacctaa aaaggtagct 1260
ttgctggcat tggctgctca tgctagtgat cctagtgaag ccgataggtt aaagttcctg 1320
gcttcaccag ccggaaaaga tgaatatgca caatggatcg tcgccaacca acgttctttg 1380
ctagaagtga tgcaaagttt tccatctgcc aagcctccat taggtgtgtt cttcgcagca 1440
gtagctccac gtttacaacc aagatactac tctatcagtt catctcctaa gatgtctcct 1500
aacagaatac atgttacatg tgctttggtg tacgagacta ctccagcagg cagaattcac 1560
agaggattgt gttcaacctg gatgaaaaat gctgtccctt taacagagtc acctgattgc 1620
tctcaagcat ccattttcgt tagaacatca aatttcagac ttccagtgga tccaaaagtt 1680
ccagtcatta tgataggacc aggcactggt cttgccccat tcaggggctt tcttcaagag 1740
agattggcct tgaaggaatc tggtacagaa ttgggttctt ctatcttttt ctttggttgc 1800
cgtaatagaa aagttgactt tatctacgag gacgagctta acaattttgt tgagacagga 1860
gcattgtcag aattgatcgt cgcattttca agagaaggga ctgccaaaga gtacgttcag 1920
cacaagatga gtcaaaaagc ctccgatata tggaaacttc taagtgaagg tgcctatctt 1980

tatgtctgtg gcgatgcaaa gggcatggcc aaggatgtcc atagaactct gcatacaatt 2040
gttcaggaac aagggagtct ggattcttcc aaggctgaat tgtacgtcaa aaacttacag 2100
atgtctggaa gatacttaag agatgtttgg taa 2133

SEQ ID NO:78
Stevia rebaudiana

MQSDSVKVSP FDLVSAAMNG KAMEKLNASE SEDPTTLPAL KMLVENRELL TLFTTSFAVL 60
IGCLVFLMWR RSSSKKLVQD PVPQVIVVKK KEKESEVDDG KKKVSIFYGT QTGTAEGFAK 120
ALVEEAKVRY EKTSFKVIDL DDYAADDDEY EEKLKKESLA FFFLATYGDG EPTDNAANFY 180
KWFTEGDDKG EWLKKLQYGV FGLGNRQYEH FNKIAIVVDD KLTEMGAKRL VPVGLGDDDQ 240
CIEDDFTAWK ELVWPELDQL LRDEDDTSVT TPYTAAVLEY RVVYHDKPAD SYAEDQTHTN 300
GHVVHDAQHP SRSNVAFKKE LHTSQSDRSC THLEFDISHT GLSYETGDHV GVYSENLSEV 360
VDEALKLLGL SPDTYFSVHA DKEDGTPIGG ASLPPPFPPC TLRDALTRYA DVLSSPKKVA 420
LLALAAHASD PSEADRLKFL ASPAGKDEYA QWIVANQRSL LEVMQSFPSA KPPLGVFFAA 480
VAPRLQPRYY SISSSPKMSP NRIHVTCALV YETTPAGRIH RGLCSTWMKN AVPLTESPDC 540
SQASIFVRTS NFRLPVDPKV PVIMIGPGTG LAPFRGFLQE RLALKESGTE LGSSIFFFGC 600
RNRKVDFIYE DELNNFVETG ALSELIVAFS REGTAKEYVQ HKMSQKASDI WKLLSEGAYL 660
YVCGDAKGMA KDVHRTLHTI VQEQGSLDSS KAELYVKNLQ MSGRYLRDVW 710

SEQ ID NO:79
Siraitia grosvenorii

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aactcctcat ttgaatctac tggtgaagtt gcctccgtta tctttgaaaa cagagaattg 120
gttgccatct tgaccacttc tattgctgtt atgattggtt gcttcgttgt cttgatgtgg 180
agaagagctg gttctagaaa ggttaagaat gtcgaattgc caaagccatt gattgtccat 240
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actggtactg ctgaaggttt tgctaaggct ttggctgatg aagctaaagc tagatacgaa 360
aaggctacct tcagagttgt tgatttggat gattatgctg ccgatgatga ccaatacgaa 420
gaaaaattga agaacgaatc cttcgccgtt ttcttgttgg ctacttatgg tgatggtgaa 480
cctactgata atgctgctag attttacaag tggttcgccg aaggtaaaga aagaggtgaa 540
tggttgcaaa acttgcacta tgctgttttt ggtttgggta acagacaata cgaacacttc 600
aacaagattg ctaaggttgc cgacgaatta ttggaagctc aaggtggtaa tagattggtt 660
aaggttggtt taggtgatga cgatcaatgc atcgaagatg atttttctgc ttggagagaa 720
tctttgtggc cagaattgga tatgttgttg agagatgaag atgatgctac tactgttact 780
actccatata ctgctgctgt cttggaatac agagttgtct ttcatgattc tgctgatgtt 840
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ccattcagat ctaacgttgt cgtcagaaaa gaattgcata cttctgcctc tgatagatcc 960
tgttctcatt tggaattcaa catttccggt tccgctttga attacgaaac tggtgatcat 1020
gttggtgtct actgtgaaaa cttgactgaa actgttgatg aagccttgaa cttgttgggt 1080
ttgtctccag aaacttactt ctctatctac accgataacg aagatggtac tccattgggt 1140
ggttcttcat tgccaccacc atttccatca tgtactttga gaactgcttt gaccagatac 1200
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aatccagttg aagctgatag attgagatac ttggcttctc cagctggtaa agatgaatat 1320
gcccaatctg ttatcggttc ccaaaagtct ttgttggaag ttatggctga attcccatct 1380
gctaaaccac cattaggtgt ttttttgct gctgttgctc caagattgca acctagattc 1440
tactccattt catcctctcc aagaatggct ccatctagaa tccatgttac ttgtgctttg 1500
gtttacgata agatgccaac tggtagaatt cataagggtg tttgttctac ctggatgaag 1560
aattctgttc caatggaaaa gtcccatgaa tgttcttggg ctccaatttt cgttagacaa 1620
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ggtttggctc cttttagagg ttttttacaa gaaagattgg ccttgaaaga atccggtgtt 1740
gaattgggtc catccatttt gtttttcggt tgcagaaaca gaagaatgga ttacatctac 1800
gaagatgaat tgaacaactt cgttgaaacc ggtgctttgt ccgaattggt tattgctttt 1860
tctagagaag gtcctaccaa agaatacgtc caacataaga tggctgaaaa ggcttctgat 1920
atctggaact tgatttctga aggtgcttac ttgtacgttt gtggtgatgc taaaggtatg 1980
gctaaggatg ttcatagaac cttgcatacc atcatgcaag aacaaggttc tttggattct 2040
tccaaagctg aatccatggt caagaacttg caaatgaatg gtagatactt aagagatgtt 2100

tggtaa 2106

SEQ ID NO:80

Siraitia grosvenorii

MKVSPFEFMS AIIKGRMDPS NSSFESTGEV ASVIFENREL VAILTTSIAV MIGCFVVLMW 60
RRAGSRKVKN VELPKPLIVH EPEPEVEDGK KKVSIFFGTQ TGTAEGFAKA LADEAKARYE 120
KATFRVVDLD DYAADDDQYE EKLKNESFAV FLLATYGDGE PTDNAARFYK WFAEGKERGE 180
WLQNLHYAVF GLGNRQYEHF NKIAKVADEL LEAQGGNRLV KVGLGDDDQC IEDDFSAWRE 240
SLWPELDMLL RDEDDATTVT TPYTAAVLEY RVVFHDSADV AAEDKSWINA NGHAVHDAQH 300
PFRSNVVVRK ELHTSASDRS CSHLEFNISG SALNYETGDH VGVYCENLTE TVDEALNLLG 360
LSPETYFSIY TDNEDGTPLG GSSLPPPFPS CTLRTALTRY ADLLNSPKKS ALLALAAHAS 420
NPVEADRLRY LASPAGKDEY AQSVIGSQKS LLEVMAEFPS AKPPLGVFFA AVAPRLQPRF 480
YSISSSPRMA PSRIHVTCAL VYDKMPTGRI HKGVCSTWMK NSVPMEKSHE CSWAPIFVRQ 540
SNFKLPAESK VPIIMVGPGT GLAPFRGFLQ ERLALKESGV ELGPSILFFG CRNRRMDYIY 600
EDELNNFVET GALSELVIAF SREGPTKEYV QHKMAEKASD IWNLISEGAY LYVCGDAKGM 660
AKDVHRTLHT IMQEQGSLDS SKAESMVKNL QMNGRYLRDV W 701

SEQ ID NO:81

Artificial Sequence

atggcagaat tagatacact tgatatagta gtattaggtg ttatcttttt gggtactgtg 60
gcatacttta ctaagggtaa attgtggggt gttaccaagg atccatacgc taacggattc 120
gctgcaggtg gtgcttccaa gcctggcaga actagaaaca tcgtcgaagc tatggaggaa 180
tcaggtaaaa actgtgttgt tttctacggc agtcaaacag gtacagcgga ggattacgca 240
tcaagacttg caaaggaagg aaagtccaga ttcggtttga acactatgat cgccgatcta 300
gaagattatg acttcgataa cttagacact gttccatctg ataacatcgt tatgtttgta 360
ttggctactt acggtgaagg cgaaccaaca gataacgccg tggatttcta tgagttcatt 420
actggcgaag atgcctcttt caatgagggc aacgatcctc cactaggtaa cttgaattac 480
gttgcgttcg gtctgggcaa caatacctac gaacactaca actcaatggt caggaacgtt 540
aacaaggctc tagaaaagtt aggagctcat agaattggag aagcaggtga gggtgacgac 600
ggagctggaa ctatggaaga ggacttttta gcttggaaag atccaatgtg ggaagccttg 660
gctaaaaaga tgggcttgga ggaaagagaa gctgtatatg aacctatttt cgctatcaat 720
gagagagatg atttgacccc tgaagcgaat gaggtatact tgggagaacc taataagcta 780
cacttggaag gtacagcgaa aggtccattc aactcccaca acccatatat cgcaccaatt 840
gcagaatcat acgaactttt ctcagctaag gatagaaatt gtctgcatat ggaaattgat 900
atttctggta gtaatctaaa gtatgaaaca ggcgaccata tcgcgatctg gcctaccaac 960
ccaggtgaag aggtcaacaa atttcttgac attctagatc tgtctggtaa gcaacattcc 1020
gtcgtaacag tgaaagcctt agaacctaca gccaaagttc cttttccaaa tccaactacc 1080
tacgatgcta tattgagata ccatctggaa atatgcgctc cagtttctag acagtttgtc 1140
tcaactttag cagcattcgc ccctaatgat gatatcaaag ctgagatgaa ccgtttggga 1200
tcagacaaag attacttcca cgaaaagaca ggaccacatt actacaatat cgctagattt 1260
ttggcctcag tctctaaagg tgaaaaatgg acaaagatac cattttctgc tttcatagaa 1320
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aaaaagatta gtattactgc tgttgtcgaa tctcagcaaa ttccaggtag agatgaccca 1440
ttcagaggtg tagcgactaa ctacttgttc gctttgaagc agaaacaaaa cggtgatcca 1500
aatccagctc cttttggcca atcatacgag ttgacaggac caaggaataa gtatgatggt 1560
atacatgttc cagtccatgt aagacattct aactttaagc taccatctga tccaggcaaa 1620
cctattatca tgatcggtcc aggtaccggt gttgcccctt ttagaggctt cgtccaagag 1680
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ggcgacaaat tcgaaatgat tacagctttt tcaagagaag gatctaaaaa ggtttatgtt 1860
caacacagac tgaaggaaag atcaaaggaa gtttctgatc ttctatccca aaaagcatac 1920
ttctacgttt gcggagacgc cgcacatatg gcacgtgaag tgaacactgt gttagcacag 1980
atcatagcag aaggccgtgg tgtatcagaa gccaagggtg aggaaattgt caaaaacatg 2040
agatcagcaa atcaatacca agtgtgttct gatttcgtaa ctttacactg taaagagaca 2100
acatacgcga attcagaatt gcaagaggat gtctggagtt aa 2142

SEQ ID NO:82
Gibberella fujikuroi

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MAELDTLDIV VLGVIFLGTV AYFTKGKLWG VTKDPYANGF AAGGASKPGR TRNIVEAMEE        60
SGKNCVVFYG SQTGTAEDYA SRLAKEGKSR FGLNTMIADL EDYDFDNLDT VPSDNIVMFV       120
LATYGEGEPT DNAVDFYEFI TGEDASFNEG NDPPLGNLNY VAFGLGNNTY EHYNSMVRNV       180
NKALEKLGAH RIGEAGEGDD GAGTMEEDFL AWKDPMWEAL AKKMGLEERE AVYEPIFAIN       240
ERDDLTPEAN EVYLGEPNKL HLEGTAKGPF NSHNPYIAPI AESYELFSAK DRNCLHMEID       300
ISGSNLKYET GDHIAIWPTN PGEEVNKFLD ILDLSGKQHS VVTVKALEPT AKVPFPNPTT       360
YDAILRYHLE ICAPVSRQFV STLAAFAPND DIKAEMNRLG SDKDYFHEKT GPHYYNIARF       420
LASVSKGEKW TKIPFSAFIE GLTKLQPRYY SISSSSLVQP KKISITAVVE SQQIPGRDDP       480
FRGVATNYLF ALKQKQNGDP NPAPFGQSYE LTGPRNKYDG IHVPVHVRHS NFKLPSDPGK       540
PIIMIGPGTG VAPFRGFVQE RAKQARDGVE VGKTLLFFGC RKSTEDFMYQ KEWQEYKEAL       600
GDKFEMITAF SREGSKKVYV QHRLKERSKE VSDLLSQKAY FYVCGDAAHM AREVNTVLAQ       660
IIAEGRGVSE AKGEEIVKNM RSANQYQVCS DFVTLHCKET TYANSELQED VWS               713
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SEQ ID NO:83
Stevia rebaudiana

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gcgatgatgt tcgaaattcg tgatctgttg ctgattttga ctacgtcagt tgctgttttg       180
gtcggatgtt tcgttgtttt ggtgtggaag agatcgtccg ggaagaagtc cggcaaggaa       240
ttggagccgc cgaagatcgt tgtgccgaag aggcggctgg agcaggaggt tgatgatggt       300
aagaagaagg ttacgatttt cttcggaaca caaactggaa cggctgaagg tttcgctaag       360
gcacttttcg aagaagcgaa agcgcgatat gaaaaggcag cgtttaaagt gattgatttg       420
gatgattatg ctgctgattt ggatgagtat gcagagaagc tgaagaagga aacatatgct       480
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aaatggttta ctgagggaga cgagaaaggc gtttggcttc aaaaacttca atatggagta       600
tttggtcttg gcaacagaca atatgaacat ttcaacaaga ttggaatagt ggttgatgat       660
ggtctcaccg agcagggtgc aaaacgcatt gttcccgttg gtcttggaga cgacgatcaa       720
tcaattgaag acgatttttc ggcatggaaa gagttagtgt ggcccgaatt ggatctattg       780
cttcgcgatg aagatgacaa agctgctgca actccttaca cagctgcaat ccctgaatac       840
cgcgtcgtat ttcatgacaa acccgatgcg ttttctgatg atcatactca aaccaatggt       900
catgctgttc atgatgctca acatccatgc agatccaatg tggctgttaa aaaagagctt       960
catactcctg aatccgatcg ttcatgcaca catcttgaat ttgacatttc tcacactgga      1020
ttatcttatg aaactgggga tcatgttggt gtatactgtg aaaacctaat tgaagtagtg      1080
gaagaagctg ggaaattgtt aggattatca acagatactt atttctcgtt acatattgat      1140
aacgaagatg gttcaccact tggtggacct tcattacaac ctccttttcc tccttgtact      1200
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cttgctctag ctgctcatgc ttccgatccc actgaagctg atcgtttaag atttcttgca      1320
tctcgcgagg gcaaggatga atatgctgaa tgggttgttg caaaccaaag aagtcttctt      1380
gaagtcatgg aagctttccc gtcagctaga ccgccacttg gtgttttctt tgcagcggtt      1440
gcaccgcgtt tacagcctcg ttactactct atttcttcct ccccaaagat ggaaccaaac      1500
aggattcatg ttacttgcgc gttggtttat gaaaaaactc ccgcaggtcg tatccacaaa      1560
ggaatctgct caacctggat gaagaacgct gtacctttga ccgaaagtca agattgcagt      1620
tgggcaccga tttttgttag aacatcaaac ttcagacttc caattgaccc gaaagtcccg      1680
gttatcatga ttggtcctgg aaccgggttg gctccattta ggggttttct tcaagaaaga      1740
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aaccgcaaag tggattacat atatgagaat gaactcaaca actttgttga aaatggtgcg      1860
ctttctgagc ttgatgttgc tttctcccgc gatggcccga cgaaagaata cgtgcaacat      1920
aaaatgaccc aaaaggcttc tgaaatatgg aatatgcttt ctgagggagc atatttatat      1980
gtatgtggtg atgctaaagg catggctaaa gatgtacacc gtacacttca caccattgtg      2040
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tcaggaagat acctccgtga tgtttggtaa                                       2130
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SEQ ID NO:84
Stevia rebaudiana

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VGCFVVLVWK RSSGKKSGKE LEPPKIVVPK RRLEQEVDDG KKKVTIFFGT QTGTAEGFAK 120
ALFEEAKARY EKAAFKVIDL DDYAADLDEY AEKLKKETYA FFFLATYGDG EPTDNAAKFY 180
KWFTEGDEKG VWLQKLQYGV FGLGNRQYEH FNKIGIVVDD GLTEQGAKRI VPVGLGDDDQ 240
SIEDDFSAWK ELVWPELDLL LRDEDDKAAA TPYTAAIPEY RVVFHDKPDA FSDDHTQTNG 300
HAVHDAQHPC RSNVAVKKEL HTPESDRSCT HLEFDISHTG LSYETGDHVG VYCENLIEVV 360
EEAGKLLGLS TDTYFSLHID NEDGSPLGGP SLQPPFPPCT LRKALTNYAD LLSSPKKSTL 420
LALAAHASDP TEADRLRFLA SREGKDEYAE WVVANQRSLL EVMEAFPSAR PPLGVFFAAV 480
APRLQPRYYS ISSSPKMEPN RIHVTCALVY EKTPAGRIHK GICSTWMKNA VPLTESQDCS 540
WAPIFVRTSN FRLPIDPKVP VIMIGPGTGL APFRGFLQER LALKESGTEL GSSILFFGCR 600
NRKVDYIYEN ELNNFVENGA LSELDVAFSR DGPTKEYVQH KMTQKASEIW NMLSEGAYLY 660
VCGDAKGMAK DVHRTLHTIV QEQGSLDSSK AELYVKNLQM SGRYLRDVW 709

SEQ ID NO:85
Artificial Sequence

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aaggttttgg acacatcgaa cgcatcggaa tcgggagaat ctgctatgct gccgactata 120
gcgatgatta tggagaatcg tgagctgttg atgatactca caacgtcggt tgctgtattg 180
atcggatgcg ttgtcgtttt ggtgtggcgg agatcgtcta cgaagaagtc ggcgttggag 240
ccaccggtga ttgtggttcc gaagagagtg caagaggagg aagttgatga tggtaagaag 300
aaagttacgg ttttcttcgg cacccaaact ggaacagctg aaggcttcgc taaggcactt 360
gttgaggaag ctaaagctcg atatgaaaag gctgtcttta aagtaattga tttggatgat 420
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ttaaaggaag ccggaactga cctcggttta tccattttat tcttcggatg taggaatcgc 1800
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agtgagaagg cttcggatat ctggaacttg ctttctgaag gagcatattt atacgtatgt 1980
ggtgatgcca aaggcatggc caaagatgta catcgaaccc tccacacaat tgtgcaagaa 2040
cagggatctc ttgactcgtc aaaggcagaa ctctacgtga agaatctaca aatgtcagga 2100
agatacctcc gtgacgtttg gtaa 2124

SEQ ID NO:86
Stevia rebaudiana

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IGCVVVLVWR RSSTKKSALE PPVIVVPKRV QEEEVDDGKK KVTVFFGTQT GTAEGFAKAL 120

VEEAKARYEK AVFKVIDLDD YAADDDEYEE KLKKESLAFF FLATYGDGEP TDNAARFYKW 180
FTEGDAKGEW LNKLQYGVFG LGNRQYEHFN KIAKVVDDGL VEQGAKRLVP VGLGDDDQCI 240
EDDFTAWKEL VWPELDQLLR DEDDTTVATP YTAAVAEYRV VFHEKPDALS EDYSYTNGHA 300
VHDAQHPCRS NVAVKKELHS PESDRSCTHL EFDISNTGLS YETGDHVGVY CENLSEVVND 360
AERLVGLPPD TYSSIHTDSE DGSPLGGASL PPPFPPCTLR KALTCYADVL SSPKKSALLA 420
LAAHATDPSE ADRLKFLASP AGKDEYSQWI VASQRSLLEV MEAFPSAKPS LGVFFASVAP 480
RLQPRYYSIS SSPKMAPDRI HVTCALVYEK TPAGRIHKGV CSTWMKNAVP MTESQDCSWA 540
PIYVRTSNFR LPSDPKVPVI MIGPGTGLAP FRGFLQERLA LKEAGTDLGL SILFFGCRNR 600
KVDFIYENEL NNFVETGALS ELIVAFSREG PTKEYVQHKM SEKASDIWNL LSEGAYLYVC 660
GDAKGMAKDV HRTLHTIVQE QGSLDSSKAE LYVKNLQMSG RYLRDVW 707

SEQ ID NO:87

Artificial Sequence

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gacggtagat acttgagaga tgtttggtga 2070

SEQ ID NO:88

Rubus suavissimus

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VPKPVTIVEE EDEFEVASGK TRVSIFYGTQ TGTAEGFAKA LAEEIKARYE KAAVKVIDLD 120
DYTAEDDKYG EKLKKETMAF FMLATYGDGE PTDNAARFYK WFTEGTDRGV WLEHLRYGVF 180
GLGNRQYEHF NKIAKVVDDL LVEQGAKRLV TVGLGDDDQC IEDDFSAWKE ALWPELDQLL 240
QDDTNTVSTP YTAVIPEYRV VIHDPSVTSY EDPYSNMANG NASYDIHHPC RANVAVQKEL 300

HKPESDRSCI HLEFDIFATG LTYETGDHVG VYADNCDDTV EEAAKLLGQP LDLLFSIHTD 360
NNDGTSLGSS LPPPFPGPCT LRTALARYAD LLNPPKKAAL IALAAHADEP SEAERLKFLS 420
SPQGKDEYSK WVVGSQRSLV EVMAEFPSAK PPLGVFFAAV VPRLQPRYYS ISSSPRFAPH 480
RVHVTCALVY GPTPTGRIHR GVCSFWMKNV VPLEKSQNCS WAPIFIRQSN FKLPADHSVP 540
IVMVGPGTGL APFRGFLQER LALKEEGAQV GPALLFFGCR NRQMDFIYEV ELNNFVEQGA 600
LSELIVAFSR EGPSKEYVQH KMVEKAAYMW NLISQGGYFY VCGDAKGMAR DVHRTLHTIV 660
QQEEKVDSTK AESIVKKLQM DGRYLRDVW 689

SEQ ID NO:89

Artificial Sequence

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SEQ ID NO:90

Arabidopsis thaliana

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LDDYAADDDQ YEEKLKKETL AFFCVATYGD GEPTDNAARF YKWFTEENER DIKLQQLAYG 180
VFALGNRQYE HFNKIGIVLD EELCKKGAKR LIEVGLGDDD QSIEDDFNAW KESLWSELDK 240
LLKDEDDKSV ATPYTAVIPE YRVVTHDPRF TTQKSMESNV ANGNTTIDIH HPCRVDVAVQ 300
KELHTHESDR SCIHLEFDIS RTGITYETGD HVGVYAENHV EIVEEAGKLL GHSLDLVFSI 360
HADKEDGSPL ESAVPPPFPG PCTLGTGLAR YADLLNPPRK SALVALAAYA TEPSEAEKLK 420
HLTSPDGKDE YSQWIVASQR SLLEVMAAFP SAKPPLGVFF AAIAPRLQPR YYSISSSPRL 480

APSRVHVTSA LVYGPTPTGR IHKGVCSTWM KNAVPAEKSH ECSGAPIFIR ASNFKLPSNP 540
STPIVMVGPG TGLAPFRGFL QERMALKEDG EELGSSLLFF GCRNRQMDFI YEDELNNFVD 600
QGVISELIMA FSREGAQKEY VQHKMMEKAA QVWDLIKEEG YLYVCGDAKG MARDVHRTLH 660
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SEQ ID NO:91
Artificial Sequence

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ttacaaactt ccggtagata cttgagagat gtctggtga 2139

SEQ ID NO:92
Arabidopsis thaliana

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AVLIGCIVML VWRRSGSGNS KRVEPLKPLV IKPREEEIDD GRKKVTIFFG TQTGTAEGFA 120
KALGEEAKAR YEKTRFKIVD LDDYAADDDE YEEKLKKEDV AFFFLATYGD GEPTDNAARF 180
YKWFTEGNDR GEWLKNLKYG VFGLGNRQYE HFNKVAKVVD DILVEQGAQR LVQVGLGDDD 240
QCIEDDFTAW REALWPELDT ILREEGDTAV ATPYTAAVLE YRVSIHDSED AKFNDITLAN 300
GNGYTVFDAQ HPYKANVAVK RELHTPESDR SCIHLEFDIA GSGLTMKLGD HVGVLCDNLS 360
ETVDEALRLL DMSPDTYFSL HAEKEDGTPI SSSLPPPFPP CNLRTALTRY ACLLSSPKKS 420
ALVALAAHAS DPTEAERLKH LASPAGKDEY SKWVVESQRS LLEVMAEFPS AKPPLGVFFA 480
GVAPRLQPRF YSISSSPKIA ETRIHVTCAL VYEKMPTGRI HKGVCSTWMK NAVPYEKSEK 540
LFLGRPIFVR QSNFKLPSDS KVPIIMIGPG TGLAPFRGFL QERLALVESG VELGPSVLFF 600

GCRNRRMDFI YEEELQRFVE SGALAELSVA FSREGPTKEY VQHKMMDKAS DIWNMISQGA 660
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SEQ ID NO:93
Artificial Sequence

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SEQ ID NO:94
S. rebaudiana

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KYGPILQLQL GYRRVLVISS PSAAEECFTN NDVIFANRPK TLFGKIVGGT SLGSLSYGDQ 120
WRNLRRVASI EILSVHRLNE FHDIRVDENR LLIRKLRSSS SPVTLITVFY ALTLNVIMRM 180
ISGKRYFDSG DRELEEEGKR FREILDETLL LAGASNVGDY LPILNWLGVK SLEKKLIALQ 240
KKRDDFFQGL IEQVRKSRGA KVGKGRKTMI ELLLSLQESE PEYYTDAMIR SFVLGLLAAG 300
SDTSAGTMEW AMSLLVNHPH VLKKAQAEID RVIGNNRLID ESDIGNIPYI GCIINETLRL 360
YPAGPLLFPH ESSADCVISG YNIPRGTMLI VNQWAIHHDP KVWDDPETFK PERFQGLEGT 420
RDGFKLMPFG SGRRGCPGEG LAIRLLGMTL GSVIQCFDWE RVGDEMVDMT EGLGVTLPKA 480
VPLVAKCKPR SEMTNLLSEL 500

SEQ ID NO:95
Rubus suavissimus

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SEQ ID NO:96
Artificial Sequence

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aaggttgtta ctatgatttt gttagaagtt ttgagattgt acccaccagt cattgagtta 1200
atcagaacca ttcataaaaa gactcaattg ggtaaattat ctttgccaga aggtgttgaa 1260
gtcagattac caaccttgtt gattcaccac gataaggaat tatggggtga cgacgctaat 1320
caatttaatc cagaaagatt ttccgaaggt gtttccaagg ctaccaaaaa ccgtttgtcc 1380
ttcttcccat ttggtgctgg tccacgtatt tgtatcggtc aaaacttttc catgatggaa 1440
gccaagttgg ctttggcttt aatcttgcaa cacttcactt tcgaattgtc tccatcccat 1500
gcccacgctc cttctcatag aatcacttta caaccacaat acggtgtcag aatcatctta 1560
cacagaagat aa 1572

SEQ ID NO:97
Rubus suavissimus

MEVTVASSVA LSLVFISIVV RWAWSVVNWV WFKPKKLERF LREQGLKGNS YRFLYGDMKE 60
NSILLKQARS KPMNLSTSHD IAPQVTPFVD QTVKAYGKNS FNWVGPIPRV NIMNPEDLKD 120
VLTKNVDFVK PISNPLIKLL ATGIAIYEGE KWTKHRRIIN PTFHSERLKR MLPSFHQSCN 180
EMVKEWESLV SKEGSSCELD VWPFLENMSA DVISRTAFGT SYKKGQKIFE LLREQVIYVT 240
KGFQSFYIPG WRFLPTKMNK RMNEINEEIK GLIRGIIIDR EQIIKAGEET NDDLLGALME 300
SNLKDIREHG KNNKNVGMSI EDVIQECKLF YFAGQETTSV LLAWTMVLLG QNQNWQDRAR 360

QEVLQVFGSS KPDFDGLAHL KVVTMILLEV LRLYPPVIEL IRTIHKKTQL GKLSLPEGVE 420
VRLPTLLIHH DKELWGDDAN QFNPERFSEG VSKATKNRLS FFPFGAGPRI CIGQNFSMME 480
AKLALALILQ HFTFELSPSH AHAPSHRITL QPQYGVRIIL HRR 523

SEQ ID NO:98
Prunus avium

atggaagcat caagggctag ttgtgttgcg ctatgtgttg tttgggtgag catagtaatt 60
acattggcat ggagggtgct gaattgggtg tggttgaggc caaagaaact agaaagatgc 120
ttgagggagc aaggccttac aggcaattct tacaggcttt tgtttggaga caccaaggat 180
ctctcgaaga tgctggaaca aacacaatcc aaacccatca aactctccac ctcccatgat 240
atagcgccac gagtcacccc atttttccat cgaactgtga actctaatgg caagaattct 300
tttgtttgga tgggccctat accaagagtg cacatcatga atccagaaga tttgaaagat 360
gccttcaaca gacatgatga ttttcataag acagtaaaaa atcctatcat gaagtctcca 420
ccaccgggca ttgtaggcat tgaaggtgag caatgggcta aacacagaaa gattatcaac 480
ccagcattcc atttagagaa gctaaagggt atggtaccaa tattttacca aagttgtagc 540
gagatgatta acaaatggga gagcttggtg tccaaagaga gttcatgtga gttggatgtg 600
tggccttatc ttgaaaattt taccagcgat gtgatttccc gagctgcatt tggaagtagc 660
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gaggcgatga aggcagggga agccactaaa gatgacttac taggaatact tatggagtcc 900
aacttcaggg aaattcagga acatgggaac aacaaaaatg ctggaatgag tattgaagat 960
gtaattggag agtgtaagtt gttttacttt gctgggcaag agaccacttc ggtgttgctt 1020
gtttggacaa tgattttact aagccaaaat caggattggc aagctcgtgc aagagaagag 1080
gtcttgaaag tctttggaag caacatccca acctatgaag agctaagtca cctaaaagtt 1140
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aagccagaga ggttttcaga gggagtttca aaggcaacaa agaacaaatt tacatactta 1380
cctttcggag ggggtccaag gatttgcatt ggacaaaact ttgccatggt ggaagctaaa 1440
ttggccttgg ccctgatttt acaacacttt gcctttgagc tttctccatc ctatgctcat 1500
gctccttctg cagttataac ccttcaacct caatttggtg ctcatatcat tttgcataaa 1560
cgttga 1566

SEQ ID NO:99
Artificial Sequence

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ttgagagaac aaggtttgac tggtaactct tacagattgt tgttcggtga taccaaggac 180
ttgtctaaga tgttggaaca aactcaatcc aagcctatca agttgtctac ctctcatgat 240
attgctccaa gagttactcc attcttccat agaactgtta actccaacgg taagaactct 300
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gctttcaaca gacatgatga tttccataag accgtcaaga acccaattat gaagtctcca 420
ccaccaggta tagttggtat tgaaggtgaa caatgggcca aacatagaaa gattattaac 480
ccagccttcc acttggaaaa gttgaaaggt atggttccaa tcttctacca atcctgctct 540
gaaatgatta acaagtggga atccttggtt tccaaagaat cttcctgtga attggatgtc 600
tggccatatt tggaaaactt cacctccgat gttatttcca gagctgcttt tggttcttct 660
tacgaagaag gtagaaagat cttccaatta ttgagagaag aagccaaggt ttactccgtt 720
gctttgagat ctgtttacat tccaggttgg agattcttgc caactaagca aaacaaaaag 780
accaaagaaa tccacaacga aatcaagggt ttgttgaagg gtatcatcaa caagagagaa 840
gaagctatga aggctggtga agctacaaaa gatgatttgt tgggtatctt gatggaatcc 900
aacttcagag aaatccaaga acacggtaac aacaagaatg ccggtatgtc tattgaagat 960
gttatcggtg aatgcaagtt gttctacttt gctggtcaag aaactacctc cgttttgttg 1020
gtttggacca tgattttgtt gtcccaaaat caagattggc aagctagagc tagagaagaa 1080
gtcttgaaag ttttcggttc taacatccca acctacgaag aattgtctca cttgaaggtt 1140
gtcactatga tcttgttgga agtattgaga ttatacccat ccgttgttgc attgccaaga 1200

actactcata agaaaactca attgggtaaa ttgtccttgc cagctggtgt tgaagtttct 1260
ttgccaattt tgttagtcca ccacgacaaa gaattgtggg gtgaagatgc taatgaattc 1320
aagccagaaa gattctccga aggtgtttct aaagctacca agaacaagtt cacttacttg 1380
ccatttggtg gtggtccaag aatatgtatt ggtcaaaatt tcgctatggt cgaagctaaa 1440
ttggctttgg ctttgatctt gcaacatttc gctttcgaat tgtcaccatc ttatgctcat 1500
gctccatctg ctgttattac attgcaacca caatttggtg cccatatcat cttgcataag 1560
agataac 1567

