



Production of Steviol Glycosides in Recombiant Hosts

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Douchin et al. (43) **Pub. Date: Aug. 3, 2017**(54) **PRODUCTION OF STEVIOL GLYCOSIDES
IN RECOMBIANT HOSTS****Related U.S. Application Data**(60) Provisional application No. 62/035,902, filed on Aug.
11, 2014.(71) Applicant: **Evolva SA**, Reinach (CH)**Publication Classification**(72) Inventors: **Veronique Douchin**, Frederiksberg
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Frederiksberg (DK)(51) **Int. Cl.**
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C12N 1/16 (2006.01)
(52) **U.S. Cl.**
CPC **C12P 19/44** (2013.01); **C12N 1/16**
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§ 371 (c)(1),

(2) Date: **Jan. 23, 2017**(57) **ABSTRACT**The invention relates to recombinant microorganisms and
methods for producing steviol glycosides and steviol gly-
coside precursors.

Figure 1

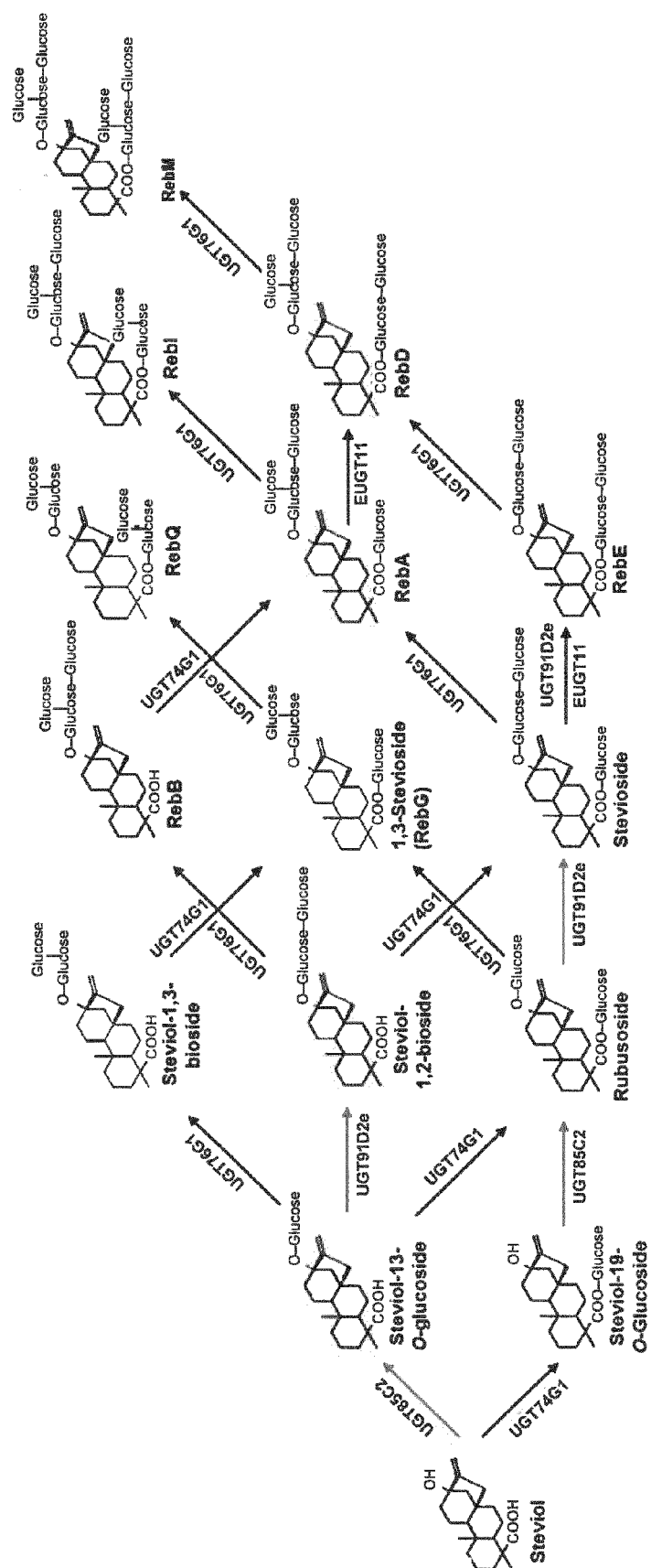


Figure 2

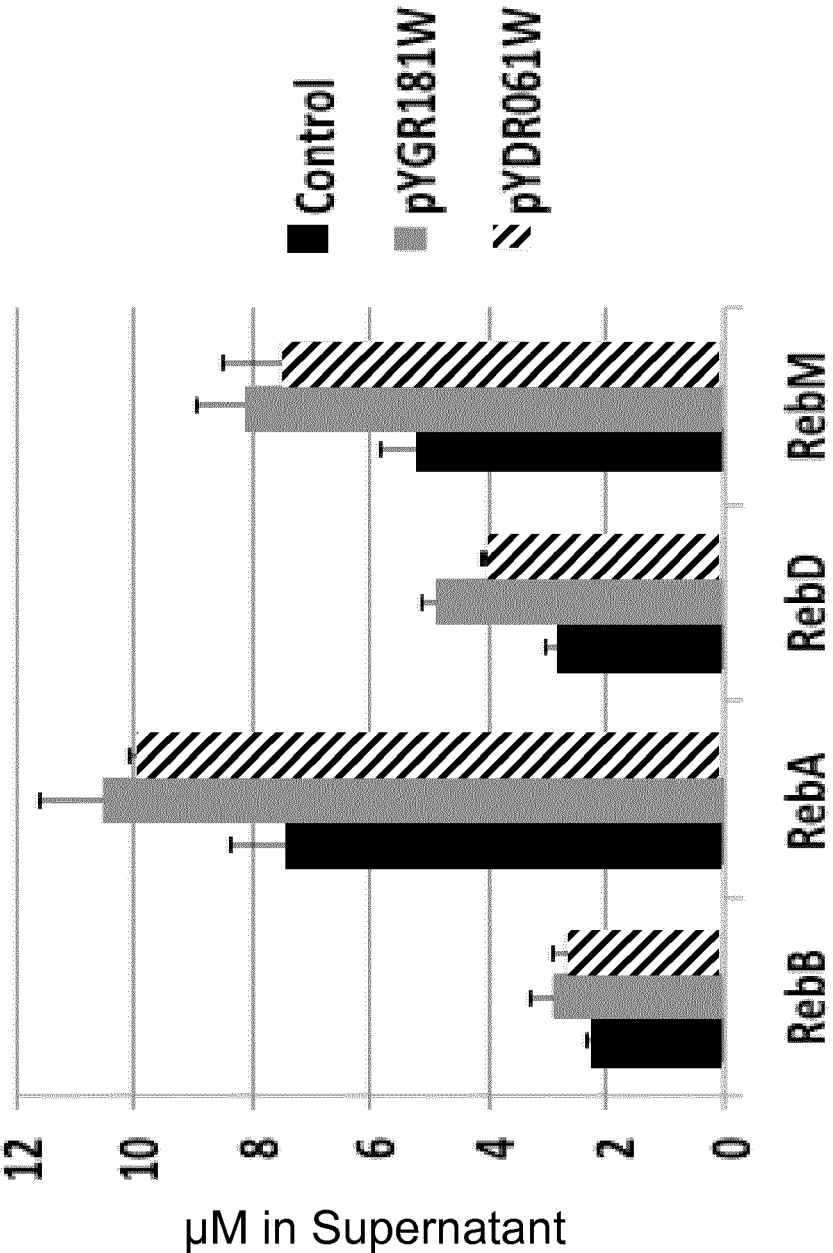


Figure 3A

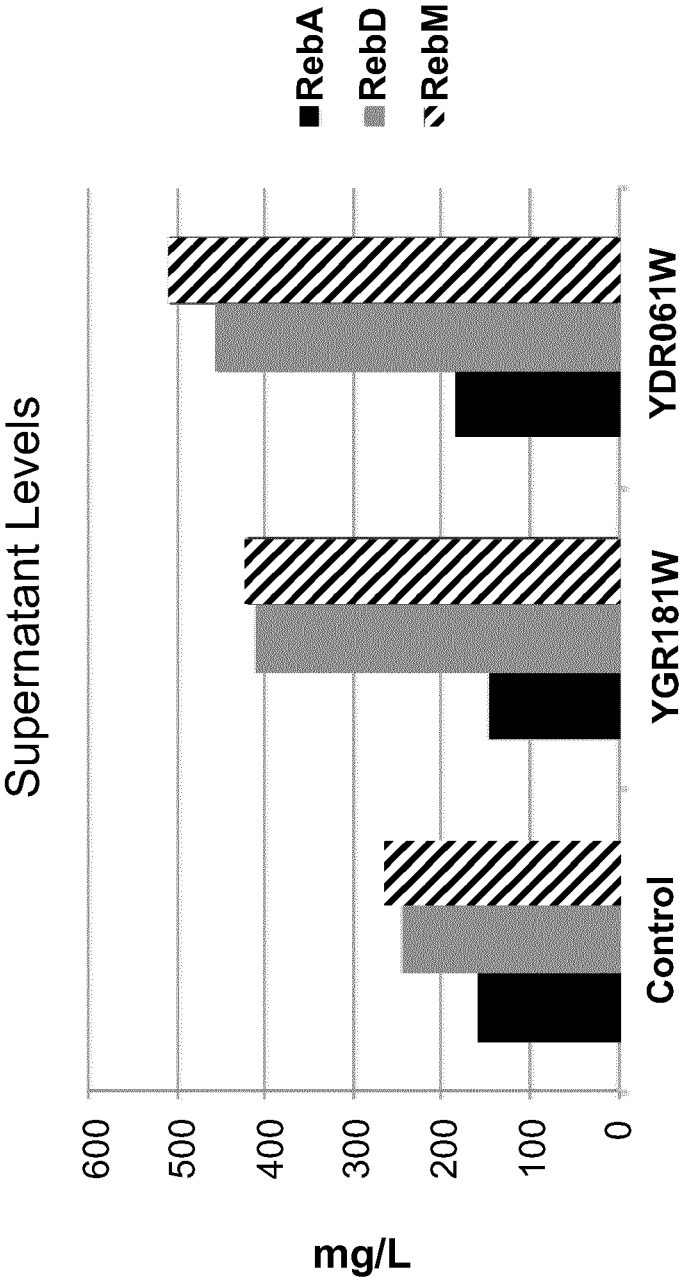


Figure 3B

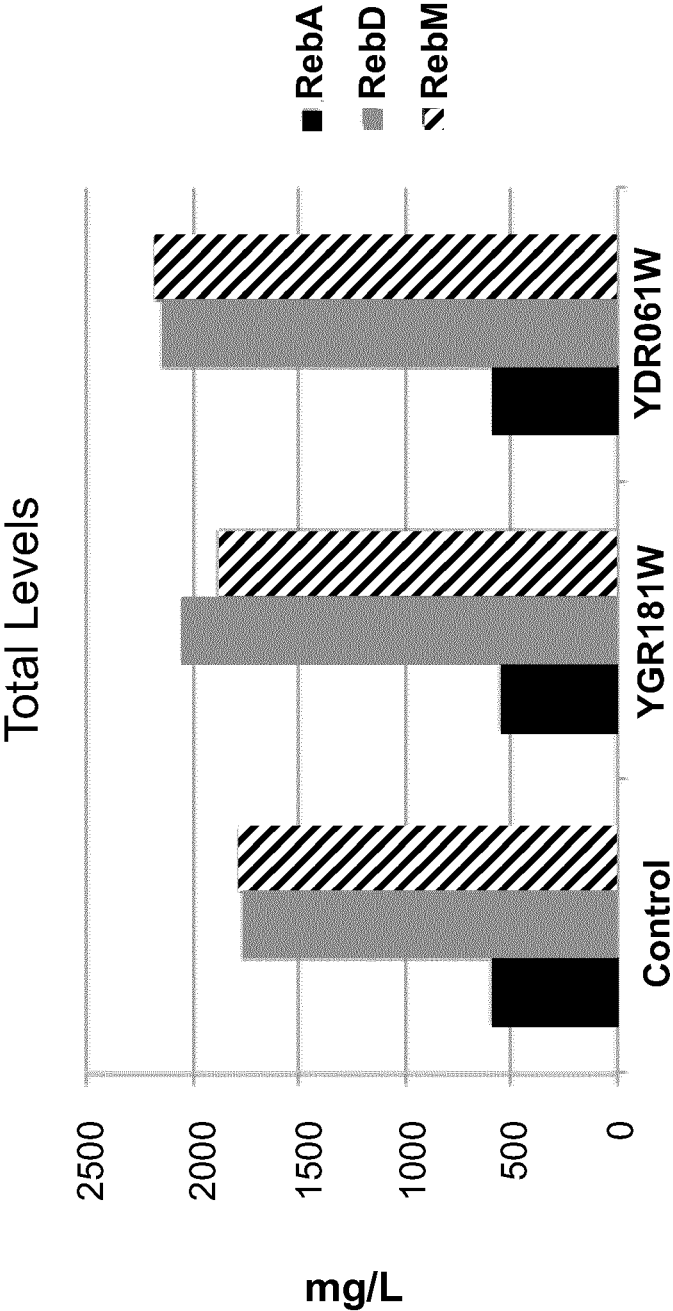
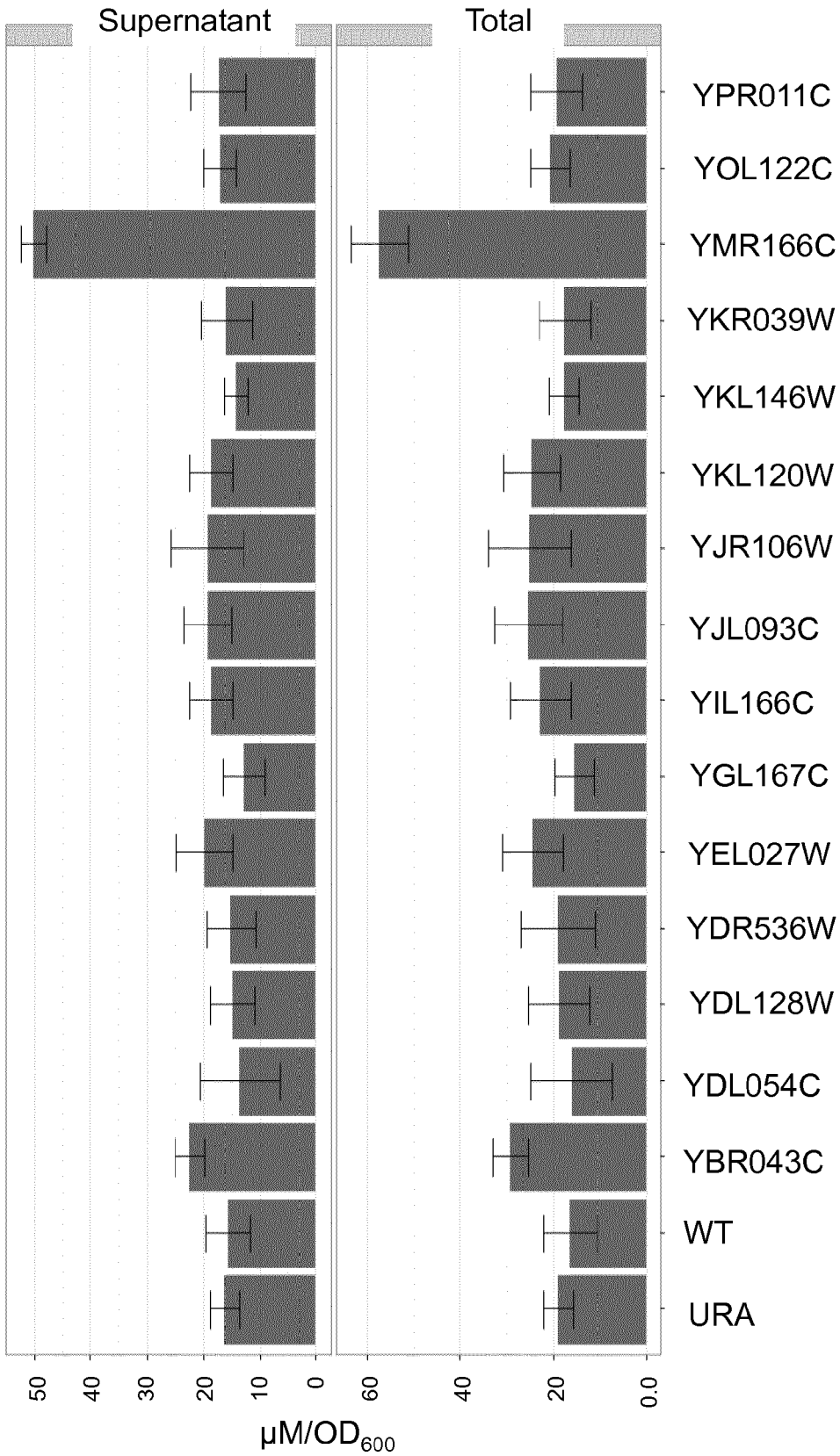
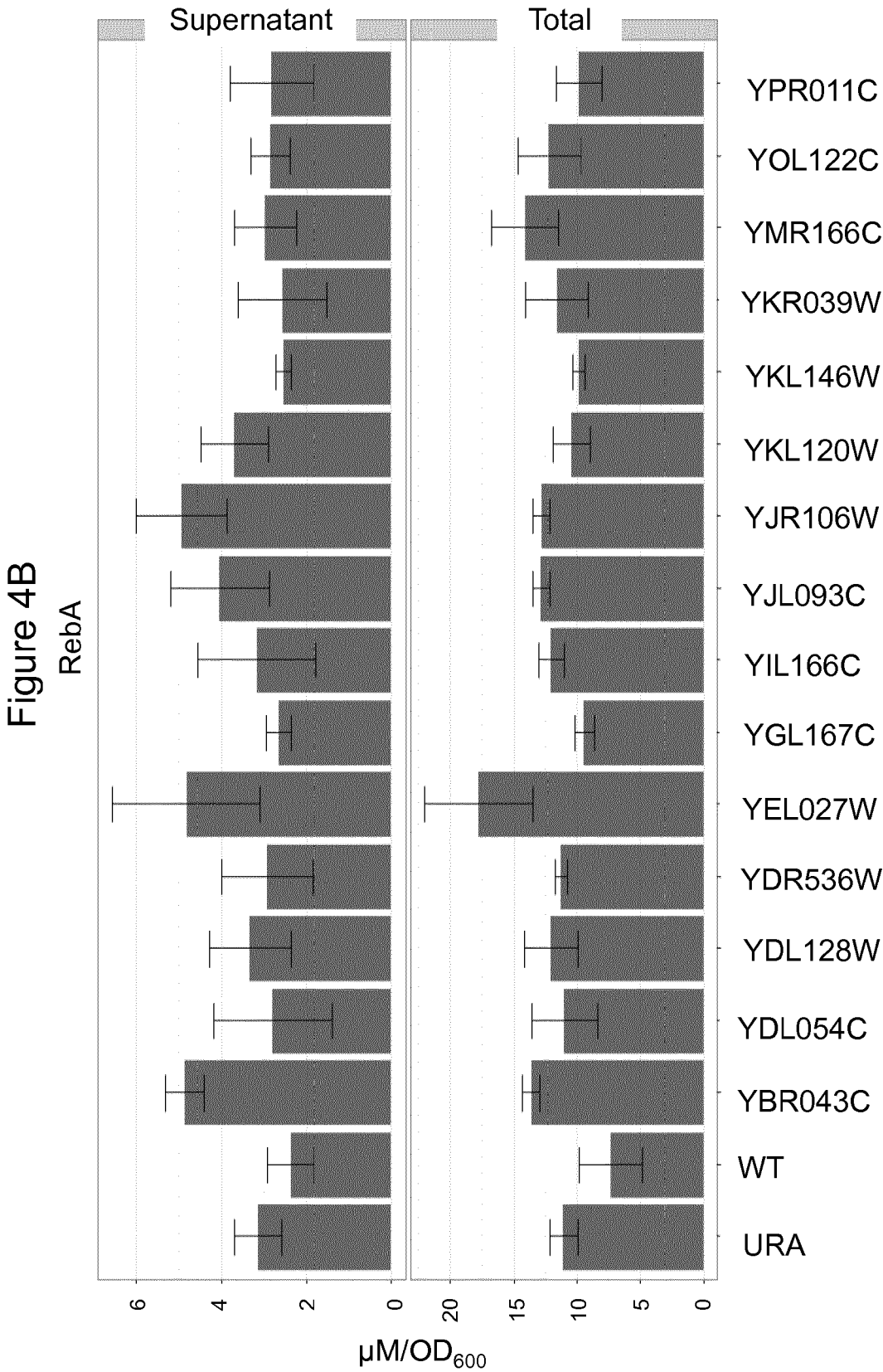
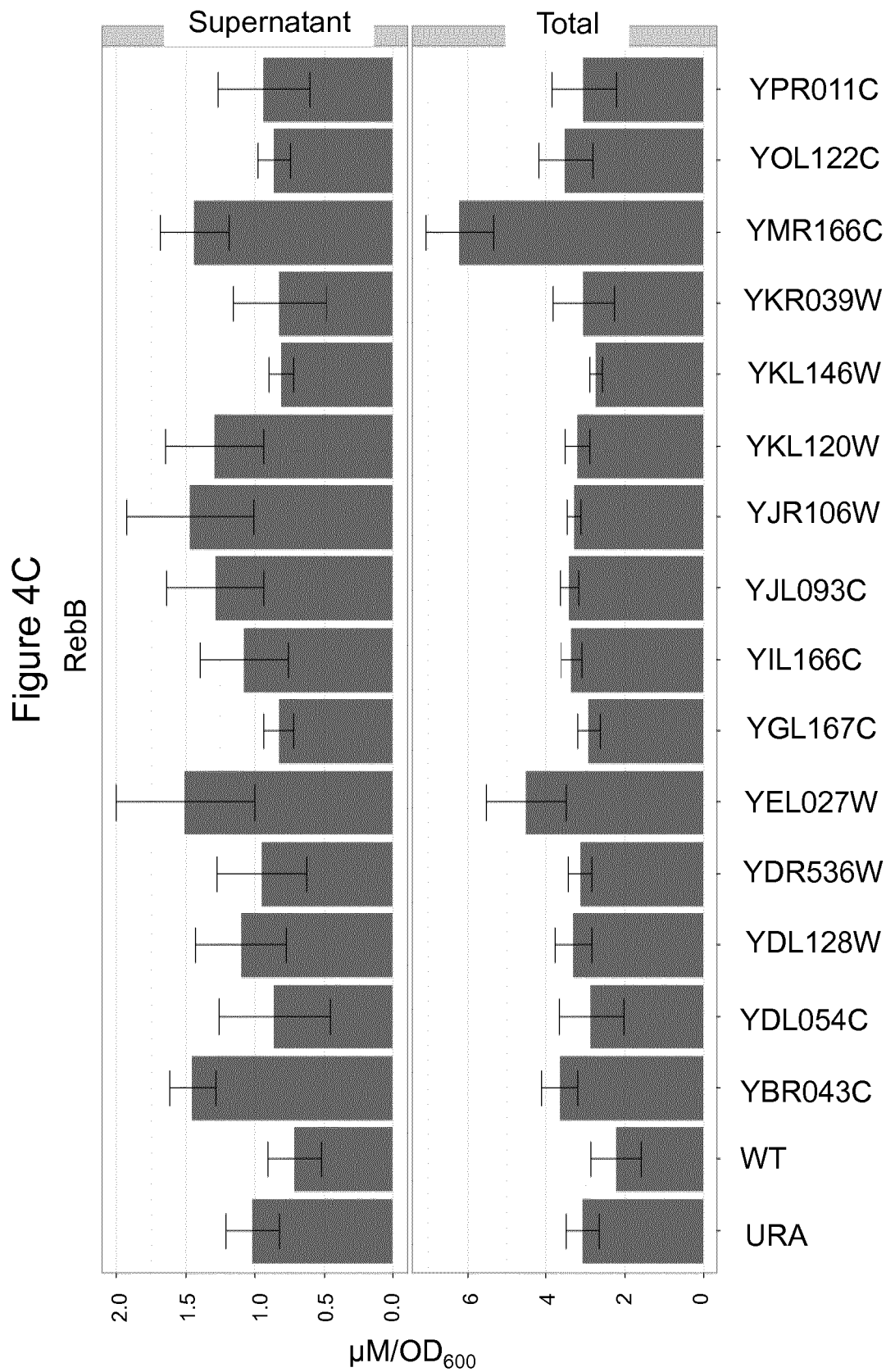
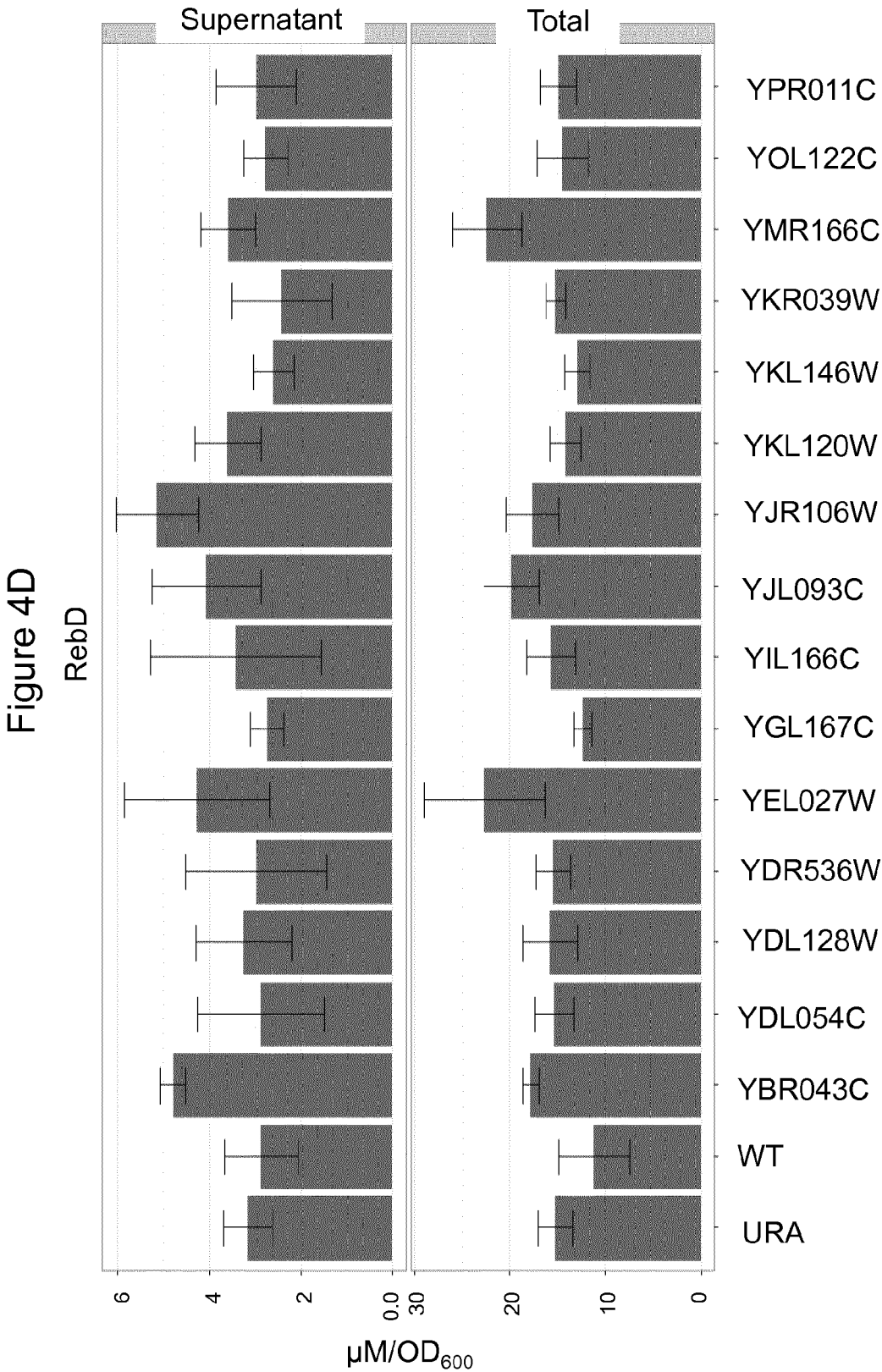


Figure 4A
13-SMG









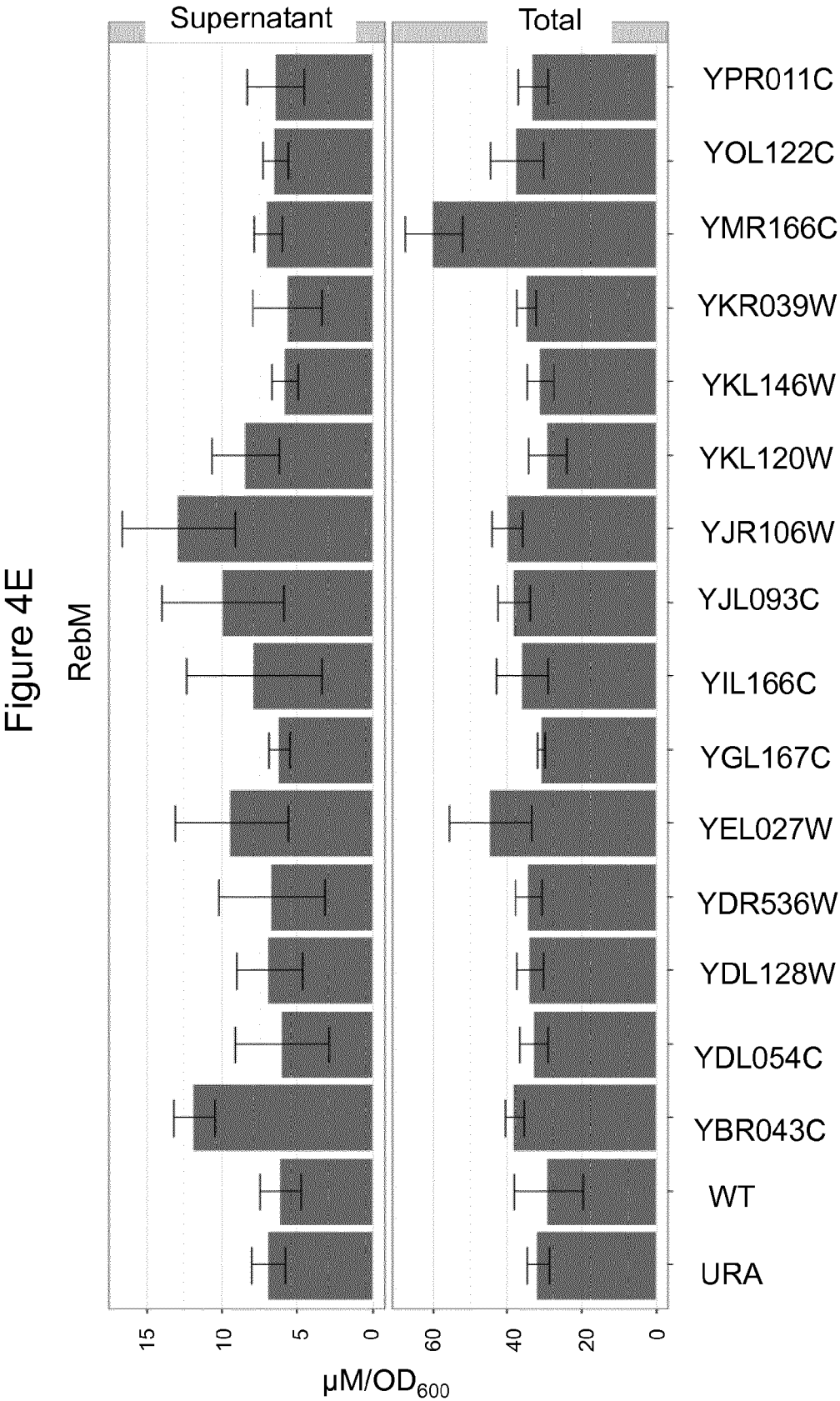


Figure 5A

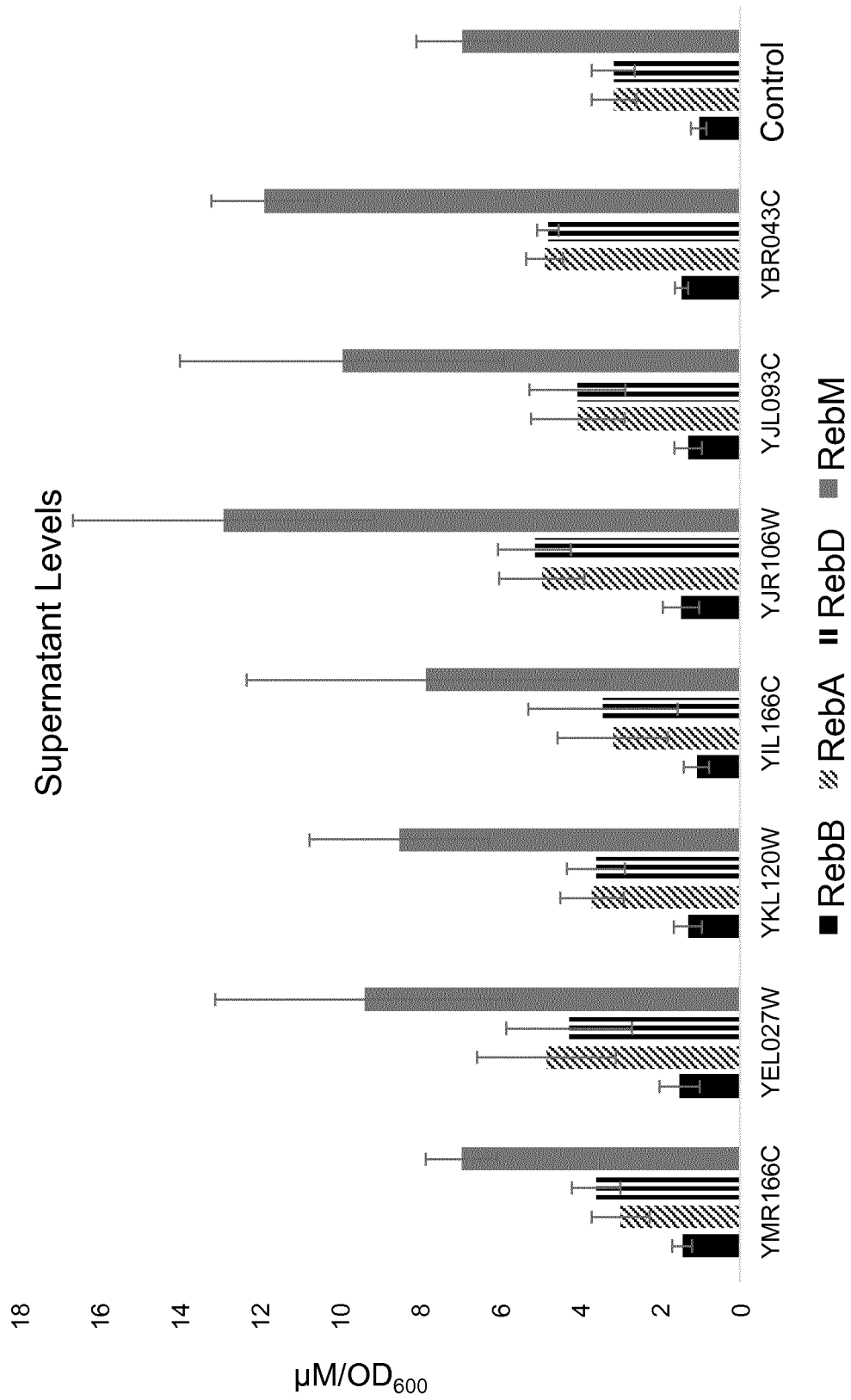
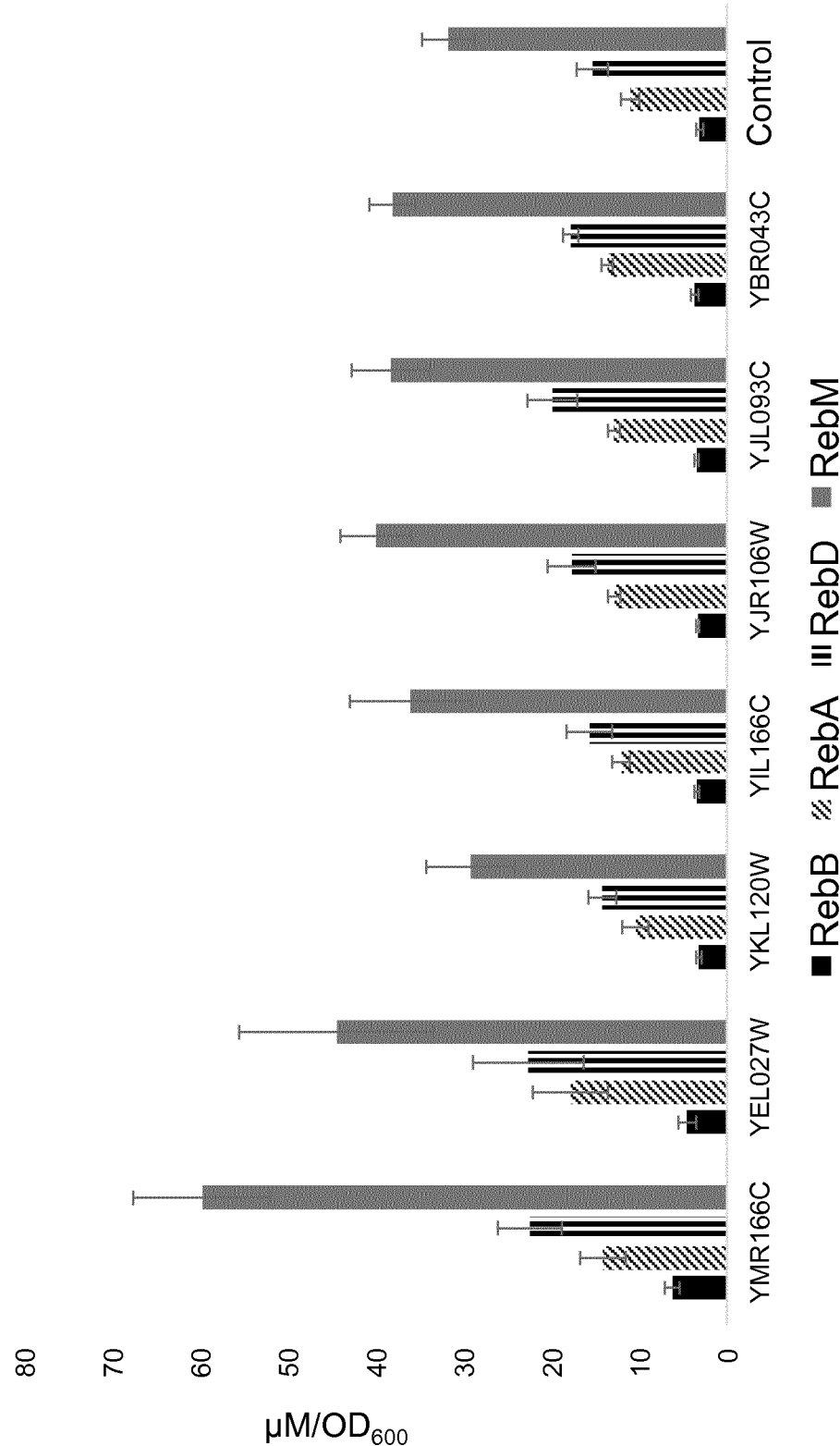


Figure 5B
Total Levels



PRODUCTION OF STEVIOL GLYCOSIDES IN RECOMBIANT HOSTS

BACKGROUND OF THE INVENTION

[0001] Field of the Invention

[0002] This disclosure relates generally to the recombinant production of steviol glycosides such as rebaudioside A (RebA), rebaudioside B (RebB), rebaudioside D (RebD), and rebaudioside M (RebM) by recombinant hosts such as recombinant microorganisms and isolation methods thereof. In particular, this disclosure relates to modifications to transport systems in a recombinant host to increase production of such steviol glycosides and/or transport of such steviol glycosides into the culture medium.

[0003] Description of Related Art

[0004] 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.

[0005] Chemical structures for several steviol glycosides are shown in FIG. 1, including the diterpene steviol and various steviol glycosides. Extracts of the *Stevia* plant generally comprise rebaudiosides and other steviol glycosides that contribute to the sweet flavor, although the amount of each steviol glycoside often varies, inter alia, among different production batches.

[0006] 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 produce high yields of desired steviol glycosides, such as RebD and RebM.

SUMMARY OF THE INVENTION

[0007] It is against the above background that the present invention provides certain advantages and advancements over the prior art.

[0008] In particular, the invention provides a recombinant host capable of synthesizing a steviol glycoside, comprising a gene encoding a transporter polypeptide and/or a gene encoding a transcription factor polypeptide that regulates expression of at least one transporter gene; wherein expression of the gene encoding the transporter polypeptide and/or the gene encoding the transcription factor polypeptide that regulates expression of at least one transporter gene is modified and the recombinant host transports at least a portion of the synthesized steviol glycoside from the host into a culture medium.

[0009] In some aspects of the recombinant host disclosed herein, the gene encoding the transporter polypeptide is an endogenous gene.

[0010] In some aspects of the recombinant host disclosed herein, the transporter polypeptide comprises an ATP-binding cassette (ABC) transporter, a major facilitator superfamily (MFS) transporter, an amino acid/auxin permease (AAP) family transporter, ATPase transporter, a sulfate permease (SulP) family transporter, a lysosomal cystine transporter (LCT) family transporter, a Ca²⁺:cation antiporter (CaCA) family transporter, an amino acid-polyamine-organocation (APC) superfamily transporter, a multidrug/oligosaccharidyl-lipid/polysaccharide (MOP) transporter, a ZRT/IRT-like protein (ZIP) metal transporter family transporter, a mitochondrial protein translocase (MPT) family transporter, a voltage-gated ion channel (VIC) family transporter, a monovalent cation:proton antiporter-2 (CPA2) family transporter, a ThrE family of putative transmembrane amino acid efflux transporter, an oligopeptide transporter (OPT) family transporter, a K⁺ transporter (Trk) family transporter, a bile acid:Na symporter (BASS) family transporter, a drug/metabolite transporter (DMT) superfamily transporter, a mitochondrial carrier (MC) family transporter, an auxin efflux carrier (AEC) family transporter, an ammonia channel transporter (Amt) family transporter, a metal ion (Mn²⁺-iron) transporter (Nramp) family transporter, a transient receptor potential Ca²⁺ channel (TRP-CC) family transporter, an arsenical resistance-3 (ACR3) family transporter, a nucleobase:cation symporter-1 (NCS1) family transporter, an inorganic phosphate transporter (PiT) family transporter, an arsenite-antimonite (ArsAB) efflux family transporter, an IISP family of transporter, a glycerol uptake (GUP) family transporter, a metal ion transport (MIT) family transporter, a copper transport (Ctr) family or a cation diffusion facilitator (CDF) family transporter.

[0011] In some aspects of the recombinant host disclosed herein, the modified expression comprises modified expression comprises:

[0012] (a) overexpressing the gene encoding the transporter polypeptide and/or the gene encoding the transcription factor polypeptide; or

[0013] (b) deleting the gene encoding the transporter polypeptide and/or the gene encoding the transcription factor polypeptide.

[0014] In some aspects of the recombinant host disclosed herein, the gene encoding the transporter polypeptide and/or the gene encoding the transcription factor polypeptide has an activity that is increased.

[0015] In some aspects of the recombinant host disclosed herein, one or more of the genes encoding the transporter polypeptide and/or one or more of the genes encoding the transcription factor polypeptide are overexpressed.

[0016] In some aspects of the recombinant host disclosed herein, the transporter polypeptide and/or transcription polypeptide comprise YAL067C set forth in SEQ ID NO:14, YBL089W set forth in SEQ ID NO:15, YBL099W set forth in SEQ ID NO:16, YBR008C set forth in SEQ ID NO:86, YBR021W set forth in SEQ ID NO:87, YBR043C set forth in SEQ ID NO:88, YBR180W set forth in SEQ ID NO:13, YBR241C set forth in SEQ ID NO:17, YBR287W set forth in SEQ ID NO:89, YBR294W set forth in SEQ ID NO:18, YBR295W set forth in SEQ ID NO:90, YBR296C set forth in SEQ ID NO:91, YCL038C set forth in SEQ ID NO:92, YCL069W set forth in SEQ ID NO:19, YCR011C set forth in SEQ ID NO:93, YCR028C set forth in SEQ ID NO:20, YCR075C set forth in SEQ ID NO:21, YDL054C set forth in SEQ ID NO:94, YDL100C set forth in SEQ ID NO:95,

YDL128W set forth in SEQ ID NO:22, YDL185W set forth in SEQ ID NO:23, YDL194W set forth in SEQ ID NO:24, YDL210W set forth in SEQ ID NO:25, YDL245C set forth in SEQ ID NO:96, YDL247W set forth in SEQ ID NO:97, YDR011W set forth in SEQ ID NO:98, YDR061W set forth in SEQ ID NO:26, YDR093W set forth in SEQ ID NO:27, YDR292C set forth in SEQ ID NO:99, YDR338C set forth in SEQ ID NO:28, YDR406W set forth in SEQ ID NO:29, YDR497C set forth in SEQ ID NO:100, YDR536W set forth in SEQ ID NO:30, YEL006W set forth in SEQ ID NO:101, YEL027W set forth in SEQ ID NO:102, YEL031W set forth in SEQ ID NO:31, YEL065W set forth in SEQ ID NO:103, YER019C-A set forth in SEQ ID NO:104, YER053C set forth in SEQ ID NO:105, YER119C set forth in SEQ ID NO:106, YER166W set forth in SEQ ID NO:32, YFL011W set forth in SEQ ID NO:33, YFL028C set forth in SEQ ID NO:107, YFR045W set forth in SEQ ID NO:108, YGL006W set forth in SEQ ID NO:34, YGL013C set forth in SEQ ID NO:35, YGL084C set forth in SEQ ID NO:109, YGL104C set forth in SEQ ID NO:110, YGL114W set forth in SEQ ID NO:111, YGL167C set forth in SEQ ID NO:112, YGL255W set forth in SEQ ID NO:36, YGR125W set forth in SEQ ID NO:37, YGR181W set forth in SEQ ID NO:38, YGR217W set forth in SEQ ID NO:39, YGR224W set forth in SEQ ID NO:40, YGR257C set forth in SEQ ID NO:113, YGR281W set forth in SEQ ID NO:41, YHL016C set forth in SEQ ID NO:42, YHL035C set forth in SEQ ID NO:114, YHL036W set forth in SEQ ID NO:115, YHR002W set forth in SEQ ID NO:116, YHR096C set forth in SEQ ID NO:117, YIL006W set forth in SEQ ID NO:118, YIL088C set forth in SEQ ID NO:43, YIL120W set forth in SEQ ID NO:119, YIL121W set forth in SEQ ID NO:120, YIL166C set forth in SEQ ID NO:121, YJL093C set forth in SEQ ID NO:44, YJL094C set forth in SEQ ID NO:45, YJL108C set forth in SEQ ID NO:46, YJL133W set forth in SEQ ID NO:122, YJL212C set forth in SEQ ID NO:47, YJL219W set forth in SEQ ID NO:123, YJR106W set forth in SEQ ID NO:48, YJR160C set forth in SEQ ID NO:49, YKL016C set forth in SEQ ID NO:124, YKL050C set forth in SEQ ID NO:125, YKL064W set forth in SEQ ID NO:50, YKL120W set forth in SEQ ID NO:126, YKL146W set forth in SEQ ID NO:127, YKL209C set forth in SEQ ID NO:128, YKR039W set forth in SEQ ID NO:129, YKR050W set forth in SEQ ID NO:51, YKR105C set forth in SEQ ID NO:52, YKR106W set forth in SEQ ID NO:53, YLR411W set forth in SEQ ID NO:130, YLR447C set forth in SEQ ID NO:54, YML038C set forth in SEQ ID NO:131, YML116W set forth in SEQ ID NO:55, YMR034C set forth in SEQ ID NO:56, YMR056C set forth in SEQ ID NO:57, YMR166C set forth in SEQ ID NO:132, YMR253C set forth in SEQ ID NO:58, YMR279C set forth in SEQ ID NO:133, YNL003C set forth in SEQ ID NO:134, YNL065W set forth in SEQ ID NO:59, YNL070W set forth in SEQ ID NO:60, YNL083W set forth in SEQ ID NO:61, YNL095C set forth in SEQ ID NO:62, YNL121C set forth in SEQ ID NO:63, YNL142W set forth in SEQ ID NO:64, YNL268W set forth in SEQ ID NO:135, YNR055C set forth in SEQ ID NO:136, YOL020W set forth in SEQ ID NO:65, YOL075C set forth in SEQ ID NO:66, YOL077W-A set forth in SEQ ID NO:67, YOL122C set forth in SEQ ID NO:68, YOL158C set forth in SEQ ID NO:137, YOR079C set forth in SEQ ID NO:69, YOR087W set forth in SEQ ID NO:70, YOR092W set forth in SEQ ID NO:71, YOR100C set forth in SEQ ID NO:138, YOR130C set forth in SEQ ID NO:72, YOR153W set forth

in SEQ ID NO:139, YOR222W set forth in SEQ ID NO:73, YOR271C set forth in SEQ ID NO:140, YOR273C set forth in SEQ ID NO:141, YOR291W set forth in SEQ ID NO:74, YOR306C set forth in SEQ ID NO:75, YOR307C set forth in SEQ ID NO:142, YOR316C set forth in SEQ ID NO:76, YOR332W set forth in SEQ ID NO:143, YOR334W set forth in SEQ ID NO:77, YOR348C set forth in SEQ ID NO:144, YPL036W set forth in SEQ ID NO:145, YPL078C set forth in SEQ ID NO:78, YPL270W set forth in SEQ ID NO:79, YPL274W set forth in SEQ ID NO:80, YPR003C set forth in SEQ ID NO:81, YPR011C set forth in SEQ ID NO:82, YPR058W set forth in SEQ ID NO:83, YPR128C set forth in SEQ ID NO:84, or YPR201W set forth in SEQ ID NO:85.

[0017] In some aspects of the recombinant host disclosed herein, YBR043C set forth in SEQ ID NO:88, YDL100C set forth in SEQ ID NO:95, YDL054C set forth in SEQ ID NO:94, YDL128W set forth in SEQ ID NO:22, YDL198C set forth in SEQ ID NO:146, YDR061W set forth in SEQ ID NO:26, YDR536W set forth in SEQ ID NO:30, YEL027W set forth in SEQ ID NO:102, YFL054C set forth in SEQ ID NO:147, YGL167C set forth in SEQ ID NO:112, YGR181W set forth in SEQ ID NO:38, YHL016C set forth in SEQ ID NO:42, YIL166C set forth in SEQ ID NO:121, YJL093C set forth in SEQ ID NO:44, YJR106W set forth in SEQ ID NO:48, YKL120W set forth in SEQ ID NO:126, YKL146W set forth in SEQ ID NO:127, YKR039W set forth in SEQ ID NO:129, YMR034C set forth in SEQ ID NO:56, YMR166C set forth in SEQ ID NO:132, YOL122C set forth in SEQ ID NO:68, YOR079C set forth in SEQ ID NO:69, YPL270W set forth in SEQ ID NO:79, and/or YPR011C set forth in SEQ ID NO:82 are overexpressed.

[0018] In some aspects, the recombinant host further comprises:

- [0019]** (a) one or more genes encoding a sucrose transporter and a sucrose synthase;
- [0020]** (b) a gene encoding a geranylgeranyl diphosphate synthase (GGPPS) polypeptide;
- [0021]** (c) a gene encoding an ent-copalyl diphosphate synthase (CDPS) polypeptide;
- [0022]** (d) a gene encoding a kaurene synthase (KS) polypeptide;
- [0023]** (e) a gene encoding a kaurene oxidase (KO) polypeptide;
- [0024]** (f) a gene encoding a steviol synthase (KAH) polypeptide;
- [0025]** (g) a gene encoding a cytochrome P450 reductase (CPR) polypeptide;
- [0026]** (h) a gene encoding a UGT85C2 polypeptide;
- [0027]** (i) a gene encoding a UGT76G1 polypeptide;
- [0028]** (k) a gene encoding a UGT91D2 functional homolog; and/or
- [0029]** (l) a gene encoding a EUGT11 polypeptide;
- [0030]** wherein at least one of the genes is a recombinant gene; and
- [0031]** wherein the host is capable of producing one or more of RebA, RebB, RebD and/or RebM.

[0032] In some aspects of the recombinant host disclosed herein, at least one of the genes is codon optimized for expression in the host.

[0033] In some aspects of the recombinant host disclosed herein, at least one of the genes is codon optimized for expression in *Saccharomyces cerevisiae*.

[0034] In some aspects of the recombinant host disclosed herein,

[0035] (a) the GGPPS polypeptide comprises a polypeptide having at least 70% identity to an amino acid sequence set forth in SEQ ID NO:149;

[0036] (b) the CDPS polypeptide comprises a polypeptide having at least 70% identity to an amino acid sequence set forth in SEQ ID NO:150;

[0037] (c) the KO polypeptide comprises a polypeptide having at least 70% identity to an amino acid sequence set forth in SEQ ID NO:152;

[0038] (d) the KS polypeptide comprises a polypeptide having at least 40% identity to an amino acid sequence set forth in SEQ ID NO:151;

[0039] (e) the KAH polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:154;

[0040] (f) the CPR polypeptide comprises a polypeptide having at least 70% identity to an amino acid sequence set forth in SEQ ID NO:153 and/or a polypeptide having at least 65% identity to an amino acid sequence set forth in SEQ ID NO:155;

[0041] (g) the UGT85C2 polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:156;

[0042] (h) the UGT76G1 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:158;

[0043] (i) the UGT74G1 polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:157;

[0044] (j) the a UGT91D2 functional homolog comprises a UGT91D2e-b polypeptide having at least 90% identity to the amino acid sequence set forth in SEQ ID NO:159; and

[0045] (k) the EUGT11 polypeptide comprises a polypeptide having at least 65% identity to an amino acid sequence set forth in SEQ ID NO:148.

[0046] In some aspects, the recombinant host disclosed herein comprises a microorganism that is a plant cell, a mammalian cell, an insect cell, a fungal cell, or a bacterial cell.

[0047] In some aspects, the bacterial cell comprises *Escherichia* bacteria cells, *Lactobacillus* bacteria cells, *Lactococcus* bacteria cells, *Cornebacterium* bacteria cells, *Acetobacter* bacteria cells, *Acinetobacter* bacteria cells, or *Pseudomonas* bacterial cells.

[0048] In some aspects, the fungal cell is a yeast cell.

[0049] In some aspects, 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 adenivorans*, *Xanthophyllomyces dendrorhous*, or *Candida albicans* species.

[0050] In some aspects, the yeast cell is a *Saccharomycete*.

[0051] In some aspects, the yeast cell is a cell from the *Saccharomyces cerevisiae* species.

[0052] The invention further provides a method of producing a steviol glycoside, comprising:

[0053] (a) growing the recombinant host disclosed herein in a culture medium, under conditions in which the genes comprising recombinant host disclosed herein are expressed,

[0054] wherein the steviol glycoside is synthesized by the host; and

[0055] (b) optionally isolating the steviol glycoside.

