Production of Steviol Glycosides in Recombiant Hosts

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(54) **PRODUCTION OF STEVIOL GLYCOSIDES IN RECOMBIANT HOSTS**

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(57) **ABSTRACT**

The invention relates to recombinant microorganisms and methods for producing steviol glycosides and steviol glycoside precursors.

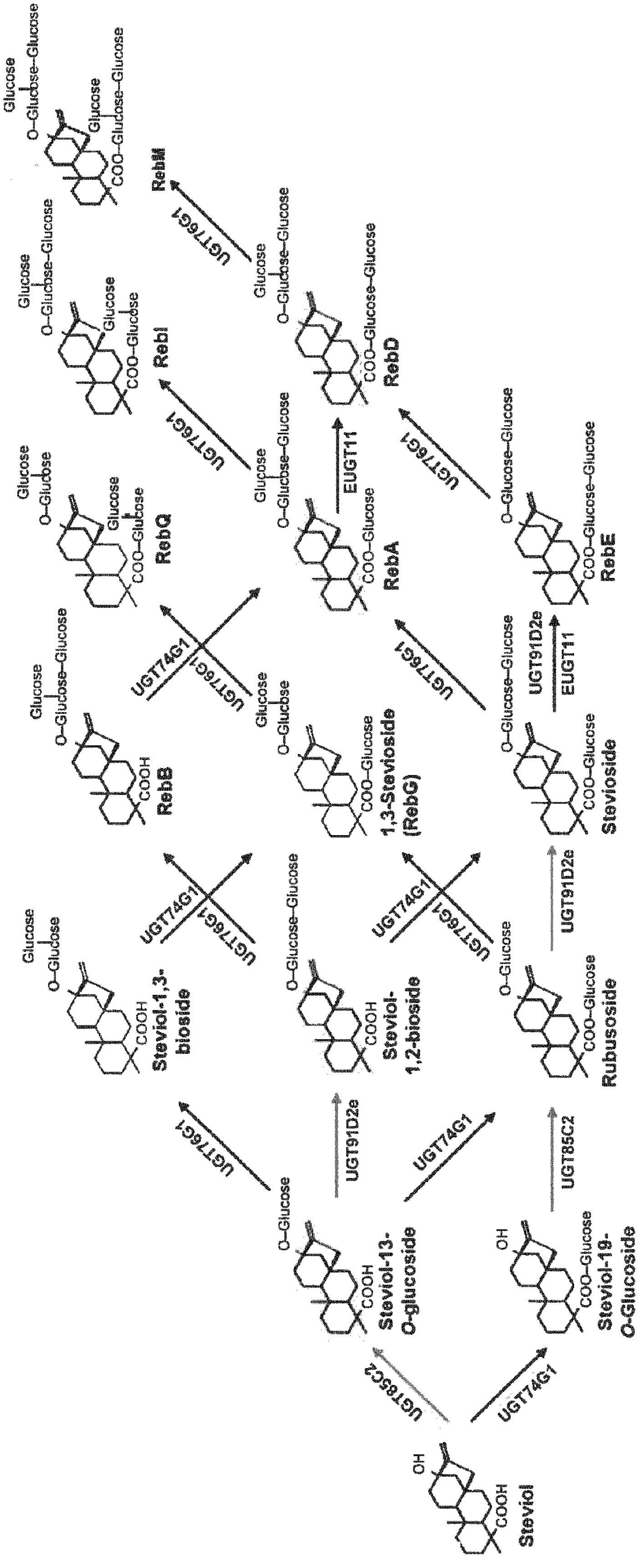

Steviol
COOH
OH
UGT85C2
UGT74G1
Steviol-13-O-glucoside
Steviol-19-O-Glucoside
O–Glucose
COO–Glucose
UGT76G1
UGT91D2e
UGT74G1
UGT85C2
Steviol-1,3-bioside
Steviol-1,2-bioside
Rubusoside
Glucose
O–Glucose–Glucose
UGT74G1
UGT76G1
UGT74G1
UGT76G1
UGT91D2e
RebB
1,3-Stevioside (RebG)
Stevioside
UGT74G1
UGT76G1
UGT76G1
UGT91D2e
EUGT11
RebQ
RebA
RebE
COO–Glucose–Glucose
UGT76G1
EUGT11
UGT76G1
RebI
RebD
UGT76G1
RebM