SEQ ID NO:100
Prunus avium

MEASRASCVA LCVVWVSIVI TLAWRVLNWV WLRPKKLERC LREQGLTGNS YRLLFGDTKD 60
LSKMLEQTQS KPIKLSTSHD IAPRVTPFFH RTVNSNGKNS FVWMGPIPRV HIMNPEDLKD 120
AFNRHDDFHK TVKNPIMKSP PPGIVGIEGE QWAKHRKIIN PAFHLEKLKG MVPIFYQSCS 180
EMINKWESLV SKESSCELDV WPYLENFTSD VISRAAFGSS YEEGRKIFQL LREEAKVYSV 240
ALRSVYIPGW RFLPTKQNKK TKEIHNEIKG LLKGIINKRE EAMKAGEATK DDLLGILMES 300
NFREIQEHGN NKNAGMSIED VIGECKLFYF AGQETTSVLL VWTMILLSQN QDWQARAREE 360
VLKVFGSNIP TYEELSHLKV VTMILLEVLR LYPSVVALPR TTHKKTQLGK LSLPAGVEVS 420
LPILLVHHDK ELWGEDANEF KPERFSEGVS KATKNKFTYL PFGGGPRICI GQNFAMVEAK 480
LALALILQHF AFELSPSYAH APSAVITLQP QFGAHIILHK R 521

SEQ ID NO:101
Prunus mume

ASWVAVLSVV WVSMVIAWAW RVLNWVWLRP KKLEKCLREQ GLAGNSYRLL FGDTKDLSKM 60
LEQTQSKPIK LSTSHDIAPH VTPFFHQTVN SYGKNSFVWM GPIPRVHIMN PEDLKDTFNR 120
HDDFHKVVKN PIMKSLPQGI VGIEGEQWAK HRKIINPAFH LEKLKGMVPI FYRSCSEMIN 180
KWESLVSKES SCELDVWPYL ENFTSDVISR AAFGSSYEEG RKIFQLLREE AKIYTVAMRS 240
VYIPGWRFLP TKQNKKAKEI HNEIKGLLKG IINKREEAMK AGEATKDDLL GILMESNFRE 300
IQEHGNNKNA GMSIEDVIGE CKLFYFAGQE TTSVLLVWTM VLLSQNQDWQ ARAREEVLQV 360
FGSNIPTYEE LSQLKVVTMI LLEVLRLYPS VVALPRTTHK KTQLGKLSLP AGVEVSLPIL 420
LVHHDKELWG EDANEFKPER FSEGVSKATK NQFTYFPFGG GPRICIGQNF AMMEAKLALS 480
LILRHFALEL SPLYAHAPSV TITLQPQYGA HIILHKR 517

SEQ ID NO:102
Prunus mume

MEASRPSCVA LSVVLVSIVI AWAWRVLNWV WLRPNKLERC LREQGLTGNS YRLLFGDTKE 60
ISMMVEQAQS KPIKLSTTHD IAPRVIPFSH QIVYTYGRNS FVWMGPTPRV TIMNPEDLKD 120
AFNKSDEFQR AISNPIVKSI SQGLSSLEGE KWAKHRKIIN PAFHLEKLKG MLPTFYQSCS 180
EMINKWESLV FKEGSREMDV WPYLENLTSD VISRAAFGSS YEEGRKIFQL LREEAKFYTI 240
AARSVYIPGW RFLPTKQNKR MKEIHKEVRG LLKGIINKRE DAIKAGEAAK GNLLGILMES 300
NFREIQEHGN NKNAGMSIED VIGECKLFYF AGQETTSVLL VWTLVLLSQN QDWQARAREE 360
VLQVFGTNIP TYDQLSHLKV VTMILLEVLR LYPAVVELPR TTYKKTQLGK FLLPAGVEVS 420
LHIMLAHHDK ELWGEDAKEF KPERFSEGVS KATKNQFTYF PFGAGPRICI GQNFAMLEAK 480
LALSLILQHF TFELSPSYAH APSVTITLHP QFGAHFILHK R 521

SEQ ID NO:103
Prunus mume

CVALSVVLVS IVIAWAWRVL NWVWLRPNKL ERCLREQGLT GNSYRLLFGD TKEISMMVEQ 60
AQSKPIKLST THDIAPRVIP FSHQIVYTYG RNSFVWMGPT PRVTIMNPED LKDAFNKSDE 120
FQRAISNPIV KSISQGLSSL EGEKWAKHRK IINPAFHLEK LKGMLPTFYQ SCSEMINKWE 180
SLVFKEGSRE MDVWPYLENL TSDVISRAAF GSSYEEGRKI FQLLREEAKF YTIAARSVYI 240
PGWRFLPTKQ NKRMKEIHKE VRGLLKGIIN KREDAIKAGE AAKGNLLGIL MESNFREIQE 300
HGNNKNAGMS IEDVIGECKL FYFAGQETTS VLLVWTLVLL SQNQDWQARA REEVLQVFGT 360
NIPTYDQLSH LKVVTMILLE VLRLYPAVVE LPRTTYKKTQ LGKFLLPAGV EVSLHIMLAH 420
HDKELWGEDA KEFKPERFSE GVSKATKNQF TYFPFGAGPR ICIGQNFAML EAKLALSLIL 480
QHFTFELSPS YAHAPSVTIT LHPQFGAHFI LHKR 514

SEQ ID NO:104

Prunus persica

MGPIPRVHIM NPEDLKDTFN RHDDFHKVVK NPIMKSLPQG IVGIEGDQWA KHRKIINPAF 60
HLEKLKGMVP IFYQSCSEMI NIWKSLVSKE SSCELDVWPY LENFTSDVIS RAAFGSSYEE 120
GRKIFQLLRE EAKVYTVAVR SVYIPGWRFL PTKQNKKTKE IHNEIKGLLK GIINKREEAM 180
KAGEATKDDL LGILMESNFR EIQEHGNNKN AGMSIEDVIG ECKLFYFAGQ ETTSVLLVWT 240
MVLLSQNQDW QARAREEVLQ VFGSNIPTYE ELSHLKVVTM ILLEVLRLYP SVVALPRTTH 300
KKTQLGKLSL PAGVEVSLPI LLVHHDKELW GEDANEFKPE RFSEGVSKAT KNQFTYFPFG 360
GGPRICIGQN FAMMEAKLAL SLILQHFTFE LSPQYSHAPS VTITLQPQYG AHLILHKR 418

SEQ ID NO:105

Artificial Sequence

atgggtttgt tcccattaga ggattcctac gcgctggtct ttgaaggact agcaataaca 60
ctggctttgt actatctact gtctttcatc tacaaaacat ctaaaaagac atgtacacct 120
cctaaagcat ctggtgaaat cattccaatt acaggaatca tattgaatct gctatctggc 180
tcaagtggtc tacctattat cttagcactt gcctctttag cagacagatg tggtcctatt 240
ttcaccatta ggctgggtat taggagagtg ctagtagtat caaattggga aatcgctaag 300
gagattttca ctacccacga tttgatagtt tctaatagac caaaatactt agccgctaag 360
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gtaagagttt ttgaactaga aaactctatg aaatctatca gagaatcatg gaaggagaaa 540
aaggatgaag agggaaaggt attagttgag atgaaaaagt ggttctggga actgaatatg 600
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gcaaagcgta tctccgagtt attcagagaa tggtttcact acactggcag atttgtcgtt 720
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ttagcgacat tgctgcaaaa cttcgaaatg tcaacaccaa acgatgcgcc agtcgatatg 1500
actgcttctg ttggcatgac aaatgccaaa gcatcacctt tagaagtctt gctatcacct 1560
cgtgttaaat ggtcctaa 1578

SEQ ID NO:106

Stevia rebaudiana

MGLFPLEDSY ALVFEGLAIT LALYYLLSFI YKTSKKTCTP PKASGEHPIT GHLNLLSGSS 60
GLPHLALASL ADRCGPIFTI RLGIRRVLVV SNWEIAKEIF TTHDLIVSNR PKYLAAKILG 120
FNYVSFSFAP YGPYWVGIRK IIATKLMSSS RLQKLQFVRV FELENSMKSI RESWKEKKDE 180
EGKVLVEMKK WFWELNMNIV LRTVAGKQYT GTVDDADAKR ISELFREWFH YTGRFVVGDA 240
FPFLGWLDLG GYKKTMELVA SRLDSMVSKW LDEHRKKQAN DDKKEDMDFM DIMISMTEAN 300
SPLEGYGTDT IIKTTCMTLI VSGVDTTSIV LTWALSLLLN NRDTLKKAQE ELDMCVGKGR 360
QVNESDLVNL IYLEAVLKEA LRLYPAAFLG GPRAFLEDCT VAGYRIPKGT CLLINMWKLH 420
RDPNIWSDPC EFKPERFLTP NQKDVDVIGM DFELIPFGAG RRYCPGTRLA LQMLHIVLAT 480
LLQNFEMSTP NDAPVDMTAS VGMTNAKASP LEVLLSPRVK WS 522

SEQ ID NO:107

Artificial Sequence

atgatacaag ttttaactcc aattctactc ttcctcatct tcttcgtttt ctggaaagtc 60
tacaaacatc aaaagactaa aatcaatcta ccaccaggtt ccttcggctg gccatttttg 120

ggtgaaacct tagccttact tagagcaggc tgggattctg agccagaaag attcgtaaga 180
gagcgtatca aaaagcatgg atctccactt gttttcaaga catcactatt tggagacaga 240
ttcgctgttc tttgcggtcc agctggtaat aagtttttgt tctgcaacga aaacaaatta 300
gtggcatctt ggtggccagt ccctgtaagg aagttgttcg gtaaaagttt actcacaata 360
agaggagatg aagcaaaatg gatgagaaaa atgctattgt cttacttggg tccagatgca 420
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tactccagta aaaaggccgc agctgccatt agaattgaat tgaaaaagct cattaaagct 720
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gctactccag ctaagggctt gccaattaga cttcatccac accaagtcta a 1431

SEQ ID NO:108

Stevia rebaudiana

MIQVLTPILL FLIFFVFWKV YKHQKTKINL PPGSFGWPFL GETLALLRAG WDSEPERFVR 60
ERIKKHGSPL VFKTSLFGDR FAVLCGPAGN KFLFCNENKL VASWWPVPVR KLFGKSLLTI 120
RGDEAKWMRK MLLSYLGPDA FATHYAVTMD VVTRRHIDVH WRGKEEVNVF QTVKLYAFEL 180
ACRLFMNLDD PNHIAKLGSL FNIFLKGIIE LPIDVPGTRF YSSKKAAAAI RIELKKLIKA 240
RKLELKEGKA SSSQDLLSHL LTSPDENGMF LTEEEIVDNI LLLLFAGHDT SALSITLLMK 300
TLGEHSDVYD KVLKEQLEIS KTKEAWESLK WEDIQKMKYS WSVICEVMRL NPPVIGTYRE 360
ALVDIDYAGY TIPKGWKLHW SAVSTQRDEA NFEDVTRFDP SRFEGAGPTP FTFVPFGGGP 420
RMCLGKEFAR LEVLAFLHNI VTNFKWDLLI PDEKIEYDPM ATPAKGLPIR LHPHQV 476

SEQ ID NO:109

Artificial Sequence

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tcactgaagc tacaaggtgt taaaggccca ccaccatcca tcttcaatgg taacgtctca 180
gaaatgcaac gtatccaatc cgaagctaaa cactgctctg gcgataacat tatctcacat 240
gattattctt cttcattatt cccacacttc gatcactgga gaaaacagta cggcagaatc 300
tacacatact ctactggatt aaagcaacac ttgtacatca atcatccaga aatggtgaag 360
gagctatctc agactaacac attgaacttg ggtagaatca cccatataac caaaagattg 420
aatcctatct taggtaacgg aatcataacc tctaatggtc ctcattgggc ccatcagcgt 480
agaattatcg cctacgagtt tactcatgat aagatcaagg gtatggttgg tttgatggtt 540
gagtctgcta tgcctatgtt gaataagtgg gaggagatgg taaagagagg cggagaaatg 600
ggatgcgaca taagagttga tgaggacttg aaagatgttt cagcagatgt gattgcaaaa 660
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cttacagcta tcacaaagag aagtgttcta ttcagattca acggattcac tgatatggtc 780
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ctgatgcaat tgattttgga aggggcaatg cgttcatgtg acggtaacct ttgggataaa 960
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gcaccaatcg tcgggagaga agcctctaaa gatatcagat tgggcgatct agttgttcct 1260
aaaggcgtct gtatatggac actaatacca gctttacaca gagatcctga gatttgggga 1320
ccagatgcaa acgatttcaa accagaaaga ttttctgaag gaatttcaaa ggcttgtaag 1380
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tctcctacct accaacatag tcctagtcac aaacttttag tagaaccaca acatggggtg 1560
gtaattagag tggtttaa 1578

SEQ ID NO:110
Arabidopsis thaliana
MESLVVHTVN AIWCIVIVGI FSVGYHVYGR AVVEQWRMRR SLKLQGVKGP PPSIFNGNVS 60
EMQRIQSEAK HCSGDNIISH DYSSSLFPHF DHWRKQYGRI YTYSTGLKQH LYINHPEMVK 120
ELSQTNTLNL GRITHITKRL NPILGNGIIT SNGPHWAHQR RIIAYEFTHD KIKGMVGLMV 180
ESAMPMLNKW EEMVKRGGEM GCDIRVDEDL KDVSADVIAK ACFGSSFSKG KAIFSMIRDL 240
LTAITKRSVL FRFNGFTDMV FGSKKHGDVD IDALEMELES SIWETVKERE IECKDTHKKD 300
LMQLILEGAM RSCDGNLWDK SAYRRFVVDN CKSIYFAGHD STAVSVSWCL MLLALNPSWQ 360
VKIRDEILSS CKNGIPDAES IPNLKTVTMV IQETMRLYPP APIVGREASK DIRLGDLVVP 420
KGVCIWTLIP ALHRDPEIWG PDANDFKPER FSEGISKACK YPQSYIPFGL GPRTCVGKNF 480
GMMEVKVLVS LIVSKFSFTL SPTYQHSPSH KLLVEPQHGV VIRVV 525

SEQ ID NO:111
Artificial Sequence
atgtacttcc tactacaata cctcaacatc acaaccgttg gtgtctttgc cacattgttt 60
ctctcttatt gtttacttct ctggagaagt agagcgggta acaaaaagat tgccccagaa 120
gctgccgctg catggcctat tatcggccac ctccacttac ttgcaggtgg atcccatcaa 180
ctaccacata ttacattggg taacatggca gataagtacg gtcctgtatt cacaatcaga 240
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gaagttgtca catctattaa ggaactatac aaattgtggg cggaaaagaa gaatgagtca 540
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SEQ ID NO:112
Vitis vinifera
MYFLLQYLNI TTVGVFATLF LSYCLLLWRS RAGNKKIAPE AAAAWPIIGH LHLLAGGSHQ 60
LPHITLGNMA DKYGPVFTIR IGLHRAVVVS SWEMAKECST ANDQVSSSRP ELLASKLLGY 120
NYAMFGFSPY GSYWREMRKI ISLELLSNSR LELLKDVRAS EVVTSIKELY KLWAEKKNES 180
GLVSVEMKQW FGDLTLNVIL RMVAGKRYFS ASDASENKQA QRCRRVFREF FHLSGLFVVA 240

DAIPFLGWLD WGRHEKTLKK TAIEMDSIAQ EWLEEHRRRK DSGDDNSTQD FMDVMQSVLD 300
GKNLGGYDAD TINKATCLTL ISGGSDTTVV SLTWALSLVL NNRDTLKKAQ EELDIQVGKE 360
RLVNEQDISK LVYLQAIVKE TLRLYPPGPL GGLRQFTEDC TLGGYHVSKG TRLIMNLSKI 420
QKDPRIWSDP TEFQPERFLT THKDVDPRGK HFEFIPFGAG RRACPGITFG LQVLHLTLAS 480
FLHAFEFSTP SNEQVNMRES LGLTNMKSTP LEVLISPRLS SCSLYN 526

SEQ ID NO:113
Artificial Sequence

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SEQ ID NO:114
Medicago truncatula

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KFIFDRMRKY SSELFKTSIV GESTVVCCGA ASNKFLFSNE NKLVTAWWPD SVNKIFPTTS 120
LDSNLKEESI KMRKLLPQFF KPEALQRYVG VMDVIAQRHF VTHWDNKNEI TVYPLAKRYT 180
FLLACRLFMS VEDENHVAKF SDPFQLIAAG IISLPIDLPG TPFNKAIKAS NFIRKELIKI 240
IKQRRVDLAE GTASPTQDIL SHMLLTSDEN GKSMNELNIA DKILGLLIGG HDTASVACTF 300
LVKYLGELPH IYDKVYQEQM EIAKSKPAGE LLNWDDLKKM KYSWNVACEV MRLSPPLQGG 360
FREAITDFMF NGFSIPKGWK LYWSANSTHK NAECFPMPEK FDPTRFEGNG PAPYTFVPFG 420
GGPRMCPGKE YARLEILVFM HNLVKRFKWE KVIPDEKIIV DPFPIPAKDL PIRLYPHKA 479

SEQ ID NO:115
Artificial Sequence

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gccttagcca actacatcgc ttacagacaa aactaa 1116

SEQ ID NO:116
Arabidopsis thaliana

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VLCIAACELV GGEESTAMPA ACAVEMIHTM SLIHDDLPCM DNDDLRRGKP TNHKVFGEDV 180
AVLAGDALLS FAFEHLASAT SSDVVSPVRV VRAVGELAKA IGTEGLVAGQ VVDISSEGLD 240
LNDVGLEHLE FIHLHKTAAL LEASAVLGAI VGGGSDDEIE RLRKFARCIG LLFQVVDDIL 300
DVTKSSKELG KTAGKDLIAD KLTYPKIMGL EKSREFAEKL NREARDQLLG FDSDKVAPLL 360
ALANYIAYRQ N 371

SEQ ID NO:117
Rubus suavissimus

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KILTADKCMV AISDYNDFHK MIKRYILSNV LGPSAQKRHR SNRDTLRANV CSRLHSQVKN 180
SPREAVNFRR VFEWELFGIA LKQAFGKDIE KPIYVEELGT TLSRDEIFKV LVLDIMEGAI 240
EVDWRDFFPY LRWIPNTRME TKIQRLYFRR KAVMTALINE QKKRIASGEE INCYIDFLLK 300
EGKTLTMDQI SMLLWETVIE TADTTMVTTE WAMYEVAKDS KRQDRLYQEI QKVCGSEMVT 360
EEYLSQLPYL NAVFHETLRK HSPAALVPLR YAHEDTQLGG YYIPAGTEIA INIYGCNMDK 420
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KLRDGEEENV DTVGLTTHKR YPMHAILKPR S 511

SEQ ID NO:126
Arabidopsis thaliana

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caagacataa tgcaattaga acaacccaag cgctag 1476

SEQ ID NO:127
Arabidopsis thaliana
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NCIIADMCLP YTNRIAKNLG IPKIIFHGMC CFNLLCTHIM HQNHEFLETI ESDKEYFPIP 180
NFPDRVEFTK SQLPMVLVAG DWKDFLDGMT EGDNTSYGVI VNTFEELEPA YVRDYKKVKA 240
GKIWSIGPVS LCNKLGEDQA ERGNKADIDQ DECIKWLDSK EEGSVLYVCL GSICNLPLSQ 300
LKELGLGLEE SQRPFIWVIR GWEKYNELLE WISESGYKER IKERGLLITG WSPQMLILTH 360
PAVGGFLTHC GWNSTLEGIT SGVPLLTWPL FGDQFCNEKL AVQILKAGVR AGVEESMRWG 420
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SEQ ID NO:132
Arabidopsis thaliana
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SEQ ID NO:133
Arabidopsis thaliana
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KPRPSCLISD WCLPYTSIIA KNFNIPKIVF HGMGCFNLLC MHVLRRNLEI LENVKSDEEY 180
FLVPSFPDRV EFTKLQLPVK ANASGDWKEI MDEMVKAEYT SYGVIVNTFQ ELEPPYVKDY 240
KEAMDGKVWS IGPVSLCNKA GADKAERGSK AAIDQDECLQ WLDSKEEGSV LYVCLGSICN 300
LPLSQLKELG LGLEESRRSF IWVIRGSEKY KELFEWMLES GFEERIKERG LLIKGWAPQV 360
LILSHPSVGG FLTHCGWNST LEGITSGIPL ITWPLFGDQF CNQKLVVQVL KAGVSAGVEE 420
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ITLLLQDIMQ LAQFKN 496

SEQ ID NO:134
Arabidopsis thaliana

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SEQ ID NO:135
Arabidopsis thaliana

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RPSCLISDFC LPYTSKIAKK FNIPKILFHG MGCFCLLCMH VLRKNREILD NLKSDKELFT     180
VPDFPDRVEF TRTQVPVETY VPAGDWKDIF DGMVEANETS YGVIVNSFQE LEPAYAKDYK     240
EVRSGKAWTI GPVSLCNKVG ADKAERGNKS DIDQDECLKW LDSKKHGSVL YVCLGSICNL     300
PLSQLKELGL GLEESQRPFI WVIRGWEKYK ELVEWFSESG FEDRIQDRGL LIKGWSPQML     360
ILSHPSVGGF LTHCGWNSTL EGITAGLPLL TWPLFADQFC NEKLVVEVLK AGVRSGVEQP     420
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SEQ ID NO:136
Arabidopsis thaliana

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gccattgagt ctggtttgcc catcaaccta gtgcaagtca agtttccata tcaagaagct     240
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actttcttgc tacaagacat aatgcaacta gcacagtcca ataattga 1488

SEQ ID NO:137

Arabidopsis thaliana

MAFEKNNEPF PLHFVLFPFM AQGHMIPMVD IARLLAQRGV LITIVTTPHN AARFKNVLNR 60
AIESGLPINL VQVKFPYQEA GLQEGQENMD LLTTMEQITS FFKAVNLLKE PVQNLIEEMS 120
PRPSCLISDM CLSYTSEIAK KFKIPKILFH GMGCFCLLCV NVLRKNREIL DNLKSDKEYF 180
IVPYFPDRVE FTRPQVPVET YVPAGWKEIL EDMVEADKTS YGVIVNSFQE LEPAYAKDFK 240
EARSGKAWTI GPVSLCNKVG VDKAERGNKS DIDQDECLEW LDSKEPGSVL YVCLGSICNL 300
PLSQLLELGL GLEESQRPFI WVIRGWEKYK ELVEWFSESG FEDRIQDRGL LIKGWSPQML 360
ILSHPSVGGF LTHCGWNSTL EGITAGLPML TWPLFADQFC NEKLVVQILK VGVSAEVKEV 420
MKWGEEEKIG VLVDKEGVKK AVEELMGESD DAKERRRRAK ELGESAHKAV EEGGSSHSNI 480
TFLLQDIMQL AQSNN 495

SEQ ID NO:138

Arabidopsis thaliana

atgtgttctc atgatcctct tcacttcgtc gtaataccct ttatggccca aggccatatg 60
atcccattgg tcgacatctc taggctcttg tcccagcgcc aaggcgtgac tgtctgcatc 120
atcacaacta ctcaaaatgt agccaagatc aagacttcac tctcattttc ctctttgttt 180
gcgactatca acatcgttga agttaagttt ctgtctcaac aaacgggttt gccagaaggg 240
tgcgagagtt tagatatgtt ggcttcaatg ggcgatatgg tgaagttctt tgatgctgcc 300
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cccaaactta tcttccatgg gttttcttgt ttcagcctca tgtctataca agtggttcga 480
gaaagcggga tcttgaaaat gatagaatca aacgacgagt attttgattt gcccggcttg 540
cctgacaaag ttgagttcac gaaacctcag gtctctgtgt tgcaacctgt tgaaggaaat 600
atgaaagaga gtacggccaa gattattgaa gctgataatg actcttatgg tgttattgtg 660
aacacttttg aagagttaga ggttgattat gcaagagaat ataggaaagc aagggctgga 720
aaagtttggt gcgttggacc tgtttccttg tgcaataggt tagggttaga caaagctaaa 780
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gatattatgg agcaatcaca aaatcaattc tag 1473

SEQ ID NO:139

Arabidopsis thaliana

MCSHDPLHFV VIPFMAQGHM IPLVDISRLL SQRQGVTVCI ITTTQNVAKI KTSLSFSSLF 60
ATINIVEVKF LSQQTGLPEG CESLDMLASM GDMVKFFDAA NSLEEQVEKA MEEMVQPRPS 120

CIIGDMSLPF TSRLAKKFKI PKLIFHGFSC FSLMSIQVVR ESGILKMIES NDEYFDLPGL 180
PDKVEFTKPQ VSVLQPVEGN MKESTAKIIE ADNDSYGVIV NTFEELEVDY AREYRKARAG 240
KVWCVGPVSL CNRLGLDKAK RGDKASIGQD QCLQWLDSQE TGSVLYVCLG SLCNLPLAQL 300
KELGLGLEAS NKPFIWVIRE WGKYGDLANW MQQSGFEERI KDRGLVIKGW APQVFILSHA 360
SIGGFLTHCG WNSTLEGITA GVPLLTWPLF AEQFLNEKLV VQILKAGLKI GVEKLMKYGK 420
EEEIGAMVSR ECVRKAVDEL MGDSEEAEER RRKVTELSDL ANKALEKGGS SDSNITLLIQ 480
DIMEQSQNQF 490

SEQ ID NO:140
Stevia rebaudiana
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gctcaaggcc atctggtacc catggtcgac atcgctcgaa tcttagccca acgtggtgca 120
acggtcacca taatcaccac accctaccat gccaaccggg tcagaccggt tatctcccga 180
gccatcgcga ccaatctcaa gatccagcta ctcgaactcc aactgcggtc aaccgaagcc 240
ggtttacccg aagggtgcga aagcttcgac caacttccgt cattcgagta ctggaaaaat 300
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ttaaaatggc tcgatgagag aaaactgggg tccgtgttat acgtttgttt aggtagcctt 900
gcacgcattt ctgccgcaca agcaatcgag ctcgggttag gactcgagtc cataaaccgt 960
ccctttatat ggtgcgtaag aaacgaaacc gatgagctca aaacatggtt tttggatggg 1020
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gaatcgatta ccgcgggtgt tccaatgatc acgtggccat tttttgcgga ccagtttttg 1200
aatgaagctt ttatagttga agttttgaag attggagtta ggattggtgt tgagagggct 1260
tgtttgtttg gggaagaaga taaggttgga gtgttggtga agaaggagga tgtgaagaag 1320
gctgttgaat gcttgatgga tgaagatgaa gatggtgatc agagaagaaa gagggtgatt 1380
gagcttgcaa aaatggcgaa gattgcaatg gcggaaggtg gatcttctta tgaaaatgta 1440
tcgtcgttga ttcgagatgt gactgaaaca gttagagcac cacattag 1488

SEQ ID NO:141
Stevia rebaudiana
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AIATNLKIQL LELQLRSTEA GLPEGCESFD QLPSFEYWKN ISTAIDLLQQ PAEDLLRELS 120
PPPDCIISDF LFPWTTDVAR RLNIPRLVFN GPGCFYLLCI HVAITSNILG ENEPVSSNTE 180
RVVLPGLPDR IEVTKLQIVG SSRPANVDEM GSWLRAVEAE KASFGIVVNT FEELEPEYVE 240
EYKTVKDKKM WCIGPVSLCN KTGPDLAERG NKAAITEHNC LKWLDERKLG SVLYVCLGSL 300
ARISAAQAIE LGLGLESINR PFIWCVRNET DELKTWFLDG FEERVRDRGL IVHGWAPQVL 360
ILSHPTIGGF LTHCGWNSTI ESITAGVPMI TWPFFADQFL NEAFIVEVLK IGVRIGVERA 420
CLFGEEDKVG VLVKKEDVKK AVECLMDEDE DGDQRRKRVI ELAKMAKIAM AEGGSSYENV 480
SSLIRDVTET VRAPH 495

SEQ ID NO:142
Arabidopsis thaliana
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accacttcct ccacccacaa ctccatcctc cgccgtgcca tcaccggcgg agccactgct 180
cttcctctct cttttgtccc cattgacgat ggattcgagg aagatcaccc atctacggac 240
acatctcccg actacttcgc aaagttccaa gaaaacgtat ctcgaagcct ctcagagctt 300
atctcctcga tggacccaaa accaaacgcc gtcgtttacg actcgtgcct gccttatgtc 360

ctcgacgttt gccggaaaca tcctggcgtt gctgcggcgt cgtttttcac tcagtcctcc 420
accgtgaacg cgacctatat tcatttcttg cgtggagagt ttaaggagtt tcaaaatgat 480
gtcgttttgc ctgcaatgcc tccgctgaag ggtaatgact taccggtgtt tctgtacgat 540
aacaatctct gccggccgtt gtttgagctc attagtagcc agttcgtgaa tgttgacgac 600
attgacttct tcttggttaa ctctttcgac gaactcgaag tcgaggtgct acaatggatg 660
aaaaaccaat ggccggtcaa gaacatagga ccgatgattc catcaatgta cttagacaaa 720
cgattagcag gtgacaaaga ctacggaatc aacctcttca atgcccaagt caacgaatgc 780
cttgattggc ttgactcaaa accgcccggt tcagtgatct acgtgtcttt tggaagcttg 840
gccgtcttaa aagacgatca aatgatagaa gtcgcggctg gtctaaaaca aactggccat 900
aacttcttat gggttgttag agaaactgaa acaaagaagc ttccaagcaa ttacatagag 960
gacatttgtg acaagggatt gatagtgaat tggagtcctc aattacaagt tcttgcacat 1020
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ttaggagttg ctttgatagg aatgccggct tatagcgacc agccgactaa tgctaagttt 1140
attgaagatg tgtggaaggt tggggttagg gttaaggcag atcaaaatgg gtttgttccg 1200
aaggaagaga ttgtgagatg tgttggagaa gttatggaag atatgtcgga gaaagggaag 1260
gagattagaa aaaatgctcg gaggttgatg gagtttgcaa gggaagcttt gtctgatgga 1320
ggaaattctg ataagaatat tgatgagttt gttgctaaaa ttgtgaggta a 1371

SEQ ID NO:143

Arabidopsis thaliana

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LPLSFVPIDD GFEEDHPSTD TSPDYFAKFQ ENVSRSLSEL ISSMDPKPNA VVYDSCLPYV 120
LDVCRKHPGV AAASFFTQSS TVNATYIHFL RGEFKEFQND VVLPAMPPLK GNDLPVFLYD 180
NNLCRPLFEL ISSQFVNVDD IDFFLVNSFD ELEVEVLQWM KNQWPVKNIG PMIPSMYLDK 240
RLAGDKDYGI NLFNAQVNEC LDWLDSKPPG SVIYVSFGSL AVLKDDQMIE VAAGLKQTGH 300
NFLWVVRETE TKKLPSNYIE DICDKGLIVN WSPQLQVLAH KSIGCFMTHC GWNSTLEALS 360
LGVALIGMPA YSDQPTNAKF IEDVWKVGVR VKADQNGFVP KEEIVRCVGE VMEDMSEKGK 420
EIRKNARRLM EFAREALSDG GNSDKNIDEF VAKIVR 456

SEQ ID NO:144

Arabidopsis thaliana

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ctccgttttg ctcgtcggct catcaaaaga accggcgcac gtgtcacttt cgtcacttgt 120
gtctccgtct tccacaactc catgatcgca aaccacaaca aagtcgaaaa tctctctttc 180
cttactttct ccgacggttt cgacgatgga ggcatttcca cctacgaaga ccgtcagaaa 240
aggtcggtga atctcaaggt taacggcgat aaggcactat cggatttcat cgaagctact 300
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aaagtagcac gtagatttca acttccctcc gctcttctct ggatccaacc ggctttggtt 420
ttcaacatct attacactca tttcatggga aacaagtccg ttttcgagtt acctaatctg 480
tcttctctgg aaatcagaga tcttccatct ttcctcacac cttccaacac aaacaaaggc 540
gcatacgatg cgtttcaaga aatgatggag tttctcataa aagaaaccaa accgaaaatt 600
ctcatcaaca ctttcgattc gctggaacca gaggccttaa cggctttccc gaatatcgat 660
atggtggcgg ttggtccttt acttcccacg gagattttct caggaagcac caacaaatca 720
gttaaagatc aaagtagtag ttatacactt tggctagact cgaaaacaga gtcctctgtt 780
atttacgttt cctttggaac aatggttgag ttgtccaaga aacagataga ggaactagcg 840
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gaaacgaaaa cagaaggaga agaagagaca gagattgaga agatagctgg attcagacac 960
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ctggaagaaa gttggaagac tggtgtgagg gtaagagaga acaaggatgg tttggtggag 1200
agaggagaga tcaggaggtg tttggaagcc gtgatggagg agaagtcggt ggagttgagg 1260
gaaaacgcaa agaaatggaa gcgtttagcg atggaagcgg gtagagaagg aggatcttcg 1320
gataagaaca tggaggcttt tgtggaggat atttgtggag aatctcttat tcaaaacttg 1380
tgtgaagcag aggaggtaaa agtacgctag 1410

SEQ ID NO:145
Arabidopsis thaliana

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LTFSDGFDDG GISTYEDRQK RSVNLKVNGD KALSDFIEAT KNGDSPVTCL IYTILLNWAP       120
KVARRFQLPS ALLWIQPALV FNIYYTHFMG NKSVFELPNL SSLEIRDLPS FLTPSNTNKG       180
AYDAFQEMME FLIKETKPKI LINTFDSLEP EALTAFPNID MVAVGPLLPT EIFSGSTNKS       240
VKDQSSSYTL WLDSKTESSV IYVSFGTMVE LSKKQIEELA RALIEGKRPF LWVITDKSNR       300
ETKTEGEEET EIEKIAGFRH ELEEVGMIVS WCSQIEVLSH RAVGCFVTHC GWSSTLESLV       360
LGVPVVAFPM WSDQPTNAKL LEESWKTGVR VRENKDGLVE RGEIRRCLEA VMEEKSVELR       420
ENAKKWKRLA MEAGREGGSS DKNMEAFVED ICGESLIQNL CEAEEVKVR                   469
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SEQ ID NO:146
Gardenia jasminoides