[0056] In some aspects of the methods disclosed herein, the steviol glycoside is RebA, RebB, RebD, and/or RebM, and wherein:

[0057] (a) RebA is capable of being synthesized in the recombinant host disclosed herein expressing UGT85C2, UGT76G1, UGT74G1, and UGT91D2;

[0058] (b) RebB is capable of being synthesized in the recombinant host disclosed herein expressing UGT85C2, UGT76G1, and UGT91D2;

[0059] (c) RebD is capable of being synthesized in the recombinant host disclosed herein expressing UGT85C2, UGT76G1, UGT74G1, and UGT91D2 and/or EUGT11; and

[0060] (d) RebM is capable of being synthesized in the recombinant host disclosed herein expressing UGT85C2, UGT76G1, UGT74G1, and UGT91D2 and/or EUGT11.

[0061] In some aspects of the methods disclosed herein a gene encoding YBR043C set forth in SEQ ID NO:88, YDL100C set forth in SEQ ID NO:95, YDL054C set forth in SEQ ID NO:94, YDL128W set forth in SEQ ID NO:22, YDL198C set forth in SEQ ID NO:146, YDR061W set forth in SEQ ID NO:26, YDR536W set forth in SEQ ID NO:30, YEL027W set forth in SEQ ID NO:102, YFL054C set forth in SEQ ID NO:147, YGL167C set forth in SEQ ID NO:112, YGR181W set forth in SEQ ID NO:38, YHL016C set forth in SEQ ID NO:42, YIL166C set forth in SEQ ID NO:121, YJL093C set forth in SEQ ID NO:44, YJR106W set forth in SEQ ID NO:48, YKL120W set forth in SEQ ID NO:126, YKL146W set forth in SEQ ID NO:127, YKR039W set forth in SEQ ID NO:129, YMR034C set forth in SEQ ID NO:56, YMR166C set forth in SEQ ID NO:132, YOL122C set forth in SEQ ID NO:68, YOR079C set forth in SEQ ID NO:69, YPL270W set forth in SEQ ID NO:79, and/or YPR011C set forth in SEQ ID NO:82 is overexpressed.

[0062] In some aspects of the methods disclosed herein the steviol glycoside is produced at a concentration of between about 500 mg/L to about 10,000 mg/L.

[0063] The invention further provides a method of increasing production or transport of a steviol glycoside into a culture medium, comprising:

[0064] (a) growing the recombinant host disclosed herein in a culture medium, under conditions in which the genes comprising the host disclosed herein are expressed,

[0065] wherein the steviol glycoside is synthesized by the host; and

[0066] (b) optionally isolating the steviol glycoside.

[0067] In some aspects of the methods disclosed herein, the steviol glycoside is RebA, RebB, RebD, and/or RebM.

[0068] The invention further provides a method increasing production of steviol or a steviol glycoside in a recombinant host, comprising modifying expression of a gene encoding a transporter polypeptide and/or a gene encoding a transcription that regulates expression of at least one transporter gene, wherein the host is capable of transporting at least a portion of the produced steviol or a steviol glycoside from the host into a culture medium.

[0069] These and other features and advantages of the present invention will be more fully understood from the following detailed description of the invention 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.

DESCRIPTION OF DRAWINGS

[0070] FIG. 1 shows the chemical structures and synthesis pathways for various steviol glycosides.

[0071] FIG. 2 is a bar graph of the amount (μM) of RebA, RebB, RebD, or RebM in the supernatant of a steviol glycoside-producing strain overexpressing transporter genes YGR181W (SEQ ID NO:38) or YDR061W (SEQ ID NO:26), compared to a control steviol glycoside-producing strain. See Example 4.

[0072] FIG. 3A and FIG. 3B are bar graphs of the amount (mg/L) of RebA, RebD, or RebM in the supernatant (FIG. 3A) or total culture (FIG. 3B) of a YGR181W (SEQ ID NO:38) or YDR061W (SEQ ID NO:26) overexpressing strain, compared to a control steviol glycoside-producing strain. See Example 4.

[0073] FIG. 4A shows levels of 13-SMG (total levels and supernatant levels; $\mu\text{M}/\text{OD}_{600}$), FIG. 4B shows levels of RebA (total levels and supernatant levels; $\mu\text{M}/\text{OD}_{600}$), FIG. 4C shows levels of RebB (total levels and supernatant levels; $\mu\text{M}/\text{OD}_{600}$), FIG. 4D shows levels of RebD (total levels and supernatant levels; $\mu\text{M}/\text{OD}_{600}$), and FIG. 4E shows levels of RebM (total levels and supernatant levels; $\mu\text{M}/\text{OD}_{600}$) in a steviol glycoside-producing *S. cerevisiae* strain with a genomically integrated transporter gene. The genomically integrated transporter genes of FIGS. 4A-E are YBR043C (SEQ ID NO:88), YEL027W (SEQ ID NO:102), YJL093C (SEQ ID NO:44), YJR106W (SEQ ID NO:48), YMR166C (SEQ ID NO:132), YIL166C (SEQ ID NO:121), YKL120W (SEQ ID NO:126), YDL054C (SEQ ID NO:94), YDL128W (SEQ ID NO:22), YDR536W (SEQ ID NO:30), YGL167C (SEQ ID NO:112), YKL146W (SEQ ID NO:127), YKR039W (SEQ ID NO:129), YOL122C (SEQ ID NO:68), and YPR011C (SEQ ID NO:82). See Example 6.

[0074] FIG. 5A shows supernatant levels of RebA, RebB, RebD, and RebM (in $\mu\text{M}/\text{OD}_{600}$) of a steviol glycoside-producing strain overexpressing YMR166C (SEQ ID NO:132), YEL027W (SEQ ID NO:102), YKL120W (SEQ ID NO:126), YJL166C (SEQ ID NO:121), YJR106W (SEQ ID NO:48), YJL093C (SEQ ID NO:44), and YBR043C (SEQ ID NO:88) by the USER cloning system. FIG. 5B shows total levels of RebA, RebB, RebD, and RebM (in $\mu\text{M}/\text{OD}_{600}$) of a steviol glycoside-producing strain overexpressing YMR166C (SEQ ID NO:132), YEL027W (SEQ ID NO:102), YKL120W (SEQ ID NO:126), YJL166C (SEQ ID NO:121), YJR106W (SEQ ID NO:48), YJL093C (SEQ ID NO:44), and YBR043C (SEQ ID NO:88) by the USER cloning system.

DETAILED DESCRIPTION

[0075] All publications, patents and patent applications cited herein are hereby expressly incorporated by reference in their entirety for all purposes.

[0076] 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.

[0077] 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.

[0078] 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.

[0079] 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, Calif.).

[0080] 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.

[0081] As used herein, the terms “microorganism,” “microorganism host,” “microorganism host cell,” “host cell,” “recombinant host,” “recombinant microorganism host,” and “recombinant host cell” can be used interchangeably. 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 the non-recombinant 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.

[0082] 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. Said recombinant genes are particularly encoded by cDNA.

[0083] As used herein, the term “engineered biosynthetic pathway” refers to a biosynthetic pathway that occurs in a recombinant host, as described herein, and does not naturally occur in the host.

[0084] 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 transporter. In some embodiments, the transporter is endogenous to *S. cerevisiae*, including, but not limited to *S. cerevisiae* strain S288C. In some embodiments, an endogenous yeast transporter 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 transporter gene 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 interchangeably 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*. In some embodiments, a deleted/knocked out gene is a transporter gene or a transcription factor gene that regulates expression of a transporter gene.

[0085] 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.

[0086] 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.

[0087] 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.

[0088] 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.

[0089] 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), 1,2-Bioside (MassBank Record: FU000299), 1,3-Bioside, Steviol-13-O-glucoside (13-SMG), Steviol-19-O-glucoside (19-SMG), a tri-glucosylated steviol glycoside, a tetra-glucosylated steviol glycoside, a penta-glucosylated steviol glycoside, a hexa-glucosylated steviol glycoside, a hepta-glucosylated steviol glycoside, di-glucosylated kaurenoic acid, tri-glucosylated kaurenoic acid, di-glucosylated kaurenol, tri-glucosylated kaurenol, and isomers thereof.

[0090] 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, each of which has been incorporated by reference herein in its entirety. See, also, Example 2. 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.

[0091] In some embodiments, steviol glycosides 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 steviol-producing recombinant host expressing one or more of a gene encoding a geranylgeranyl diphosphate synthase (GGPPS) polypeptide, a gene encoding an ent-copalyl diphosphate synthase (CDPS) polypeptide, a gene encoding a kaurene synthase (KS) polypeptide, a gene encoding a kaurene oxidase polypeptide (KO), a gene encoding a steviol synthase (KAH) polypeptide, a gene encoding a cytochrome P450 reductase (CPR) polypeptide,

and a gene encoding a UGT polypeptide can produce a steviol glycoside and/or steviol glycoside precursors in vivo. See Example 2.

[0092] In some embodiments, a recombinant host comprises a nucleic acid encoding a UGT85C2 polypeptide, a nucleic acid encoding a UGT76G1 polypeptide, a nucleic acid encoding a UGT74G1 polypeptide, a nucleic acid encoding a UGT91D2 polypeptide, and/or a nucleic acid encoding a EUGT11 polypeptide. 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 microorganism. In a particular embodiment, a steviol-producing recombinant microorganism comprises exogenous nucleic acids encoding UGT85C2, UGT76G1, or UGT91D2 polypeptides. In another particular embodiment, a steviol-producing recombinant microorganism comprises exogenous nucleic acids encoding UGT85C2, UGT76G1, UGT74G1, and UGT91D2 polypeptides. In yet another particular embodiment, a steviol-producing recombinant microorganism comprises exogenous nucleic acids encoding UGT85C2, UGT76G1, UGT74G1, and UGT91D2 (including inter alia 91D2e, 91D2m, 91D2e-b, and functional homologs thereof), and EUGT11 polypeptides. See Example 2.

[0093] In certain embodiments, the steviol glycoside is RebA, RebB, RebD, and/or RebM. RebA can be synthesized in a steviol-producing recombinant microorganism expressing UGT85C2, UGT76G1, UGT74G1, and UGT91D2. RebB can be synthesized in a steviol-producing recombinant microorganism expressing UGT85C2, UGT76G1, and UGT91D2. RebD can be synthesized in a steviol-producing recombinant microorganism expressing UGT85C2, UGT76G1, UGT74G1, and UGT91D2 and/or EUGT11. RebM can be synthesized in a steviol-producing recombinant microorganism expressing UGT85C2, UGT76G1, UGT74G1, and UGT91D2 and/or EUGT11 (see FIG. 1, Example 2).

[0094] In some embodiments, steviol glycosides 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 a UGT polypeptide 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 KAH enzyme can result in production of steviol in vitro.

[0095] 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 a steviol glycoside precursor in the cell; following modification in vivo, a steviol glycoside remains in the cell and/or is excreted into the culture medium. For example, a host cell expressing a gene encoding a UGT polypeptide 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 some embodiments, the cell is permeabilized to take up a substrate to be modified or to excrete a modified product.

[0096] In some embodiments, a steviol glycoside or steviol glycoside precursor composition produced in vivo, in vitro, or by whole cell bioconversion comprises less contaminants than a *stevia* extract from, inter alia, a *stevia* plant. Contaminants 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 - and β -amyrin, lupeol, β -amyrin acetate, pentacyclic triterpenes, centauredin, quercetin, epialpha-cadinol, carophyllenes and derivatives, beta-pinene, beta-sitosterol, and gibberellin.

[0097] As used herein, the terms “detectable amount,” “detectable concentration,” “measurable amount,” and “measurable concentration” refer to a level of steviol glycosides measured in AUC, $\mu\text{M}/\text{OD}_{600}$, 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 nuclear magnetic resonance spectroscopy (NMR).

[0098] 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.

Transporters and Transcription Factor Expression

[0099] This document describes reagents and methods that can be used to efficiently produce steviol glycoside compositions. Modification of transport systems in a recombinant host that are involved in transport of steviol glycosides into culture medium can allow more effective production of steviol glycosides in recombinant hosts.

[0100] As set forth herein, recombinant cells having modifications to cellular transport are capable of producing steviol. Recombinant hosts described herein can produce steviol and have altered expression of at least one endogenous transporter gene. Recombinant hosts described herein

can produce steviol and have altered expression of a transcription factor that regulates expression of at least one endogenous transporter gene. Altering expression of endogenous transporter genes can be useful for increasing production of steviol and/or excretion of steviol into the culture medium.

[0101] As set forth herein, recombinant cells having modifications to cellular transport are capable of producing at least one steviol glycoside, including, but not limited to, RebA, RebB, RebD, and/or RebM. Recombinant hosts described herein can produce at least one steviol glycoside such as RebA, RebB, RebD, and/or RebM and have altered expression of at least one endogenous transporter gene. Recombinant hosts described herein can produce at least one steviol glycoside such as RebA, RebB, RebD, and/or RebM and have altered expression of a transcription factor that regulates expression of at least one endogenous transporter gene. Recombinant hosts described herein can produce at least one steviol glycoside such as RebA, RebB, RebD, and/or RebM and have altered expression of a plurality of endogenous transporter genes and/or of a plurality of transcription factor genes that regulate expression of a plurality of endogenous transporter genes. Altering expression of endogenous transporter genes and/or transcription factors regulating expression of at least one transporter gene can be useful for increasing production of steviol glycosides and/or excretion of steviol glycosides into the culture medium.

[0102] Recombinant hosts disclosed herein can include one or more biosynthesis genes, such as one or more genes encoding a sucrose transporter and a sucrose synthase; a gene encoding a geranylgeranyl diphosphate synthase (GG-PPS) polypeptide; a gene encoding an ent-copalyl diphosphate synthase (CDPS) polypeptide; a gene encoding a kaurene synthase (KS) polypeptide; a gene encoding a kaurene oxidase (KO) polypeptide; a gene encoding a steviol synthase (KAH) polypeptide; a gene encoding a cytochrome P450 reductase (CPR) polypeptide; a gene encoding a UGT85C2 polypeptide; a gene encoding a UGT76G1 polypeptide; a gene encoding a UGT74G1 polypeptide; a gene encoding a UGT91D2 functional homolog; and/or a gene encoding a EUGT11 polypeptide; wherein expression of one or more of these genes results in production of steviol steviol glycosides such as RebA, RebB, RebD, and/or RebM.

[0103] As used herein, the terms “transport of a steviol glycoside,” “steviol glycoside transport,” “excretion of a steviol glycoside,” and “steviol glycoside excretion” can be used interchangeably.

[0104] As used herein, the term “transporter” (also referred to as a membrane transport protein) refers to a membrane protein involved in the movement of small molecules, macromolecules (such as carbohydrates), and ions across a biological membrane. Transporters span the membrane in which they are localized and across which they transport substances. Transporter proteins can assist in the movement (i.e., transport or excretion) of a substance from the intracellular space to the culture medium. Transporters are known to function as passive transport systems, carrying molecules down their concentration gradient, or as active transport systems, using energy to carry molecules uphill against their concentration gradient. Active transport is mediated by carriers which couple transport directly to the use of energy derived from hydrolysis of an ATP molecule or by carriers which make use of a pre-established electro-

chemical ion gradient to drive co-transport of the nutrient molecule and a co-transported ion. The latter category comprises symporters and antiporters, which carry the ion in the same or opposite direction, respectively, as the transported substrate.

[0105] Transport proteins have been classified according to various criteria at the Transporter Classification Database (on the world wide web at tcdb.org). See, Saier Jr. et al., Nucl. Acids Res., 42(1):D251-258 (2014). Non-limiting examples thereof include, among others, the family of Multiple Drug Resistance (MDR) plasma membrane transporters that is thought to be ubiquitous among living organisms. The MDR transporter superfamily can be further subdivided according to the mode of operation by which the substrate is transported from one side of the membrane to the other. Transporters can operate to move substances across membranes in response to chemiosmotic ion gradients or by active transport. ATP-binding cassette transporters (ABC transporters) are transmembrane proteins that utilize the energy of adenosine triphosphate (ATP) hydrolysis to carry out translocation of various substrates across membranes. They can transport a wide variety of substrates across the plasma membrane and intracellular membranes, including metabolic products, lipids and sterols, and drugs. Particular non-limiting examples of endogenous ABC transporter genes include PDR5, YDR061W, PDR15, SNQ2, YOR1, YOL075C, MDL2, ADP1, CAF16, VMR1 and STE6 (or a functional homolog thereof). In some aspects, ABC transporters transport steviol glycosides.

[0106] A second group of MDRs is further subdivided based on the nature of the chemiosmotic gradient that facilitates the transport. Saier, Jr. et al., J. Mol. Microbiol. Biotechnol. 1:257-279 (1999). In some aspects, MDR transporters transport steviol glycosides.

[0107] Another transporter family, the Major Facilitator Superfamily (MFS) transporters are monomeric polypeptides that can transport small solutes in response to proton gradients. The MFS transporter family is sometimes referred to as the uniporter-symporter-antiporter family. MFS transporters function in, inter alia, in sugar uptake and drug efflux systems. MFS transporters typically comprise conserved MFS-specific motifs. Non-limiting examples of endogenous MFS transporter genes include DTR1, SEO1, YBR241C, VBA3, FEN2, SNF3, STL1, HXT10, AZR1, MPH3, VBA5, GEX2, SNQ1, AQR1, MCH1, MCH5, ATG22, HXT15, MPH2, ITR1, SIT1, VPS73, HXT5, QDR1, QDR2, QDR3, SOA1, HXT9, YMR279C, YIL166C, HOL1, ENB1, TPO4 and FLR1 (or a functional homolog thereof). In some aspects, MFS transporters transport steviol glycosides.

[0108] Other transporter families include the SMR (small multidrug resistant) family, RND (Resistance-Nodulation-Cell Division) family, and the MATE (multidrug and toxic compound extrusion) family. The SMR family members are integral membrane proteins characterized by four alpha-helical transmembrane strands that confer resistance to a broad range of antiseptics, lipophilic quaternary ammonium compounds (QAC), and aminoglycoside resistance in bacteria. See, Bay & Turner, 2009, BMC Evol Biol., 9:140. In some aspects, SMR transporters transport steviol glycosides.

[0109] The MATE family members comprise 12 transmembrane (TM) domains. Members of the MATE family have been identified in prokaryotes, yeast such as *S. cerevisiae* and *Schizosaccharomyces pombe*, and plants. See Diener et al., 2001, Plant Cell. 13(7):1625-8. The MATE

family members are sodium or proton antiporters. In some aspects, MATE transporters transport steviol glycosides.

[0110] Additional transporter families include the amino acid/auxin permease (AAP) family (for example, YKL146W/AVT3, YBL089W/AVT5, YER119C/AVT6 and YIL088C/AVT7), the ATPase family (for example, YBL099W/ATP1, YDL185W/VMA1, YLR447C/VMA6, YOL077W/ATP19, YPL078C/ATP4, YEL027W/VMA3, YKL016C/ATP7, and YOR332W/VMA4), the sulfate permease (SuP) family (for example, YBR294W/SUL1, YGR125W and YPR003C), the lysosomal cystine transporter (LCT) family (for example, YCR075C/ERS1), the Ca²⁺:cation antiporter (CaCA) family (for example, YDL128W/VCX1 and YJR106W/ECM27), the amino acid-polyamine-organocation (APC) superfamily (for example, YDL210W/UGA4, YOL020W/TAT2, YPL274W/SAM3, YNL268W/LYP1, YHL036W/MUP3, YKR039W/GAP1 and YOR348C/PUT4), multidrug/oligosaccharidyl-lipid/polysaccharide (MOP) (for example, YDR338C), the ZRT/IRT-like protein (ZIP) metal transporter family (for example, YGL225W/ZRT1 and YOR079C/ATX2), the mitochondrial protein translocase (MPT) family (for example, YGR181W/TIM13, YNL070W/TOM7, YNL121C/TOM70, the voltage-gated ion channel (VIC) family (for example, YGR217W/CCH1 and YJL093C/TOK1), the monovalent cation:proton antiporter-2 (CPA2) family (for example, YJL094C/KHA1), the ThrE family of putative transmembrane amino acid efflux transporters (for example, YJL108C/PRM10), the oligopeptide transporter (OPT) family (for example, YJL212C/OPT1 and YGL114W), the K⁺ transporter (Trk) family (for example, TKR050W/TRK2), the bile acid:Na symporter (BASS) family (for example, YMR034C), the drug/metabolite transporter (DMT) superfamily (for example, YMR253C, YML038C/YMD8, and YOR307C/SLY41), the mitochondrial carrier (MC) family (for example, YMR056C/AAC1, YNL083W/SAL1, YOR130C/ORT1, YOR222W/ODC2, YPR011C, YPR058W/YMC1, YPR128C/ANT1, YEL006W/YEA6, YER053C/PIC2, YFR045W, YGR257C/MTM1, YHR002W/LEU5, YIL006W/YIA6, YJL133W/MRS3, YKL120W/OAC1, YMR166C, YNL003C/PET8 and YOR100C/CRC1), the auxin efflux carrier (AEC) family (for example, YNL095C, YOR092W/ECM3 and YBR287W), the ammonia channel transporter (Amt) family (for example, YNL142W/MEP2), the metal ion (Mn²⁺-iron) transporter (Nramp) family (for example, YOL122C/SMF1), the transient receptor potential Ca²⁺ channel (TRP-CC) family (for example, YOR087W/YVC1), the arsenical resistance-3 (ACR3) family (for example, YPR201W/ARR3), the nucleobase:cation symporter-1 (NCS1) family (for example, YBR021W/FUR4), the inorganic phosphate transporter (PiT) family (for example, YBR296C/PHO089), the arsenite-antimonite (ArsAB) efflux family (for example, YDL100C/GET3), the IISP family of transporters, the glycerol uptake (GUP) family (for example, YGL084C/GUP1), the metal ion transport (MIT) family (for example, YKL064W/MNR2, YKL050C and YOR334W/MRS2), the copper transport (Ctr) family (for example, YLR411W/CTR3) and the cation diffusion facilitator (CDF) family (for example, YOR316C/COT1). Particular members of any of these transporter families are included within the scope of the disclosed invention to the extent that altered expression in a cell capable of producing steviol glycoside increases production

of said steviol glycoside from the cell; exemplary members are disclosed above and in Tables 5, 6, and 14.

[0111] As used herein, the term “transcription factor” refers to a DNA-binding protein that regulates gene expression. Preferably, the transcription factor regulates expression of at least one transporter gene.

[0112] Methods for identifying a gene affecting production or transport of steviol glycosides and steviol glycoside pathway intermediates are disclosed herein. Such methods can involve inactivating at least one endogenous transporter gene or modifying expression of at least one transporter gene. Typically, a library of mutant microorganisms is prepared, each mutant in the library having a different endogenous transporter gene inactivated. Methods of inactivating genes and determining their effect in a microorganism are known to a person having ordinary skill in the art; additional methods are disclosed in WO 2014/122328, the disclosure of which is incorporated by reference in its entirety. The mutant microorganisms comprising one or more steviol glycoside pathway genes are cultured in a medium under conditions in which steviol or a steviol glycoside is synthesized, and the amount of total, supernatant, and/or intracellular steviol glycosides produced by the microorganism is measured (e.g., using LC-MS) as described herein.

[0113] The disclosure is directed to recombinant host cells in which expression of endogenous transporter or transcription factor genes is modified. In some embodiments, the transporter or transcription factor gene is endogenous to *S. cerevisiae*, including, but not limited to *S. cerevisiae* strain S288C. In some embodiments, expression of an endogenous transporter or transcription factor can be modified by replacing the endogenous promoter with a different promoter that results in increased expression of the transporter protein (e.g., at least a 5% increase in expression, such as at least a 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, or 50%, 100%, 200% increase or more in expression). For example, an endogenous promoter can be replaced with a constitutive or inducible promoter that results in increased expression of the transporter. Homologous recombination can be used to replace the promoter of an endogenous gene with a different promoter that results in increased expression of the transporter. In other embodiments, the inducible or constitutive promoter and endogenous transporter or transcription factor can be integrated into another locus of the genome using homologous recombination. In other embodiments, the transporter or transcription factor gene can be introduced into a microorganism using exogenous plasmids with a promoter that results in overexpression of the transporter or transcription factor in the microorganism. In yet another embodiment, the exogenous plasmids may also comprise multiple copies of the transporter or transcription factor gene. In a further embodiment, the endogenous transporter or transcription factor can be induced to be overexpressed using native mechanisms to the recombinant microorganism (e.g. heat shock, stress, heavy metal, or antibiotic exposure). In yet a further embodiment, the activity of an endogenous gene product is enhanced or increased (for example, by mutation). In yet another embodiment, a homologous or orthologous gene of an endogenous yeast transporter or transcription factor gene is overexpressed.

[0114] In certain other embodiments, modified expression of a target gene in a recombinant microorganism comprises overexpressing a transporter gene and/or a transcription

factor gene involved in expression of said transporter gene. In yet other embodiments, a plurality of endogenous transporter genes or transcription factor genes is overexpressed in said recombinant microorganism.

[0115] Modification of transcription factor expression can be used to increase transporter expression. For example, yeast transcription factor PDR1 regulates expression of the genes encoding ABC transporters PDR5, SNQ2 and YOR1. Therefore, in some embodiments, promoters for the endogenous PDR1 locus can be replaced with a different promoter that results in increased expression of the transcription factors, which can increase production of endogenous transporters.

[0116] In some embodiments, the transporter gene or transcription factor gene is (using Uniprot Ordered Locus Name for each): YAL067C, YBL089W, YBL099W, YBR008C, YBR021W, YBR043C, YBR180W, YBR241C, YBR287W, YBR294W, YBR295W, YBR296C, YCL038C, YCL069W, YCR011C, YCR028C, YCR075C, YDL054C, YDL100C, YDL128W, YDL185W, YDL194W, YDL210W, YDL245C, YDL247W, YDR011W, YDR061W, YDR093W, YDR292C, YDR338C, YDR406W, YDR497C, YDR536W, YEL006W, YEL027W, YEL031W, YEL065W, YER019C-A, YER053C, YER119C, YER166W, YFL011W, YFL028C, YFR045W, YGL006W, YGL013C, YGL084C, YGL104C, YGL114W, YGL167C, YGL255W, YGR125W, YGR181W, YGR217W, YGR224W, YGR257C, YGR281W, YHL016C, YHL035C, YHL036W, YHR002W, YHR096C, YIL006W, YIL088C, YIL120W, YIL121W, YIL166C, YJL093C, YJL094C, YJL108C, YJL133W, YJL212C, YJL219W, YJR106W, YJR160C, YKL016C, YKL050C, YKL064W, YKL120W, YKL146W, YKL209C, YKR039W, YKR050W, YKR105C, YKR106W, YLR411W, YLR447C, YML038C, YML116W, YMR034C, YMR056C, YMR166C, YMR253C, YMR279C, YNL003C, YNL065W, YNL070W, YNL083W, YNL095C, YNL121C, YNL142W, YNL268W, YNR055C, YOL020W, YOL075C, YOL077W-A, YOL122C, YOL158C, YOR079C, YOR087W, YOR092W, YOR100C, YOR130C, YOR153W, YOR222W, YOR271C, YOR273C, YOR291W, YOR306C, YOR307C, YOR316C, YOR332W, YOR334W, YOR348C, YPL036W, YPL078C, YPL270W, YPL274W, YPR003C, YPR011C, YPR058W, YPR128C, and/or YPR201W. SEQ ID NOs, Uniprot Accession Numbers, and gene names for each Ordered Locus can be found in Tables 5, 6, and 14. In some embodiments, the above transporter genes and transcription factor genes regulate excretion of steviol glycosides.

[0117] In some embodiments, deletion in a steviol glycoside-producing strain of YDL128W (SEQ ID NO:22), YDL194W (SEQ ID NO:24), YDL210W (SEQ ID NO:25), YDR536W (SEQ ID NO:30), YFL011W (SEQ ID NO:33), YGL006W (SEQ ID NO:34), YGL013C (SEQ ID NO:35), YGL255W (SEQ ID NO:36), YGR181W (SEQ ID NO:38), YGR217W (SEQ ID NO:39), YHL016C (SEQ ID NO:42), YIL088C (SEQ ID NO:43), YJL094C (SEQ ID NO:45), YJR106W (SEQ ID NO:48), YKR050W (SEQ ID NO:51), YNL065W (SEQ ID NO:59), YNL083W (SEQ ID NO:61), YNL121C (SEQ ID NO:63), YNL142W (SEQ ID NO:64), YOR291W (SEQ ID NO:74), YOR306C (SEQ ID NO:75), YOR334W (SEQ ID NO:77), YPL270W (SEQ ID NO:79), YPR011C (SEQ ID NO:82), YPR128C (SEQ ID NO:84) results in a measurable decrease of RebD excreted into the culture medium, indicating that each plays a role in RebD excretion. See Example 3 and Tables 7-10.

[0118] In some embodiments, deletion in a steviol glycoside-producing strain of YBR180W (SEQ ID NO:13), YAL067C (SEQ ID NO:14), YBR241C (SEQ ID NO:17), YCL069W (SEQ ID NO:19), YCR075C (SEQ ID NO:21), YDL128W (SEQ ID NO:22), YDL194W (SEQ ID NO:24), YDR093W (SEQ ID NO:27), YDR338C (SEQ ID NO:28), YDR406W (SEQ ID NO:29), YER166W (SEQ ID NO:32), YFL011W (SEQ ID NO:33), YGL006W (SEQ ID NO:34), YGL013C (SEQ ID NO:35), YGL255W (SEQ ID NO:36), YGR217W (SEQ ID NO:39), YHL016C (SEQ ID NO:42), YJL094C (SEQ ID NO:45), YJL212C (SEQ ID NO:47), YJR106W (SEQ ID NO:48), YJR160C (SEQ ID NO:49), YKR050W (SEQ ID NO:51), YKR106W (SEQ ID NO:53), YML116W (SEQ ID NO:55), YMR034C (SEQ ID NO:56), YMR056C (SEQ ID NO:57), YMR253C (SEQ ID NO:58), YNL070W (SEQ ID NO:60), YNL083W (SEQ ID NO:61), YNL095C (SEQ ID NO:62), YNL121C (SEQ ID NO:63), YOL075C (SEQ ID NO:66), YOL122C (SEQ ID NO:68), YOR087W (SEQ ID NO:70), YOR222W (SEQ ID NO:73), YOR291W (SEQ ID NO:74), YOR306C (SEQ ID NO:75), YPL274W (SEQ ID NO:80), YPR003C (SEQ ID NO:81), YPR011C (SEQ ID NO:82), or YPR201W (SEQ ID NO:85) results in a measurable decrease of RebM, indicating that each plays a role in RebM excretion. See Example 3 and Tables 7-10.

[0119] In some embodiments, overexpression of YGR181W (SEQ ID NO:38) or YDR061W (SEQ ID NO:26) improves RebD and RebM transport into the culture medium by approximately 2-fold (~400-500 mg/L of supernatant RebD and RebM in YGR181W (SEQ ID NO:38) and YDR061W (SEQ ID NO:26) overexpression strains versus ~250 mg/L of supernatant RebD and RebM in a control steviol glycoside-producing strain). See Example 4, FIG. 2, and FIG. 3.

[0120] In some embodiments, overexpression of a transporter of Table 11 increases excretion of RebA, RebB, RebD, and/or RebM by at least 20%. In some embodiments, overexpression of a transporter of Table 12 increases production of RebA, RebB, RebD, and/or RebM by at least 40%. See Example 5.

[0121] In some embodiments, a transporter gene is integrated into the genome of a steviol glycoside-producing host. In some embodiments, the integrated transporter is YBR043C (SEQ ID NO:88), YEL027W (SEQ ID NO:102), YJL093C (SEQ ID NO:44), YJR106W (SEQ ID NO:48), YMR166C (SEQ ID NO:132), YIL166C (SEQ ID NO:121), YKL120W (SEQ ID NO:126), YDL054C (SEQ ID NO:94), YDL128W (SEQ ID NO:22), YDR536W (SEQ ID NO:30), YGL167C (SEQ ID NO:112), YKL146W (SEQ ID NO:127), YKR039W (SEQ ID NO:129), YOL122C (SEQ ID NO:68), or YPR011C (SEQ ID NO:82). In some embodiments, integration of YBR043C (SEQ ID NO:88), YEL027W (SEQ ID NO:102), YJL093C (SEQ ID NO:44), YJR106W (SEQ ID NO:48), YKL120W (SEQ ID NO:126), or YMR166C (SEQ ID NO:132) improves excretion and/or total production of 13-SMG. In some embodiments, integration of YBR043C (SEQ ID NO:88), YEL027W (SEQ ID NO:102), or YMR166C (SEQ ID NO:132) improves excretion and/or total production of RebA. In some embodiments, integration of YBR043C (SEQ ID NO:88), YEL027W (SEQ ID NO:102), or YMR166C (SEQ ID NO:132) improves excretion and/or total production of RebB. In some embodiments, integration of YBR043C of SEQ ID NO:88, YEL027W of SEQ ID NO:102, YJL093C of SEQ ID

NO:44, YJR106W of SEQ ID NO:48, and YMR166C of SEQ ID NO:132 improves excretion and/or total production of RebD, and YBR043C of SEQ ID NO:88, YEL027W of SEQ ID NO:102, YIL166C (SEQ ID NO:121), YJL093C of SEQ ID NO:44, YJR106W of SEQ ID NO:48, and YMR166C of SEQ ID NO:132 improves excretion and/or total production of RebM, as measured by an increase in RebD and RebM levels in the supernatant compared to a control steviol glycoside-producing strain. See Example 6.

[0122] In some embodiments, steviol glycoside-producing *S. cerevisiae* strains overexpressing YJL093C (SEQ ID NO:44) or YBR043C (SEQ ID NO:88) produce higher levels of RebD+RebM, compared to a steviol glycoside-producing *S. cerevisiae* strain that does not overexpress YJL093C or YBR043C. See Example 7.

[0123] In some embodiments, a transporter that is knocked out can also have specificity for transport of larger molecular weight steviol glycosides (for example, RebD and the knockout of YGR181W of SEQ ID NO:38 or YOR291W of SEQ ID NO:74), and therefore, can be useful to overexpress in strains where transport of RebD into the culture medium is desired. With appropriate balancing of the rate of glycosylation activity through expression of pathway UGTs, smaller molecular weight steviol glycosides are further glycosylated before they are transported into the culture medium. For example, higher expression levels of a UGT76G1 and UGT91D2e and/or EUGT11, as compared to the UGT74G1 and UGT85C2 enzymes, can prevent accumulation of the steviol monoglucosides that are transported more readily. If the UGT activity level is higher (so the glycosylation rate is faster) than the rate of transport, then greater amounts of larger molecular weight steviol glycosides will be produced.

Steviol and Steviol Glycoside Biosynthesis Nucleic Acids

[0124] 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.

[0125] 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. 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 trans-

formed 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.

[0126] 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.

[0127] 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 comprises an origin of replication, and one or more selectable markers for maintenance of the construct in appropriate species.

[0128] 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.

[0129] 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 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. As another example, expression of membrane transporters involved in transport of steviol glycosides can be activated, such that transportation of steviol glycosides is increased. Such regulation can be beneficial in that transportation of steviol glycosides can be increased for a desired period of time during culture of the microorganism, thereby increasing the yield of glycoside product(s) at harvest. 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.

Recombinant Hosts

[0130] 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).

[0131] Typically, the recombinant microorganism is grown in a fermenter at a defined temperature(s) for a desired period of time. 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, kaurene and kaurenoic acid, can be determined by extracting samples from culture media for analysis according to published methods.

[0132] 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, carbon 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.

[0133] After the recombinant microorganism has been grown in culture for the desired period of time, 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.

[0134] 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 produce steviol and/or steviol glycosides.

[0135] 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.

[0136] 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*, *Rhodotulula*, *Saccharomyces*, *Schizosaccharomyces*, *Sphaceloma*, *Xanthophyllomyces* or *Yarrowia*. Exemplary species from such genera include *Lentinus tigrinus*, *Laetiporus sulphureus*, *Phanerochaete chrysosporium*, *Pichia pastoris*, *Cyberlindnera jadinii*, *Physcomitrella patens*, *Rhodotulula glutinis*, *Rhodotulula mucilaginosa*, *Phaffia rhodozyma*, *Xanthophyllomyces dendrorhous*, *Fusarium fujikuroi*/*Gibberella fujikuroi*, *Candida utilis*, *Candida glabrata*, *Candida albicans*, and *Yarrowia lipolytica*.

[0137] In some embodiments, a microorganism can be a prokaryote such as *Escherichia coli*.

[0138] 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*.

[0139] 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.

[0140] 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.

[0141] *Saccharomyces* 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.

[0142] *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

[0143] *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.

[0144] *Agaricus*, *Gibberella*, and *Phanerochaete* spp.

[0145] *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*)

[0146] *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

[0147] *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 microorganism. *Yarrowia lipolytica* 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.

[0148] *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).

[0149] *Rhodospiridium toruloides*

[0150] *Rhodospiridium 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

[0151] *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*)

[0152] *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, *Viral Sin.* 29(6):403-9.

Kluyveromyces lactis

[0153] *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

[0154] *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.

[0155] *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.

Steviol Glycoside Compositions

[0156] 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) and have a consistent taste profile. 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. Hosts described herein do not produce the 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.

[0157] The amount of an individual steviol glycoside (e.g., RebA, RebB, RebD, or RebM) produced can be from about 1 mg/L to about 2,800 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 1,400 mg/L, at least about 1,600 mg/L, at least about 1,800 mg/L, or at least about 2,800 mg/L. In some aspects, the amount of an individual steviol glycoside can exceed 2,800 mg/L. The amount of a combination of steviol glycosides (e.g., RebA, RebB, RebD, or RebM) produced can be from about 1 mg/L to about 6,000 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, or at least about 6,000 mg/L. In some aspects, the amount of a combination of steviol glycosides can exceed 6,000 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.

[0158] 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 steviol and null mutations in a first group of endogenous transporters, while a second microorganism comprises steviol glycoside biosynthesis genes and null mutations in a second group of endogenous transporters. 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.

[0159] 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. The microorganisms can have the same or a different group of mutations in endogenous transporters. 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.

[0160] 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) and have a consistent taste profile. Thus, the recombinant microorganisms 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. Microorganisms described herein do not produce the undesired plant byproducts found in *Stevia* extracts. Thus, steviol glycoside compositions produced by

the recombinant microorganisms described herein are distinguishable from compositions derived from *Stevia* plants.

[0161] 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, each of which has been incorporated by reference in its entirety.

[0162] 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. For example, recombinant microorganisms described herein can express transporters specific for transport of a particular rebaudioside into the culture medium. When a transporter is specific for a particular rebaudioside it will enrich the concentration of that compound in the fermentation broth, preventing it from being further reacted to a different compound, and by selectively transporting the rebaudioside into the fermentation broth it will make it easier to recover from the other rebaudiosides and therefore making the process more efficient.

[0163] 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, e.g., 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.

[0164] 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 a 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.

[0165] For example, such a steviol glycoside composition can have from 90-99% 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.

[0166] Such a steviol glycoside composition can be a RebB-enriched composition having greater than 3% 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.

[0167] Such a steviol glycoside composition can be a RebD-enriched composition having greater than 3% 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.

[0168] Such a steviol glycoside composition can be a RebE-enriched composition having greater than 3% 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.

[0169] Such a steviol glycoside composition can be a RebM-enriched composition having greater than 3% 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.

[0170] 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.

[0171] The invention will be further described in the following examples, which do not limit the scope of the invention described in the claims.

EXAMPLES

[0172] 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

[0173] The LC-MS methods described here are oriented towards the separation, general detection and potential identification of chemicals of particular masses (i.e. steviol glycosides) in the presence of a mixture (i.e. culture media). LC-MS analyses were performed on: (A) an UltiMate® 3000-TSQ (Thermo Fisher Scientific); (B) a 1290 Infinity—6130SQ (Agilent); or (C) an Acquity—XevoTQD (Waters) system. Specific methods used for each system are described below.

[0174] Method A:

[0175] LC-MS analyses were performed using an UltiMate® 3000 UPLC system (Dionex) fitted with a waters ACQUITY UPLC® BEH shield RP18 column (2.1×50 mm, 1.7 µm particles, 130 Å pore size) connected to a TSQ Quantum® Access (ThermoFisher Scientific) triple quadrupole mass spectrometer with a heated electrospray ion (HESI) source, unless otherwise indicated. Elution was carried out using a mobile phase of eluent B (MeCN with 0.1% Formic acid) and eluent A (water with 0.1% Formic acid) by increasing the gradient from 25% to 47% B from min. 0.0 to 4.0, increasing 47% to 100% B in min. 4.0 to 5.0, holding 100% B from min. 5.0 to 6.5 re-equilibration. The flow rate was 0.4 mL/min and the column temperature 35° C. The steviol glycosides were detected using SIM (Single Ion Monitoring) with the following m/z-traces.

TABLE 1

MS analytical information for Steviol Glycosides			
Description	Exact Mass	m/z trace	compound (typical t_R in min)
Steviol + 1 Glucose	[M + H] ⁺	481.2 ± 0.5	19-SMG (2.29),
	481.2796	503.1 ± 0.5	13-SMG (3.5)
Steviol + 2 Glucose	[M + Na] ⁺	665 ± 0.5	Rubusoside (2.52)
	665.3149		Steviol-1,2-bioside (2.92)
Steviol + 3 Glucose	[M + Na] ⁺	827.4 ± 0.5	Steviol-1,3-bioside (2.28)
	827.3677		1,2-Stevioside (2.01)
Steviol + 4 Glucose	[M + Na] ⁺	989.4 ± 0.5	1,3-Stevioside (2.39)
	989.4200		RebB (2.88)
Steviol + 5 Glucose	[M + Na] ⁺	1151.4 ± 0.5	RebA (2.0)
	1151.4728		RebD (1.1)
Steviol + 6 Glucose	[M + Na] ⁺	1313.5 ± 0.5	RebM (1.3)
	1313.5257		

[0176] The levels of steviol glycosides were quantified by comparing with calibration curves obtained with authentic standards from LGC Standards. For example, standard solutions of 0.5 to 100 µM RebA were typically utilized to construct a calibration curve.

[0177] Method B:

[0178] A second analytical method was performed on the Agilent system 1290 Infinity fitted with a waters ACQUITY UPLC® BEH shield RP18 column (2.1×50 mm, 1.7 µm particles, 130 Å pore size, Waters) was connected to a 6130 single quadrupole mass detector (Agilent) with a APCI ion source. Elution was carried out using a mobile phase of eluent B (MeCN with 0.1% Formic acid) and eluent A (water with 0.1% Formic acid) by increasing the gradient from 23% to 47% B from min. 0.0 to 4.0, increasing 47% to 100% B in min. 4.0 to 5.0, holding 100% B from min. 5.0 to 6.5 re-equilibration. The flow rate was 0.6 mL/min and the column temperature 50° C. The steviol glycosides were detected using SIM (Single Ion Monitoring) with the following m/z-traces.

TABLE 2

MS analytical information for Steviol Glycosides					
SIM trace No	time window	m/z trace	Exact Mass	Description	compound (typical t_R in min)
1	0.0-1.51 min	1289.5	[M - H] ⁻ 1289.5281	Steviol + 6 Glucose	RebM (0.91)
	1.51-1.90 min	687.3	[M + HCOOH - H] ⁻ 687.3217	Steviol + 2 Glucose	Rubusoside
	1.90-5.0 min	641.0	[M - H] ⁻ 641.3168	Steviol + 2 Glucose	1,2-Stevioside (1.44) 1,3-stevioside (1.74)
2	0.0-1.0 min	1127.4	[M - H] ⁻ 1127.4752	Steviol + 5 Glucose	RebD (0.81)
	1.0-5.0 min	525.3	[M - HCOOH - H] ⁻ 525.2689	Steviol + 1 Glucose	19SMG (2.49) 13SMG (2.65)
3	0.0-2.8 min	965.4	[M - H] ⁻ 965.4224	Steviol + 4 Glucose	RebA (1.42)
4	0.0-3.2 min	803.4	[M - H] ⁻ 803.3696	Steviol + 2 Glucose	1,2-Stevioside (2.16) 1,3-Stevioside (2.34) RebB (2.13)

[0179] The levels of steviol glycosides were quantified by comparing with calibration curves obtained with authentic standards from LGC Standards. For example, standard solutions of 0.3 to 25 μ M RebA were typically utilized to construct a calibration curve.

[0180] Method C:

[0181] A third analytical method used was LC-MS analyses performed using a Waters ACQUITY UPLC (Waters Corporation, Milford, Mass.) with Waters ACQUITY UPLC® BEH C18 column (2.1×50 mm, 1.7 μ m particles, 130 Å pore size) coupled to a Waters ACQUITY TQD triple quadrupole mass spectrometer with electrospray ionization (ESI) in negative mode. Compound separation 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-equilibrate for another 0.6 min. The flow rate was 0.6 mL/min and the column temperature 55° C. RebD (m/z 1127.5), RebM (m/z 1289.5), rebaudioside A (m/z 965.4) and RebB (m/z 803.4) were monitored using SIM (Single Ion Monitoring) and quantified by comparing with authentic standards.

Example 2. Construction of a Steviol Glycoside-Producing Yeast Strain

[0182] Steviol glycoside-producing *S. cerevisiae* strains were constructed as described in WO 2011/153378, WO 2013/022989, WO 2014/122227, and WO 2014/122328, each of which is incorporated by reference in its entirety. For example, a yeast strain comprising a recombinant gene encoding a *Synechococcus* sp. GGPPS polypeptide (SEQ ID NO:1, SEQ ID NO:149), a recombinant gene encoding a truncated *Zea mays* CDPS polypeptide (SEQ ID NO:2, SEQ ID NO:150), a recombinant gene encoding an *A. thaliana* KS polypeptide (SEQ ID NO:3, SEQ ID NO:151), a recombinant gene encoding a recombinant *S. rebaudiana* KO1 polypeptide (SEQ ID NO:4, SEQ ID NO:152), a recombinant gene encoding an *A. thaliana* ATR2 polypeptide (SEQ ID NO:5, SEQ ID NO:153), a recombinant gene encoding an *O. sativa* EUGT11 polypeptide (SEQ ID NO:12; SEQ ID NO:148), a recombinant gene encoding an SrKAHe1 polypeptide (SEQ ID NO:6, SEQ ID NO:154), a recombinant gene encoding an *S. rebaudiana* CPR8 polypeptide (SEQ ID

NO:7, SEQ ID NO:155), a recombinant gene encoding an *S. rebaudiana* UGT85C2 polypeptide (SEQ ID NO:8, SEQ ID NO:156), a recombinant gene encoding an *S. rebaudiana* UGT74G1 polypeptide (SEQ ID NO:9, SEQ ID NO:157), a recombinant gene encoding an *S. rebaudiana* UGT76G1 polypeptide (SEQ ID NO:10, SEQ ID NO:158), and a recombinant gene encoding an *S. rebaudiana* UGT91D2 variant (or functional homolog), UGT91D2e-b (SEQ ID NO:11, SEQ ID NO:159) polypeptide produced steviol glycosides. As analyzed by LC-MS (Method C) following DMSO-extraction of total steviol glycosides from the whole cell and broth mixture (total production), the strain produced between 18-21 μ g/mL or 1-1.5 μ g/mL/OD₆₀₀ RebM after growth for five days in 1 mL SC (Synthetic Complete) media at 30° C. with 400 rpm shaking in deep-well plates. See Table 3.

TABLE 3

Steviol glycoside production in a representative <i>S. cerevisiae</i> strain comprising genes encoding GGPPS, truncated CDPS, KS, KO, ATR2, EUGT11, SrKAHe1, CPR8, UGT85C2, UGT74G1, UGT76G1, and EUGT11 polypeptides.				
RebB (μ g/mL/ OD ₆₀₀)	RebA (μ g/mL/ OD ₆₀₀)	RebD (μ g/mL/ OD ₆₀₀)	RebM (μ g/mL/ OD ₆₀₀)	Normalized by OD ₆₀₀
0.21	0.33	0.33	1.3	Average
0.028	0.054	0.032	0.14	Std Deviation
RebB (μ g/mL)	RebA (μ g/mL)	RebD (μ g/mL)	RebM (μ g/mL)	
3.1	4.9	5.0	19.0	Average
0.42	0.81	0.48	2.1	Std Deviation

[0183] A second strain, which comprised additional copies of the genes of the first strain, was analyzed for steviol glycoside production. The second strain produced RebD and RebM as primary steviol glycosides, although at higher levels than the first strain.

[0184] As analyzed by LC-MS (Method C) following DMSO-extraction of total steviol glycosides from the whole cell and broth mixture (total production), the second strain produced between 60-80 μ g/mL or 4-6 μ g/mL/OD₆₀₀ RebM, after growth for five days in 1 mL SC media at 30° C. with

400 rpm shaking in deep-well plates. Production of RebA, RebB, RebD and RebM by the second strain is shown in Table 4.

TABLE 4

Steviol glycoside production in an <i>S. cerevisiae</i> strain comprising additional copies of genes encoding GGPPS, truncated CDPS, KS, KO, ATR2, EUGT11, SrKAHe1, CPR8, UGT85C2, UGT74G1, UGT76G1, and EUGT11 polypeptides.				
RebA ($\mu\text{g/mL}/\text{OD}_{600}$)	RebB ($\mu\text{g/mL}/\text{OD}_{600}$)	RebD ($\mu\text{g/mL}/\text{OD}_{600}$)	RebM ($\mu\text{g/mL}/\text{OD}_{600}$)	Normalized by OD_{600}
2.1	0.67	1.6	4.8	Average
0.66	0.21	0.75	2.3	Std Deviation
RebA ($\mu\text{g/mL}$)	RebB ($\mu\text{g/mL}$)	RebD ($\mu\text{g/mL}$)	RebM ($\mu\text{g/mL}$)	
31.0	10.1	23.7	72.5	Average
9.9	3.1	11.3	34.4	Std Deviation

Example 3. Knockout of Yeast Endogenous Transport Genes and Transport-Related Genes

[0185] Observations from deep-well studies of Example 2 and similar strains indicated that the fraction of RebA, RebB, RebD or RebM in the supernatant changes with time, and the effect was determined not to be the result of cell lysis. To determine the effect of various transporters on steviol glycoside excretion in *S. cerevisiae*, deletion cassettes for homologous recombination were obtained by designing primers annealing approximately 200 bp upstream and downstream of the open reading frame (ORF) and then amplifying the ORF-specific deletion cassette from the *S. cerevisiae* deletion collection. The candidate genes selected include identified ORFs with relation to transport or comprising membrane spanning domains, regardless of subcellular localization. In the resulting colonies, the presence of the deletion cassette at the correct locus was verified by colony PCR. A maximum of 6 clones of each deletion was frozen down as freezer stock. All samples for analysis were initiated from the freezer stock and grown in SC medium for 5 days (30° C., shaking 400 rpm) prior to harvest and extraction of samples for LC-MS. Samples were analyzed for the presence of RebA, RebB, RebD and RebM in the culture broth lacking cells (Supernatant) as well as in the whole cell and broth mixture (Total production).

[0186] Concentrations of total and supernatant RebA, RebB, RebD and RebM were compared to the levels in a control steviol glycoside-producing strain. The amounts of RebA, RebB, RebD and RebM in each sample were normalized to the control strain by dividing the value of a particular steviol glycoside with the corresponding value for the control strain, thereby calculating a percentage to the

control strain, where 1 equals 100 percent. The “ideal candidate” would exhibit a decrease in RebA, RebB, RebD and/or RebM levels in the supernatant, as compared to the control steviol glycoside-producing strain, without decreasing RebA, RebB, RebD, and/or RebM total production.

[0187] The effect of yeast gene knockouts on transport of higher molecular weight steviol glycosides into the culture medium was tested in a strain that produces steviol glycosides, such as the strains described in Example 2. Disruption of each specific transporter gene was performed by homologous recombination. After 5 days of growth in 1 mL SC medium at 30° C. and 400 rpm, cells were harvested. A 50 μL aliquot of the culture was mixed with an equal volume of 100% DMSO, vortexed, and heated to 80° C. for 10 min. The suspension was then centrifuged to remove cell debris. 60 μL of the mixture were analyzed by LC-MS as the “Total” sample. The remaining culture was then centrifuged to pellet cells. An aliquot of 50 μL was removed from the supernatant (i.e., the culture medium) and mixed with an equal volume of 100% DMSO. The suspension was heated to 80° C. for 10 min and centrifuged. 60 μL of the mixture were analysed by LC-MS as the “Supernatant” sample. The amounts of higher molecular weight steviol glycosides (including RebA, RebB, RebD, RebM) were measured by LC-MS (Method C), as described in Example

[0188] The data demonstrate that disruption of a single endogenous yeast transporter gene in a steviol glycoside-producing strain resulted in a decrease in the level of various steviol glycosides in the supernatant of the culture media, as evaluated by the normalized amount transported into the supernatant (see Tables 5-10). Tables 5-10 comprise lists of transport related genes that were knocked out in a steviol glycoside-producing strain. More specifically, Table 5 comprises a compiled list of genes by ordered locus name found to affect steviol glycoside excretion in steviol glycoside-producing strains and are therefore identified as having a role in steviol glycoside excretion. When the specified genes were knocked out, a more than 40% decrease in either the supernatant alone or in the ratio of supernatant/total production of RebA, RebB, RebD, and/or RebM was observed. This corresponded approximately to more than 2 standard deviations removed from the mean of a control steviol glycoside-producing strain (a value of 1 equals 100 percent of the control strain, whereas a value of 0.5 indicates a 50% decrease).

[0189] Table 6 comprises a compiled list of genes by ordered locus name found to affect steviol glycoside excretion in steviol glycoside-producing strains and are therefore identified as having a role in steviol glycoside excretion. When knocked out, these genes caused a mean of between 20-40% decrease in either the supernatant alone or in the ratio of supernatant/total production. This corresponded to approximately between 1 and 2 standard deviations removed from the mean of the control strain (a value of 1 equals 100 percent of the control strain, whereas a value of 0.5 indicates a 50% decrease).