Figure 1

Figure 2

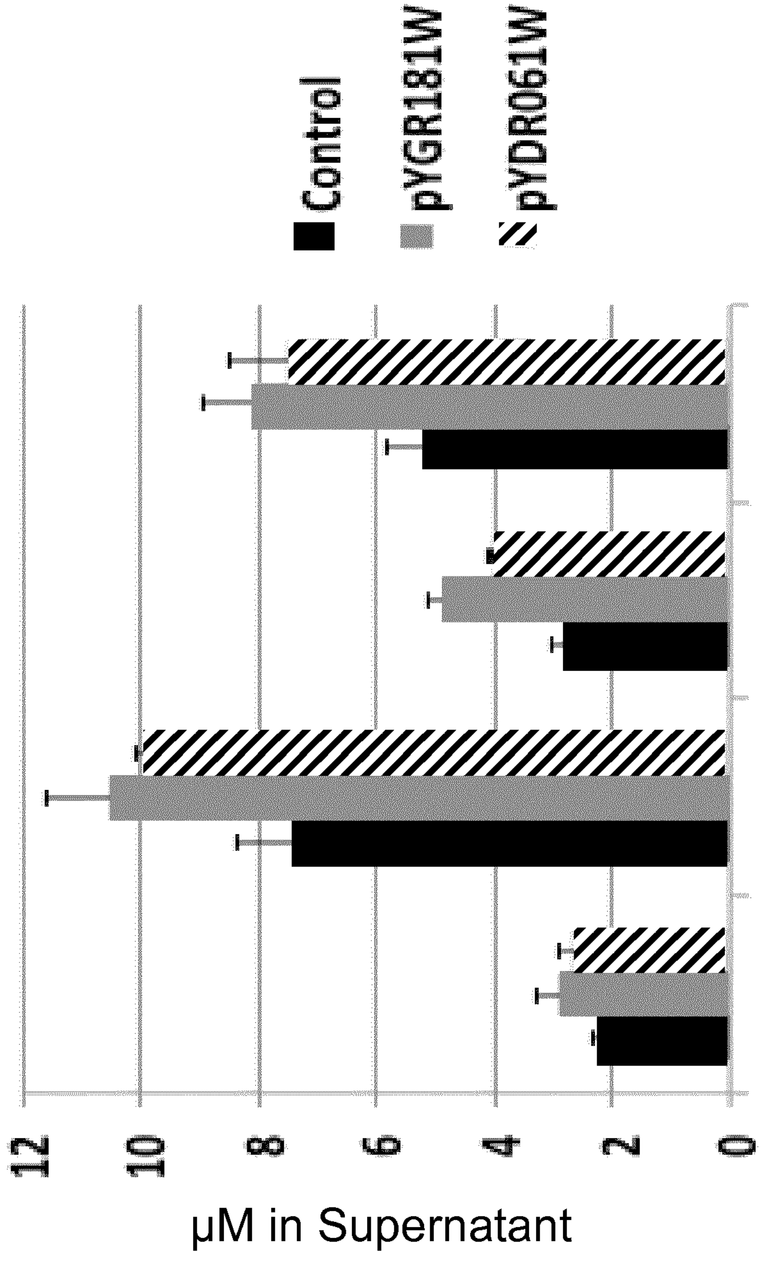

Control
pYGR181W
pYDR061W
12
10
8
6
4
2
0
µM in Supernatant
RebB
RebA
RebD
RebM

Figure 3A

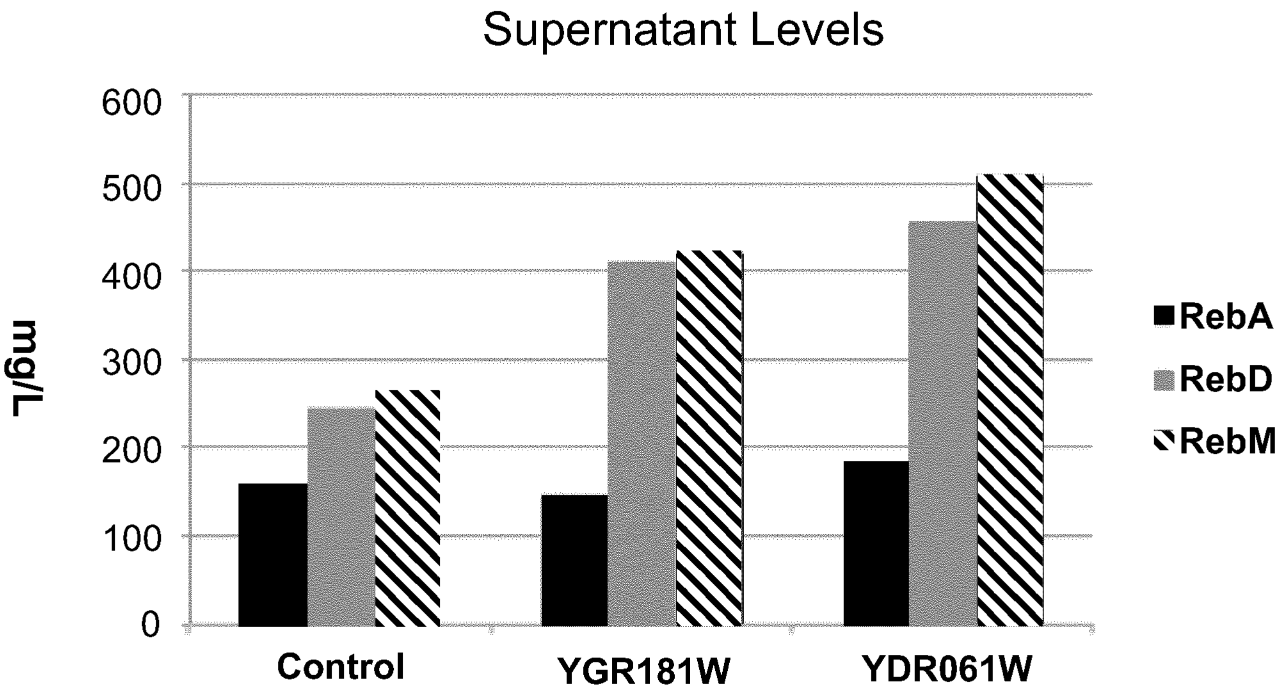

Supernatant Levels
mg/L
600
500
400
300
200
100
0
Control
YGR181W
YDR061W
■RebA
▨RebD
▧RebM