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gtttatgcct tgtccagaat gaagaagtca tctggttcta ctccaaaggg tttgactttt       180
gctactttct ctgatggtta cgatgatggt tttagaccta agggtgttga tcacaccgaa       240
tatatgtcat ctttggctaa gcaaggttcc aacactttga gaaacgttat taacacctct       300
gctgatcaag gttgtccagt tacttgtttg gtttacactt tgttgttgcc atgggctgct       360
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gatccaacct ggtccattca atttccaggt ttgccatcta tgaaggctaa agatttgcct       540
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caattggaaa ctttggacga agaagaaaga ccaaaggttt tggttaatac cttcgatgct       660
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tacgtttctt ttggttcctt gttgaccttg ccaaagcaac aaatggaaga aattgctaga       900
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gttccatggt gctcccaaat tgaagttttg actcatccat ctttgggttg cttcgttact      1080
cattgtggtt ggaatagtac tttggaaacc ttggtttgtg gtgttccagt tgttgcattt      1140
ccacattgga ccgatcaagg tactaatgcc aaattgattg aagatgtttg ggaaaccggt      1200
gttagagttg ttccaaatga agatggtact gtcgaatctg acgaaatcaa gagatgtatc      1260
gaaaccgtta tggatgatgg tgaaaaaggt gtcgaattga agagaaatgc caagaagtgg      1320
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SEQ ID NO:147
Gardenia jasminoides

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ATFSDGYDDG FRPKGVDHTE YMSSLAKQGS NTLRNVINTS ADQGCPVTCL VYTLLLPWAA       120
TVARECHIPS ALLWIQPVAV MDIYYYYFRG YEDDVKNNSN DPTWSIQFPG LPSMKAKDLP       180
SFILPSSDNI YSFALPTFKK QLETLDEEER PKVLVNTFDA LEPQALKAIE SYNLIAIGPL       240
TPSAFLDGKD PSETSFSGDL FQKSKDYKEW LNSRPAGSVV YVSFGSLLTL PKQQMEEIAR       300
GLLKSGRPFL WVIRAKENGE EEKEEDRLIC MEELEEQGMI VPWCSQIEVL THPSLGCFVT       360
HCGWNSTLET LVCGVPVVAF PHWTDQGTNA KLIEDVWETG VRVVPNEDGT VESDEIKRCI       420
ETVMDDGEKG VELKRNAKKW KELAREAMQE DGSSDKNLKA FVEDAGKGYQ AESN             474
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SEQ ID NO:152
Arabidopsis thaliana

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gttcagacta agttcaatta ctttagccct tcagatgact tcactcatga ttttcagttc       180
gtcaccattc cagaaagctt accagagtct gatttcaaga atctcggacc aatacagttt       240
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gctgcagcca aagagtgtaa gcttccaaac atcattttca gcacaacaag tgccacggct 420
ttcgcttgcc gctctgtatt tgacaaacta tatgcaaaca atgtccaagc tcccttgaaa 480
gaaactaaag gacaacaaga agagctagtt ccggagtttt atcccttgag atataaagac 540
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gacaaacgga cagcttcctc ggtgataatc aacactgcga gctgtctaga gagctcatct 660
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gtggtcgaga gagctgtgaa gaggttaatg gttgacgaag aaggagagga gatgaggaag 1260
agagctttca gtttaaaaga gcaacttaga gcctctgtta aaagtggagg ctcttcacac 1320
aactcgctag aagagtttgt acacttcata aggactgcct ag 1362

SEQ ID NO:153

Arabidopsis thaliana

MEEKPARRSV VLVPFPAQGH ISPMMQLAKT LHLKGFSITV VQTKFNYFSP SDDFTHDFQF 60
VTIPESLPES DFKNLGPIQF LFKLNKECKV SFKDCLGQLV LQQSNEISCV IYDEFMYFAE 120
AAAKECKLPN IIFSTTSATA FACRSVFDKL YANNVQAPLK ETKGQQEELV PEFYPLRYKD 180
FPVSRFASLE SIMEVYRNTV DKRTASSVII NTASCLESSS LSFLQQQQLQ IPVYPIGPLH 240
MVASAPTSLL EENKSCIEWL NKQKVNSVIY ISMGSIALME INEIMEVASG LAASNQHFLW 300
VIRPGSIPGS EWIESMPEEF SKMVLDRGYI VKWAPQKEVL SHPAVGGFWS HCGWNSTLES 360
IGQGVPMICR PFSGDQKVNA RYLECVWKIG IQVEGELDRG VVERAVKRLM VDEEGEEMRK 420
RAFSLKEQLR ASVKSGGSSH NSLEEFVHFI RTA 453

SEQ ID NO:168

Catharanthus roseus

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tacttctaca tttgtagtac tccaattaat ttggactcta ttaaaaataa gataaaccaa 180
aactattctt catccataca attggttgat ttgcatttgc caaacagtcc tcaattgcca 240
ccttctttac atactacaaa tggtttgcca cctcacttaa tgtctacatt gaaaaacgct 300
ttgatcgatg caaatccaga cttatgcaag attatagcct caattaaacc agatttgatc 360
atctatgact tacatcaacc ttggaccgaa gcattggctt ctagacacaa cattcctgct 420
gttagttttt ctactatgaa tgccgtatcc tttgcttacg ttatgcacat gttcatgaat 480
ccaggtatag aatttccttt caaagcaatc cacttatcag attttgaaca agccagattc 540
ttggaacaat tagaatcagc taagaacgat gcctccgcta aagacccaga attgcaaggt 600
agtaagggtt tctttaactc taccttcatt gttagaagtt ctagagaaat cgagggtaaa 660
tacgttgatt acttgtcaga aatcttaaag tccaaggtca ttccagtatg tcctgttata 720
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tgggtattga gattcccaaa gggtgaagat acaaaaattg aagaagtttt gcctgaaggt 960
ttcttggaca gagttaaaac caagggtaga attgtccacg gttgggcacc acaagccaga 1020
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aaattaaaga gagaaagaat cggtgaagtt atcaaggaag tcgctatagg taaaaagggt 1260
gaaaaattga gaaagacagc aaaagatttg ggtcaaaaat tgagagatag agaaaaacaa 1320
gactttgacg aattagcagc aactttgaaa caattatgcg tatga 1365

SEQ ID NO:169

Catharanthus roseus

MATEQQQASI SCKILMFPWL AFGHISSFLQ LAKKLSDRGF YFYICSTPIN LDSIKNKINQ 60
NYSSSIQLVD LHLPNSPQLP PSLHTTNGLP PHLMSTLKNA LIDANPDLCK IIASIKPDLI 120
IYDLHQPWTE ALASRHNIPA VSFSTMNAVS FAYVMHMFMN PGIEFPFKAI HLSDFEQARF 180
LEQLESAKND ASAKDPELQG SKGFFNSTFI VRSSREIEGK YVDYLSEILK SKVIPVCPVI 240
SLNNNDQGQG NKDEDEIIQW LDKKSHRSSV FVSFGSEYFL NMQEIEEIAI GLELSNVNFI 300
WVLRFPKGED TKIEEVLPEG FLDRVKTKGR IVHGWAPQAR ILGHPSIGGF VSHCGWNSVM 360
ESIQIGVPII AMPMNLDQPF NARLVVEIGV GIEVGRDENG KLKRERIGEV IKEVAIGKKG 420
EKLRKTAKDL GQKLRDREKQ DFDELAATLK QLCV 454

SEQ ID NO:172

Arabidopsis thaliana

atgaccaaat tctccgagcc aatcagagac tcccacgtgg cagttctcgc gtttttcccc 60
gttggcgctc atgccggtcc tctcttagcc gtcactcgcc gtctcgccgc cgcttctccc 120
tccaccatct tttctttctt caacaccgca agatcaaacg cgtcgttgtt ctcctctgat 180
catcccgaga acatcaaggt ccacgacgtc tctgacggtg ttccggaggg aaccatgctc 240
gggaatccac tggagatggt cgagctgttt ctcgaagcgg ctccacgtat tttccggagc 300
gaaatcgcgg cggcagagat agaagttgga aagaaagtga catgcatgct aacagatgcc 360
ttcttctggt tcgcagcgga catagcggct gagctgaacg cgacttgggt tgccttctgg 420
gccggcggag caaactcact ctgtgctcat ctctacactg atctcatcag agaaaccatc 480
ggtctcaaag atgtgagtat ggaagagaca ttagggttta taccaggaat ggagaattac 540
agagttaaag atataccaga ggaagttgta tttgaagatt tggactctgt tttcccaaag 600
gctttatacc aaatgagtct tgctttacct cgtgcctctg ctgttttcat cagttccttt 660
gaagagttag aacctacatt gaactataac ctaagatcca aacttaaacg tttcttgaac 720
atcgcccctc tcacgttatt atcttctaca tcggagaaag agatgcgtga tcctcatggc 780
tgctttgctt ggatggggaa gagatcagct gcttctgtag cgtacattag cttcggcacc 840
gtcatggaac ctcctcctga agagcttgtg gcgatagcac aagggttgga atcaagcaaa 900
gtgccgtttg tttggtcgct gaaggagaag aacatggttc atctaccaaa agggtttttg 960
gatcggacaa gagagcaagg gatagtggtt ccttgggctc cacaagtgga actgctgaaa 1020
cacgaggcaa tgggtgtgaa tgtgacacat tgtggatgga actcagtgtt ggagagtgtg 1080
tcggcaggtg taccgatgat cggcagaccg attttggcgg ataataggct caacggaaga 1140
gcagtggagg ttgtgtggaa ggttggagtg atgatggata atggagtctt cacgaaagaa 1200
ggatttgaga agtgtttgaa tgatgttttt gttcatgatg atggtaagac gatgaaggct 1260
aatgccaaga agcttaaaga aaaactccaa gaagatttct ccatgaaagg aagctcttta 1320
gagaatttca aaatattgtt ggacgaaatt gtgaaagttt ag 1362

SEQ ID NO:173

Arabidopsis thaliana

MTKFSEPIRD SHVAVLAFFP VGAHAGPLLA VTRRLAAASP STIFSFFNTA RSNASLFSSD 60
HPENIKVHDV SDGVPEGTML GNPLEMVELF LEAAPRIFRS EIAAAEIEVG KKVTCMLTDA 120
FFWFAADIAA ELNATWVAFW AGGANSLCAH LYTDLIRETI GLKDVSMEET LGFIPGMENY 180
RVKDIPEEVV FEDLDSVFPK ALYQMSLALP RASAVFISSF EELEPTLNYN LRSKLKRFLN 240
IAPLTLLSST SEKEMRDPHG CFAWMGKRSA ASVAYISFGT VMEPPPEELV AIAQGLESSK 300
VPFVWSLKEK NMVHLPKGFL DRTREQGIVV PWAPQVELLK HEAMGVNVTH CGWNSVLESV 360
SAGVPMIGRP ILADNRLNGR AVEVVWKVGV MMDNGVFTKE GFEKCLNDVF VHDDGKTMKA 420
NAKKLKEKLQ EDFSMKGSSL ENFKILLDEI VKV 453

SEQ ID NO:176

Streptomyces antibioticus

atgacttctg aacatagatc cgcttccgtt actccaagac atatttcatt cttcaacatc 60
ccaggtcatg gtcatgttaa tccatctttg ggtatcgttc aagaattggt tgctagaggt 120
cacagagttt cttacgctat taccgatgaa tttgctgctc aagttaaggc tgctggtgct 180
actccagttg tttatgattc catcttgcca aaagaatcca acccagaaga atcttggcca 240
gaagatcaag aatctgctat gggtttgttc ttggatgaag ctgttagagt cttgccacaa 300

ttagaagatg cttacgctga tgatagacca gatttgatcg tttacgatat tgcttcttgg 360
ccagctccag ttttgggtag aaaatgggat attccattcg tccaattatc cccaactttc 420
gttgcttacg aaggttttga agaagatgtt ccagcagttc aagatccaac tgctgataga 480
ggtgaagaag ctgctgctcc agcaggtact ggtgatgctg aagaaggtgc tgaagctgaa 540
gatggtttgg ttagattctt cactagattg tccgctttct tggaagaaca tggtgttgat 600
actccagcta ccgaattttt gattgctcca aacagatgca tcgttgcttt gccaagaact 660
tttcaaatca agggtgatac cgttggtgat aactacactt ttgttggtcc aacttacggt 720
gatagatctc atcaaggtac ttgggaaggt ccaggtgatg gtagaccagt tttgttgatt 780
gctttgggtt ctgctttcac tgatcacttg gatttctaca gaacctgttt gtctgctgtt 840
gatggtttgg attggcatgt tgttttgtct gttggtagat ttgttgatcc agcagatttg 900
ggtgaagttc caccaaatgt tgaagttcat caatgggttc cacaattaga tattttgacc 960
aaggcttccg ccttcattac tcatgctggt atgggttcta ctatggaagc cttgtctaat 1020
gctgttccaa tggttgctgt tccacaaatt gctgaacaaa ctatgaacgc cgaaagaata 1080
gtcgaattgg gtttgggtag acatatccca agagatcaag ttactgccga aaaattgaga 1140
gaagctgttt tggctgttgc ttctgatcca ggtgttgctg aaagattggc tgctgttaga 1200
caagaaatta gagaagccgg tggtgctaga gctgctgctg atattttgga aggtattttg 1260
gctgaagccg gttaa 1275

SEQ ID NO:177
Streptomyces antibioticus
MTSEHRSASV TPRHISFFNI PGHGHVNPSL GIVQELVARG HRVSYAITDE FAAQVKAAGA 60
TPVVYDSILP KESNPEESWP EDQESAMGLF LDEAVRVLPQ LEDAYADDRP DLIVYDIASW 120
PAPVLGRKWD IPFVQLSPTF VAYEGFEEDV PAVQDPTADR GEEAAAPAGT GDAEEGAEAE 180
DGLVRFFTRL SAFLEEHGVD TPATEFLIAP NRCIVALPRT FQIKGDTVGD NYTFVGPTYG 240
DRSHQGTWEG PGDGRPVLLI ALGSAFTDHL DFYRTCLSAV DGLDWHVVLS VGRFVDPADL 300
GEVPPNVEVH QWVPQLDILT KASAFITHAG MGSTMEALSN AVPMVAVPQI AEQTMNAERI 360
VELGLGRHIP RDQVTAEKLR EAVLAVASDP GVAERLAAVR QEIREAGGAR AAADILEGIL 420
AEAG 424

SEQ ID NO:180
Oryza sativa
atgaagcaaa ccgtcgtcct gtaccccggc ggcggcgtcg gccacgtcgt ccccatgctg 60
gagctcgcca aggtcttcgt caagcacggg cacgacgtca ccatggtgct gctggagccg 120
cccttcaagt cgtccgactc cggcgccctc gccgtcgagc gcctcgtcgc ctccaaccct 180
tccgtctcct tccacgtcct cccgccactc cccgcccccg acttcgccag cttcggcaag 240
cacccgttcc tcctcgtcat ccagctcctg cgccagtaca acgagcggct cgagagcttc 300
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gccatcgacg tgtgcgcaaa gctcggcgtg ccggtgtaca cgttcttcgc ctcgggcgtc 420
tcggtgctgt ccgtcttgac ccagctccca ccgtttcttg ccggtaggga gacgggcctg 480
aaggagcttg gcgacacgcc gcttgatttc ctcggtgttt cgccgatgcc ggcgtctcat 540
ctcgtcaagg aattgctcga gcatccggag gacgagttgt gcaaggccat ggtgaaccgc 600
tgggagcgca acacggaaac catgggcgtc ctggtgaact cgttcgaatc gttggagagc 660
cgggcggctc aggcgctcag ggacgacccg ctctgcgtcc caggcaaggt gctgcctccg 720
atctactgcg tcgggccttt ggtcggcggc ggcgcggagg aggcggccga gaggcacgag 780
tgcctcgtct ggctcgacgc tcagccggag cacagcgtcg tgttcctctg cttcgggagc 840
aagggcgtgt tctccgcgga gcagctcaag gagatcgccg tcggcttgga gaactccagg 900
caacggttca tgtgggtcgt gcgcacgccg ccgacaacca ccgaaggctt gaagaagtac 960
ttcgagcaac gcgcggcgcc ggacctcgac gcgctcttcc cggatgggtt cgtggagcgt 1020
accaaggacc gtggcttcat cgtcacgacg tgggcgccgc aggtggacgt gctccgccac 1080
cgggcgaccg gcgcgttcgt gacgcactgc gggtggaact cggcgctgga gggcatcacg 1140
gcgggggtgc cgatgctgtg ctggccgcag tacgcggagc agaagatgaa caaggtgttc 1200
atgacggcgg agatgggcgt cggggtggag ctggacgggt acaactcgga ctttgtcaaa 1260
gcggaggagt tggaggccaa ggtgaggctg gtgatggagt cggaggaagg gaagcagctc 1320
agggctcgtt cggctgcgcg gaagaaggag gcagaggcgg cgctggagga agggggctcg 1380
tcgcacgctg cgttcgtcca gttcctgtcc gatgtggaga atcttgtcca gaactaa 1437

SEQ ID NO:181

Oryza sativa

MKQTVVLYPG GGVGHVVPML ELAKVFVKHG HDVTMVLLEP PFKSSDSGAL AVERLVASNP 60
SVSFHVLPPL PAPDFASFGK HPFLLVIQLL RQYNERLESF LLSIPRQRLH SLVIDMFCVD 120
AIDVCAKLGV PVYTFFASGV SVLSVLTQLP PFLAGRETGL KELGDTPLDF LGVSPMPASH 180
LVKELLEHPE DELCKAMVNR WERNTETMGV LVNSFESLES RAAQALRDDP LCVPGKVLPP 240
IYCVGPLVGG GAEEAAERHE CLVWLDAQPE HSVVFLCFGS KGVFSAEQLK EIAVGLENSR 300
QRFMWVVRTP PTTTEGLKKY FEQRAAPDLD ALFPDGFVER TKDRGFIVTT WAPQVDVLRH 360
RATGAFVTHC GWNSALEGIT AGVPMLCWPQ YAEQKMNKVF MTAEMGVGVE LDGYNSDFVK 420
AEELEAKVRL VMESEEGKQL RARSAARKKE AEAALEEGGS SHAAFVQFLS DVENLVQN 478

SEQ ID NO:182

Nicotiana tabacum

atgactactc aaaaagctca ttgcttgatc ttaccatatc cagctcaggg tcatatcaac 60
cctatgctcc aattctccaa acgtttgcaa tccaaaggtg tcaaaatcac tatagcagcc 120
accaaatcat tcttgaaaac catgcaagaa ttgtcaactt ctgtgtcagt cgaggctatc 180
tccgatggct atgatgatgg cggacgcgag caagctggaa cctttgtggc ctatattaca 240
agattcaaag aagttggctc ggatactttg tctcagctta ttggaaagtt aacaaattgt 300
ggttgtcctg tgagttgcat agtttacgat ccatttcttc cttgggctgt tgaagtggga 360
aataattttg gagtagctac tgctgctttt ttcactcaat cttgtgcagt ggataacatt 420
tattaccatg tacataaagg ggttctaaaa cttcctccaa ctgacgttga taaagaaatc 480
tcaattcctg gattattaac aattgaggca tcagatgtac ctagttttgt ttctaatcct 540
gaatcttcaa gaatacttga aatgttggtg aatcagttct cgaatcttga gaacacagat 600
tgggtcctaa tcaacagttt ctatgaattg gagaaagagg taattgattg gatggccaag 660
atctatccaa tcaagacaat tggaccaact ataccatcaa tgtacctaga caagaggcta 720
ccagatgaca aagaatatgg ccttagtgtc ttcaagccaa tgacaaatgc atgcctaaac 780
tggttaaacc atcaaccagt tagctcagta gtatatgtat catttggaag tttagccaaa 840
ttagaagcag agcaaatgga agaattagca tggggtttga gtaatagcaa caagaacttc 900
ttgtgggtag ttagatccac tgaagaatcc aaacttccca acaacttttt agaggaatta 960
gcaagtgaaa aaggattagt cgtgtcatgg tgtccacaat tacaagtctt ggaacataaa 1020
tcaatagggt gttttctcac gcactgtggc tggaattcaa ctttggaagc aattagtttg 1080
ggagtaccaa tgattgcaat gccacattgg tcagaccagc caacaaatgc gaagcttgtg 1140
gaagatgttt gggagatggg aattagacca aaacaagatg aaaaaggatt agttagaaga 1200
gaagttattg aagaatgtat taagatagtg atggaggaaa agaaaggaaa aaagattagg 1260
gaaaatgcaa agaaatggaa ggaattggct aggaaagctg tggatgaagg aggaagttca 1320
gatagaaata ttgaagaatt tgtttccaag ttggtgacta ttgcctcagt ggaaagctaa 1380

SEQ ID NO:183

Nicotiana tabacum

MTTQKAHCLI LPYPAQGHIN PMLQFSKRLQ SKGVKITIAA TKSFLKTMQE LSTSVSVEAI 60
SDGYDDGGRE QAGTFVAYIT RFKEVGSDTL SQLIGKLTNC GCPVSCIVYD PFLPWAVEVG 120
NNFGVATAAF FTQSCAVDNI YYHVHKGVLK LPPTDVDKEI SIPGLLTIEA SDVPSFVSNP 180
ESSRILEMLV NQFSNLENTD WVLINSFYEL EKEVIDWMAK IYPIKTIGPT IPSMYLDKRL 240
PDDKEYGLSV FKPMTNACLN WLNHQPVSSV VYVSFGSLAK LEAEQMEELA WGLSNSNKNF 300
LWVVRSTEES KLPNNFLEEL ASEKGLVVSW CPQLQVLEHK SIGCFLTHCG WNSTLEAISL 360
GVPMIAMPHW SDQPTNAKLV EDVWEMGIRP KQDEKGLVRR EVIEECIKIV MEEKKGKKIR 420
ENAKKWKELA RKAVDEGGSS DRNIEEFVSK LVTIASVES 459

SEQ ID NO:184

Siraitia grosvenorii

atggagaaag gcgatacgca tattctagtg tttcctttcc cttcacaagg ccacataaac 60
cctcttcttc aactatcgaa gcgcctaatc gccaagggaa tcaaggtttc gctggtcaca 120
accttacatg ttagcaatca cttgcagttg cagggtgctt attccaactc cgtgaagatc 180
gaagtcattt ccgatggctc tgaggatcgt ctggaaaccg atactatgcg ccaaactctg 240
gatcgatttc ggcagaagat gacgaagaac ttggaagatt tcttgcagaa agccatggtt 300
tcttcaaatc cgcctaaatt cattctgtat gattcgacaa tgccgtgggt tttggaggtc 360

gccaaggagt tcggactcga tagggccccg ttctacactc agtcttgtgc gcttaacagt 420
atcaattatc atgttcttca tggtcaattg aagcttcctc ctgaaacccc cacgatttcg 480
ttgccttcta tgcctctgct tcgccccagc gatctcccgg cttatgattt tgatcctgcc 540
tccactgaca ccatcatcga tcttcttacc agtcagtatt ctaatatcca ggatgcaaat 600
ctgcttttct gcaacacttt tgacaagttg gaaggcgaga ttatccaatg gatggagacc 660
ctgggtcgcc ctgtgaaaac cgtaggacca actgttccat cagcctactt agacaaaagg 720
gtagagaacg acaagcacta tgggctgagt ctgttcaagc ccaacgagga cgtctgcctc 780
aaatggcttg atagcaagcc ctctggttct gttctgtatg tgtcttatgg cagtttggtt 840
gaaatggggg aagagcagct gaaggagttg gctctgggaa tcaaggaaac tggcaagttc 900
ttcttgtggg tggtgagaga cactgaagca gagaagcttc ctcccaactt tgtggagagt 960
gtggcagaga aggggcttgt ggtcagctgg tgctcccagc tggaggtatt ggctcacccc 1020
tccgtcggct gcttcttcac gcactgtggc tggaactcga cgcttgaggc gctgtgcttg 1080
ggcgtcccgg tggtcgcttt cccacagtgg gctgatcagg taaccaatgc aaagttttta 1140
gaagatgttt ggaaggttgg gaagagggtg aagcggaatg agcagaggct ggcaagtaaa 1200
gaagaagtaa ggagttgcat ttgggaagtg atggagggag agagagccag cgagttcaag 1260
agcaactcca tggagtggaa gaagtgggca aaagaagctg tggatgaagg tgggagctct 1320
gataagaaca ttgaggagtt tgtggctatg ctcaagcaaa cttga 1365

SEQ ID NO:185

Siraitia grosvenorii

MEKGDTHILV FPFPSQGHIN PLLQLSKRLI AKGIKVSLVT TLHVSNHLQL QGAYSNSVKI 60
EVISDGSEDR LETDTMRQTL DRFRQKMTKN LEDFLQKAMV SSNPPKFILY DSTMPWVLEV 120
AKEFGLDRAP FYTQSCALNS INYHVLHGQL KLPPETPTIS LPSMPLLRPS DLPAYDFDPA 180
STDTIIDLLT SQYSNIQDAN LLFCNTFDKL EGEIIQWMET LGRPVKTVGP TVPSAYLDKR 240
VENDKHYGLS LFKPNEDVCL KWLDSKPSGS VLYVSYGSLV EMGEEQLKEL ALGIKETGKF 300
FLWVVRDTEA EKLPPNFVES VAEKGLVVSW CSQLEVLAHP SVGCFFTHCG WNSTLEALCL 360
GVPVVAFPQW ADQVTNAKFL EDVWKVGKRV KRNEQRLASK EEVRSCIWEV MEGERASEFK 420
SNSMEWKKWA KEAVDEGGSS DKNIEEFVAM LKQT 454

SEQ ID NO:198

Crocus sativus

atggggtcag aagataggtc cttgtccatc ttattctttc cttttatggc acaaggtcac 60
atgttaccta tgctagatat ggctaagtta tttgctctgt atggtgtcaa atcaacagta 120
gtgaccactc cagctaatgt accaatagtc aactcagtaa ttgatcagcc tgatgtttct 180
actttgcacc caatccaatt acgactgata ccatttccat ctgacacggg cttgcctgaa 240
ggttgtgaaa acgtatcatc aattcctcca agagacatgc caactgttca tgtcactttc 300
ttcagcgcta cagcaaaact tagagaacct tttggtaagg tgctagagga tctaagacca 360
gattgtattg ttactgacat gtttttccct tggacctacg atgtggccgc agaattaggt 420
atcccaagga ttgttttcca tgggacaaat ttcttttctc tctgcgtaac agattctctt 480
gaaagatata aaccagttga aaacttgcga agtgatgccg agtctgtagt gatcccagga 540
ctcccacaca gaatcgaggt attgcgttct caaataccag aatacgaaaa atcaaaagca 600
gattttgtta gagaagttag ggaatcagaa tctaagtctt acggagcggt ggttaattct 660
ttctttgaat tggaacctga ctacgctaga cattacagag aggttgtcgg cagacgtgct 720
tggcatatcg ggccacttgc tctggtcaat aactctacta cagacaaaag ctcaagagga 780
tacaagacag cgatcgatag aaacgattgt ttgaaatggc tcgattctaa aagactaaga 840
tccgttgtat atgtgtgctt tggctcaatg tctgactttt ccgatgccca attacgtgaa 900
atggcaagtg gtctagaggc atccaatcat cctttcattt gggtggttag aaaatctggc 960
aaggaatggt taccagaagg atttgaggaa agagtccagg agagaggttt gattatcaga 1020
ggctgggctc cacaaatctt aatactcaac catagagcag tgggaggctt catgacccat 1080
tgtgggtgga atagtagttt ggaagcagtt tctgccggac tgcctcttgt tacatggcct 1140
ctatttgcag aacaatttta caatgaaaga ttcatggttg atgttttgag aattggtgta 1200
tcagtgggtg cgaagagaca cggtatgaaa gccgaagaga gagaagtcgt agaagccaaa 1260
atggttaagg aagctgttga tggcttgatg gacgacggtg aagaggctga gggtagaagg 1320
cgtagagcta gagaactggg cgaaaaagct agaaaggccg tcgaaaaagg tggttcatcc 1380
tacgaggaca tgagaaatct tttgcaagag cttaagggtg atagcaagtt aactgtcgga 1440
tgctaa 1446

SEQ ID NO:199

Crocus sativus

MGSEDRSLSI LFFPFMAQGH MLPMLDMAKL FALYGVKSTV VTTPANVPIV NSVIDQPDVS 60
TLHPIQLRLI PFPSDTGLPE GCENVSSIPP RDMPTVHVTF FSATAKLREP FGKVLEDLRP 120
DCIVTDMFFP WTYDVAAELG IPRIVFHGTN FFSLCVTDSL ERYKPVENLR SDAESVVIPG 180
LPHRIEVLRS QIPEYEKSKA DFVREVRESE SKSYGAVVNS FFELEPDYAR HYREVVGRRA 240
WHIGPLALVN NSTTDKSSRG YKTAIDRNDC LKWLDSKRLR SVVYVCFGSM SDFSDAQLRE 300
MASGLEASNH PFIWVVRKSG KEWLPEGFEE RVQERGLIIR GWAPQILILN HRAVGGFMTH 360
CGWNSSLEAV SAGLPLVTWP LFAEQFYNER FMVDVLRIGV SVGAKRHGMK AEEREVVEAK 420
MVKEAVDGLM DDGEEAEGRR RRARELGEKA RKAVEKGGSS YEDMRNLLQE LKGDSKLTVG 480
C 481

SEQ ID NO:200

Crocus sativus

atggaggctg gaggtgacaa acttcacatt gttgtctttc catggttagc ttttggccac 60
atgttgccat ttctagagct gtctaagtct ttggctaaaa gaggtcactt aatcagtttt 120
gtttctacac ctaaaaacat tcaaagattt cctaatcttc caccacaaat ctcaccactt 180
atcaacttta tcccattaag tctacctaaa gtggagggca tgccaggtga cgtagaagct 240
accacagacc taccacctgc caacctacaa tatctgaaaa aggcacttga cgggttagaa 300
caacctttca gatcattcct aagagaggcc tccccaaaac ctgattggat aatccaagat 360
cttttacaac attggatacc tccaattgcc gcagaacttc atgttccttc catgtacttt 420
ggcacagtgc cagctgccgc cttgaccttt ttcggtcatc catcacaact tagttcaaga 480
gggaagggat tggaaggctg gctggcttca ccaccatggg ttccattccc atctaaggtg 540
gcatacagat tgcacgaact aatcgttatg gctaaagatg ccgctggtcc attgcattcc 600
ggtatgactg atgctagaag gatggaagct gcaatagttg gatgctgtgc agtcgctatt 660
agaacatgta gagaattgga atcagaatgg ttacctattc tggaggagat ctacggaaag 720
cctgtgatac cagttggatt acttttacct actgctgatg aatctactga tggaaactct 780
atcatagact ggttaggcac aagatcccag gaatcagtag tgtacattgc tctgggttca 840
gaagtttcta ttggtgtgga attgatacat gaattggcct tgggtcttga attagcaggt 900
ttgccattcc tatgggcact acgtagacct tatggactgt ctagtgatac tgagattttg 960
cctggtggat tcgaggagag aactagaggc tatggaaagg tagtcatggg ctgggttcct 1020
caaatgagag tcttggcaga tcgttctgta ggcggctttg tcacacactg tggttggtca 1080
tctgtagttg aatcattaca ttttgggcat ccactagttt tactgccaat cttcggtgac 1140
caaggattga atgcaagatt gctggaggaa aagggaattg gggtcgaagt agaaaggaag 1200
ggtgatgggt cttttacccg taatgaagtt gcaaaagcaa tcaatttgat catggtcgaa 1260
ggtgacggtt ctggttcctc ctacaggaaa aaggcaaagg aaatgaaaaa gattttcgct 1320
gataaggaat gccaggagaa atacgtggat gaatttgtgc agttcctgtt atcaaatggt 1380
actgctaaag gctaa 1395

SEQ ID NO:201

Crocus sativus

MEAGGDKLHI VVFPWLAFGH MLPFLELSKS LAKRGHLISF VSTPKNIQRF PNLPPQISPL 60
INFIPLSLPK VEGMPGDVEA TTDLPPANLQ YLKKALDGLE QPFRSFLREA SPKPDWIIQD 120
LLQHWIPPIA AELHVPSMYF GTVPAAALTF FGHPSQLSSR GKGLEGWLAS PPWVPFPSKV 180
AYRLHELIVM AKDAAGPLHS GMTDARRMEA AIVGCCAVAI RTCRELESEW LPILEEIYGK 240
PVIPVGLLLP TADESTDGNS IIDWLGTRSQ ESVVYIALGS EVSIGVELIH ELALGLELAG 300
LPFLWALRRP YGLSSDTEIL PGGFEERTRG YGKVVMGWVP QMRVLADRSV GGFVTHCGWS 360
SVVESLHFGH PLVLLPIFGD QGLNARLLEE KGIGVEVERK GDGSFTRNEV AKAINLIMVE 420
GDGSGSSYRK KAKEMKKIFA DKECQEKYVD EFVQFLLSNG TAKG 464

SEQ ID NO:202

Arabidopsis thaliana

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accactttta tcttcaacac aatccacctc gacccatcta gtcctatctc catagccaca 180

atctccgatg gctatgacca gggagggttc tcatcagccg gttctgtccc ggagtaccta 240
caaaacttca aaaccttcgg ctccaaaacc gtcgctgata tcatccgcaa acaccagagt 300
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agcatcaagg aagtgatgga aggagagaag agcaaagaga tgaaagagaa tgcgggaaaa 1260
tggagagact tggctgtgaa gtcactcagt gaaggaggtt ctacagatat caacattaac 1320
gaatttgtat caaaaattca aatcaaataa 1350