TABLE 5

Transport related genes with over a 40% decrease in Reb A, RebB, RebD or RebM levels compared to a control steviol glycoside-producing strain.					
A.					
SEQ ID No.	Ordered Locus Name	Family	Description	Gene name	Uniprot Accession No.
13	YBR180W	MFS	Secondary Transporter	DTR1	P38125
14	YAL067C	MFS	Secondary Transporter	SEO1	P39709

TABLE 5-continued

Transport related genes with over a 40% decrease in Reb A, RebB, RebD or RebM levels compared to a control steviol glycoside-producing strain.					
15	YBL089W	AAAP	Secondary Transporter	AVT5	P38176
16	YBL099W	F-ATPase	ATP-Dependent	ATP1	P07251
17	YBR241C	MFS	Secondary Transporter		P38142
18	YBR294W	SulP	Secondary Transporter	SUL1	P38359
19	YCL069W	MFS	Secondary Transporter	VBA3	P25594
20	YCR028C	MFS	Secondary Transporter	FEN2	P25621
21	YCR075C	LCT	Secondary Transporter	ERS1	P17261
22	YDL128W	CaCA	Secondary Transporter	VCX1	Q99385
23	YDL185W	F-ATPase	ATP-Dependent	VMA1	P17255
24	YDL194W	MFS	Secondary Transporter	SNF3	P10870
25	YDL210W	APC	Secondary Transporter	UGA4	P32837
26	YDR061W	ABC	ATP-Dependent		Q12298
27	YDR093W	P-ATPase	ATP-Dependent	DNF2	Q12675
28	YDR338C	MOP/MATE	Secondary Transporter		Q05497
29	YDR406W	ABC	ATP-Dependent	PDR15	Q04182
30	YDR536W	MFS	Secondary Transporter	STL1	P39932
31	YEL031W	P-ATPas	ATP-Dependent	SPF1	P39986
32	YER166W	P-ATPase	ATP-Dependent	DNF1	P32660
33	YFL011W	MFS	Secondary Transporter	HXT10	P43581
34	YGL006W	P-ATPase	ATP-Dependent	PMC1	P38929
35	YGL013C		Transcription factor	PDR1	P12383
36	YGL255W	ZIP	Secondary Transporter	ZRT1	P32804
37	YGR125W	SulP	Secondary Transporter		P53273
38	YGR181W	MPT	ATP-Dependent	TIM13	P53299
39	YGR217W	VIC	Ion Channels	CCH1	P50077
40	YGR224W	MFS	Secondary Transporter	AZR1	P50080
41	YGR281W	ABC	ATP-Dependent	YOR1	P53049
42	YHL016C	SSS	Secondary Transporter	DUR3	P33413
43	YIL088C	AAAP	Secondary Transporter	AVT7	P40501
44	YJL093C	VIC	Ion Channels	TOK1	P40310
45	YJL094C	CPA2	Secondary Transporter	KHA1	P40309
46	YJL108C	ThrE	Secondary Transporter	PRM10	P42946
47	YJL212C	OPT	Secondary Transporter	OPT1	P40897
48	YJR106W	CaCA	Secondary Transporter	ECM27	P47144

B.

No.	Ordered Locus Name	Family	Description	Gene name	Uniprot Accession No.
49	YJR160C	MFS	Secondary Transporter	MPH3	POCE00
50	YKL064W	MIT	Ion Channels	MNR2	P35724
51	YKR050W	Trk	Secondary Transporter	TRK2	P28584
52	YKR105C	MFS	Secondary Transporter	VBA5	P36172
53	YKR106W	MFS	Secondary Transporter	GEX2	P36173
54	YLR447C	F-ATPase	ATP-Dependent	VMA6	P32366
55	YML116W	MFS	Secondary Transporter	SNQ1/ATR1	P13090
56	YMR034C	BASS	Secondary Transporter		Q05131
57	YMR056C	MC	Secondary Transporter	AAC1	P04710
58	YMR253C	DMT	Secondary Transporter		Q04835
59	YNL065W	MFS	Secondary Transporter	AQR1	P53943
60	YNL070W	MPT	ATP-Dependent	TOM7	P53507
61	YNL083W	MC	Secondary Transporter	SAL1	D6W196
62	YNL095C	AEC	Secondary Transporter		P53932
63	YNL121C	MPT	ATP-Dependent	TOM70	P07213
64	YNL142W	Amt	Ion Channels	MEP2	P41948
65	YOL020W	APC	Secondary Transporter	TAT2	P38967
66	YOL075C	ABC	ATP-Dependent		Q08234
67	YOL077W-A	F-ATPase	ATP-Dependent	ATP19	P81451
68	YOL122C	Nramp	Secondary Transporter	SMF1	P38925
69	YOR079C	ZIP	Secondary Transporter	ATX2	Q12067
70	YOR087W	TRP-CC	Ion Channels	YVC1	Q12324
71	YOR092W	AEC	Secondary Transporter	ECM3	Q99252
72	YOR130C	MC	Secondary Transporter	ORT1	Q12375
73	YOR222W	MC	Secondary Transporter	ODC2	Q99297
74	YOR291W	P-ATPase	ATP-Dependent	YPK9	Q12697
75	YOR306C	MFS	Secondary Transporter	MCH5	Q08777
76	YOR316C	CDF	Secondary Transporter	COT1	P32798
77	YOR334W	MIT	Ion Channels	MRS2	Q01926
78	YPL078C	F-ATPase	ATP-Dependent	ATP4	P05626
79	YPL270W	ABC	ATP-Dependent	MDL2	P33311
80	YPL274W	APC	Secondary Transporter	SAM3	Q08986
81	YPR003C	SulP	Secondary Transporter		P53394

TABLE 5-continued

Transport related genes with over a 40% decrease in Reb A, RebB, RebD or RebM levels compared to a control steviol glycoside-producing strain.					
82	YPR011C	MC	Secondary Transporter		Q12251
83	YPR058W	MC	Secondary Transporter	YMC1	P32331
84	YPR128C	MC	Secondary Transporter	ANT1	Q06497
85	YPR201W	ACR3	Secondary Transporter	ARR3	Q06598

TABLE 6

Transport related genes with a 20-40% decrease in Reb A, RebB, RebD or RebM levels compared to a control steviol glycoside-producing strain.					
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A.

SEQ ID No.	Ordered Locus Name	Family	Description	Gene name	Uniprot Accession No.
86	YBR008C	MFS	Secondary Transporter	FLR1	P38124
87	YBR021W	NCS1	Secondary Transporter	FUR4	P05316
88	YBR043C	MFS	Secondary Transporter	QDR3	P38227
89	YBR287W	AEC	Secondary Transporter		P38355
90	YBR295W	P-ATPase	ATP-Dependent	PCA1	P38360
91	YBR296C	PiT	Secondary Transporter	PHO89	P38361
92	YCL038C	MFS	Secondary Transporter	ATG22	P25568
93	YCR011C	ABC	ATP-Dependent	ADP1	P25371
94	YDL054C	MFS	Secondary Transporter	MCH1	Q07376
95	YDL100C	ArsAB	ATP-Dependent	GET3	Q12154
96	YDL245C	MFS	Secondary Transporter	HXT15	P54854
97	YDL247W	MFS	Secondary Transporter	MPH2	P0CD99
98	YDR011W	ABC	ATP-Dependent	SNQ2	P32568
99	YDR292C	IISP	ATP-Dependent	SRP101	P32916
100	YDR497C	MFS	Secondary Transporter	ITR1	P30605
101	YEL006W	MC	Secondary Transporter	YEA6	P39953
102	YEL027W	F-ATPase	ATP-Dependent	VMA3	P25515
103	YEL065W	MFS	Secondary Transporter	SIT1	P39980
104	YER019C-A	IISP	ATP-Dependent	SBH2	P52871
105	YER053C	MC	Secondary Transporter	PIC2	P40035
106	YER119C	AAAP	Secondary Transporter	AVT6	P40074
107	YFL028C	ABC	ATP-Dependent	CAF16	P43569
108	YFR045W	MC	Secondary Transporter		P43617
109	YGL084C	GUP	Secondary Transporter	GUP1	P53154
110	YGL104C	MFS	Secondary Transporter	VPS73	P53142
111	YGL114W	OPT	Secondary Transporter		P53134
112	YGL167C	P-ATPase	ATP-Dependent	PMR1	P13586
113	YGR257C	MC	Secondary Transporter	MTM1	P53320
114	YHL035C	ABC	ATP-Dependent	VMR1	P38735
115	YHL036W	APC	Secondary Transporter	MUP3	P38734

B.

No.	Ordered Locus Name	Family	Description	Gene name	Accession No.
116	YHR002W	MC	Secondary Transporter	LEU5	P38702
117	YHR096C	MFS	Secondary Transporter	HXT5	P38695
118	YIL006W	MC	Secondary Transporter	YIA6	P40556
119	YIL120W	MFS	Secondary Transporter	QDR1	P40475
120	YIL121W	MFS	Secondary Transporter	QDR2	P40474
121	YIL166C	MFS	Secondary Transporter	SOA1	P40445
122	YJL133W	MC	Secondary Transporter	MRS3	P10566
123	YJL219W	MFS	Secondary Transporter	HXT9	P40885
124	YKL016C	F-ATPase	ATP-Dependent	ATP7	P30902
125	YKL050C	MIT	Ion Channels		P35736
126	YKL120W	MC	Secondary Transporter	OAC1	P32332
127	YKL146W	AAAP	Secondary Transporter	AVT3	P36062
128	YKL209C	ABC	ATP-Dependent	STE6	P12866
129	YKR039W	APC	Secondary Transporter	GAP1	P19145
130	YLR411W	Ctr	Ion Channels	CTR3	Q06686
131	YML038C	DMT	Secondary Transporter	YMD8	Q03697
132	YMR166C	MC	Secondary Transporter		Q03829
133	YMR279C	MFS	Secondary Transporter		Q03263

TABLE 6-continued

Transport related genes with a 20-40% decrease in Reb A, RebB, RebD or RebM levels compared to a control steviol glycoside-producing strain.					
134	YNL003C	MC	Secondary Transporter	PET8	P38921
135	YNL268W	APC	Secondary Transporter	LYP1	P32487
136	YNR055C	MFS	Secondary Transporter	HOL1	P53389
137	YOL158C	MFS	Secondary Transporter	ENB1	Q08299
138	YOR100C	MC	Secondary Transporter	CRC1	Q12289
139	YOR153W	ABC	ATP-Dependent	PDR5	P33302
140	YOR271C	MTC	Secondary Transporter	FSF1	Q12029
141	YOR273C	MFS	Secondary Transporter	TPO4	Q12256
142	YOR307C	DMT	Secondary Transporter	SLY41	P22215
143	YOR332W	F-ATPase	ATP-Dependent	VMA4	P22203
144	YOR348C	APC	Secondary Transporter	PUT4	P15380
145	YPL036W	P-ATPase	ATP-Dependent	PMA2	P19657

[0190] Steviol glycoside exporter candidates were selected from the data based on two selection criteria for each steviol glycoside measured (L e., two methods of normalizing expression).

[0191] Transporter selection criterion 1 corresponded to selection based on the level of high molecular weight steviol glycosides (RebA, RebB, RebD, or RebM) available in the supernatant, as well as the total production of the said steviol glycoside. Both values were normalized to the value of the corresponding steviol glycoside-producing control strain. The control level was set to 1, and the corresponding steviol glycoside level was calculated as a percentage of the control. For Ordered Locus Names (i.e., genes) of interest, the steviol glycoside available in the supernatant should be below 0.6 (below 60% of the control) or between 0.8-0.6 (80-60% of the control). To avoid false positives or a bias towards transporters that decrease the production in general, the calculation had an additional requirement that the total production had to be similar to the control. In the current calculation, production was set to be between 0.85 and 1.15 of the control, when the control is set to 1. In this regard, steviol glycoside production levels did not affect results. Table 7 shows the supernatant/total ratio for each candidate that fulfills the selection criteria.

[0192] Transporter selection criterion 2 corresponded to selection based on the ratio of high molecular weight steviol glycosides (RebA, RebB, RebD, or RebM) in the supernatant relative to total production of the said steviol glycoside. The supernatant-to-total production ratio was normalized to the ratio of the corresponding steviol glycoside-producing strain control. The control level was set to 1, and the corresponding steviol glycoside ratio was calculated as a percentage of the control. For Ordered Locus Names (i.e., genes) of interest, the supernatant-to-total production ratio for a given steviol glycoside should be below 0.6 (below 60% of the control) or between 0.8-0.6 (80-60% of the control). To avoid false positives or a bias towards transporters that decrease the production in general, the calculation had an additional requirement that the total production had to be similar to the control. In the current calculation, production was set to be between 0.85 and 1.15 of the control, when the control is set to 1. In this regard, steviol glycoside production levels did not affect results. Table 8 shows the supernatant/total ratio for each candidate that fulfills the selection criteria.

[0193] The data demonstrate that disruption of a single endogenous yeast transporter gene in a steviol glycoside-producing strain resulted in a decrease in the level of various

steviol glycosides in the supernatant of the culture media, as evaluated by the normalized amount transported into the supernatant (see Tables 5-10), and are therefore identified as having a role in steviol glycoside excretion.

[0194] For example, deletion in a steviol glycoside-producing strain of YDL128W (SEQ ID NO:22), YDL194W (SEQ ID NO:24), YDL210W (SEQ ID NO:25), YFL011W (SEQ ID NO:33), YGL006W (SEQ ID NO:34), YGL013C (SEQ ID NO:35), YGL255W (SEQ ID NO:36), YGR181W (SEQ ID NO:38), YGR217W (SEQ ID NO:39), YIL088C (SEQ ID NO:43), YJL094C (SEQ ID NO:45), YJR106W (SEQ ID NO:48), YNL065W (SEQ ID NO:59), YNL083W (SEQ ID NO:61), YNL121C (SEQ ID NO:63), YNL142W (SEQ ID NO:64), YOR306C (SEQ ID NO:75), or YPR011C (SEQ ID NO:82) led to a measurable decrease of RebD excreted into the culture medium, indicating that each plays a role in RebD excretion. This was confirmed by transporter selection criteria 1 and 2 (see Tables 7 and 8, RebD column).

[0195] Furthermore, for example, deletion in a steviol glycoside-producing strain of YBR180W (SEQ ID NO:13), YBR241C (SEQ ID NO:17), YCL069W (SEQ ID NO:19), YCR075C (SEQ ID NO:21), YDL128W (SEQ ID NO:22), YDL194W (SEQ ID NO:24), YDR093W (SEQ ID NO:27), YDR338C (SEQ ID NO:28), YER166W (SEQ ID NO:32), YFL011W (SEQ ID NO:33), YGL006W (SEQ ID NO:34), YGL013C (SEQ ID NO:35), YGL255W (SEQ ID NO:36), YGR217W (SEQ ID NO:39), YJL094C (SEQ ID NO:45), YJR106W (SEQ ID NO:48), YJR160C (SEQ ID NO:49), YKR106W (SEQ ID NO:53), YML116W (SEQ ID NO:55), YMR056C (SEQ ID NO:57), YNL070W (SEQ ID NO:60), YNL083W (SEQ ID NO:61), YNL095C (SEQ ID NO:62), YNL121C (SEQ ID NO:63), YOR087W (SEQ ID NO:70), YOR291W (SEQ ID NO:74), YOR306C (SEQ ID NO:75), YPL274W (SEQ ID NO:80), or YPR011C (SEQ ID NO:82) led to a measurable decrease of RebM, indicating that each plays a role in RebM excretion. This was confirmed by transporter selection criteria 1 and 2 (see Tables 7 and 8, RebM column).

[0196] Table 7 represents the calculated ratio, normalized to a steviol glycoside-producing strain comprising genes encoding GGPPS, truncated CDPS, KS, KO, ATR2, EUGT11, SrKAHe1, CPR8, UGT85C2, UGT74G1, UGT76G1, and EUGT11 polypeptides, of supernatant/total production for each gene (by ordered locus name) deleted in the steviol glycoside-producing strain. The supernatant or supernatant/total ratio of less than 0.6 represented a more than 40% decrease in either the supernatant alone or in the ratio of supernatant/total production of RebA, RebB, RebD,

or RebM, which corresponded approximately to more than 2 standard deviations removed from the mean of the control steviol glycoside-producing strain and indicates the gene as having a role in steviol glycoside transportation (Table 7). The supernatant or ratio supernatant/total of between 0.6 and 0.8 represents a 40-20% decrease in either the supernatant alone or in the ratio of supernatant/total production of RebA, RebB, RebD, or RebM, which corresponds to approximately

between 1 and 2 standard deviations removed from the mean of the control steviol glycoside-producing strain, and indicates the gene as having a role in steviol glycoside transportation and/or production (Table 8). Total production of each steviol glycoside was between 0.85 and 1.15 compared to the steviol glycoside-producing strain. Table 8 shows the supernatant/total ratio for each candidate that fulfills the selection criteria.

TABLE 7

Transport related genes with over a 40% decrease in RebA, RebB, RebD or RebM compared to a control steviol glycoside-producing strain comprising genes encoding GGPPS, truncated CDPS, KS, KO, ATR2, EUGT11, SrKAHe1, CPR8, UGT85C2, UGT74G1, UGT76G1, and EUGT11 polypeptides.							
Transporter selection criterion 1 Total vs. Supernatant				Transporter selection criterion 2 Ratio Sup/Total vs. Total			
RebA	RebB	RebD	RebM	RebA	RebB	RebD	RebM
YBR180W			0.486				0.486
YBR241C			0.529				0.529
YCL069W			0.519				0.519
YCR075C			0.448				0.448
YDL128W		0.459	0.405			0.459	0.405
YDL194W		0.652	0.482				0.482
YDL210W		0.000				0.000	
YDR093W			0.569				0.569
YDR338C			0.451				0.451
YEL031W	0.488				0.488		
YER166W			0.495				0.495
YFL011W		0.581	0.547			0.581	0.547
YGL006W						0.410	0.424
YGL013C		0.673	0.507				0.507
YGL255W		0.669	0.632				
YGR181W		0.419				0.419	
YGR217W		0.598	0.429			0.598	0.429
YIL088C		0.135				0.135	
YJL094C		0.568	0.525			0.568	0.525
YJR106W		0.470	0.432			0.470	0.432
YJR160C			0.689				
YKL064W	0.337				0.337		
YKR106W			0.509				0.509
YML116W			0.706				
YMR056C							0.591
YNL065W						0.571	
YNL070W			0.633				
YNL083W			0.481			0.592	0.481
YNL095C			0.610				
YNL121C		0.620	0.456				0.456
YNL142W	0.561	0.369		0.561		0.369	
YOR087W			0.611				
YOR291W			0.681				
YOR306C		0.596	0.559			0.596	0.559
YOR334W		0.520			0.520		
YPL078C		0.590			0.590		
YPL270W		0.665					
YPL274W			0.561				0.561
YPR011C		0.542	0.611			0.542	

TABLE 8

Transport related genes with a 20-40% decrease in Reb A, RebB, RebD or RebM compared to a control steviol glycoside-producing strain comprising genes encoding GGPPS, truncated CDPS, KS, KO, ATR2, EUGT11, SrKAHe1, CPR8, UGT85C2, UGT74G1, UGT76G1, and EUGT11 polypeptides.							
Transports cal 1; total vs sup				Transports cal 2; ratio sup/total vs total			
RebA	RebB	RebD	RebM	RebA	RebB	RebD	RebM
YBL089W			0.739				0.739
YBR008C	0.784		0.640	0.784			0.640

TABLE 8-continued

Transport related genes with a 20-40% decrease in Reb A, RebB, RebD or RebM compared to a control steviol glycoside-producing strain comprising genes encoding GGPPS, truncated CDPS, KS, KO, ATR2, EUGT11, SrKAHe1, CPR8, UGT85C2, UGT74G1, UGT76G1, and EUGT11 polypeptides.							
Transports cal 1; total vs sup				Transports cal 2; ratio sup/total vs total			
RebA	RebB	RebD	RebM	RebA	RebB	RebD	RebM
YBR021W	0.731				0.731		
YBR043C	0.755		0.796	0.755			0.796
YBR180W		0.747				0.747	
YBR241C		0.688		0.798		0.688	
YBR287W	0.781	0.823	0.768	0.781		0.768	
YBR295W		0.885	0.876				
YBR296C		0.724	0.799		0.724	0.799	0.790
YCL038C		0.709	0.752		0.709		0.752
YCL069W		0.785				0.785	
YCR075C		0.634				0.634	
YDL054C		0.920					
YDL100C		0.867					
YDL194W						0.652	
YDL210W			0.834				
YDL245C	0.852						
YDL247W			0.682				0.682
YDR011W		0.852					
YDR093W	0.792	0.775	0.704	0.792	0.775	0.704	
YDR338C	0.711	0.695	0.680	0.711	0.695	0.680	
YDR497C			0.694				0.694
YEL006W			0.657			0.774	0.657
YEL065W		0.635				0.635	
YER119C			0.872				
YER166W	0.771	0.843	0.687	0.771		0.687	
YFL011W		0.787			0.787		
YFL028C		0.641				0.641	
YFR045W		0.779				0.779	
YGL006W		0.410	0.424				
YGL013C						0.673	
YGL084C		0.804					
YGL104C	0.628	0.731	0.683	0.628	0.731		0.683
YGL114W					0.796		
YGL167C	0.829						
YGL255W						0.669	0.632
YGR217W		0.801					
YGR257C	0.842						
YHL035C		0.900	0.792				0.792
YHL036W			0.798				0.798
YHR096C		0.879	0.798				0.798
YIL006W	0.763		0.689	0.763		0.791	0.689
YIL120W			0.814				
YIL121W		0.903					
YIL166C		0.844					
YIL212C		0.817	0.682				0.682
YJR106W	0.719			0.719			
YJR160C		0.781	0.985		0.781		0.689
YKL050C			0.896				
YKL120W			0.706				0.706
YKL146W		0.890					
YKR039W	0.763			0.763			
YKR106W		0.785	0.738		0.785	0.738	
YLR411W	0.852		0.782			0.782	
YML038C		0.724				0.724	
YML116W		0.898					0.706
YMR056C		0.675	0.591		0.786	0.675	
YMR279C			0.885				
YNL065W	0.710	0.792	0.571	0.710	0.792		
YNL070W	0.893		0.892				0.633
YNL083W		0.592					
YNL095C		0.726				0.726	0.610
YNL121C						0.620	
YNL268W		0.920					
YNR055C		0.643				0.643	
YOL122C			0.935				
YOL158C		0.848	0.728				0.728
YOR087W							0.611
YOR100C		0.916					
YOR271C		0.889	0.758			0.758	0.608

TABLE 8-continued

Transport related genes with a 20-40% decrease in Reb A, RebB, RebD or RebM compared to a control steviol glycoside-producing strain comprising genes encoding GGPPS, truncated CDPS, KS, KO, ATR2, EUGT11, SrKAHe1, CPR8, UGT85C2, UGT74G1, UGT76G1, and EUGT11 polypeptides.								
	Transports cal 1: total vs sup				Transports cal 2: ratio sup/total vs total			
	RebA	RebB	RebD	RebM	RebA	RebB	RebD	RebM
YOR273C	0.726	0.916	0.635		0.726		0.635	
YOR291W								0.681
YOR307C								0.765
YOR348C				0.644				0.644
YPL036W	0.763		0.698		0.763		0.698	
YPL078C			0.798				0.798	
YPL270W			0.746			0.665	0.746	
YPL274W	0.817	0.807	0.721				0.721	
YPR011C	0.763				0.763			0.611

[0197] The effect of yeast gene knockouts on transport of higher molecular weight steviol glycosides into the culture medium (i.e., supernatant) also was tested in a steviol glycoside-producing strain comprising additional copies of genes encoding GGPPS, truncated CDPS, KS, KO, ATR2, EUGT11, SrKAHe1, CPR8, UGT85C2, UGT74G1, UGT76G1, and EUGT11 polypeptides, which was described in Example 2. The data demonstrated that disruption of a single endogenous yeast transporter gene in the steviol glycoside-producing strain resulted in a decrease in the level of various steviol glycosides in the supernatant of the culture media, as evaluated by the normalized amount transported or by the supernatant-to-total-production ratio (see Tables 9 and 10, RebD column). For example, deletion in the steviol glycoside-producing strain of YDR536W (SEQ ID NO:30), YHL016C (SEQ ID NO:42), YKR050W (SEQ ID NO:51), YOR291W (SEQ ID NO:74), YOR334W (SEQ ID NO:77), YPL270W (SEQ ID NO:79), YPR058W (SEQ ID NO:83), or YPR128C (SEQ ID NO:84) led to a measurable decrease of RebD transported into the supernatant, indicating that they play a role in RebD excretion. This was confirmed by transporter selection criteria 1 and 2 (see Tables 9 and 10, RebD column).

[0198] Furthermore, for example, deletion of YAL067C (SEQ ID NO:14), YDR406W (SEQ ID NO:29), YHL016C (SEQ ID NO:42), YJL212C (SEQ ID NO:47), YKR050W (SEQ ID NO:51), YMR034C (SEQ ID NO:56), YMR253C (SEQ ID NO:58), YOL075C (SEQ ID NO:66), YOL122C (SEQ ID NO:68), YOR222W (SEQ ID NO:73), YPR003C (SEQ ID NO:81), or YPR201W (SEQ ID NO:85) led to a measurable decrease of RebM transported into the superna-

tant, indicating that they play a role in RebM excretion. This was confirmed by transporter selection criteria 1 and 2 (see Tables 9 and 10, RebM column).

[0199] Table 9 represents the calculated ratio, normalized to a steviol glycoside-producing strain comprising additional copies of genes encoding GGPPS, truncated CDPS, KS, KO, ATR2, EUGT11, SrKAHe1, CPR8, UGT85C2, UGT74G1, UGT76G1, and EUGT11 polypeptides, of supernatant/total production for each gene (by ordered locus name) deleted in the steviol glycoside-producing strain. The supernatant or ratio supernatant/total of less than 0.6 represents a more than 40% decrease in either the supernatant alone or in the ratio of supernatant/total production of RebA, RebB, RebD, or RebM, which corresponds approximately to more than 2 standard deviations removed from the mean of a control steviol glycoside-producing strain, and indicates the gene as having a role in steviol glycoside transportation and/or production (Table 9). The supernatant or ratio supernatant/total of between 0.6 and 0.8 represents a 40-20% decrease in either the supernatant alone or in the ratio of supernatant/total production of RebA, RebB, RebD, or RebM, which corresponds to approximately between 1 and 2 standard deviations removed from the mean of the control strain, and indicates the gene as having a role in steviol glycoside transportation and/or production, and indicates the gene as having a role in steviol glycoside transportation and/or production (Table 10). Total production of each steviol glycoside was between 0.85 and 1.15 compared to the control steviol glycoside-producing strain. Table 10 shows the supernatant/total ratio for each candidate that fulfills the selection criteria.

TABLE 9

Transport related genes with over a 40% decrease in Reb A, RebB, RebD or RebM compared to a control steviol glycoside-producing strain comprising additional copies of genes encoding GGPPS, truncated CDPS, KS, KO, ATR2, EUGT11, SrKAHe1, CPR8, UGT85C2, UGT74G1, UGT76G1, and EUGT11 polypeptides.								
	Transporter selection criterion 1 total vs sup				Transporter selection criterion 2 ratio sup/total vs total			
	RebA	RebB	RebD	RebM	RebA	RebB	RebD	RebM
YAL067C				0.541				0.541
YBL089W	0.433	0.416			0.433	0.416		

TABLE 9-continued

Transport related genes with over a 40% decrease in Reb A, RebB, RebD or RebM compared to a control steviol glycoside-producing strain comprising additional copies of genes encoding GGPPS, truncated CDPS, KS, KO, ATR2, EUGT11, SrKAHe1, CPR8, UGT85C2, UGT74G1, UGT76G1, and EUGT11 polypeptides.								
	Transporter selection criterion 1 total vs sup				Transporter selection criterion 2 ratio sup/total vs total			
	RebA	RebB	RebD	RebM	RebA	RebB	RebD	RebM
YBL099W	0.523				0.523			
YBR294W	0.495				0.495			
YCR028C		0.419				0.419		
YDL185W	0.551				0.551			
YDL210W	0.626	0.469				0.469		
YDR061W	0.482		0.471		0.482		0.471	
YDR406W				0.288				0.288
YDR536W	0.715		0.365				0.365	
YFL011W		0.444				0.444		
YGR125W		0.400				0.400		
YGR224W		0.361				0.361		
YGR281W		0.596				0.596		
YHL016C			0.427	0.296			0.427	0.296
YJL093C		0.499				0.449		
YJL108C	0.589				0.589			
YJL212C	0.442			0.461	0.442			0.461
YKR050W	0.554		0.378	0.304	0.554		0.378	0.304
YLR447C	0.512				0.512			
YMR034C	0.331			0.316	0.331			0.316
YMR253C	0.389			0.375	0.389			0.375
YOL020W	0.371				0.371			
YOL075C	0.494			0.471	0.494			0.471
YOL077W-A	0.531				0.531			
YOL122C				0.457				0.457
YOR079C	0.552				0.552			
YOR092W	0.407				0.407			
YOR130C	0.588				0.588			
YOR222W	0.469			0.457	0.469			0.457
YOR291W			0.428				0.428	
YOR334W			0.327				0.327	
YPL270W			0.375				0.375	
YPR003C	0.400			0.418	0.400			0.418
YPR058W			0.461				0.461	
YPR128C			0.342				0.342	
YPR201W	0.376			0.353	0.376			0.353

TABLE 10

Transport related genes with a 20-40% decrease in Reb A, RebB, RebD or RebM compared to a control steviol glycoside-producing strain comprising additional copies of genes encoding GGPPS, truncated CDPS, KS, KO, ATR2, EUGT11, SrKAHe1, CPR8, UGT85C2, UGT74G1, UGT76G1, and EUGT11 polypeptides.								
	Transport cal 1; total vs sup				Transport cal 2; ratio sup/total vs total			
	RebA	RebB	RebD	RebM	RebA	RebB	RebD	RebM
YCR011C				0.654				0.654
YDL210W			0.729		0.626		0.729	
YDR292C	0.724				0.724			
YDR536W					0.715			
YEL027W		0.799				0.799		
YER019C-A	0.789				0.789			
YER053C	0.651				0.651			
YGR256W	0.744				0.744			
YHR002W	0.795				0.795			
YJL133W	0.691				0.691			
YJL219W	0.674				0.674			
YKL016C	0.627				0.627			
YKL209C	0.721				0.721			
YKR105C					0.646			

TABLE 10-continued

Transport related genes with a 20-40% decrease in Reb A, RebB, RebD or RebM compared to a control steviol glycoside-producing strain comprising additional copies of genes encoding GGPPS, truncated CDPS, KS, KO, ATR2, EUGT11, SrKAHe1, CPR8, UGT85C2, UGT74G1, UGT76G1, and EUGT11 polypeptides.							
Transports cal 1; total vs sup				Transport cal 2; ratio sup/total vs total			
RebA	RebB	RebD	RebM	RebA	RebB	RebD	RebM
YMR166C		0.924					
YNL003C		0.814					
YOR153W	0.801						
YOR316C				0.640			
YOR332W	0.700			0.700			

[0200] Knockouts of YDL210W (SEQ ID NO:25) and YPL270W (SEQ ID NO:79) resulted in decreased RebD excretion in the steviol glycoside-producing strain comprising genes encoding GGPPS, truncated CDPS, KS, KO, ATR2, EUGT11, SrKAHe1, CPR8, UGT85C2, UGT74G1, UGT76G1, and EUGT11 polypeptides and the steviol glycoside-producing strain comprising additional copies of genes encoding GGPPS, truncated CDPS, KS, KO, ATR2, EUGT11, SrKAHe1, CPR8, UGT85C2, UGT74G1, UGT76G1, and EUGT11 polypeptides. As well, knockouts of YJL212C (SEQ ID NO:47) and YOL122C (SEQ ID NO:68) resulted in decreased RebM transport in both strains.

Example 4. Confirmation of Knockout of Yeast Endogenous Transport Genes by Overexpression in a RebD/M-Producing Strain

[0201] Overexpression of a subset of the initial candidate transporters from Example 3 was performed using both plasmid-based expression and an integration cassette. First, deep-well microtiter plate culture experiments were carried out. Two transport genes were overexpressed using a plasmid in a RebD/M-producing strain in order to confirm the results from the knockout experiments. YGR181W (SEQ ID NO:38), a TIM complex, helper protein for insertion of mitochondrial inner membrane proteins, and YDR061W (SEQ ID NO:26) an ABC-like transporter were overexpressed. The data shown in FIG. 2 demonstrate that the phenotype based on the knockout studies was confirmed with a plasmid based overexpression phenotype for YGR181W (SEQ ID NO:38) and YDR061W (SEQ ID NO:26) in deep-well plates.

[0202] Next, confirmation of the phenotype in fermenters was performed in additional steviol glycoside-producing strains, which were characterized by integration of YGR181W (SEQ ID NO:38) or YDR061W (SEQ ID NO:26) on chromosome XII. The steviol glycoside-producing strains were grown on defined media at 30° C. in a fed-batch fermentation for about 5 days under glucose-limited conditions, and the levels of RebA, RebB, RebD, and RebM were measured using LC-MS (Method B, Example 1). The graphs shown in FIG. 3 illustrate an approximate 2-fold increase in RebD and RebM transported in the culture medium for the new integration constructs, and little change in RebA and RebB transport. Overexpression of YGR181W (SEQ ID NO:38) or YDR061W (SEQ ID NO:26) resulted in improved (~2-fold) RebD and RebM transport into the culture medium (~400-500 mg/L of supernatant RebD and RebM in YGR181W (SEQ ID NO:38) and YDR061W (SEQ ID NO:26) overexpression strains versus ~250 mg/L of supernatant RebD and RebM in a control

steviol glycoside-producing strain). See FIG. 3A. The ratio of transported RebD as compared to the total RebD increased from 0.158 in the control strain to 0.21-0.25 with the candidate genes overexpressed. RebM transport into the culture medium was also simultaneously improved. See FIG. 3.

Example 5. Overexpression of Selected Yeast Endogenous Transport Genes

[0203] Overexpression in a steviol glycoside-producing strain (as described in Example 2) using a plasmid with a constitutive promoter of the transporter genes shown in Table 11 resulted in greater than a 20% increase in excretion of RebA, RebB, RebD, and/or RebM. Results were analyzed using criterion 2 described in Example 3. Additionally, overexpression of the transporter genes shown in Table 12 resulted in greater than a 40% improvement in production of RebA, RebB, RebD, and/or RebM. Table 11 shows the supernatant/total ratio for each candidate that fulfills the selection criteria.

TABLE 11

Transport related genes with over a 20% increase in RebA, RebB, RebD or RebM excretion, compared to a control steviol glycoside-producing strain.				
Ratio Supernatant/Total				
	RebB	RebA	RebD	RebM
YOR079C			1.21	
YMR166C		1.36	1.53	1.38
YEL027W		1.62	1.82	1.52
YDL054C		1.45	1.38	1.31
YKL120W		1.83	1.89	1.93
YDR536W		1.79	1.80	1.76
YBL099W				1.22
YML116W		1.32	1.31	1.42
YIL166C			1.27	1.22
YKR039W			1.26	1.41
YOR307C				1.23
YKL146W		1.36	1.47	1.66
YGL167C				1.33
YJL093C				1.29
YOR306C	1.67			
YDL128W	1.85		1.29	
YOR153W	1.42		1.21	
YKL050C	1.59	1.22		
YJL094C	1.71	1.24	1.24	
YCL069W	1.59			
YOL158C	1.52			
YFL011W	1.44			

TABLE 11-continued

Transport related genes with over a 20% increase in RebA, RebB, RebD or RebM excretion, compared to a control steviol glycoside-producing strain.				
Ratio Supernatant/Total				
	RebB	RebA	RebD	RebM
YJR106W			1.38	1.33
YBR043C				1.20
YPR011C				1.27

TABLE 12

Transport related genes with over a 40% increase in RebA, RebB, RebD or RebM production, compared to a control steviol glycoside-producing strain.				
Increases in Production				
	RebB	RebA	RebD	RebM
YMR166C				1.52
YIL166C		1.41	1.50	1.55
YKR039W			1.48	1.52
YKL146W				1.42
YJL093C			1.46	1.43
YOR306C				1.59
YDL128W				1.49
YOL122C			1.41	1.59
YIL006W			1.64	2.03
YFL028C				1.55
YBR021W			1.51	1.87
YHR002W			1.51	1.73
YEL031W			1.45	1.66
YCL069W				1.53
YOL158C			1.42	1.63
YKL064W			1.40	1.44
YHR096C				1.42
YOR332W				1.44
YDR338C			1.50	1.55
YJR106W			1.41	1.44
YBR043C			1.55	1.49
YPR011C				1.43
YFR045W			1.44	

Example 6. Genomic Integration of Transporter Genes

[0204] DNA of the transporter genes selected for integration into the genome of a RebD/M-producing *S. cerevisiae* strain (see Example 2) was amplified from an S288C background by PCR and cloned into a plasmid with homology regions for the integration site and a PGK1 promoter for overexpression, using the USER cloning system. See, e.g., Nour-Eldin et al., 2010, Methods Mol Biol. 643:185-200. The USER cloning construct including the homology regions and the transporter was cut out from the plasmid using restriction enzymes, and the linear piece of DNA was integrated into the genome of the receiving RebD/M-producing strain by standard LiAc method. The genomically integrated transporters were tested in plates that release glucose from a polymer after addition of a growth medium. A polymer that releases 20 g/L glucose over 3 days was used to mimic the feed profile during fermentation. Steviol glycoside levels were measured by LC-MS (see Example 1), and OD₆₀₀ was measured on a Perkin Elmer 2104 Multilabel reader. YBR043C (SEQ ID NO:88), YEL027W (SEQ ID NO:102), YJL093C (SEQ ID NO:44), YJR106W (SEQ ID NO:48), YKL120W (SEQ ID NO:126), and YMR166C

(SEQ ID NO:132) showed improved excretion of 13-SMG. (FIG. 4A). YBR043C (SEQ ID NO:88), YEL027W (SEQ ID NO:102), and YMR166C (SEQ ID NO:132) showed improved excretion of RebA (FIG. 4B). YBR043C (SEQ ID NO:88), YEL027W (SEQ ID NO:102), and YMR166C (SEQ ID NO:132) showed improved excretion of RebB (FIG. 4C). YBR043C of SEQ ID NO:88, YEL027W of SEQ ID NO:102, YJL093C of SEQ ID NO:44, YJR106W of SEQ ID NO:48, and YMR166C of SEQ ID NO:132 showed improved production of RebD, and YBR043C of SEQ ID NO:88, YEL027W of SEQ ID NO:102, YIL166C (SEQ ID NO:121), YJL093C of SEQ ID NO:44, YJR106W of SEQ ID NO:48, and YMR166C of SEQ ID NO:132 showed improved production of RebM, as measured by an increase in RebD and RebM levels in the supernatant compared to a control steviol glycoside-producing strain. See FIGS. 4D and 4E. Controls with a URA marker are also shown in FIG. 4.

[0205] FIG. 5A shows supernatant levels of RebA, RebB, RebD, and RebM of an additional steviol glycoside-producing strain overexpressing YMR166C (SEQ ID NO:132), YEL027W (SEQ ID NO:102), YKL120W (SEQ ID NO:126), YJR106W (SEQ ID NO:48), YJL093C (SEQ ID NO:44), and YBR043C (SEQ ID NO:88) by the USER cloning system. The strain of FIG. 5 comprised a recombinant gene encoding a *Synechococcus* sp. GGPPS polypeptide (SEQ ID NO:1, SEQ ID NO:149), a recombinant gene encoding a truncated *Zea mays* CDPS polypeptide (SEQ ID NO:2, SEQ ID NO:150), a recombinant gene encoding an *A. thaliana* KS polypeptide (SEQ ID NO:3, SEQ ID NO:151), a recombinant gene encoding a recombinant *S. rebaudiana* KO1 polypeptide (SEQ ID NO:4, SEQ ID NO:152), a recombinant gene encoding a KO polypeptide (SEQ ID NO:XX, SEQ ID NO:XX), a recombinant gene encoding an *A. thaliana* ATR2 polypeptide (SEQ ID NO:5, SEQ ID NO:153), a recombinant gene encoding an *O. sativa* EUGT11 polypeptide (SEQ ID NO:12, SEQ ID NO:148), a recombinant gene encoding an SrKAHe1 polypeptide (SEQ ID NO:6, SEQ ID NO:154), a recombinant gene encoding an *S. rebaudiana* CPR8 polypeptide (SEQ ID NO:7, SEQ ID NO:155), a recombinant gene encoding an *S. rebaudiana* UGT85C2 polypeptide (SEQ ID NO:8, SEQ ID NO:156), a recombinant gene encoding an *S. rebaudiana* UGT74G1 polypeptide (SEQ ID NO:9, SEQ ID NO:157), a recombinant gene encoding an *S. rebaudiana* UGT76G1 polypeptide (SEQ ID NO:10, SEQ ID NO:158), and a recombinant gene encoding an *S. rebaudiana* UGT91D2 variant (or functional homolog), UGT91D2e-b (SEQ ID NO:11, SEQ ID NO:159) polypeptide. FIG. 5B shows total levels of RebA, RebB, RebD, and RebM of the above described steviol glycoside-producing strain overexpressing YMR166C (SEQ ID NO:132), YEL027W (SEQ ID NO:102), YKL120W (SEQ ID NO:126), YIL166C (SEQ ID NO:132), YJR106W (SEQ ID NO:48), YJL093C (SEQ ID NO:44), and YBR043C (SEQ ID NO:88) by the USER cloning system.

Example 7. Production of RebD and RebM by Fermentation of Steviol Glycoside-Producing *S. cerevisiae* Strains Overexpressing YJL093C or YBR043C

[0206] YJL093C (SEQ ID NO:44) and YBR043C (SEQ ID NO:88) were individually overexpressed in the steviol glycoside-producing strain described in Example 3. The strains were cultivated by fermentation (fed-batch, minimum medium, glucose-limiting) for approximately 130 h. Production of RebD and RebM was measured by LC-MS. As shown in Table 13, the strains overexpressing YJL093C or YBR043C produced higher levels of RebD and RebM, as compared to a control steviol glycoside-producing strain.

TABLE 13

Production of RebD and RebM in <i>S. cerevisiae</i> strains overexpressing YJL093C and YBR043C.						
Strain	Ferm. Length (h)	Final Cell Dry Weight	RebD Titer (g/L)	RebM Titer (g/L)	RebD + RebM	RebD/RebM Ratio (g/g)
Control	126.83	104.53	1.38	4.47	5.85	0.31
YJL093C	130.10	114.40	3.42	2.80	6.22	1.22
YBR043C	129.17	112.00	3.56	2.72	6.28	1.31

TABLE 14

Sequences disclosed herein.						
SEQ ID NO: 1						
<i>Synechococcus</i> sp. GGPPS (GenBank ABC98596.1)						
atggctgcac	aaactttcaa	cctggatacc	tacttatccc	aaagacaaca	acaagttgaa	60
gaggccctaa	gtgctgctct	tgtgccagct	tatcctgaga	gaatatacga	agctatgaga	120
tactccctcc	tggcaggtgg	caaaagatta	agacctatct	tatgtttagc	tgcttgcgaa	180
ttggcaggtg	gttctgttga	acaagccatg	ccaactgcgt	gtgcacttga	aatgatccat	240
acaatgtcac	taattcatga	tgacctgcca	gccatggata	acgatgattt	cagaagagga	300
aagccaacta	atcacaaggt	gttcggggaa	gatatagcca	tcttagcggg	tgatgcgctt	360
ttagcttagc	cttttgaaca	tattgcttct	caaacagag	gagtaccacc	tcaattggtg	420
ctacaagtta	ttgctagaat	cggacacgcc	gttgctgcaa	caggcctcgt	tgagggccaa	480
gtcgtagacc	ttgaatctga	aggtaaagct	atttccttag	aaacattgga	gtatattcac	540
tcacataaga	ctggagccct	gctggaagca	tcagttgtct	caggcgggtat	tctcgcaggg	600
gcagatgaag	agctttttggc	cagattgtct	cattacgcta	gagatatagg	cttggctttt	660
caaatcgtcg	atgatatcct	ggaatgttact	gctacatctg	aacagttggg	gaaaaccgct	720
ggtaagagcc	aggcagccgc	aaaggcaact	tatccaagtc	tattgggttt	agaagcctct	780
agacagaaag	cgggaagagt	gattcaatct	gctaaggaag	ccttaagacc	ttacggttca	840
caagcagagc	cactcctagc	gctggcagac	ttcatcacac	gtcgtcagca	ttaa	894
SEQ ID NO: 2						
<i>Zea mays</i> truncated CDPS						
atggcacagcaca	catcagaatc	cgcagctgtc	gcaaagggca	gcagtttgac	ccctatagtg	60
agaactgaag	ctgagttcaag	gagaacaaga	tggccaacog	atgacgatga	cgccgaacct	120
ttagtggaag	agatcagggc	aatgcttact	tccatgtctg	atggtgacat	ttcctgagac	180
gcatacgata	cagcctgggt	cggattgggt	ccaagattag	acggcgggtga	aggtcctcaa	240
tttccagcag	ctgtgagatg	gataagaaat	aaccagttgc	ctgacgggaag	ttggggcgat	300
gccgcattat	tctctgcta	tgacaggtct	atcaataccc	ttgcctgcgt	tgtaactttg	360
acaaggtggg	ccctagaacc	agagatgaga	ggtagaggac	tatctttttt	gggtaggaac	420
atgtggaaat	tagcaactga	agatgaagag	tcaatgccta	ttggcttcga	attagcattt	480
ccatctttga	tagagcttgc	taagagccta	ggtgtccatg	acttccctta	tgatcaccag	540
gccctacaag	gaatctaact	ttcaagagag	atcaaaatga	agaggattcc	aaaagaagtg	600
atgcataccg	ttccaactac	aatattgcac	agtttggagg	gtatgcctgg	cctagattgg	660
gctaactac	ttaaactaca	gaggagcgac	ggaagttttt	tggtctcacc	agctgccact	720
gcataatgctt	taagtgaatc	cggagatgac	aggtgtttta	gctacatcga	tagaacagta	780
aagaaattca	acggcggcgt	ccctaattgt	tatccagtg	atctatttga	acatatgttg	840
gccgttgata	gacttgaaag	attaggaatc	tccaggtact	tccaaaagga	gatcgaaaca	900
tgcatggatt	atgtaaacag	gcattggact	gaggacggta	tttgttgggc	aaggaactct	960
gatgtcaaaag	aggtgggaaga	cacagctatg	gcctttagac	ttcttaggtt	gcacggctac	1020
agcgtcagtc	ctgatgtggt	taaaaacttc	gaaaaggacg	gtgaattttt	cgcatttgtc	1080
ggacagtcta	atcaagctgt	taccggtatg	tacaacttaa	acagagcaag	ccagatatcc	1140
ttcccaggcg	aggaatgtgt	tcataagact	ggtgccttct	catatgagtt	cttgaggaga	1200
aaagaagcag	agggagcttt	gagggacaag	tggatcattt	ctaaagatct	acctggtgaa	1260
gtttgtgata	ctttggattt	tccatgggtac	ggcaacttac	ctagagtcga	ggccagagac	1320
tacctagagc	aataccgagg	tgggtgatgac	gttttgattg	gcaagacatt	gtataggatg	1380
ccacttgtaa	acaatgatgt	atatttggaa	ttggcaagaa	tggatttcaa	ccactgccag	1440
gctttgcatc	agttagagtg	gcaaggacta	aaaagatggg	atactgaaaa	taggttgatg	1500
gactttgggtg	tgcgccaaaga	agatgccctt	ttcttgagc	cgcatctggt	1560	
tacgagcctt	gtagagctgc	cgaagaggtt	gcattgggcta	gagccgcaat	actagctaac	1620
gccgtgagca	cccacttaag	aaatagccca	tcattcagag	aaagggtaga	gcattctctt	1680
aggtgtagac	ctagtgaaga	gacagatggc	tccctgggtta	actcctcaag	tggctctgat	1740
gcagttttag	taaaggctgt	cttaagactt	actgattcat	tagccaggga	agcacagcca	1800
atccatggag	gtgaccacaga	agatatata	cacaagttgt	taagatctgc	ttgggcccag	1860
tgggttaggg	aaaaggcaga	cgctgccgat	agcgtgtgca	atggtagtct	tgcatagaaa	1920
caagagggat	caagaatggg	ccatgataaa	cagacctgtc	tattattggc	tagaatgatc	1980
gaaattttctg	ccggttagggc	agctggtgaa	gcagccagtg	aggacggcga	tagaagaata	2040
attcaattaa	caggctccat	ctgcgacagt	cttaagcaaa	aaatgctagt	ttcacaggac	2100
cctgaaaaaa	atgaagagat	gatgtctcac	gtggatgacg	aattggaagt	gaggattaga	2160
gagttcgttc	aatatttgct	tagactaggt	gaaaaaaaga	ctggatctag	cgaaccagg	2220
caaacatttt	taagtattag	gaaatcatgt	tactatgctg	ctcattgccc	acctcatgtc	2280
gttgatagac	acattagtag	agtgattttc	gagccagtaa	gtgcgcgcaa	gtaaccgcgg	2340

TABLE 14-continued

Sequences disclosed herein.

SEQ ID NO: 3

Arabidopsis thaliana KS (similar to GenBank AEE36246.1)

atgtctatta	atttgagatc	tcccggttgt	agctcccaaa	taagcgcaac	tttggaaagg	60
ggcttagact	ctgaagttca	aacaagagca	aacaatgtat	cttttgagca	gaccaaaagag	120
aagatcagga	aaatgcttga	gaaggctcag	ttgagcgtga	gtgcctatga	cactagtgttg	180
gtagctatgg	tcccatcacc	atccagtcac	aacgcacctc	ttttccacac	gtgcgtcaaaa	240
tggctacttg	ataatcaaca	tgaggacggc	tcttggggat	tggataacca	cgaccatcag	300
agcttaaaga	aagatgtgtt	gtcatccaca	ttagcctcta	tcctagctct	taagaaatgg	360
ggaataggcg	aaagacagat	caataagggt	ctacagtcca	ttgaattaaa	ctctgcacta	420
gttaccgatg	aaactataca	aaaacctaca	ggtttcgaca	tcatttttcc	aggaatgalt	480
aagtacgcca	gggaccttaa	tttgaccata	cctcttggct	cagaagtagt	cgacgatatg	540
atcaggaaaa	gagatctaga	cttaaaagtgt	gatagcgaga	aattcagcaa	aggtagagag	600
gcttatcttg	cctatgttct	tgaaggaaat	aggaacttga	aggactggga	cttaatttgt	660
aaatatcaga	gaaagaacgg	tagtctatct	gatagtccag	ctacaaccgc	cgcagctttc	720
actcaatttg	gcaatgacgg	ttgcttgagg	tacttatgtt	cactttttaca	gaaattcgag	780
ggcgagtg	ctagtgtata	tccatttgat	caatacgcta	gattaagcat	aatcgctact	840
ttagaatcat	tgggaattga	cagagatttc	aagactgaga	taaaaagcat	attggatgag	900
acctataggt	actggcttag	aggtgacgaa	gaaattttgcc	tagattttggc	cacatgtgca	960
cttgctttta	gggtgctttt	agccacggc	tatgacgtgt	catacgatcc	tctaaagcca	1020
tttgacaggg	aatctggttt	cagcgatacc	cttgagggat	atgttaaaaa	caccttttcc	1080
gtatttagag	ttttcaaggc	tgcccaaatg	tacctctatg	agagtgtctt	gaaaaagcag	1140
tgttgctgga	caaaacaata	tctagaaatg	gaactaagtt	catgggttaa	aacaagcgtt	1200
agggacaagt	acttgaaaaa	ggaagtggag	gatgctttgg	catttccatc	atatgcctct	1260
ttaaaaagaa	gtgaccacag	aaggaaaatt	cttaattggct	cagcagttga	aaacacaaga	1320
gtaaccaaga	cctcttacag	gttgacataat	atatgtacat	cagatatctt	aaaacttgct	1380
gtcgacgatt	tcaacttttg	ccaactctat	catagagagg	aaatggaaag	attggataga	1440
tggatagtag	agaatagact	acaggaatta	aagttcgcca	gacaaaaatt	ggcttactgt	1500
tacttttagt	gcgctgccac	actattctct	ccagaattgt	ctgacgcaag	gatctcatgg	1560
gctaaggag	gtgtttcaac	cacagtagtc	gatgactttt	ttgatgttgg	cggtagttaa	1620
gaagagcttg	agaacttaat	tcacttggtg	caaaagtggg	atcttaattg	agttcctgaa	1680
tactcttcag	agcatgtaga	aataattttc	tctgtcctaa	gagacacat	cttagaaacc	1740
gggtataaag	cctttacata	tcagggcaga	aacgttactc	accatattgt	gaaaaatagg	1800
ttggacttac	ttaagagcat	gctaaggggag	gctgaatgg	ccagtgcaca	atcaacccca	1860
tctttggaag	attacatgga	gaatgcctat	atcagcttcg	cattaggtcc	tattgtattg	1920
ccagctacat	accttatagg	acctccacta	cctgaaaaga	ctgtcgactc	ccaccaatat	1980
aatcaattat	acaaacttgg	tagtaccatg	ggtagactat	taaacgat	ccagggtctt	2040
aagaggggaat	cagccgaggg	aaaacttaat	gcagtgtctc	tacatatgaa	gcataaaaga	2100
gacaacagaa	gcaaaagagg	tattatagaa	tccatgaaa	gattggctga	aaggaaaaga	2160
gaggaaattac	caaaaacttg	actagaagag	aaaggtatgt	tcgttccaag	agaatgcaag	2220
gaagccttct	taaaaatgtc	aaaagtgttg	aacctttttt	ataggaagga	tgatggcttc	2280
acatctaacg	acttgatgag	ccttgtgaaa	tccgtcatct	acgagcctgt	ttcacttcaa	2340
aaggagagtc	taacttga					2358

SEQ ID NO: 4

S. rebaudiana K01 (codon optimized)

atggatgctg	tgacgggttt	gttaactgtc	ccagcaaccg	ctataactat	tggtggaact	60
gctgtagcat	tggcggtagc	gctaactctt	tggtacctga	aatcctacac	atcagctaga	120
agatcccaat	caaatcatct	tccaagagtg	cctgaagtc	caggtgttcc	attgttagga	180
aatctgtttac	aattgaagga	gaaaaagcca	tacatgactt	ttacgagatg	ggcagcgaca	240
tatggaccta	tctatagtat	caaaaactgg	gctacaagta	tggttgtggt	atcatctaat	300
gagatagcca	aggaggcatt	ggtgaccaga	ttccaatcca	tatctacaag	gaacttatct	360
aaagccctga	aagtacttac	agcagataag	acaatggtcg	caatgtcaga	ttatgatgat	420
tatcataaaa	cagttaagag	acacatactg	accgccgtct	tgggtcctaa	tgacacagaaa	480
aagcatagaa	ttcacagaga	tatcatgatg	gataacatat	ctactcaact	tcatgaattc	540
gtgaaaaaca	accagaaca	ggaagaggta	gaccttagaa	aaatctttca	atctgagtta	600
ttcggtttag	ctatgagaca	agccttagga	aaggatgttg	aaagtttgta	cgttgaagac	660
ctgaaaaatca	ctatgaatag	agacgaaatc	tttcaagtcc	ttgttgttga	tccaatgatg	720
ggagcaatcg	atgttgattg	gagagacttc	tttccatacc	taaagtgggt	cccaaacaaa	780
aagttcgaaa	atactattca	acaaatgtac	atcagaagag	aagctgttat	gaaatcttta	840
atcaaaagag	acaaaagag	aatagcgtca	ggcgaagagc	taaatagtta	tatcgattac	900
cttttatctg	aagctcaaac	tttaaccgat	cagcaactat	tgatgtcctt	gtgggaacca	960
atcattgaat	cttcagatca	aacaatgggtc	acaacagaat	gggcaatgta	cgaattagct	1020
aaaaacccta	aattgcaaga	taggtgtgtac	agagacatta	agtcgctctg	tggtctgaa	1080
aagataaccg	aagagcatct	atcacagctg	ccttacatta	cagctatctt	ccacgaaaca	1140
ctgagaagac	actcaccagt	tctatcatct	cctctaagac	atgtacatga	agataccgtt	1200
ctagggcggt	acctgttcc	tgctggcaca	gaacttgccg	ttaacatcta	cgttgcaaac	1260
atggacaaaa	acgtttggga	aaatccagag	gaatggaacc	cagaaagatt	catgaaagag	1320
aatgagacaa	ttgattttca	aaagacgatg	gccttcggtg	gtggtaagag	agtttgtgct	1380
ggttccttgc	agaacctttt	aactgcactc	attgggattg	ggagaatggt	tcaagagttc	1440
gaatggaaac	tgaaggatat	gactcaagag	gaagtgaaca	cgataggcct	aactacacaa	1500
atgttaagac	cattgagagc	tattatcaaa	cctaggtatc	aa		1542

TABLE 14-continued

Sequences disclosed herein.