Figure 3B

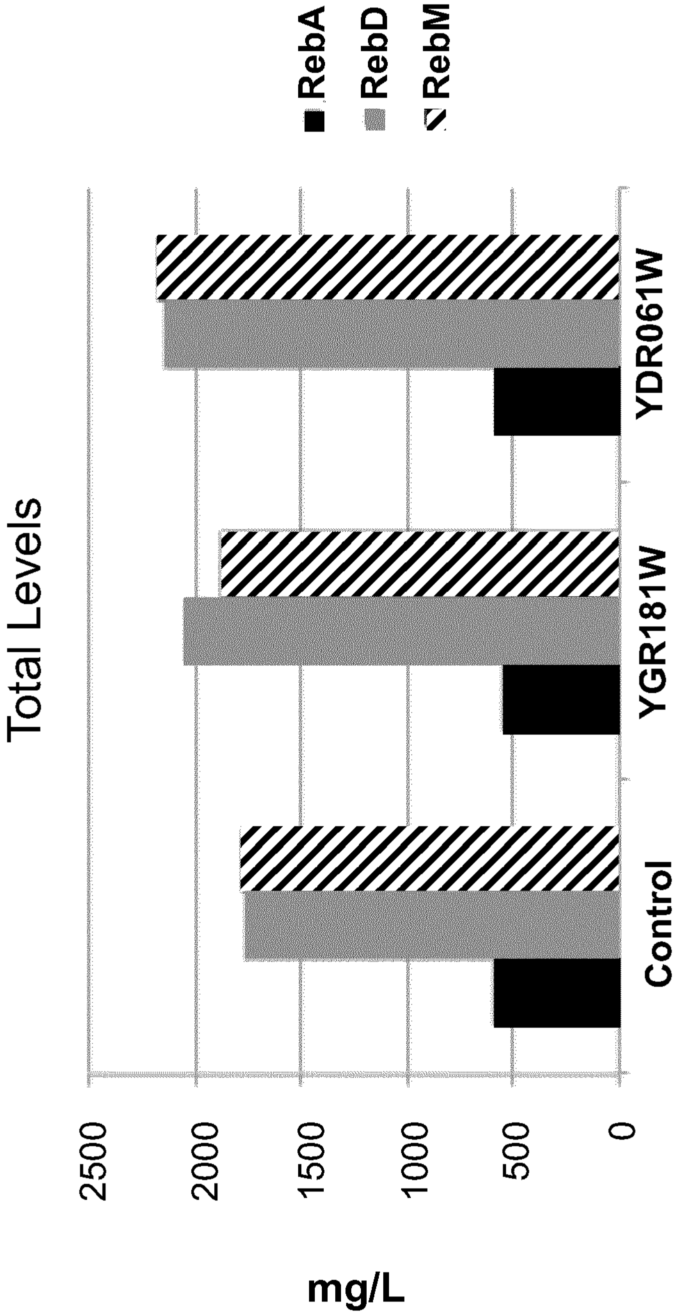

Total Levels
■ RebA
▨ RebD
▧ RebM
mg/L
2500
2000
1500
1000
500
0
Control
YGR181W
YDR061W