SEQ ID NO:203
Arabidopsis thaliana

MEKMRGHVLA VPFPSQGHIT PIRQFCKRLH SKGFKTTHTL TTFIFNTIHL DPSSPISIAT 60
ISDGYDQGGF SSAGSVPEYL QNFKTFGSKT VADIIRKHQS TDNPITCIVY DSFMPWALDL 120
AMDFGLAAAP FFTQSCAVNY INYLSYINNG SLTLPIKDLP LLELQDLPTF VTPTGSHLAY 180
FEMVLQQFTN FDKADFVLVN SFHDLDLHEE ELLSKVCPVL TIGPTVPSMY LDQQIKSDND 240
YDLNLFDLKE AALCTDWLDK RPEGSVVYIA FGSMAKLSSE QMEEIASAIS NFSYLWVVRA 300
SEESKLPPGF LETVDKDKSL VLKWSPQLQV LSNKAIGCFM THCGWNSTME GLSLGVPMVA 360
MPQWTDQPMN AKYIQDVWKV GVRVKAEKES GICKREEIEF SIKEVMEGEK SKEMKENAGK 420
WRDLAVKSLS EGGSTDININ EFVSKIQIK 449

SEQ ID NO:204
Arabidopsis thaliana

atggccaaca acaattccaa ctctcccacc ggtccacact ttctattcgt aacatttcca 60
gcccaaggtc acatcaaccc atctctcgag ctagccaaac gcctcgccgg aacaatctct 120
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atgagacgac gtggcaaaga gacactaacc gaactaatcg aagataaccg gaaacaaaac 360
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gagtttcatc ttccttctgc tcttctttgg gtccaaccag taacagtctt ctccattttt 480
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aaagcgttga tacaaagtcg gagaccattc ttgtgggtga ttacggataa gtcgtacaga 960
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gttccggtgg tggcgtttcc gcaatggaat gatcagatga tgaacgcgaa gcttttagaa 1200
gattgttgga aaacaggtgt aagagtgatg gagaagaagg aagaagaagg agttgtggtg 1260
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tcttccttta atcatctcaa agcttttgtc gatgagcaca tctag 1425

SEQ ID NO:205
Arabidopsis thaliana
MANNNSNSPT GPHFLFVTFP AQGHINPSLE LAKRLAGTIS GARVTFAASI SAYNRRMFST 60
ENVPETLIFA TYSDGHDDGF KSSAYSDKSR QDATGNFMSE MRRRGKETLT ELIEDNRKQN 120
RPFTCVVYTI LLTWVAELAR EFHLPSALLW VQPVTVFSIF YHYFNGYEDA ISEMANTPSS 180
SIKLPSLPLL TVRDIPSFIV SSNVYAFLLP AFREQIDSLK EEINPKILIN TFQELEPEAM 240
SSVPDNFKIV PVGPLLTLRT DFSSRGEYIE WLDTKADSSV LYVSFGTLAV LSKKQLVELC 300
KALIQSRRPF LWVITDKSYR NKEDEQEKEE DCISSFREEL DEIGMVVSWC DQFRVLNHRS 360
IGCFVTHCGW NSTLESLVSG VPVVAFPQWN DQMMNAKLLE DCWKTGVRVM EKKEEEGVVV 420
VDSEEIRRCI EEVMEDKAEE FRGNATRWKD LAAEAVREGG SSFNHLKAFV DEHI 474

SEQ ID NO:206
Arabidopsis thaliana
atgggaagta atgagggtca agaaacacat gtcctaatgg tagcattagc attccaaggt 60
catctcaatc caatgctcaa attcgcaaaa catctcgcac gaaccaatct acacttcact 120
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ccggtggacc tcgctttctt ctcagacggt ctacctaaag acgatccaag agatcccgac 240
actctcgcaa agtcattgaa aaaagatgga gccaagaact tgtcaaaaat catcgaagaa 300
aagagatttg attgcatcat ctctgtgcct tttactccct gggttccagc tgttgcagct 360
gcacataaca ttccttgtgc aatcctctgg atccaagctt gtggagcttt ttctgtttat 420
taccgttatt acatgaagac aaatcctttc cccgaccttg aagatctgaa tcaaacagtg 480
gagttaccag ctttaccatt gttggaagtc cgagatctcc cgtcattgat gttaccttct 540
caaggagcta atgtcaatac cctaatggcg gaatttgcag attgtttgaa agatgtgaaa 600
tgggttttgg ttaactcgtt ttacgaactc gaatcagaga tcatcgagtc tatgtctgat 660
ttaaaaccta taatcccaat tggtcctctt gtttctccat tcctgttggg aaatgatgaa 720
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gctaggtctt cagttgttta catatctttc ggaagcatac tcaaatcatt ggagaatcaa 840
gttgagacca tagcaacggc attaaaaaac agaggagttc catttctttg ggtgatacgg 900
ccgaaggaga aaggcgaaaa cgtccaggtt ttgcaggaga tggttaaaga aggtaaaggg 960
gttgtaactg aatggggtca acaagaaaag atattgagcc acatggcgat ttcttgcttc 1020
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gcgtatccga cttggataga tcagccgctt gatgcgagac tgcttgtgga tgtgtttgga 1140
atcggagtaa ggatgaagaa cgacgctatc gatggagagc ttaaggttgc agaggtggag 1200
agatgcattg aggccgtgac agagggacct gccgccgcgg atatgaggag gagagcgacg 1260
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gactcgttca ttagtgatat cccaatcact tga 1353

SEQ ID NO:207
Arabidopsis thaliana
MGSNEGQETH VLMVALAFQG HLNPMLKFAK HLARTNLHFT LATTEQARDL LSSTADEPHR 60
PVDLAFFSDG LPKDDPRDPD TLAKSLKKDG AKNLSKIIEE KRFDCIISVP FTPWVPAVAA 120
AHNIPCAILW IQACGAFSVY YRYYMKTNPF PDLEDLNQTV ELPALPLLEV RDLPSLMLPS 180
QGANVNTLMA EFADCLKDVK WVLVNSFYEL ESEIIESMSD LKPIIPIGPL VSPFLLGNDE 240
EKTLDMWKVD DYCMEWLDKQ ARSSVVYISF GSILKSLENQ VETIATALKN RGVPFLWVIR 300
PKEKGENVQV LQEMVKEGKG VVTEWGQQEK ILSHMAISCF ITHCGWNSTI ETVVTGVPVV 360
AYPTWIDQPL DARLLVDVFG IGVRMKNDAI DGELKVAEVE RCIEAVTEGP AAADMRRRAT 420
ELKHAARSAM SPGGSSAQNL DSFISDIPIT 450

SEQ ID NO:208
Catharanthus roseus
atggttaatc agctccatat tttcaacttc ccattcatgg cacagggcca tatgttaccc 60
gccttagaca tggccaatct attcacttct cgtggagtca aagtaacatt aatcacaacc 120
catcaacatg ttcccatgtt tacaaaatcc atagaaagga gcagaaattc tggatttgat 180

atatccattc aatccatcaa attcccagct tcagaagttg gtttacctga aggaatcgaa 240
agtctagatc aagtttcagg ggacgacgaa atgcttccta agttcatgag aggagttaat 300
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gagatgagaa acagagcaaa agatttgaag gaaaaggcaa gaaaagcttt ggaagaagat 1380
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gttgaaagaa agcaacaaga ctag 1464

SEQ ID NO:209

Catharanthus roseus

MVNQLHIFNF PFMAQGHMLP ALDMANLFTS RGVKVTLITT HQHVPMFTKS IERSRNSGFD 60
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DMFFPWTTES AAKFGIPRLL FHGSCSFALS AAESVRRNKP FENVSTDTEE FVVPDLPHQI 180
KLTRTQISTY ERENIESDFT KMLKKVRDSE STSYGVVVNS FYELEPDYAD YYINVLGRKA 240
WHIGPFLLCN KSRAEDKAQR GKKSAIDADE CLNWLDSKQP NSVIYLCFGS MANLNSAQLH 300
EIATALESSG QNFIWVVRKC VDEENSSKWF PEGFEERTKE KGLIIKGWAP QTLILEHESV 360
GAFVTHCGWN STLEGICAGV PLVTWPFFAE QFFNEKLITE VLKTGYGVGA RQWSRVSTEI 420
IKGEAIANAI NRVMVGDEAV EMRNRAKDLK EKARKALEED GSSYRDLTAL IEELGAYRSQ 480
VERKQQD 487

SEQ ID NO:210

Solanum lycopersicum

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acaaaatcct gtttgaaaac aatgcaagaa ttgtcaactt cagtatcaat cgaggcgatt 180
tctgatggct acgatgatgg tggtttccat caagcagaaa atttcgtagc ctacataaca 240
cgattcaaag aagttggttc ggatactctg tctcagctta ttaaaaaatt ggaaaatagt 300
gattgtcctg taaattgcat agtatatgat ccattcattc cttgggctgt tgaagttgca 360
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gattatgttc taatcaatag cttctatgag ttggagaaag aggtaaatga atggatgtca 660
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gtgaaagatg tttgggaaat aggtgttaga gccaaacaag atgaaaaagg ggtagttaga 1200
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agagaaaatg caaagaaatg gaaggaaata gctagaaatg ttgtgaatga aggaggaagt 1320
tcagataaaa acattgaaga atttgtttcc aagttggtta ctatttccta a 1371

SEQ ID NO:211
Solanum lycopersicum
MTTHKAHCLI LPFPGQGHIN PMLQFSKRLQ SKRVKITIAL TKSCLKTMQE LSTSVSIEAI 60
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KQFGLISAAF FTQNCVVDNL YYHVHKGVIK LPPTQNDEEI LIPGFPNSID ASDVPSFVIS 180
PEAERIVEML ANQFSNLDKV DYVLINSFYE LEKEVNEWMS KIYPIKTIGP TIPSMYLDKR 240
LHDDKEYGLS VFKPMTNECL NWLNHQPISS VVYVSFGSIT KLGDEQMEEL AWGLKNSNKS 300
FLWVVRSTEE PKLPNNFIEE LTSEKGLVVS WCPQLQVLEH ESTGCFLTHC GWNSTLEAIS 360
LGVPMVAMPQ WSDQPTNAKL VKDVWEIGVR AKQDEKGVVR REVIEECIKL VMEEDKGKLI 420
RENAKKWKEI ARNVVNEGGS SDKNIEEFVS KLVTIS 456

SEQ ID NO:212
Artificial Sequence
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ggtcacaaag tctcgtttct ttctaccacc agaaacattc aacgtctctc ttctcatatc 180
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gcagaggcga ccactgacgt ccaccctgaa gatattccat atctcaagaa ggcttctgat 300
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gagataccaa gaaatgagga agatggttgc ttgaccaagg agtcggttgc tagatcactg 1260
aggtccgttg ttgtggaaaa agaaggggag atctacaagg cgaacgcgag ggagctgagt 1320
aaaatctata acgacactaa ggttgaaaaa gaatatgtaa gccaattcgt agactatttg 1380
gaaaagaatg cgcgtgcggt tgccatcgat catgagagtt aa 1422

SEQ ID NO:213
Stevia rebaudiana
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acaacacttg ttaccaccat ccacacctta aactcaaccc taaaccacag taacaccacc 180
accacctcca tcgaaatcca agcaatttcc gatggttgtg atgaaggcgg ttttatgagt 240
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gatagtgatg tcaacttctt gtgggttatc aaacataaag aagagggaaa gctcccagaa 960
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catgaaggtg gtagctcaga caatgatatt gtcgaatttg taagtgagct aattaaggct 1380
taa 1383

WHAT IS CLAIMED IS:

1. A recombinant host cell capable of producing one or more steviol glycosides and/or glycosylated steviol precursors, or a composition thereof, comprising:

(a) a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position;

(b) a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position;

(c) a gene encoding a polypeptide capable of beta-1,2-glycosylation of the C2' and/or beta-1,3-glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside; and/or

(d) a gene encoding a polypeptide capable of glycosylating a steviol precursor at its C-19 carboxyl or C-19 hydroxyl position;

wherein at least one of the genes is a recombinant gene.

2. The recombinant host cell of claim 1, wherein:

(a) the polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position is a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73E1 polypeptide, a UGT75B1 polypeptide, a UGT75L6 polypeptide, a OleI polypeptide, a UGT5 polypeptide, a SA Gtase polypeptide, a UDPG1 polypeptide, a UN1671 polypeptide, a UGT74F1 polypeptide, a UGT84B2 polypeptide, and/or a UGT74F2-like UGT polypeptide;

(b) the polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position is a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73C7 polypeptide, a UGT73E1 polypeptide, and/or a UGT76E12 polypeptide;

(c) the polypeptide capable of beta-1,2-glycosylation of the C2' and/or beta-1,3-glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside is a UGT73C6 polypeptide, a CaUGT3 polypeptide, a UN32491 polypeptide, and/or a UN1671 polypeptide; and/or

(d) the polypeptide capable of glycosylating a steviol precursor at its C-19 carboxyl or C-19 hydroxyl position is a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73E1 polypeptide, a UGT74D1 polypeptide, a UGT75B1 polypeptide, a UGT75L6 polypeptide, a UGT76E12 polypeptide, a OleI polypeptide, a UGT5 polypeptide, a SA Gtase, a UDPG1 polypeptide, a UGT74F1 polypeptide, a UGT75D1 polypeptide, a UGT84B2 polypeptide, a CaUGT2 polypeptide, and/or a UGT74F2-like UGT polypeptide.

3. The recombinant host cell of claim 2, wherein:

the UGT73C1 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:127, the UGT73C3 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:133, the UGT73C5 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:135, the UGT73C6 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:137, the UGT73E1 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:141, the UGT74D1 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:143, the UGT75B1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:145, the UGT75L6 polypeptide comprises a polypeptide having at least 60% sequence identity to an amino acid sequence set forth in SEQ ID NO:147, the UGT76E12 polypeptide comprises a polypeptide having at least 60% sequence identity to an amino acid sequence set forth in SEQ ID NO:153, the OleI polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:177, the UGT5 polypeptide comprises a polypeptide having at least 65% identity to an amino acid sequence set forth in SEQ ID NO:181, the SA Gtase polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:183, the UDPG1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:185, the

UN1671 polypeptide comprises a polypeptide having at least 45% identity to an amino acid sequence set forth in SEQ ID NO:201, the UGT74F1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:203, the UGT75D1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:205, the UGT84B2 polypeptide comprises a polypeptide having at least 40% sequence identity to an amino acid sequence set forth in SEQ ID NO:207, the UGT74F2-like UGT polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:211, the UGT73C7 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:139, the CaUGT3 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:169, the UN32491 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:199, and/or the CaUGT2 polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:209.

4. The recombinant host cell of any one of claims 1-3, wherein the recombinant host cell further comprises:

(a) a gene encoding a polypeptide capable of synthesizing geranylgeranyl pyrophosphate (GGPP) from farnesyl diphosphate (FPP) and isopentenyl diphosphate (IPP);

(b) a gene encoding a polypeptide capable of synthesizing ent-copalyl diphosphate from GGPP;

(c) a gene encoding an a polypeptide capable of synthesizing ent-kaurene from ent-copalyl diphosphate;

(d) a gene encoding a polypeptide capable of synthesizing ent-kaurenoic acid from ent-kaurene;

(e) a gene encoding a polypeptide capable of reducing cytochrome P450 complex;

(f) a gene encoding a polypeptide capable of synthesizing steviol from ent-kaurenoic acid;

(g) a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position thereof;

(h) a gene encoding a polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside;

(i) a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position; and/or

(k) a gene encoding a polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside;

wherein at least one of the genes is a recombinant gene.

5. The recombinant host cell of claim 4, wherein:

(a) the polypeptide capable of synthesizing GGPP comprises a polypeptide having at least 70% sequence identity to the amino acid sequence set forth in SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, or SEQ ID NO:116;

(b) the polypeptide capable of synthesizing ent-copalyl diphosphate comprises a polypeptide having at least 70% sequence identity to the amino acid sequence set forth in SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, or SEQ ID NO:120;

(c) the polypeptide capable of synthesizing ent-kaurene comprises a polypeptide having at least 70% sequence identity to the amino acid sequence set forth in SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, or SEQ ID NO:52;

(d) the polypeptide capable of synthesizing ent-kaurenoic acid comprises a polypeptide having at least 70% sequence identity to the amino acid sequence set forth in SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:117, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, or SEQ ID NO:76;

(e) the polypeptide capable of reducing cytochrome P450 complex comprises a polypeptide having at least 70% sequence identity to the amino acid sequence set forth in SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82,

SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92;

(f) the polypeptide capable of synthesizing steviol comprises a polypeptide having at least 70% sequence identity to the amino acid sequence set forth in SEQ ID NO:94, SEQ ID NO:97, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, or SEQ ID NO:114;

(g) the polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position thereof comprises a polypeptide having at least 55% sequence identity to the amino acid sequence set forth in SEQ ID NO:7;

(h) the polypeptide capable of beta 1,3 glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside comprises a polypeptide having at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:9;

(i) the polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position comprises a polypeptide having at least 55% sequence identity to the amino acid sequence set forth in SEQ ID NO:4; and/or

(k) the polypeptide capable of beta 1,2 glycosylation of the C2' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside comprises a polypeptide having 80% or greater identity to the amino acid sequence set forth in SEQ ID NO:11; a polypeptide having 80% or greater identity to the amino acid sequence set forth in SEQ ID NO:13; or a polypeptide having at least 65% sequence identity to the amino acid sequence set forth in SEQ ID NO:16.

6. The recombinant host cell of any of claims 1-5, wherein expression of the one or more recombinant genes increases an amount of the one or more steviol glycosides and/or glycosylated steviol precursors, or a composition thereof accumulated by the cell relative to a corresponding host lacking the one or more recombinant genes.

7. The recombinant host cell of claim 6, wherein expression of the one or more recombinant genes increases the amount of the one or more steviol glycosides and/or

glycosylated steviol precursors, or the composition thereof, accumulated by the cell by at least about 5%, at least about 10%, at least about 25%, at least about 50%, at least about 75%, or at least about 100% relative to a corresponding host lacking the one or more recombinant genes.

8. The recombinant host cell of claim 6 or 7, wherein expression of the one or more recombinant genes increases the amount of *ent*-kaurenoic acid+2Glc (#7), *ent*-kaurenoic acid+3Glc (isomer 1), *ent*-kaurenoic acid+3Glc (isomer 2), steviol-13-*O*-glucoside (13-SMG), Rebaudioside A (RebA), Rebaudioside B (RebB), Steviol+4Glc (#36), Steviol+6Glc (isomer 1), Steviol+7Glc (isomer 2), and/or *ent*-Kaurenol+3Glc (isomer 1 and/or isomer 2) accumulated by the cell relative to a corresponding host lacking the one or more recombinant genes.

9. The recombinant host cell of any one of claims 1-8, wherein the one or more steviol glycosides and/or glycosylated steviol precursors are, or the composition thereof comprises, steviol-13-*O*-glucoside (13-SMG), steviol-19-*O*-glucoside (19-SMG), steviol-1,2-bioside, steviol-1,3-bioside, 1,2-stevioside, 1,3-stevioside, rubusoside, Rebaudioside A (RebA), Rebaudioside B (RebB), Rebaudioside C (RebC), Rebaudioside D (RebD), Rebaudioside E (RebE), Rebaudioside F (RebF), Rebaudioside M (RebM), Rebaudioside Q (RebQ), Rebaudioside I (RebI), dulcoside A, a mono-glycosylated *ent*-kaurenoic acid, a di-glycosylated *ent*-kaurenoic acid, a tri-glycosylated *ent*-kaurenoic acid, a mono-glycosylated *ent*-kaurenols, a di-glycosylated *ent*-kaurenol, a tri-glycosylated *ent*-kaurenol, a tri-glycosylated steviol glycoside, a tetra-glycosylated steviol glycoside, a penta-glycosylated steviol glycoside, a hexa-glycosylated steviol glycoside, a hepta-glycosylated steviol glycoside, or an isomer thereof.

10. The recombinant host cell of claim 9, wherein the mono-glycosylated *ent*-kaurenoic acid comprises KA1.58 of Table 1 and/or the penta-glycosylated steviol comprises Compound 5.24 of Table 1.

11. The recombinant host cell of claim 1-10, wherein the recombinant host cell comprises a plant cell, a mammalian cell, an insect cell, a fungal cell, an algal cell, or a bacterial cell.

12. A method of producing in a cell culture one or more steviol glycosides and/or glycosylated steviol precursors, or a composition thereof, comprising growing the recombinant host cell of any one of claims 1-11 in the cell culture, under conditions in which the genes are expressed, and wherein the one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof is produced by the recombinant host cell.

13. The method of claim 12, wherein the genes are constitutively expressed and/or expression of the genes is induced.

14. The method of claim 12 or 13, wherein an amount of *ent*-kaurenoic acid+2Glc (#7), *ent*-kaurenoic acid+3Glc (isomer 1), *ent*-kaurenoic acid+3Glc (isomer 2), 13-SMG, RebA, RebB, Steviol+4Glc (#36), Steviol+6Glc (isomer 1), Steviol+7Glc (isomer 2), and/or *ent*-Kaurenol+3Glc (isomer 1 and/or isomer 2) accumulated by the recombinant host cell is increased by at least about 5% relative to a corresponding host lacking the one or more recombinant genes.

15. The method of any one of claims 12-14, further comprising isolating from the cell cultures the one or more steviol glycosides and/or glycosylated steviol precursors or the composition thereof produced thereby.

16. The method of claim 15, wherein the isolating step comprises:

(a) providing the cell culture comprising the one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof;

(b) separating a liquid phase of the cell culture from a solid phase of the cell culture to obtain a supernatant comprising the produced one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof;

(c) providing one or more adsorbent resins, comprising providing the adsorbent resins in a packed column; and

(d) contacting the supernatant of step (b) with the one or more adsorbent resins in order to obtain at least a portion of the produced one or more steviol glycosides and/or glycosylated steviol precursors, or the

composition thereof, thereby isolating the produced one or more steviol glycosides or the steviol glycoside composition;

or

(a) providing the cell culture comprising the one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof;

(b) separating a liquid phase of the cell culture from a solid phase of the cell culture to obtain a supernatant comprising the produced one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof;

(c) providing one or more ion exchange or ion exchange or reversed-phase chromatography columns; and

(d) contacting the supernatant of step (b) with the one or more ion exchange or ion exchange or reversed-phase chromatography columns in order to obtain at least a portion of the produced one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof, thereby isolating the produced one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof;

or

(a) providing the cell culture comprising the one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof;

(b) separating a liquid phase of the cell culture from a solid phase of the cell culture to obtain a supernatant comprising the produced one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof;

(c) crystallizing or extracting the produced one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof, thereby isolating the produced one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof.

17. The method of any one of claims 12-14, further comprising recovering from the cell culture the one or more steviol glycosides and/or glycosylated steviol precursors or the composition thereof from the cell culture, wherein the cell culture is enriched for the one or more steviol glycosides and/or glycosides of a steviol presursor, or the composition

thereof relative to a steviol glycoside composition from a Stevia plant and has a reduced level of Stevia plant-derived components relative to a plant-derived Stevia extract.

18. The method of claim 17, wherein the recovered one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof are present in relative amounts that are different from a steviol glycoside composition recovered from a Stevia plant and have a reduced level of Stevia plant-derived components relative to a plant-derived Stevia extract.

19. A method for producing one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof, comprising whole cell bioconversion of plant-derived or synthetic steviol, steviol precursors and/or steviol glycosides in a cell culture medium of a recombinant host cell using:

(a) a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position;

(b) a gene encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position;

(c) a gene encoding a polypeptide capable of beta-1,2-glycosylation of the C2' and/or beta-1,3-glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside; and/or

(d) a gene encoding a polypeptide capable of glycosylating a steviol precursor at its C-19 carboxyl or C-19 hydroxyl position;

wherein at least one of the polypeptides is a recombinant polypeptide expressed in the recombinant host cell; and producing the one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof, thereby.

20. The method of claim 19, wherein:

(a) the polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position is a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73E1 polypeptide, a UGT75B1 polypeptide, a UGT75L6 polypeptide, a OleI polypeptide, a UGT5 polypeptide, a SA Gtase polypeptide, a

UDPG1 polypeptide, a UN1671 polypeptide, a UGT74F1 polypeptide, a UGT84B2 polypeptide, and/or a UGT74F2-like UGT polypeptide;

(b) the polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position is a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73C7 polypeptide, a UGT73E1 polypeptide, and/or a UGT76E12 polypeptide;

(c) the polypeptide capable of beta-1,2-glycosylation of the C2' and/or beta-1,3-glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside is a UGT73C6 polypeptide, a CaUGT3 polypeptide, a UN32491 polypeptide, and/or a UN1671 polypeptide; and/or

(d) the polypeptide capable of glycosylating a steviol precursor at its C-19 carboxyl or C-19 hydroxyl position is a UGT73C1 polypeptide, a UGT73C3 polypeptide, a UGT73C5 polypeptide, a UGT73C6 polypeptide, a UGT73E1 polypeptide, a UGT75B1 polypeptide, a UGT75L6 polypeptide, a UGT76E12 polypeptide, a OleI polypeptide, a UGT5 polypeptide, a SA Gtase, a UDPG1 polypeptide, a UGT74F1 polypeptide, a UGT75D1 polypeptide, a UGT84B2 polypeptide, and/or a UGT74F2-like UGT polypeptide.

21. The method of claim 20, wherein:

the UGT73C1 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:127, the UGT73C3 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:133, the UGT73C5 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:135, the UGT73C6 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:137, the UGT73E1 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:141, a UGT74D1 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:143, the UGT75B1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in

SEQ ID NO:145, the UGT75L6 polypeptide comprises a polypeptide having at least 60% sequence identity to an amino acid sequence set forth in SEQ ID NO:147, the UGT76E12 polypeptide comprises a polypeptide having at least 60% sequence identity to an amino acid sequence set forth in SEQ ID NO:153, the OleI polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:177, the UGT5 polypeptide comprises a polypeptide having at least 65% identity to an amino acid sequence set forth in SEQ ID NO:181, the SA Gtase polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:183, the UDPG1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:185, the UN1671 polypeptide comprises a polypeptide having at least 45% identity to an amino acid sequence set forth in SEQ ID NO:201, the UGT74F1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:203, the UGT75D1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:205, the UGT84B2 polypeptide comprises a polypeptide having at least 40% sequence identity to an amino acid sequence set forth in SEQ ID NO:207, the UGT74F2-like UGT polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:211, the UGT73C7 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:139, the CaUGT3 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:169, the UN32491 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:199, or the CaUGT2 polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:209.

22. The method of any one of claims 12-21, wherein the recombinant host cell is a plant cell, a mammalian cell, an insect cell, a fungal cell, an algal cell or a bacterial cell.

23. An *in vitro* method for producing one or more steviol glycosides and/or glycosylated steviol precursors, or a composition thereof comprising adding:

(a) a UGT85C2 polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:7;

(b) a UGT76G1 polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:9;

(c) a UGT74G1 polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:4;

(d) a UGT91D2 functional homolog polypeptide comprising a UGT91D2e polypeptide having 90% or greater identity to an amino acid sequence set forth in SEQ ID NO:11 or a UGT91D2e-b polypeptide having 90% or greater identity to an amino acid sequence set forth in SEQ ID NO:13;

(e) a EUGT11 polypeptide having at least 65% identity to an amino acid sequence set forth in SEQ ID NO:16; and/or

(f) a UGT73C1 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:127, a UGT73C3 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:133, a UGT73C5 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:135, a UGT73C6 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:137, a UGT73E1 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:141, a UGT74D1 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:143, a UGT75B1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:145, a UGT75L6 polypeptide comprises a polypeptide having at least 60% sequence identity to an amino acid sequence set forth in SEQ ID NO:147, a UGT76E12 polypeptide comprises a polypeptide having at least 60% sequence identity to an amino acid sequence set forth in SEQ ID NO:153, a OleI polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:177, a UGT5 polypeptide comprises a polypeptide having at least 65% identity to an amino acid sequence set forth in SEQ ID NO:181, a SA Gtase polypeptide comprises

a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:183, a UDPG1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:185, a UN1671 polypeptide comprises a polypeptide having at least 45% identity to an amino acid sequence set forth in SEQ ID NO:201, a UGT74F1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:203, a UGT75D1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:205, a UGT84B2 polypeptide comprises a polypeptide having at least 40% sequence identity to an amino acid sequence set forth in SEQ ID NO:207, a UGT74F2-like UGT polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:211, a UGT73C7 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:139, a CaUGT3 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:169, a UN32491 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:199, or a CaUGT2 polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:209;

and a plant-derived or synthetic steviol glycoside precursor or a plant-derived or synthetic steviol precursor to a reaction mixture;

wherein at least one of the polypeptides is a recombinant polypeptide; and

producing the one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof, thereby.

24. The method of claim 23, wherein the reaction mixture comprises:

(a) glucose, fructose, sucrose, xylose, rhamnose, uridine diphosphate (UDP)-glucose, UDP-rhamnose, UDP-xylose, and/or N-acetyl-glucosamine; and/or

(b) reaction buffer and/or salts.

25. The method of any one of claims 12-24, wherein the one or more steviol glycosides and/or glycosylated steviol precursors are, or the composition thereof comprises, 13-SMG, 19-SMG, steviol-1,2-bioside, steviol-1,3-bioside, 1,2-stevioside, 1,3-stevioside, rubusoside, RebA, RebB, RebC, RebD, RebE, RebF, RebM, RebQ, RebI, dulcoside A, a mono-glycosylated *ent*-kaurenoic acid, a di-glycosylated *ent*-kaurenoic acid, a tri-glycosylated *ent*-kaurenoic acid, a mono-glycosylated *ent*-kaurenols, a di-glycosylated *ent*-kaurenol, a tri-glycosylated *ent*-kaurenol, a tri-glycosylated steviol glycoside, a tetra-glycosylated steviol glycoside, a penta-glycosylated steviol glycoside, a hexa-glycosylated steviol glycoside, a hepta-glycosylated steviol glycoside, or an isomer thereof.

26. The method of claim 25, wherein the mono-glycosylated *ent*-kaurenoic acid comprises KA1.58 of Table 1 and/or the penta-glycosylated steviol comprises Compound 5.24 of Table 1.

27. A cell culture, comprising the recombinant host cell of any one of claims 1-11, the cell culture further comprising:

(a) one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof produced by the recombinant host cell,

(b) glucose, fructose, sucrose, xylose, rhamnose, UDP-glucose, UDP-rhamnose, UDP-xylose, and/or N-acetyl-glucosamine; and

(c) supplemental nutrients comprising trace metals, vitamins, salts, yeast nitrogen base (YNB), and/or amino acids;

wherein the one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof is present at a concentration of at least 1 mg/liter of the cell culture;

wherein the cell culture is enriched for the one or more steviol glycosides and/or glycosides of a steviol presursor, or the composition thereof relative to a steviol glycoside composition from a Stevia plant and has a reduced level of Stevia plant-derived components relative to a plant-derived Stevia extract.

28. A cell lysate from the recombinant host cell of any one of claims 1-11 grown in the cell culture, comprising:

(a) one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof produced by the recombinant host cell;

(b) glucose, fructose, sucrose, xylose, rhamnose, UDP-glucose, UDP-rhamnose, UDP-xylose, and/or N-acetyl-glucosamine; and/or

(c) supplemental nutrients comprising trace metals, vitamins, salts, yeast nitrogen base, YNB, and/or amino acids;

wherein the one or more steviol glycosides and/or glycosylated steviol precursors, or the composition thereof produced by the recombinant host cell is present at a concentration of at least 1 mg/liter of the cell culture.

29. A reaction mixture, comprising:

(a) a UGT85C2 polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:7;

(b) a UGT76G1 polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:9;

(c) a UGT74G1 polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:4;

(d) a UGT91D2 functional homolog polypeptide comprising a UGT91D2e polypeptide having 90% or greater identity to an amino acid sequence set forth in SEQ ID NO:11 or a UGT91D2e-b polypeptide having 90% or greater identity to an amino acid sequence set forth in SEQ ID NO:13;

(e) a EUGT11 polypeptide having at least 65% identity to an amino acid sequence set forth in SEQ ID NO:16; and/or

(f) a UGT73C1 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:127, a UGT73C3 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:133, a UGT73C5 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:135, a UGT73C6 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:137, a UGT73E1 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:141, a UGT75B1 polypeptide comprises a polypeptide having at least 50%

sequence identity to an amino acid sequence set forth in SEQ ID NO:145, a UGT75L6 polypeptide comprises a polypeptide having at least 60% sequence identity to an amino acid sequence set forth in SEQ ID NO:147, a UGT76E12 polypeptide comprises a polypeptide having at least 60% sequence identity to an amino acid sequence set forth in SEQ ID NO:153, a OleI polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:177, a UGT5 polypeptide comprises a polypeptide having at least 65% identity to an amino acid sequence set forth in SEQ ID NO:181, a SA Gtase polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:183, a UDPG1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:185, a UN1671 polypeptide comprises a polypeptide having at least 45% identity to an amino acid sequence set forth in SEQ ID NO:201, a UGT74F1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:203, a UGT75D1 polypeptide comprises a polypeptide having at least 50% sequence identity to an amino acid sequence set forth in SEQ ID NO:205, a UGT84B2 polypeptide comprises a polypeptide having at least 40% sequence identity to an amino acid sequence set forth in SEQ ID NO:207, a UGT74F2-like UGT polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:211, a UGT73C7 polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:139, a CaUGT3 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:169, or a UN32491 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:199;

and further comprising:

(g) one or more steviol glycosides and/or glycosylated steviol precursors, or a composition thereof;

(h) glucose, fructose, sucrose, xylose, rhamnose, uridine diphosphate (UDP)-glucose, UDP-rhamnose, UDP-xylose, and/or N-acetyl-glucosamine; and/or

(i) reaction buffer and/or salts.