SEQ ID NO: 5

A. thaliana ATR2 (codon optimized)

atgtcttcct	cttctctctc	cagtacctct	atgattgatt	tgatggctgc	tattattaaa	60
ggtgaaccag	ttatcgctct	cgaccagca	aatgcctctg	cttatgaatc	agttgctgca	120
gaattgtctt	caatgttgat	cgaaaacaga	caattcgcca	tgatcgtaac	tacatcaatc	180
gctgttttga	tccgtttgat	tgtcatgttg	gtatggagaa	gatccggtag	tggttaattct	240
aaaagagtcg	aacctttgaa	accattagta	attaagccaa	gagaagaaga	aatagatgac	300
ggtagaaaaga	aagttacaat	atttttcggg	acccaaactg	gtacagctga	aggttttgca	360
aaagccttag	gtgaagaagc	taaggcaaga	tacgaaaaga	ctagattcaa	gatagtcgat	420
ttggatgact	atgccgctga	tgacgatgaa	tacgaagaaa	agttgaagaa	agaagatggt	480
gcatttttct	ttttggcaac	ctatgggtgac	ggtgaaccaa	ctgacaatgc	agccagattc	540
tacaaatggt	ttcacagagg	taatgatcgt	ggtgaatggt	tgaaaaactt	aaagtacggt	600
gttttcgggt	tgggttaacg	acaatacgaa	catttcaaca	aagttgcaaa	ggttgtcgac	660
gatattttgg	tcaacaagg	tgtcacaaga	ttagtccaag	taggtttggg	tgacgatgac	720
caatgtatag	aagatgactt	tactgcctgg	agagaagcct	tgtggcctga	attagacaca	780
atcttgagag	aaagaaggta	caccgcggt	gctaccccat	atactgctgc	agtattagaa	840
tacagagttt	ccatccatga	tagtgaagac	gcaaagttaa	atgatatac	tttgcccaat	900
ggtaacgggt	atacagtttt	cgtgcacaaa	cacccttaca	aagctaactg	tcagtcacaa	960
agagaattac	atacacaga	atccgacaga	agttgtatatac	acttggaatt	tgatagcgt	1020
ggttccgggt	taaccatgaa	gttgggtgac	catgtaggtg	ttttatgcga	caattttgct	1080
gaaactgttg	atgaagcatt	gagattgttg	gatattgtccc	ctgacactta	ttttagtttg	1140
cacgctgaaa	aagaagatgg	tacaccaatt	tccagttctt	taccacctcc	attccctcca	1200
tgtaaactaa	gaacagcctt	gaccagatac	gcttgcttgt	tatcatcccc	taaaagttcc	1260
gccttggttg	cttttagccg	tcatgctagt	gatcctactg	aagcagaaag	attgaaacac	1320
ttagcatctc	cagccggtaa	agatgaatat	tcaaagtggg	tagttgaatc	tcaaagatca	1380
ttgttagaag	ttatggcaga	atttccatct	gccaaagcct	cattaggtgt	cttctttgct	1440
gggttagcac	ctagattgca	accaagattc	tactcaatca	gttcttcacc	taagatcgct	1500
gaaactagaa	ttcatgttac	atgtgcattac	gtctacgaaa	agatgccaac	cggtagaatt	1560
cacaaggggtg	tatgctctac	ttggatgaaa	aatgtgtgtc	cttacgaaaa	atcagaaaaag	1620
ttgttcttag	gtagaccaat	cttcgtaaga	caatcaaaact	tcaagttgcc	ttctgattca	1680
aaggttccaa	taatcatgat	aggtcctggt	acaggttttag	ccccattcag	aggtttcttg	1740
caagaaagat	tggctttagt	tgaatctggt	gtcgaattag	gtccttcagt	tttgttcttt	1800
gggtgtagaa	acgaagaagt	ggatttctac	tatgaagaag	aattgcaaaag	attcgtcgaa	1860
tctggtgcat	tggccgaatt	atctgtagct	ttttcaagag	aaggtccaac	taaggaatac	1920
gttcaacata	agatgatgga	taaggcatcc	gacatattgga	acatgatcag	tcaagggtgct	1980
tattttgtacg	tttgccgtga	cgcgaagggt	atggccagag	atgtccatag	atctttgcac	2040
acaattgtctc	aagaacaagg	ttccattggat	agtaccaaaag	ctgaaggttt	cgtaaaagaac	2100
ttacaaactt	ccggtagata	cttgagagat	gtctggtgta			2139

SEQ ID NO: 6

Stevia rebaudiana KAHe1 (codon-optimized)

atggaagcct	cttacctata	cattttctatt	ttgcttttac	tggcatcata	cctgttcacc	60
actcaactta	gaaggaagag	cgctaactta	ccaccaacog	tgtttccatc	aataccaatc	120
attggacact	tatacttact	caaaaagcct	ctttatagaa	ctttagcaaa	aattgcccgt	180
aagtacggac	caatactgca	attacaactc	ggctacagac	gtgttctggt	gatttccctca	240
ccatcagcag	cagaagagtg	ctttaccaat	aacgatgtaa	tcttcgcaaa	tagacctaag	300
acattgtttg	gcaaaatagt	gggtggaaca	tcccttgcca	gtttatccta	cggcgatcaa	360
tggcgtaatc	taaggagagt	agcttctatc	gaaatcctat	cagttcatag	gttgaacgaa	420
tttcatgata	tcagagtggga	tgagaacaga	ttgttaatta	gaaaaactag	aagttcatct	480
tctcctgtta	ctcttataac	agtcttttat	gctctaact	tgaacgtcat	tatgagaatg	540
atctctggca	aaagatat	cgacagtggg	gatagagaat	tggaggagga	aggtaagaga	600
tttcgagaaa	tcttagacga	aacgttgctt	ctagccggtg	cttctaattg	tggcgactac	660
ttaccaatat	tgaactgggt	gggagttaag	tctcttgaaa	agaaattgat	cgcttgcag	720
aaaaagagag	atgacttttt	ccaggggttg	attgaacagg	ttagaaaaatc	tcgtggtgct	780
aaagttaggca	aaggtagaaa	aacgatgac	gaactcttat	tatctttgca	agagtcagaa	840
cctgagtact	atacagatgc	tatgataaga	tcttttgtcc	taggtctgct	ggctgcaggt	900
agtgatactt	cagcgggcac	tatggaatgg	gccatgagct	tactgggtcaa	tcaccacatc	960
gtattgaaga	ctagagtgac	tgaaatcgat	agagttatcg	gtaataacag	attgattgac	1020
gagtcagaca	ttggaaatat	cccttacatc	gggtgtatta	tcaatgaaac	tctaagactc	1080
tatccagcag	ggccattggt	gttcccacat	gaaagtctcg	ccgactgcgt	tatttccgggt	1140
tacaatatac	ctagagtgac	aatgtttaac	gtaaaccaat	gggcgattca	tcacgactct	1200
aaagtcttygg	atgatcttga	aacctttaa	cctgaaagat	tcaaggatt	agaaggaaact	1260
agagatggtt	tcaaaacttat	gccattccgt	tctggggagaa	gaggatgtcc	agggtgaagg	1320
ttggcaataa	ggctgttagg	gatgacacta	ggctcagtg	tccaatgttt	tgattgggag	1380
agagtaggag	atgagatggt	tgacatgaca	gaaggtttgg	gtgtcacact	tcctaaggcc	1440
gttccattag	ttgccaaatg	taagccacgt	tccgaaatga	ctaatactct	atccgaactt	1500
ttaa						1503

SEQ ID NO: 7

Stevia rebaudiana CPR8

ATGCAATCTAATCCGTGAAGATTTCCGCGCTTGATCTGGTAACTGCGCTGTTTAGCGGCAAGGTTTT
 GGACACATCGAACGCATCGGAATCGGGAGAATCTGCTATGCTGCCGACTATAGCGGATGATTATGGAGA
 ATCGTGAGCTGTGATGATGATCTACCAACGTCGGTTGCTGTATTGATCGGATCGGTTGCTGCTTTGGTG
 TGGCGGAGATCGTCTACGAAGAAGTCGCGCTTCGAGCCACCGGTGATTGTGGTTCCGAAGAGAGTGCA

TABLE 14-continued

Sequences disclosed herein.

AGAGGAGGAAGTTGATGATGGTAAGAAGAAAGTTACGGTTTTCTTCGGCACCCAACTGGAACAGCTG
AAGGCTTCGCTAAGGCACTTGTGAGGAAGCTAAAGCTCGATATGAAAAGGCTGTCTTTAAAGTAATT
GATTTGTCATGATTATGCTGCTGATGACDATGAGTATGAGGAGAACTAAAGAAAGAACTTTTGGCCTT
TTTTTTTTTGGCTACGTATGGAGATGGTGAGCCAACAGATAATGCTGCCAGATTTTATAAATGGTTTA
CTGAGGGAGATGCGAAAGGAGAATGGCTTAATAAGCTTCAATATGGAGTATTGGTTTGGGTAACAGA
CAATATGAACATTTTAAAGAAATCGCAAAAGTGGTTGATGATGGTCTTGTAGAACAGGGTGCAAAGCG
TCTTGTTCTCTGTTGGACTTGGAGATGATGATCAATGTATTGAAGATGACTTCACCGCATGGAAAGAGT
TAGTATGGCCGGAGTTGGATCAATTACTTCGTGATGAGGATGACACAACCTGTGCTACTCCATACACA
GCTGCTGTTGCAAGATATCGCGCTGTTTTTCATGAAAACAGACGCGGTTCTGAAGATTATAGTTA
TACAAATGGCCATGCTGTTTCATGATGCTCAACATCCATGCAGATCCACGCTGGCTGTCAAAAAGGAAC
TTCATAGTCTGAAATCTGACCGGCTTGCACCTCATCTTGAATTTGACATCTCGAACACCGGACTATCA
TATGAAACTGGGGACCATGTTGGAGTTTACTGTGAAAACCTGAGTGAAGTTGTGAATGATGCTGAAAG
ATTAGTAGGATTACACCAGACACTTACTCTCCATCCACACTGATAGTGAAGACGGGTGCGCACTTG
GCGGAGCCTCATTTGCCGCTCCTTTCCCGCATGCACTTAAGGAAAGCATTGACGTGTTATGCTGAT
GTTTTGAGTTCTCCCAAGAGTCGGCTTGTCTGCACTAGCTGCTCATGCCACCGATCCCAGTGAAGC
TGATAGATTGAAATTTCTTGATCCCCCGCGGAAAGGATGAATATTCTCAATGGATAGTTGCAAGCC
AAAGAAGTCTCCTTGAAGTCAATGGAAGCATTCCTGTCAGCTAAGCCTTCACTTGGTGTCTTTCTTGCA
TCTGTTGCCCCGCGTTACACCAAGATACTACTTATTTCTCTCCTCAAGATGACACCGGATAG
GATTCATGTTACATGTGCTATTAGTCTATGAGAAAACCTGCAGGCCCATCCCAAAGGAGTTTGT
CAACTTGGATGAAGAACGCACTGCTATGACCGAGAGTCAAGATTGCAAGTTGGGCCCAATATACGTC
CGAACATCCATTTTCACTACCATCTGACCTAAGGTCCCGGTTATCATGATTGGACCTGGCACTGG
TTTGCTCCTTTTAGAGGTTTCTTCAAGAGCGGTTAGCTTTAAGGAAGCCGGAACCTGACCTCGGTT
TATCCATTTTATCTTCGGATGTAGGAATCGCAAAGTGGATTTCATATATGAAAACGAGCTTAACAAC
TTTGTGGAGATCGGTGCTCTTCTGAGCTTATGTTGCTTCTCCGTTGAAGGCCGCTAAGGAATA
TGTGCAACACAAGATGAGTGAGAAGGCTTCGGATATCTGGAACCTGCTTCTGAAGGAGCATATTTAT
ACGTATGTGGTGATGCCAAAGGCATGGCCAAAGATGTACATCGAACCTCCACACAATTGTGCAAGAA
CAGGGATCTCTTGATCTGTCAAAGGCAGAACTCTACGTGAAGAATCTACAAATGTCAGGAAGATACCT
CCGTGACGTTTGGTAA

SEQ ID NO: 8

Stevia rebaudiana UGT85C2 (codon optimized)

atggatgcaa	tggcaactac	tgagaaaaag	cctcatgtga	tcttcattcc	atttcctgca	60
caatctcaca	taaaggcaat	gctaaaagta	gcacaaactat	tacaccataa	gggattacag	120
ataactttcg	tgaataccga	cttcacccat	aatcaatttc	tggaaactag	tggccctcat	180
tgcttggacg	tgcgtccagg	gtttagattc	gaacaaattc	ctgacggtgt	ttcacattcc	240
ccagaggcct	ccatcccaat	aagagagagt	ttactgaggt	caatagaaac	caactttttg	300
gatcgtttca	tgaacttggg	cacaaaaact	ccagaccac	caacttgcat	aatctctgat	360
ggcgtttctg	ctagtgattac	tatcgacgt	gccaaaaagt	tgggtatccc	agttatgatg	420
tactggactc	ttgctgcatg	cggtttccatg	ggtttctatc	acatccattc	tcttatcgaa	480
aagggttttg	ctccactgaa	agatgcatca	tacttaacca	acggctacct	ggatactggt	540
attgactggg	taccaggtat	ggaaggtata	agaacttaag	attttccttt	ggattggtct	600
acagacctta	atgataaagt	attgatgttt	actacagaag	ctccacaaag	atctcataag	660
gtttcacatc	atatctttca	cacctttgat	gaattggaac	catcaatcat	caaaaccttg	720
tctctaagat	acaactcatat	ctacactatt	ggtccattac	aattacttct	agatcaaat	780
cctgaagaga	aaaagcaaac	tggattataca	tccttacacg	gctactcttt	agtgaagag	840
gaaccagaat	gttttcaatg	gctacaaaag	aaagagccta	attctgtggt	ctacgtcaac	900
tctggaagta	ctcgttgga	gtccttgga	gatatgactg	aatttggttg	gggacctgct	960
aattcaaatc	attactttct	atggattatc	aggtccaatt	tggtaatagg	ggaaaacgcc	1020
gtattacctc	cagaattgga	ggaacacatc	aaaaagagag	gtttcattgc	ttcctgggtg	1080
tctcaggaaa	aggtatgtga	acatccttct	gttggtggtt	tccttactca	ttgcggttgg	1140
ggctctacaa	tcgaatcact	aagtgcagga	gttccaatga	ttgttggtgc	atattcatgg	1200
gaccaactta	caaattgtag	gtatatctgt	aaagagtggg	aagttggatt	agaaatggga	1260
acaaaggtta	taccaggtga	agtgaaaaga	ttggttcagg	agttgatggg	ggaaggtggc	1320
cacaagatga	gaaacaaggc	caaagattgg	aaggaaaaag	ccagaattgc	tattgctcct	1380
aacgggtcat	cctctctaaa	cattgataag	atgggtcaag	agattacagt	cttaggcaga	1440
aactaa						1446

SEQ ID NO: 9

S. rebaudiana UGT74G1 (GenBank AAR06920.1)

atggcggaac	aacaaaagat	caagaaatca	ccacacgttc	tactcatccc	attcccttta	60
caaggccata	ttaacccttt	catccagttt	ggcaaacgat	taatctccaa	aggtgtcaaa	120
acaaacttgg	ttaaccacct	ccacacctta	aactcaaccc	ttaaccacag	taacaccacc	180
accacctcca	tcgaatcca	agcaatttcc	gatggttgtg	atgaaggcgg	ttttatgagt	240
gcaggagaat	catatttggg	aacattcaaa	caagttgggt	ctaaatcact	agctgactta	300
atcaagaagc	tccaagatga	aggaaccaca	attgatgcaa	tcatttatga	ttctatgact	360
gaatgggttt	tagatgttgc	aattgagttt	ggaatcgatg	gtggttcggt	tttcaactca	420
gcttgtgttg	ttaacagctt	atattatcat	gttcataagg	gtttgatttc	tttgccattg	480
gggtgaaactg	tttcggttcc	tggatttcca	gtgcttcaac	ggttggagac	accgttaatt	540
ttgcagaatc	atgagcaaat	acagagccct	tggctctcaga	tggtgtttgg	tcagtttget	600
aatattgac	aaagcagttg	ggtcttccca	aatagttttt	acaagctcga	ggaagaggtg	660
atagagtggg	cgagaaaagt	atggaaactg	aggttaactg	ggccaacact	tccatccatg	720
taccttgaca	aacgacttga	tgatgataaa	gataacggat	ttaatctcta	caaagcaaac	780
catcatgagt	gcgtgaactg	gttagacgat	aagccaaaag	aatcagttgt	ttacgtagca	840
tttgtagacc	tgttgaaaac	tggaccggag	caagtggag	aaatcacacg	ggctttaata	900
gatagtgatg	tcaacttctt	gtgggttatc	aaacataaag	aagagggaaa	gctcccagaa	960

TABLE 14-continued

Sequences disclosed herein.						
aatcttttcgg	aagtaataaa	aaccggaaa	ggtttgattg	tagcatgggtg	caaacaattg	1020
gatgtgttag	cacacgaatc	agtaggatgc	tttgttacac	attgtggggtt	caactcaact	1080
cttgaagcaa	taagtcttgg	agtccccgtt	gttgcaatgc	ctcaattttc	ggatcaaact	1140
acaaatgcc	agcttctaga	tgaattttg	ggtgttggag	ttagagttaa	ggctgatgag	1200
aatgggtag	tgagaagagg	aaatcttgcg	tcatgtatta	agatgattat	ggaggaggaa	1260
agaggagtaa	taatccgaaa	gaatgcggta	aaatggaagg	atttggctaa	agtagccgtt	1320
catgaagggtg	gtagctcaga	caatgatatt	gtcgaatttg	taagtgaagt	aattaaaggct	1380
taaatTTTTTg	ttgctttgta	ttttatgtgt	tatgggtttt	tgatttagat	gtattcaatt	1440
aatattggaat	cataactaaa	ttcaagatta	ttgtttgtaa	tattctttgt	cctaaaattt	1500
tgcgacttaa	aacctttagt	ttataaaaag	aaattagaaa	atactattgc	acgga	1555

SEQ ID NO: 10

S. rebaudiana UGT76G1 (codon optimized)

atggaaaaca	agaccgaaac	aacagttaga	cgtaggcgta	gaatcattct	gtttccagta	60
ccttttcaag	ggcacatcaa	tccaatacta	caactagcca	acgttttgta	ctctaaagggt	120
ttttctatta	caatctttca	caccaatttc	aacaaccaa	aaacatccaa	ttaccacat	180
ttcacattca	gattcactac	tgataatgat	ccacaagatg	aacgtatttc	aaacttacct	240
acccacggtc	ctttagctgg	aatgagaatt	ccaatcatca	atgaacatgg	tgccgatgag	300
cttagaagag	aatttagagt	acttatgttg	gcatccgaag	aggacgagga	agtcctctgt	360
ctgattactg	acgctctatg	gtactttgcc	caatctgtgg	ctgatagtgt	gaatttgagg	420
agattgggtac	taatgacatc	cagtctgttt	aactttcacg	ctcatgttag	tttaccacaa	480
tttgacgaat	tgggatactt	ggaccctgat	gacaagacta	ggtttagagga	acaggcctct	540
ggttttccta	tgttgaaagt	caaagatata	aagtctgcct	attctaattg	gcaaatcttg	600
aaagagatct	taggaaagat	gatcaaacag	acaaaggctt	catctggagt	gatttggaac	660
agtttcaaa	agtttagaaga	gtctgaattg	gagactgtaa	tcagagaaa	tcacgacact	720
tcattcctga	taccattacc	aaaacatttg	actgcttcct	cttcctcttt	gttggatcat	780
gacagaacag	tttttcaatg	gttggaccaa	caaccaccta	gttctgtttt	gtacgtgtca	840
tttggtagta	cttctgaagt	cgatgaaaag	gacttccctg	aaatcgcaag	aggcttagtc	900
gatagtaagc	agtcattcct	ttgggtcggt	cgctccaggtt	tcgtgaaagg	ctcaacatgg	960
gtcgaaccac	ttccagatgg	ttttctaggc	gaaagaggta	gaatagtcaa	atgggttcct	1020
caacaggaag	ttttagctca	tggcgctatt	ggggcattct	ggactcattc	cggatggaat	1080
tcacactttag	aattcagtag	cgaaggggta	cctatgatct	tttcagattt	tggtcttgat	1140
caaccactga	acgcaagata	catgtctgat	gttttgaaag	tgggtgtata	tctagaaaat	1200
ggctgggaaa	ggggtgaaat	agctaattga	ataagacgtg	ttatggttga	tgaagagggg	1260
gagtatatca	gacaaaacgc	aagagtgtgt	aagcaaaagg	cgcacgtttc	tctaataagg	1320
ggaggctctt	catacgaatc	cttagaatct	cttgtttcct	acatttcac	actgtaa	1377

SEQ ID NO: 11

S. rebaudiana UGT91D2e-b (codon optimized)

atggctactt	ctgattccat	cgttgacgat	agaaagcaat	tgcattgtgc	tacttttcca	60
tggttgggtt	tcggtccatc	tttgccatc	ttgcaattgt	ccaagttgat	tgctgaaaag	120
gggtcacagg	tttcattctt	gtctaccacc	agaaacatcc	aaagattgtc	ctctcatatc	180
tccccattga	tcaacgttgt	tcaattgatc	ttgccaagag	tccaagaatt	gccagaagat	240
gctgaagcta	ctactgatgt	tcacccagaa	gatatacctt	acttgaaaaa	ggcttccgat	300
ggtttacaa	cagaagttag	tagattcttg	gaacaacatt	cccagattg	gatcatctac	360
gattatactc	attactgggt	gccatccatt	gctgcttcat	tgggtatttc	tagagcccat	420
ttctctgtta	ctactctatg	ggctattgct	tatatgggtc	catctgctga	tgctatgatt	480
aacggttctg	atggtagaac	taccgttgaa	gatttgacta	ctccaccaaa	gtgggtttcca	540
tttccaacaa	aagtcctgtg	gagaaaacac	gatttggcta	gatttggttc	atacaaaagt	600
ccaggtattt	ctggtgtgta	cagaattggg	atgggtttga	aaggttccga	ttgcttgggt	660
tctaagtgtc	atcatgaatt	cgttactcaa	tgggtgcctt	tgttggaaac	attgcatcaa	720
gttccagttg	ttccagtagg	ttgtttgcca	ccagaaatcc	caggtgacga	aaaagacgaa	780
acttgggttt	ccatcaaaaa	gtgggtggat	ggtaagcaaa	agggttctgt	tgtttatggt	840
gctttgggtt	ccgaagcttt	ggtttctcaa	accgaagttg	tgaattggc	tttgggtttg	900
gaattgtctg	gtttgccatt	tgtttgggtc	tacagaaaac	ctaaaggctc	agctaaagtct	960
gattctgttg	aattgccaga	tggtttcgtt	gaaagaacta	gagatagagg	tttggtttgg	1020
acttcttggg	ctccacaatt	gagaattttg	tctcatgaat	ccgtctgtgg	tttcttgact	1080
cattgtgggt	ctggttctat	cgttgaaggt	ttgatgtttg	gtcaccattc	gattatgttg	1140
ccaatctttg	gtgaccgaac	attgaacgct	agattattgg	aagataagca	agtcggatct	1200
gaaatcccaa	gaaatgaaga	agatggttgc	ttgaccaaag	aatctgttgc	tagatctttg	1260
agatccgttg	tcgttgaaaa	agaaggtgaa	atctacaagg	ctaaccgtag	agaattgttc	1320
aagatctaca	acgataccaa	ggtcgaaaaa	gaatacgttt	cccaattcgt	tgactacttg	1380
gaaaagaatg	ctagagctgt	tgccattgat	catgaattct	ga		1422

SEQ ID NO: 12

Oryza sativa sequence encoding EUGT11 (codon optimized)

atggatagtg	gctactcctc	atcttatgct	gctgccgctg	gtatgcacgt	tgtgatctgc	60
ccttgggttg	ccttgggtca	cctgttacca	tgtctggatt	tagcccaaa	actggcctca	120
agaggccata	gagtatcatt	tgtgtctact	cctagaaaata	tctctcgttt	accaccagtc	180
agacctgtc	tagtctctct	agttgcattc	gttgcctctc	cacttccaag	agtagaagga	240
ttgcagacg	gcgctgcaat	tactaatgac	gtaccacatg	atagacctga	catggctgaa	300
ttgcatagaa	gagcctttga	tggattggca	gctccatttt	ctgagttcct	gggcacagca	360
tgtgcagact	gggttatagt	cgatgtattt	catcactggg	ctgctgcagc	cgcattggaa	420
cataaggctc	cttgtgctat	gatgttgta	gggtcagcac	acatgatcgc	atccatagct	480
gatagaagat	tggaaagagc	tgaacagaa	tccccagccg	cagcaggaca	aggtaggcca	540

TABLE 14-continued

Sequences disclosed herein.			
gctgccgccc	caacctttga	agtggtctaga	atgaaattga
gggatgagtc	ttgctgaaag	gttttctctg	acattatcta
agatcctgcg	tcgagttcga	acctgaaaca	gtacctttac
cctattactt	tccttggtct	aatgcctcca	ttacatgaag
gatgctactg	ttaggtggtt	agatgcccaa	cctgctaagt
ggttctgagg	taccactagg	ggtggaaaag	gtgcatgaat
gccggaacaa	gattcctttg	ggctttgaga	aaaccaaccg
ctaccagctg	ggttogaaga	gagaacaaga	ggccgtggtg
ccacaaatga	gtattctagc	tcatgcagct	gtaggggcct
aactcaacaa	tagaaggact	gatgtttgg	catccactta
gatcagggac	ctaacgcaag	attgattgag	gcaaagaacg
aatgatggtg	atggttcctt	tgatagagaa	ggcgttgcag
gttgaggaag	agtcactctaa	agttttccaa	gctaaggcca
gctgacatgg	cttgctcacga	aagatacatc	gatggtttca
aaagactaa			

600
660
720
780
840
900
960
1020
1080
1140
1200
1260
1320
1380
1389

SEQ ID NO: 13

YBR180W

>sp|P38125|DTR1_YEAST Dityrosine transporter 1 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = DTR1 PE = 1 SV = 1
MGSEPFQKKNLGLQNSQESGTRSTRFHSLEDLGDVINESWDQVNQKRANIDHDFHEH
PDSSPSLSAQKAKTKEEVAVKSSNSQSRDPSDPTQAHIPYTYFSKDQRLIIFGIIIFIG
FLGPMGNIYIPALPLLQREYDVSATTINATVSVFMAVFSVGPLFWGALADFGGRKFLYM
VSLSLMLIVNLLAAVPVNIALLFVLRIFQAFASSSVISLGAGTVTDVVPKHRGKAIAY
FMMGPNMGPIIAPIVAGLILMKGNVWRWLFGFTSMTGIALILVALLPETLRCIVGNND
PKWGDKKDERENNESPPFEGNKISHRRLEFPDGIIRKPVNNDAFFQENFPKPKAGLTLYW
KMIKCPPIIITSVSTALLFSSYYAFSVTFSSYLEHDYRFTMLEIGAAVYCPGVAMLLGSQ
SGGHLSDYLRSRWIKSHPKKKFPAEFRLLNLIIGILLTCGTIGYGWAIFFHYHFVLLV
FSALTAFGMTWCSTMTYLTTELFPKRAAGTVAVSSFFRNVGAAISSAIILQLCNAMGIG
WCFTGLGLCSSISLIGILYLLIFQRKYTAKEF

SEQ ID NO: 14

YAL067C

>sp|P39709|SE01_YEAST Probable transporter SE01 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = SE01 PE = 1 SV = 1
MYSIVKEIIVDPYKRLKWGFIPVKRQVEDLPDDLNSTEIVTISNSIQSHETAENFITTS
EKDQLHFETSSYSEHKDNVNVTRSYEYRDEADRPWWRFDEQEYRINEKERSHNKWSWF
KQGTSPKEKLLIKLDVLLAFYSCIAVWVKYLDVTNINNAVSGMKEDLGFQGNLDLVHTQ
VMYTVGNIIIFQLPFLIYLNKLPLNYVLPSLDLWLLTVGAAYVNSVPHLKAIRFFIGAF
EAPSYLAYQYLFSGFYKHDEMVRSAFYVLGQYIGILSAGGIQSAVYSSSLNGVNGLEGWR
WNFIIDATVSVVVLIGFYSLPGDPYNCYSIFLTDEIRLARKRLKENQTKSDFETKVF
DIKLWKTIFSDWKIYILTLWNIFCWNSDNVSSGAYLLWLKSLKRYSI PKLNQLSMITPGL
GMVYLMLTGIIADKLHSRWFIIIFTQVFNIIIGNSILAANDVAEGAKWFAFMLQCFGWAMA
PVLYSWQNDICRRDAQTRAITLVMTNIMAQSSSTAWISVLVWKTAEAPRYLKGFTEFTACSA
FCLSIWTFVVLIFYKRDERNNAKNGIVLYNSKHGVEKPTSKDVETLSVSEK

SEQ ID NO: 15

YBL089W

>sp|P38176|AVT5_YEAST Vacuolar amino acid transporter 5
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = AVT5
PE = 3 SV = 2
MPSNVRSGVLTLTLHTACGAGVLAMPFAFKPFLMPGLITLTFCGICSLCGLLLQTRIAKY
VPKSENASFALKTQLINPSISVVPDFAIAVKCFGVGVSYLIIIVGDLVPQIVQSIIFYRND
NMSGSQEHMFLDRRLYITLIIVFVISPLCFKRSLSLSRYASMIIVSVAYLSGLIIYHF
VNRHQLERQGVYFVMPHGDSSQSHPLTLTLPFVFAYTCHNMFSVINEQVDKSKFVIRRI
PIFAIVLAYFLYIIIGGTGYMTFGENIVGNILTLYPNSISTTIGRLAMLLVMLAPPLQC
HPCRSSVKNIIFIENFRKGKLYDNRASFIPLDNFNSQEDPQEAPTQONNEEPNLRSESLR
HINIITLCILLFSYLLAISITSLAKVLAIVGATGSTSISFILPGLFGYKLGSEFTGTNE
RVPTSIIKIFKYLSSLFVWGIAMVASLSAIVFLGTSSH

SEQ ID NO: 16

YBL099W

>sp|P07251|ATPA_YEAST ATP synthase subunit alpha, mitochondrial
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = ATP1
PE = 1 SV = 5
MLARTAAIRSLRSTLINSTKARPAAAAALASTRRLASTKAQPTVESSILEERIKGVSD
NLNETGRVLAVGDGIARVFLMNIQAELVEFSSGVKGMALNLEPGQGVIVLFGSDRLVK
EGELVKRTGNIVDVVPGGLLGRVVDALGNPIDGKGPIDAGRSRAQVKAPGILPRRSVH
EPVQTGLKAVDALVPIGRGQRELIIIGDRQTGKTAVALDTIILNQKRWNNNGSDSKLYCVY
VAVGQKRSTVAQLVQTLQHDAMKYSIIAATASEAAPLQYLAPPTAASIGWFRDNGKH
ALIVYDLSKQAVAYRQLSLLRRPPGREAYPGDVLYLHSLRLERAALKSEKEGSGSLTA
LPVLETQGGDVSAYIPTNVISITDQGFLEAELFYKGIKIRPAINVGLSVSRVGSAAQVKAL
KQVAGSLKFLAQYREVAFAQFGSDLDASTKQTLVLRGERLTQLLKQNYSPATEEQVP
LIYAGVNGHLDIELSRIGEFESSFLSYLKNHNLLEIREKGELSKELLASLSKATES
FVATF

TABLE 14-continued

Sequences disclosed herein.

SEQ ID NO: 17
YBR241C
>sp|P38142|YB91_YEAST Probable metabolite transport protein YBR241C
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YBR2410
PE = 1 SV = 1
MAETERLMPNGGSRETKPLITGHLILGTIVACLGSIQYGYHIAELNAPQEFLSCSRFEAP
DENISYDDTWVGQHGKQCIALTDSQYGAIITSIFSIGGLFGSYAGNWNARYGRKYVSMG
ASAMCMVSSLLFFNSYQLFLGFRFLVGMSCGTAIVITPLFINEIAPVWVRGAMGSMNQ
VSINLGILLTQTALAKYADSYNWRWLLFSGSVIAVANILAWLKVDSPRWLVSHGFVSEA
ETALFKLRPGTYQQAKQEIQDWQRSHGHNRPESSEETHSGPTLWQYVTDPSYKKPRTVI
LAILSCQQFCGINSIIFYGVKVGKILPDYSIQVNFAISILNVVTLAASAIIDHVGRRP
LLLASTTVMTAMSLISVGLTSLVSFLLVTATFVYIAAFAIGLGPPIPLIIGELSYPPQDA
ATAQSFQVTCNWLATFIVGYLFPIGHGLMGYVFAIFAAIAAMPATVYVYKRPETKKGKT
YSEVWAGY

SEQ ID NO: 18
YBR294W
>sp|P38359|SUL1_YEAST Sulfate permease 1 OS = *Saccharomyces cerevisiae*
(strain ATCC 204508 / S288c) GN = SUL1 PE = 1 SV = 2
MSRKSTSTYVHNQEDADIEVFSEYRTYRESEAAENRDGLHNGDEENWKNVSSKQKFGVT
KNELSDVLYDSIPAYEESTVTLKEYYDHSIKNNLTAKSAGSYLVSLFPPIKWFPHYNFTW
GYADLVAGITVGCVLVPPQSMQSYAQIASLSPEYGLYSSFIGAFIYSLFATSKDVCIGPVAV
MSLQTAKVIAEVLKKYPEDQTEVTAPIIATTLCLLCGIVATGLGILRLGLVELISLNAV
AGFMTGSAFNIWQIPALMGYNLSLVNTREATYKVVINTLKLHPNTKLDVFLIPLVIL
YVKKWCGTFGITLADRYRNQPKVANRLKSFYFYAQAMRNAVIVVFTAISWSITRNKS
SKDRPISILGTVPVPSGLNEVGVMKIPDGLLSNMSSSEIPASIIVLVLEHIAISKSFRINDY
KVVPDQELIAIGVTNLIGTFPHSYPATGSPFSRSALKACNVTRPFGSVFTGGCVLLALYC
LTDAPFFIPKATLSAVI IHAVSDLLTSYKTTWTFWKTNPDCISFIVTVFTVFSIENG
IFYFAMCWCAMLLLKQAFPAKFLGRVEVAEVLNPTVQEDIDAVISSNELPNELNKQVKS
TVEVLPAPEYKFSVQWVPFDHGYSRELNINTTVRPPPGVIVYRLGDSFTYVNCNRHYDI
IFDRKEETRGQLITLRRKSDRPWNPDGEWKMPDLSKSLFKFKRHSATTNSDLPI SNGS
SNGETYKPLLVKVDLDFSQVAQVDSTAVQSLVDRKAVNRYADRQVEFHAGIISPWIK
RSLLSVKFGTTNNEYSDDSIAGHSSPHVAKVLKDDVDYTDDESRISTSYSNYETLCAAT
GTNLPPFFHIDIPDFSQWV

SEQ ID NO: 19
YCL069W
>sp|P25594|VBA3_YEAST Vacuolar basic amino acid transporter 3
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = VBA3
PE = 1 SV = 1
MNMILVGRVVASVGGSLQTLFCFVIGCTMVGERSRPLVISILSCAFVAAIVGPIIGGAF
TTHVTRWCFYINLPIGLLAIIMPLLTAKENKILQKIDAGTISSTFSKFRHQVNF
KRLMNGIIFKDFDFGFALCSAGLVFLGLTFGGNKYSWNSGQVIAYLVGLVLFIFSLV
YDFPLFDKFNPEPDNISYRPLLLRRLVAKPAIIINMVTFLCTGYNGQMIYSVQFFQLI
PASSAWKAGLHLIPIVITNVIAAASGVITKKLGLVKPLLIFFGGVLGVIGAGLMTLMTNT
STKSTQIGVLLLPFGSLGFALQASLMSAQLQITKDRPEAAMDPIEVTAFTFMKSLGTTL
GGVLSTTVFSAFHNKVSRAHLEPYEGKTVDDMILYRLQNYDGSHTIGNILSDSIKNVF
WMDLGFYALGFLFCFSNNKKLIIPKDETPEDNLEDK

SEQ ID NO: 20
YCR028C
>sp|P25621|FEN2_YEAST Pantothenate transporter FEN2 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = FEN2 PE = 1 SV = 1
MMKESKLTQHEVERESVSSKRAIKRLLLFKIDLVLSFVCLQYWINYVDRVGFTNAYI
SGMKEDLKMVGNDLTVSNTVFMIGYIVGMVNNLMLLCVPPRIWLSFCTFAWGLLTLGMY
KVTSFKHICAIRFPQALFESCTFSGTHFVLGSGWYKEDELPIRSAIFTGSGVLGSMFSGFM
QTSIFTHLNGRNLGAWRWLFIIIDFCITLPIAIYGFIFFPGLPDQTSASVSKFSMTRYIFN
EQELHYARRRLPARDESTRLDWSTIPRVLKRWHWMMFSLVWVLGGENLGFASTFALWL
QNQKYTLAQRNNYPSGIFAVGIVSTLCSAVYMSKIPRARHWHVSVFISLVMVIVAVLIRA
DPLNPKVVFSAQYLGGVAYAGQAVFFSWANII CHADLQERAIVLASMMNMFSGAVNAWWSI
LFFASDMVPKFERGCYALLATAISSGIVSVIRSLQIKENLSKKQVPYIDANDMPGEDDD
DDNQDNENDGDDESMEVELHNEEMAEISNPFR

SEQ ID NO: 21
YCR075C
>sp|P17261|ERS1_YEAST Cystine transporter OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = ERS1 PE = 1 SV = 1
MVSLDDILGIVVTSWSISMYPPITNWRHKSASAIMDFVMLNTAGYSYLVISIFLQLY
CWKMTGDESDLRPKLTQDFWYCLHGCLMNVLLTQVAVAGIWRFPKGHRKMNPNWYL
RILLASLAIFSLLTQVQFMYSNYWDWHSRTLAYCNNLFLKKISMSLIKIYQVTHNSTR
KSMDCFPPIQGVFLDVTGGLASLLQLIWLQSLNDQGFSLDTFVTNFGKVLGSMVTLIFNFI
IMQWFPVYRSRGHDLASEYPL

TABLE 14-continued

Sequences disclosed herein.

SEQ ID NO: 22
YDL128W
>sp|Q99385|VCX1_YEAST Vacuolar calcium ion transporter
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = VCX1
PE = 1 SV = 1
MDATPTLLTVANSHPARNPKHTAWRAAVYDLQYILKASPLNFLLVFVPLGLIWHGFQLSH
TLTFLFNFLAIIPLAAILANATEELADKAGNTIGGLLNATFGNAVELIVSIIALKKGQVR
IVQASMLGSLLSNLLVLGLCFIFGGYNRVQQTFFNQTAQTMSLLAIACASLLIPAAFR
ATLPHGKEDHFIDGKILELSRGTSIVILIVYVFLYFQLGSHHALFEQQEETDEVMSTI
SRNPHHSLSVKSSVLVLLGTTVIISFCADFLVGTIDNVVESTGLSKTFIGLIVIPVGN
AEHVTSLVAMKDKMDLALGVAIGSSSLQVLFVTPFMVLVGMIDVPMTLNFSTFETATL
FIAVFLSNYLILDGESNWLEGVMSLAMYILIAMAFFYYPDEKTLDSIGNSL

SEQ ID NO: 23
YDL185W
>sp|P17255|VATA_YEAST V-type proton ATPase catalytic subunit A
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = VMA1
PE = 1 SV = 3
MAGAIENARKEIKRISLEDHAEEYGAISVSGPVVIAENMIGCAMYELVKVGHNDLVGE
VIRIDGDKATIQVYEETAGLTVGDPVLRTGKPLSVELGPGLMETIYDGIQRPLKAIKEES
QSIYIPRGIDTPALDRTIKWQFTPGKPFQVGDHISGGDIYGSVFENSLISSHKILLPPRSR
GTITWAPAGEYTLDEKILEVEFDGKSDFTLYHTWPVRVPRPVTEKLSADYPLLTGQVR
LDALFPCVQGGTTCIPGAFGCGKTVISQSLSKYSNSDAIIVVGCFAKGTNVLMADGSIEC
IENIEVGKNVGMKGRPREVIKLPRGRETMYSVVQKSQRAHKS DSSREVPELLKFTCNA
THELVVRTPRSVRRLSRTIKGVEYFEVITFEMGQKAPDGRIVELVKEVSKSYPISEGPE
RANELVESYRKASNKAYFEWTIEARDLSLLGSHVRKATYQTYAPILYENDHFFDYMQSKS
FHLTIEGPKVLAAYLLGLWIGDGLSDRATFSVDSRDTSLMERVTEYAEKLNLCAYKDRKE
PQVAKTVNLVSKVVRNGIRNNLNTENPLWDAIVGLGFLKDGVKNIIPSLSTDNIGTRET
FLAGLIDSDGVVTDHEGIKATIKTIHTSVRDGLVSLARSLGLVSVNAEPKVDMMNGTKH
KISYAIYMSGGDVLLNVLKSCAGSKKFRPAPAAAFARECRGFYFELQELKEDDYGITLS
DDSDHQFLLAQVQVHVHNCGERGNEMAELMEEPELYTEMSTKEPIMKRTTLVANTSMP
VAAREASTYTGITLAEYFRDQGNVSMIADSSRWAEALREISGRLGEMPADQGFPAVLG
AKLASFYERAGKAVALGSPDRTGVSIVAAVSPAGGDFSDPVTTATLGI TQVFWGLDKKL
AQRKHPSPINTSVSYSKYTNVNLKFYDSNYPEFPVLRDRMKEILSNAEELEQVVLQVGKS
ALSDSDKITLVDATLIKEDFLQQNGYSTYDAFCPIWKTFFMMRAFISYHDEAQKAVANGA
NWSKLADSTGDVHKAVSSSKFFEPSRGEKEVHGEFEKLLSTMQERFAESTD

SEQ ID NO: 24
YDL194W
>sp|P10870|SNF3_YEAST High-affinity glucose transporter SNF3
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = SNF3
PE = 1 SV = 3
MDPNSNSSSETLRQEKQGLDKALQRVKGIALRRNNSNKDHTDDTTGSIRTPSLQRQN
SDRQSNMTSVTDDISTIDDNSILFSEPPQKQSMMSICVGVFVAVGGFLFGYDTGLINS
ITSMNYVKSHVAPNHDSFTAQMSILVSFLSLGTFFGALTAPFISDSYGRKPTIIFSTIF
IFSIGNSLQVGAGGITLLIVGRVISGIGIGAISAVVPLYQAEATHKSLRGAIISTYQWAI
TWGLLVSSAVSQGTHARNDASSYRIPIGLQYVWSSFLAIGMFFLPESPRYVVLKDKLDEA
AKSLSFLRGVPVHDGSLLEELVEIKATYDYEASEGSSNFIDCFISSKSRPKQTLRMFTGI
ALQAFQQSGINFIYYGVNFPNKTGVNSVLSVFIYAVNVVFNVPGLFFVEFPGRKRV
LVVGGVIMTIANFIVAIVGCSLKTVAACKVMIAFICLFIAAFSATWGGVWVISAELYPL
GVRSKCTAICAAANWLVNFIICALITPYIVDTGSHTSSLGAKIFFIWGSLNAMGVIVVYLT
VYETKGLTLEEIDELIYIKSSTGVVSPKFNKDIRERALKFQYDPLQRLLEDGKNTFVAKRNN
FDETPRNDFRNTISGEIDHSPNQKEVHSIPERVDIPTSTEILES PNKSSGMTVPVSPSL
QDVP IPQTTEPAEIRTKYVDLGNGLGLNTYNRGPPSLSDSSEDTYDEIIGGPSSQGDQS
NRSTMNNDINDYMARLIHSTASTNTDKFSGNQSTLRYHTASSHSDTTEEDSNLMDLNG
LALNAYNRGPPSILMNSDDEEANGGETSDNLNTAQDLAGMKERMAQFAQSYIDKRGGLEP
ETQSNILSTLSVMADTNEHNNEILHSSEENATNPVNENNDLK

SEQ ID NO: 25
YDL210W
>sp|P32837|UGA4_YEAST GABA-specific permease OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = UGA4 PE = 1 SV = 1
MSMSSKNENKISVEQRISTDIGQAYQLQGLGSNLRSIRSKTGAGEVNNYIDAAKSVNDNQL
LAEIGYKQELKRQFSTLQVFGIAFSIMGLLPSIASVMGGGLGGGPATLVWGWFWVAFFIL
LVGITMAEHASSIPTAGGLYWTYYYAPEGYKEIISFIIGCSNSLALAAAGVCSIDYGLAE
ETAAAVTLTKDGNFEVTSGLYIGIPAGAVVMCITCTCVASGAIALRLQTLISIFANLFIIVL
LFIALPIGTHRMGGFNDGDFIFGKYENLSDWNNGWQFCLAGEMPVAVTIGSFDSCVHQ
EEAKDAKKSVPIGISSIAVCWILGWLIICLMACINPDIDSVLDSKYGFALAQIIYDSL
GKKWAI AFMSLIAFCQFLMGASITTA VSRQVWAFSRDNGLPLSKYIKRVDSKYVPPFAI
LAACVGSLLILGLLCLIDDAATDALPSLAVAGNNLAWSTPTVFRLTSGRDLFRPGPFYLGK
IWSPIVATGVAFQLFIILVMFPSSQQHGIKTSTMNACVIGPGIWLAGIYYKYKKKY
YHGPNATLSDDDYTEAVGADVITIMSKQEP

TABLE 14-continued

Sequences disclosed herein.

SEQ ID NO: 26

YDR061W

>sp|Q12298|YD061_YEAST Uncharacterized ABC transporter ATP-binding protein YDR061W OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YDR061W PE = 1 SV = 1

MSTNKFVVRITNALFKSSLASNSPPVYPKRIHFILPNEKWVIWGPKGKFLDVLNNKY
 ICEPPLSLRFGFLKSSNILPRIEQVAFKGVMPHTAHLARSYEYFKDDYDQCKQFIDKA
 SGNNAVSVKVTNNRQINMELYNALVENLNLSSLQDRWVMGLSNGQMRRLARSILKEP
 DLLLIDDPFLGLDPAAIATISQFLAKYDSIEVSGGCPVIGLRYQDTIPAWCTHICCVDE
 KNGILFEGPIEKLQSKMDETRSRALKELEQLKASNSKEDISINDLICIHPMYGKKEHEI
 IKMPHLIELDGLSVSYKGEAVLENLHWKVQPGSKWHIRGDNBSGKSTLLSLTAEHPQSW
 NSRVIDNGVPRRTGKTNFYDLNSKIGMSSPELHAIFLKNAGGRNLNIRESVATGYHEASSN
 NYLPWIKRLDKNSQEIWNMYLKYFGLDKDADSVLFEQLSVSDQKLVLFVRSLLIKMPQILI
 LDEAFSGMEVEPMRCHFEFLEEWPGTVLVVAHVAETPKCAHYLRLLISPGYEIGDMEN

SEQ ID NO: 27

YDR093W

>sp|Q12675|ATC4_YEAST Phospholipid-transporting ATPase DNF2 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = DNF2 PE = 1 SV = 1

MSSPSKPTSPFVDDIEHESGSASNLSSMSPFDDSFQFEKPSSAHGNIEVAKTGGSVLKR
 QSKPMKDIPTDLSKVTFDGIDDDYSNDNDINDDDDELNGKKEIHEHENEVDDDLHSPQAT
 PMPNTGGFEDVELDNNEGSNNDSQADHKLKRVRFGRTRNKSGRIDINRSKTLKWAKKNFH
 NAIDFESTKEDSLNSALQNRSEDLRTVYNNLPLPEDMLDEDGLPLAVYPRNKIRTTKYT
 PLTFPPKNILFQFHNFIYFLILLILGAFQIFGVNTNPGFASVPLIVIVIIITAKDGIED
 SRRTVLDLEVNNTRTHILSGVKNENVAVDNVS LWRRFKKANTRALIKIFEYFSENLTAAAG
 REKKLQKKREELRRKRNSRSPGRGSLDSIGSYRMSADFGRPSLDYENLNQMTSQANRYN
 DGENLVDRTLQPNPECRFAKDYWKNVKVGDI VRVHNNDEI PADMILLSTSDVDGACYVET
 KNLDGETNLKVRQSLKCSKIIKSSRDI TRTKFWVESEGPHANLYSYQGNFKWQDTQNGNI
 RNEPVNINLLRGCTLRNTKWAMGMVIFTGDDTKIMINAGVTPTKKSRISELNFSVIL
 NFVLLFILCFPAGI NGVYKQKPRSDYFEFGTIGGSASTNGFVSFWAVILYQSLVPI
 SLYISVEI IKTAQAIPIYTDVLLYNALDYPTPKSWNISDDLGGQIEYIFSDKGTGLTQN
 VMEFKKCTINGVSYGRAYTEALAGLRKQGVDSVESEGRREKEEIAKDRETMIDELRMSD
 NTQCPEDLTPVSKIEVEDLKGSSGDHQKCEHFLALALCHSVLVLEPNKDDPKKLDIK
 AQSPDESALVSTARQLGYSFVGSKSSGLIVEIQGVQKEFQVLNVLEFNSSRKRMSCIIKI
 PGSTPKDEPKALLICKGADSVIYSLRDLRTQNDATLLEKTAHLHEEYATEGLRTLCLAQRE
 LTWSYERWVTYDVAASVTNREEELDKVTDVIERELILGGTAIEDRLQDGVDPDSIAL
 LAEAGIKLWVLTDGKVETAINIGFSCNVLNNDMELLVVKASGEDVEEFGSDPIQVNNLV
 TKYLREKFGMSGSEELKEAKREHGLPQGNFAVIDGDALKVALNGEEMRRKFLLLCKNC
 KAVLCCRVSPAQAQAAVVKLVKKTLDVMTLAI GDSNDVAMIQSADVGVIAGEEGRQAVM
 CSDYAIGQFRVYTRVLVHVGKWCYKRLAEMIPQFFYKNVIFTLSLFWYGIYNNFDGSLF
 EYTYLTFYNLAFTSPVPILLAVLDQDVSDTSMVSLVPQLYRVGILRKEWNQTKFLWYMLDG
 VYQSVICFPFFPYLASHKNNMVTENGLGLDHRIFVGVFVTAIAVTS CNFYVFMEQYRWDF
 CGLFICLGLAVFYGTGIWTSSSSSNEFYKGAARVFAQPAYWAVLVGVFLCLPRFTID
 CIRKIFYPKDIIEIVREMWLRGDFDLYPQGYDPTDPSRPRINEIRPLTDFKEPISLDTHFD
 GVSHSQETIVTEEI PMSILNGEQSRKGYRVSTTLERRDQLSPVTTNNLPRRSMASARG
 NKLRTSLDRTREMLANHQLDTRYSEVERARASLDLPGINHAETLLSQSRDR

SEQ ID NO: 28

YDR338C

>sp|Q05497|YD338_YEAST Uncharacterized transporter YDR338C OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YDR338C PE = 1 SV = 1

MAGILSKTLSEVHPSLRTNGMIGINTHRRISLGFLPPNKKNPLVRKFRARTRNIDQRSFR
 SLTDDFGSNVHEPNPYLGNIDEEPDLYYHDEEDGELSRTISLPSRVSETPELSPQDWDWI
 LHEHERRYSSVCNSDNEEASQSNTPDRIQEYSGRELEYDEFMNLQAQKQKLTSAVTDA
 KGTSHHRRPSFVSVTSRGSVPTIYQEIENDSEALAEASHVTFKSEARVLASYSFPLI
 FTFLLEQIFPMVCSLTGVHGLGKNELAAVSLASMTSNITLAI FEGIATSLDLCQAYGSG
 RFYSVGVHLQRCIAFSLVIYIPFAVMWYSEPLLSYIIEPEKELINLTSRFLRVLLILGAPA
 YIFFENLKRFLQAQGFIDAGIYVLTICAPLNVLSYTLVWNKYIGVGFIAAIAVVLNFW
 LMFFLLLFYALYIDGRKCWGGFSRKAFTHWNLDGLHAFSGIIMLEAEELSYELLTFSAY
 YGVSYLAAQSAVSTMAALLYMIPFAIGISTRIANFI GAKRTDFAHSSQVGLSFSFIA
 GFINCCILVFGNRLIANIYSKDPEVIKLAQVPLVGVIGVQNFDSLNAVAGSCLRGQGMQS
 LGSIVNLMAYLFGIPLALILSWFFDMKLYGLWIGISAMLLIGLVEAYYVLPFDWDKIM
 TYAEILKETEDDEVDSDYELTSDDPDENTALLGA

SEQ ID NO: 29

YDR406W

>sp|Q04182|PDR15_YEAST ATP-dependent permease PDR15 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = PDR15 PE = 1 SV = 1

MSSDIRDVEERNRSRSSSSSSSSNSAAQSIGQHPYRGFDSEAEVHEHARTLTSQSLLYT
 ANSNSSSSNNHNAHADSRSVFTDMEGVNPFVTPNPTPGYNPKLDPNSDQFSSTAWVQN
 MANICTSDPDYFYKYSYLGCVWKNLSASGDSADVSQSTFANIVPKLLTKGLRLLKPSKEE
 DTFQLKPMDCGLNPGELLVVLGRPGSGCTTLKSISSNSHGFKIAKDSIVSYNGLSSD

TABLE 14-continued

Sequences disclosed herein.