Figure 4A

13-SMG

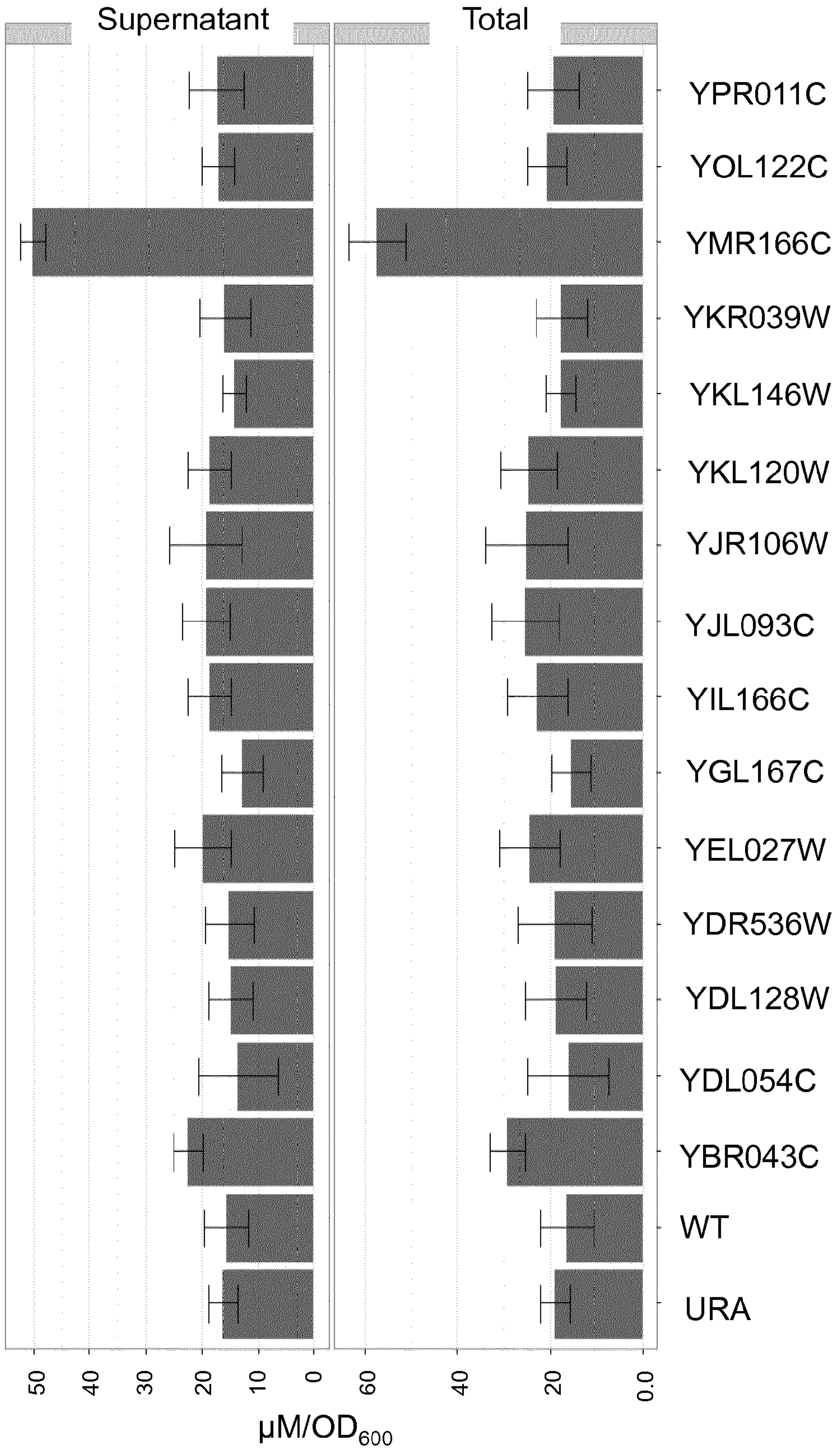


Figure 4B
RebA

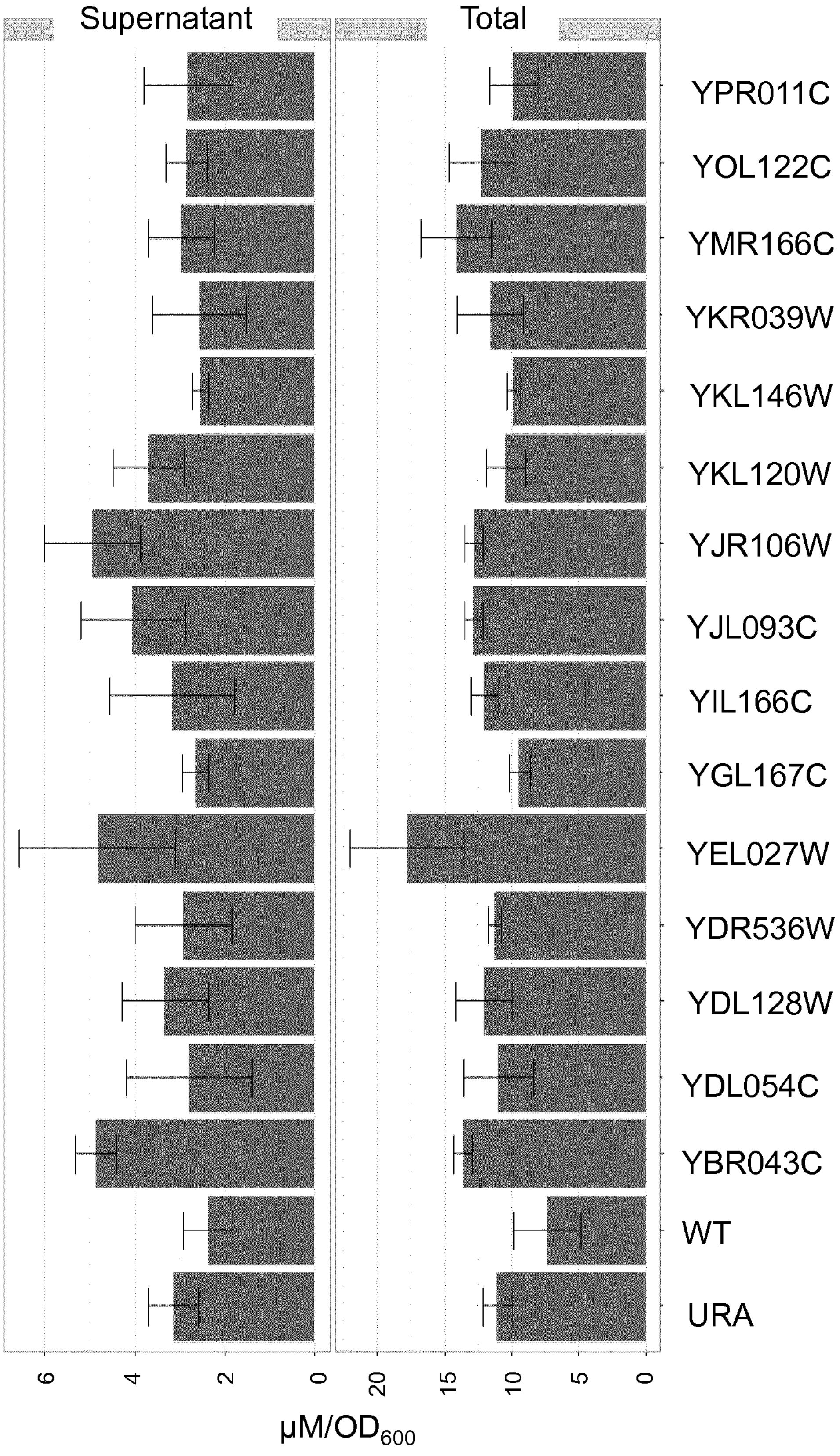