30. A composition of one or more steviol glycosides and/or glycosylated steviol precursors produced by the recombinant host cell of any one of claims 1-11;

wherein the one or more steviol glycosides and/or glycosylated steviol precursors produced by the recombinant host cell are present in relative amounts that are different from a steviol glycoside composition from a Stevia plant and have a reduced level of Stevia plant-derived components relative to a plant-derived Stevia extract.

31. A composition of one or more steviol glycosides and/or glycosylated steviol precursors produced by the method of any one of claims 12-26;

wherein the one or more steviol glycosides and/or glycosylated steviol precursors produced by the recombinant host cell are present in relative amounts that are different from a steviol glycoside composition from a Stevia plant and have a reduced level of Stevia plant-derived components relative to a plant-derived Stevia extract.

32. A sweetener composition, comprising one or more steviol glycosides and/or glycosylated steviol precursors of claim 30 or 31.

33. A food product, comprising the sweetener composition of claim 32.

34. A beverage or a beverage concentrate, comprising the sweetener composition of claim 32.

35. An isolated nucleic acid molecule encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position or a catalytically active portion thereof, wherein the encoded polypeptide capable of glycosylating steviol or a steviol glycoside at its C-19 carboxyl position or the catalytically active portion thereof has at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:127, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:133, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:135, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:137, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:141, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:145, at

least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:147, at least 55% sequence identity to the amino acid sequence set forth in SEQ ID NO:177, at least 65% sequence identity to the amino acid sequence set forth in SEQ ID NO:181, at least 55% sequence identity to the amino acid sequence set forth in SEQ ID NO:183, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:185, at least 45% sequence identity to the amino acid sequence set forth in SEQ ID NO:201, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:203, at least 40% sequence identity to the amino acid sequence set forth in SEQ ID NO:207, or at least 55% sequence identity to the amino acid sequence set forth in SEQ ID NO:211.

36. An isolated nucleic acid molecule encoding a polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position or a catalytically active portion thereof, wherein the encoded polypeptide capable of glycosylating steviol or a steviol glycoside at its C-13 hydroxyl position or the catalytically active portion thereof has at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:127, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:133, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:135, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:137, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:139, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:141, or at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:153.

37. An isolated nucleic acid molecule encoding a polypeptide capable of beta-1,2-glycosylation of the C2' and/or beta-1,3-glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside or a catalytically active portion thereof, wherein the encoded polypeptide capable of beta-1,2-glycosylation of the C2' and/or beta-1,3-glycosylation of the C3' of the 13-*O*-glucose, 19-*O*-glucose, or both 13-*O*-glucose and 19-*O*-glucose of a steviol glycoside or the catalytically active portion thereof has at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:137, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:169, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:199, or at least 45% sequence identity to the amino acid sequence set forth in SEQ ID NO:201.

38. An isolated nucleic acid molecule encoding a polypeptide capable of glycosylating a steviol precursor at its C-19 carboxyl or C-19 hydroxyl position or a catalytically active portion thereof, wherein the encoded polypeptide capable of glycosylating a steviol precursor at its C-19 carboxyl or C-19 hydroxyl position or the catalytically active portion thereof has at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:127, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:133, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:135, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:137, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:141, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:145, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:147, at least 60% sequence identity to the amino acid sequence set forth in SEQ ID NO:153, at least 55% sequence identity to the amino acid sequence set forth in SEQ ID NO:177, at least 65% sequence identity to the amino acid sequence set forth in SEQ ID NO:181, at least 55% sequence identity to the amino acid sequence set forth in SEQ ID NO:183, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:185, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:203, at least 50% sequence identity to the amino acid sequence set forth in SEQ ID NO:205, at least 40% sequence identity to the amino acid sequence set forth in SEQ ID NO:207, or at least 55% sequence identity to the amino acid sequence set forth in SEQ ID NO:211.

39. The isolated nucleic acid of any one of claims 35-38, wherein the nucleic acid is cDNA.

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Figure 1

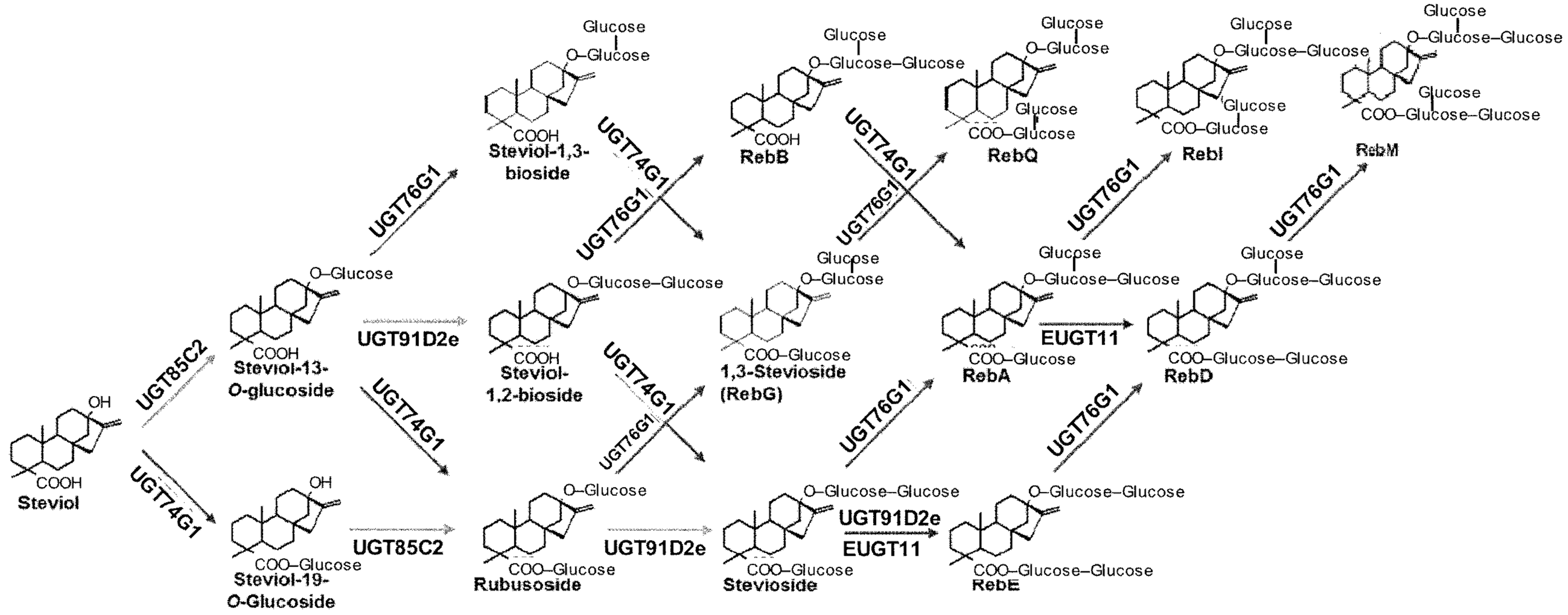


Figure 2

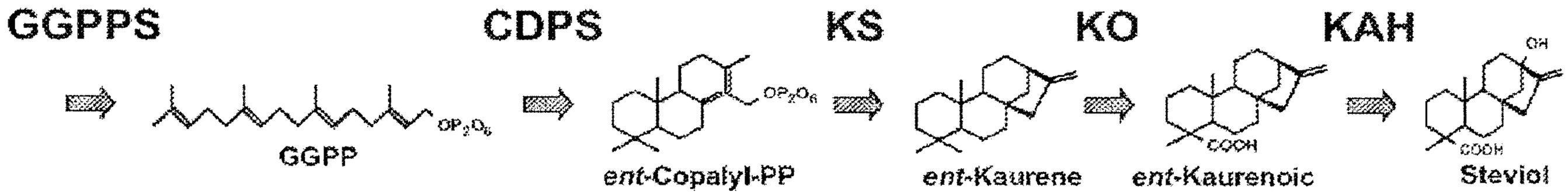
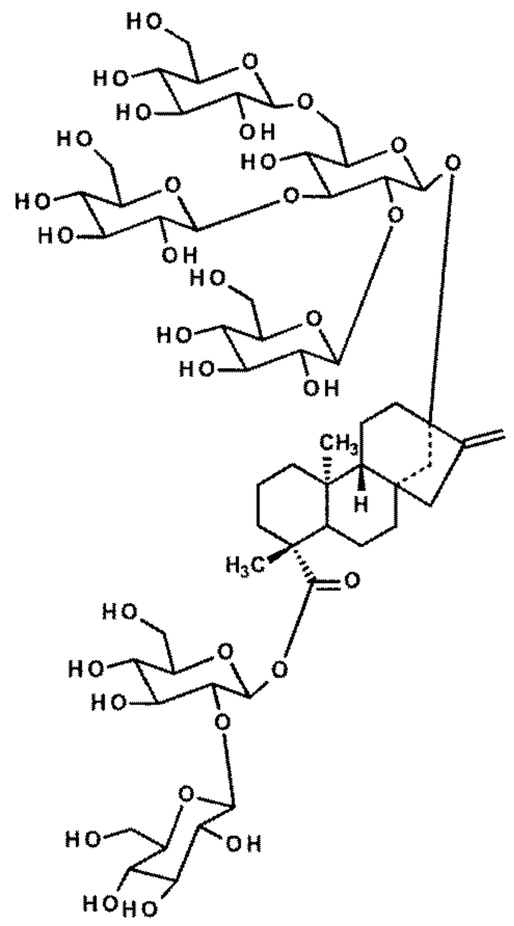
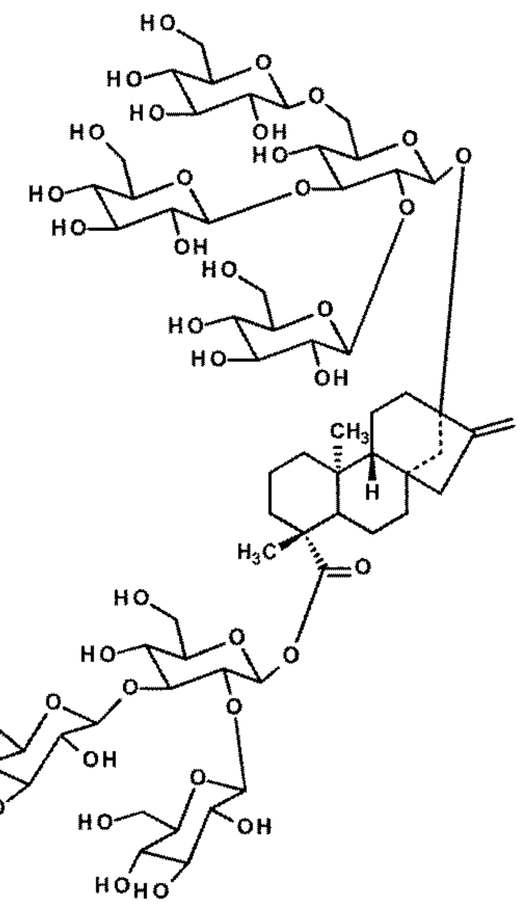

GGPPS
CDPS
KS
KO
KAH
OPP
GGPP
ent-Copalyl-PP
ent-Kaurene
COOH
ent-Kaurenoic acid
OH
COOH
Steviol

Figure 3

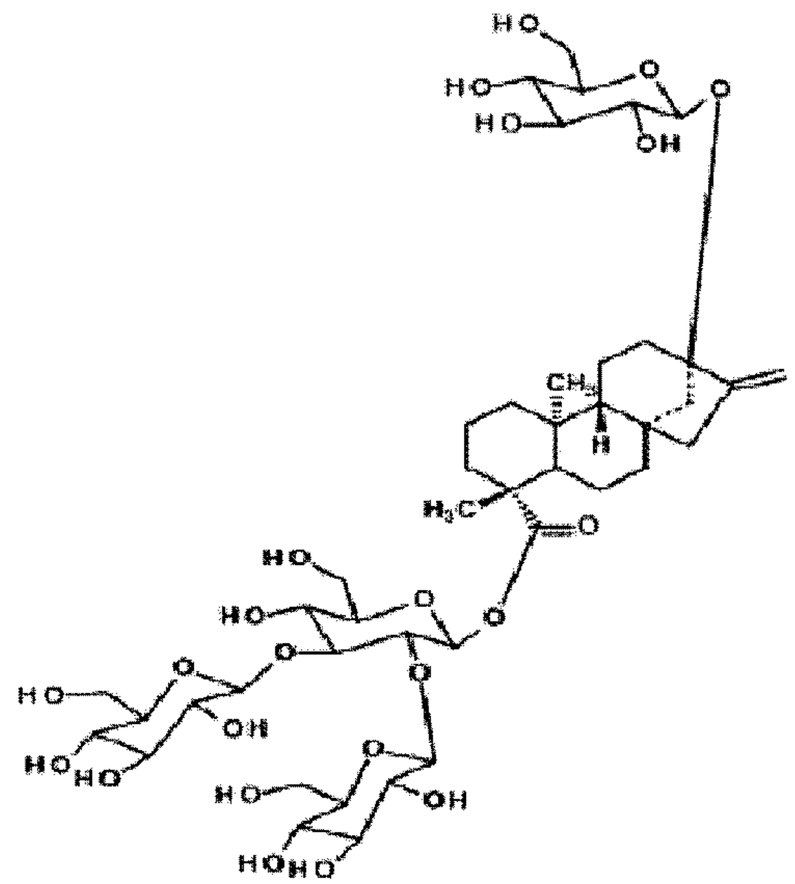


Steviol+6Glc (isomer 1)
[Compound 6.1]

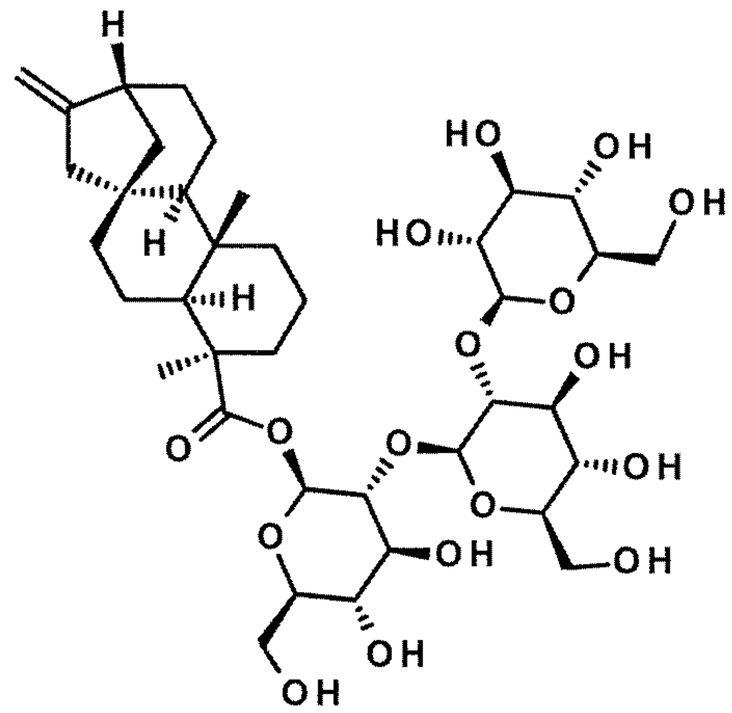


Steviol+7Glc (isomer 2)
[Compound 7.2]

Figure 4

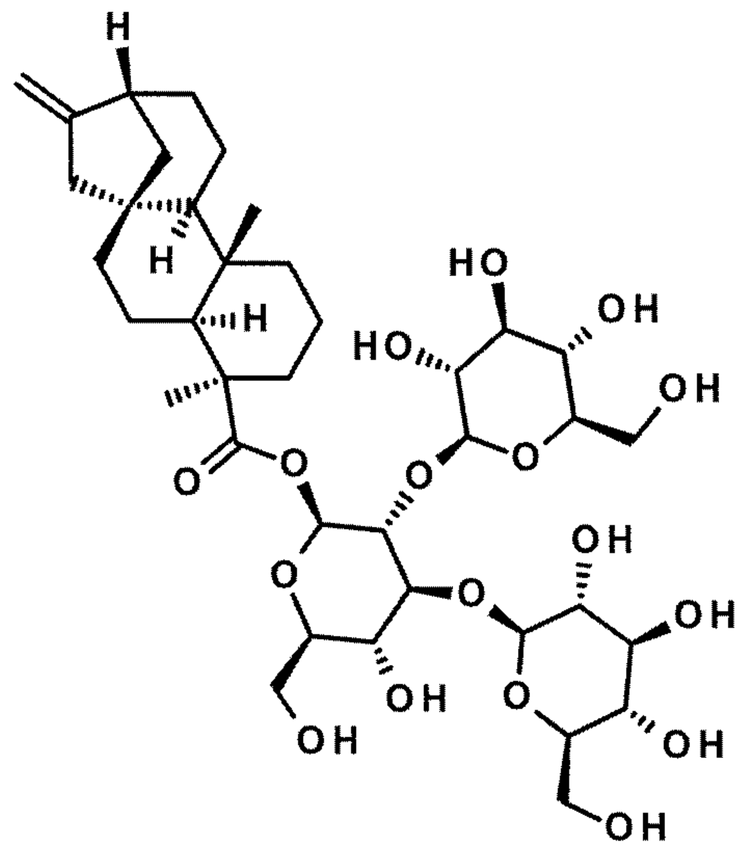


Steviol+4Glc (#26)
[Compound 4.26]

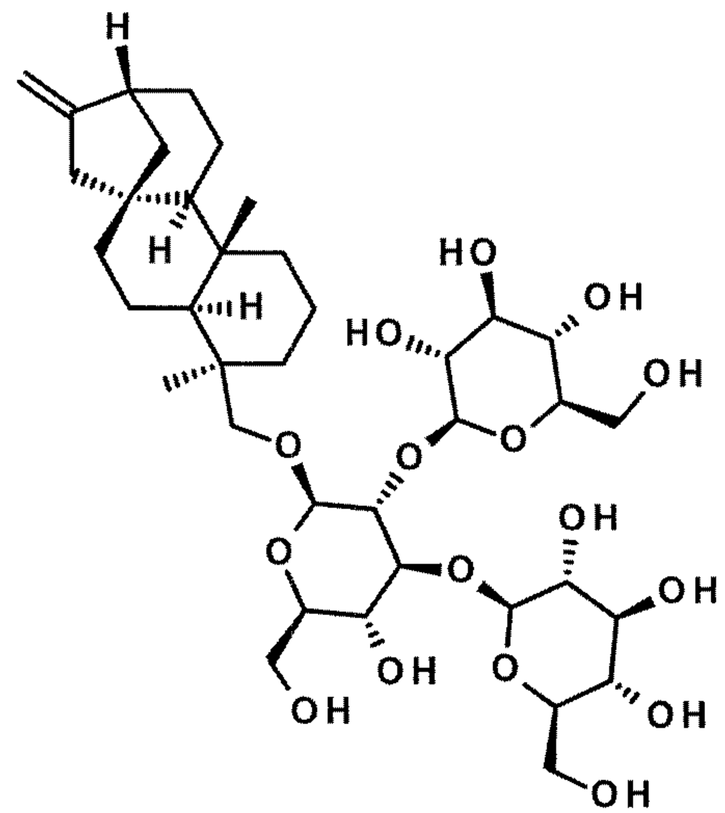


ent-Kaurenoic Acid+3Glc
(isomer 1) [KA 3.1]

Figure 5



ent-Kaurenoic Acid+3Glc
(isomer 2) [KA3.2]



ent-Kaurenol+3Glc
(isomer 1) [KL3.1]

Figure 6A

Kaurenoic Acid+3Glc (isomer 1)

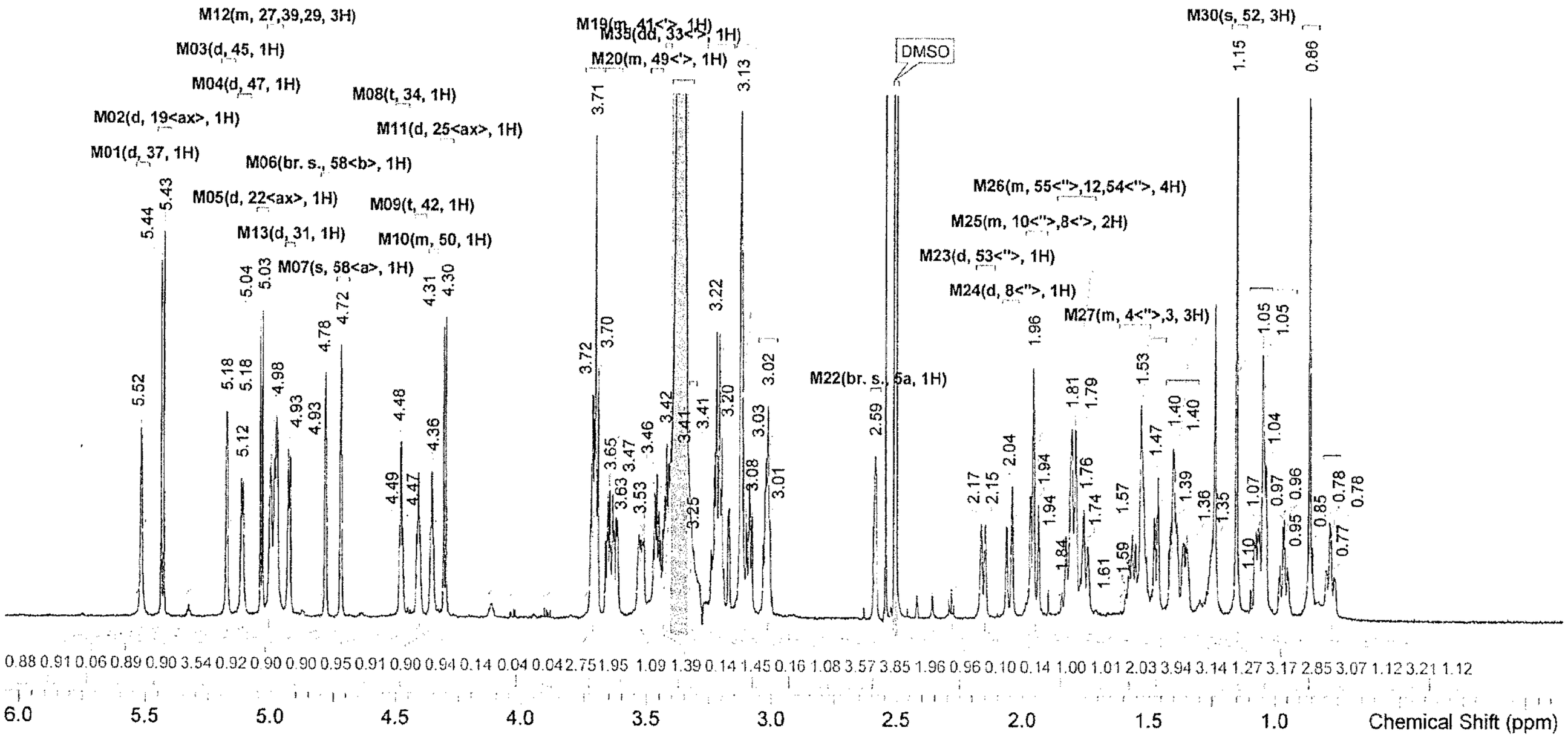


Figure 6B

Atom1	Shift1 (ppm	H's	Type	J (Hz)	Multiplet1	(ppm)
55<'>	0.78	1	m	-	M34	[0.74 .. 0.81]
57	0.86	3	m	-	M33	[0.83 .. 0.90]
53<'>	0.97	1	td	13.33, 4.16	M32	[0.92 .. 1.00]
13a, 2a, 10<'>	1.07	3	m	-	M31	[1.02 .. 1.10]
52	1.15	3	s	-	M30	[1.12 .. 1.18]
11<'>, 4<'>, 54<'>	1.38	3	m	-	M29	[1.30 .. 1.44]
11<">	1.47	1	m	-	M28	[1.44 .. 1.50]
4<">, 3	1.56	3	m	-	M27	[1.50 .. 1.62]
55<">, 12, 54<">	1.79	4	m	-	M26	[1.72 .. 1.87]
10<">, 8<'>	1.95	2	m	-	M25	[1.91 .. 1.99]
8<">	2.06	1	d	17.12	M24	[2.02 .. 2.08]
53<">	2.16	1	d	12.72	M23	[2.12 .. 2.19]
5a	2.59	1	br. s.	-	M22	[2.57 .. 2.61]
38<ax>, 26<ax>	3.02	2	m	-	M14	[2.98 .. 3.06]
30<ax>, 40<ax>, 28<ax>, 32<ax	3.10	4	m	-	M15	[3.07 .. 3.15]
46<ax>, 23<ax>, 48<ax>	3.22	3	m	-	M16	[3.16 .. 3.26]
36<ax>	3.32	1	m	-	M21	[3.30 .. 3.33]
33<'>	3.42	1	dd	11.00, 5.14	M35	[3.41 .. 3.43]
49<'>	3.46	1	m	-	M20	[3.44 .. 3.49]
41<'>	3.52	1	m	-	M19	[3.50 .. 3.55]
44<ax>, 49<">	3.64	2	m	-	M18	[3.60 .. 3.67]
41<">, 33<">, 20<ax>	3.71	3	m	-	M17	[3.68 .. 3.75]
25<ax>	4.31	1	d	7.82	M11	[4.28 .. 4.33]
50	4.35	1	m	-	M10	[4.34 .. 4.37]
42	4.41	1	t	5.38	M09	[4.39 .. 4.43]
34	4.48	1	t	5.62	M08	[4.45 .. 4.51]
58<a>	4.72	1	s	-	M07	[4.69 .. 4.74]
58<b>	4.78	1	br. s.	-	M06	[4.76 .. 4.81]
31	4.93	1	d	5.38	M13	[4.91 .. 4.95]
27, 39, 29	4.99	3	m	-	M12	[4.96 .. 5.02]
22<ax>	5.04	1	d	7.83	M05	[5.02 .. 5.06]
47	5.12	1	d	5.38	M04	[5.09 .. 5.14]
45	5.18	1	d	2.45	M03	[5.15 .. 5.21]
19<ax>	5.43	1	d	7.83	M02	[5.40 .. 5.46]
37	5.52	1	d	2.45	M01	[5.49 .. 5.54]

Kaurenoic Acid+3Glc (isomer 1)

^{1}H NMR (800 MHz, *DMSO-d_6*) δ ppm 0.74 - 0.81 (m, 1 H) 0.83 - 0.90 (m, 3 H) 0.97 (td, *J*=13.33, 4.16 Hz, 1 H) 1.02 - 1.10 (m, 3 H) 1.15 (s, 3 H) 1.30 - 1.44 (m, 3 H) 1.44 - 1.50 (m, 1 H) 1.50 - 1.62 (m, 3 H) 1.72 - 1.87 (m, 4 H) 1.91 - 1.99 (m, 2 H) 2.06 (d, *J*=17.12 Hz, 1 H) 2.16 (d, *J*=12.72 Hz, 1 H) 2.59 (br. s., 1 H) 2.98 - 3.06 (m, 2 H) 3.07 - 3.15 (m, 4 H) 3.16 - 3.26 (m, 3 H) 3.30 - 3.33 (m, 1 H) 3.42 (dd, *J*=11.00, 5.14 Hz, 1 H) 3.44 - 3.49 (m, 1 H) 3.50 - 3.55 (m, 1 H) 3.60 - 3.67 (m, 2 H) 3.68 - 3.75 (m, 3 H) 4.31 (d, *J*=7.82 Hz, 1 H) 4.34 - 4.37 (m, 1 H) 4.41 (t, *J*=5.38 Hz, 1 H) 4.48 (t, *J*=5.62 Hz, 1 H) 4.72 (s, 1 H) 4.78 (br. s., 1 H) 4.93 (d, *J*=5.38 Hz, 1 H) 4.96 - 5.02 (m, 3 H) 5.04 (d, *J*=7.83 Hz, 1 H) 5.12 (d, *J*=5.38 Hz, 1 H) 5.18 (d, *J*=2.45 Hz, 1 H) 5.43 (d, *J*=7.83 Hz, 1 H) 5.52 (d, *J*=2.45 Hz, 1 H)

^{13}C NMR (201.21 MHz, *DMSO-d_6*) δ ppm 175.4 (1C), 155.3 (1C), 104.6 (1C), 103.6 (1C), 99.8 (1C), 92.4 (1C), 83.4 (1C), 77.6 (1C), 77.5 (1C), 77.2 (1C), 76.9 (1C), 76.2 (1C), 76.1 (1C), 75.8 (1C), 75.2 (1C), 70.8 (1C), 70.0 (1C), 69.8 (1C), 61.5 (1C), 61.4 (1C), 60.6 (1C), 56.7 (1C), 54.6 (1C), 48.7 (1C), 43.9 (1C), 43.4 (1C), 43.3 (1C), 41.2 (1C), 40.4 (1C), 40.0 (1C), 39.4 (1C), 37.8 (1C), 32.9 (1C), 28.5 (1C), 21.6 (1C), 19.1 (1C), 18.5 (1C), 16.1 (1C)

Figure 6C

Kaurenoic Acid+3Glc (isomer 1)

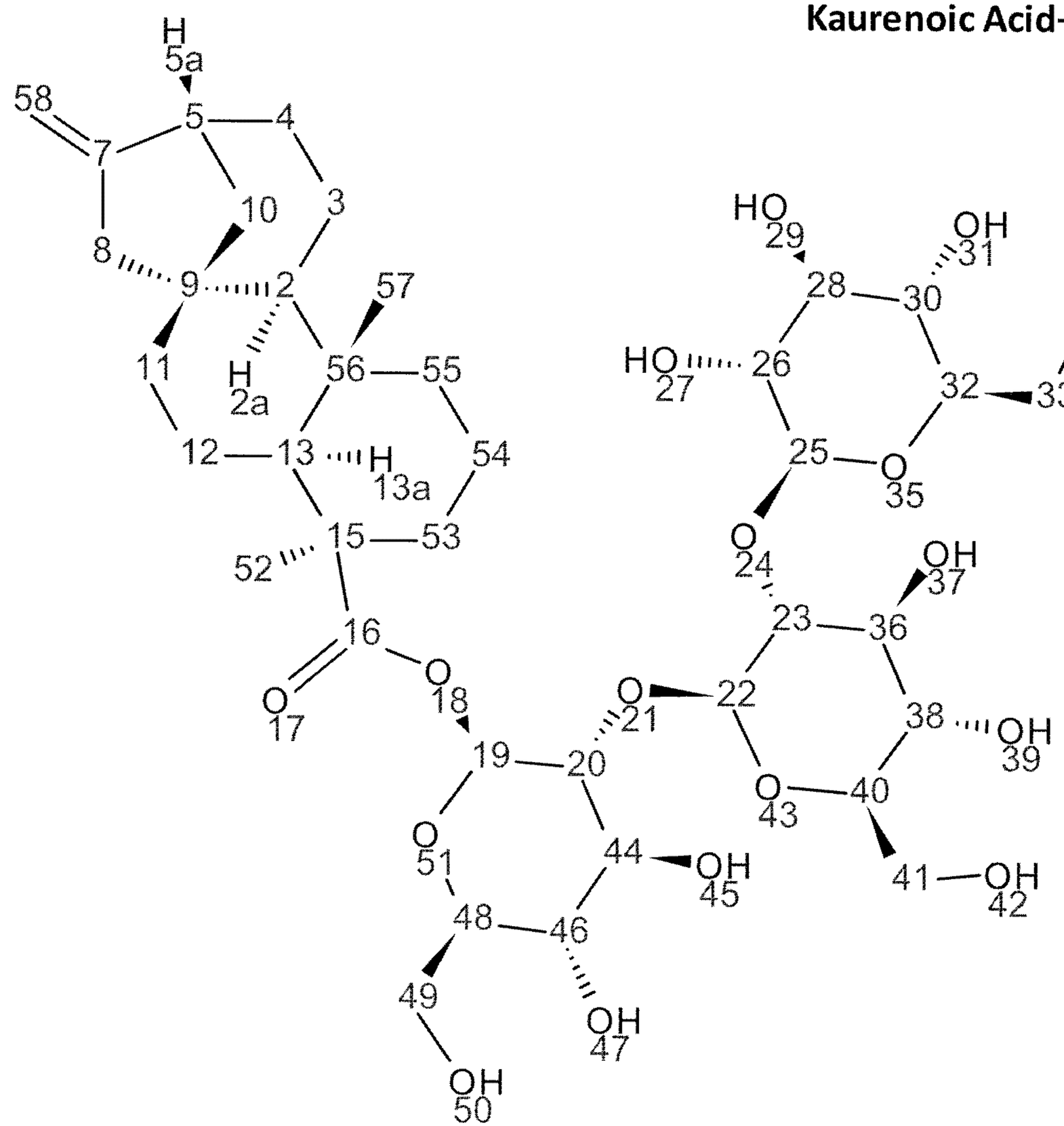


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Figure 6D

Kaurenoic Acid+3Glc (isomer 2)