IRKHYRGEVVYNAESDIHLPHLTVYQTLFTVARMKTPQNRIGKVDREAYANHVTEVAMAT
YGLSHTRDTKVGNDLVRGVSGGERKRVSAEVAICGARFQCWDNATRGDLSATALEFIRA
LKTQADIGKTAATVAIYQCSQDAYDLFDKVCVLDGQYLYFGPAKDAKKYFQDMGYGCPP
RQTTADFLTSTITSPTERII SKEFIEKGTRVPQTPKDMAEYWLQSESYKNLIKIDIDSTLEK
NTDEARNIIRDAHAKQAKRAPSSPYVVNYGMQVKYLLIRNFWRMKQASVTLWQVIGN
SVMAFILGSMFYKVMKNDTSTFYFRGAAMFFAILFNAFSCLEIFISLYETRPITEKHRT
YSLYHPSADAFASVLSEMPPKLITAVCFNIIFYFLVDPRRNGGVFFYYFLINVIATFTLS
HLFRVCVGLTKTLQEAMVPASMLLLAISMTYGFAPKTKILGWSIWIWYINPLAYLFESL
MINEFHDRRFPQAQYIPAGPAYQNI TGTQRVCSAVGAYPGNDYVLGDDFLKESYDYEHKH
KWRGFGIGMAYVVFVFFVYLLICEYNEGAQKQGMVVFRLRSKI KQLKKEGKLQEKHRPGD
IENNAGSSPDSATTEKKILDDSSSESDSSDNAGLGLSKSEAI FHWRLCYDVPKGGQR
RILNNVDGWVKPGTTLTALMGASGAGKTTLLDCLAERVMTMGVITGNI FVDGRLRDESFPRS
IGYCCQQDLHLKATATVRESLRFSAYLRQPSVSVIEEKNYVEEVIKILEMQQYSDAVVGV
AGEGLNVEQRKRLTIGVELAARPKLLVFLDEPTSGLDSQTAWDTQCLMRKLATHGQAILC
TIHQPSAILMQQFDRLLFLQKGGQTVYFGDLGEGCKTMDYFESKGAHKCPCPDANPAEWM
LEVVGAAAGSHATQDYNVWRNSDEYKAVQEELDWMENLPGRSKEPTAEHKKPFAASLY
YQFMVITRLPQQYVRS PDYLWSKFILTI FNQVFIGFTFFKADRS LQGLQNLQMSIFMYT
VIFNPI LQYVLP SFVQQRDL YEARERPSRTFSWLAFFLSQIIVEIPWNILAGTIAICYIY
YAVGFYANASAAQQLHERGALFWLFSIAFYVYIGSMGLLMISFNEVAETA AHMGTLLFTM
ALSFCGVMATPKVMPERFWI FMYRVSP LTYMIDALLALGVANVDVKCSNYEMVKFTPPSGT
TCGDYMASYIKLAGTGYLSDPSATDICSFCAVSTTNAFLATFSSHYRWRWNYGIFICYI
APDYIAATFLYWSRVPPKNGKIKSEKPKK

SEQ ID NO: 30

YDR536W

>sp|P39932|STL1_YEAST Sugar transporter STL1 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = STL1 PE = 1 SV = 2
MKDLKLSNFKGKFSIRTSWGLTGKKLRYFITIASMTGFSLFGYDQGLMASLITGKQFN
EFPATKENGDDHRAHATVVQGATTSCYELGCFAGSLFVFMFCGERIGRKLILMGSVITII
AVISTCAFRGVALGQFIIGRVVTGVGTGLNTSTIPVQSEMSKAENRGLLVNLEGSTIA
FGTMIAIYWDIFGLSYTNSSVQWRFPVSMQIVFALFLAFMIKLPESPRWLISQSRTTEAR
YLVGLDDADPNDEEVI TEVAMLHDAVNRTKHEKHSLSLFSRGRSQNLQRLALIAASTQF
FQQFTGCNAAYIYS TVLFNKT IKLDYRLSMIIGGVFATIALSTIGSFFLIEKLGRRLF
LLGATGQAVSTFI TFAFLVKENKENARGAAGVGLFLFITFFGLSLLSLPWIYPPEIASMKV
RASTNAFSTCTNWL CNFAVVMFTPIFIGSGWGCYLPFAVMNYLYIPVIFFFYPETAGRS
LEEIDIFI KAYEDGTQPRVANHLPKLSLQEVEDHANALGSYDDEMEKEDFGEDRVEDT
YNQINGDNSSSSSNIKNEDTVNDKANFEG

SEQ ID NO: 31

YEL031W

>sp|P39986|ATC6_YEAST Manganese-transporting ATPase I
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = SPF1
PE = 1 SV = 1
MTKKS FVSSPIVRDSTLLVPKSLIAKPYVLPFFPLYATFAQLYFQQYDRIYKGPWFVY
LGTLSVSLNILVMLPAWNVKIKAKFNYSTTKNVNEATHILYITTPNNGSDGIVEIQRVTE
AGSLQTFQFQKRLFWHENEQVFSSPKFLVDES PKIGDFQKCKGHSGLDTHLKRLYGEN
SFDIPIPTFMELFKEHAVAPLFVFPQVFCVALWLLDEFWYSLFNLPMIISMEAAVFPQL
TALKEFRMTGKIPYITINVRNKKWVALQTNELLPMDLVSI TRTAESAI PCDLILLDGS
IVNEAMLSGESTPLKESIKLRPSEDNLQLDGVDKIAVLUGGT KALQVTPPEHKS DIPPP
PDGGALATVTTKGFTSQGSLVRVMIYSAERVSVDNKEALMFI LFLIFAVIASWYVVE
GTKMGRIOQSKLLD CILII TSVVPELPMELTMAVNSSLAALAKFYVYCTEFPRI PFAGR
IDVCCFDKTGTLTGEDLVFEGLAGISADSENIRHLYSAAEPESTILVIGAAHALVKLED
GDIVGDPMEKATLKAVGWAVERKNSNYREGTGKLDI IRRFQFSSALKRSASIASHNDALF
AAVKGAPETIRERLSDIPKNYDEIYKSFTRSGSRVLALASKSLPKMSQSKIDDLNRDDVE
SELTFNGLIFHCPKDKDAIETIKMLNESSHRSIMITGDNPLTAVHVAKEVGIVGETLI
LDRAGKSDDNQLLFRDVEETVSI PFDPSKDTFDHSLKLPDRYDI AVTGYALNALEGHSQRL
DLLRHTWVYARVSPSQKEFLNTLTKDMGYQTL MCGDGTNDVGALKQAHVGIALLNGTEEG
LKKLGEQRRLLEGKMMYIKQTEFMARWNPQPPVPEIAHLFPFGPKPNPHYLKALESGT
VITPEIRKAVEEANSKPVVEVIKPNGLSEKKPADLASLLNSAGDAQGDEAPALKLGASC
AAPFTSKLANVASVNTIIRQGRCALVNTIQMYKILALNCLISAYSLSIIMAGVKFGDGQ
ATVSGLLLSVCFLSISRKPLEKLSKQRPQSGIFNVYIMSGILSQFAVHIATLVYITTEI
YKLEPREPQVLDKEFAPSLNLTGIFIIQLVQQVSTFAVNYQGEPPFRENIRSNKMGMYGL
LGVTGLALASATEFLPELNEAMKFVPMTD DFKIKLTLTLLDFFGSGWGEHFFKFFFMDD
KPSDISVQQVKIASK

SEQ ID NO: 32

YER166W

>sp|P32660|ATC5_YEAST Phospholipid-transporting ATPase DNF1
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = DNF1
PE = 1 SV = 2
MSGTFHGDGHAPSPFEDTFQFEDNSSNEDTHIAPHFDDGATSNKYSRPQVSNDET
PKNKREDAEEFTFNDDTEYDNHSFQPTPKLNNSGT FDDVELDNDSGEPHTNYDGMKFRFMG
TKRNKKGNPIMGRSKTLKWKRNIPNPFEDFTKDDIDPGAINRAQELRTVYYNMPLPKDM
IDEEGNPI MQYRNI RTTKY TPLIFLPKNILFQFHNFAVYFLVLIILGAFQIPGVNTN
GLSAVPLVVIVITAIKDAIEDSRRTVLDELVNNTKTHILEGVENENVSTDNISLWRRPK

TABLE 14-continued

Sequences disclosed herein.

KANSRLLFKFIQYCKEHLTEEGKKKRMQRKHEL RVQKTVGTSGPRSSLDSDSYRVSAD
YGRPSLDYDNLEQGAGEANIVDRSLPPRTDCKFAKNYWKGVKVGDIVRIHNNDI PADII
LLSTSDTDGACVYETKNLDGETNLKVRQSLKCTNTIRTSKDIARTKFWIESEGPSNLYT
YQGNMKWRNLADGEIRNEPITINNVLRLGCTLRNTKWAMGVVMFTGGDTKIMLNSGITPT
KKSRI SRRLNFSVVINFVLLFILCFVSGIANGVYD KKGSRFSYEFGTIAGSAATNGFV
SFWVAVILYQSLVPI SLYI SVEI IKTAQAAP IYGDVLLYNALDYPCTPKSWNI SDDLQ
VEYIFSDKTGTLTQNVMEFKKCTINGVSYGRAYTEALAGLRKRQGDVETEGRRKAEIA
KDRDTMIDELRALSGNSQFYPEEVTFFVSKFVRDLKGASGEVQQRCCEHFMALALCHSV
LVEANPDNPKKLDLKAQSPDEAALVATARDVGFSGVKGTKKGLI IEMQGIQKEFEILNIL
EFNSSRKRMSCIVKIPGLNPGDEPRALLICKGADSI IYSRLSRQSGSSEAEILEKTALHL
EQYATEGLRRLTLCIAQRELSWSEYEKWNKYDIAAASLANREDELEVVDSDIERELI LGG
TAIEDRLQDGVPCDIELLAEAGIKLWVLTGDKVETAINIGFSCNLLNNEMELLVIKTTGD
DVKEFGSEPS EIVDALLSKYLKEYFNLTGSEEEIFEAKDHEFPKGNYAIVIDGALKLA
LYGEDIRKFLLLCKNCRAVLCCRVSPSKAAVVKLVKDSLDMVTLAIGDGSNDVAMIQS
ADVGTIGIAGEGRQAVMCSDYAIGQFRYLARLVLVHGRWSYKRLAEMIPEFFYKNI MFAL
ALFWYGIYNDFDGSYLYEYTYMMFYNAFTSLPVI FLGILDQDVNDTISLVVPQLYRVGI
LRKEWNQRKFLWYMLMDGLYQSIICFFPPYLVYMKNMIVISNGLGLDHRYPVGVYVTTIAV
ISCNTYVLLHQYRWVWFSGLFIALSCLVVFANTGIWSSAIASREFFKAAARIYGAPSPWA
VFFVAVLFLCLLPRTYDSFQKFFYP T DVEIVREMWMQMGHFDHYPPGYDPIDPNRPKVTKA
GQHGEKIEGLALS DNLGGSNYSRDSVTEETI PMTFMHGEDGSPSGYQKQETWMTSPKET
QDLLQSPQFQQAQTFRGFSINVRSSLDRTREQMIATNQLDNRYSVRARTSLDLPGVIN
AASLIGTQQNN

SEQ ID NO: 33

YFL011W

>sp|P43581|HXT10_YEAST Hexose transporter HXT10 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = HXT10 PE = 1 SV = 1
MVSSSVSILGTSKASTSLSRKDEIKLTPETREASLDIPYKPIIAYWTVMGLCLMIAFGG
FIFGWD TGTISGFINQTD FKRFRGELQRDG SFQLSDVRTGLIVGIFNIGCALGGLTLGRLL
GDIYGRKIGLMLCVILVYVYVIGIYQIASSDKWYQYFGRIVSGMGVGGVAVLSPTLISEIS
PKHLRGTCVSYFQYLMITLGIPLGYCTNYGTTKYSNSIQWRVPLGLCFAWAIFMVIGMVMV
PESPRYLVEKGYEARRSLAKSNKVTVDPGVVFEPTIIVANMELERAVGNASWHELFS
NKGAILPRVIMGIVIQSLQQLTGCNYFFYYGTTIFNAVGMQDSFETSIVLGA VNFASFV
ALYIVDKFGRKCLLWGSASMAICFVIFATVGVTRLWPQKQDQPSQSAGNVMIVFTCF
IFSAITWAPLAYVIVAETYP LRVKNRAMAIAVAGNWMWGFLIGFTTFFITRSIGFSYGY
VFMGCLIFSYFYVFFVFCETKGLTLEEVNEMYERIKPWKSGGWIPSSRRTPQPTSSSTPL
VIVDSK

SEQ ID NO: 34

YGL006W

>sp|P38929|ATC2_YEAST Calcium-transporting ATPase 2 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = PMC1 PE = 1 SV = 1
MSRQDENSALLANNENKPSYTGNGVYDNFKLSKSQLDLHNPKSIRSFVRLFGYESN
SLFKYLKTDKNAGISLPEISNYRKTNRKYN YGDNLSLPERIPKSFQLVWAAFNDKTMQLL
TVAAVVSFVLGLYELWMPQPYDPEGNKIKQVDWIEGVAIMIAV FVVVLVSAANDYQKEL
QFALNKKKKENRKIIIVIRNDQEI LISIHHVLVGDVISLQTDGVVPADCVMI SGKCEADES
SITGESNTIQKFPVDNSLRDPKKNFISDSHNHSPKPLDIDGVNEDGNKIADCM LISGSRIL
SGLGRGVITSGVINSVYGTMTSLNAEPES TPLQLHLSQLADNISVYGCVSAIILFLVLF
TRYLFYIIPEDGRFHDLDP AQKGSKFMNIFITSITVIVVAVPEGLPLAVTLALAFATTRM
TKDGNLVRVLRSCETMGSAATVCSDKTGLTENVMVTVVRGFPKSKFDKSKLVPSEQRK
LNSKKVFEENCSSSLRNDLLANIVLNSTAFENRDYKKNDKNTNGSKNMSKNLSFLDKCKS
RLSFFKKNRDEDDQLFKNVNKG RQEPF IGSKTETALLSLARLSLGLQPGELQYLRLDQ
MEKFNI EKVVQTI PFESSRKWAGLVVYKKEGKNKKPFYRFFIKGAAEIVSKNCSYKRNSD
DTLEEINEDNKKETDDEIKNLASDALRAISVAHKDFCECD SWPPEQLRDKDSPNIAALDL
LFNSQKGLILDGLLGIQDPLRAGVRESVQQCQRAGVTVRMVTDGNIL TAKAIARNCAILS
TDISSEAYSAMEGTEFRKLT KNERIRIILPNLRVLARSSPEDKRLLVETLKGMDVAVTG
DGTNDAPALKLADVGFSGMISGTEVAREASDIILMTDDFSAIVNAIKWGRCVSVSIKKFI
QFQLIVNITAVILTFVSSVASSDETSVLTA VQLLWINLIMDTLALALATDKPDNIMDR
KPRGRSTLSISVSTWKMLLSQATLQLIVTFILHFYGP ELFFKKHEDEITSHQQQLNAMT
FNTFVWLQFFTMLVSRKLDEGDG ISNWRGRISAANLNFFQDLGRNYYFLTIMAIIGSCQV
LIMFFGGAPFSIARQTKSMWITAVLCGMLSLIMGVLRICPDEAVAVKFPAAVFQRFKYV
FGLEFLRKNHTGKHDEEALLEESDSPESTAFY

SEQ ID NO: 35

YGL013C

>sp|P12383|PDR1_YEAST Transcription factor PDR1 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = PDR1 PE = 1 SV = 2
MRGLTPKNGVHETGPDTESSADSNFSTGFSGKIRKPRSKVSKACDNCRKRKIKCNGKF
PCASCEIYSCETFTSTRQGGARIKNLHKTSLEGTTVQVKEETDSSSTSFSPQRC T DGPC
AVEQPTKFFENFKLGGRSSGDSGSGDKNDDVNRFYEDDESQATLTSLQTLTKNLK
EMAHLGTHVTS AIESIELQISDLLKRWEKVRTELATTKFYPNKS IETQLMKNYCDV
HLTRYAAWNNKDKQDTSSQPLIDEIFGLYSPFQFLSLQIGIKCFQNYRSKSKCEIFPRT
AKETIYIMLRFVDVCFHHINQGCVS IANPLENYLQKMNLLPSTPSSISSAGSPNTAHTKS
HVALVINHLQPFPVFNITGISNSELSEMNNDISMFGILLKMLDMHKNSYQNFLEMTSN
PSVAKNTQSIDVLQEFIIHYCQAGEALIALCYSYNSNTLYNVVDFTCDITHLEQLLYFLDL

TABLE 14-continued

Sequences disclosed herein.

LFWLSEIYGFEKVLNVAVHFVSRVGLSRWEFYVGLDENFAERRRNLWKAIFYFEKTLASK
 LGYPSNIDDSKINCLLPKNFRDVGFLDNDRDFIENVHLVRRSEAFDNMCI SDLKYYGELAV
 LQIVSHFSSSVLFNEKFTSIRNTSKPSVVRKLLFEVLEIFNETEMKYDAIKEQTGKLFED
 IAFSKDSTELKVSREDKIMASKFVLFYEHHPFCRMVNESDNIVARLCVHRRPSILIENTKI
 YLHKIYKSWTDMNKILLDFDNDYSVYRSFAHYSISCIIILVSQAFSVAEFIKVNDVVMIR
 VFKRFLDIKIPSENETNEHVNSQSFKDYTRAFSLTIVTRIMLLAYGESSTNLDVISK
 YIDENAPDLKGIIELVLDTNSCAYRFLLEPVQKSGFHLTVSQMLKNRKFQEPLMSNEDNK
 QMKHNSGKLNLPDLPSLKTGTSCLLNGIESPOLPFNGRSAPSPVRNNSLPEFAQLPSFRS
 LSVSDMINPDYAQPTNGQNTQVQSNKPINAQQQIPTSVQVPPMNTNEINNNNNNNNNK
 NNINNNNNNNNNFSATSFNLGTLDEFVNGDLEDLYSILWSDVYPDS

SEQ ID NO: 36

YGL255W

>sp|P32804|ZRT1_YEAST Zinc-regulated transporter 1 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = ZRT1 PE = 1 SV = 1
 MSNVTTPWWKQWDPSEVTLADKTPDDVWKTCLVQGVYFGGNEYNGNLGARISSVFVILFV
 STFFTMFPLISTKVKRLRIPLYVYLFAKYFGSGVIVATAFIHMDPAYGAIGGTTTCVGQT
 GNMGLYSWCPAIMLTSLTFTLTDLFSSVWVERKYGLSHDHTHDEIKDVTVRNTAAVSSE
 NDNNGTANGSHDTKNGVEYYEDSDATSMDDVQSPQAQFYAFILFEGVIFHSMIGLNL
 GSVGDEFSSLYPVLVPHQSFEGLGIGARLSAIEFPRSKRWFPWALCVAYGLTTPICVAIG
 LGVTRTRYVSGSYTALVISGVLDASAGILLYTGLVELLARDFIENPQRTKDLRELSFNVI
 CTFLGAGIMALIGKWA

SEQ ID NO: 37

YGR125W

>sp|P53273|YG35_YEAST Uncharacterized vacuolar membrane protein
 YGR125W OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)
 GN = YGR125W PE = 1 SV = 1
 MGRTIRRRRSNSLSEASISVSLGINQDSSVNMHRASVSAMSPPLCRSYMGGFTTGGNSP
 MINNLSDSKLPISNKQHPKVIHGSENLHRQTAQLSNEFCSSSVEENSPTIKDYMDIIGNG
 DRKDDQSMRTIEENIDEEYSDEYSRLLSLPASSNVDDDRNRLQNSSLPELEDGYAGGYQ
 SLRPSHNLRFRPRNLWHMCTSFPSKFAHYLPAAVLGLLNLILDALSYGMIIFPITEPVFS
 HLGP TGISMFIYIISQAVYSGGSSPSPSGISEMIEITPFYHTMALAIKEALAGNDDE
 IITTTIFCYVISSMLTGUVFYALGKLRGKIVGFPFRHILIGCIGGVGYFLIITGIEVTT
 RVAKFEYSWPFPSGLFTDYDTLAKWLLPVLLTVVLIGTQRYFKNSLVLPSPYIILTLVLFH
 FIVAIIPITLSLDALRQAGWIFPIANSDSKWYDHYRLFNVHKVHWSLVLQQTPTMALTFF
 GILHVPINVPALAMSLQMDKYDVDELIAHGYSNFFSGLLGSVQNYLVYTNVSLFIRAGA
 DSPFAGFLLIALTICIMIIIGPVIISFIPICIVGSLIFLLGYELLVEALVDWTKLNRFY
 LTVVIIIVTMTGIFDFVLGIIVGILIACSFLVDSTKLQTINGEYNGNVARSTVYRDYVQT
 KFLDGI GEQIYVVLKQNLFPFGTIIISIEEKIERLLQISNKDATKRRIKYLIIDFPKINAD
 NIDYSAABGFNRKIRFTETKRIKLIISIKERDRIYNAFNNVGLLNDVELFADLNSALEW
 CENEFLFQYKQLRKAKERLEEGKQNNVVS AVIAATKNKKIDTIGNGLNRGSGD TARNL
 MSLPTNTPRNYQILSVAQNVFVNDEQAVKNFKKEYKDDEPVLPIILLFALKQYRPDIISEV
 QKVRKEIKFWAQLCPYFTRRLASQSHLLHADNIFPLVETGMLKATYELPQGTLYEIFS
 NGTCFGKIIAPGNAMPREQKLTIEETDSVLWVIDSSSLNKLKEDNLALYVEALVMVCI
 KDRFKELLGYTLVSA

SEQ ID NO: 38

YGR181W

>sp|P53299|TIM13_YEAST Mitochondrial import inner membrane
 translocase subunit TIM13 OS = *Saccharomyces cerevisiae* (strain ATCC
 204508 / S288c) GN = TIM13 PE = 1 SV = 1
 MGLSSI FGGGAPSQQKEAATAKTTPNPIAKELKNQIAQELAVANATELVNKISENCFEK
 CLTSPYATRNDA CIDQCLAKYMRSWNVISKAYISRIQNASASGEI

SEQ ID NO: 39

YGR217W

>sp|P50077|CCH1_YEAST Calcium-channel protein CCH1 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = CCH1 PE = 1 SV = 1
 MQGRKRTLTEPPEPNTNPFGDNAAVMTENVEDNSETDGNRLSEKQALVPPALNIVPPES
 SIHSTEEKKGDEYNGNDKSSLI SNIFRTRVGRSSHENLSRPKLSLKTASFGAAESSRRN
 VSPSTKSAKSSQYIDLNDERLRRRSFSSYSRSSRRVSNPSSTDRPPRS AKVLSLIAA
 DDMDFEDLQKGFKAIDEGLTWLPQLKSEKSRPVSDVGEDRGEQEISIPDVHTPNVG
 ASATPGSIHLTPAQNGSVSEGLEGSINNSRKKPSPKFFHHLSPQKEDKDQTEVIEYAE
 DILDPETLQRKLESPPFVLGHSLGVFSPTNPLRIKARFLHRRYSLLYNTLLTFYAIL
 LAIRTYNPHNVFLYRFSNWTDFIFILSACFTGNDIAKI IAFGFWDSEMFKAYGREYK
 SILQRSGIMKLYIYLREKYGRKLIDFIIPFRIISPGREETKYQRSSLSLTKPKYAKENQ
 RPFGTTPRAFARSWNRIDLVSSVSFWLGMFLSIKSYDTKTGIRIFKPLAILRI LRLVNVD
 TGMPSILRGLKYGIPQLVNVSSMLVYFWIFFGILGVQIFQGSFRRCQCVWFNPEPTDTYQ
 YDMQFCGGYLDPVTKRKQNYIYEDGSEGSVSKGFLCPQYSKCVSNANPYNGRISFDNIVN
 SMELVFVIMSANTFFDLMYTMSDEMAACLFIVCIVFLTIWLLNLLIAVLVSSFEIAN
 EYKKKKFIYGRKTYGVARIIVTGYWKYFKLANKQTKFPNWSQKGLAIYSHVEFIFVILI
 ICDIGMRASVKVSTSANCNILLKTDRGISIVLFIESLARLVLYLPNMWKFLTKPSYVYD
 FTIISITLVISCLAVEGLGHMYAWLSIFHISRFYRVIISFNLTKLWKQLLSNGVMWIN
 LSSFFYFFTFVLVAIMAVYFEGVIPPEEMADQPFQMYSLPNSFLSLFIIGSTENWTDILY

TABLE 14-continued

Sequences disclosed herein.

ALQKHSPNISSTFFCSVFFIIWFLLSNSVILNIFIALISESMEVKEEEKRPQQIKHYLKF
 VYPQKIQEYTHASLVARIRKKFFGGHRNEDTRDFKQFLMRGTAIMNIAQNMGELADEFK
 PPSENLFFKKGLSKLTIGVPSLKRLRMFANNPFYKNSDVVFTETNDINGRTYILELNEYED
 EKLDYLKKYPLFNYSYFFSQHRFRRCQRLVPPSTGKRTDGSRRFFEDSTDLYNKRSYF
 HHIERDVFVFI PALATILLIVCSYVTPLYRMHHKMGTTWNWSSALDCAFIGAFSIEFIVK
 TVADGFIYSPNAYLRNPWNFIDFCVLISMWINLIAYLKNNGNLSRIFKGLTALRALRCLT
 ISNTARQTFNLVMPDGLNKIFEAGLISLSLLFPPTVWGLSIFKGRGLGTCNDGSLGRADCY
 NEYSNSVFWQDIMS PRVYQQPYLHLDSPASAFSSLYQIISLEGWVDLLENMMNSSGIGTP
 ATVMGSAGNALFLVLFNFLSMVFILNLFVSVIVNNQARTTGSAYFTIEEKAWLESQKLLS
 QAKPKAIPNLIELSRVRQFFYQLAVEKKNFYASFLQVVLVYLHIIMLLSRSYNPNGLIGY
 QGVYFMFSTSVFLIQEALHMCGEGRPLYFRQKWN SIRLSIIIIAFIMNAVAFHVPASHYW
 FHNKIGKFFLLVIFLPIIQNDTLTLELTAMASLPPILSLTYTWGVLPVYAIALNQIFG
 LTRLGNSNTDINFRFTVKSIMIVLFRCSFGEGWNYIMADLTVSEPYCSDDDNSTYTDCGS
 ETYAYLLLSMNIIISMYIFVNMVSLIIGNFSYVYRSGGSRSGINRSEIKKYIEAWSKFD
 TDGTGELELSYLPRIHMSFDGPLSFKIWEGRLLTIKSLVENYMEVNPDDPYDKIDLIGLN
 KELNTIDKAKIIQRKLQYRRFVQSIIHYTNAYNGCIRFSDLLQLIPLYTAYSARECLGIDQ
 YVHHLYILGKVDKYLENQRNFDVLEMVVRWKFHCRMKRTIEPEWDVKDPTVSSHISININ
 VNLEPAPGILEREP IATPRMDYGVNNFMWSPRMNQDSTMEPPEPIDNNDSDANDLIDR

SEQ ID NO: 40

YGR224W

>sp|P50080|AZR1_YEAST Azole resistance protein 1 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = AZR1 PE = 1 SV = 1
 MKGEPKTYSMSDLSSYGEKAQQQKQKQVVRNRNSTQSTSKQNVSVVLEDNASESNEL
 PKGFILYASLIALALSLFLAALDIMIVSTIIIEEVAKQFGSYSEIGWLTGYSLPNALLAL
 IWGR IATPIGPKFTMLFAIVIFEIGSLISALANSMSMLIGGRVIAAGVGCGCIQSLSPVIG
 STLVEESQRGLLIAVLSCSFAIASVVGPFLLGGVFTSSVTRWCFYVNLPIGGLAFFFLFLF
 FYNPGLSTFQETMDNIRKFPSPQFIEIVRNVAHYHLKIKGFSKLNQWPKPMELIFMYDII
 EBFVCSAGFTCILLAFTPGGNRYAWNSASIIILFIIIGIVLVLAGIYDFLVFPKFNIVKA
 TPHYQPLMSWNTIKKPGIFTVNIALFLTCAGYISQFTYIVQYFQLIYNDSAWRAAVHLVA
 CIISTVVTAILCGAITDKTRQIKPIIVISSIFGVVGAGILTLLNNNANNSAHIGLLILPG
 VAFGLAQSSMLASIQLDKKSPTFRSDFVSIITFTNTFCNLGQALGGVINTSVFSAAAI
 KKLTKANIQLPDGTTVDNLVIYRQTNFDGSHSKLGNIISES LTDVFYMALGFYALSILIPA
 VFASNKKVTASLR

SEQ ID NO: 41

YGR281W

>sp|P53049|YOR1_YEAST Oligomycin resistance ATP-dependent permease
 YOR1 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)
 GN = YOR1 PE = 1 SV = 1
 MTITVGDAVSETELENKSNQNVVLSPKASASSDISTDVKDTSSSWDDKSLLPTEGYIVDR
 NKPQTYLNSDDIEKVTESDIFPQKRLFSFLHKKIPEVPQTDDERKIYPLFHTNII SNMF
 FWWVLPILRVGYKRTIQPNDLFKMDPRMSIETLYDDFEKNMIYYFEKTRKKYRKRHPEAT
 EEEVMENAKLPKHTVLRALLFTFKKQYFMSIVFAILANCTSGFNPMI TKRLIEFVEEKAI
 FSHMHVNGKIGYAIACGLMMFVNGLTFNHFFHTSQLTGVAQKSLTKAAMKMFNASNYA
 RHCFFNGKVTSPVTTDLARIEFALSFPQFLAGFPAILAICIVLLIVNLGPALVIGIGIF
 GGFFISLFAFKLILGFRIAANIFTDARVTMMREVLNNIKMIKYTWEDAYEKNIQDIRTK
 EISKVRKMQLSRNFILAMASLPSTIASLVTFLAMYKVNKGGRQPGNIFASLSLQVLSLQ
 MPFLPIAIGTGIDMIIGLGRQLSLEAPEDDPNQMIEMKPSPGFDPKLALKMTHCSEFEW
 DYELNDATBEAKGEAKDEGKKNKKRKDWTGKPSASTNKA KRLDNMLKDRDGPEDLEKTS
 FRGFKDLNFDIKKGEFIMI TGPIGTGKSSLLNAMAGSMRKTDGKVEVNGDLLMCGYPWIQ
 NASVRDNIIFGSPFNKEKYDEVVRVCSLKADLDILPAGDMTEIGERGITLSGGQKARINL
 ARSVYKKKDIYLFDDVLSAVDSRVGKHIMDECLTGMLANKTRILATHQLSLIERASRVIV
 LGTDGQVDIGTVDELKARNQTLINLLQFSSQNSEKEDEEQEAVVAGELGQLKYSEVKEKEL
 TELKKKATEMSQTANSKIVADGHTSSKEERAVNSISLKIYREYIKAAVGKWFIALPLY
 AILVVGTTFFCSLFSVWLSYWTENKFKNRPPSFYMGLYSFFVFAAFIFMNGQFTILCAGM
 IMASKWLNLRVAKRILHTPMSYIDTTPLGRIILNRFTKDTSLDNELTESLRMTSQFANI
 VGVVCMCIVYLPWFIAIPFLLVIFVLIAHYQSSGREIKRLEAVQSFVYNNLNEVLGG
 MDTIKAYRSQRFRLAKSDFLINKMNEAGYLVVLRQWVGIFLDMVAIAFALIIITLLCVTR
 APPI SAASVGVLLTYVLQPLGLLNTILRAMTQTENDMNSAERLVTYATELPLEASYRKPE
 MTPPESWPSMGEIIFENVDFAYRPLPVLKLNLLNLIKSGEKIGICGRTGAGKSTIMSAL
 YRLNELTAGKLIIDNVDISQLGLFDLRRKLAIIPQDPVLFRGTIRKNDLPFNERTDDELW
 DALVRGGAIKADDLPEVKLQKPDENGTHGKMHKPHLDQAVEEGSNFSLGERQLLALTRA
 LVRQSKILILDEATSSVDYETDGGIKQTRIVEEFGDCTILCIAHRLKTIIVNYDRILVLEKG
 EVAEPDTPWTLFSQEDSIFRSMCSRSGIVENDFENRS

SEQ ID NO: 42

YHL016C

>sp|P33413|DUR3_YEAST Urea active transporter OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = DUR3 PE = 1 SV = 2
 MGEFPKPLPQAGAYIVLGLGAVFAGMMVLTYYLLKRYQKEIITAEETPTAGRSVKTLGV
 AAASVSSWIWSTLTSTSTKEYADGIFGGYAYAAGACFQIIAFAILAIKTKQMAPNAHTY
 LELVRTRYGKIGHGCGYLFYAIATNIVLSMLLTSGSAVFSDLTGMMNTIASCFLLPVGVVV
 YTLFGGIKATPLTDYHMTCVIIIVLVFAFKVYATSDVLGSPGKVYDYLVRBAKRHPVDG
 NYQGEYMTMTSKSAGILLIINLIGNFGTVFLDNGYWNKAISASPAASLKAYAIIGGLAWFA

TABLE 14-continued

Sequences disclosed herein.

VPSLISLTMGLACLAVETSPNFPPTYDPDLTSFQANSGLVLPAAAIAMGKGAVASLLMI
FMAVTSAMSALIAVSSVFTYDIYREYIDPRASGKKLIYTSHVACIFFGLAMSGFSVGLY
YGGISMGYIYEMMGIISSAVLPVVLTLCSKDMNLVAAVSPILGTGLAIMSWLVCTESL
YKELTVDTTFMDYPMLTGNLVALLSPAIFIPILTYVFKPQNFDEKMKDITRVEDTAELV
QADPDIQLYDAEANDKEQEEETNSLVSDSEKNDVRVNNKLEPNLGVVISNAIFQEDDT
QLQNELDEEQRELARGLKIAYFLCVFFALAPLVVWPMMPYGSKYIFSKKFFTGWVVMII
WLFFSAFVAVCIYPLWEGRGIYTTLRGLYWDLSGQTYKLREWQNSNPQDLHVVTQSISAR
AHRQSSHFGQVDEII

SEQ ID NO: 43

YIL088C

>sp|P40501|AVT7_YEAST Vacuolar amino acid transporter 7

OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = AVT7

PE = 1 SV = 1

MEATSSALSSSTANLVKTIIVGAGTLAIPYSFKSDGVLVGVILTLAAVTSGLGLFVLSKCS
KTLINPRNSSFTLCLMITYPTLAPIFDLAMIYQCFGVGLSYLVLIGDLFPGLFGGERNYW
IIASAVIIIPLCVLVKLDQLKYSSILGLFALAYISILVFSHFVFELGKGLTNILRNDIC
WKKIHDFKGLLSTFSIIIFAPTGMNLFPMINELKDNMENITFVINNSISLSTALFLIV
GLSGYLTFGNETLGNLMLNYPNSIWIWIGKFCGLSMLILSPPLLFHPLRIAVNNVWIWI
EITYGGANPEEDPQVSEYTRASNLRPISMTVEDPAQPSDALDATSYNQECLLPNGNFDN
GSIESQENNNDRGTMAVAGDNEHHAPFVKSRFYWITALLISMYTLALSQSFALVLSF
VGATGSTSISFTLPLGLGYKLIGLDSLAIKMIPPKDRFYKRCSLLLVFYGLSVMFLSLY
VTVFNRSDEA

SEQ ID NO: 44

YJL093C

>sp|P40310|TOK1_YEAST Outward-rectifier potassium channel TOK1

OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = TOK1

PE = 1 SV = 1

MTRFMNSFAKQTLGYGNMATVEQESSAQAVDSHSNNTPKQAKGVLAELKDALRFRDERV
SIINAEPSSTLFVFWFVSCYFPVITACLGVPVANTISACVVEKWRSLKNNSVVTNPRSN
DTDVLMMNQVKTVFDPGIFAVNIISLVLGFTSNIILMLHFSKLLTYLKSQNLINITGWITIA
GGMLLVVDVIVCSLNDMPSTIYKTIIGFWFACISSGLYLVCTIILTIHFYIGYKLGKYPPTFN
LLPNERSIMAYTVLLSLWLWIGAGMFSGLLHITYGNALYFCTVSLTTLVGLGDIPLKSVGA
KIMVLI FSLSGVVLMLIVFMTRSI IQKSSGPIFFHFRVEKGRSKSWKHMYMDSKNLSE
EAFDLMKCIQTASRKQHWFSLSVTIAIFMAFWLLGALVFKFAENWSYFNCIYFCFLCLL
TIGYGDYAPRTGAGRAFFVIWALGAVPLMGAILSTVGDLLFDISTSLDIKIGESFNKVK
SIVFNGRQRALSFMVNTGEI FEESDTADGDLEENTSSQSSQISEFNDDNNSEENDSGVTS
PPASIQESFSSLSKASSPEGILPLEYVSSAEYALQDSGTCNLRNLQELLKAVKKLHRICL
ADKDYTLFSFSDWSYIHKHLHRNITDIEEYTRGPFEWISPDTPLPPLNEPHFAPMMLFKN
IEELVGNLVEDEELKYKISKRKFLGHRKTL

SEQ ID NO: 45

YJL094C

>sp|P40309|KHA1_YEAST K(+)/H(+) antiporter 1 OS = *Saccharomyces**cerevisiae* (strain ATCC 204508 / S288c) GN = KHA1 PE = 1 SV = 1

MANTVGGLLSGVNPVPHYSSSPLTLFLFQAQLILVLCNLIHIPFSMMRQPKVISEVISGV

ILGPTIFGQIPNYTNTIPTSSIPGLNLVANLGIILFMFFLGLFVDIAFIKKHKKALVI

GIVTLAVPFGGCLLAIPLFHTYANKTEGERHIKFSVFMVFIASVISVTAFFVLCLRIINE

LRLIKDRAGIVVLAAGIINDIMGWILLALSIISSAEGSPVNTVYILLITPAWFLIYFPP

LKYLLRWVLIIRTHELDRSKPSPLATMCIILFIMFISAYFTDIIIGVHPIFGAFIAGLVVPRD

DHYVVKLTERMEDIPNIVFIPIYFAVAGLVNVDLTLNNEGRDWGVVFATIGIAIFTKIISG

TLTAKLTGLFWREATAAGVLMSCKGIVEIVLTVGLNAGISRKIFGMFVLMALVSTFVT

TPLTQLVYPDSYRDGVRKSLSTPAEDDGAADGLDSEGVDKTEINTQLNSLADVSKYRIGE

LTTVINTTEAISPSLKLNLNLSLGVSPKPKNNKHNETSLSRMTTATDSTLKSNTFKIKK

MVHIWSKVDVDVTLNLSVIDEKLTPFEGVGALRAIHLRLTERTDQLQSSSLYNDDPHF

TANTDSLLQIFDIFSNLSKIPFSSEVIFSTMREKAANIATMKMDSLDLILLPLKGASYEY

RGSPVFIDEKYANFDHIYSHLLGLNELSSSTFFKSIQSLKANFAVQISNTYGRNLNADRFK

RKRFNLLLPKPYLTQSDYLGYLILLI CYRDGYNNNDNASCSIFINSKNIDFAKDLSTAPA

EHDWLNRESTIKIIVDIPFETKVPEEAIEKPSFIETVLDVGLSDTALADIEETFTIIGEDLP

DESEFPFSEEVRTVIFEGSNRRFDTLIVHHFSSE

SEQ ID NO: 46

YJL108C

>sp|P42946|PRM10_YEAST Pheromone-regulated membrane protein 10

OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = PRM10

PE = 1 SV = 1

MIVSFGDATTRTSEVQLVRCQGLNLWKLHQVHAVYKRKVVDHDLGADEGNALLDQILADT

NLYPPWMCVLLYAFCSAMVTPYAFGGDWVNLAISFFMGLCVGSLQFILSQKSYMSNVFE

ISASIVVSFCGRAFGSIPRSHICFAGVATQGSLLALILPGYIILCGALELQSRSLVAGAVRM

FYAIYSLFLGFGITLGSALPGWYHNNATNEISCPQLISPWFRFLVPAFTISISLLNQA

HISQLPVMVFISCTGYVVTYWAGKHANSTEFATAALAAVIGVLGNLYSRIWKGLAVSAM

LPAIFVQVPFGIASQNSLLSGLQSANITVNNANETITTSSTDPSSSMSFGMTMIQVCVGIS

VGLFASSLFLVYFPFGKKKGTLFSL

TABLE 14-continued

Sequences disclosed herein.

SEQ ID NO: 47

YJL212C

>sp|P40897|OPT1_YEAST Oligopeptide transporter 1 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = OPT1 PE = 1 SV = 1
 MSTIYRESDSLESEPSPTPTTIPIQINMEEKKDAFVKNIDEDVNNLTATTDEEDRDPES
 QKFDHRHSIQEGLVWKGDPITYLPNSPYPEVRSASVISEDPTIRLNHWRTWFLTTVFVVVF
 AGVNOFFSLRYPSELEINFLVAQVVCYPIGRILALLPDWCKSKVPFFDLNPGPFKKEHAV
 VTIAVALTSSTAYAMYILNAQGSFYNMKLNVGQYQLLVWTSQMIGYGAAGLIRRVVNPA
 SSIWPQTLISVSLFDSLHRSRVEKTVANGWTMPRYRFFLIVLIGSFIWYVWPGFLFTGLS
 YFNVILWGSKTRHNFIANTIPGTQSGGLGALPITFDYTQVVSQAMSGSVFATPPFYVSANTYA
 SVLIFFVIVLPCLYFTNTWYAKYMPVISGSTDYNTQNKYNVTKILNEDYSINLEKYKEYS
 PVFVFPFSLLSYALNFAAVIAVVFVHCILYHGKDIVAKFKDRKNGGTDIHMRIYSKNYKDC
 PDWWYLLQLQIVMIGLGFVAVCCFDTKFPAAVAFVIAILISLVNFIPQGILEAMTNQHVGLN
 IITELICGYMLPLRPMANLLPKLYGFIVMRQGLNLSRDLKLAMYMKVSPRLIFAVQIYAT
 IISGMVNVGVQEWMMHNIDGLCTTDQPNGFTCANGRTVFENASIIWSLPKYLFSGRIYNP
 LMWFFLIGLLFPLAVYAVQWKFPKFKFAKHIHTPVFFTGPGNIPPSTPYNSYSLFFAMSF
 LNLIRKRWRAWFNKYNFVMGAGVEAGVAISVVIIFLCVQYPGGKLSWGWNNVWKRTYDND
 YKKFYTLKKGETFGYDKWW

SEQ ID NO: 48

YJR106W

>sp|P47144|ECM27_YEAST Protein ECM27 OS = *Saccharomyces cerevisiae*
 (strain ATCC 204508 / S288c) GN = ECM27 PE = 1 SV = 2
 MDWAINVAHPRLLYKDPKLSVTFIVPSLPHIIIAFVLLGICASDFLCPNVAHISDPNSLR
 SNGSLVSKTASHASHTGALMAVLLSWCNSSPDLFNLMSWATSTRETRSTSVLSIGEVL
 GACGIIICIVEGSIPIIIMSRTHIEISQIKLSIMRDLFLSLAAMCVMSYVSLMNQVTVLN
 CLLMAFLYAFYLVVKLTFKLNHSAETPDETAADTSLRENSVSPFLDDSLMASGLLPPIQP
 GFDISNSTHGIKPSLLSAMDENFSLMLENSLSEEDSRNEMAEINLTLSMTPGQHWSA
 SATVAGEATSAGRPFSEPTNAFTEYRDSERAINSSPAVFAPYRDNPDDEESQEQLVLETT
 THGHFGAQEMRRFRFSKRSLGWIIKIFIPHLNFSQKSISDAIFSIIITVPFFIIFKLSQP
 PSDILSYDPILNRYSLTTLPIILLFIQSITAPFLCSILSVLLTYHLGYLVYLFPLILAM
 ALILLLTAFITKVNLNHNKFTLSLDSNLIQEKQLQRKLLERLNTSIQIIFLAIGIINI
 WISLLANGLIEMNEIYQKILGLSKAILGLTIFAWGNSVGDLSINISMCRLYKTQTHYQDR
 VRLATKPFMISCASCLGGVMLNSMGGIGFSGLVSMFLIGAFNDNEWVFLRKVKLQETSQ
 DNILNYKFIVSCVFIILQIILLLLFFGGPNNIKRRLTKEMKLVGISMCGWLALATLINIL
 LELFS

SEQ ID NO: 49

YJR160C

>sp|P0CE00|MPH3_YEAST Alpha-glucosides permease MPH3
 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = MPH3
 PE = 1 SV = 1
 MKNLSFLINRRKENTSDSNVYPGKAKSHEPSWIEMDQTKKDGLDIVHVEFSPDTRAPSD
 SNKVITEIEDATEDAKEADESERGMPLATALNTYPKAAWSLLVSTTLIMEGYDTAILGA
 FYALPIFQRKFGSQNDKTGEWEISASWQIGLTLCYMAGEIVGLQLTGSPVDLVGNRYTLI
 IALFFLAAFTFIFYFCNSLGMIAVGQALCGMPWGCFCQCLTVSYASEICPLALRYLLTYS
 NLCWLFQGLFAAGIMKNSQKKYADSELGYKLPALQWILPVPLALGIFAPESPWWLVKK
 GRFDEARRSLRRTLSGKGPEKEILVLEVDKIKVTIDKEKRLTSKEGSYSDCFEDKINRR
 RTRITCLCWAQATCGSILIGYSTYFYEKAGVSTEMSFTFSIIQYCLGI CATFLSWWASK
 YFGRVDLYAFAGLAFQTI VFFIIGGLGCSSTHGSKMGSGLLMAVAFFYNLGIAPVVFCLV
 SEMPSSRLRTKTIILARNTYNVVSIIICSVLILYQLNSKKWNWGA KSGFFWGVLCFCTLIW
 AVVDLPETAGKTFVEINELFKLGVSARKFKSTKVDPPFVVKTPPKDVSHNDPKGDIEASIA
 EE

SEQ ID NO: 50

YKL064W

>sp|P35724|MNR2_YEAST Manganese resistance protein MNR2
 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = MNR2
 PE = 1 SV = 1
 MSTDNSQKDEGVPLLSPYSSSPQLRKKRNQKRRKDKFVGHLSDSRRPTQLLHDNLQHN
 HGQITDFDQIDSWGMLHESDTSNDIIKSEDP SLKGAFIDHRPMSQPREGQSVSSTVQ
 PQPIMKFTSPSYKKPAGLRPSDQNRSLVSDLSPELESWLKRRKS VHKSFVDENSPTDRR
 QSNANNDVVVIDDALMNHVNNNASTGVNDNSKRRKKRGSDDSSNKNKSSTSSDSNDEED
 EYNSRPSSLSNNSSLDVCLVLDDEGEVPAWPDCTVLEEFSEETERLRSQAIQDA
 EAFHPQYDEDEEDGTSNEDGILFSKPIVINIDVPELGNRRVNETENLKNGLRPKRIAPW
 HLIQRPMVLGSNSTKDSKSRIQSGLDNLLVGRNIQYPPHIIISNPEHFRFTYFRVLDLS
 TVHSPTISGLLQPGQKFDLFAVSIYSQDNSAGHIKTHPNSPTPGIKAETVSQLOGLTAK
 NPSTLSSMSVANIEDVPPFWLDVSNPTBEEEMKILSKAFGIHPLTTEDIFLGEVREKVELF
 RDYILI CFRSPDIVAEKHVRRRRKEKQESAILDHESISRRKSQAYGATMSNESNANNNS
 TSNASRSKWLP SILRARRRSSANRTNTSSSSYKRRVKSEKKMEENEKFKRKS GDRHKK
 REGELEPLNVYIIVRTGVLTFHFAPT PHPINVRRLARLLKDYLNVTSDWIAAYALIDDIT
 DAFAPMIELIEDEVYEIEDAILKMQSDSDSDSDSDSDSGASDEDAFPDVSYSKTS

TABLE 14-continued

Sequences disclosed herein.

YSSAKSSVSSSRMSTSEASFANLIGWKRKGDMLRRIGECRKRVMSILRLLGSKADVIKG
FAKRYNEQWEASPQSEIAMYLGDIQDHIVTMVSSLNHYEKLRSRSHSNYLAQINIDMTKV
NNDMNDVLGKITILGTIVLPMNVITGLWGMNVIVPGQYRDSLTFIGIVLFCMLACSAY
MYTKRRFGF

SEQ ID NO: 51

YKR050W

>sp|P28584|TRK2_YEAST Low-affinity potassium transport protein
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = TRK2
PE = 1 SV = 1

MPTAKRTSSRASLALPFQLRLVHKKSWGHLRDFISGFLKSCRPIAKYVFPNFIVVHYIY
LITLSIIGSILLYPCKNTAFIDVFLAAGASTQGGLATKSTNDFNLYQQIVVYVITLLST
PILIHGFLAFVRLYWFERYFDNIIRDISKQNFKLRRMTLQQRELSGSSGNAARSRSFKDN
LFRGKFVSREDPRQSASDVPMDSPTLSALSSISPLNVSSSKESSDTQSSPPNFSSKRQP
SDVDPRDIYKSIMMLQKQEKSNANSTDSFSSETNGPAFIVQERHERRAPHCSLKRHSVL
PSSQBLNKLQTKSFQKLLGLRRDEGDHDYDFDGAHPKYMVTKKKISRTQSCNIPTYTAS
PSPKTSQGQVVENHRNLAKSAPSSFVDEEMSFSPQESLNLQFQAHPKPKRREGDIGHPFT
RTMSTNYLSWQPTFGRNSVFI GLTKQQKEELGGVEYRALRLCCILMVYYIGFNILAFVT
IVPWACTRHHSYSEIIRNGVSPFTWWGFFTAMSAFNSNLGLSLTADSMVSFDTAPYPLIFMM
FFIIIGNTGFPIMLRFI IWIMFKTSRDLSQFKESLGFLLDHPRRCFTLLFPSPGTWWLFT
TLVVLNATDNLFI ILDFNSAVVRQVAKGYRALMGLFQSVCTR TAGFNVVDLSKLHPSIQ
VSYMLMMYVSVLPLAISIRRTNVYEEQSLGLYDSGQDDENITHEDDIKETDHDGSEERD
TVSTKSKPKKQSPKSFVGAHLRRQLSFDLWYLFGLFI ICICEGRKIEDVKNPDPNVFAI
LFEVVSAYGTVGLSGYPNTNTSLSAQFTVLSKLVI IAMLIRGRNRLPYTLDRAIMLPS
DKLEQIDRLQDMKAKGKLLAKVGEDPMTTYVKKRSHKLLKIATKFWGKH

SEQ ID NO: 52

YKR105C

>sp|P36172|VBA5_YEAST Vacuolar basic amino acid transporter 5
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = VBA5
PE = 3 SV = 1

MEETKYSSQQEIEGACGSDASLNARGSNDSMPGLSLYLCLASLILVLFITALDILIVGTI
IDVVAEQFGNYSKTNGLVLTGYSLPNAILSLIWGRFASIIIGFQHSILAILIFEAGSLIAA
LASSMNLIFGRVAVAGVGGSLQTLFCFVIGCTMVGERSRPLVISILSCAFAVAIVGPPII
GGAFTHVTWRWCFYINLP IIGGLAI IMFLITYKAENKILQKIDAI GTISSFTFSKFRH
QVNFKRLMNGIIFKFPDFGFCALCSAGLVFLLLGLTFGGNKYSWNSGQVITYLVLVGLLFI
FSLVYDFPLFDKFNPEPDNISYRPLLLRRLVAKPAIIIVNMVTFLLCTGYNGQMIYSVQF
FQLIFASSAWKAGLHLIPIVITNVIAAIASGVITKKLGLVKPLLI FGGVLGVIGAGLMTL
MTNTSTKSTQIGVLLLPFGFSLGFALQASLMSAQLQITKDRPEAMDFIEVTAFTNFMKSL
GTTLGGVLTSTVFSASFHNKVSRAHLEPYEGKTVDDMILYRLQNYDGSHTIGNILSDSI
KNVFWMDLGFYALGFLFCSFSSNKKLIIPKKDDTPEDNLEDK

SEQ ID NO: 53

YKR106W

>sp|P36173|GEX2_YEAST Glutathione exchanger 2 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = GEX2 PE = 1 SV = 1

MSSSVVGASSNKSGIRQSCETIERERHSNDDTYSMTSTFFKLKENEIMSAQFDSLKYKI
LLISTAFVCGPGISLDYTLRSTYTGATNSYEHSLSTVQVINAVVSVGSQVYSRLSD
HPGRRLRFLVATIFYIMGTIIQSQATRLTMYAAGSVFYNGYVGTNLLTLILSDFSSLK
WRMFYQYASYWPIYIIPWISGNI ITAANPQKNWSNIIAMWAFIYPLSTLPIIFLILYMKY
KSSKTAEWRSKKEQARKERTGGLFENLVFLFWKLDIVGILLITVSLGCI LVPLTLANETS
QKWHNSKI IATLVSGGCLFFIFLYWEAKFAKSPLLPFLKLSDRGIWAPLGVTFNFFFTFF
ISCDLYLPVLLVSMKESSTSAARIVNLPDFVAATASPFYSLLVAKTRKLKLSVIGGCAAW
MVCMLGFYKYRGGSGSHEGVIAASVIMGLSGLLCSNSVIVILQAMTTHSRMAVITGIQYT
FSKLGAAGASVSGAIWQTMPNQLYKNLGNLTLAEIAYASPYTFISDYPWGSPPERDAVV
ESYRYVQRIIMTVGLACTVPFFFTFMFMRNPELIDKATHEEFTEDGLVLPDEENIFSQI
KALFRHNRSNKKSGC

SEQ ID NO: 54

YLR447C

>sp|P32366|VA0D_YEAST V-type proton ATPase subunit d
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = VMA6
PE = 1 SV = 2

MEGVYFNIDNNGFIEGVVGRYRNGLLSNQYINLTQCDTLEDLKLQLSSTDYGNFLSSVSS
ESLTSLIQEYASSKLYHEFNIRYDQSSGSTRKFMDYITYGYMIDNVALMITGTIHDRDK
GEILQRCHPLGWDFTLPTLSVATDLESLEYTVLVDTPLAYPKNCFDTAEELDDMNIEII
RNKLYKAYLEDYFNVTBEIPEPAKECMQTLTGFEADRRSINIALNSLQSSDIDPDLKSD
LLPNIGKLYPLATPHLAQAQDFEGVRAALANVVEYRGFLETGNLEHDHFQYLEMELCRDAF
TQQFAISTVWAWMKSEQEVNRNITWIAECIAQNQRERINNYISVY

TABLE 14-continued

Sequences disclosed herein.