Figure 4C

RebB

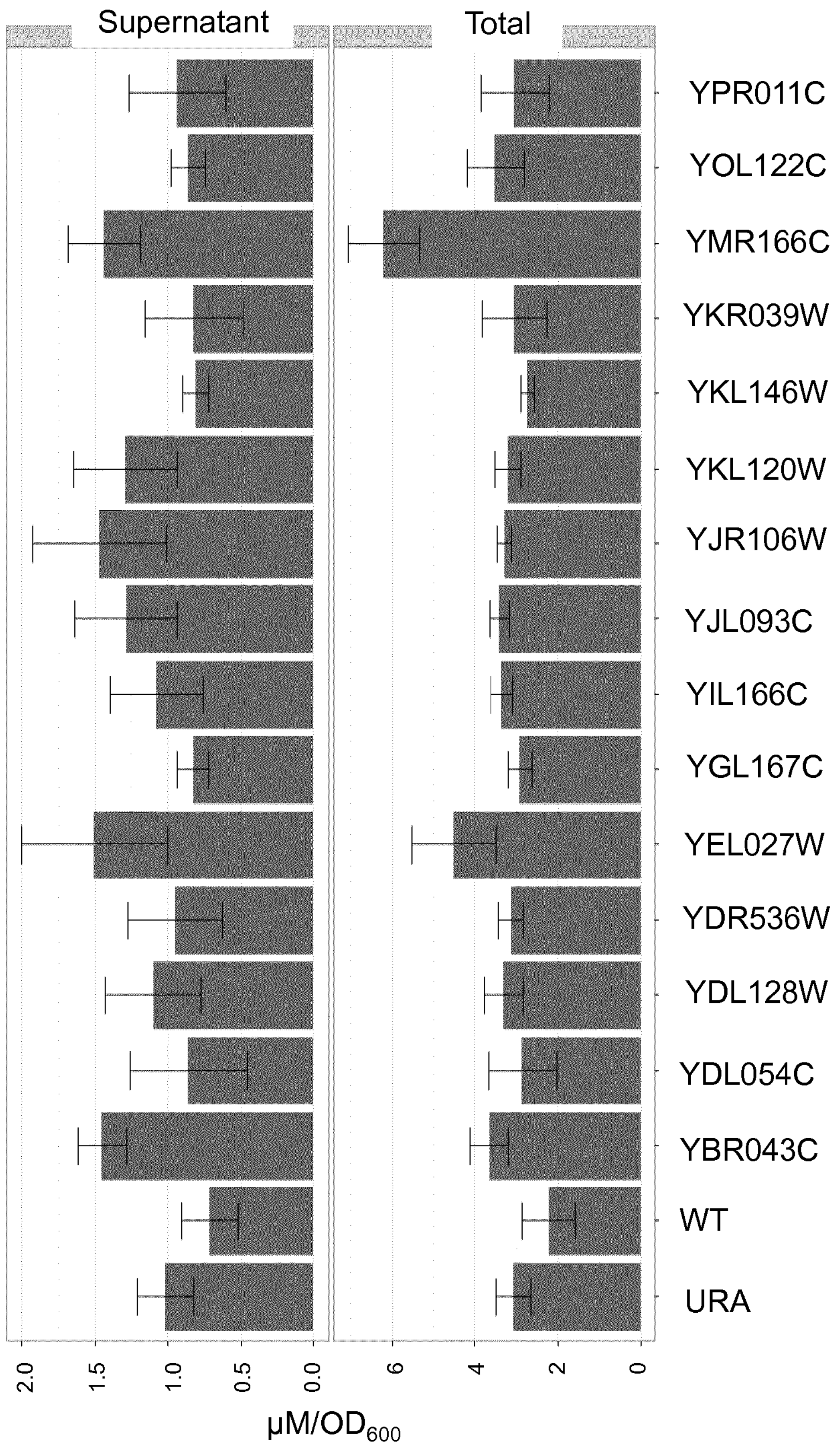


Figure 4D

RebD

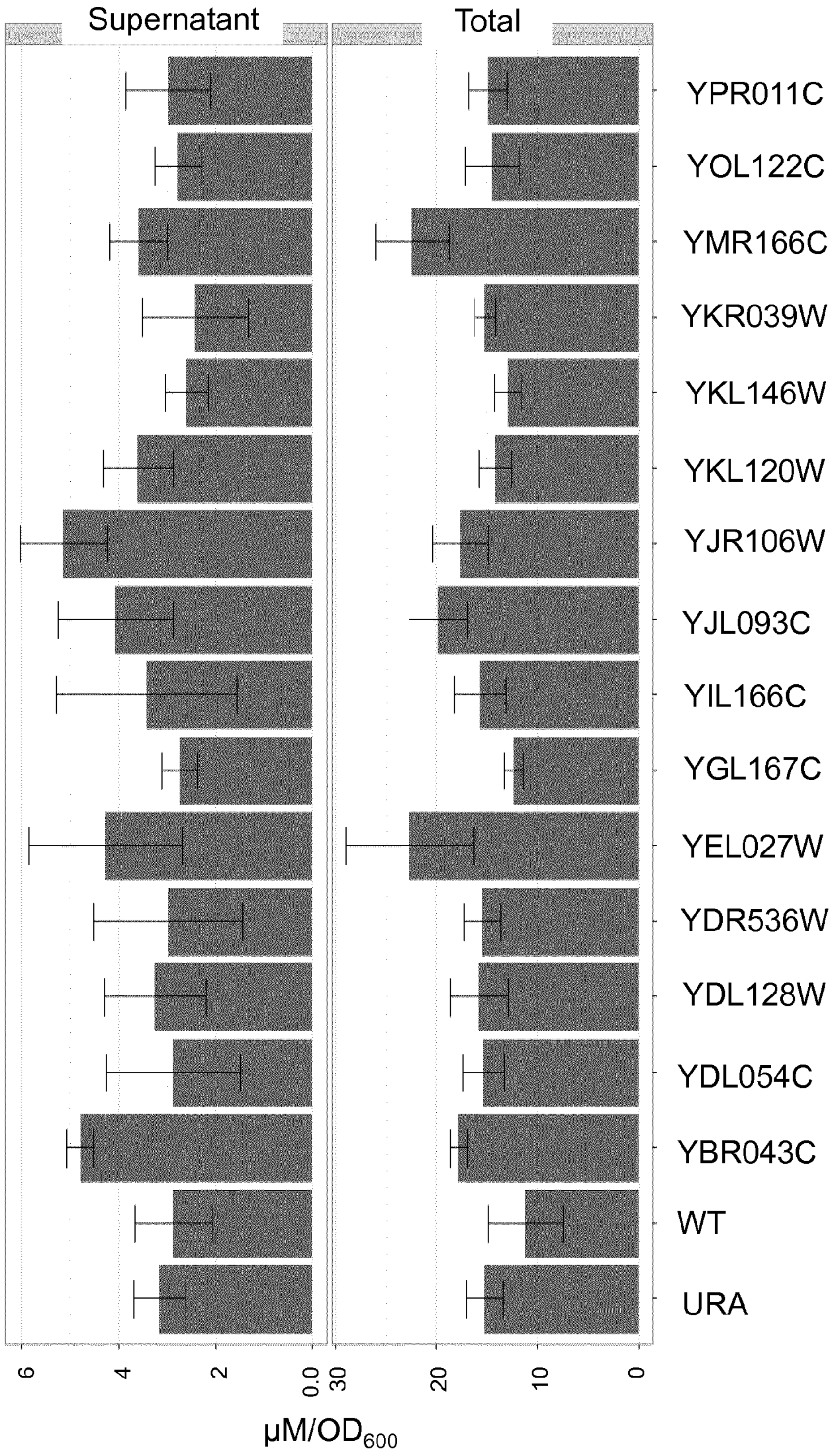