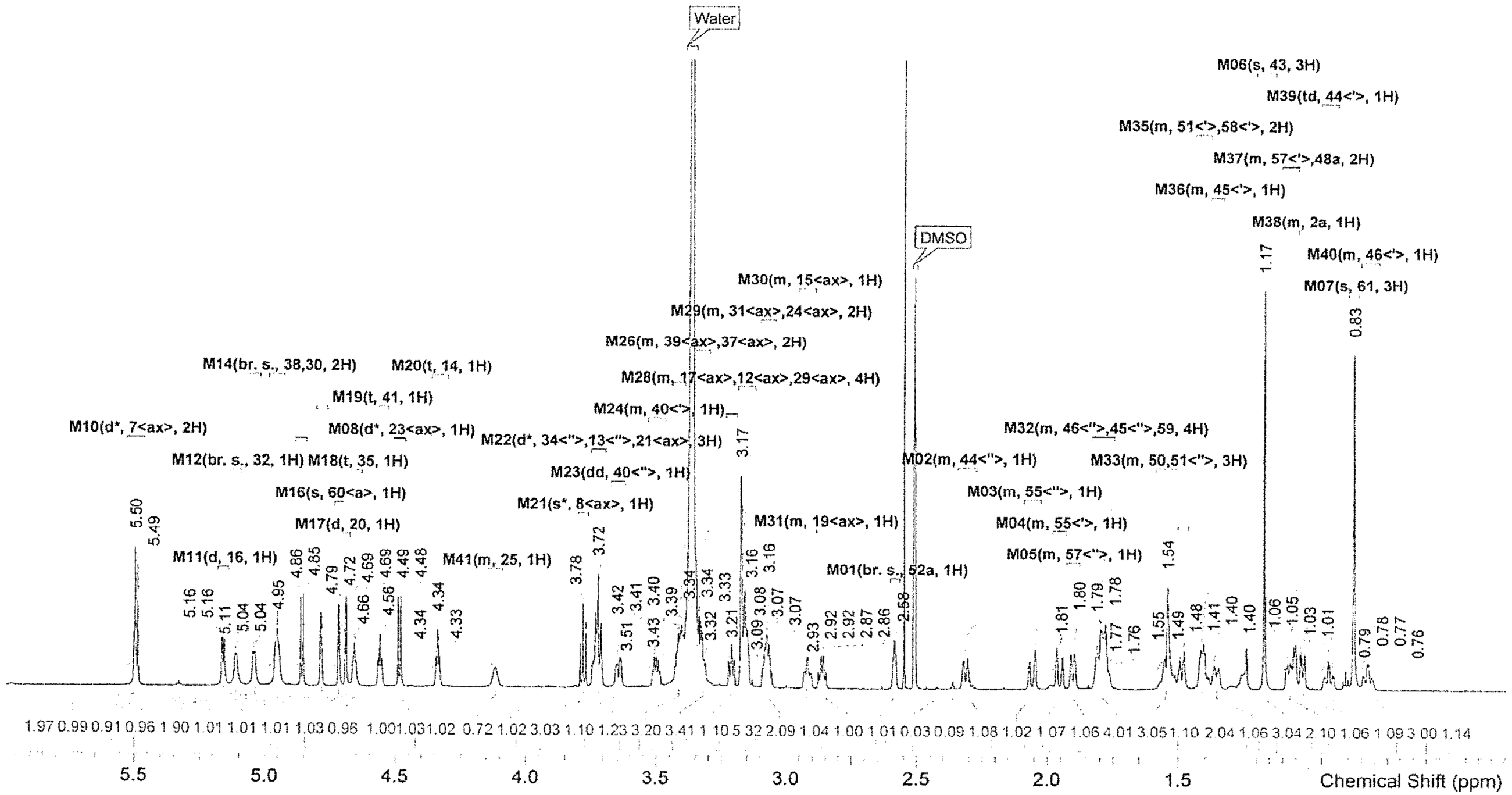


Figure 6E

Atom1	Shift1 (ppm	H's	Type	J (Hz)	Multiplet1	(ppm)
46<'>	0.77	1	m	-	M40	[0.73 .. 0.80]
61	0.83	3	s	-	M07	[0.81 .. 0.85]
44<'>	0.92	1	td	13.33, 4.16	M39	[0.89 .. 0.96]
2a	1.03	1	m	-	M38	[1.00 .. 1.04]
57<'>, 48a	1.07	2	m	-	M37	[1.04 .. 1.10]
43	1.17	3	s	-	M06	[1.13 .. 1.21]
45<'>	1.36	1	m	-	M36	[1.33 .. 1.38]
51<'>, 58<'>	1.40	2	m	-	M35	[1.38 .. 1.44]
58<">	1.49	1	d	12.72	M34	[1.46 .. 1.50]
50, 51<">	1.54	3	m	-	M33	[1.51 .. 1.59]
46<">, 45<">, 59	1.78	4	m	-	M32	[1.75 .. 1.83]
57<">	1.90	1	m	-	M05	[1.88 .. 1.93]
55<'>	1.95	1	m	-	M04	[1.93 .. 1.98]
55<">	2.06	1	m	-	M03	[2.03 .. 2.09]
44<">	2.31	1	m	-	M02	[2.27 .. 2.34]
52a	2.58	1	br. s.	-	M01	[2.56 .. 2.60]
19<ax>	2.86	1	m	-	M31	[2.83 .. 2.88]
15<ax>	2.92	1	m	-	M30	[2.89 .. 2.95]
31<ax>, 24<ax>	3.07	2	m	-	M29	[3.04 .. 3.10]
17<ax>, 12<ax>, 29<ax>	3.16	4	m	-	M28	[3.12 .. 3.19]
33<ax>	3.21	1	m	-	M27	[3.19 .. 3.23]
39<ax>, 37<ax>	3.32	2	m	-	M26	[3.30 .. 3.35]
34<'>, 13<'>	3.41	2	m	-	M25	[3.39 .. 3.44]
40<'>	3.50	1	m	-	M24	[3.47 .. 3.53]
40<">	3.64	1	dd	10.51, 4.16	M23	[3.62 .. 3.67]
34<">, 13<">, 21<ax>	3.73	3	d	7.83	M22	[3.70 .. 3.75]
8<ax>	3.78	1	s	-	M21	[3.76 .. 3.80]
25	4.12	1	m	-	M41	[4.09 .. 4.14]
14	4.34	1	t	5.14	M20	[4.30 .. 4.36]
23<ax>	4.48	1	d	7.83	M08	[4.46 .. 4.51]
41	4.56	1	t	5.62	M19	[4.53 .. 4.59]
35	4.66	1	t	4.89	M18	[4.63 .. 4.67]
20	4.69	1	d	2.45	M17	[4.67 .. 4.70]
60<a>	4.72	1	s	-	M16	[4.70 .. 4.73]
60<b>	4.79	1	br. s.	-	M15	[4.76 .. 4.80]
10<ax>	4.86	1	d	7.83	M09	[4.84 .. 4.88]
38, 30	4.95	2	br. s.	-	M14	[4.93 .. 4.99]
18	5.04	1	d	4.89	M13	[5.02 .. 5.06]
32	5.11	1	br. s.	-	M12	[5.09 .. 5.13]
16	5.16	1	d	6.36	M11	[5.14 .. 5.18]
7<ax>	5.49	2	d	8.31	M10	[5.46 .. 5.53]

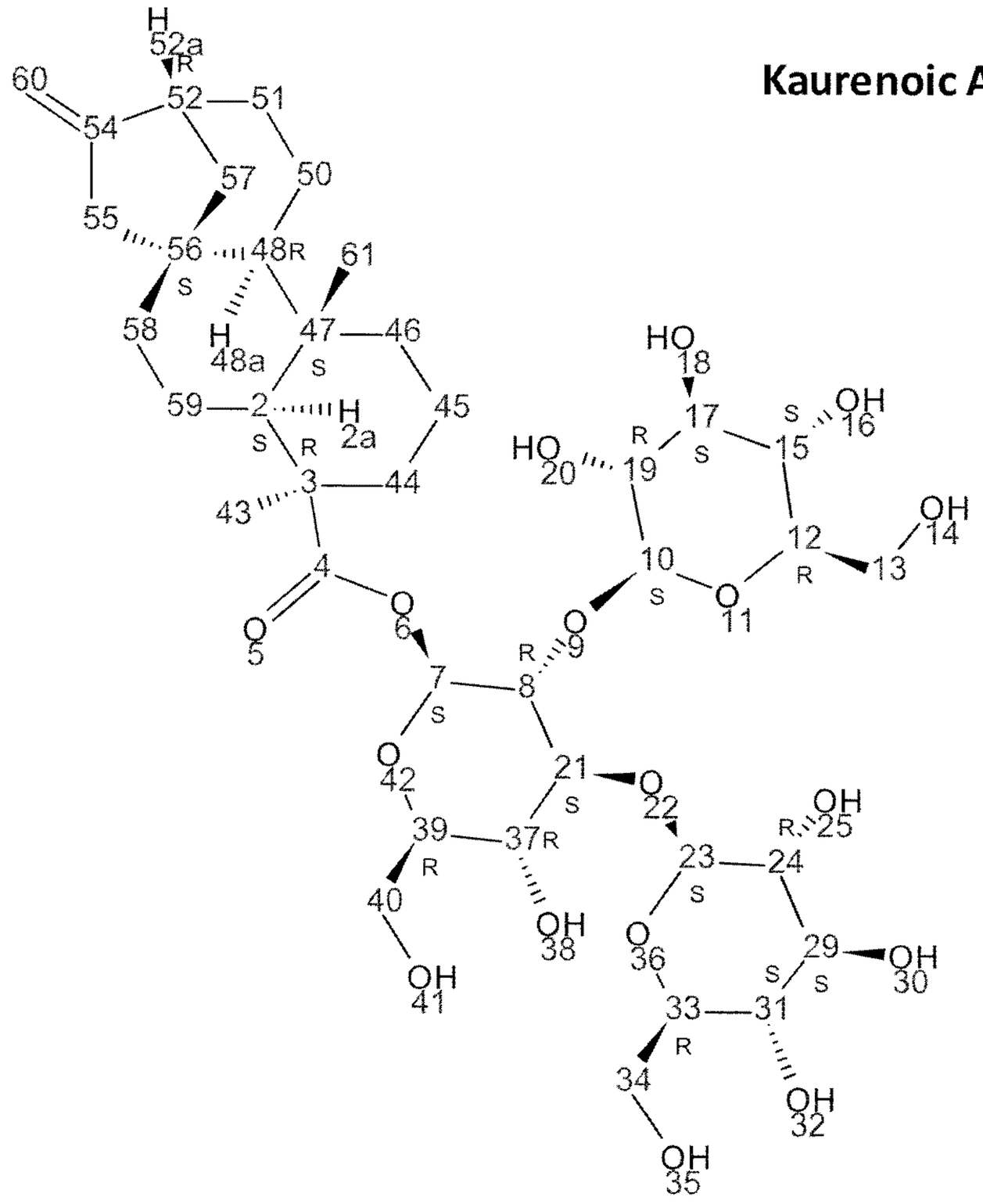
Kaurenoic Acid+3Glc (isomer 2)

^{1}H NMR (800 MHz, *DMSO-d_6*) δ ppm 0.73 - 0.80 (m, 1 H) 0.83 (s, 3 H) 0.92 (td, *J*=13.33, 4.16 Hz, 1 H) 1.00 - 1.04 (m, 1 H) 1.04 - 1.10 (m, 2 H) 1.17 (s, 3 H) 1.33 - 1.38 (m, 1 H) 1.38 - 1.44 (m, 2 H) 1.49 (d, *J*=12.72 Hz, 1 H) 1.51 - 1.59 (m, 3 H) 1.75 - 1.83 (m, 4 H) 1.88 - 1.93 (m, 1 H) 1.93 - 1.98 (m, 1 H) 2.03 - 2.09 (m, 1 H) 2.27 - 2.34 (m, 1 H) 2.58 (br. s., 1 H) 2.83 - 2.88 (m, 1 H) 2.89 - 2.95 (m, 1 H) 3.04 - 3.10 (m, 2 H) 3.12 - 3.19 (m, 4 H) 3.19 - 3.23 (m, 1 H) 3.30 - 3.35 (m, 2 H) 3.39 - 3.44 (m, 2 H) 3.47 - 3.53 (m, 1 H) 3.64 (dd, *J*=10.51, 4.16 Hz, 1 H) 3.73 (d, *J*=7.83 Hz, 3 H) 3.78 (s, 1 H) 4.09 - 4.14 (m, 1 H) 4.34 (t, *J*=5.14 Hz, 1 H) 4.48 (d, *J*=7.83 Hz, 1 H) 4.56 (t, *J*=5.62 Hz, 1 H) 4.66 (t, *J*=4.89 Hz, 1 H) 4.69 (d, *J*=2.45 Hz, 1 H) 4.72 (s, 1 H) 4.79 (br. s., 1 H) 4.86 (d, *J*=7.83 Hz, 1 H) 4.95 (br. s., 2 H) 5.04 (d, *J*=4.89 Hz, 1 H) 5.11 (br. s., 1 H) 5.16 (d, *J*=6.36 Hz, 1 H) 5.49 (d, *J*=8.31 Hz, 2 H)

^{13}C NMR (201.21 MHz, *DMSO-d_6*) δ ppm 175.1 (1C), 155.4 (1C), 103.7 (1C), 103.2 (1C), 101.5 (1C), 92.1 (1C), 86.8 (1C), 77.9 (1C), 77.3 (1C), 77.1 (1C), 77.0 (1C), 76.8 (1C), 76.7 (1C), 74.4 (1C), 73.9 (1C), 71.2 (1C), 70.2 (1C), 68.2 (1C), 61.8 (1C), 61.1 (1C), 60.6 (1C), 56.7 (1C), 54.6 (1C), 48.8 (1C), 44.0 (1C), 43.6 (1C), 43.4 (1C), 41.1 (1C), 40.0 (1C), 39.5 (1C), 39.4 (1C), 37.1 (1C), 32.8 (1C), 28.4 (1C), 21.6 (1C), 19.3 (1C), 18.2 (1C), 16.2 (1C)

Figure 6F

Kaurenoic Acid+3Glc (isomer 2)



Kaurenol+3Glc (isomer 1)

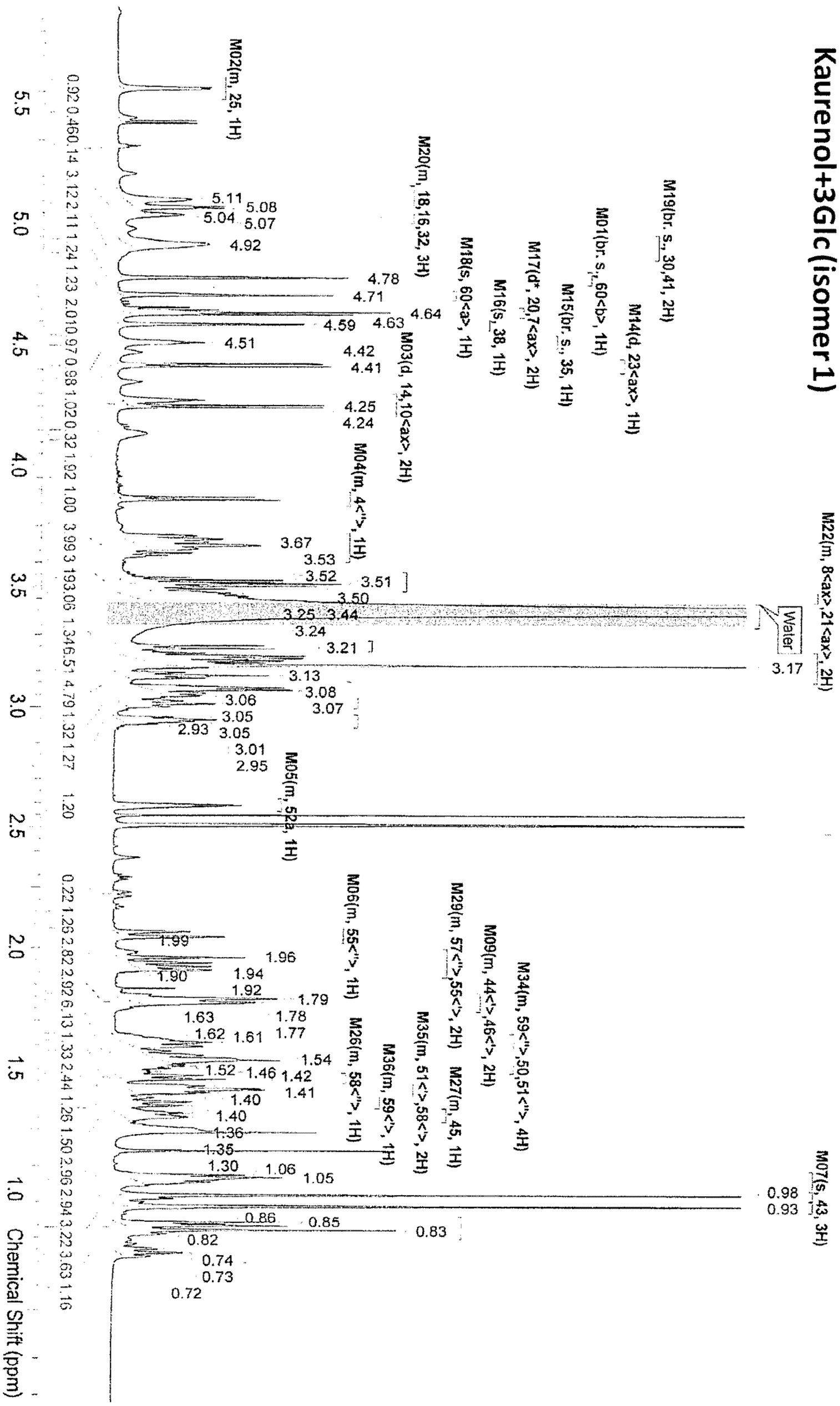


Figure 6G

Figure 6H

Kaurenol+3Glc (isomer 1)

Atom1	Shift1 (ppm	H's	Type	J (Hz)	Multiplet1	(ppm)
46<">	0.74	1	m	-	M32	[0.70 .. 0.76]
44<">, 2a	0.84	2	m	-	M25	[0.79 .. 0.89]
61	0.93	3	s	-	M08	[0.91 .. 0.96]
43	0.98	3	s	-	M07	[0.96 .. 1.00]
48a, 57<'>	1.04	2	m	-	M28	[1.01 .. 1.08]
45	1.32	1	m	-	M27	[1.28 .. 1.34]
59<'>	1.36	1	m	-	M36	[1.34 .. 1.39]
51<'>, 58<'>	1.41	2	m	-	M35	[1.39 .. 1.44]
58<">	1.46	1	m	-	M26	[1.44 .. 1.48]
59<">, 50, 51<">	1.56	4	m	-	M34	[1.48 .. 1.65]
44<'>, 46<'>	1.78	2	m	-	M09	[1.74 .. 1.82]
57<">, 55<'>	1.94	2	m	-	M29	[1.88 .. 2.00]
55<">	2.06	1	m	-	M06	[2.02 .. 2.09]
52a	2.59	1	m	-	M05	[2.57 .. 2.62]
19<ax>	2.94	1	m	-	M24	[2.91 .. 2.97]
37<ax>	3.02	1	m	-	M23	[2.99 .. 3.04]
31<ax>, 24<ax>	3.07	2	m	-	M30	[3.04 .. 3.11]
15<ax>	3.13	1	t	9.05	M11	[3.11 .. 3.15]
17<ax>, 29<ax>, 12<ax>, 33<ax>, 39<ax>	3.19	5	m	-	M31	[3.15 .. 3.23]
4<'>	3.24	1	m	-	M33	[3.23 .. 3.28]
8<ax>, 21<ax>	3.46	2	m	-	M22	[3.44 .. 3.48]
13<'>, 34<'>, 40<'>	3.51	3	dd	11.74, 7.82	M21	[3.48 .. 3.56]
13<">, 34<">, 40<">	3.67	3	br. s.	-	M12	[3.60 .. 3.72]
4<">	3.86	1	m	-	M04	[3.83 .. 3.89]
14, 10<ax>	4.25	2	d	7.34	M03	[4.21 .. 4.30]
23<ax>	4.42	1	d	7.83	M14	[4.39 .. 4.45]
35	4.51	1	br. s.	-	M15	[4.49 .. 4.54]
38	4.59	1	s	-	M16	[4.56 .. 4.61]
20, 7<ax>	4.63	2	d	8.31	M17	[4.62 .. 4.66]
60<a>	4.71	1	s	-	M18	[4.69 .. 4.73]
60<b>	4.78	1	br. s.	-	M01	[4.75 .. 4.81]
30, 41	4.92	2	br. s.	-	M19	[4.86 .. 4.96]
18, 16, 32	5.07	3	m	-	M20	[5.01 .. 5.17]
25	5.57	1	m	-	M02	[5.52 .. 5.62]

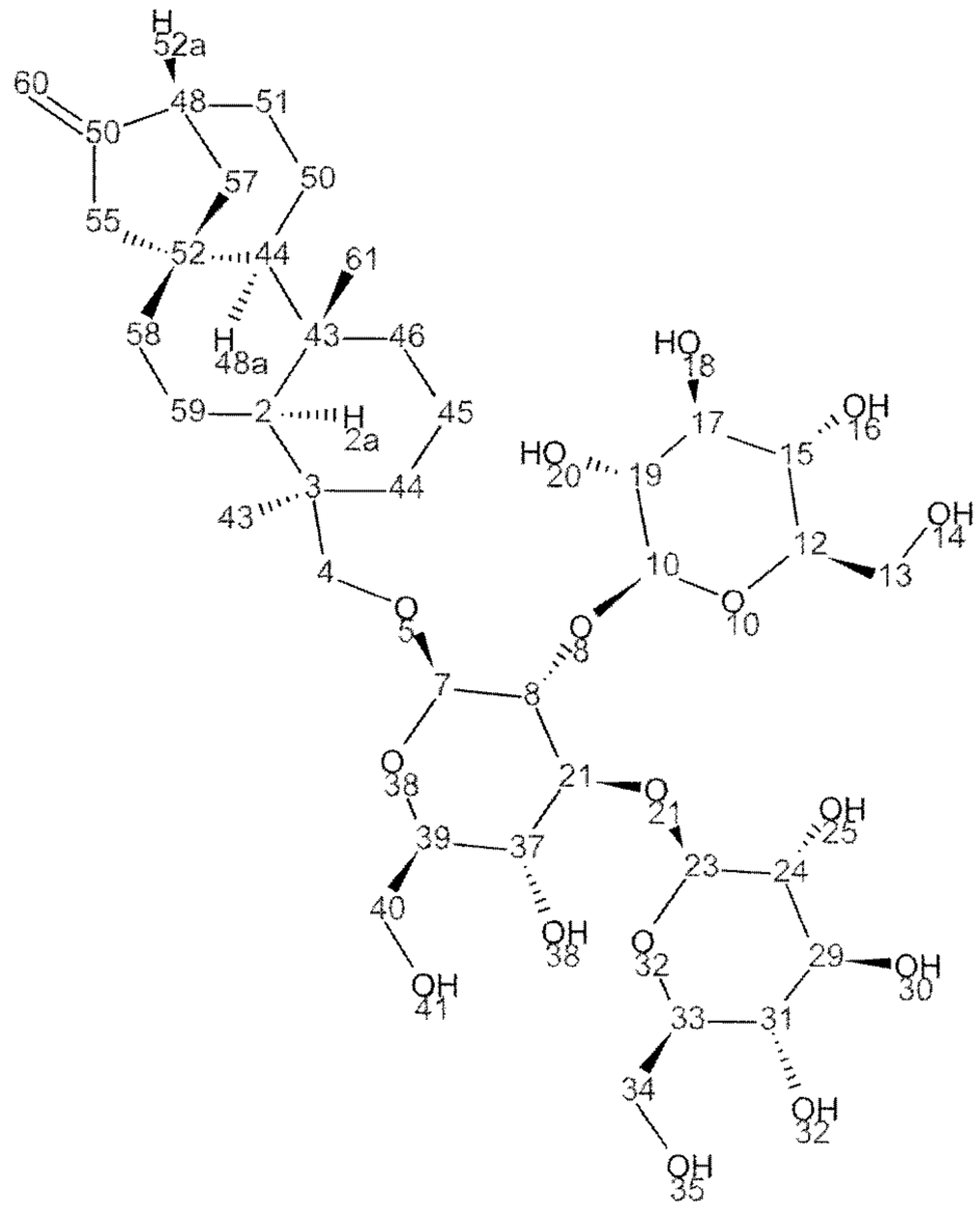


Figure 6l

Kaurenol+3Glc (isomer 1)

^{1}H NMR (800 MHz, *DMSO-d_6*) δ ppm 0.70 - 0.76 (m, 1 H) 0.79 - 0.89 (m, 2 H) 0.93 (s, 3 H) 0.98 (s, 3 H) 1.01 - 1.08 (m, 2 H) 1.28 - 1.34 (m, 1 H) 1.34 - 1.39 (m, 1 H) 1.39 - 1.44 (m, 2 H) 1.44 - 1.48 (m, 1 H) 1.48 - 1.65 (m, 4 H) 1.74 - 1.82 (m, 2 H) 1.88 - 2.00 (m, 2 H) 2.02 - 2.09 (m, 1 H) 2.57 - 2.62 (m, 1 H) 2.91 - 2.97 (m, 1 H) 2.99 - 3.04 (m, 1 H) 3.04 - 3.11 (m, 2 H) 3.13 (t, *J*=9.05 Hz, 1 H) 3.15 - 3.23 (m, 5 H) 3.23 - 3.28 (m, 1 H) 3.44 - 3.48 (m, 2 H) 3.51 (dd, *J*=11.74, 7.82 Hz, 3 H) 3.67 (br. s., 3 H) 3.83 - 3.89 (m, 1 H) 4.25 (d, *J*=7.34 Hz, 2 H) 4.42 (d, *J*=7.83 Hz, 1 H) 4.51 (br. s., 1 H) 4.59 (s, 1 H) 4.63 (d, *J*=8.31 Hz, 2 H) 4.71 (s, 1 H) 4.78 (br. s., 1 H) 4.92 (br. s., 2 H) 5.01 - 5.17 (m, 3 H) 5.52 - 5.62 (m, 1 H)

^{13}C NMR (201.21 MHz, *DMSO-d_6*) δ ppm 155.8 (1C), 103.6 (1C), 103.4 (1C), 102.3 (1C), 102.1 (1C), 86.7 (1C), 78.6 (1C), 77.1 (1C), 77.0 (1C), 76.5 (1C), 76.4 (1C), 76.2 (1C), 74.7 (1C), 73.8 (1C), 72.2 (1C), 70.5 (1C), 70.2 (1C), 68.8 (1C), 61.5 (1C), 61.3 (1C), 61.1 (1C), 56.7 (1C), 55.9 (1C), 48.9 (1C), 44.1 (1C), 43.6 (1C), 41.4 (1C), 40.4 (1C), 39.4 (1C), 39.1 (1C), 37.7 (1C), 36.4 (1C), 33.1 (1C), 28.0 (1C), 20.4 (1C), 18.4 (1C), 18.2 (1C), 18.1 (1C)

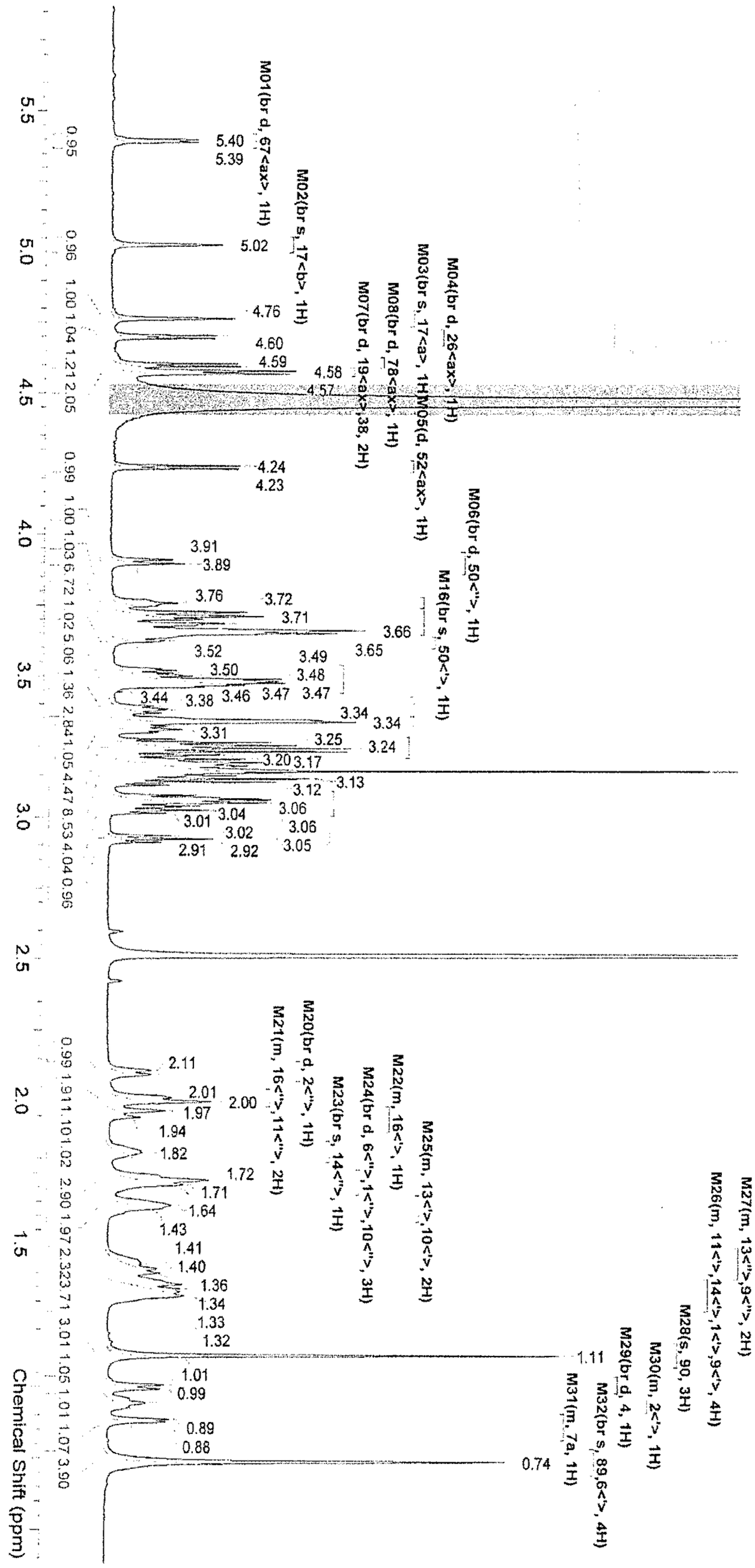
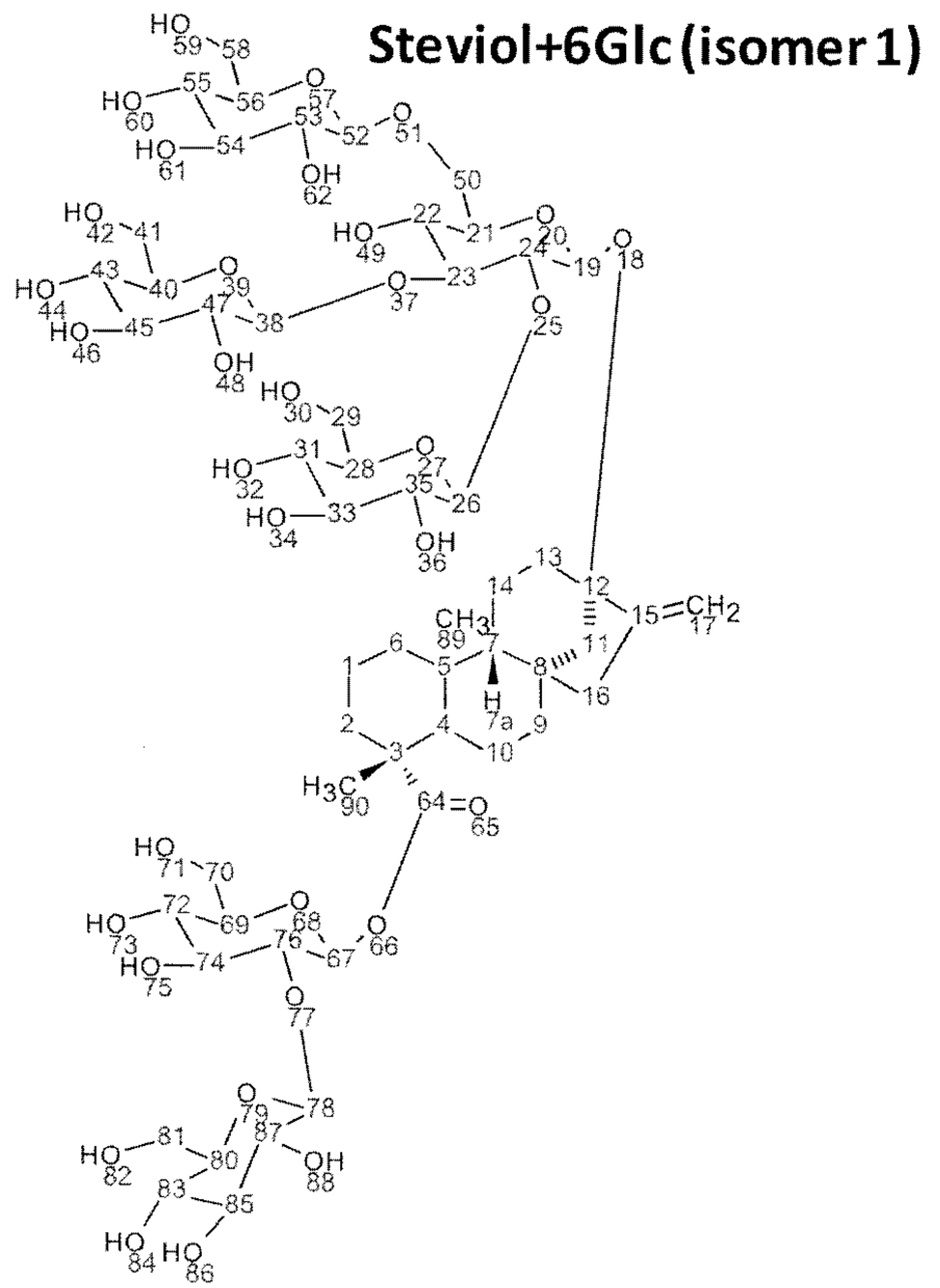

Steviol+6Glc (isomer 1)
M01(br d, 67<ax>, 1H)
M02(br s, 17<b>, 1H)
M03(br s, 17<a>, 1H)
M04(br d, 26<ax>, 1H)
M05(d, 52<ax>, 1H)
M06(br d, 50<'>, 1H)
M07(br d, 19<ax>, 38, 2H)
M08(br d, 78<ax>, 1H)
M11(m, 40<ax>, 1H)
M16(br s, 50<'>, 1H)
M20(br d, 2<">, 1H)
M21(m, 16<">, 11<">, 2H)
M22(m, 16<'>, 1H)
M23(br s, 14<">, 1H)
M24(br d, 6<">, 1<">, 10<">, 3H)
M25(m, 13<'>, 10<'>, 2H)
M26(m, 11<'>, 14<'>, 1<'>, 9<'>, 4H)
M27(m, 13<">, 9<">, 2H)
M28(s, 90, 3H)
M29(br d, 4, 1H)
M30(m, 2<'>, 1H)
M31(m, 7a, 1H)
M32(br s, 89, 6<'>, 4H)
Chemical Shift (ppm)