SEQ ID NO: 55

YML116W

>sp|P13090|ATR1_YEAST Aminotriazole resistance protein

OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = ATR1

PE = 1 SV = 2

MGNQSLVVLTESKGEYENETELPVKKSSRDNNIGESLTATAFTQSEDEMVDNQNQWQNP
 YFKYAWQEYLFIFTCMISQLLNQAGTTQTLSIMNILSDSFGSEGNKSWLMASFPLVSGS
 FILISGRGLGDIYGLKMLLVGYVLVLIWSLICGITKYSGSDIFFIISRAFAQGLGIAFVLP
 NVLGIIGNIYVGGTFRKNIVISFVGAMAPIGATLGCLFAGLIGTEDPKQWPWAFYAYSIA
 AFINFVLSTIYAIPTIPTNIHHFSMDWIGSVLGVIGLILLNFVWNQAPISGWNQAYIIVI
 LIISVIFLVVFIIEIRFAKTPLLPRAVIKDRHMIQIMLALFFGWSFGIFTFYTQFQL
 NIRQYALWAGGTYFMFLIWGIIAALLVGFTIKNVSPSVFLFFSMVAFNVGSIMASVTPV
 HETYPRTQLGTMIIISFGMDLSFPASSIIFSDNLPMEYQGMAGSLVNTVVNYSMLCLGM
 GATVETQVNSDGKHLKGYRGAQYLGIGLASLACMISGLYMVESFIKGRRARAAEYDCT
 VA

SEQ ID NO: 56

YMR034C

>sp|Q05131|YMS4_YEAST Uncharacterized membrane protein YMR034C

OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YMR034C

PE = 1 SV = 1

MKTQYSLIRKIWAHSVTEFLKSQWFFICLAILIVIAFAPNFARDGGLIKQYSIGYGCV
 AWIFLQSGGLMKSRSLMANMLNWRHAHATILVLSFLITSSIVYGCCAVKAANDPKIDDWV
 LIGLILTATCPTTVASNVIMTNAGGNSLLCVCEVFIGNLLGAFITPALVQMFTNRAPFA
 YGNPATGNGIGALYGRVMKQVGLSVFVPLFVGQVIQNCFPKGTAYYLGLKKYHIKIGSY
 MLLLMFSSSFSTAFYQDAFTSVSHVCIIFLCFFNLGIYIFFTGLSYLCARPWFILKLPFH
 EPIEGKSTRLVRYSYNI FRPFYYSKEDAICIMFCGPAKTAALGVSLITSQYGDKEHLGK
 LLVPLVLVYQVEQVMATANFFVSLFKRWIQKDAQADGSESSCANENEVDLEKIIISIGTGEN
 QSVLSNNVPYPTQPR

SEQ ID NO: 57

YMR056C

>sp|P04710|ADT1_YEAST ADP, ATP carrier protein 1 OS = *Saccharomyces**cerevisiae* (strain ATCC 204508 / S288c) GN = AAC1 PE = 1 SV = 1

MSHTETQTQSHFGVDFLMGGVSAIAKTGAAPIERVKLLMQNQEMLKQGLDTRYKGI
 LDCFRTATHTGIVSFWRGNTANVLRYPPTQALNFAFKDKIKSLSYDRERDGYAKWFAG
 NLFSGGAAGGLSLLFVYSLDYARTRLAADARGSKSTSQRQFNGLLDVYKKTLLKTDGLLGL
 YRGFVPSVLGIIIVYRGLYFGLYDSFKPVLLTGALEGSFVASFLLGWVITMGASTASYPLD
 TVRRRMMMTSGQTIKYDGALDCLRKIVQKEGAYSLFKGCGANI FRGVAAAGVISLYDQLQ
 LIMFGKKFK

SEQ ID NO: 58

YMR253C

>sp|Q04835|YM87_YEAST Uncharacterized membrane protein YMR253C

OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YMR253C

PE = 1 SV = 1

MNPSVPKVMKRENNTHLLVSKEMNDTSLQLPSTTRSLSPKESNSNEDFNVDGNETTQRI
 SKDYLKPNIGLVLLTVSYFFNSAMVSTKVLENDPDDIANDRQIKPLQILLVRMVITYIG
 TLIYMYINKSTISDVPPGKPEVRKWLVLRGCTGFFGVFGMYYSMLYLTISDAVLITFLAP
 SLTIPLSWVILRERFTKVEALGSLISLGLVVLIVRPSFLFGTPELTDSSSQIVESSDPKS
 RLIAITLVGLWGLVGMSCVYIIIRYIGKRAHAIMSVSYFSLITAIVSFIGINTIPSMKFI
 PHSKKQWILFGNLGVSGFIFQLLLTMGIQERAGRGLMTYTQLLYAVFWDVALYKHWP
 IWSWIGMIIISATLWVIRAANNETTAKDLTPIIDDEENSIPLTEFDLSDSK

SEQ ID NO: 59

YNL065W

>sp|P53943|AQR1_YEAST Probable transporter AQR1 OS = *Saccharomyces**cerevisiae* (strain ATCC 204508 / S288c) GN = AQR1 PE = 1 SV = 1

MSRSNSIYTEIDIEMYPHNEQHLTREYTKPDGQTKSEKLNFEAGYINSHGTLSTTTREI
 EGDLDSETSSHSDDKVDPTQQTAEKAPYTLLSYGQKWMVAILTMCGFWSLGSPIY
 YPALRQLEKQFNVDENMVNTVVVYLLFQGISPTVSGGLADCFGRPIILAGMLIYVIAS
 IGLACAPSYGVIIFLRCIQSIGISPTIAISSGVVGDFTLKHERGTFFVGATSGFVLLGQCF
 GSLIGAVLTAARDWRAIFWFLTIGCGSCFLIAFLILPETKRTIAGNLISI KPKRFINRAPI
 FLLGPVRRRFKYDNPDIETLDPTIPKLDLSSAGKILVLP EIIISLFPSSGLLFAMWTMLLS
 SISSGLSVAPYNYHLVIGVCYLPGGIGGLMGSPFTGRIIDMYFKRKIKKFEQDKANGLI
 PQDAEINMFKVRLVCLLQNF LAVVAYLLFGWSIDKGWRIESILITSFVCSYCAMSTLST
 STTLVDLYPTKSS TASSCFNFVRCSLSTIFMGCFAPKMAAMTVGGTFTFLCALVFFNF
 LMFIPMKYGMKWREDRLKQQRQSWLNTLAVKAKKGTQRDQNDNHN

TABLE 14-continued

Sequences disclosed herein.

SEQ ID NO: 60

YNL070W

>sp|P53507|TOM7_YEAST Mitochondrial import receptor subunit TOM7
 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = TOM7
 PE = 1 SV = 2
 MSFLPSFILSDESKERISKILTLTHNVAHYGWIPFVLYLGWAHTSNRPNFLNLLSPLPSV

SEQ ID NO: 61

YNL083W

>sp|D6W196|CMC1_YEAST Truncated non-functional calcium-binding
 mitochondrial carrier SAL1-1 OS = *Saccharomyces cerevisiae* (strain
 ATCC 204508 / S288c) GN = SAL1 PE = 1 SV = 2
 MLLKNCETDKQDIRYACLFKELDVKGNGQVTLDNLISAFEKNDHPLKGNDEAIKMLPTA
 MDVVKDSVVLDLSDFKKYASNAESQIWNQFQRIIDLHDGKIGINEINRYLSDLDNQSIENN
 ELNHELSEKVNKFSRFFFEWAFFPKRKANIALRGQASHKNTDNDRSKKTDSLDLYVTYDQ
 WRDFLLLVPKQGSRLHTAYSFYLFNEDVDLSSEGDVTLINDFIRGFGFFIAGGISGVI
 SRTCTAPFDRLKVFLIARTDLSSILLNSKTDLLAKNPADINKISSPLAKAVKSLYRQGG
 IKAFYVGNGLNVIKVFPESIKFGSFEVTKKIMTKLEGCRDTKDLSKPFSTYIAGGLAGMA
 AQFSVYPIDTLKFRVQCAPLDTKLKGNLLFPQAKDMFREGGGQIILQRCHSRYSGHISL
 CCIRFGDFFLCKKMYCQTGKDEPTTRSGHSKQPGCTSNQCIQWNCRSFCCLSNQSPKN
 KTTSPRNICTSLCV

SEQ ID NO: 62

YNL095C

>sp|P53932|YNJ5_YEAST Uncharacterized transporter YNL095C
 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YNL095C
 PE = 1 SV = 1
 MVHITLGQAIWVSVKPIIKIYLIIGVGFLMAKMGILTVEATRIISDIVLTVLLPSLSFNK
 IVANIEDKDIKSVGIIICLSALLIFGSGFFAYVVRFLFPVPKQWYGGILAGGMFPNISDL
 PIAYLQSMQDLGVFSEEEGNKGVANVIFLTMFLICIFNLGGFRLIESDFEYNDDESARV
 VSETTKTPAVSANTNTDTSERFFSNEQQLFNKYTARDSLTEAIGTKGENADVPPIISR
 RSTNSIAPLSLPDTSNSKITKPVQVKARNTIACTQSEESQATRGSNPLDSQSSASTIHS
 YNTSESYESSIDTMRARRTASQPRAYNTTTLLEENCLDEKCPKNMSMAALEPIRSIDMRA
 LPSQNIHHILIREYSNVDQYGHQRRNSSLRGADMNDVHSISSNSTLQTIKTANLTRILTS
 ATVSKKDIETSGESLPQWMRKPSLTPLLVFFLKNCLRPCSMAVIIALTVAIPWVKALFV
 TTANTPHISQAPDNAPPLSFFMDFTGYVGAACVPFGLILLGATLGRLLKIGNLYPGFWKAA
 VTLVLIRQCVMPIFGVLWCDRLVKAGVWNWQDRMLLFVIAISWNLPTMTTLIYFTASFT
 PPETTAPIQMCVSVFLLMLQYPLMVVSLPFLVSYFLKVQMMNL

SEQ ID NO: 63

YNL121C

>sp|P07213|TOM70_YEAST Mitochondrial import receptor subunit TOM70
 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = TOM70
 PE = 1 SV = 2
 MKSFITRNKTAITVAATGTAIGAYYYNQLQQQQQQRGKNTINKDEKKDTKDSQKETE
 GAKKSTAPSNPPIYVPSNNGEPDFSNKANFTAEEDKYALALKDKGNQFPRNKKYDDAIK
 YYNWALELKEDPVFYSNLSACYVSVGDLKKVEMSTKALELKPDSKVLRRASANEGLG
 KPADAMPDLSVLSLNGDFNDASIEPMLERNLNKQAMSKLKEKFGDIDTATATPTELSTQP
 AKERDKQENLPSVTSMSASFFGIFKPELTFANYDESNEADKELMNGLSNLYKRSPEYDK
 ADESFTKAARLFEEQLDKNNEDEKLKEKLAISLEHTGIFKFLKNDPLGAHEDIKKAIELF
 PRVNSYIYMALIMADRNDSTEYNYFDKALKLDSNNSSVYHRGQMFILQNYDQAGKDF
 DKAKELDPENIFPFIQLACLAYRENKFDDECETLFSEAKRKFPPEPEVNPFFAEILTDKND
 FDKALKQYDLAIELENKLDGIYVGIAPLVGKATLLTRNPTVENFIEATNLLEKASKLDP
 SEQAKI GLAQMKLQOQEDIDEAITLFEESADLARTMEEKLQAITFAEAAKVQQRIRSDPVL
 AKKIQTLLAKLREQGLM

SEQ ID NO: 64

YNL142W

>sp|P41948|MEP2_YEAST Ammonium transporter MEP2 OS = *Saccharomyces*
cerevisiae (strain ATCC 204508 / S288c) GN = MEP2 PE = 1 SV = 1
 MSYNFTGTPTGEGTGGNSLTDLNTQFDLANMGWIGVASAGVWIMVPGIGLLYSGLSRKK
 HALSLWASMMASAVCIFQWFFWGSYSLAFSHNTRNGNFIGTFEFGFRNVLGAPSSVSSL
 PDILFAVYQGMFAAVTGLMLGGACERARLFPMVFLFLWMTIVYCPACWVWNAEGWL
 KLGLDYAGGLCVHLTSGHGLVYALILGKRNDPVTRKGMKPKPHSVTSVVLGTVFLWF
 GWMFFNGGSAGNATIRAWYSIMSTNLAAACGGLTWMVIDYFRCGRKWTVGLCSGIIAGL
 VGITPAAGFVPIWSAVVIGVVTGAGCNLAVDLKSLRLRDDGLDCYSIHVGVGCTGSVLGT
 IFAADYVNATAGSYISPIDGGWINHHYKQVGYQLAGICAALAWTVTVTSILLTMMNAIPF
 LKRLLSADEELGTDAAQIGFTYEESTAYIPEIRSKTSAQMPPPHENIDDKIVGNLDA
 EKNSTPSDASSTKNTDHIV

TABLE 14-continued

Sequences disclosed herein.

SEQ ID NO: 65

YOL020W

>sp|P38967|TAT2_YEAST Tryptophan permease OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = TAT2 PE = 1 SV = 1
 MTEDFISSVKRSNEELKERKSNFGFVEYKSKQLTSSSSHNSSSHDDDNQHGKRNIQOR
 CVDSPKSPLDGSDFTSNLKRITLKRHLIMIAIGGSGTGLFVSGSKAIAEGGPLGVVIGW
 AIAGSQIIGTIHGLGEITVRFPVVGAFANYGTRFLDPSISFVSTIYVLQWFFVLPLEII
 AAAMTVQVWNSIDPVIWVAIFYAVIVSINLFGVRGFGAEFAFSTIKAITVCGFIILCV
 VLICGGGPDHEFIGAKYWHDPGCLANGFPGLVSLVSVASYSLGGIEMTCLASGETDPKGL
 PSAIKQVFWRLFFFLISLTLVGFPLVPYTNQNLGGSSVDNSPFVIAIKLHHIKALPSIV
 NAVILISVLSVSGNSCIFASSRSLCSMAHQGLIPWWFGYIDRAGRPLVGIMANSLFGLLAF
 LVKSGSMSEVFNWLMIAIAGLATCIVWLSINLSHIRFLAMKAQKSLDELEFVSAVGIWG
 SAYSALINCLLLIAQFYCSLWPIGGWTSKGERAKIFFQNYLCALIMLFIFIVHKIYYKQ
 TKGWVGKALKDIDLETRKIDIEIVKQEIAEKKMYLDSRPWVVRQPHFWC

SEQ ID NO: 66

YOL075C

>sp|Q08234|Y0075_YEAST Uncharacterized ABC transporter ATP-binding protein/permease YOL075C OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YOL075C PE = 1 SV = 3
 MSQQENGDVATELIEENRLSFSRIPRISLHVRLDSIVASKTNTTLVNTFSMDLPSGSMVAV
 MGGSGSGKTTLLNLVASKISGGLTHNGSIRYVLEDTGSEPNETEPKRAHLDGQDHPKQH
 VIMAYLPQQDVLSPRLTCRETLKFAADLKLNSERTKKLMVEQLIEELGLKDCADTLVGD
 NSHRLGSGGKRRLSIGTQMISNPSIMFLDEPTTGLDAYSAPLVIKTLKKLAKEDGRFTFI
 MSIHQPRSDILFLLDQVCILSKGNVVCYCDKMDNTIPYFESIGYHVPQLVNPADYFIDLSS
 VDSRSDKEEAATQSRNLSDHWHYDERTHLQLQAESYISNATEIQIQNMTRLPFWKQV
 TVLTRRNFKLNFSDYVTLISTFAEPLIGTVCGWIYKPKDKSSIGGLRTTACLYASTIL
 QCYLVLFPDTRYRLCQDIALYDRERAEGSVTPLAIFIVARKISLFLSDDFAMTMIFVSTY
 FMFGLLEADARKEFFYQFAVFLCQLSCSGLSMLSVAVSRDFSKASLVGNMTFTVLSMGC
 FVNAKVMPPVYVRWIKYIAFTWYSFGTLMSSFTNSYCTDNLDECLGNQILEVYGFPRNW
 ITVPVAVLLCWSVGVYFVVGAILLYLHKIDITLQNEVKSQKKIKKSPGTMKPEIQLDD
 VYHQDLEAEKGNHITIKLEIDLRLVIFSAPFSNWKEGNFHETKEILQSVNAIFKpG
 MINAIMGPSGSGKSSLLNLISGRKSSVFAPDFTSGSIMFNDIQVSELMFKNVCSYVSQD
 DDHLAALATVKTETLYAAALRLHLHTEAERMERTDNLIRSLGLKHCENNIIIGNEFVKIS
 GGEKRRVTMGVQLLNDPPIILLDEPTSGLDSTSATILEILEKLCREQGKTIITIHQPR
 SELFRFPGNVLLAKSGRTAFNGSPDEMIAYFTELGYNCPSFTNVADFFLDLISVNTQNE
 QNEISSRARVREKILSAWKNMNDNESLPTPISEKQYSQESFFTEYSFVRKPNLVLA
 IVNVRQPTTTRRSDSLMARIAQIPGLGVIFALFFAPVKHNTISISNRLGLAQESTALY
 FVGMLGNLACYPTERDIFYEYNDNVYGIAPFFLAYMTLELPLSALASVLYAVETVLACG
 LPTAGNFFATVYCSFIPTCCGEALGIMTNTFFERPGFVVNCISILSIGTQMSGLMSGL
 MSRVLKGFNLYLNPVGYSMIIINFAPPGNLKLTCEGGKNSDGTCEFANGHDVLSYGLV
 RNTQKYLGIIIVCAIIRYLAFFILKAKLEWIKW

SEQ ID NO: 67

YOL077W-A

>sp|P81451|ATP19_YEAST ATP synthase subunit K, mitochondrial OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = ATP19 PE = 1 SV = 1
 MGAAYHFMGKAIPPHQLAIGTLGLLGLLVVNPFFKSAKPKTVDIKTDNKDEEKFIENYLK
 KHSEKQDA

SEQ ID NO: 68

YOL122C

>sp|P38925|SMF1_YEAST Manganese transporter SMF1 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = SMF1 PE = 1 SV = 2
 MVNVPASHAAVAVDASEARKRNISEEVFELRDKKDSTVVIIEGAPVRTFTSSSNHERED
 TYVSKRQVMRDIFAKYLFKIFGPGMLVSVAYIDPGNYSTAVDAGASNQFSLLCIILLSNFI
 AIFLQCLCIKLGSVTGLDLRACREYLPRWLNWTLFFFAECAVIATDIAEVIPTAIALNI
 LKIVPLPAGVAITVVDVFLIMFTYKPGASSIRFIRIFECFVAVLVVGVICIFAIELAYIP
 KSTSVKQVFRGFVPSAQMFHDHNGIYTAISILGATVMPHSLFLGSALVQPRLLDYDVKHGN
 YTVSEQDKVKKSKSTEIIEEKYFNRYRPTNAAIKYCMKYSMVELSITLFTLALFVNCAI
 LVVAGSTLYNSPEADGADLFTIHELLSRNLAPAAGTIFMLALLLSGQAGVVTMSGGIV
 SEGHINWKLQWPQRRLATRCISIIIPCLVISICIGREALSKALNASQVLSIVLPFLVAPL
 IFTCKSKIMKTEITVDHTEEDSHNHQNNDRSAGSVIEQDGSNGMEIENGKDVKIYVMA
 NNWITVTIAIIVWLFLSLNLNVYAIIVQLGMSHGDIGS

SEQ ID NO: 69

YOR079C

>sp|Q12067|ATX2_YEAST Metal homeostasis factor ATX2 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = ATX2 PE = 1 SV = 1
 MKFLGVILLASELLIATFLIGLIPLYYIDKQKSSIVTNQEGADSIDFTTNADTQTINDD
 VSSYRVKIAVLSQFGIGMLLGTSMFLVPIPEGIKACVEHDGNVGVNLLIGFLGINVLDRLV
 TLWVSRKQTVYTHDAVKFQSQWKDIINHPRQIWMNLIQNNVVFALFIHGLSDGIALGTTTN
 NDSLLIIVVLIAIVIHKIPAVLSLTSLMVSRLNLMKWEVICNVELPASSTPIGYIVLSLLN

TABLE 14-continued

Sequences disclosed herein.

LSHSPMDWISGNLLMSGGSLLYASFTAFVGGDSHDHLSVEQEVVLPHDSESVYVLIGV
CIPLVISYCISEE

SEQ ID NO: 70

YOR087W

>sp|Q12324|YVC1_YEAST Calcium channel YVC1 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YVC1 PE = 1 SV = 2
MVSANGDLHLPLISNEQCMPENNGLGFEAPTFRQILRVTLNLKYLDKVVPIVYDPNDIV
CDHSEILSPKVVKLAYEACGGNPKDKANKRKYQSVIIFSLLKVCEWYSILATMEVHNAKL
YETRNLASQQCLCKLLIEREETRDQLFLFMQLLLRRYVINENDEQEPNLAELELATDMHCT
TVIGSSGFQRCCLKWIRGWIVQNGLDPTTFIKDDSLAEVSLISHFNPVRLKAPVYQNYLQ
MIFSFLFLGLYTLVVNGKDSERVQSFDDLLESIFYVFNTGFILDELTKLYYIGYAHLSFWN
LFNDTTYLIITFAMGFRAMSVTPLNAKYSSSEDWDKISYRVLSCAAPFVWSRLLLYLESQR
FIGIMLVILKHMKEISIVFFLLFLIMIGFTQGFLGLDSADGKRDIITGPILGNLTIITVLG
LGSFVDFEFAFPYAAILYGYFYFIVSVILLNILIALYSTAYQKVIDNADDEYMALMSQK
TLRYIRAPDEDDVYVSPNLNIEVFMTPIFRILPPKRAKDLSYVTMTIVYSPFLLISVKET
REARRIKYNRMKRLNDDANEYDTPWDLTDGYLDDDDGLFSDNRNSGMRATQLKNSRSLKL
QRTAEQEDVHFVKVPKKWYKNVKKCSPSPEQYDNDTDEDDAGEDKDEVKELTKKVENLTAV
ITDLEKLDIKDKKE

SEQ ID NO: 71

YOR092W

>sp|Q99252|ECM3_YEAST Protein ECM3 OS = *Saccharomyces cerevisiae*
(strain ATCC 204508 / S288c) GN = ECM3 PE = 1 SV = 1
MTHITLGGAIWASVRPIIKIYLIIGVGFLCKMNLTVQATRSISDIVLTILLPCLSPNK
IVANEDNDIKDVGIICTSVILFATGLGFATVRSVLPVPKRWGGILAGGMFPNIDSL
PIAYLQSDMQGFIFTEAEGEKGANVIFLAMFLICVFNLGGFRLEIENDFHYKGGDDDEEN
TLTNDSSAQQPTQPIEGNSSSSSQDILKEPNESVTPNSSQASYISEKNKKEKTELSVPK
PHTTAPPAIDRRSSNSSAVVSIDSITHSLRTHNVDAQSVSELNDPTYRTRSQPIAYTTES
RTSHVHNRRNSITGSLRSIDMRELPAGMSDLIREYSNVDOYGRRRKSSISSQGAPSVL
QADGTISPNLTRTSTLQRVKTSNLTRIITS DATVSKKDIETSGSSSLPKWLQKPLTKFFV
FPLKNCCLRPCSMAVILALI IAFIPWVKALFVTTSTNPKIKQAPDNAPALTFIMDFTSYVG
AASVPFGLILLGATIGRLKIGKLYPGFWKSAVVLVFLRQCIMPFGVLWCDRLVKAGWLN
WENDKMLLFVTAITWNLPTMTTLIYFTASYTPEDETEPVQMECTSFLLMLQYPLMVVSLP
FLVSFYIKVQMKL

SEQ ID NO: 72

YOR130C

>sp|Q12375|ORT1_YEAST Mitochondrial ornithine transporter 1
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = ORT1
PE = 1 SV = 2
MEDSKKKGLIEGAILDIINGSIAGACGKVIEFPFDTVKVRLQTQASNVFPTTWSCIKFTY
QNEGIARGFFQGIASPLVGACLENATLFVSYNQCSKFLEKHINVSPLGQILISGGVAGSC
ASLVLTVPVELVKCKLQVANLQVASAKTKHTKVLPTIKAIITERGLAGLWQQSGTFIRES
FGGVAWFATYETVKKSLKDRHSLDDPKRDESKIWELLSGGSAGLAFNASIFPADTVKSV
MQTEHISLTNAVKKIFGKFGKGFYRGLGITLFRAPVANAAYFYIFETLSAL

SEQ ID NO: 73

YOR222W

>sp|Q99297|ODC2_YEAST Mitochondrial 2-oxodicarboxylate carrier 2
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = ODC2
PE = 1 SV = 1
MSSDSNAKPLPFIYQFISGAVAGISELTVMYPLDVVKTRFQLEVTTPTAAAVGKQVERYN
GVIDCLKKIVKKEGFSRLYRGISSPMLMEAPKRATKFACNDQYQKIFKNLFNTNETTQKI
SIAAGASAGMTEAAVIVPFELIKIRMDQVKSSYLGPMDCLKTIKNEGIMGLYKGIESTM
WRNALWNGGYFGVIYQVRNSMPVAKTKGQKTRNDLIAGAIAGTVGTMNTPFDDVVKSRIQ
SVDVSSAVKKYNWCLPSLLVIYREEGFRALYKGFVVKVCR LAPGGSMLLVFTGMNNFF
RDLKYGH

SEQ ID NO: 74

YOR291W

>sp|Q12697|YPK9_YEAST Vacuolar cation-transporting ATPase YPK9
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YPK9
PE = 1 SV = 1
MDIPSSNQIQHGQSRERNRMPRASFSSTATTTSTAATLTSAMVLDQNNSEPYAGATFEAV
PSSIVSFHHPHSFQSSNLPSPHSSGNLEQRGRRLTESEPLVLSAEQSRSSSRNP SHFRF
FTQEQISNAEGASTLENTDYDMAWDATPAYEQDRIYGTGLSSRRSSIRSFSSRASSLSNAK
SYGFSKRGSRGSRAPQRLGENSDTGFVYHSATHSSSLSRYTTRERIPIELESQTDAIL
EDESSTHSLSSDSRRSASENNRGSFSGHDDVHNQHSYLYKPDYHEKFYPQYAPNLHYQR
FYIAEEDLVIGIAAYQTSKFYWIYNLCCFLTFLGLVYLLTRWPLHLKVLYGVKVPLAKA
EWWVITENEFGEFVIQPIDRQWYNRPLSTVLPFENYPNPSYEPNDINLSHHANEINPNVP
ILITEYRYIKFIYSPLDDLFTKTNNNWIDPDWVDLSTVSNGLTKGVQEDRELAFGKNQIN
LRMKTTSSEILFNEVLHPFYVQVFSIILWGIDEYVYAAACIFLISVLSIFDSLNEQKKVS
RNLAEMSHFHCDVRVLRDKFWTTISSSELVPGDIYEVSDPNITILPCDSILLSSDCIVNE
SMLTGESVPVSKFPATEETMYQLCDDFQSTQISSFVSKSFLYNGTNIIRARIAPGQTAAL

TABLE 14-continued

Sequences disclosed herein.

AMVVRTGFSTTKGSLVRSMVFPKPTGFKFYRDSFKYIGFMSLIAIFGFCVSCVQFIKGLGL
DKKTMILRALDIITIVPPALPATLTIGTNFALSRLKEKGIFCISPTRLNISGKIDVMCF
DKTGTLTDEGLDVLGVQISEPNVGRQKFGELLSDIRQVFPKFSLNDCSSPLDFKSRNFF
MSLLTCHSLRSDVGNLLGDPLDFKMFQFTGWSFEEDFQKRAFHSLEYEGRHEDDVFPENSE
IIPAVVHPDSNNRENTFTDNDPHNFLGVVRSFEFLSELRRMSVIVKTNDDVYWSFTKGA
PEVISEICNKTSLPADFEVLRCYTHNGYRVIAACAGKTLPKRTWLVSQKVSREEVESNLE
FLGFIIFQNKLLKKTSETLKSLODANIRTIMCTGDNILTASVGREAGLIQCSRVYVPSI
NDTPLHGEFPIVWRDVNEPDKILDTKTLKPVKLGNNSVESLRECNYTLAVSGDVFRLLFR
DENEIPEEYLNELNLSIYARMSPEKHELMIQQLDLYTVGFCGDGANDCGALKAADV
GISLSEAEASVAAPFTSKI FNISCVLDVIREGRAALVISFACFQYMSLYSAIQFITITIL
YSRGSNLGDFQFLYIDLILLVPIAICMSWSKSYEKIDKKRPSANLVS PKILVPLLSVFL
VFLFQFIPIWIVQKMSWYIKPIVGGDDAVQSSDNTVLFVSNFQYILTAIVLSVGGPPYRE
PMSKNFEFIVDITVSIGASLLMLTLDTESYLGKMLQLTPISNSFTMFIIVVILNYYAQL
YIPPSIKGWLKKKSSKKYKLLIQEEMKLKEV

SEQ ID NO: 75

YOR306C

>sp|Q08777|MCH5_YEAST Riboflavin transporter MCH5 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = MCH5 PE = 1 SV = 2
MSSDSLTPKDTIVPEEQTNQLRQPDLDDEDSIHYDPEADDLESLETTASYASTSVSAKVYT
KKEVNGKGDIESQPHWGENTSSTHSDKEDSNEEIESFPEGGFKAUVVTFGCFGLGIAC
FGLLNSTGVIESHLQDNQLSSESSTIGWLSFLFLVCSASCIISGTYFDRNGFRTIMIV
GTVFHVAGLFPATANSTKYWHFILSFAIVCGFNGIVLSPLVSVPAHYFFKRRGTALAMAT
IGGSVGGVFPIMLSRFSFMSKSDTPTYGFWGIRTLGFLDLALLTSLIILVKERLPHVI
ENSKDGESRWRYILRVYILQCFDAKAPLDMKYLFCVLGTVFSELSINSALTYGGSYATSH
GISANDATYTLIMIINVCGIPGRWVPGYLSDKFGRFNVAIALTLTLFIVMFVGWLPFGTNL
TMYVVISALYGFCSGSVFSLLPVCCGQISKTEEFKGRYSTMYFVVVGFTLVGIPITGAI
SIKTTADYQHYIIFCGLATFVSACVYIISRAYCVGFKWVRP

SEQ ID NO: 76

YOR316C

>sp|P32798|COT1_YEAST Cobalt uptake protein COT1 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = COT1 PE = 1 SV = 2
MKLGSKQVKIISLLLDLTVFFGIEITTGYSLSHLALDIADSPHMLNDIISLVVALWAVNVA
KNRNPDSYTYGKRAEILGALINAVFLIALCVSLIEALQRIAPPVIEPKFVLYVGV
AGLIISNTVGLFLPHDNDQEHGHHGHSHGGIFADHEMHMPSSTHTTHAHVDGIENTTPMD
STDNISEIMPNAIVDSFMNENTRLTTPENASKTPSYSTSSHTIASGGNYTEHNKRKRS LN
MHGVFLHVLGDALGNIGVMSLAFPIWKTDYSWKYTDPLVSLIITGIIFSSALPLSCKAS
KILLQATPSTLSGDQVEGDLKIPGIIAHDHFIWNLTESIPIASLHIQLDISPEQFTDL
AKIVRSKLHRYGIHSATLQPEFITREVTSTERAGDSQGDHLQNDPLSLRPKTYGTGISGS
TCLIDDAANCNTADCLEDH

SEQ ID NO: 77

YOR334W

>sp|Q01926|MRS2_YEAST Magnesium transporter MRS2, mitochondrial OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = MRS2 PE = 1 SV = 2
MNRRLVRSISCFQPLSRITFGRPNTPFLRKYADTSTAANTNSTILRKQLLSLKPISASD
SLFISCTVFNSKGNIIISMSEKFPKWSFLTEHSLFPRDLRKIDNSSIDIPTIMCKPNCIV
INLLHIKALIERDKVYVFDTPNPSAAKLSVLMYDLESKLSSTKNNSQFYEHRALESIFI
NVMSALETDFKLHSQICIQILNDLENEVNRLKLRHLLIKSKDLTLFYQKTLIRDLDEL
LENDDDLANMYLTVKSKPKDNFSDLEMLIETYYTQCDEYVQQSES LIQDIKSTEEIVNII
LDANRNSLMLLELKVITYTLGFTVASVLPAPYGMNLKNFIEESEWGFSTSVAVFSIVSALY
ITKKNFNSLSRVTKMTMPNSPANSSVYPKTSASIALTNKLRKRKWKWKSTKQRLGVLLY
GSSYTNKANLSNNKINKGFSKVKKFNMENTDIKNQNRDMIWKWLIEDKKN

SEQ ID NO: 78

YPL078C

>sp|P05626|ATP4_YEAST ATP synthase subunit 4, mitochondrial OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = ATP4 PE = 1 SV = 2
MSMSMGVRLALRSVSKTLFSQGVRCPSMVIGARYMSSTPEKQTPKAKANSIINAIPGN
NILTKTGLVLTSAAGVYIAISNELYVINDESI LLLTFLGFTGLVAKYLAPAYKDFADARM
KKVSDVLNASRNKHVEAVKDRIDSVSQQLQNAETTKVLFVDVSKETVELESEAFELKQKVE
LAHEAKAVLDSWVRYEASLRQLEQRQLAKSVISRVSQSELGNPKFQEKVLQQSISEIEQLL
SKLK

SEQ ID NO: 79

YPL270W

>sp|P33311|MDL2_YEAST ATP-dependent permease MDL2, mitochondrial OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = MDL2 PE = 1 SV = 3
MLNGRLPLRLGLICRNMLSRPRLAKLPSIRFRSLVTPSSSQLIPLSRICLRSAPVAGKSLI
LQSFRCNSKTVPTSLPSASPIKSGARSAAHAKQSKTDDYKDIIRLFMLAKRDWKL LLL
TAILLLTISCSIGMSIPKIVIGIVLDTLKTSSGSDFFDLKIPISPLPYEFLSFFTVALLI

TABLE 14-continued

Sequences disclosed herein.

GCAANFGRFILLRILSERVVARLRANVIKKTLLHQDAEFFDNHKVGDLSRLGSDAYVVS
 SMTQKVSQVKGALICGVVGVGMMCSLSPQLSILLFFTEPEWLFSAVFGKQIRNTSKDLQ
 EATGQLTRVAEEQLSGIKTVQSFVAEGNELSRYNVAIRDIQVVGKTAFTNAKFFTTSL
 LGDLNFLVLAAGSYLVLSQSLSIGDLTAFMLYTEYTGNAVFGLSTFYSEIMQGAGAASR
 LFELTDRKPSISPTVGHKYPDRGVIEFKDVSFSYPTRPVQIFKNLNFKIAPGSSVCIV
 GPSGRGKSTIALLLRLRYNPTTGTITIDNQDISKLNCKSLRRHIGIVQOEPVLMSTIRD
 NITYGLTYPTKEIRSVAKQCFCHNFITKFPNTYDVTVIGPHGTLTLLSGGQKQRIAIARAL
 IKKPTILILDEATSALDVESEGAINYTFGQLMKSKSMTIVSIAHRLSTIRSENIVLGH
 DGSVVMGKFKELYANPTSALSQLLNEKAAPGPSDQQLQIEKVIEWEDLNESKEHDDQKK
 DDNDNDNNHNDNSNNQSPETKONNSDDIEKSVEHLLKDAKEANPIKITPQP

SEQ ID NO: 80

YPL274W

>sp|Q08986|SAM3_YEAST S-adenosylmethionine permease SAM3

OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = SAM3

PE = 1 SV = 1

MDILKRGNESDKFTKIETESTTIPNDSDRSGSLIRMKDSFKQSNLHVIPEDLENSEQTE
 QEKIQWKLASQPYQVLSQRHLTMIAIGGTGLTGLFGLGYSLASGPAALLIGFLLVGT
 MFCVVSQAELSCQFPVSGSYATHVSRFIDESVGFVATNYALAWLISFSPSELIGCALTI
 SYWNQTVNPAVWVAIFYVFMVLNLFVGRGFAETEFALSIKIVIAIFIFIIIGIVLIAGG
 GPNSTGYIGAKYWHDPGAFAPVFKNLNTFVSAAFSPGGSELVLLTSTESKNISAISSRA
 AKGTFWRIAFIYITTVVIGCLVPYNDPRLLSGSNSDVSAFPVIALSNTGSMGAKVSN
 FMNVVILVAVVSVCSNVCYASSRLIQLGASGQLPSVCSYMDRKGRLVIGIGISGAFGLL
 GFLVASKKEDEVFTWLFALCSISSPFTWFCICMSQIRFRMALKAGRSNDEIAYKSILGV
 YGGILGCVNLALLIAGEIYVSAAPVGPSSAEAFYEYCLSIPIIMIVVYFAHRFYRRDWKH
 FYIKRSEIDLDTGCSVENLELFKAQKEAEEQLIASKPFYIKYIRFWC

SEQ ID NO: 81

YPR003C

>sp|P53394|SULX_YEAST Putative sulfate transporter YPR003C

OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YPR003C

PE = 1 SV = 1

MTSNNLLGRGRMSYSSTAPPFRKRSVDQRTFSDNFDYDKDSSNRGRTYIAASNSTTG
 PPPNNSRSGCTNNTNNTNNTSNTSNTNNDSDVENTVFETLPYYLPCFSWLPEYTFNKLW
 GDVIAGISVASFQIPLALSYYTSIAHVPPCLGLYSLAISPFVYGLGSPQIMIVGPESAI
 SLVVGQAVESITLHKENVSLIDISTVITFVSGTILLFSGISRFGFLGNVLSKALLRGFIS
 SVGLVMIINSLISELKLKFLVSLPQHYHTPFEKILFLIDYAPAYHIPTAIFSGCCLIV
 LFLRLRLKRLKMKYHKSIAFFPDILLVVIVTILISMKNLKHRYGISIIGDFSMDFDEL
 KNPLTRPRKRLIPDLFSASLIVAMLGFFESTASKSLGTTYNLTVSSNRELVALGFMNIV
 ISLFGALPAFGGYGRSKINALSGAQSVMSGVFMGVITLITMNLQLQVHYIPNCVLSVIT
 TIIGISLLEEVPGDIKPHLRGCGFSELFVFAVTFCTTIFYSIEAGICIGCNNSIINIHK
 SAKSRIQLARVAGTSNFTNLDDYMMNMKRNSLDVEGTEEIEGCMIVRIPEPLTFNSED
 LKQRLDRIERYGSSKIHPGRKSLRSKDSIKYVIFDLGGMTSIDSSAAQVLEEIITSYKRR
 NVFIYLVNVSINDKVRRLFKAGVAASVERAQQANNENNTSNTFSDAGETYSPTYDSIDA
 ALYEIEKMKIKGNVNPNDSEFSMNTLNFSSLV

SEQ ID NO: 82

YPR011C

>sp|Q12251|YPR011_YEAST Uncharacterized mitochondrial carrier YPR011C

OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YPR011C

PE = 1 SV = 1

MAEVLTVLEQPNISKDFLKQDSNIAFLAGGVAGAVSRTVVSPPFERVKILLQVQSSTTSYN
 RGIFSSIRQVYHEEGTKGLFRGNGLNCIRIFPYSVAVQVVEACKKLFHVNGNNGQEQ
 TNTQRLFSGALCGGCSVATYPLDLIKTRLISQITANLSSLNRKAKSISKPPGIWQLLSE
 TYRLEGGRLGLYRGVWPTSLGVVPYVALNFAVYEQLEFGVNSSDAQPSWKSNNLYKLITIG
 AISGGVAQTITYPFDLLRRRQVQLAMGGNELGFRYTSVWDALVTIGRAEGVSGYKGLAA
 NLFKVVPTAVSWLVYEVVCDSVRNW

SEQ ID NO: 83

YPR058W

>sp|P32331|YMC1_YEAST Carrier protein YMC1, mitochondrial

OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YMC1

PE = 1 SV = 2

MSEEFPSQLIDDLLEHPQHDNARVVKDLLAGTAGGIAQVLVGQPFDTTKVRLQTSSTPT
 TAMEVVRKLLANEGPRGFYKGTLTPLIGVGACVSLQFGVNEAMKRFPHHRNADMSSTLSL
 PQYYACGTGIVNSFLASPIEHVRIQLQTQSGTNAEFKGPLECIKKLRHNNKALLRGL
 TPTILREGHGCGTYFLVYBALIANQMNKRRGLERKDIKAWKLCIFGALSGLTALWLMVYPL
 DVIKSMQTDNLQKPKFGNSISSVAKTLYANGGIGAFFKFGPTMLRAAPANGATFATFE
 LAMRLLG

TABLE 14-continued

Sequences disclosed herein.

SEQ ID NO: 84
YPR128C
>sp|Q06497|ANT1_YEAST Peroxisomal adenine nucleotide transporter 1
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = ANT1
PE = 1 SV = 1
MLTLESALTGAVASAMANIAYVPLDLSKTIIQSQVSPSSSEDSNEGKVLNRRYKNVVD
MINIFKEKGLGLYQGMTVTTVATFVQNFVYFFWYTFIRKSYMCHKLLGLQSLKNRDGP
TPSTIEELVLGVAAASISQLFTSPMAVVATRQQTVHSAESAKFTNVIKDIYRENNGDIT
A FWKGLRTGLALTINPSITYASFQRLKEVFFHDHSDNAGSLSAVQNFILGVLSKMISTLVT
QPLIVAKAMLQSAGSKFTTFQEALLYLYKNEGLKSLWKGVLPQLTKGVIVQGLLFAFRGE
LTKSLKRLIFLYSSPFLKHNGQRKLAST

SEQ ID NO: 85
YPR201W
>sp|Q06598|ARR3_YEAST Arsenical-resistance protein 3
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = ARR3
PE = 1 SV = 1
MSEDQKSENSVPSKVMVNRDILTITIKSLSWLDLMLPFTIILSIIIAVIISVYVPSSRH
TFDAEGHPNLMGVSIPLTVGMIVMMIPICKVSWESIHKYPYRSYIRKQLALSFLNWI
GPLLMTALAWMALFDYKEYRQGIIMIGVARIAMVLIWNQIAGGDNDCVVLVITNSLLQ
MVLYAPLQIFYCYVISHDHLNNTSNRVLPFEEVAKSVGVFLGIPLGIGIIRLGSLLTIAGKS
NYEKYILRFISPWAMIGFHYTLFVIFISRGYQFIHEIGSAILCFVPLVLYFFIAWFLTFA
LMRYLSISRSQTQRECSQDQELLLKRVWGRKSCASFSITMTQCFMASNNFELSIAIAI
SLYGNNSKQAIATATFGPLLEVPILLILAIVARILKPYIYWNRN

SEQ ID NO: 86
YBR008C
>sp|P38124|FLR1_YEAST Fluconazole resistance protein 1
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN=FLR1
PE = 1 SV = 1
MYYTSTYRHTIVVDLLEYLGIIVSNLETLQSAREDETRKPENTDKKECKPDYDIECGPNRS
CSESSTDSDSGSGSIEKNDPFRVDWNGSPDPENPQNWPLKKSLVVFQIMLLTCVTYMG
SIYTPGQEYIEQEFHVGHVATLNLNLSLVGLYGLGPIIFSPLESTARYGRNLNLYMVTLFF
FMIFQVGCATVHNIIGGLIVMRFIGILCSPSLATGGGTVADIIISPEMVPLVGMNSAGAV
AAPVLAPLGAAMVDKNWRFIFWLLMWLSAATFILLAFFFPETQHNNILYRRALKLRKE
TGDDRYYTEQDKLDREVDARTFLINTLYRPLKMIKEPAIADFLLYIAVAYGCFYLFPEA
FPFIVFVGIYHPSLVVGLAYMGFCVGCVLAYGLFGILNMR IIVPRFRNGTFTPEAFLLI
VAVCVCCLPLSLFLFGLTARVHWILPVISEVFFVLAVFNIFQATFAYLATCYPKYVASVFA
GNGFCRASFCACAPLFGAMYDNLATKNYPVAVWGSSLVGFLTLGLAIIPFILYKYGPSLR
TRSSYTEE

SEQ ID NO: 87
YBR021W
>sp|P05316|FUR4_YEAST Uracil permease OS = *Saccharomyces cerevisiae*
(strain ATCC 204508 / S288c) GN = FUR4 PE = 3 SV = 2
MPDNLSLHLSGSKRLNSRQLMESSNETFAPNNVDLEKEYKSSQSNITTEVYEASSFEEK
VSSEKPYSSFWKKIYYEYVVDKSLIGVSLDSFMYNQDLKPVEKERRVSWYNYCYFW
LAECFNINTWQIAATGLQLGLNWWQCWITIIWIGYGFVAVVLASRVGSAYHLSFPPISSR
ASFGLPFLSLWVINRVVMAIVWYSVQAYIAATPVSLMLKSIIPGKDLQDKIPDHFGSPNAT
TYEFMCFPIFWAASLPFLLVPPHKIRHLFTVKAVLVFPASFGFLIWAIRRAHGRALGSL
TDVQPHGSFAFWAFRLSLMGMANFSTMVINAPDFSRSFKNPNSALWSQLVCIPFLFSIT
CLIGILVTAAGYEIYGINYWSPLDVLEKFLQTTYNKGTAGVFLISFVFAVAQLGTNISA
NSLSCGTDMSAIFPKFINIKRGSFLCAAMALCICPWNLMATSSKFTMALSAYAIFLSSIA
GVVCSDFVVRRGYIKLTHIYSHQKGSFYMYGNRFGINWRAALYLCGVAPCLPGFIAEV
GAPAIKVDGAMKLYLSYVWGYGLSFSSYTALCYFFPVPGCPVNNI IKDKGWQFORWANV
DDFEEBWKDITERRDDLVDNLSVYEHEHEKTFI

SEQ ID NO: 88
YBR043C
>sp|P38227|QDR3_YEAST Quinidine resistance protein 3
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = QDR3
PE = 1 SV = 2
MQAQGSQSNVGSRLSNCSNLSLNNHVMHCDSESGSPHSEHNDYSYEKTNLESTASNSR
EHRDNQLSRLKSEYVVPKNQRRGLLPQLAIIPEFKDARDYPPMMKKMIIVLIAFSSMMG
PMGTSIIFPAINSITTEFKTSVIMVNVSIGVYLLSLGVFPLWSSLSLEGRRTTYITSF
ALLFAFNIGSALAPDINSFIALRMLCGAASASVQSVGAGTVADLYISEDGRKNLSYYLGL
PLLAPLLSPIPGSLLVNRWPRSTQWFMVILSGCNVILLTVLLPETLRKQDSKGAIAQIL
AERRIQVDNNEERGEIQEDYQGEDETDRLENQVATLSTEKHNYVGEVRDQDSLDESSES
PNTYDGRAGETQLQRIYTEASRSLYEYQLDDSGIDATTAQVTRIRSTDPKLARSIRENSL
RKLQTNLEEQVKVLLSSNGGETAPKQVSAVRKVWDTFVYFIKPLKSLHFLEYPPVALAI
TFSATSFSTVYFVNMTVEYKYSRPPYNFKPLYIGLLYIPNSVTYFFASTYGGRWVDMLLK
RYKEYGILAPPEARISWNVVTSVISFPFIALLI FGWCLDKKCHWVTP LIGTALFGYAAAMMT
IGATLSYLVDSLPGKATGVALNNLIRQILAATAVFVTPMLNGMG TGWAFMTLAFIVLG
ASSVLIILKKHGDYWRNYDLQKLYDKID

TABLE 14-continued

Sequences disclosed herein.

SEQ ID NO: 89

YBR287W

>sp|P38355|YB8B_YEAST Uncharacterized transporter YBR287W
 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YBR287W
 PE = 1 SV = 1
 MVETPSFAHLAYLVFESVLQVVI IALAGFWSASSGLLPKQSQKIISLLNVDLFTPCCLIFS
 KLAKSLSMAKIFEIAI IPIFFGLTTGISFISGKIMSRILDLDDKDETNFVANSVFGNSNS
 LPVSLTSLAYLTPNLTDQIPNDNRDNVARGILYLLIFQQIGQMLRWSWGYNKLKMKWS
 GENTQHMPPSQVQSLLERTPNIDNEELVNEEQEEQELLEENNRNMSFLSSSSIGDKIW
 QKSCTVFERIRANLNPPLYSMIFAVVVAIGPLQRELFMEDGFINNTFAEAVTQLGVSISI
 PLILVVLGSNLYPSAEVFPKTVHHSKLLIGSIIGRMILPSCFLLPITIAIAVKYINVSIID
 DPIFLVVGFLTLTSPPAIQLTQITQLNEFFEAEMADILFWGYAVLSLPVSIIVVSGAIYV
 LQWANPT

SEQ ID NO: 90

YBR295W

>sp|P38360|ATU1_YEAST P-type cation-transporting ATPase
 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = PCA1
 PE = 1 SV = 2
 MKPEKLFSGGLTSDGEYGVVNSENISIDAMQDNRGECRRSIEMHANDNLGLVSRQDCTN
 RPKITPQECCLSETEQICHGGENRTKAGLDVDDAETGGDHTNESRVDECCAELKVNDETGL
 DVDSCCGDAQTGGDHTNESCVDGCCVRDSSVMVEEVTGSCAEVSSKEQLTSFEVVPKSKS
 EGLQSIHDIRTTRCNTNSNQHTGKGRLCIESDSTLKKRSCVKSRQKIEVSSKPECCNI
 SCVERIASRSECKRTFKGSTNVGISGSSSTDSLSEKFFSEQYSRMNYRYSILKNLGCIC
 NYLRTLKESCCPLKVRFCSEGBGASKTKYSYRNSSGCLTKKTHGDKERLSDNDNGHADP
 VCSKSCCTKMKDCAVTSTISGHSSSEISRIVSMPEIENHLNLEAGSTGTEHIVLSVSGMS
 CTGCESEKLLKSPGALKCVHGLKTSLLLSQAEEFNLDLAQGSVKDVIKHLKSTEFKYEQIS
 NHGSTIDVVVYPAAKDFINEEWPQGVTELKIVERNIRIYFDPKVI GARDLVNEGWSVPV
 STAPFSCPTIEVGRKHLVRVGCCTTALSIIITIPILVMAWAPQLREKISTISASMLATI
 IQFVIAGPFYLNALKSLIFSRLIEMDLLIVLSTSAAYIFSIVSFGYFVVGRLSTEQFPE
 TSSLLVLTIMVGRFVSELARHRAVKSISVRSLQASSAILVDKTKETEINIRLLQYGDIF
 KVLPSRSRPTDGTVLSGSSEVDEALITGESMPVKKQCSIVVAGSVNGTGTLFVLSKLP
 GNTTISTITATMVDEAKLTKPKIQNIADKIASYFVPTIIGITVVTFCVWIAVGIRVEKQSR
 SDAVIQAI IYAITVLIVSCPCVIGLAVPIVFIASGVAAKRGVIFKSAESI EVAHNTSHV
 VFDKGTGLTEGKLTVVHETVRGDRHNSQSLLLGLTEGI KHPVSMIAISYLKEKGVSAQNV
 SNTKAVTGKRVEGTSYSGLLKQGGNCRWLGHNNDDPVRKALEQGYSVFCFSVNGSVTAVY
 ALEDSLRAVSTINLLRQGISLHILSGDDDGAVRSMAARLGISSNIRSHATPAEKSE
 YIKDIVEGRNCDSSSQSKRPVVVFCGDTNDAIGLTQATIGVHINEGSEVAKLAADVML
 KPCLNNILMTITVSQKAMFRVKLNFLWSFTYNLFAILLAAAGAFVDFHIPPEYAGLGELVS
 ILPVIFVAILLRYAKI

SEQ ID NO: 91

YBR296C

>sp|P38361|PHO89_YEAST Phosphate permease PHO89 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = PHO89 PE = 1 SV = 1
 MALHQFDYIFAIAMLFAFLDAFNIGANDVANSFASSISSRLKYWQAMVLAGLCEFLGAV
 LAGARVSGTIKNNIIDSSIFTNDPAVLMMLTMSALIGSSCWLTFATAIGMPVSTTHSIVG
 GTIGAGIAAGGANGVVGWGSVSI IASWFIAPILAGAIAAIVFSISRFSVLEVKSLERS
 IKNALLLVGVLVFATFSILTMLIVWKGSPNLHLLDSETETAVSIVLTGAIASIVYFIF
 YPFYRRKVLDDQDWTLLKIDIFRGPSFYFKSTDDIPPMPEGHQLTIDYIEGRNRLGTTVS
 EDEENKAASNSNDVKNKEDIQEVDLVRTETEPETKLS TKQYVWSLLKGPKKWPLFLFWL
 VISHGWTQDVIHAQVNDRLMSGLDKGMYERSKFYDNRVEYIYSVLQAITAATMSFAHGA
 NDVANATGPLSAVYVIWKTNTIGAKSEVPVWVLA YGGVALVIGCWYGYNI IKNLGNKMI
 LQSPSRGFSIELAVAITVMATQLGIPTSTTQIAGGVIAVGLCNKDLKSVNWRMVANCY
 SGWFLTLPIAGLIAGIINGIILNAPRFGVEYQMT

SEQ ID NO: 92

YCL038C

>sp|P25568|ATG22_YEAST Autophagy-related protein 22 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = ATG22 PE = 1 SV = 1
 MSYGTINDMNESVTNRYIKKAQNNIKGWYAYSFSSEPPVVS AVSTYIPLLLQQFASINGV
 KVHDHSIPCLSETGSDSKCVLGLFNNRIFVDTSSFALYVFSLSVLFQTIIVISVSGIVD
 LWGSKVKGRILVWFGIVGALSTVAISKLNLTQIYSLAGLYIVANGCPGVINVVGNLSLP
 IFVKDSLCKCQSQGAYEPDKVDSLTTVISGRGASLGYSSALIVQIVSMFLVASKKGSQKDV
 QVAVLFVGIWVFWQLPMIWLIDDVTIPIRVDDSTLASARSPYGEQDALGQLNWKNYLS
 YGWSLFSFSPKHARLLKDVMI FLIAWFIISDSITTINSTAVLFSKAEHLMSLTNLIMITSV
 LIVVNAMLGAFM1PQFLATKFRWTSSQTLMYII IAWSFIPFYGILGFFNFAGLKHKPFEM
 PLLAIWYGLSLGGLSAVRSVFSLVIPPGKSTFFSMFSITDKGSSILGPFLVGLLTDKT
 HNIRYSFYFFFLMLSLPVLNCLDVKRGREAEELSQVLPESERRLD

TABLE 14-continued

Sequences disclosed herein.