Figure 4E

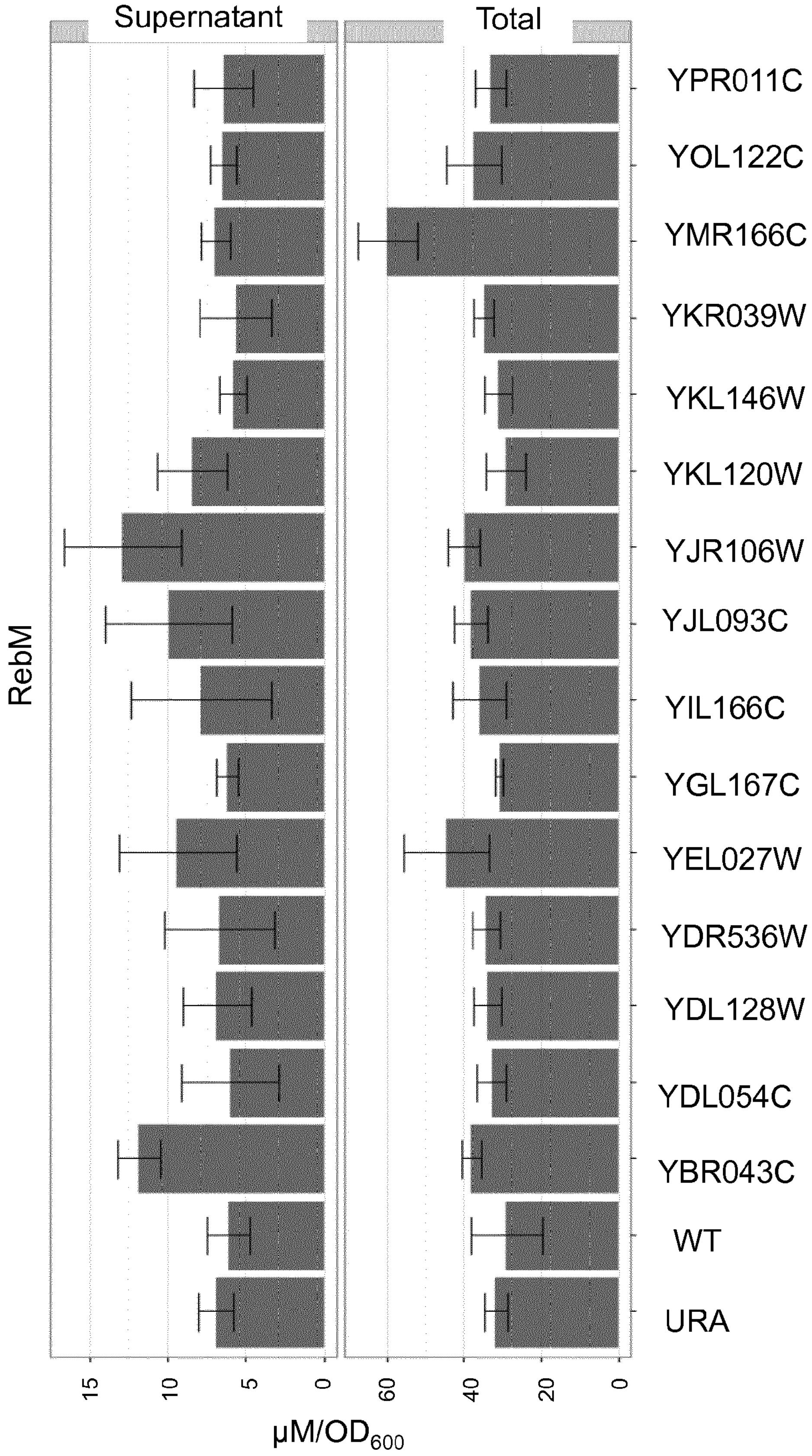

RebM
Supernatant
Total
YPR011C
YOL122C
YMR166C
YKR039W
YKL146W
YKL120W
YJR106W
YJL093C
YIL166C
YGL167C
YEL027W
YDR536W
YDL128W
YDL054C
YBR043C
WT
URA
15
10
5
0
60
40
20
0
μM/OD600