Figure 6J

Figure 6K

No.	Atom1	Shift1 (ppm)	H's	Type	J (Hz)	Multiplet1	(ppm)
1	89, 6<'>	0.74	4	br s	-	M32	[0.69 .. 0.78]
2	7a	0.88	1	m	-	M31	[0.81 .. 0.91]
3	2<'>	0.94	1	m	-	M30	[0.91 .. 0.98]
4	4	1.00	1	br d	12.72	M29	[0.98 .. 1.04]
5	90	1.11	3	s	-	M28	[1.07 .. 1.15]
6	11<'>, 14<'>, 1<'>, 9<'>	1.34	4	m	-	M26	[1.27 .. 1.38]
7	13<">, 9<">	1.42	2	m	-	M27	[1.38 .. 1.49]
8	13<'>, 10<'>	1.64	2	m	-	M25	[1.58 .. 1.67]
9	6<">, 1<">, 10<">	1.72	3	br d	12.23	M24	[1.67 .. 1.76]
10	14<">	1.82	1	br s	-	M23	[1.79 .. 1.86]
11	16<'>	1.96	1	m	-	M22	[1.89 .. 1.98]
12	16<">, 11<">	2.00	2	m	-	M21	[1.98 .. 2.04]
13	2<">	2.10	1	br d	11.49	M20	[2.07 .. 2.14]
14	31<ax>	2.92	1	m	-	M15	[2.90 .. 2.95]
15	85<ax>, 87<ax>, 35<ax>, 53<ax>	3.05	4	m	-	M14	[3.00 .. 3.09]
16	80<ax>, 83<ax>, 43<ax>, 55<ax>, 56<ax>, 28<ax>, 47<ax>, 33<ax>	3.16	8	m	-	M13	[3.10 .. 3.21]
17	45<ax>, 54<ax>, 74<ax>, 72<ax>	3.25	4	br dd	17.24, 8.93	M19	[3.21 .. 3.28]
18	40<ax>	3.31	1	m	-	M11	[3.30 .. 3.32]
19	69<ax>, 21<ax>, 22<ax>	3.34	3	br d	4.65	M18	[3.32 .. 3.35]
20	29<'>	3.38	1	m	-	M12	[3.36 .. 3.43]
21	81<'>, 41<'>, 58<'>, 70<'>, 24<ax>	3.48	5	m	-	M10	[3.44 .. 3.54]
22	50<'>	3.62	1	br s	-	M16	[3.59 .. 3.64]
23	81<">, 41<">, 58<">, 76<ax>, 70<">, 29<">	3.68	6	m	-	M09	[3.64 .. 3.74]
24	23<ax>	3.75	1	br d	8.56	M17	[3.74 .. 3.78]
25	50<">	3.90	1	br d	11.25	M06	[3.86 .. 3.94]
26	52<ax>	4.24	1	d	7.82	M05	[4.22 .. 4.26]
27	19<ax>, 38	4.57	2	br d	7.83	M07	[4.56 .. 4.59]
28	78<ax>	4.60	1	br d	7.58	M08	[4.59 .. 4.63]
29	26<ax>	4.70	1	br d	7.82	M04	[4.67 .. 4.72]
30	17<a>	4.76	1	br s	-	M03	[4.73 .. 4.79]
31	17<b>	5.02	1	br s	-	M02	[5.00 .. 5.05]
32	67<ax>	5.39	1	br d	7.34	M01	[5.37 .. 5.42]



^{1}H NMR (800 MHz, *DMSO-d*$_6$) δ ppm 0.74 (br s, 4 H) 0.81 - 0.91 (m, 1 H) 0.91 - 0.98 (m, 1 H) 1.00 (br d, *J*=12.72 Hz, 1 H) 1.11 (s, 3 H) 1.27 - 1.38 (m, 4 H) 1.38 - 1.49 (m, 2 H) 1.58 - 1.67 (m, 2 H) 1.72 (br d, *J*=12.23 Hz, 3 H) 1.82 (br s, 1 H) 1.89 - 1.98 (m, 1 H) 1.98 - 2.04 (m, 2 H) 2.10 (br d, *J*=11.49 Hz, 1 H) 2.90 - 2.95 (m, 1 H) 3.00 - 3.09 (m, 4 H) 3.10 - 3.21 (m, 8 H) 3.25 (br dd, *J*=17.24, 8.93 Hz, 4 H) 3.30 - 3.32 (m, 1 H) 3.34 (br d, *J*=4.65 Hz, 3 H) 3.36 - 3.43 (m, 1 H) 3.44 - 3.54 (m, 5 H) 3.62 (br s, 1 H) 3.64 - 3.74 (m, 6 H) 3.75 (br d, *J*=8.56 Hz, 1 H) 3.90 (br d, *J*=11.25 Hz, 1 H) 4.24 (d, *J*=7.82 Hz, 1 H) 4.57 (br d, *J*=7.83 Hz, 2 H) 4.60 (br d, *J*=7.58 Hz, 1 H) 4.70 (br d, *J*=7.82 Hz, 1 H) 4.76 (br s, 1 H) 5.02 (br s, 1 H) 5.39 (br d, *J*=7.34 Hz, 1 H)

Figure 6L

F2 Atom	F2 (ppm)	F2 Atom	F2 (ppm)	F1 Atom	F1 (ppm)	F1 Atom	F1 (ppm)
1<">	1.71	31<ax>	2.91	1	19.9	31	71.5
1<'>	1.31	33<ax>	3.18			33	77.2
2<">	2.09	35<ax>	3.01	2	37.7	35	75.4
2<'>	0.93	38<ax>	4.56			38	103.3
		40<ax>	3.33	3	44.8	40	77.8
4	0.99	41<">	3.69	4	57.4	41	61.9
		41<'>	3.46	5	40.3		
6<">	1.71	43<ax>	3.24	6	40.8	43	70.3
6<'>	0.73	45<ax>	3.23			45	76.9
7a	0.87	47<ax>	3.12	7	54	47	74.4
		50<">	3.89	8	42.2	50	69.3
9<">	1.39	50<'>	3.62	9	42.1		
9<'>	1.31	52<ax>	4.23			52	103.9
10<">	1.72	53<ax>	3.04	10	22.7	53	74.2
10<'>	1.62	54<ax>	3.18			54	77.2
11<">	2	55<ax>	3.33	11	44.4	55	69.1
11<'>	1.34	56<ax>	3.3			56	77.2
		58<">	3.68	12	88.4	58	62
13<">	1.81	58<'>	3.46	13	38.3		
13<'>	1.36					64	178
14<">	1.62	67<ax>	5.38	14	20.6	67	93.6
14<'>	1.43	69<ax>	3.23			69	76.9
		70<">	3.64	15	153.2	70	61.6
16<">	1.99	70<'>	3.5	16	47.4		
16<'>	1.94	72<ax>	3.15			72	70.8
17<a>	4.75	74<ax>	3.65	17	105.8	74	77.2
17<b>	5.02	76	3.65			76	78.4
19<ax>	4.57	78<ax>	4.59	19	96.4	78	103.3
21<ax>	3.15	80<ax>	3.33	21	77.6	80	75.6
22<ax>	3.12	81<">	3.66	22	70.8	81	62.7
23<ax>	3.75	81<'>	3.37	23	86.5		
24<ax>	3.48	83<ax>	3.06	24	79.6	83	71.3
26<ax>	4.69	85<ax>	3.18	26	103	85	77.2
28<ax>	3.3	87<ax>	3.05	28	77.2	87	75.1
29<">	3.71	89	0.73	29	62.1	89	17.1
29<'>	3.69	90	1.1			90	29.2

^{13}C NMR (201 MHz, *DMSO-d_6*) δ ppm 17.1, 19.9, 20.6, 22.7, 29.2, 37.7, 38.3, 40.3, 40.8, 42.1, 42.2, 44.4, 44.8, 47.4, 54.0, 57.4, 61.6, 61.9, 62.0, 62.1, 62.7, 69.1, 69.3, 70.3, 70.8, 70.8, 71.3, 71.5, 74.2, 74.4, 75.1, 75.4, 75.6, 76.9, 76.9, 77.2, 77.2, 77.2, 77.2, 77.2, 77.2, 77.6, 77.8, 78.4, 79.6, 86.5, 88.4, 93.6, 96.4, 103.0, 103.3, 103.3, 103.9, 105.8, 153.2, 178.0

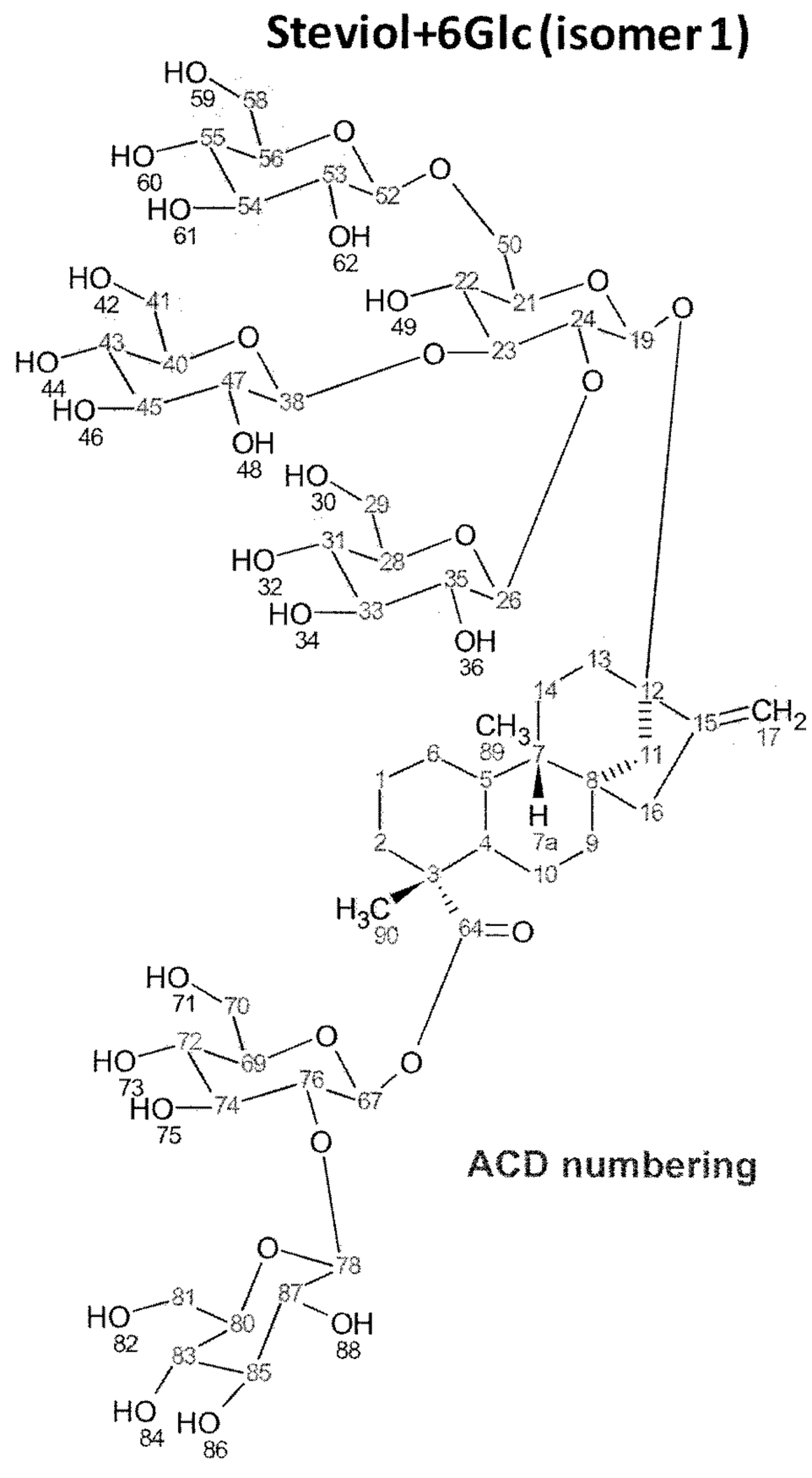
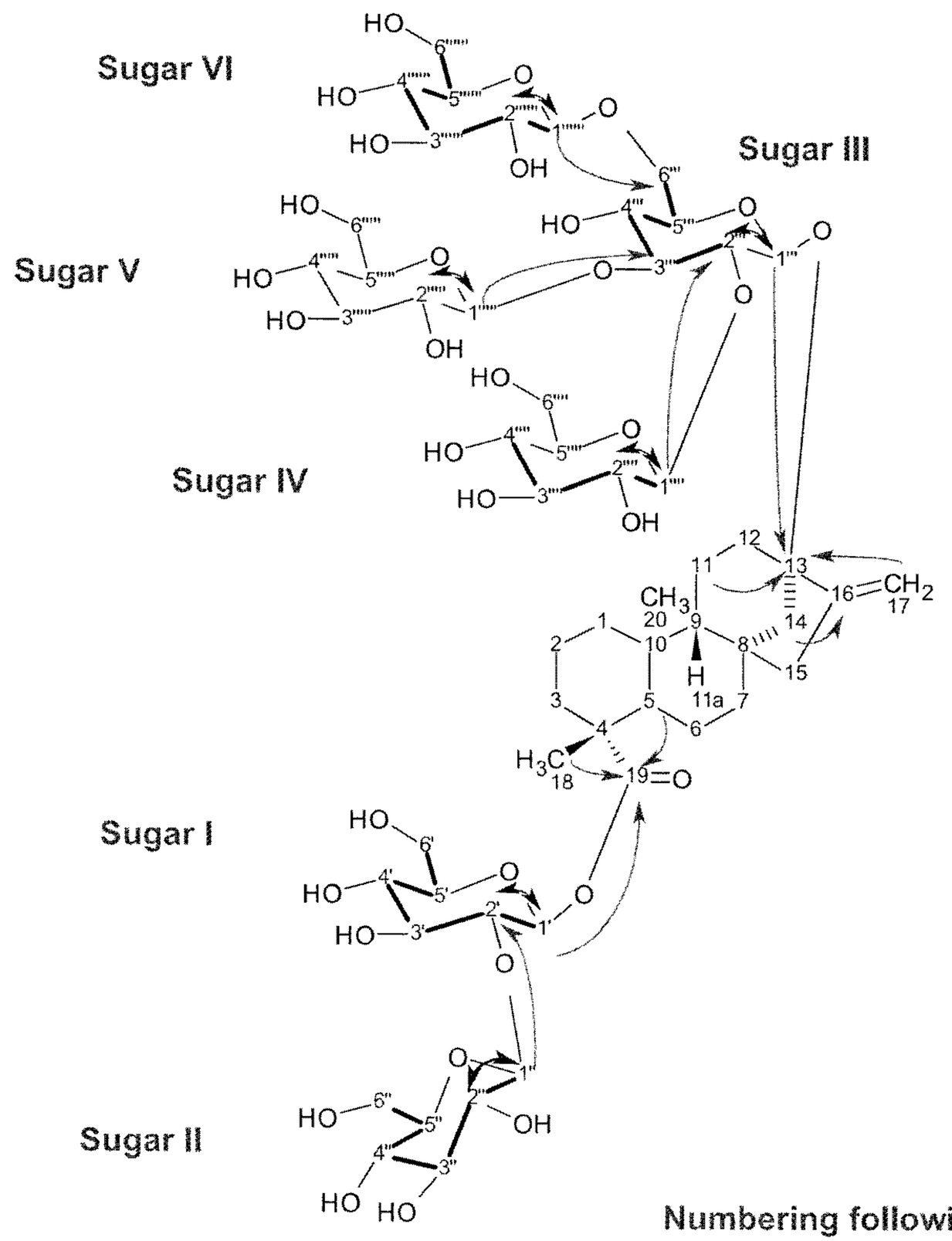


Figure 6M



= ^{1}H-^{13}C HMBC

= ^{1}H-^{1}H COSY

= ^{1}H-^{1}H TOCSY spin system

Assigments were made on the basis of ^{1}H-^{1}H COSY, ^{1}H-^{1}H TOCSY, ^{1}H-^{13}C HSQC-DEPT, ^{1}H-^{13}C HMBC.

Figure 6N

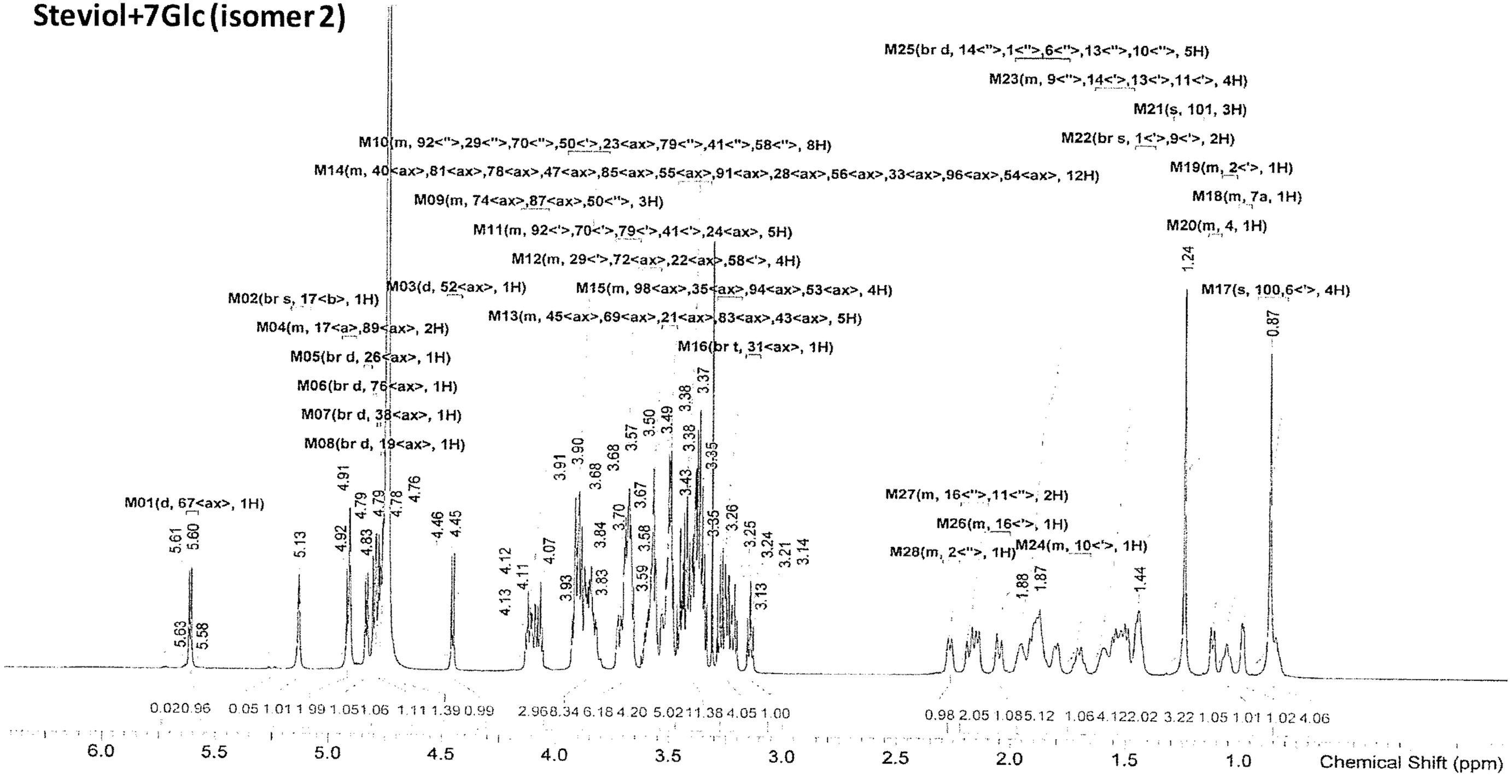
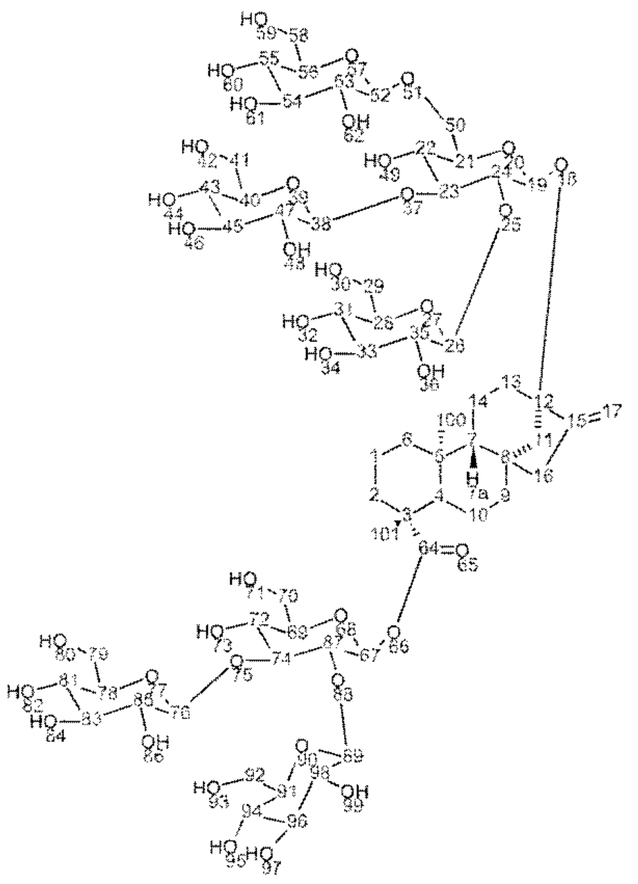

Steviol+7Glc (isomer 2)
M25(br d, 14<''>,1<''>,6<''>,13<''>,10<''>, 5H)
M23(m, 9<''>,14<'>,13<'>,11<'>, 4H)
M21(s, 101, 3H)
M22(br s, 1<'>,9<'>, 2H)
M10(m, 92<''>,29<''>,70<''>,50<'>,23<ax>,79<''>,41<''>,58<''>, 8H)
M19(m, 2<'>, 1H)
M14(m, 40<ax>,81<ax>,78<ax>,47<ax>,85<ax>,55<ax>,91<ax>,28<ax>,56<ax>,33<ax>,96<ax>,54<ax>, 12H)
M18(m, 7a, 1H)
M09(m, 74<ax>,87<ax>,50<''>, 3H)
M20(m, 4, 1H)
M11(m, 92<'>,70<'>,79<'>,41<'>,24<ax>, 5H)
M12(m, 29<'>,72<ax>,22<ax>,58<'>, 4H)
M03(d, 52<ax>, 1H)
M15(m, 98<ax>,35<ax>,94<ax>,53<ax>, 4H)
M17(s, 100,6<'>, 4H)
M02(br s, 17<b>, 1H)
M13(m, 45<ax>,69<ax>,21<ax>,83<ax>,43<ax>, 5H)
M04(m, 17<a>,89<ax>, 2H)
M16(br t, 31<ax>, 1H)
M05(br d, 26<ax>, 1H)
M06(br d, 76<ax>, 1H)
M07(br d, 38<ax>, 1H)
M08(br d, 19<ax>, 1H)
M01(d, 67<ax>, 1H)
M27(m, 16<''>,11<''>, 2H)
M26(m, 16<'>, 1H)
M28(m, 2<''>, 1H)
M24(m, 10<'>, 1H)
0.020.96 0.05 1.01 1.99 1.05 1.06 1.11 1.39 0.99 2.96 8.34 6.18 4.20 5.02 11.38 4.05 1.00
0.98 2.05 1.08 5.12 1.06 4.12 2.02 3.22 1.05 1.01 1.02 4.06
6.0
5.5
5.0
4.5
4.0
3.5
3.0
2.5
2.0
1.5
1.0
Chemical Shift (ppm)

Figure 60

Steviol+7Glc (isomer 2)

No.	Atom1	Shift1 (ppm)	H's	Type	J (Hz)	Multiplet1	(ppm)
1	100, 6<'>	0.87	4	s	-	M17	[0.80 .. 0.93]
2	7a	0.99	1	m	-	M18	[0.96 .. 1.02]
3	2<'>	1.06	1	m	-	M19	[1.02 .. 1.09]
4	4	1.12	1	m	-	M20	[1.09 .. 1.15]
5	101	1.24	3	s	-	M21	[1.17 .. 1.30]
6	1<'>, 9<'>	1.44	2	br s	-	M22	[1.38 .. 1.47]
7	9<">, 14<'>, 13<'>, 11<'>	1.56	4	m	-	M23	[1.47 .. 1.65]
8	10<'>	1.70	1	m	-	M24	[1.65 .. 1.75]
9	14<">, 1<">, 6<">, 13<">, 10<">	1.88	5	br d	10.51	M25	[1.76 .. 1.99]
10	16<'>	2.05	1	m	-	M26	[2.00 .. 2.09]
11	16<">, 11<">	2.16	2	m	-	M27	[2.10 .. 2.22]
12	2<">	2.26	1	m	-	M28	[2.23 .. 2.30]
13	31<ax>	3.14	1	br t	9.41	M16	[3.10 .. 3.17]
14	98<ax>, 35<ax>, 94<ax>, 53<ax>	3.24	4	m	-	M15	[3.19 .. 3.30]
15	40<ax>, 81<ax>, 78<ax>, 47<ax>, 85<ax>, 55<ax>, 91<ax>, 28<ax>, 56<ax>, 33<ax>, 96<ax>, 54<	3.40	12	m	-	M14	[3.32 .. 3.47]
16	45<ax>, 69<ax>, 21<ax>, 83<ax>, 43<ax>	3.50	5	m	-	M13	[3.47 .. 3.54]
17	29<'>, 72<ax>, 22<ax>, 58<'>	3.58	4	m	-	M12	[3.54 .. 3.63]
18	92<'>, 70<'>, 79<'>, 41<'>, 24<ax>	3.69	5	m	-	M11	[3.63 .. 3.74]
19	92<">, 29<">, 70<">, 50<'>, 23<ax>, 79<">, 41<">, 58<">	3.86	8	m	-	M10	[3.77 .. 3.95]
20	74<ax>, 87<ax>, 50<">	4.09	3	m	-	M09	[4.04 .. 4.16]
21	52<ax>	4.45	1	d	7.82	M03	[4.42 .. 4.49]
22	19<ax>	4.77	1	br d	8.07	M08	[4.76 .. 4.77]
23	38<ax>	4.78	1	br d	8.07	M07	[4.78 .. 4.79]
24	76<ax>	4.80	1	br d	8.07	M06	[4.79 .. 4.81]
25	26<ax>	4.83	1	br d	7.83	M05	[4.81 .. 4.85]
26	17<a>, 89<ax>	4.91	2	m	-	M04	[4.88 .. 4.95]
27	17<b>	5.13	1	br s	-	M02	[5.09 .. 5.17]
28	67<ax>	5.61	1	d	7.83	M01	[5.58 .. 5.63]



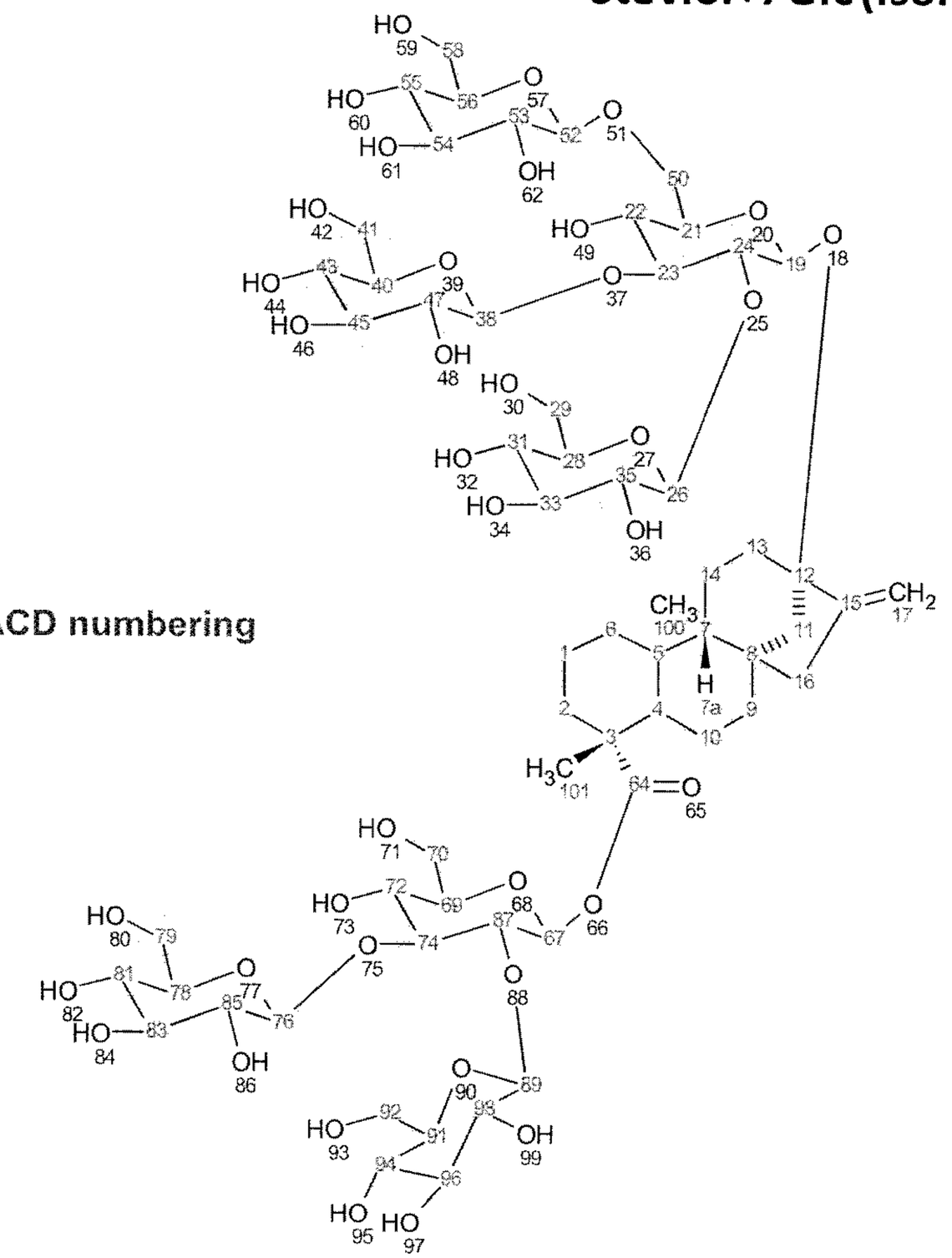
^{1}H NMR (800 MHz, *DEUTERIUM OXIDE*) δ ppm 0.87 (s, 4 H) 0.96 - 1.02 (m, 1 H) 1.02 - 1.09 (m, 1 H) 1.09 - 1.15 (m, 1 H) 1.24 (s, 3 H) 1.44 (br s, 2 H) 1.47 - 1.65 (m, 4 H) 1.65 - 1.75 (m, 1 H) 1.88 (br d, *J*=10.51 Hz, 5 H) 2.00 - 2.09 (m, 1 H) 2.10 - 2.22 (m, 2 H) 2.23 - 2.30 (m, 1 H) 3.14 (br t, *J*=9.41 Hz, 1 H) 3.19 - 3.30 (m, 4 H) 3.32 - 3.47 (m, 12 H) 3.47 - 3.54 (m, 5 H) 3.54 - 3.63 (m, 4 H) 3.63 - 3.74 (m, 5 H) 3.77 - 3.95 (m, 8 H) 4.04 - 4.16 (m, 3 H) 4.45 (d, *J*=7.82 Hz, 1 H) 4.77 (br d, *J*=8.07 Hz, 1 H) 4.78 (br d, *J*=8.07 Hz, 1 H) 4.80 (br d, *J*=8.07 Hz, 1 H) 4.83 (br d, *J*=7.83 Hz, 1 H) 4.88 - 4.95 (m, 2 H) 5.13 (br s, 1 H) 5.61 (d, *J*=7.83 Hz, 1 H)

Figure 6P

F2 Atom	F2 (ppm)	F1 Atom	F1 (ppm)
1<">	1.87	1	19.3
1<'>	1.45		
2<">	2.27	2	37.1
2<'>	1.06		
		3	44.3
4	1.12	4	57.1
		5	39.8
6<">	1.88	6	40.3
6<'>	0.84		
7a	0.99	7	53.5
		8	42
9<">	1.55	9	41.5
9<'>	1.44		
10<">	1.91	10	22.1
10<'>	1.7		
11<">	2.15	11	44
11<'>	1.5		
		12	88.6
13<">	1.96	13	37.5
13<'>	1.52		
14<">	1.81	14	20.3
14<'>	1.6		
		15	153.1
16<">	2.19	16	47
16<'>	2.06		
17<a>	4.91	17	104.9
17<b>	5.14		
19<ax>	4.77	19	95.7
21<ax>	3.54	21	74.8
22<ax>	3.57	22	68.5
23<ax>	3.92	23	85.4
24<ax>	3.68	24	78.9
26<ax>	4.84	26	102.4
28<ax>	3.39	28	76.6
29<">	3.87	29	62
29<'>	3.6		
31<ax>	3.15	31	70.9
33<ax>	3.44	33	76.2
35<ax>	3.25	35	74.6
38<ax>	4.79	38	102.4