SEQ ID NO: 93
YCR011C
>sp|P25371|ADP1_YEAST Probable ATP-dependent permease
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = ADP1
PE = 1 SV = 2
MGSHRRYLYSILSFLLLSCSVVLAKQDKTPFFEGTSSKNSRLTAQDKGNDTCPPCFNCM
LPIFECKQFSECNSYTGRCCEIEGFAGDDCSLPLCGGLSPDESGNKDRPIRAQNDTCHCD
NGWGGINCDCQEDFVCDAMPDPDSIKGTCTYKNGMIVDKVPSGCNVTNEKILQILNGKIP
QITFACDKPNQECNQFQWIDQLESFYCGLSDCAFEYDLEQNTSHYKCNNDVQCKCVPDPTVL
CGAKGSIDISDFLTETIKGPGDFSCDLETRQCKFSEPSMNDLILTVFGDPYITLKESGE
CVHYSEIPGYKSPSKDPTVSWQGLVLALTAVMVLALFTFATFYISKSPFRNGLGSSKS
PIRLPDEDAVNNFLQNEDDTLATLSFENITYSVPSINSIDGVEETVLNEISGIVKPGQILA
IMGGSGAGKTTLLDILAMKRKTGHVSGSIKVNIGISMDRKSFSKIIIGFVDQDDFLLPTLTV
FETVLNSALLRLPKALSPEAKKARVYKVLLEELRIIDIKDRIIGNEFDRGISGGEKRRVSI
ACELVTSPLVLFLDEPTSGLDASNANNVIECLVRLSSDYNRTLVLVLSIHQPRSNIFYFLFDK
LVLLSKGEMVYSGNAKKVSEFLRNEGYICPDNYNIADYLDITFEAGPQKRRRIRNISD
LEAGTDTNDINDINTIHQTFTTSSDGTQREWAHLAHRDEIRSLRDEEDVEGTDGRAGAT
EIDLNTKLLHDKYKDSVYYAELSQEIEEVLSEGDSESNVLNGDLPTGQQSAGFLQQLSIL
NSRSFKNNMYRNPFLKLLGNLYLLTILLSLFLGLTYLVNSNDISGFQNRMGLEFFFIITYFGFV
TFTGLSSPALERIIPIKERSNNYYSPLAYYISKIMS EVVPLRVVPPILLSLIVYPMTGLN
MKDNAPFKCIGILILFNLGISLEILTIGIIFEDLNNSIILSVLVLLGSLFLSGLFINTKN
ITNVAFKYLKNFSVFYYAYESLLINEVKTMLLKERKYGLNIEVPGATILSTFGFVVQNLV
FDIKILALFNVVFLIMGYLALKWIVVEQK

SEQ ID NO: 94
YDL054C
>sp|Q07376|MCH1_YEAST Probable transporter MCH1 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = MCH1 PE = 1 SV = 1
MPLSKVEHYLSYHTRLLLPHVLSLQSSSHRVAYIFSLLSAVSTGFTITLSLYSQPWQKHLN
YSSWQINTIASMTNLGMYLTPPILGMIADSHGPIITLSLLAIIGFIPSYSLAYVFNHPEL
SLGNGDSSPNLSIICFVFIGISTALYFSALLTCTKLYPHTKLLSISLPTCYGISSV
GSQLLRLIKWFSSSNASSSSSDNLNLGRVFTFALVYVYVIGLLAWIATSVVSLHLFNEEQ
DNQKRLDDQTDVEQSPLLERSNHVQEKFTQTMRLIFSDPVIYILAVSILLSLGLPLEMFIA
NMGSLINLLVQLDAPTLSTKLLSTYALSSFTRLTGTIVADFFAKKISIKWILLTFLSL
GVCAQLFLLKMTSSASPWGLVPTGSLVGIYVGGFTVYPTLVLLVWGGERSFGTVYGSLLI
APAIGSMIFCMLYAKFYDSRCMSGGDLRNPSCISAVYKYSSIAFVVS AVLSAVVFWKLK
SRKLRI

SEQ ID NO: 95
YDL100C
>sp|Q12154|GET3_YEAST ATPase GET3 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = GET3 PE = 1 SV = 1
MDLTVEPNLHSLITSTTHKWIFVGGKGVGKTSSSCSIAIQMALSQPNKQFLLISTDPAH
NLSDAFGKFKGDKARKVTGMNLS CMEIDPSAALKDMNDMAVSRANNNGSDGQDGLGSL
LQGGALADLTGSIPIGIDEALSFMVEMKHIKRQEQEGETFDTVIFDTAPTGHTRLRFLQLP
NTLSKLEKFGELITNKLGPMLNSFMGAGNVDSGKLNELKANVETIRQQFTDPDLTTFFVC
VCISFELSLEYETERLIQELISYDMDVNSIIVNQLLFAENDQEHNCRCQARWKMKKKYLD
QIDELYEDFHVVKMPLCAGEIRGLNMLTKFSQFLNKEYNPITDGKVIYELEDKE

SEQ ID NO: 96
YDL245C
>sp|P54854|HXT15_YEAST Hexose transporter HXT15 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = HXT15 PE = 1 SV = 1
MASEQSSPEINADNLNSSAADVHVQPPGKEKWSDFYDKEVINGNTPDAPKRGFLGYLII
YLLCYPVSFGGFLPGWDSGITAGFINMDNFKMNFSGYKHSTGEYYLSNVRMGLLVAMFSV
GCSIGGVAFARLADTLGRRLAIVIVLVYMGAI IQISSNHKWYQYFVGKI IYGLGAGGC
SVLCPMLLSEIAPTDLRGLVSLYQLNMTFGIFLGYCSVYGTRKYSNTAQWRIPVGLCFL
WALI IIVGMMLVPESPRYLIECERHEEACVSIKINKVSPEDPWVWKQADEINAGVLAQR
ELGEASWKEKLSVVKTKVLQRLITGILVQTFQLTGNEYFFFYGTTFKSVGLTDGFETSI
VLGTVNFFSTIIIVMVVDKIGRRKCLLFGAASMMACMVIFASIGVKCLYPHQDGPSSKG
AGNAMI VFTCFYIFCFATTWAPVAYIVVAESFPSPKVKSKAMSI STAFNWLWQFLIGFFTP
FITGSIHFYGYVVGCLVAMFLYVFFFLPETIGLSLEEIQLLYEEGKIPWKSASWVPPS
RRGASSRETEAKKKSWEVLKFPKFSFN

SEQ ID NO: 97
YDL247W
>sp|P0CD99|MPH2_YEAST Alpha-glucosides permease MPH2
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = MPH2
PE = 2 SV = 1
MKNLSFLINRRKENTSDSNVYPGKAKSHEPSWIEMDQTKKDGLDIVHVEFSPDTRAPSD
SNKVITEIFDATEDAKEADESERGMPLATALNTYKAAAWSLVSTTLIMEGYDTAILGA
FYALPIFORKEGSDNDKTGEWEISASWQIGLTLCYMAGEIVGLQLTGPSVDLVGNRYTLI
IALFFLAFTFLYPCNSLGMIAVGQALCGMPWGCFOCLTVSYASEICPLALRYLTTYS
NLCWLFGQLFAAGIMKNSQKKYADSELGYKLPFALQWILVPLALGIFAPAPESPWWLVKK

TABLE 14-continued

Sequences disclosed herein.

GRFDEARRSLRRTLSGKGPEKEILVLTLEVDKIKVTIDKEKRLTSKEGYSYSCFEDKINRR
 RTRITCLCWAGQATCGSILIGYSTYFYEKAGVSTEMSFTFSIIQYCLGICATFLSWWASK
 YFGRYDLAYAGLAFQTIIVFFIIGGLGCSSTHGSKMGSGSLLMAVAFFYNLGIAPVVFCLV
 SEMPSRRRTKTIILARNTYNVVSIIICSVLILYQLNSKKWNWGAKS GFFWGVLCFCTLIW
 AVVDLPETAGTKTFVEINELFKLGVSARKFKSTKVDPFVVKPLKTSLITTPREISKPLQ
 RNSNVSHHL

SEQ ID NO: 98

YDR011W

>sp|P32568|SNQ2_YEAST Protein SNQ2 OS = *Saccharomyces cerevisiae*
 (strain ATCC 204508 / S288c) GN = SNQ2 PE = 1 SV = 2
 MSNIKSTQDSSHNAVARSSSASFASEESFTGITHDKDEQSDTPADKLTKMLTGPARDTA
 SQISATVSEMAPDVVSKVESPADALSRHTTRSGAFNMDSDDDGFDHAIFESFVRDADE
 QGIHIRKAGVTIEDVSAGVDASALEGATFGNILCLPLTIFKGIAKRRHQMKRQIISNVN
 ALAEAGEMILVLRPGAGCSSFLKVTAGEIDQFAGGVSGEVAYDGIPOEEMMKRYKADVI
 YNGELDVHFPYLTVKQTLDFAIACKTPALRVNNVSKKEYIASRRDLATIFGLRHTYNTK
 VGNDFVRGVSGGERKRVSI AEALAAKGSICYWDNATRGDASTALEYAKAIRIMTNLLKS
 TAFVTIYQASENIYETFDKVTVLVYSGKQIYFGLIHEAKPYPAKMGYLCPPRQATAEFLTA
 LTDPNGFHILKPGYENKVPRTAEFEFETYWLNSEPAQMKKDIAAYKEKVNTTEKTKEVYDE
 SMAQKSKYTRKKSYYTVSYWEQVKLCTQRGFQRIYGNKSYTVINVCSAIIQSFITGSLF
 YNTPSSTSGAFSRGVLVYFALLYYSLMGLANISFEHRPILQKHKGYSLYHPSAEAI GSTL
 ASFPFRMIGLTCFFIILFFLSGLHRTAGSFFTIYLFITMCSEAINGLFEMVSSVCDTLSQ
 ANSISGILMMSISMYSTYMIQLPSMHPWFKWISYVLPYRYAFESMLNAEFHGRHMDCANT
 LVPSPGGDYDNLSDDYKVCFAVGSKPGQSYVLGDDYLNQFQYVYKHTWRNFGILWCFLLG
 YVVLKVIFTEYKRPVKGGDALIFKKGSKRFIAHADEESPDNVNDIDAKEQFSSESSGAN
 DEVFDDLEAGVFIWKDVCFITPYEGGKRMLLDNVSGYCIPTMTALMGESGAGKTTLLN
 TLAQRNVGIIITGDMLVNRPIDASFERRTGYYVQQQDIHIAELTVRESLQFSARMRRPQHL
 PDSEKMDYVEKIIIRVLGMEEYAEALVGEVGCGLNVEQRKKSIGVELVAKPDLFLFLDEP
 TSGLDSQSSWAIQLLRKLSKAGQSILCTIHQPSATLFEEDRLLLRKGGQT VYFGDIG
 KNSATILNYFERNGARKCDSENPAEYILEAIGAGATASVKEDWHEKWLNSVEFEQTKEK
 VQDLINDLSKQETKSEVGDKPSKYATSYAYQFRYVLI RTSTSPWRSLNYIMSKMMLMLVG
 GLYIGFTFFNVGKSYVGLQNAMFAAFISIIISAPAMNQIQGRAIASRELFEVRESQSNMF
 HWSLVLTQYLSSELPYHLFFSTIFFVSSYFPLRIFFEASRSAYVFLNYCIMFQLYYVGLG
 LMILYMSPNLPSANVILGLCLSFMLSPCGVTQPVSLMPGFWTFMWKASPYTYFVQNLVGI
 MLHKKPVVCKKKELNYFNPNPGSTCGEYMKPFLEKATGYIENPDATSDCAYCIEVGDNY
 LTHISKSYSLWRNFGIFWIIYIFFNIIAMVCVYYLFHVRQSSFLSPVSI LNKIKNIRKKK
 Q

SEQ ID NO: 99

YDR292C

>sp|P32916|SRPR_YEAST Signal recognition particle receptor subunit
 alpha homolog OS = *Saccharomyces cerevisiae* (strain ATCC 204508 /
 S288c) GN = SRP101 PE = 1 SV = 2
 MPDQLAVFTPGQVLYQYNCLGKKFSEIQINSFISQLITSPVTRKESVANANTDGFDFNL
 LTINSEHKNSPSFNALFYLNKQPELYFVVTFAEQTLLELNQETQQTALVLKLNLSHLSE
 SILKNRQQQNEKNKHNYVDILQGIEDDLKKFEQYFRIKYEESI QKDHINPDNFTKNGSVP
 QSHNKNTKKLRDITKGGKQSTGNVGSGRKWGRDGMGLDEMNHEDA AKLDFSSSNHNSSQ
 VALDSTINKDSFGDRTEGGDFLIKEIDDLSSHKDEITSGNEAKNSGYVSTAFGLQKHV
 LGNKTTINESDLKSVLEKLTQQLITKNVAPEAADYLTQQVSHDLVGSKTANWTSVENTARE
 SLTKALTQILTPGVSVDLLREIQSKRSKKDEEGKCDPYVFSIVGVNGVGKSTNLSKLAFW
 LLQNNFKVLIVACDTFRSGAVEQLRVHVENLAQLMDDSHVRGSKNKRKGTGNDYVELFEA
 GYGGSDLVTIKAKQAIKYSRDQNFIVLMDTAGRRHNDPTLMSPLKSPADQAKPKIIMV
 GEALVGTDSVQQAKNFNDAFGKGRNLDFFIISKCDTVGEMLGTVMNMVYATGIPILFVG
 GQTYTDLRLTSVKWAVNTLMS

SEQ ID NO: 100

YDR497C

>sp|P30605|ITR1_YEAST Myo-inositol transporter 1 OS = *Saccharomyces*
cerevisiae (strain ATCC 204508 / S288c) GN = ITR1 PE = 1 SV = 2
 MGIHTPYLTSTKTSQNVGDVAGNADSVFNEHDSPSKRGKITLESHEIQRAPASDDEDR
 IQIKPVNDEDDTSVMITFNQSLSPFIITLTFVASISGPMFGYDTGYISSALISIGTDLDH
 KVLTYGEKEIYTAATSLGALITSIFAGTAADIFGRKRCMLGNSLMFVIGAILQVSAHTFW
 QMAVGRLIMFGVGLGSLIAPLFISEIAPKMIRGRLTVINSLWLTLGGQLVAYGCGAGLNy
 VNNGWRILVGLSLIPTAVQFTCLCFLPDTPRYVVMKGDARATEVLKRSYTDTSSEIIER
 KVEELVTLNQSIGPNVPEKVWNTIKELHTVPSNLRALII GCGLQAIQQFTGWNSLMYFS
 GTIFETVGFKNSSAVSIIVSGTNFIFTLVAFPSIDKIGRRTILLIGLPGMTMALVVCISIA
 FHFLGIKPDGAVAVVVSSGFSWGIVII VFII VFAAFYALGIGTVPWQQSELPQNVIRGI
 GTSYATATNWAGSLVIASFTLTMQNITPAGTFAFFAGLSCLSTIFCYFCYPELSGLELE
 EVQTLILKDGFNISKALAKKRKQQVARVHELKYEPTQBEIIEDI

TABLE 14-continued

Sequences disclosed herein.

SEQ ID NO: 101

YEL006W

>sp|P39953|YEA6_YEAST Mitochondrial nicotinamide adenine dinucleotide transporter 2 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YEA6 PE = 1 SV = 1
 MNNGNKNTLENSKNASLANGNYAIPTKLNRLKKNADPRVAAISGALSGALSAMLVCPFD
 VAKTRLQAQGLQNMTHQSQHYKGFFGTATIFKDEGAAGLYKGLQPTVLGYIPTLMIYFS
 VYDFCRKYSVDIFPHSPFLSNASSAITAGAISTVATNPWVVKTRMLQGTGIGKYSTHYK
 GTIDTFRKIIQQEGAKALYAGLVPALLGMLNVAIQFPLYENLKIRFGYSESTDVSTDVTS
 SNFQKLILASMLSKMVASTVTYPHEILRTRMQLKSDLPNTVQRHLLPLIKITYRQEGFAG
 FYSGFATNLVRTVPAAVVTLVSFEYSKKYLTTFQ

SEQ ID NO: 102

YEL027W

>sp|P25515|VATL1_YEAST V-type proton ATPase subunit c OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = VMA3 PE = 1 SV = 1
 MTELCPVYAPFFGAIGCASAIIFTSLGAAYGTAKSGVGICATCVLRPDLLFKNIVPVIMA
 GIIAIYGLVSVLVYCYSLGQKQALYTGFIQLGAGLSVGLSGLAAGFAIGVGDAGVRGSS
 QQPRLFVGMILILIFAENVGLYGLIVALLNSRATQDVVC

SEQ ID NO: 103

YEL065W

>sp|P39980|SIT1_YEAST Siderophore iron transporter 1 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = SIT1 PE = 3 SV = 1
 MDPGIANHTLPEEFEEVVPEMLEKEVGAKVDVKPTLTSSPAPSYIELIDPGVHNIEIY
 AEMYNRPITYRVALFFSLFLIAYAYGLDGNIRYTFQAYATSSYSQHSLLSTVNCIKTVIAA
 VGQIFFARLSDFGRFSTMIVSIIFYSMGTIIESQAVNITRAVGCGCYQLGLTGIIILIL
 EVIASDFSNLNRLLALFIPALPFIINTWISGNVTSIDANWKKWIGMWAFILPLACIPL
 GICMLHMRYLARKHAKDRLKPEFEALNKLKWSFCIDIAFWKLDIIGMLLITVFFGCVLV
 PFTLAGGLKEEWKTAHIIVPEVIGWVVVLPLYMLWEIKYSRHLPTPWLIDQDRGIFFALL
 IAFFINFNWYMQGDYMYTVLVVAVHESIKSATRITSLYSFVSVIVGTILGFILIKVRATK
 PFIIFGISCWIVSGFLLVHYRGDSGAHSGIIGSLCLLGFGAGSFTYVTVQASIQASAKTHA
 RMAVVTSLYLATYNIIGSAFGSSVSGAVWTNLPKEISKRI SDPTLAAQAYGETTFITTY
 TWGTPERIALVMSYRYVQKILCIIGLVFCFPLLGCAFMRLRNHKLTDSTIALEGNHLESKN
 TFEIEEKEESFLKNKFFTHFTSSSKDRKD

SEQ ID NO: 104

YER019C-A

>sp|P52871|SC6B2_YEAST Protein transport protein SBH2 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = SBH2 PE = 1 SV = 1
 MAASVPPGGQRILQKRRQAQSIKEKQAKQTPPTSTRQAGYGGSSSSILKLYTDEANGFRVD
 SLVVLFSLVGFIFSVIALHLLTKFTHII

SEQ ID NO: 105

YER053C

>sp|P40035|PIC2_YEAST Mitochondrial phosphate carrier protein 2 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = PIC2 PE = 1 SV = 1
 MESNKQPRKIQLYTKFYTCTLGIIACGPTHSSITPLDLVKCRLQVNPKLYTSNLQGF
 RKIIANEGWKKVYTGFGATFVGYSLQAGKYGGEYFKHLYSSWLSPGVTVYLMASATAE
 FLADIMLCPEFAIKVKQQTTPPPFCNNVVDGWKKMYAESGGMKAFYKGIIVPLWCRQIPYT
 MCKFTSFEKIVQKIYSVLPPKKKEEMNALQQISVSVGGYLAGILCAAVSHPADVMVSKIN
 SERKANESMSVASKRIYQKIGFTGLWNGLMVRIVMIGTLTSFQWLIYDSFKAYVGLPTTG

SEQ ID NO: 106

YER119C

>sp|P40074|AVT6_YEAST Vacuolar amino acid transporter 6 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = AVT6 PE = 1 SV = 1
 MVASIRSGVLTLLHTACGAGILAMPYAFKPFGLIPGVIMIVLCGACAMQSLFIQARVAKY
 VPQGRASFALTRLINPNLGI VFDLAIKCFGVGVSYMIVVGLDMPQIMSVWTRNAWLL
 NRNVQISLIMLFFVAPLSFLKLNLSRLYASMAISSVAYLCVLVLLHYVAPSDELRLKG
 RISYLLPPQSHDLNVLNLTLPFVFAITCHNMFSIINEQRSSRFHEVMKIPLIAISLALI
 LYIATGCAGYLTFGDNIIIGNIIMLYPQAVSSTIGRIAVLLVMLAFPLQCHPARASIHQI
 LQHFAEENVISATSADPTVATESSPILRDSLDLNEVIEESIYQPKETPLRGKSFIV
 ITCSILVASYLVAISVSLARVLAVGATGSTSISFILPGLFGYKLIGTEHKTAVPLTTK
 IFKYTGLLLFIWGLIIMITCLTAALKLN

TABLE 14-continued

Sequences disclosed herein.

SEQ ID NO: 107

YFL028C

>sp|P43569|CAF16_YEAST CCR4-associated factor 16 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = CAF16 PE=1 SV=1
MVSQFAIEVRNLTYPKKESSDPSVVDINLQIPWNTSLVVGANGAGKSTLLKLLSGKHLCLD
GKILVNLDPFSPLSMNQVDDDESVEDSTNYQTYYLGTVEWCHMSIINRDIQVLELLK
SIGFDHFRERGERLVRILIDVVRWRMRLSDGQKRRVQLAMGLLKPWRVLLDEVTVLDD
VIARARLLEFLKWTETRRCSVVYATHIFDGLAKWPNQVYHMKSGKIVDNLQYQKDVESF
EVVNAKVNQVAFENDNNKVVISKVNSLHPLALEWLKRDNQIPDKEIGI

SEQ ID NO: 108

YFR045W

>sp|P43617|YFL5_YEAST Uncharacterized mitochondrial carrier YFR045W
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YFR045W
PE = 1 SV = 3
MANQNSDLYKQITAGSVAAPVQTTMTYPFEYLKTGLQLQPKGTAFEIIIPQIKSYFVGC
SALNVAAPGKTIILRFVTFDKLCHSLNNIDNNDNFQRLTGYNLLIAGTLTGIVESLFIFP
ENIKTTLIQSAMIDHKKLEKNQPVVNAKATPHKVATKSTPVARIEKLLPAVKHMYQTRGP
AAVQGTATATIFRQIANTSIQFTAYTAFKRLQARNDKASSVITGLATSFTLVAMTQPID
VVKTRMMSQNAKTEYKNTLNCMYRIFVQEGMATFWKSGIFRPMKVGISGGLTFTVYEQVS
LLGFSSRS

SEQ ID NO: 109

YGL084C

>sp|P53154|GUP1_YEAST Glycerol uptake protein 1 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = GUP1 PE = 1 SV = 1
MSLISILSPLITSEGLDSRIKPSPKKDASTTTKPSLWKTTEFKFYIAFLVVPLMFYAG
LQASSPENPNYARYERLLSQGWLFGKVDNDSQYRFFRDNFALLSVLMLVHTSIKRIVL
YSTNITKLRFDLIFGLIFLVAAGVNSIRILAHMLILYIAHVLKNFRRIATISIWYIGI
STLFINDNFRAYPPGNICSFSLPLDHWYRGIIIPRDVFFNFLLRVLSYNLDFLERWENL
QKKKSPSYESKEAKSAILLNERARLTAHPIDQYSLMNYIAYVYTYPLFIAGPIITFNDY
VYQSKHTLPSINFKFIFYAVRFVIALLSMEFILHFLHVVAISKTKAWENDTPFQISMIG
LFNLNI IWLKLLIPWRLFRLWALLDGDITPENMIRCVDNVSSLAFWRAWHRSYNKWVVR
YIYIPLGSGKNRVLTSLAVFSFVAIWHDIELKLLWGLVIVLFLLEIFATQIFSHYTD
AVYRHVCAVGAVFNIVWMMIANLFGFCLGSDGTTKLLSDMFTVSGFKFVILASVSLFIA
VQIMFEIREEEKRHGIYKLC

SEQ ID NO: 110

YGL104C

>sp|P53142|VPS73_YEAST Vacuolar protein sorting-associated protein 73 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = VPS73
PE = 1 SV = 1
MNRILSSASLLSNVSMPRQNKHKITKALCYAIVASIGSIQGYHLSELNAPQQVLSCE
FDIPMEGYPPYDRTWLGRGKYKQCIPLNDEQIGIVTSVFCIGGILGSYFATSLANIYGRKF
SSLINCLNIYVGLIIIFNSNSYRGLIIGRILVIGISGSLVILPLFIKEVAPSGWEGLLG
SMTQICIRLGVLLTQGIAPLTDSYRWRWILFGSPLIIVLNFMMFIVDESPKWLALHGR
VTDALSLCKLRGVTFDEAAQEIQDWQLQIESGDPLIEPTTNSISGNSLWKYLRDRTN
VKSRHVITVLLFGQFQCGINSIVLYGTKIISQLYPQHAIRINFFISMVNVLTIVLSLLI
HSLPRKPLLMSTVLVSVTAFIMGIAMNHNKMNLLIVFSFIYMGVFTMGLNPLPFIMRE
VSKPQDMVLAQRYGTICNVVGTFTIAYTFPIIHDLVLSGYVFIIFAIIACSI SAFIWKKVP
ETKRSG

SEQ ID NO: 111

YGL114W

>sp|P53134|YGL4_YEAST Putative oligopeptide transporter YGL114W
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YGL114W
PE = 1 SV = 1
MPQSTPSQEVQRVPWDNKPALKQITLRATIAGIAGSLVLTSNFQFGLQTGWVSMMSLPS
ALLACAFFKNWPLIFPNDRPFSDEVNVVQSMVAVGTGPLAFGVGVIPAIEKFLTND
ESGGLREQQQSFTFRELLIWSTALAFFGIFFAVPLRKQVIVREKLFPFSGSATAFLISVL
NGTEILQEVSKSELEMRQRLNECPEVLQPNRDPPEADYLMNSSHSELGDTATSDQGS
SILSTGSENRYRANI ILLKTFVSSLYTMVSYFVPVIRSIPVFGKYLNNYLWNFQPSA
YIGQGIIMGLPTVSYMLIGCFLGWGLAPLARYKRWVPPDADVHDWEQVQGWILWSSLS
IMVADSVVAFIVVTVKSVKFIIDDKAALLNNI IDDTFQSMLEEEERAINSSRRNTYVD
GRQDTRVLVSRDNEIEVDSKHLVRYTTVISGCLVSSIICIVSIIYLFQIPIYAIITA
LILALFLSILGIRALGETDLNPVSGIGKISQLIFAFIIPRDRPGSVLMNVVSGGIAEASA
QQAGDLMDLKTGHLGLASPRQAQFCAQLIGACWSIILSSFMVLCYNKVYSIPSEQFRIPT
AVVWIDCARLVGKGLPKALECSMILGVIFAVLSLRNTYRDYGYGWILYIPSGVAVGV
GIFNSPSTFIARFIGGWASHFWLKNHRGDLNAKTMIVFSSGLVLGEGIFSVINMLFICL
NVPHY

TABLE 14-continued

Sequences disclosed herein.

SEQ ID NO: 112
YGL167C
>sp|P13586|ATC1_YEAST Calcium-transporting ATPase 1 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = PMR1 PE = 1 SV = 1
MSDNPFNASLLDEDSNREREILDATAEALS KPSPSLEYCTLSVDEALEKLDTDKNGGLRS
SNEANNRRSLYGPNEITVEDDES LFKKFLSNFIEDRMILLIGSAVVSFLFMGNIDDAVSI
TLAIFIVVTGFGVQYRSEKSLAENKLVPAECHLMRCGQESHVLASTLVPGDLVHFRIG
DRIPADIRII EAIDLSIDESNLGTGENEPVHKTSQTIEKSSFPNDQPNISIVPISERSCIAYM
GTLVKEGHGKGIIVGTGTNTSFGAVFEMMNNIEKPKTLPQLTMDKLGKDL SLVSFVIGM
ICLVGI IQGRSWLEMFQISVSLAVAAI PEGLP IIVTVTLALGVLRMAKRKAIVRRLPSVE
TLGSSVNVICSDKTGTLTNSHMTVSKLWC LDSMSNKLNVLSLDKNKKT KNSGNLKNYLTE
DVRETLTIGNLCNNASFQEHAI FLGNPTDVALLEQLANFEMPDIRNTVQKVQELPFNSK
RKLMA TKILNPVDNKCTVYVKGAFERILEYSTSYLKS GKKTEKLEAQKATINECANSM
ASEGLRVPGFAKLT LSDSSTPLTEDLIKDLTFTGLIGMNDPPRPNVKFAIEQLQGGVHI
IMITGDSSENTAVNIAKQIGIPVIDPKLSVLSGDKLDEMSDDQLANVIDHVNI FARATPEH
KLNIVRALRKRGDVVAMTGDGVNDAPALKLSDIGVSMGRIGTDVAKEASDMVLTDDDFST
ILTAIEEGKGI FNNI QNFLT FQLSTSVAA LSLVALSTAFKLPNPLNAMI LWINILMDGP
PAQSLGVEPVDHEVMKKPPRKRTDKILTHDVMKRLTTAACIIVGTVYI FVKEMAEDGKV
TARDTMTFTCFVFFDMFNALACRHNTKSI FEIGFFT NKMFN YAVGLSLLGQMCAIYIPF
FQSIFKTEKLGISDILL LLISSSVFIVDELRLKLWTRKKNEDSTYFSNV

SEQ ID NO: 113
YGR257C
>sp|P53320|MTM1_YEAST Mitochondrial carrier protein MTM1
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = MTM1
PE = 1 SV = 1
MSDRNTSNSLTLKERMLSAGAGSVLTS LILTPMDVVRI RLQQQMIPDCSCDGAAEVPNA
VSSGSKMKTFTTNVGGQNLNNAKI FWESACFQELHCKNSSLKFNGLTLEAFTKIASVEGITS
LWRGISTLTLMAIPANMVYFSGY EYIRDVSP IASTYPTLNLPLFCGAIARVFAATSIAPLE
LVKTKLQSI PRSSKSTKTWMMVKDLLNETRQEMKMVGPSRALFKGLEITLWRDVPFSAIY
WSSYELCKERLWLDSTRFASKDANWVHFINSFASGCISGMIAAICTHPFDVGKTRWQISM
MNSNDPKGGRSRNMFKFLETIWRTEGLAALYTGLAARVIRKIRPSCAIMISSYEISKVVF
GNKLHQ

SEQ ID NO: 114
YHL035C
>sp|P38735|VMR1_YEAST ABC transporter ATP-binding protein/permease
VMR1 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)
GN = VMR1 PE = 2 SV = 1
MGTDPLIIRNNGSFWEVDDFTRLGR TQLLSYYLPLAIIASIGIFALCRSGLSRYVRSAC
DLVNEYLFAGAEERKEDNSIERLLRNSNTQANYVNVKKQGRILKLRHFDITIDVKQIDA
KNHGGLTFSRPSTSDHLRKSSEIVLMSLQIIGLSFLRVTKINIELTNRDVTLLFWLIL
LSLSILRVYKSTNLWAICTAHTTIWISTWIPRSVYIGNIDVPSQIFYIFEVITST
LQPIKLTSP IKDSSIIYVRDHTSPSREHSSILSCITWSWITNFIWEAQNTIKLKDI
WGLSMEDYSIFILKGFTRRNKHINNLTLALFESFKTYLLIGMLWVLVNSIVNLLPTILMK
RPLEIVDNPNRSSSCMNLAWLYIIGMFICRLTLAICNSQGGQFVSDKICLRIRAILIGIY
AKGLRRRLFTSPKTSDDSDSISANLGTIINLISIDSPKVS ELANYLYVTQAVIMIIVVV
GLLFNFLGVSAFAGISIIILVMFPLNFLLANLLGKFKQKTLKCTDQRI SKLNECLQNIRIV
KYFAWERNI INEIKSIRQKELRSL LKSLVWSVTSFLWVFTPTLVGTVTFICTFVQHED
LNAPLAF T TLLSFTLLKTPLDQLSNMLSFINQSKVSLKRISDFLRMDTEKYNQLTISPD
KNKIEFKNATLTWNENDSDMNAFKL CGLNIFQIGKLNLI LGSTGSGKSALLGLLGELN
LISGSIIVPSLEPKHDLIPDCEGLTNSFAYCSQS AWLLNDTVKNNIIFDNFYNE DRYNKV
IDACGLKRDLEILPAGDLTEIGEGKITLSGGQKQRI SLARAVYSSAKHVLLDDCLS AVDS
HTAVWIYENCITGPLMKNR TCILVTHNVSLTLRNAHFAIVLENGKVKNQGTITELQSKGL
FKEKYVQLSSRDSINEKNANRLKAPRKND SQKIEPV TENINFDANFVNDGQLIEEEKSN
GAISPDVYKWLKFFGGFKALTALFALYIT AQILFISQSWIRHWVNDTNVRINAPGFAM
DTLPLKGMTDSSKNKHNAFYLYTVYFLIGI IQAMLGGFKTM TFLSGMRASRKIFNNLLD
LVLHAQIRFFVTPVGRIMNRFSKDIEGV DQELI PYLEVTFCLIQCASII FLITVITPR
FLTVAIVFVLYFFVGKWL TASRELKR LDSITKSPIQHFS ETLVGVC TIRAFGDERRF
ILENMNKIDQNNRAFFYLSVTWKFSFRVDMIGAFIVLASGSFILLN IANIDSGLAGISL
TYAIFLTDGALWLVRLYSTFEMNMNSVERLKEYSSI EQENYLGHDEGRILLN EPSPWKD
GEIEIENLSLRYPANLPPVIRNV SFKVPDQSKIGIVGR TGAGKSTIITALFRLL EPITGC
IKIDGQDISKIDLVTLRRSIT IIPQDPILFAGTIKSNVDPYDEYDEKKIFKALSQVNLIS
SHEPEEVLNS EERFNSTHNKPLNLHTEIAEGGLNLSQGERQLLF IARSLLEPKIILLDE
ATSSIDYSDHLIQGIRSEFNKSTILTIAHRLRSVIDYDRIIVMDAGEVK EYDRPSELL
KDERGIFYSMCRDSSGGLLELLKQIAKQSSKMMK

SEQ ID NO: 115
YHL036W
>sp|P38734|MUP3_YEAST Low-affinity methionine permease
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = MUP3
PE = 1 SV = 1
MEPLLFNSGKANPSQDV FIDVEVGDIITKYGSTNTG SFSSMDTVEAQAIKAETARFMEVP
QGRHLGVFSTVVL FVSIRMGSGIFAVPSVILLNTGGNKLIYFAI WVFSAAIAPAGLYIFL

TABLE 14-continued

Sequences disclosed herein.

EFGSWIPKSGGRKNFLERSFERPRLLISVVFSCYSVLTGYALTGSIVFGKYVLSAFGVT
 DSWSKYVSISFIIFAVLIHGVSVRHGVFIQNALGGLKLIMIVLMCFAGLYTLFFYKSTGQ
 VAWDLPTQVEKDSLLSVSSIAATAFISSFFCFSGWDTVHTVTSEIKNPVKTLKVSGLPLSL
 IICFVCYTMNMNAVLYKVLTYEEIVSAGPLVGSVLFTEKLFGRVGGKFIASFIAISAASNI
 LVVIYSISRNVQEIPEGYLPFSIHMSKNWPFDAPLPSISLCGFITIAWILILPKEGESF
 NYLVSMDDGYGNQFFLLVAIGLFIWRFKHKNEVPEIRASTFGVLAITTLSLYMLMAPFFA
 DPDLNRVGFLLPPYQIMSLLVIVACFFFWLVKFVLLPKFFHYKLLPKITYLHDLGLIVTEWV
 KKPCLC

SEQ ID NO: 116

YHR002W

>sp|P38702|LEU5_YEAST Mitochondrial carrier protein LEU5
 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = LEU5
 PE = 3 SV = 1
 MTRDSPDSNDYVKHINKNTTQKTSFDRNSFDYIVRSGLAGGISGCAKTLIAPLDRIKIL
 FQTSNPHYTKYTGSLIGLVEAAKHIWINDGVRGFFQGHSAATLLRIFPYAAVKFVAYEQIR
 NTLIPSEKFEFESHWRRLVSGSLAGLCSVFITYPLDLVRVRLAYETEHKRVKLGRIIKKIYK
 EPASATLTKNDYIPNWFCHWCNFYRGYVPTVLGMIPYAGVSFFAHDLLHDLKSPFFAPY
 SVLELSEDEDELERVQKKQRRLRTWAEILISGGLAGMASQTAAYPFEIIRRLQVSALSPK
 TMYDHKQSQSISEIAHIIKFERGVRGFFVGLSIGYIKVTPMVACSFNNRMKWNFGI

SEQ ID NO: 117

YHR096C

>sp|P38695|HXT5_YEAST Probable glucose transporter HXT5
 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = HXT5
 PE = 1 SV = 1
 MSELNAHQGLEGSATVSTNSNSYNEKSGNSTAPGTAGYNDNLAQAKPVSSYISHEGPP
 KDELEELQKEVDKQLEKKSDDLFPVSVCCLMVAPGGFVFGWDTGTISGFVRQTDFFIRRF
 GSTRANGTTLSDVRTGLMVSIFNIGCAIGGIVLSKLGDMYGRKIGLMTVVVIYSIGII
 QIASIDKHYQYFIGRIISGLGVGGITVLAPMLISEVSPKQLRGTLVSCYQLMITFGIFLG
 YCTNFGTKNYSNSVQWRVPLGLCFAWSIFMIVGMTFVPESPRYLVEVGKIEAKRSLARA
 NKTTEDSLPLVTLEMENYQSSIEAERLAGSASWGLVLTGKPMFRRTLGMMMIQSLQQLTG
 DNYFFYYGTTIFQAVGLEDSFETAIVLGVNVFVSTFFSLYTVDRFGRNCLLWGCVMIC
 CYVVYASVGVTRLWPNGQDQPSKSGAGNCMIVFACFYIFCFATTWAPVAVVLISESYPLR
 VRGKAMSIASACNWIWGLISFFTPFITSAINFYGYVFMGCMVFAYFYVFFVFPETKGL
 TLEEVNEMYENNVLPWKSTKWIPPSRRTTDYDLDATRNDPRPFYKRMPTKEK

SEQ ID NO: 118

YIL006W

>sp|P40556|YIA6_YEAST Mitochondrial nicotinamide adenine
 dinucleotide transporter 1 OS = *Saccharomyces cerevisiae* (strain ATCC
 204508 / S288c) GN = YIA6 PE = 1 SV = 1
 MTQTDNPVNCGLLPEQQYCSADHEEPLLLHHEQLIFPDHSSQLSSADIIEPIKMNSSTE
 SIIGTTLRKKWVPLSSTQITALSAGAFAGFLSGVAVCPDVDVAKTRLQAQGLQTRFENPYR
 GIMGTLSTIVRDEGRGLYKGLVPIVLGYFPTWMIYFSVYEFSSKKFFHGFQDFDFAQS
 CAAITAGAASTTLTNPIVWVKTRLMLQSNLGEHPHGYKGTDFDAFRKLFYQEGFKALYAGL
 VPSLLGLFHFVAIHFFIYEDLKVRFHCYSRENNNTNSINLQRLIMASSVSKMIASAVTYPHE
 ILRTRMQLKSDIPDSIQRLFLPLIKATYAQEGKGFYSGFTTNLVRTIPASAITLVSPFEY
 FRNRLNENISTMVI

SEQ ID NO: 119

YIL120W

>sp|P40475|QDR1_YEAST Quinidine resistance protein 1
 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = QDR1
 PE = 1 SV = 1
 MTKQQTSMVRNASIAKEEREGSDNNNVDRSSSDAISDNDNAERSNSHSEIDNESNFMV
 SRFSHKQKMLLVVQCAFTGFFSTVAGSIYYPVLTIIERKFNITEELANVTIVVYFIFQGV
 APSIMGGLADTFGRRPVILWAILAYFCACIGLACAHNYAQILALRCLQAAGISPVIAINS
 GIMGDVTTKVERGGYVGLVAGFQVVGTAFGALIGAGLSSKKGWRAIFWFLAIGSGICLVF
 STLLMPETKRTLGVNGSVTPRSFLNRSLLILHVGSVKKTLLHLDLDDPETLEPRTSVDLAP
 LKILHIREIDILLSIAGLQFSTWTHQTALTIVLSKKYNLSVAKIGLCFLPAGISTLTSI
 ISAGRYLWNSYRTRKVKYNRWIKEQELQMEKYKGDKNKVAELIHSNSHYAFNLVEARLH
 PAFVTLLLSSIGFTAFGWCISVKTPLAAVLCTSAFASLFSNCILTFSTTLIVDLFPKAS
 TATGCLNLFRCLLSAIFIAALTKMVEKMRVGGVFTFLSAITSSSSLLLFYLLKNGKQLSF
 DRI RANDKSAGRSVGKNSEKST

SEQ ID NO: 120

YIL121W

>sp|P40474|QDR2_YEAST Quinidine resistance protein 2
 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = QDR2
 PE = 1 SV = 1
 MAGATSSIIRENDFEDELAESMQSYNRETADKLALTRTESVKPEEITAPPHSRFSRSFK
 TVLIAQCAFTGFFSTIAGAIYYPVLSVIERKFDIDEELVNVTVVVYFVQGLAPTFMGGF
 ADSLGRRPVVLVAIVVIYFGACIGLACAQTYAQIIVLRCLQAAGISPVIAINSIMGDVTT
 RAERGGYVGYVAGFQVLGSAGFALIGAGLSSRWGWAIFWFLAIGSGICFLASFLILPET

TABLE 14-continued

Sequences disclosed herein.

KRNISGNGSVTPKSYLNRAPILVLPTRKSLHLDNPDYETLELPTQLNLLAPPFKILKAYE
 ICILMLVAGLQFAMYTTHLTALSTALSQYHLTVAKVGLCYLPSGICTLCSIVIAGRYLN
 WNYRRLKYYQNWLGKKRSKLEEHNDNLNVQRIIENDPKYTFNIFKARLQPAFVTLLL
 SSSGFCAYGWCITVKAPLAAVLCMSGFASLFSNCILTFTSTTLIVDLFPKTSTATGCLNL
 FRCILSAVFIAALSVMVEKMKFGGVFTFLGALTSSSSILLFILLRKKGKELAFKRKKQELG
 VN

SEQ ID NO: 121
 YIL166C
 >sp|P40445|YIQ6_YEAST Uncharacterized transporter YIL166C
 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YIL166C
 PE = 1 SV = 1
 MSVQKEEYDIVEKAQLSVSAESLTSDESISHNPFDDFHKAERWRKVYESSGYEGLSKFD
 PEFTWIKDEEKKLVKMDLKIPLWVFIMFAFLDLIRKNIARAVSDNFIVDLKMTNDYNL
 GQTVVLVIFLASELPGNLLSKRFGPERVIPVQIVLWSVICITQAGLKNRGQFIATRCLLG
 MVQGGFIPDNILYLSYYTGAELTFRLSFFWCAPLPLFQILGSLASGIIEMRGIHNLGAW
 QYLFIIIEGFLSLSVGASFYLMRRGPTQTGESAFHKGKSLFTEYEKIMVNRILRDDPSK
 GDMSNRQPVTFKEILYTLTEPDLWPLFIQGITAFISLQTVGSYLSLILKSLNYSTFLSNI
 LAIPGQALLINLPLAALLSRKLKEKSLCVGIANVWVLPFIVSLVALPTDINPWIKYILL
 TGILGLPYTHSILAGWVSEISNSVRSRTVGTALYNMSAQVGAIASNMVRNDDKPYTRG
 NKILLGFCFNICMAVATKFYIISRNYKDRKWNMTKEEQINYLDTTKDKGMKRLDYRF
 IH

SEQ ID NO: 122
 YJL133W
 >sp|P10566|MRS3_YEAST Mitochondrial RNA-splicing protein MRS3
 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = MRS3
 PE = 1 SV = 4
 MVENSSNNSTRPIPAIPMDLPDYALPHTAPLYHQLIAGAFAGIMEHSVMFPIDALKTR
 IQSANAKSLSAKNMLSQISHISTSEGTALWKGVSILGAGPAHAVYFGTYEFCKKNLI
 DSSDTQTHHPKTAISGACATTASDALMNPFDTIKQRIQLNTSASVWQTTKQIYQSEGLA
 AFYYSYPTTLVMNIPFAAFNFVIESSTKFLNPSNEYNPLIHCLGSGISGSTCAAITTPL
 DCIKTVLQIRGSQTVSLEIMRKADTFSKAASAIYQVYGWKGFWRGWKPRIVANMPATAIS
 WTAYECAKHFLMTY

SEQ ID NO: 123
 YJL219W
 >sp|P40885|HXT9_YEAST Hexose transporter HXT9 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = HXT9 PE = 1 SV = 1
 MSGVNNTSANDLSTTESNSNVANAPSVKTEHNDSKNSLNLDATEPPIDLPQKPLSAYTT
 VAILCLMIAFGGFI PGWDTGTISGFVNLSDFIRRFQKNDKGTYYLSKVRMGLIVSIFNI
 GCAIGGIYLSKVGDYIGRRIGLITVTAIYVVGILIQITSINKWYQYFIGRIISGLGVGGI
 AVLSPMLISEVAPKQIRGTLVQLYQLMCTMGIFLGYCTNYGKKNYHNATQWRVGLGLCFA
 WTTFMVSGMMFVPESPRYLIEVGKDEEAKRSLSKSNKVSVDPAALAEYDTIKAGIELEK
 LAGNASWSELSTTKTKVQFQVLMGVMIQSLQQLTGDNYFFYGTTFKSVGLKDSFQTSI
 IIGVNVFSSFIAYTIERFGRRTCLLWGAASMLCCFAVFASVGVTKLWPQGS SHQDITS
 QGAGNCMI VFTMFFIFSPATTWAGGCYVIVSETPLRVKSRGMAIATAANWVGFLISFF
 TPFITGAINFYGYVFLGCLVFAYFYVFFVPETKGLTLEEVNTMWLEGVPAWKSASWVP
 PERRTADYDADAIDHDDRPIYKRFSS

SEQ ID NO: 124
 YKL016C
 >sp|P30902|ATP7_YEAST ATP synthase subunit d, mitochondrial
 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN=ATP7
 PE = 1 SV = 2
 MSLAKSAANKLDWAKVISSLRITGSTATQLSSFKKRNDEARRQLELQSQPTEVDFSHYR
 SVLKNTSVIDKIESYVKQYKPKIDASKQLQVIESFEKHAMTNAKETESLVSKEKLDLQS
 TLDNIQSARPFDELTVDDLTKIKPEIDAKVEEMVKKGKWDVPGYKDRFGNLNV

SEQ ID NO: 125
 YKL050C
 >sp|P35736|YKF0_YEAST Uncharacterized protein YKL050C
 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YKL050C
 PE = 1 SV = 1
 MSLISALQTTDVESVQTSPEQITERKAVRVSTLQESLHSSMHRAAPETPRISNSVHKL
 KTIYSTYQSQGQPLSKEAIFRAKQKYGILNTPANYKTLGLGDSKSESVDLAARLASKRTK
 VSPDDCVETAIEQKARGEAFKVTFSKIPLTPPEDVPITVNLGLKGRDFLTRLAQKALA
 FSPSLDNMKGTSDDSSSVKKRFSGAPIGNEFDANLVNPQHPAGFKSLDLKVLDAERR
 AISRVNDRLYPQKVNFKNLQSSDQSGVSKANKEVFKGTLEKLEHSAEQFLES HAGNER
 QRLSDQQYMCAGAADAVKDLDPKTLEDPDFAAREAQKLYIKQVASPVVLNEAQKLANR
 KLQIDSRDVTYMLLFGNQAYNKLAVNIALQHYSVKQEEKKKIYLGGLWMTPEEVNAVAK
 KLISPVVNEIDERASRQRDVKDIERRSRVLDQYEDGNSMERAKEQNDGQLLLAMASKQ
 QQEKAAKAEEGQRYDQFVQKMNILKQKEKELENARENRENRLNELQERLSKNLSGEND
 BLNDWNDACERDLKNSSIEHYAVRSHFDNLGNSERGYDELEERSKIQVEIERLVASIA
 EHKTAIHGFGETADAGGAIPAVQKQKI PTRKDLLDATVNDPLVISAEMAKEEAEATEEC

Sequences disclosed herein.

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>sp|P19145|GAP1_YEAST General amino-acid permease GAP1
OS = Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN = GAP1
PE = 1 SV = 2
MSNTSSYEKNNPNDNLKHNGITIDSEFLTQEPITIPSNGSAVSIDETGSGSKWQDFKDSFK
RVKPIEDVDPNLSAEKVAIITAQPTLKHLLNRRHLQMIAGGATGGLLVGSGGTAIRTGG
PASLLIGWPGSGTGMIIYAMVMALGELAVIPISGSGFTTYATRFIDESFGYNNFNMYMLQLWL
VVLPLEIVSASITVNFWGTDPKYRQDGFVALFWLAIVIIINMPGVKGYGEAEFVFSFIKVIT
VVGFIILIGLNLSCGGGTGGYIGGKYNHDPGAFAGDTPGAKFKVCSVFVTAASFSPAGE
LVGLAAGESVEPRKSPGAAKOVFWRITLFLYLLSLMLGLLVPVNDKSLTGAASVDAAAS
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TABLE 14-continued

Sequences disclosed herein.

PFVIAIKTHGIKGLPSVVNVVILIAVLSVGNSAIYACSRMTVALAEQRFLPEIFS YVDRK
GRPLVGI AVTSAFGLIAFVAASKKEGEVFNWLLALSLGLSSLTWGGICICIRFRKALAA
QGRGLDELSEFKSPTGVWGSYWGLFMVIMFIAQFYVAVFPVGDSPSAEGFFEAYLSFPLV
MVMYIGHKIYKRNWKLFI PAEKMDIDTGRREVDDLKQEI AEEKAIMATKPRWYRIWNF
WC

SEQ ID NO: 130

YLR411W

>sp|Q06686|CTR3_YEAST Copper transport protein CTR3 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = CTR3 PE = 1 SV = 1
NMNMGSSSTAACKATCKISMLWNWYTIDTCFIARSWRNDTKGKFAGSCIGCFALVVVAQW
LTRFRSQPDVELLKRQIKHLASYSPEEYVVKCGEEDAKSDIEELQGFPYNEPSWKTTLIS
LQKSFYISFYVWGPRLNEPEDDLLKKVLSCTLTITPVDLYPTFLDHMIRVTIFVLQWGL
SYIIMLLPMYNYGIIISCLIGAIVGRFIFCYEPLGSLGANGSAQGTVS YDKESDDRKC
L

SEQ ID NO: 131

YML038C

>sp|Q03697|YMD8_YEAST Putative nucleotide-sugar transporter YMD8
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YMD8
PE = 1 SV = 1
MNRTVFLAFVFGWYFCSIALSIYNRMWFDPKDGLGIGYPVLVTTFHQATLWLLSGIYIKL
RHKPVKNVLRKNNGFNWSFFLKFLPTAVASAGDIGLSNVSFQYVPLTIYTIKSSSIAF
VLLFGCIPKLEKPHWKLALSVIIMFVGVALMVFKPSDSTSTKNDQALVIFGSFLVLASSC
LSGLRWVYTQMLRNNPIQNTAAVEESDGLFTENEDVDNEPVDNLANKNMLENFGE
SKPHPIHTIHQLAPIMGITLTLTSLLEKPPGIFSSIFRLDTSNGGVGTETTVLSIVR
GIVLLILPGFAVFLITICEFSILEQTPVLTVSIVGIVKELLTVIFGIIILSERLSGFYNW
LGMLIIMADVCCYNYFRYKQDLLQKYHSVSTQDNRELKGFQDFEQLGSKKIAPYSISVD
LTNQEYELDMIAQNVSRSSQQV

SEQ ID NO: 132

YMR166C

>sp|Q03829|YM39_YEAST Uncharacterized mitochondrial carrier YMR166C
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YMR166C
PE-1 SV = 1
MNSWNLSSSIPIIHTPHDHPPTSEGTDPQPNNRKDDKLHKRGDSDEDLSPWIHCVVSG
GIGGKIGDSAMHSLDVTKTRQQGAPNVKKYRNMISAYRTIWLEEGVRRGLYGGYMAAMLG
SFPSAAIFPGTYEYTKRMTIEDWQINDTITHLSAGFLGDFISSFVYVPSVLKTRLQLQG
RFNNPFQSGYNYNSLNRNAIKTVIKEEGFRLFFGYKATLARDLPFSALQFAFYKFRQL
AFKIEQKQGRDGELSIPNEILTACAGGLAGIITTPMDVVKTRVQTQQPPSQSNKSYST
HPHV TNGRPAALSNSISLSLRTVYQSEGVLGFFSGVGPFRFVWTSVQSSIMLLLYQMTLRG
LSNAPPTD

SEQ ID NO: 133

YMR279C

>sp|Q03263|YM8M_YEAST Uncharacterized transporter YMR279C
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YMR279C
PE = 1 SV = 1
MFSIFKKKTSVQGTDSIDEKITVKAKDKVVSTEEDEVTTIVSSTKSTQVTNDS PWQDP
TYFSSFGKELMFIAICMLAQLLNQAGQTHALCINNVLSKSFNSEANNQAWLMASFPPLAAG
SFILISGR LGDIYGLKMLIVGYVIVVWSIISGLSKYSNSDAFFITSRAFOGVGIAFIL
PNIMGLVGHVYKVGFSFRKNIVISFIGACAPTGGMFGGLFGLIVTEDPNQWPWFYAFGI
ATFLSLMAWYSIPNNVPTNIHGLSMDWTGSALAIIGLILFNFVWNQAPIVGWDKPYIIV
LLIISVIFLVAFVYVESKYAEVPLPRAMTKNRHMIMILLAVFLGWGSFGIWTFFYVSFQ
LNLRHYSVPVWTTGGTYFVFVIFGSM AAFVAFS IKRLGPALLLCFSLMAFDAGS IMFSVLP
VEQSYWKLNFAMQAILCFGMDSLFPASSIILSDGLPMQYQGMAGSLVNTVINYSASLCG
MGGTVEHQINKSGNDLLKGYRAAVYLGVLASLGVVISVTYMLENLWNRHRKSEDRSLEA

SEQ ID NO: 134

YNL003C

>sp|P38921|PET8_YEAST Putative mitochondrial carrier protein PET8
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = PET8
PE = 1 SV = 1
MNTFFLSLLSGAAAGTSTDVFFPIDTIKTRLQAKGGFFANGGYKGIYRGLGS AVVASAP
GASLFFISYDYMVKSRPYISKLYSQGSEQLIDTTHMLSSSIGEACLVVPVPAEVVKQ
RTQVHSTNSSWQTLQSI LRNDNKEGLRKNLYRGWSTTIMREIPFICIQFPLYEYLKKTWA
KANGQSQVEPWKAICGSIAGGIAAATTPDLFLKTRMLNKTITASLGSVIRIYREEGP
AVFFSGVGPRTMWISAGGAIFLGM YETVHSLLSKSFPTAGEMRA

SEQ ID NO: 135

YNL268W

>sp|P32487|LYP1_YEAST Lysine-specific permease OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = LYP1 PE = 1 SV = 2
MGRFSNIITSNKWDEKQNNIGEQSMQELPEDQIEHEMEAIDPSNKTTPYSIDEKQYNTKK
KHGSLQGGAIADVNSITNSLTRLQVVSHETDINEDEEHAHYEDKHVKRALKQRHGMIAL

TABLE 14-continued

Sequences disclosed herein.