F2 Atom	F2 (ppm)	F1 Atom	F1 (ppm)
40<ax>	3.44	40	76.2
41<">	3.89	41	61.1
41<'>	3.7		
43<ax>	3.51	43	69.9
45<ax>	3.51	45	76.3
47<ax>	3.35	47	73.8
50<">	4.1	50	68.9
50<'>	3.83		
52<ax>	4.46	52	103.1
53<ax>	3.28	53	73.5
54<ax>	3.44	54	76.2
55<ax>	3.39	55	69.9
56<ax>	3.44	56	76.2
58<">	3.89	58	61.1
58<'>	3.7		
		64	178.8
67<ax>	5.62	67	92.9
69<ax>	3.51	69	76.3
70<">	3.89	70	61.1
70<'>	3.7		
72<ax>	3.54	72	68.5
74<ax>	4.13	74	85.1
76<ax>	4.8	76	102.4
78<ax>	3.39	78	76.6
79<">	3.89	79	61.1
79<'>	3.7		
81<ax>	3.39	81	69.9
83<ax>	3.51	83	76.3
85<ax>	3.37	85	73.8
87<ax>	4.07	87	76.3
89<ax>	4.92	89	101.9
91<ax>	3.39	91	76.6
92<">	3.92	92	62
92<'>	3.67		
94<ax>	3.26	94	70.9
96<ax>	3.44	96	76.2
98<ax>	3.22	98	74.2
100	0.87	100	16.4
101	1.25	101	28.6

Steviol+7Glc (isomer 2)



ACD numbering

^{13}C NMR (201 MHz, *DEUTERIUM OXIDE*) δ ppm 16.4, 19.3, 20.3, 22.1, 28.6, 37.1, 37.5, 39.8, 40.3, 41.5, 42.0, 44.0, 44.3, 47.0, 53.5, 57.1, 61.1, 61.1, 61.1, 61.1, 62.0, 62.0, 68.5, 68.5, 68.9, 69.9, 69.9, 69.9, 70.9, 70.9, 73.5, 73.8, 73.8, 74.2, 74.6, 74.8, 76.2, 76.2, 76.2, 76.2, 76.2, 76.3, 76.3, 76.3, 76.3, 76.6, 76.6, 76.6, 78.9, 85.1, 85.4, 88.6, 92.9, 95.7, 101.9, 102.4, 102.4, 102.4, 103.1, 104.9, 153.1, 178.8

Figure 6Q

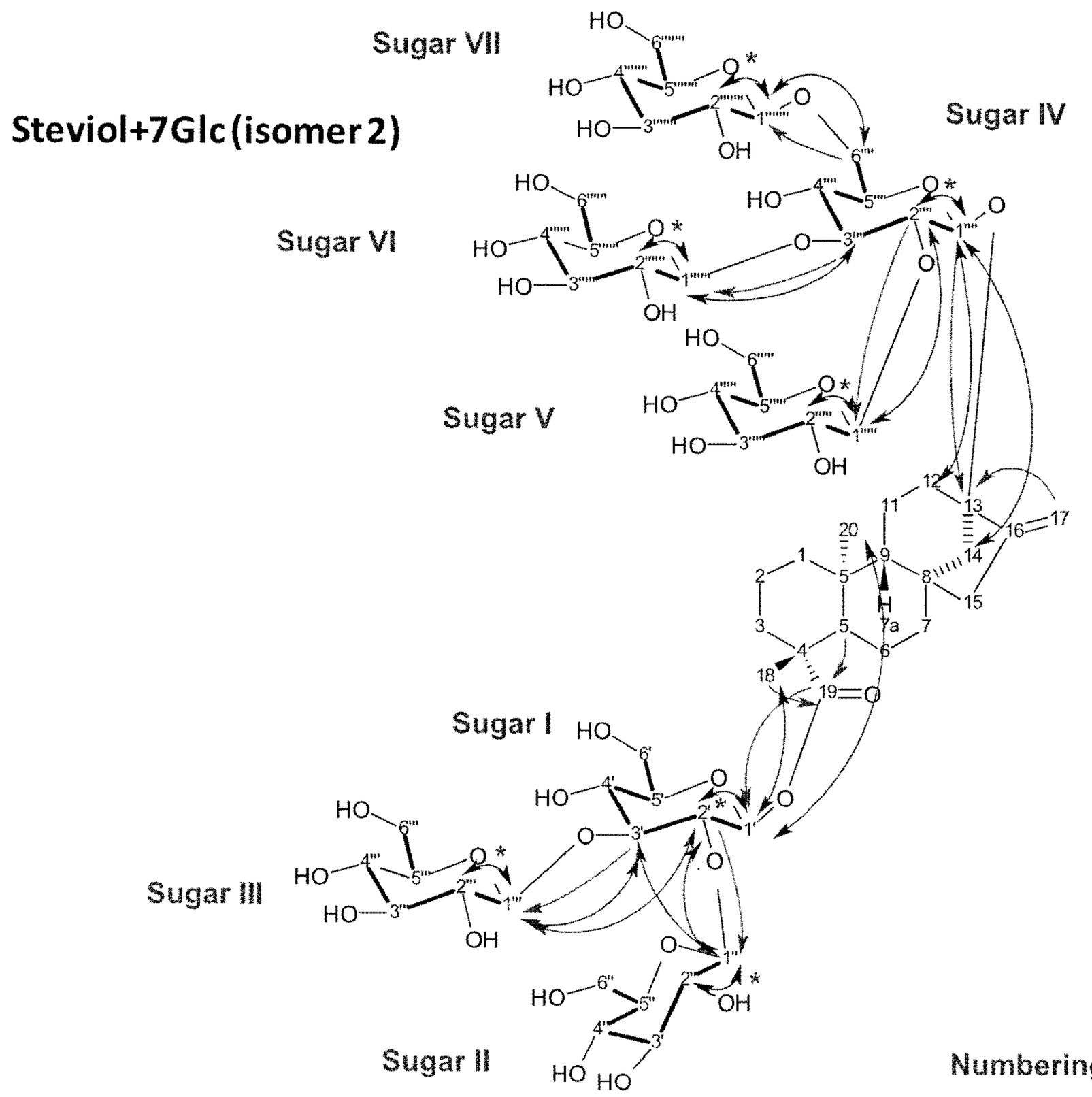

Steviol+7Glc (isomer 2)
Sugar VII
Sugar IV
Sugar VI
Sugar V
Sugar I
Sugar III
Sugar II
= ^{1}H-^{13}C HMBC
= ^{1}H-^{1}H COSY
= ^{1}H-^{1}H TOCSY spin system
= ^{1}H-^{1}H dipolar correlation (ROESY)
Assigments were made on the basis of ^{1}H-^{1}H COSY, ^{1}H-^{1}H TOCSY, ^{1}H-^{13}C HSQC-DEPT, ^{1}H-^{13}C HMBC and ^{1}H-^{1}H ROESY.
Numbering following IUPAC

Figure 6R

Steviol+4Glc (#26)

Homonuclear diploar correlations between:
H-2 and Me-53, Me-54
H-11 and H-3, H-18
H-18 and H-4
H-68 and H-28, Me-53, H-38'
H-28 and H-38', Me-53
Me-54 and H-32"

Heteronuclear scalar correlations between:
C=O(-8) and H-2, Me-53, H-28
H-11 and C-3 (H-3 and C-11)
H-18 and C-4 (H-4 and C18)
H-56 and C-33

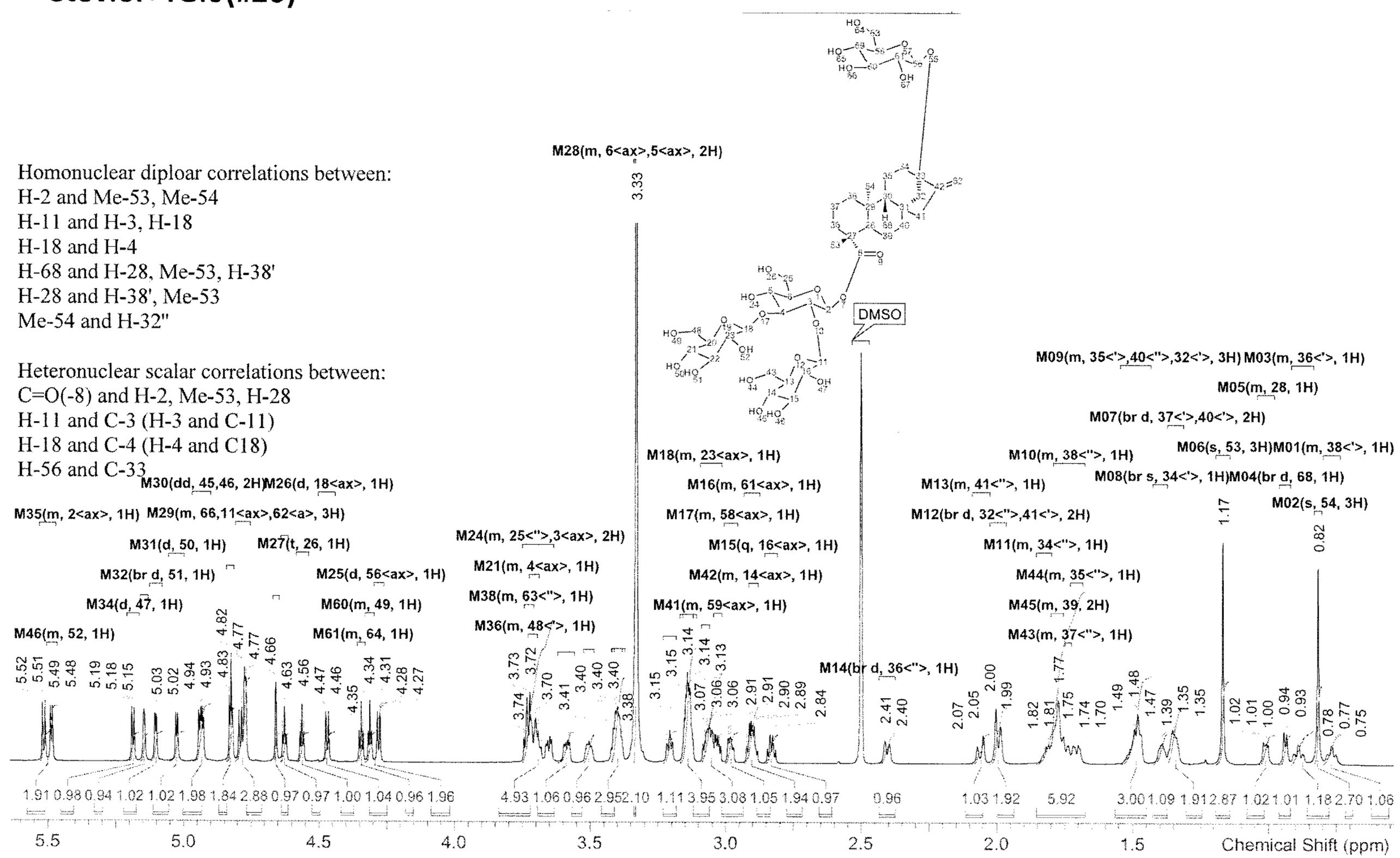
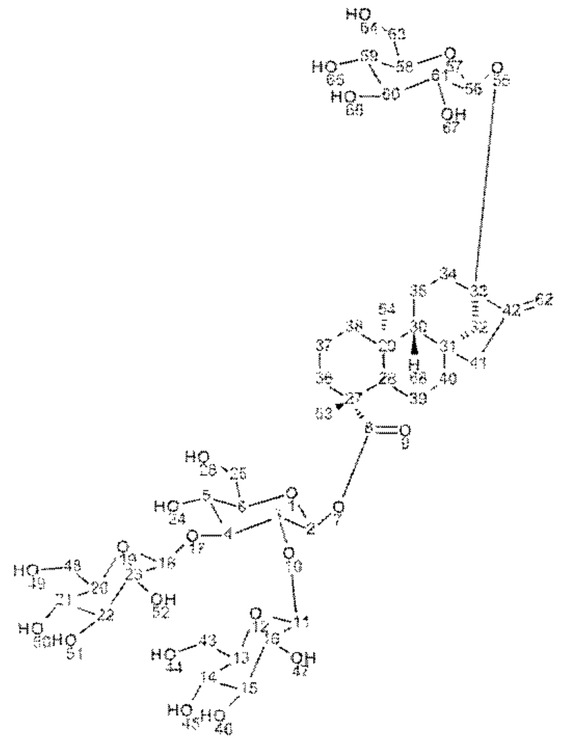


Figure 6S

Steviol+4Glc (#26)

Multiplet1	Shift1 (ppm	Atom1	H's	Type	J (Hz)	(ppm)
M35	5.50	2<ax>	1	m	-	[5.47 .. 5.53]
M46	5.49	52	1	m	-	[5.47 .. 5.50]
M34	5.19	47	1	d	6.60	[5.16 .. 5.21]
M33	5.15	62<b>	1	br s	-	[5.13 .. 5.16]
M32	5.10	51	1	br d	4.89	[5.08 .. 5.13]
M31	5.03	50	1	d	5.38	[5.00 .. 5.06]
M30	4.93	45, 46	2	dd	8.80, 4.89	[4.90 .. 4.97]
M58	4.83	65, 67	2	m	-	[4.81 .. 4.84]
M29	4.78	66, 11<ax>, 62<a>	3	m	-	[4.75 .. 4.81]
M59	4.66	24	1	m	-	[4.65 .. 4.67]
M62	4.63	44	1	m	-	[4.61 .. 4.64]
M27	4.56	26	1	t	5.50	[4.54 .. 4.58]
M26	4.47	18<ax>	1	d	7.83	[4.44 .. 4.50]
M61	4.34	64	1	m	-	[4.33 .. 4.36]
M60	4.31	49	1	m	-	[4.30 .. 4.33]
M25	4.28	56<ax>	1	d	7.82	[4.26 .. 4.30]
M38	3.73	63<">	1	m	-	[3.71 .. 3.74]
M36	3.71	48<'>	1	m	-	[3.69 .. 3.73]
M21	3.71	4<ax>	1	m	-	[3.69 .. 3.72]
M24	3.70	25<">, 3<ax>	2	m	-	[3.63 .. 3.75]
M23	3.59	43<">	1	br dd	9.90, 5.50	[3.56 .. 3.62]
M22	3.50	25<'>	1	m	-	[3.49 .. 3.52]
M47	3.40	43<'>	1	m	-	[3.38 .. 3.42]
M37	3.40	48<">	1	m	-	[3.38 .. 3.42]
M39	3.39	63<'>	1	m	-	[3.37 .. 3.41]
M28	3.33	6<ax>, 5<ax>	2	m	-	[3.33 .. 3.34]
M20	3.21	20<ax>	1	m	-	[3.18 .. 3.23]
M19	3.14	60<ax>, 15<ax>, 22<ax>	3	m	-	[3.11 .. 3.17]
M48	3.14	13<ax>	1	m	-	[3.12 .. 3.16]
M40	3.07	21<ax>	1	m	-	[3.06 .. 3.09]
M18	3.05	23<ax>	1	m	-	[3.01 .. 3.09]
M41	3.03	59<ax>	1	m	-	[3.01 .. 3.05]
M17	2.98	58<ax>	1	m	-	[2.96 .. 3.00]
M16	2.90	61<ax>	1	m	-	[2.87 .. 2.93]
M42	2.90	14<ax>	1	m	-	[2.88 .. 2.91]
M15	2.83	16<ax>	1	q	7.99	[2.81 .. 2.85]
M14	2.40	36<">	1	br d	12.47	[2.38 .. 2.43]
M13	2.06	41<">	1	m	-	[2.03 .. 2.09]
M12	1.99	32<">, 41<'>	2	br d	13.45	[1.96 .. 2.03]
M11	1.82	34<">	1	m	-	[1.80 .. 1.85]
M45	1.78	39	2	m	-	[1.75 .. 1.80]
M10	1.75	38<">	1	m	-	[1.68 .. 1.79]
M43	1.74	37<">	1	m	-	[1.72 .. 1.75]
M44	1.71	35<">	1	m	-	[1.68 .. 1.73]
M09	1.49	35<'>, 40<">, 32<'>	3	m	-	[1.43 .. 1.54]
M08	1.39	34<'>	1	br s	-	[1.37 .. 1.42]
M07	1.35	37<'>, 40<'>	2	br d	4.40	[1.31 .. 1.37]
M06	1.17	53	3	s	-	[1.14 .. 1.19]
M05	1.01	28	1	m	-	[0.98 .. 1.04]
M04	0.94	68	1	br d	8.07	[0.92 .. 0.96]
M03	0.89	36<'>	1	m	-	[0.83 .. 0.91]
M02	0.82	54	3	s	-	[0.80 .. 0.83]
M01	0.77	38<'>	1	m	-	[0.73 .. 0.80]

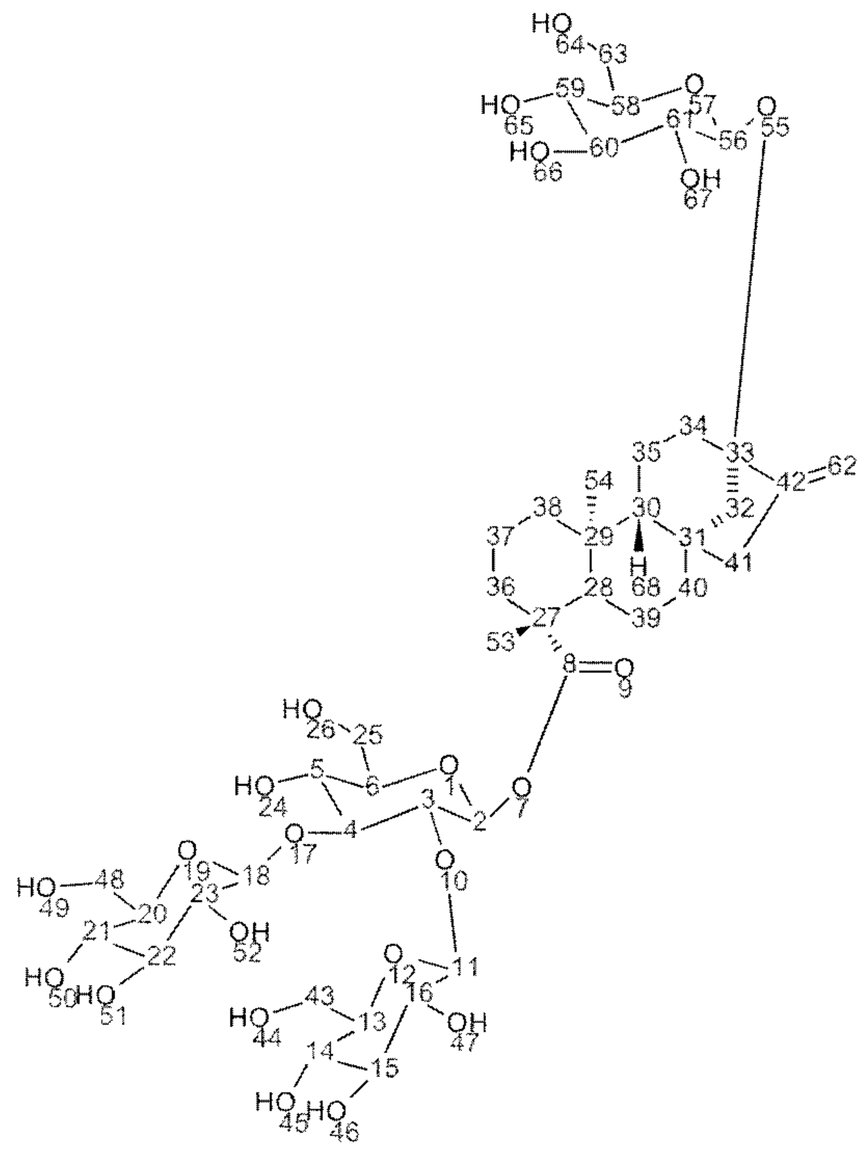


^{1}H NMR (800 MHz, *DMSO-d_6*) δ ppm 0.73 - 0.80 (m, 1 H) 0.82 (s, 3 H) 0.83 - 0.91 (m, 1 H) 0.94 (br d, *J*=8.07 Hz, 1 H) 0.98 - 1.04 (m, 1 H) 1.17 (s, 3 H) 1.35 (br d, *J*=4.40 Hz, 2 H) 1.39 (br s, 1 H) 1.43 - 1.54 (m, 3 H) 1.68 - 1.79 (m, 1 H) 1.68 - 1.73 (m, 1 H) 1.72 - 1.75 (m, 1 H) 1.75 - 1.80 (m, 2 H) 1.80 - 1.85 (m, 1 H) 1.99 (br d, *J*=13.45 Hz, 2 H) 2.03 - 2.09 (m, 1 H) 2.40 (br d, *J*=12.47 Hz, 1 H) 2.83 (q, *J*=7.99 Hz, 1 H) 2.87 - 2.93 (m, 1 H) 2.88 - 2.91 (m, 1 H) 2.96 - 3.00 (m, 1 H) 3.01 - 3.09 (m, 1 H) 3.01 - 3.05 (m, 1 H) 3.06 - 3.09 (m, 1 H) 3.11 - 3.17 (m, 3 H) 3.12 - 3.16 (m, 1 H) 3.18 - 3.23 (m, 1 H) 3.33 - 3.34 (m, 2 H) 3.37 - 3.41 (m, 1 H) 3.38 - 3.42 (m, 1 H) 3.38 - 3.42 (m, 1 H) 3.49 - 3.52 (m, 1 H) 3.59 (br dd, *J*=9.90, 5.50 Hz, 1 H) 3.63 - 3.75 (m, 2 H) 3.69 - 3.72 (m, 1 H) 3.69 - 3.73 (m, 1 H) 3.71 - 3.74 (m, 1 H) 4.28 (d, *J*=7.82 Hz, 1 H) 4.30 - 4.33 (m, 1 H) 4.33 - 4.36 (m, 1 H) 4.47 (d, *J*=7.83 Hz, 1 H) 4.56 (t, *J*=5.50 Hz, 1 H) 4.61 - 4.64 (m, 1 H) 4.65 - 4.67 (m, 1 H) 4.75 - 4.81 (m, 3 H) 4.81 - 4.84 (m, 2 H) 4.93 (dd, *J*=8.80, 4.89 Hz, 2 H) 5.03 (d, *J*=5.38 Hz, 1 H) 5.10 (br d, *J*=4.89 Hz, 1 H) 5.15 (br s, 1 H) 5.19 (d, *J*=6.60 Hz, 1 H) 5.47 - 5.50 (m, 1 H) 5.47 - 5.53 (m, 1 H)

Figure 6T

Steviol+4Glc (#26)

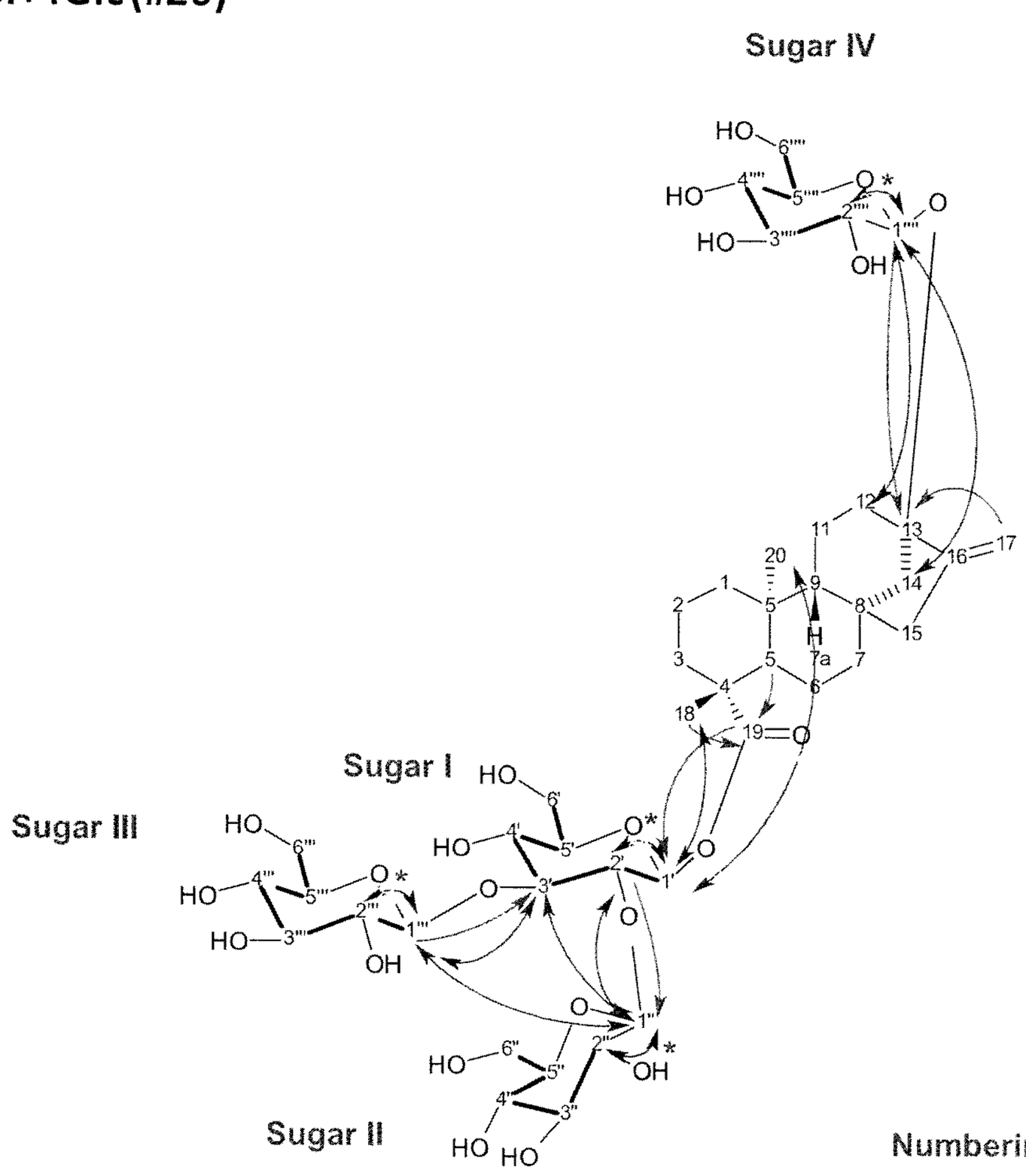
F2 Atom	δ(1H) (ppm)	F1 Atom	δ(13C) (ppm)
2<ax>	5.52	2	91.9
3<ax>	3.73	3	75.5
4<ax>	3.69	4	87
5<ax>	3.34	5	68.3
6<ax>	3.33	6	77.8
		8	174.9
11<ax>	4.79	11	101.8
13<ax>	3.14	13	77.3
14<ax>	2.89	14	71.4
15<ax>	3.14	15	77
16<ax>	2.83	16	74.3
18<ax>	4.47	18	103.3
20<ax>	3.21	20	77.3
21<ax>	3.07	21	70.3
22<ax>	3.14	22	77
23<ax>	3.06	23	74
25<''>	3.65	25	60.7
25<'>	3.5		
		27	43.6
28	1.01	28	56.7
		29	39.1
		31	41.6
32<''>	2	32	43.6
32<'>	1.48		
		33	85.8
34<''>	1.82	34	37.9
34<'>	1.39		
35<''>	1.7	35	20.1
35<'>	1.5		
36<''>	2.4	36	36.6
36<'>	0.89		
37<''>	1.74	37	19.5
37<'>	1.35		
38<''>	1.78	38	40.2
38<'>	0.77		
39	1.78	39	21.4
40<''>	1.49	40	41.3
40<'>	1.35		
41<''>	2.06	41	47.8
41<'>	2		
		42	152.6
43<''>	3.59	43	61.4
43<'>	3.39		
48<''>	3.4	48	61.3
48<'>	3.71		
53	1.17	53	28.5
54	0.82	54	16.4
56<ax>	4.28	56	98.1
58<ax>	2.98	58	76.9
59<ax>	3.03	59	70.5
60<ax>	3.14	60	77
61<ax>	2.91	61	74
62<a>	4.77	62	104.8
62<b>	5.15		
63<''>	3.73	63	62
63<'>	3.39		
68	0.94	30	53.4



^{13}C NMR (201 MHz, *DMSO-d_6*) δ ppm 174.9 (1C), 152.6 (1C), 104.8 (1C), 103.3 (1C), 101.8 (1C), 98.1 (1C), 91.9 (1C), 87.0 (1C), 85.8 (1C), 77.8 (1C), 77.3 (2C), 77.0 (3C), 76.9 (1C), 75.5 (1C), 74.3 (1C), 74.0 (2C), 71.4 (1C), 70.5 (1C), 70.3 (1C), 68.3 (1C), 62.0 (1C), 61.4 (1C), 61.3 (1C), 60.7 (1C), 56.7 (1C), 53.4 (1C), 47.8 (1C), 43.6 (2C), 41.6 (1C), 41.3 (1C), 40.2 (1C), 39.1 (1C), 37.9 (1C), 36.6 (1C), 28.5 (1C), 21.4 (1C), 20.1 (1C), 19.5 (1C), 16.4 (1C)

Figure 6U

Steviol+4Glc (#26)



= ^{1}H-^{13}C HMBC

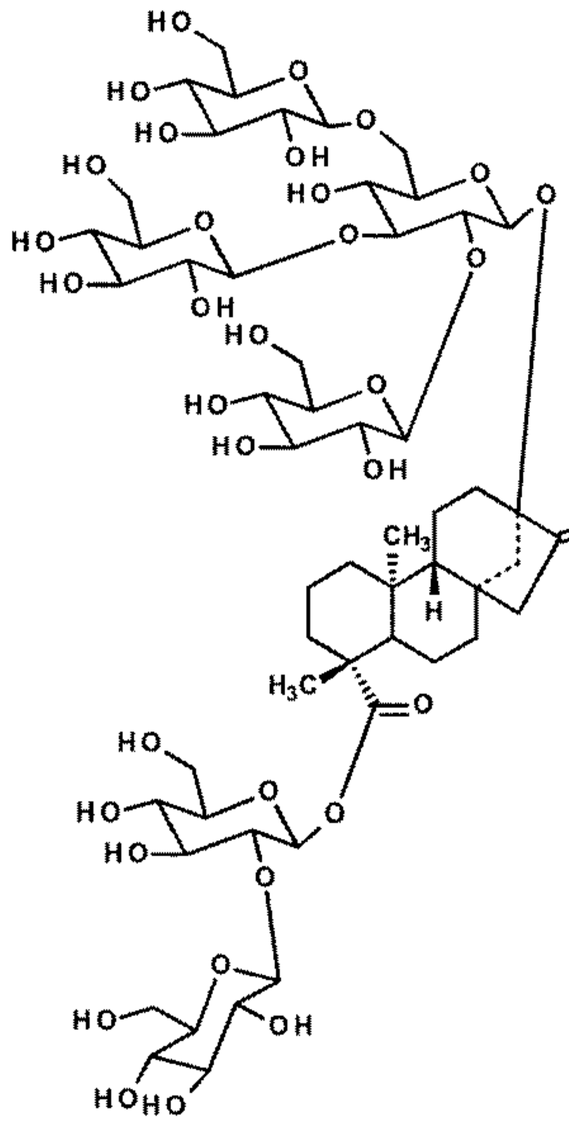
= ^{1}H-^{1}H COSY

= ^{1}H-^{1}H TOCSY spin system

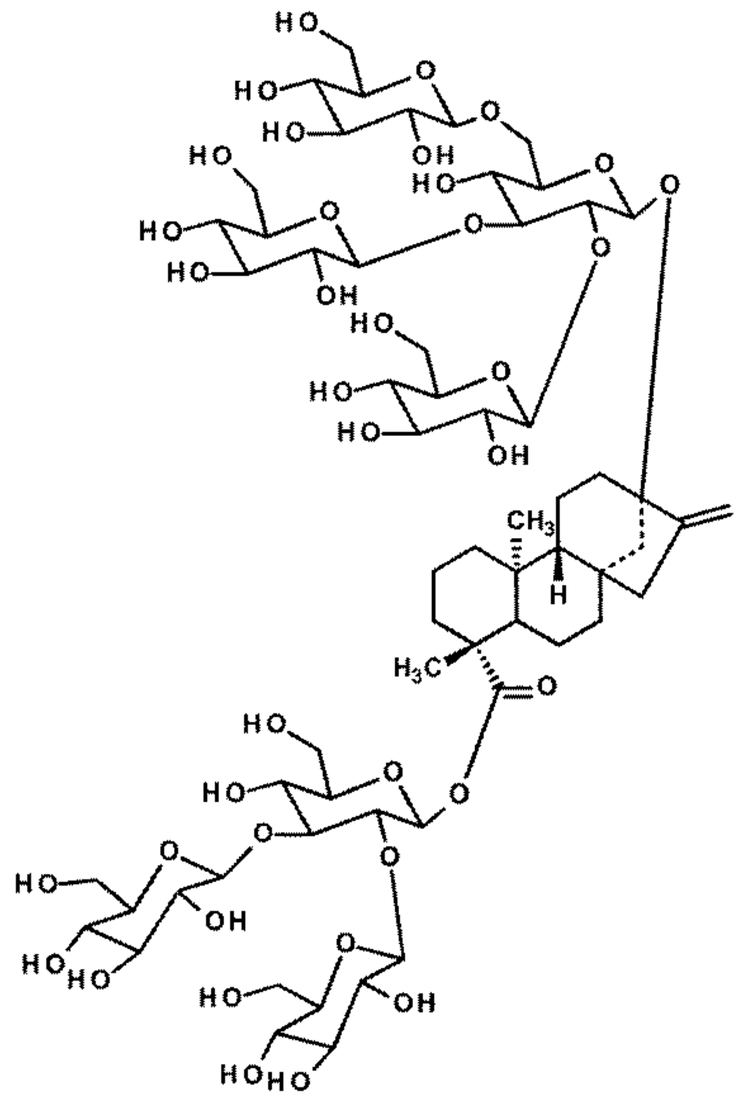
= ^{1}H-^{1}H dipolar correlation (ROESY)

Assigments were made on the basis of ^{1}H-^{1}H COSY, ^{1}H-^{1}H TOCSY, ^{1}H-^{13}C HSQC-DEPT, ^{1}H-^{13}C HMBC and ^{1}H-^{1}H ROESY.

Figure 3



Steviol+6Glc (isomer 1)
[Compound 6.1]



Steviol+7Glc (isomer 2)
[Compound 7.2]