GGTIGTGLFVGISTPLSNAGPVGSLIAYIFMGITIVYFVTQSLGEMATFIPVISSITVFSK
 RFLSPAFGVSNNGMYWFWNIAIYAVEVSVIGQVIEYWDKVPAAWIAIFWVIITLMNFF
 PVKVYGEFEFVWASVKVLAIMGYLIYALIIVCGGSHQGPIGFRYWRNPGAWGPGIISDDK
 SEGRFLGWVSSLINAAFTYQGTELVGITAGEAANPRKTVPRAINKVFRIVLFYIMSLFF
 IGLLVYPYNDRLSASSAVIASSPFVISIQNAGTYALPDIFNAVVLITVVSAAANSNVYVGS
 RVLVSLARTGNAPKQFGYVTRQGVYPYLVGVCTAALGLLAFLVNNNANTAFNWLINISTL
 AGLCAWLFISLAHIFRMQALKHRGISRDDLPFKAKLMPYGAyyAAFFVTVIIIFIQGFQAF
 CFPKVSEFFTSYISLILLAVVFIGCQIYYKCRFIWKLEDIDIDSDRREIEAIWEDDEPK
 NLWEKFWAAVA

SEQ ID NO: 136

YNR055C

>sp|P53389|HOL1_YEAST Protein HOL1 OS = *Saccharomyces cerevisiae*
 (strain ATCC 204508 / S288c) GN = HOL1 PE = 1 SV = 1
 MDKYTNRDHPYIPGTFNIIYSSQNLENGIIYESKLKKTSSGVVLIPQPSYSFNDPLNWSS
 WRKLAHFLGMAFITAFATAATSDAGAAQDSLNEIYGISYDSMNTGAGVFLFLGIGWSTLFL
 APFANLYGRKITYIVCTTLGLFGALWFALAKRTSDTIWSQLFVGISESCAEAQVQLSLSD
 IFQHQQLGSLVLTIVYIMCTSIGTFLGPLIAGYISAFNTFRWVGWVAVIISGGLLITIIIFGC
 EETYPDRGQYMTPLTSCQSGYEDGTTLQNSDNTAVSRKRHLDAKLSTPGAMGEKGVDSL
 ETAEFVNNEEVEVTIPETRELIDGSKHLKPYPKRVAILTKATNLKGYGFKQYFKYLKIN
 LRMFLFPVWVLSGMFWGIQDVLFTLYLTQESAYEPPWNYSDFGVAIMNVPTLIGAVIG
 CICAGIVSDYFVLWMARHNRGILEAEFRLYFSIATAIIGPAGLLMFGIGTARQWPWQAIY
 VGLGVGFAGWCGSGDIAMAYLMDCCYPMVLEGMVCTAIINNTISCIFTFTCSDWLAASGT
 ENTYIALAVINFGITAFALPMYIYGRIRLWTKRWYLSVNLRDGV

SEQ ID NO: 137

YOL158C

>sp|Q08299|ENB1_YEAST Siderophore iron transporter ENB1
 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = ENB1
 PE = 1 SV = 1
 MLETDHSRNDNLDDKSTVCYSEKTDSDNVEKSTTSGLRRIDAVNKVLSYSSFTAFGVTFPS
 SLKTALLVALFLQGYCTGLGGQISQSIQTYAANSFGKHSQVGSINTVKSIVASVAVPYA
 RISDRFGRIECWIFALVLYTIGEIISAATPTFSGLFAGIIVIQQFGYSGFRLLATALTGDL
 SGLADRTFAMNIFLIPVIINTWVSGNIVSSVAGNVAPYKWRWGYGIFCIIVPISTLILVL
 PYVYAQYISWRSGKLPLPLKKEKGQTLRQTLWKFADDINLIGVILFTAFVLVLPLTIA
 GGATSKWREGHIAMIVVGGCLGFIFLIWELKFAKNPFIIPRVYLGDPITIVYALLMEFVWR
 LGLQIELEYLVTVMVAFGESTLSAQRIAQLYNFLQSCCTNIVVGIMLHFYHPKVFVAVG
 SLLGVIGMGLLYKYRVVYDGSGLIGAEIVVGIAGGMIRFPMWTLVHASTTHNEMATVG
 LLMVSYQIGDAVGASIAAGIWTQRLAKELIQLRGSSLGMAIYKSPNLVLYKKYPIGSEVRV
 QMIESYSKIQRLLIIVSISFAFNAVLCFFLRGFTVNKKQSLSAEEREKEKLKIKQQSWL
 RRVIGY

SEQ ID NO: 138

YOR100C

>sp|Q12289|CRC1_YEAST Mitochondrial carnitine carrier
 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = CRC1
 PE = 1 SV = 1
 MSSDTSLSSESLLKEESGSLTKSRPPIKSNPVRENIKSFVAGGVGVCAVFTGHPFDLIK
 VRCQNGQANSTVHAITNIIKEAKTQVKGTFLTNSVKGFYKGVIPPLLGVTPIFAVSWFGY
 DVGKKLVTFNNKQGSNELTMGQMAAGFISAIPTTLVTAPTERVKVVLQTSKGSFIQA
 AKTIVKEGGIASLFGKSLATLARDGPGSALYFASYEISKNYLNSRQPRQDAGKDEPVNIL
 NVCLAGGIAGMSMWLAVFPIDTIKTKLQASSTRQNMLSATKEIYLQRGGIKGFFPGLGPA
 LLRSFPANAATFLGVEMTHSLFKKYGI

SEQ ID NO: 139

YOR153W

>sp|P33302|PDR5_YEAST Pleiotropic ABC efflux transporter of multiple
 drugs OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)
 GN = PDR5 PE = 1 SV = 1
 MPEAKLNNNVNDVTSYSSASSSTENAADLHNYNGFDEHTEARIQKLARTLTAQSMQNSTQ
 SAPNKSDAQSFSSGVEGVNPIFSDPEAPGYDPKLPDPSNENFSSAAWKNMAHLSAADPD
 FYKPYSLGCWKNLSASGASADVAYQSTVVNIYPKILKSGLRKFQRSKETNTFQILKPM
 GCLNPGELLVLVLRPGSGCTTLLKISSNTHGFDLGADTKISYSGYSGDDIKKHFRGEVV
 YNAEADVHLPHLTVFETLVTVARLKTQPNRIKGVDRSYANHLAEVAMATYGLSHTRNTK
 VGNDIVRGVSGGERKRVSAEVSICGSKFQCWDNATRGDLSATALEFIRALKTQADISNT
 SATVAIYQCSQDAYDLFNKVCVLDGQYIYGPADKAKKYFEDMGYVCPSPQTADFLTS
 VTSPSERTLNKMDLKKGIHIPQTPKEMNDYVWVSPNYKELMKEVDQRLNNDDEASREAIK
 EAHIAKQSKRARPSPTYVSYMMQVKYLLIRNMWRLRNIGFTLFMILGNCSMALILGSM
 FFKIMKKGDTSTFYFRGSAMFFAILFNAFSSLLIFSLYEAPITEKHRTYSLYHPSADA
 FASVLSEIPSKLIIAVCFNIIIFYFLVDFRRNGGVFFYLLINIVAVFMSHLFRVCVGLT
 KTLSEAMVPASMLLLALSMTYGFAPKKKILRWSKIWIYNPLAYLFESLLINEPHGKIF
 PCAEYVPRGPAYANISSTESVCTVVGAVPGQDYVLGDDFIRGTQYQYHKDKWRGFGIGMA
 YVVFVFFVYFLCEYNAGAKQKGEILVFPFSIVKRMKKRGVLTEKNANDPENVGERSDLS
 SDRKMLQSSSEESDYGEIGLSKSEAFHWRNLCEVQIKAEITRIINNVDGWKPGTL
 TALMGASGAGKTTLLDCLAERVMTGVIITGDIIVNGIPRDKSPFISYGCQQQLHLKKTAT

TABLE 14-continued

Sequences disclosed herein.

VRESLRFSAYLRQPAEVSIEEKNRYVEEVIKILEMEKYADAVVGVAGEGLNVEQKRRLTI
 GVELTAKPKLLVFLDEPTSGLDSTQAWSICQLMKKLANHGQAILCTIHQPSAILMQEFDR
 LLFMQRGGKTVYFGDLGEGCKTMIDYFESHGAHKCPADANPAEWMLEVVGAAPGSHANQD
 YVEVWRNSEEYRAVQSELDWMERELPKKGSITAAEDKHEFSQSIIYQTKLVSIRLFQQYW
 RSPDYLWSKFLITIFNQLFIGFTFFKAGTSLQGLQNLAVFMFTVIFNPILQQYLPSFV
 QQORDLYEARERPSRTFSWISFIFAQIFVEVPWNILAGTIAYFIYYPYIGFYSNASEAGQL
 HERGALFWLFSCAFVYVVGSMGLLVISFNQVAESAANLASLLFTMSLSFCGVMTPPSAMP
 RFWIFMYRVSPITYFIQALLAVGVANVDVKADYELLEFTPPSGMTGCGYMEPYLQAKT
 GYLTDENATDTCSCFCQISTTNDYLANVNSFYSERWRNYGIFICYIAFNFIAGVFFYWLAR
 VPKNKGKLSKK

SEQ ID NO: 140

YOR271C

>sp|Q12029|FSF1_YEAST Probable mitochondrial transport protein FSF1
 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = FSF1
 PE = 1 SV = 1
 MASSVPGPIDLPESRYDLSTYWGRIHCAEISDPTMLLTTEKDLAHAREIISAYRHGELK
 ETTPEFFWRRAKQLDSTVHPDTGKTVLLPFRMSSNVLSNLVTVGMLTPGLGTAGTVFWQW
 ANQSLNVAVNSANANKSHPMSTSQLLTNYAAAVTASCGVALGLNNLVPRLNKISPHSKLI
 LGRLVPFAAVVSAGIVNVFLMRGNEIRKGISVFDSENGDEVGKSKAAFMVGETALSRVI
 NATPTMVIPLPLLVRLQRGVLKKSGLGQTLANLGLISVTMFSALPFALGIFPQRQAHL
 NKLEPELHGKKDKDGKPIEKVYFNIRGI

SEQ ID NO: 141

YOR273C

>sp|Q12256|TPO4_YEAST Polyamine transporter 4 OS = *Saccharomyces*
cerevisiae (strain ATCC 204508 / S288c) GN = TPO4 PE = 1 SV = 1
 MPSSLTKTESNDPRTNIQQVPKALDKNVTNSGNLDSSTSSSTGSI TEDEKRSEPNADSN
 MTGGEPIDPRDLWDGPDPPDNPHNWSLKKWYTTMTSAFLCLVVTMGSSLYVSSVPELV
 ERYHVSQTLALAGLTFYLLGLSTVIGAPLSEVFGRKPVYLFSLPVSMLFTMGVGLSNGHM
 RIILPLRFLSGVFASPALSVMGSGTILDFDQVSVAMTYFVLSPFLGPVLSPIMAGFAT
 EAKGWRWSEWQLIAGGLILPFIALMPETHKGIIILRKRAKRNIALKKFSREAQKEFLKT
 TVTITILRPLKMLVVEPIVVFVSVYVAFIFAILFGFEEAYAVIYRGVYHMSMIGSLPFI
 GIGVGLWIGAFFYLYIDRKYLFPPKPPAGTQPLTEKERTSKRTPPYRGARDAETGELLPVV
 PEKFLIACKFGSVALPIGLFWQAWTARSDVHMAPVAAGVPFGFGLIILFFSVLMYFSTC
 YPPLTVASCLAANNLLRYVMSVPLFTIQMYTKMKIKWASTLFALVCVVMIPWPVFEEK
 WSKLRHKSQFGYAAMEKEAETEGGIDVDNAVDELNLTRMTTLTMTEDPSTREKPKGER
 LSLRTHTQVPVASFREDGQHAQNRNEPISNSLYSAIKDNEDGYSYTEMATDASARMV

SEQ ID NO: 142

YOR307C

>sp|P22215|SLY41_YEAST Uncharacterized transporter 5LY41
 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = SLY41
 PE = 1 SV = 2
 MIQTQSTAIKRRNSVHKNLFDPSLYQIPEPPRGGFQHQKKEYSKETFSNQVFGYDITSLK
 KRFTQLFPSNIIQGYLPEVDLRITIIICSIWYVTSSISSNLSKAILRTFNHPIALTELQFLV
 SAVLCVGFASIVNLFRPLRLKHTKFSKALNSFPDGLPEYLDGNFRSSI LHKFLVPSKLV
 LMTTFPMGIFQFIGHITSHKAVSMIPVSLVHVSVKALSPIITVGYKFFEHRYNSMTYYT
 LLLLIFGVMTTCWSTHSGSKRASDNKSGSSLIGLLFAFISMIIFVAQNIFAKNILTIRKV
 GILPSSSTDDVTSKEGQPSLDKTRFSPQVDKITILFYCSIGFSLTLPLTLTGELMHGG
 SVINDLTLETVALVAIHGIAHFFQAMLAFLIGLLSSINSYVANIMKRIVVISVALFWET
 KLNFFQVFGVILTIAGLYGDKWGLSKKDKGRQA

SEQ ID NO: 143

YOR332W

>sp|P22203|VATE_YEAST V-type proton ATPase subunit E
 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = VMA4
 PE = 1 SV = 4
 MSSAITALTPNQVNDENLNMQAFIRKEAEBEKAKEIQLKADQEYEIEKTNIVRNETNNIDG
 NFKSLKKKAMLSQQITKSTIANKMRLKVLASAREQSLDGIFEETKEKLSGIANNRDEYKPI
 LQSLIVEALLKLEPKAIVKALERDVLIESMKDDIMREYGEKAQRAPLLEEIVISNDYLN
 KDLVSGGVVSNASDKIEINNTLEERLKLSEALPAIRLELYGPSKTRKFFD

SEQ ID NO: 144

YOR348C

>sp|P15380|PUT4_YEAST Proline-specific permease OS = *Saccharomyces*
cerevisiae (strain ATCC 204508 / S288c) GN = PUT4 PE = 1 SV = 2
 MVNIIPLPFHKNRHSAGVVTCADDVSGDGGSGDTKKEEDVVQVTESSPSGSRNNHRSNNEK
 DDAIRMEKISKNSASSNGTIREDLIMDVLDLEKSPSVDDGSEPHKLKQGLQSRHVQLIAL
 GGAIGTGLLVGTSSTLHTCGPAGLFISYIIISAVIYPIMCALGEMVCFPLPGDGSAGST
 ANLVTRYVDPGLGFATGWNYPYCYVILVAAECTAASGVVEYWTAVPKGVWITIFLCVTV
 ILNFSAVKVYGESEFWFASIKILCIVGLIILSFILFWGGGPNHDLRGFRYWQHPGAFAHH
 LTGSLGNFTDIYTGIIKGAFAFILGPELVCMSTSAECADQRRNIAKASRRFVWRLIFFYV
 LGTLAI SVIVPNPTLVNALAQGKPGAGSSPFVIGIQNAGIKVLPHINGCILTSAWSA
 ANAFMFASSTRSLTMAQTQAPKCLGRINKWGPVYAVGVSLCCLAYLNVSSSTADV

TABLE 14-continued

Sequences disclosed herein.

NWFSNISTISGFLGWMCGCIAYLRFKKAIFYNGLYDRLPFKTWGQPYTVWFSLIVIGIIT
ITNGYAIPIKYWRVADFIAAYITLPIFLVLWFGHKLYTRTWQWVLPVSEIDVTGLVE
IEEKSREIEEMRLPPTGFKDKFLDALL

SEQ ID NO: 145

YPL036W

>sp|P19657|PMA2_YEAST Plasma membrane ATPase 2 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = PMA2 PE = 1 SV = 3
MSSTEAKQYKEKPSKEYLHASDGDPPANNSAASSSSSSSTSTSASSSAAVPRKAAAASA
ADDSDSDEDIDQLIDELQSNYGEDESSEEVRVDGVHAGQRVVEKDLSTDPXYGLTSD
EVARRRKKYGLNQMAEENESLIVKFLMFFVGPIQFVMEAAAILAAGLSDWVDVGVCALL
LLNASVGFIQEFQAGSIVDELKKTANTATVIRDGQLIEIPANEVVPGEILQLES GTIAP
ADGRIVTEDCFQLIDQSAITGESLAAEKHYGDEVFSSSTVKTGEAFMVVTTATGDNTFVGR
AAALVGQASGVGEGHTEVLNGIGIILLVLVIATLLLVWTACFYRTVGIVSILRYTLGITI
IGVPVGLPAVVTMTMAVGAAYLAKKQAIQVQLSAIESLAGVEILCSDKTGTLTKNKLSDH
EPYTVGEGVSPDDLMLTACLAASRKKKGLDAIDKAFKLSLIEYPAKAKDALTKYKVLPHFPF
DPVSKKVTAVVESPEGERIVCVKGAPLFLVKTVEEDHPIPEDVHENYENKVAELASRGFR
ALGVARKREGGHEWELGVMPMCDPPRDDTAQTINEARNLGLRIKMLTGDAVGIAKETCRQ
LGLGTNIYNAERLGLGGGDMPGSELADFVENADGFAEVFPQHKYRVVEILQNRGYLVAM
TGDGVNDAPSLNKADTGIAVEGATDAARSAADIVFLAPGLSAI IDALKTSRQIFHRMYSY
VVYRIALSLHLEIFLGLWIAILNNSLDINLIVFIAIFADVATLTITAYDNAPYAPEPVKWN
LPRLWGMSIILGIVLAIGSWITLTMTFLPNGGIIQNFAMGMVFMFLQISLTENWLI FVTR
AAGPFWSSIPSWQLAGAVFAVDIATMTPLFGWWSSENWTDIVSVVRVWISIGIFCVLGG
FYYIMSTSQAQFDRMLNGKSLKEKKSTRSVEDFMAAMQRVSTQHEKSS

SEQ ID NO: 146

YDL198C

MPHTDKKQSG LARLLGSASA GIMEIAVFHP VDTISKRLMS NHTKITSGQE LNRVIFRDHF
SEPLGKRLFT LFPPLGYAAS YKVLQRVYKY GGQPFANEFL NKHYKDFDN LPGEKTGKAM
RSAAAGSLIG IGEIVLPLD VLKIKRQTNP ESFKGRGFIK LLRDEGLFNL YRGWGWTAAAR
NAPGSFALFG GNAFAKEYIL GLKDYSQATW SQNFISSIVG ACSSLIVSAP LDVIKTRIQN
RNFDNPEGL RIVKNTLKNE GVTAPFKGLT PKLLTTGPKL VFSFALAQSL IPRFDNLLSK

SEQ ID NO: 147

YFL054C

MSYESGRSSS SSESTRPPTL KEEPNGKIAW EESVKKSRN NENDSTLLRR KLGETRKAIE
TGGSSRNKLS ALTPLKKVVD ERKDSVQPV PSMGFTYSLP NLKTLNSFSD AEQARIMQDY
LSRGNVQNS NNYVDPYLRQ LNPTMGSSRN RPVWSLNQPL PHVLDRLGLAA KMIQKNMDAR
SRASSRRGST DISRGGTTS VKDWKRLLRG AAPGKKLGDI EAQTQRDNTV GADVKTCKLE
PENPQKPSNT HIENVSRKKK RTSHNVNFSL GDESAYSSIA DAESRKLKNN QTLDGSTPVY
TKLPEELIEE ENKSTSALDG NEIGASEDED ADIMTFPNFW AKIRYHMRPFAEFLGTLVL
VIFGVGNLQ ATVTKGSGGS YESLSFAWGF GCMLGVYVAG GISGGHINPA VTISMAIFRK
FPWKVKPVYI VAQIIGAYFG GAMAYGYFWS SITEFEGGPH IRTTATGACL FTDPKSVYTW
RNAFFDEFIG ASILVGLCMA LLDSSNAPP NGMTALII GF LVAAIGMALG YQTSFTINPA
RDLGPRIFAS MIGYGPHAFH LTHWWWTGGA WGGPIAGGIA GALIYDIFIF TGCESPVNYP
DNGYIENRVG KLLHAEFHQN DGTVSDESGV NSNSNTGSKK SVPTSS

SEQ ID NO: 148

Oryza sativa sequence encoding EUGT11

MDSGYSSSYA AAAGMHVVIC PWLAFGHLLP CLDLAQRLAS RGHRSVFVST PRNISRLPPV
RPALAPLVAF VALPLPRVEG LPDGAESTND VPHDRPDMVE LHRRAFGLA APFSEPLGTA
CADWVIDVVF HHWAAAAALE HKVPCAMMLL GSAHMIASIA DRRLERAE TE SPAAAGQGRP
AAAPTFEVAR MKLIRTKGSS GMSLAERFSL TLRSSSLVVG RSCVEFEPET VPLLSTLRGK
PITFLGLMPP LHGRRREDGE DATVRWLDAQ PAKSVVYVAL GSEVPLGVEK VHELALGLEL
ACTRFLWALR KPTGVSDADL LPAGFEERTR GRGVVATRWV PQMSILAHAA VGAFLTHCGW
NSTIEGLMFG HPLIMLPFG DQGNARLIE AKNAGLQVAR NDGDGSPDRE GVAAAIRAVA
VEEESKVFQ AKAKKLQEV ADMACHERYI DGFIIQQLRSY KD

SEQ ID NO: 149

Synechococcus sp. GGPPS

MVAQTFNLDT YLSQRQQQVE EALSALVPA YPERIYEAMR YSLLAGGKRL RPILCLAACE
LAGGSVEQAM PTACALEMIH TMSLIHDDL AMDNDDFRRG KPTNHKVFE DIALLAGDAL
LAYAFEHIAS QTRGVPPQLV LQVIARIGHA VAATGLVGGQ VVDLESEGKA ISLETLEYIH
SHKTGALLEA SVVSGGILAG ADEELLARLS HYARDIGLAF QIVDDILDVT ATSEQLGKTA
GKDQAAAKAT YPSLLGLEAS RQKAELIQS AKEALRPVGS QAEPLLALAD FIITRRQH

SEQ ID NO: 150

Zea mays truncated COPS

MAQHTSESAA VAKGSSLTPI VRTDAESRRT RWPTDDDDAE PLVDEIRAML TSMSDGDIVS
SAYDTAWVGL VPRLDGGEGP QFPAAVRWIR NNQLPDGWSG DAALFSAYDR LINTLACVVT
LTRWLEPEM RGRGLSPLGR NMWKLATEDE ESMPIGFELA FPSLIELAKS LGVHDFPYDH
QALQGIYSSR EIKMKRIPKE VMHTVPTSIL HSLEGMPGLD WAKLLKLQSS DGSFLFSPAA
TAYALMNTGD TRCFSYIDRT VKKFNGGVVN VYPVDLFEHI WAVDRLERLG ISRYFQKEIE
QCMDYVNRHW DEDGICWARN SDVKEVDATA MAFRLRLRHG YSVSPDVFKN FEKDGEFFAF
VGQSNQAVTG MYNLNRSQI SFPGEDVLHR AGAFSYEFLR RKEAEGALRD KWIISKDLPG

TABLE 14-continued

Sequences disclosed herein.				
EVVYTLDFPW	YGNLPRVEAR	DYLEQYGGGD	DVWIGKTLR	MPLVNNDVYL ELARMDFNHC
QALHQLEWQ	LKRWYTENRL	MDFGVAQEDA	LRAYFLAAS	VYEP CRAAER LAWARAAILA
NAVSTHLRNS	PSFRERLEHS	LRCRPSEETD	GSWFNSSSGS	DAVLVKAVLR LTDSLAREAQ
PIHGGDPEDI	IHKLLRSABA	EWVREKADAA	DSVCNGSSAV	EQEGSRMVHD KQTCLLLARM
IEISAGRAAG	EAASEDGDRI	IIQLTGSI CD	SLKQKMLVSQ	DPEKNEEMMS HVDDELKLRI
REFVQYLLRL	GEKKTGSSET	RQTFLSIVKS	CYYAAHCPPH	VVDRHISRVI FEPVSAAK
SEQ ID NO: 151				
<i>Arabidopsis thaliana</i> KS (similar to GenBank AEE36246.1)				
MSINLRSSGC	SSPISATLER	GLDSEVQTRA	NNVSFEQTKE	KIRKMLEKVE LSVSAYDTSW
VAMVPSPPSQ	NAPLFPQCVK	WLLDNQHEDG	SWGLDNHDHQ	SLKKDVLSSST LASILALKKW
GIGERQINKG	LQFIELNSAL	VTDETIQKPT	GFDIIFPGMI	KYARDLNLTI PLGSEVVDDM
IRKRDLDLKC	DSEKFSKGRE	AYLAYVLEGT	RNLKDWDLI	KYQRKNGSLF DSPATTAAAF
TQFGNDGCLR	YLCSSLQKFE	AAVPSVYFPD	QYARLSIIVT	LESLGIDRDF KTEIKSILDE
TRYWLRGDE	EICDLATCA	LAFLRLLAHG	YDVSYDPLKP	FAEESGFSDT LEGYVKNFTS
VLELFKAAQS	YPHESALKKQ	CCWTKQYLEM	ELSSSVWKTVS	RDYLYKKEVE DALAFPSYAS
LESDHRRKI	LNGSAVENTR	VTKTSYRLHN	ICTSDILKLA	VDDFNFCQSI HREEMERLDR
WIVENRLQEL	KFARQKLAYC	YFSGAATLFS	PELSDARISW	AKGGVLTTVV DDFDVGGSK
EELNLIHLV	EKWDLNGVPE	YSSEHVEIIF	SVLRDTILET	GDKAFITYQGR NVTHHIVKIW
LDLLKSMLE	REWSSDKSTP	SLEDYMNAY	ISFALGPVL	PATYLGPPPL PEKTVDSHQY
NQLYKLVTM	GRLLNDIQGF	KRESAEGKLN	AVSLHMKHER	DNRSKEVII E SMKGLAERKR
EELHKLVL EE	KGSVVPRECK	EAPLKMSKVL	NLFYRKDDGF	TSNDLMSLVK SVIYEPVSLQ
KESLT				
SEQ ID NO: 152				
<i>S. rebaudiana</i> KO1				
MDAVTGLLTV	PATAITIGGT	AVALAVALIF	WYLKSYTSAR	RSQSNHLPRV PEVPGVPLL G
NLLQLKEKKP	YMTFTRWAAT	YGPIYSIKTG	ATSMVVVSSN	EIAKEALVTR FQSISTRNLS
KALKVLTADK	TMVAMSDDY	YHKTVKRHIL	TAVLGPNAQK	KHRIHRDIMM DNISTQLHEF
VKNNEPQEEV	DLRKIFQSEL	FGLAMRQALG	KDVESLYVED	LKI TMNRDEI FQVLVVDPM
GAIDVDWRDF	PPYLKWVPNK	KFENTIQQMY	IRREAVMKSL	IKHEKKRIAS GEKLSYIDY
LLSEAQTLD	QQLMSLWEP	IIESSDTTMV	TTEWAMYELA	KNPKLQDRLY RDIKSVCGSE
KITEEHLSQL	PYITAI PHET	LRHSPVPII	PLRHVHEDTV	LGGYHVPA GT ELAVNIYGCN
MDKNVWENPE	EWNPERPMKE	NETIDFQKTM	AFGGGKRVCA	GSLQALLTAS IGIGRMVQEF
EWKLKDMTQE	EVNTIGLTTQ	MLRPLRAI IK	PRI	
SEQ ID NO: 153				
<i>A. thaliana</i> ATR2				
MSSSSSSSTS	MIDLMAAIK	GEPVIVSDPA	NASAYESVAA	ELSSMLIENR QFAMIVTTSI
AVLIGCIVML	VWRRSGSGNS	KRVEPLKPLV	IKPREEEIDD	GRKKVTIFFG TQTGTAE GFA
KALGEEAKAR	YEKTRFKIVD	LDDYAADDDE	YEEKLKKEDV	APFFLATYGD GEPTDNAARF
YKWFTEGNDR	GEWLKKNLYG	VFGLGNRQYE	HFNKVAKVVD	DILVEQGAQR LVQVGLGDDD
QCIEDDFTAW	REALWPELDT	ILREEGDTAV	ATPYTAAVLE	YRVSIHSDSE AKFNDITLAN
NGGYTVFDAQ	HPYKANVAVK	RELHTPESDR	SCIHLFEDIA	GSGLTMKLG D HVGVLCDNLS
ETVDEALRL	DMSPDITYFSL	HA EKEDGTPI	SSSLPPPPFP	CNLRALTTRY ACLLSPPKKS
ALVALAAHAS	DPTAERLKH	LASPAGKDEY	SKWVVESQRS	LLEVMAEFPS AKPPLGVFFA
GVAPRLQPRF	YSISSSPKIA	ETRIHVTCAL	VYEKMPGTGR	HKGVCSTWMK NAVPYEKSEK
LFLGRPIFVR	QSNFKLPSDS	KVP IIMIGPG	TGLAPFRGFL	QERLALVESG VELGPSVLFF
GCRNRMDFI	YEEELQRFVE	SGALAELSVA	FSREGPTKEY	VQHKMMDKAS DIWNMISQGA
LYLYCGDAKG	MARVDHRS LH	TIAEQGSM D	STKAEGFVKI	LQTSGRYL RD VW
SEQ ID NO: 154				
<i>Stevia rebaudiana</i> KAHEL				
MEASYLYISI	LLLLASYLFT	TQLRRKSANL	PPTVFPSIPI	IGHLYLLKKP LYRTLAKIAA
KYGPILQLQL	GYRRVLVISS	PSAAEECF TN	NDVIFANRPK	TLFGKIVGGT SLGSLSYGDQ
WRNLRRVASI	EILSVHRLNE	FHDIRVDENR	LLIRKLRS SS	SPVTLITV FY ALTLNVIMRM
ISGKRYFDSG	DRELEEEGKR	FREILDETLL	LAGASNVGDY	LPILNWLGVK SLEKKLIALQ
KKRDDFFQGL	IEQVRKSRGA	KVGKGRKMTI	ELLLSLQESE	PEYYTDAMIR SFVLGLLAA G
SDTSAGTM EW	AMSLLVNHPH	VLKKAQAEID	RVIGNNRLID	ESDIGNIPYI GCIINETLRL
YPAGPLLPFH	ESSADCVISG	YNI PRGTMLI	VNQWAIHHPD	KVWDDPETFK PERFQGLEGT
RDGFKLMPFG	SGRGCPGEG	LAIRLLGM TL	GSVIQCFDWE	RVGDEMVDMT EGLGVTL PKA
VPLVAKCKPR	SEMTNLLSEL			
SEQ ID NO: 155				
<i>Stevia rebaudiana</i> CPRS				
MQSNVVKISP	LDLVTALFSG	KVLDTSNASE	SGESAMLPTI	AMIMENRELL MILTTSVAVL
IGCVVVLVWR	RSSTKKSAL E	PPVIVVPKRV	QEEEVDDGKK	KVTVFPGTQT GTAEGFAKAL
VEEAKARYEK	AVFKVIDLDD	YAADDEYEE	KLKKE SLAFF	FLATYGDGEP TDNAARFYKW
FTEGDAKG EW	LNKLQYGVFG	LGNRQYEHFN	KIAKVVD DGL	VEQGA KRLVP VGLGDD DQCI
EDDFTAWKEL	VWPELDQLLR	DEDDTTVATP	YTA AVAEYRV	VFHEKPDALS EDYSYTN GHA
VHDAQHPCRS	NVAVVKELHS	PESDRSCTHL	EPDISNTGLS	YETGDHVG VY CENLSEVVND
AERLVGLPPD	TYSSIHTDSE	DGSPLGGASL	PPPPFPCTLR	KALTCYADVL SSPKKSALLA
LAAHATDPSE	ADRLKFLASP	AGKDEYSQWI	VASQRSLL EV	MEAFPSAKPS LGVFFASVAP
RLQPRYYSIS	SSPKMAPDRI	HVTALVYEEK	TPAGRIHKG V	CSTWMKNAPV MTESQDCSWA
PIYVRTSNFR	LPSDPKVPVI	MIGPGTGLAP	FRGFLQERLA	LKEAGTDLGL SILFFGCRNR

TABLE 14-continued

Sequences disclosed herein.					
KVDFIYENEL	NNFVETGALS	ELIVAFSREG	PTKEYVQHKM	SEKASDIWNL	LSEGAYLYVC
GDAKGMADKV	HRTLHTIVQE	QGSLDSSKAE	LYVKNLQMSG	RYLRDVM	

SEQ ID NO: 156

Stevia rebaudiana UGT85C2

MDAMATTEKK PHVIFIPFPA QSHIKAMLKL AQLLHHKGLQ ITFVNTDFIH NQFLESSGPH
 CLDGAPGFRF ETIPDGVSHS PEASIPRES LLRSIETNFL DRFIDLVTKL PDPPTCIISD
 GFLSVFTIDA AKKLGIPVMM YWTLAACGFM GFYHIHSLIE KGFAPLKDAS YLTNGYLDTV
 IDWVPGMEGI RLKDFPLDWS TDLNDKVLMP TTEAPQRSHK VSHHIFHTFD ELEPSIIKTL
 SLRYNHIYTI GPLQLLLDQI PEEKKQTGIT SLHGYSLVKE EPECFQWLQS KEPNSVVYVN
 FGSTTVMSLE DMTEFGWGLA NSNHYFLWII RSNLVIGENA VLPPELEEH I KRGFIASWC
 SQEKVLKHP S VGGFLTHCGW GSTIESLSAG VPMICWPYSW DQLTNCRYIC KEWEVGLEM
 TKVKRDEVKR LVQELMGEGG HKMRNKAKDW KEKARIAIAP NGSSSLNIDK MVKEITVLAR

N

SEQ ID NO: 157

S. rebaudiana UGT74G1 (GenBank AAR06920.1)

MAEQQKIKKS PHVLLIPFPL QGHINPFIQF GKRLISKGVK TTLVTTIHTL NSTLNHSNTT
 TTSIEIQAIS DGCDEGGFMS AGESYLETFK QVGSKSLADL IKKLQSEGTT IDAIYDSMT
 EWVLDVAIEF GIDGGSFFTQ ACVNSLYYH VHKGLISLPL GETVSVPGFP VLQRWETPLI
 LQNHQIQSP WSQMLFQQA NIDQARWVFT NSFYKLEEV IEWTRKIWNL KVIGTPLPSM
 YLDKRLDDDK DNGFNLYKAN HHECMNWLDD KPKEVSVVVA FGSLVKHGP QVEEITRALI
 DSDVNFLLWVI KHKEEGKLPE NLSEVIKTGK GLIVAWCKQL DVLAHESVGC FVTHCGFNST
 LEAISLGVVP VAMPQFSDQT TNAKLLDEIL GVGVRVKADE NGIVRRGNLA SC: KMIMEEE
 RGVIRKNAV KWKDLAKVAV HEGGSSDNDI VEFVSELIKA

SEQ ID NO: 158

S. rebaudiana UGT76G1

MENKTETTFR RRRRIILFPV PFQGHINPIL QLANVLYSKG FSITIFHTNF NKPKTSNYPH
 FTFRILNDND PQDERISNLP THGPLAGMRI PIINEHGADE LRRELELML ASEDEEVSC
 LITDALWYFA QSVADSLNLR RLVLMTSSLF NFHAHVSLPQ FDELGYLDPD DKTRLEEQAS
 GPPMLKVVDI KSAYSNQPIEL KEILGKMIQ TKASSGVWN SFKELEESL ETVIREIPAP
 SFLIPLPKHL TASSSSLLDH DRTVFQWLDQ QPPSSVLVVS FGSTSEVDEK DFLEIARGLV
 DSKQSFLWVW RPFVVKGSTW VEPLPDGFLG ERGRIVKWVP QQEVLAHGAI GAFWTHSGWN
 STLESVCEGV PMIFSDFLD QPLNARYMSD VLKGVVYLEN GWERGEIANA IRRVMVDEEG
 EYIRQNARVL KQKADVSLMK GSSSYESLES LVSYSLSL

SEQ ID NO: 159

S. rebaudiana UGT91D2e-b

MATSDSIVDD RKQLHVATFP WLAFGHILPY LQLSKLIAEK GHKVSFLSTT RNIQRLSSH
 SPLINVQLT LPRVQELPED AEATTDVHPE DIPYLKASD GLQPEVTRFL EQHSPDWIY
 DYTHYWLPSI AASLGISRAH FSVTTPWAI A YMGPSADAMI NGSDGRITVE DLTTPPKWFP
 FPTKVCWRKH DLARLVYKA PGISDGYRMG MVLKGSDDL SKCYHEFGTQ WLPLETLHQ
 VPVVPVGLLP PEIPGDEKDE TWVSIKKWLD GKQKGSVVYV ALGSEALVSQ TEVVELALGL
 ELSGLPFWA YRKPKGPAKS DSVLPDGFV ERTRDRGLVW TSWAPQLRIL SHESVCGFLT
 HCGSGSIVEG LMFHGPLIML PIFGDQPLNA RLLEDKQVGI EIPRNEEDGC LTKESVARSL
 RSVVVEKEGE IYKANARELS KIYNDTKVEK EYVSQFVDYL EKNARAVAI HES

SEQ ID NO: 160

atggctacct tgggtgaaca ttttcaagct atgccattcg ctattccaat tgccttggtc
 gctttgtctt ggttgttttt gttctacatc aaggtttctt tcttctccaa caaatccgct
 caagctaaat tgcaccagct tccagttgtt ccaggtttgc cagttattgg taatttggtg
 caattgaaag aaaagaagcc ataccaaacc ttcactagat gggctgaaga atatgggtcca
 atctactcta ttagaactgg tgcttctact atggttgtct tgaacactac tcaagttgcc
 aaagaagcta tgggtaccag atacttgtct atctctacca gaaagttgtc caacgccttg
 aaaattttga ccgctgataa gtgcatgggt gccatttctg attacaacga tttccacaag
 atgatcaaga gatatactct gtctaactgt ttgggtccat ctgccccaaa aagacataga
 tctaacagag ataccttgag agccaactgt tgttctagat tgcattccca agttaagaac
 tctccaagag aagctgtcaa ctttagaaga gttttcgaat gggaattatt cggtatcgct
 ttgaaacaag cttcggtaa ggatattgaa aagccaactc acgtcgaaga attgggtact
 actttgtcca gagatgaaat cttcaagggt ttggtcttgg acattatgga aggtgccatt
 gaagttgatt ggagagattt tttccatc tgctgttggg ttccaaacac cagaatggaa
 actaagatcc aaagattata ctttagaaga aaggccgtta tgaccgcctt gattaacgaa
 caaaagaaaa gaattgcctc cgggtgaagaa atcaactgct acatcgattt cttgttgaaa
 gaagtgaaag ccttgaccat ggaccaaact tctatgtgtg tgtgggaaac cgttattgaa
 actgctgata ccacaatggt tactactgaa tgggctatgt acgaagtgc taaggattct
 aaaagacaag acagattata ccaagaaatc caaaaggctc gcggttctga aatgggttaca
 gaagaatact tgcctcactg gccatacttg aatgctgttt tccacgaaac tttgagaaaa
 cattctccag ctgctttggt tccattgaga tatgctcatg aagatactca attgggtggt
 tattacattc cagccggtac tgaattgcc attaacatct acggttgcaa catggacaaa
 caccatggg aatctccaga agaattggaag ccagaaagat ttttgatcc taagttgac
 ccaatggact tgtacaaaac tatggctttt ggtgctggtta aaagagtttg cgtggttct
 ttacaagcta tgttgattgc ttgtccaacc atcggttagat tgggtcaaga atttgaatgg
 aagttgagag atgggtgaaga agaaaacggt gatactgttg gtttgaccac ccataagaga
 tatccaatgc atgctatttt gaagccaaga tcttaa

TABLE 14-continued

Sequences disclosed herein.

SEQ ID NO: 161
 MATLLEHFQA MPFAIPIALA ALSWLFLFYI KVSFFSNKSA QAKLPPVPV PGLPVIGNLL
 QLKEKKPYQT FTRWAEYGP IYSIRTGAST MVVLNTQVA KEAMVTRYLS ISTRKLSNAL
 KILTADKCMV AISDYNDPHK MIKRYILSNV LGPSAQKRHR SNRDTLRANV CSRLHSQVKN
 SPREAVNFRF VFWEWELFGIA LKQAFGKDIE KPIYVEELGT TLSRDEIFKV LVLIDIMEGAI
 EVDWRDFFPY LRWIPNTRME TKIQRLYFRR KAVMTALINE QKKRIASGEE INCYIDFLLK
 EGKTLTMDQI SMLLWETVIE TADTTMVTE WAMYEVAKDS KRQDRLYQEI QKVCGSEMT
 EYLSQLPYL NAVFHETLRK HSPAALVPLR YAHEDTQLGG YYIPAGTEIA INIYGCNMDK
 QWESPEEWK PERFLDPKFD PMDLYKTMAF GAGKRVKAGS LQAMLIACPT IGRLVQEFEW
 KLRDGEENV DTVGLTTHKR YPMHAILKPR S

[0207] 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.

SEQUENCE LISTING

The patent application contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (<http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US20170218418A1>). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

What is claimed is:

1. A recombinant host capable of synthesizing a steviol glycoside, comprising a gene encoding a transporter polypeptide and/or a gene encoding a transcription factor polypeptide that regulates expression of at least one transporter gene;

wherein expression of the gene encoding the transporter polypeptide and/or the gene encoding the transcription factor polypeptide that regulates expression of at least one transporter gene is modified and the recombinant host transports at least a portion of the synthesized steviol glycoside from the host into a culture medium.

2. The recombinant host of claim 1, wherein the gene encoding the transporter polypeptide is an endogenous gene.

3. The recombinant host of any one of claim 1 or 2, wherein the transporter polypeptide comprises an ATP-binding cassette (ABC) transporter, a major facilitator superfamily (MFS) transporter, an amino acid/auxin permease (AAP) family transporter, an ATPase transporter, a sulfate permease (SulP) family transporter, a lysosomal cystine transporter (LCT) family transporter, a Ca²⁺:cation antiporter (CaCA) family transporter, an amino acid-polyamine-organocation (APC) superfamily transporter, a multidrug/oligosaccharidyl-lipid/polysaccharide (MOP) transporter, a ZRT/IRT-like protein (ZIP) metal transporter family transporter, a mitochondrial protein translocase (MPT) family transporter, a voltage-gated ion channel (VIC) family transporter, a monovalent cation:proton antiporter-2 (CPA2) family transporter, a ThrE family of putative transmembrane amino acid efflux transporter, an oligopeptide transporter (OPT) family transporter, a K⁺ transporter (Trk) family transporter, a bile acid:Na symporter (BASS) family transporter, a drug/metabolite transporter (DMT) superfamily

transporter, a mitochondrial carrier (MC) family transporter, an auxin efflux carrier (AEC) family transporter, an ammonia channel transporter (Amt) family transporter, a metal ion (Mn²⁺-iron) transporter (Nramp) family transporter, a transient receptor potential Ca²⁺ channel (TRP-CC) family transporter, an arsenical resistance-3 (ACR3) family transporter, a nucleobase:cation symporter-1 (NCS1) family transporter, an inorganic phosphate transporter (PiT) family transporter, an arsenite-antimonite (ArsAB) efflux family transporter, an IISF family of transporter, a glycerol uptake (GUP) family transporter, a metal ion transport (MIT) family transporter, a copper transport (Ctr) family transporter, or a cation diffusion facilitator (CDF) family transporter.

4. The recombinant host of any one of claims 1-3, wherein modified expression comprises:

- overexpressing the gene encoding the transporter polypeptide and/or the gene encoding the transcription factor polypeptide; or
- deleting the gene encoding the transporter polypeptide and/or the gene encoding the transcription factor polypeptide.

5. The recombinant host of any one of claims 1-4, wherein the gene encoding the transporter polypeptide and/or the gene encoding the transcription factor polypeptide has an activity that is increased.

6. The recombinant host of any one of claims 1-5, wherein one or more of the genes encoding the transporter polypeptide and/or one or more of the gene encoding the transcription factor polypeptide is overexpressed.

7. The recombinant host of claim 6, wherein the transporter polypeptide and/or transcription polypeptide comprise YAL067C set forth in SEQ ID NO:14, YBL089W set forth in SEQ ID NO:15, YBL099W set forth in SEQ ID

NO:16, YBR008C set forth in SEQ ID NO:86, YBR021W set forth in SEQ ID NO:87, YBR043C set forth in SEQ ID NO:88, YBR180W set forth in SEQ ID NO:13, YBR241C set forth in SEQ ID NO:17, YBR287W set forth in SEQ ID NO:89, YBR294W set forth in SEQ ID NO:18, YBR295W set forth in SEQ ID NO:90, YBR296C set forth in SEQ ID NO:91, YCL038C set forth in SEQ ID NO:92, YCL069W set forth in SEQ ID NO:19, YCR011C set forth in SEQ ID NO:93, YCR028C set forth in SEQ ID NO:20, YCR075C set forth in SEQ ID NO:21, YDL054C set forth in SEQ ID NO:94, YDL100C set forth in SEQ ID NO:95, YDL128W set forth in SEQ ID NO:22, YDL185W set forth in SEQ ID NO:23, YDL194W set forth in SEQ ID NO:24, YDL210W set forth in SEQ ID NO:25, YDL245C set forth in SEQ ID NO:96, YDL247W set forth in SEQ ID NO:97, YDR011W set forth in SEQ ID NO:98, YDR061W set forth in SEQ ID NO:26, YDR093W set forth in SEQ ID NO:27, YDR292C set forth in SEQ ID NO:99, YDR338C set forth in SEQ ID NO:28, YDR406W set forth in SEQ ID NO:29, YDR497C set forth in SEQ ID NO:100, YDR536W set forth in SEQ ID NO:30, YEL006W set forth in SEQ ID NO:101, YEL027W set forth in SEQ ID NO:102, YEL031W set forth in SEQ ID NO:31, YEL065W set forth in SEQ ID NO:103, YER019C-A set forth in SEQ ID NO:104, YER053C set forth in SEQ ID NO:105, YER119C set forth in SEQ ID NO:106, YER166W set forth in SEQ ID NO:32, YFL011W set forth in SEQ ID NO:33, YFL028C set forth in SEQ ID NO:107, YFR045W set forth in SEQ ID NO:108, YGL006W set forth in SEQ ID NO:34, YGL013C set forth in SEQ ID NO:35, YGL084C set forth in SEQ ID NO:109, YGL104C set forth in SEQ ID NO:110, YGL114W set forth in SEQ ID NO:111, YGL167C set forth in SEQ ID NO:112, YGL255W set forth in SEQ ID NO:36, YGR125W set forth in SEQ ID NO:37, YGR181W set forth in SEQ ID NO:38, YGR217W set forth in SEQ ID NO:39, YGR224W set forth in SEQ ID NO:40, YGR257C set forth in SEQ ID NO:113, YGR281W set forth in SEQ ID NO:41, YHL016C set forth in SEQ ID NO:42, YHL035C set forth in SEQ ID NO:114, YHL036W set forth in SEQ ID NO:115, YHR002W set forth in SEQ ID NO:116, YHR096C set forth in SEQ ID NO:117, YIL006W set forth in SEQ ID NO:118, YIL088C set forth in SEQ ID NO:43, YIL120W set forth in SEQ ID NO:119, YIL121W set forth in SEQ ID NO:120, YIL166C set forth in SEQ ID NO:121, YJL093C set forth in SEQ ID NO:44, YJL094C set forth in SEQ ID NO:45, YJL108C set forth in SEQ ID NO:46, YJL133W set forth in SEQ ID NO:122, YJL121C set forth in SEQ ID NO:47, YJL219W set forth in SEQ ID NO:123, YJR106W set forth in SEQ ID NO:48, YJR160C set forth in SEQ ID NO:49, YKL016C set forth in SEQ ID NO:124, YKL050C set forth in SEQ ID NO:125, YKL064W set forth in SEQ ID NO:50, YKL120W set forth in SEQ ID NO:126, YKL146W set forth in SEQ ID NO:127, YKL209C set forth in SEQ ID NO:128, YKR039W set forth in SEQ ID NO:129, YKR050W set forth in SEQ ID NO:51, YKR105C set forth in SEQ ID NO:52, YKR106W set forth in SEQ ID NO:53, YLR411W set forth in SEQ ID NO:130, YLR447C set forth in SEQ ID NO:54, YML038C set forth in SEQ ID NO:131, YML116W set forth in SEQ ID NO:55, YMR034C set forth in SEQ ID NO:56, YMR056C set forth in SEQ ID NO:57, YMR166C set forth in SEQ ID NO:132, YMR253C set forth in SEQ ID NO:58, YMR279C set forth in SEQ ID NO:133, YNL003C set forth in SEQ ID NO:134, YNL065W set forth in SEQ ID NO:59, YNL070W set forth in SEQ ID NO:60, YNL083W set forth in SEQ ID NO:61, YNL095C set forth in SEQ ID NO:62, YNL121C set forth in SEQ ID NO:63, YNL142W set forth in SEQ ID NO:64, YNL268W set forth in SEQ ID NO:135, YNR055C set forth in SEQ ID NO:136, YOL020W set forth in SEQ ID NO:65, YOL075C set forth in SEQ ID NO:66, YOL077W-A set forth in SEQ ID NO:67,

YOL122C set forth in SEQ ID NO:68, YOL158C set forth in SEQ ID NO:137, YOR079C set forth in SEQ ID NO:69, YOR087W set forth in SEQ ID NO:70, YOR092W set forth in SEQ ID NO:71, YOR100C set forth in SEQ ID NO:138, YOR130C set forth in SEQ ID NO:72, YOR153W set forth in SEQ ID NO:139, YOR222W set forth in SEQ ID NO:73, YOR271C set forth in SEQ ID NO:140, YOR273C set forth in SEQ ID NO:141, YOR291W set forth in SEQ ID NO:74, YOR306C set forth in SEQ ID NO:75, YOR307C set forth in SEQ ID NO:142, YOR316C set forth in SEQ ID NO:76, YOR332W set forth in SEQ ID NO:143, YOR334W set forth in SEQ ID NO:77, YOR348C set forth in SEQ ID NO:144, YPL036W set forth in SEQ ID NO:145, YPL078C set forth in SEQ ID NO:78, YPL270W set forth in SEQ ID NO:79, YPL274W set forth in SEQ ID NO:80, YPR003C set forth in SEQ ID NO:81, YPR011C set forth in SEQ ID NO:82, YPR058W set forth in SEQ ID NO:83, YPR128C set forth in SEQ ID NO:84, or YPR201W set forth in SEQ ID NO:85.

8. The recombinant host of any one of claims 1-7, wherein YBR043C set forth in SEQ ID NO:88, YDL100C set forth in SEQ ID NO:95, YDL054C set forth in SEQ ID NO:94, YDL128W set forth in SEQ ID NO:22, YDL198C set forth in SEQ ID NO:146, YDR061W set forth in SEQ ID NO:26, YDR536W set forth in SEQ ID NO:30, YEL027W set forth in SEQ ID NO:102, YFL054C set forth in SEQ ID NO:147, YGL167C set forth in SEQ ID NO:112, YGR181W set forth in SEQ ID NO:38, YHL016C set forth in SEQ ID NO:42, YIL166C set forth in SEQ ID NO:121, YJL093C set forth in SEQ ID NO:44, YJR106W set forth in SEQ ID NO:48, YKL120W set forth in SEQ ID NO:126, YKL146W set forth in SEQ ID NO:127, YKR039W set forth in SEQ ID NO:129, YMR034C set forth in SEQ ID NO:56, YMR166C set forth in SEQ ID NO:132, YOL122C set forth in SEQ ID NO:68, YOR079C set forth in SEQ ID NO:69, YPL270W set forth in SEQ ID NO:79, and/or YPR011C set forth in SEQ ID NO:82 are overexpressed.

9. The recombinant host of any one of claims 1-8, further comprising:

- (a) one or more genes encoding a sucrose transporter and a sucrose synthase;
 - (b) a gene encoding a geranylgeranyl diphosphate synthase (GGPPS) polypeptide;
 - (c) a gene encoding an ent-copalyl diphosphate synthase (CDPS) polypeptide;
 - (d) a gene encoding a kaurene synthase (KS) polypeptide;
 - (e) a gene encoding a kaurene oxidase (KO) polypeptide;
 - (f) a gene encoding a steviol synthase (KAH) polypeptide;
 - (g) a gene encoding a cytochrome P450 reductase (CPR) polypeptide;
 - (h) a gene encoding a UGT85C2 polypeptide;
 - (i) a gene encoding a UGT76G1 polypeptide;
 - (j) a gene encoding a UGT74G1 polypeptide;
 - (k) a gene encoding a UGT91D2 functional homolog; and/or
 - (l) a gene encoding a EUGT11 polypeptide;
- wherein at least one of the genes is a recombinant gene; and wherein the host is capable of producing one or more of RebA, RebB, RebD and/or RebM.

10. The recombinant host of claim 9, wherein at least one of the genes is codon optimized for expression in the host.

11. The recombinant host of claim 10, wherein at least one of the genes is codon optimized for expression in *Saccharomyces cerevisiae*.

12. The recombinant host of claim 9, wherein:

- (a) the GGPPS polypeptide comprises a polypeptide having at least 70% identity to an amino acid sequence set forth in SEQ ID NO:149;

- (b) the CDPS polypeptide comprises a polypeptide having at least 70% identity to an amino acid sequence set forth in SEQ ID NO:150;
- (c) the KO polypeptide comprises a polypeptide having at least 70% identity to an amino acid sequence set forth in SEQ ID NO:152;
- (d) the KS polypeptide comprises a polypeptide having at least 40% identity to an amino acid sequence set forth in SEQ ID NO:151;
- (e) the KAH polypeptide comprises a polypeptide having at least 60% identity to an amino acid sequence set forth in SEQ ID NO:154;
- (f) the CPR polypeptide comprises a polypeptide having at least 70% identity to an amino acid sequence set forth in SEQ ID NO:153 and/or a polypeptide having at least 65% identity to an amino acid sequence set forth in SEQ ID NO:155;
- (g) the UGT85C2 polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:156;
- (h) the UGT76G1 polypeptide comprises a polypeptide having at least 50% identity to an amino acid sequence set forth in SEQ ID NO:158;
- (i) the UGT74G1 polypeptide comprises a polypeptide having at least 55% identity to an amino acid sequence set forth in SEQ ID NO:157;
- (j) the a UGT91D2 functional homolog comprises a UGT91D2e-b polypeptide having at least 90% identity to the amino acid sequence set forth in SEQ ID NO:159; and
- (k) the EUGT11 polypeptide comprises a polypeptide having at least 65% identity to an amino acid sequence set forth in SEQ ID NO:148.

13. The recombinant host of any one of claims **1-12**, wherein the recombinant host comprises a microorganism that is a plant cell, a mammalian cell, an insect cell, a fungal cell, or a bacterial cell.

14. The recombinant host of claim **13**, wherein the bacterial cell comprises *Escherichia* bacteria cells, *Lactobacillus* bacteria cells, *Lactococcus* bacteria cells, *Cornebacterium* bacteria cells, *Acetobacter* bacteria cells, *Acinetobacter* bacteria cells, or *Pseudomonas* bacterial cells.

15. The recombinant host of claim **13**, wherein the fungal cell is a yeast cell.

16. The recombinant host of claim **15**, 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 adenivorans*, *Xanthophyllomyces dendrorhous*, or *Candida albicans* species.

17. The recombinant host of claim **16**, wherein the yeast cell is a *Saccharomycete*.

18. The recombinant host of claim **17**, wherein the yeast cell is a cell from the *Saccharomyces cerevisiae* species.

19. A method of producing a steviol glycoside, comprising:

- (a) growing the recombinant host of any one of claims **1-18** in a culture medium, under conditions in which the genes discussed in any one of claims **1** to **18** are expressed, wherein the steviol glycoside is synthesized by the host; and
 - (b) optionally isolating the steviol glycoside.
- 20.** The method of claim **19**, wherein the steviol glycoside is RebA, RebB, RebD, and/or RebM, and wherein:
- (a) RebA is capable of being synthesized in the recombinant host of any one of claims **1-18** expressing UGT85C2, UGT76G1, UGT74G1, and UGT91D2;
 - (b) RebB is capable of being synthesized in the recombinant host of any one of claims **1-18** expressing UGT85C2, UGT76G1, and UGT91D2;
 - (c) RebD is capable of being synthesized in the recombinant host of any one of claims **1-18** expressing UGT85C2, UGT76G1, UGT74G1, and UGT91D2 and/or EUGT11; and
 - (d) RebM is capable of being synthesized in the recombinant host of any one of claims **1-18** expressing UGT85C2, UGT76G1, UGT74G1, and UGT91D2 and/or EUGT11.

21. The method of claim **19** or **20**, wherein a gene encoding YBR043C set forth in SEQ ID NO:88, YDL100C set forth in SEQ ID NO:95, YDL054C set forth in SEQ ID NO:94, YDL128W set forth in SEQ ID NO:22, YDL198C set forth in SEQ ID NO:146, YDR061W set forth in SEQ ID NO:26, YDR536W set forth in SEQ ID NO:30, YEL027W set forth in SEQ ID NO:102, YFL054C set forth in SEQ ID NO:147, YGL167C set forth in SEQ ID NO:112, YGR181W set forth in SEQ ID NO:38, YHL016C set forth in SEQ ID NO:42, YIL166C set forth in SEQ ID NO:121, YJL093C set forth in SEQ ID NO:44, YJR106W set forth in SEQ ID NO:48, YKL120W set forth in SEQ ID NO:126, YKL146W set forth in SEQ ID NO:127, YKR039W set forth in SEQ ID NO:129, YMR034C set forth in SEQ ID NO:56, YMR166C set forth in SEQ ID NO:132, YOL122C set forth in SEQ ID NO:68, YOR079C set forth in SEQ ID NO:69, YPL270W set forth in SEQ ID NO:79, and/or YPR011C set forth in SEQ ID NO:82 is overexpressed.

22. The method of any one of claims **19-21**, wherein the steviol glycoside is produced at a concentration of between about 500 mg/L to about 10,000 mg/L.

23. A method of increasing production or transport of a steviol glycoside into a culture medium, comprising:

- (a) growing the recombinant host of any one of claims **1-18** in a culture medium, under conditions in which the genes discussed in any one of claims **1** to **18** are expressed, wherein the steviol glycoside is synthesized by the host; and
- (b) optionally isolating the steviol glycoside.

24. The method of claim **23**, wherein the steviol glycoside is RebA, RebB, RebD, and/or RebM.

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