Figure 5A

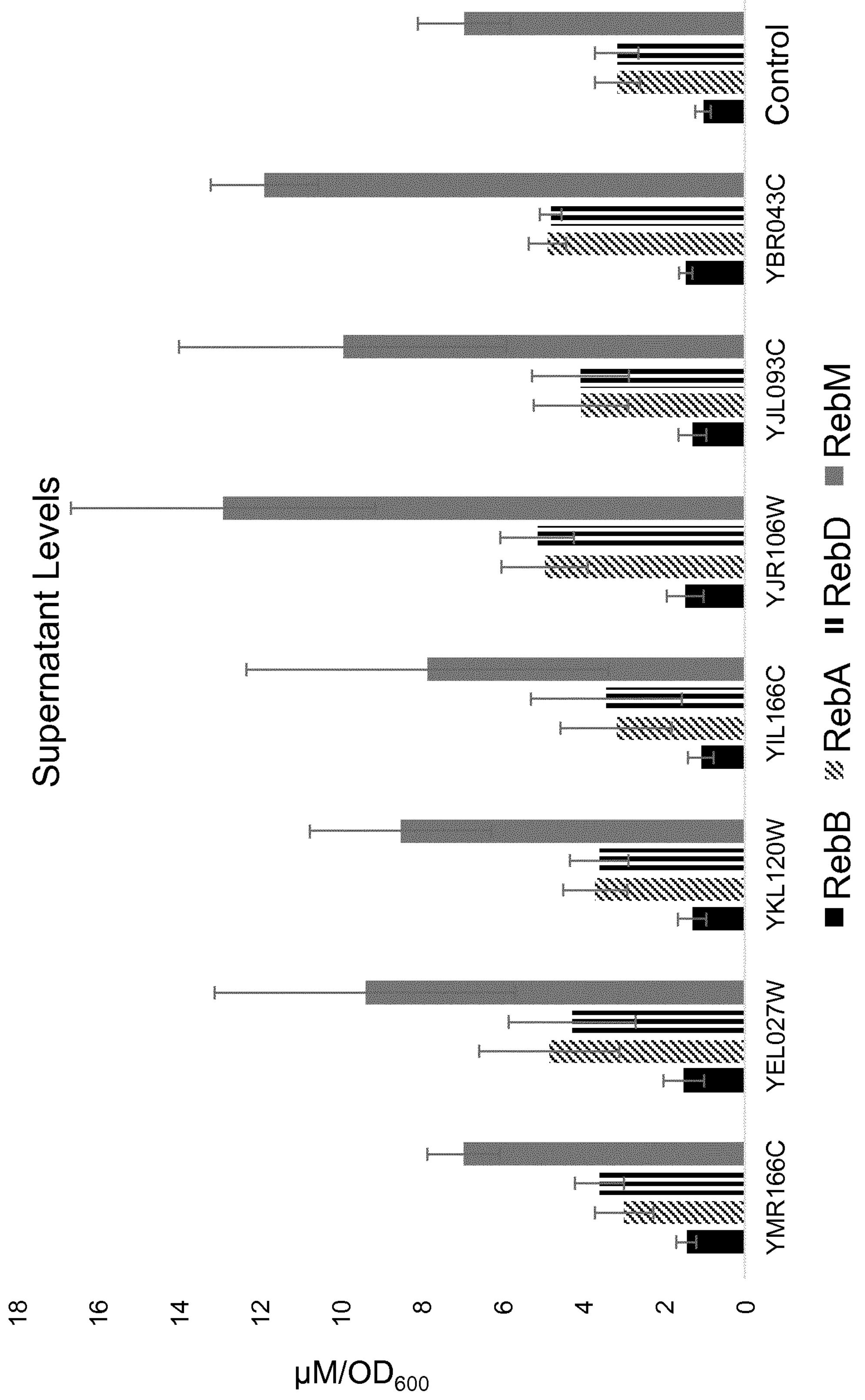
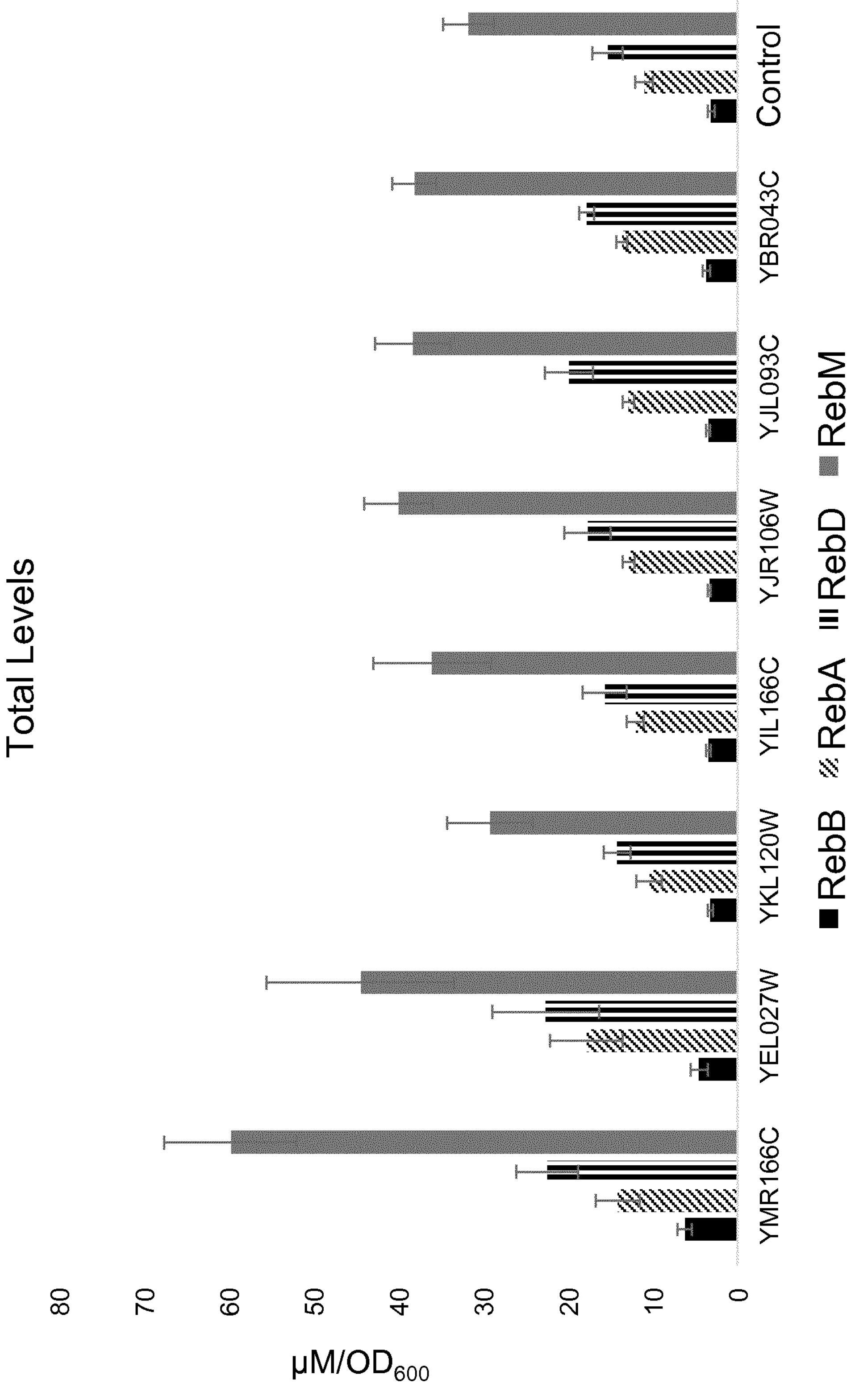

Supernatant Levels
μM/OD600
0
2
4
6
8
10
12
14
16
18
YMR166C
YEL027W
YKL120W
YIL166C
YJR106W
YJL093C
YBR043C
Control
■ RebB
▨ RebA
▤ RebD
■ RebM

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 (AAAP) 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 (Mn^{2+}-iron) transporter (Nramp) family transporter, a transient receptor potential Ca^{2+} 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 adeninivorans, 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. **3**A and FIG. **3**B are bar graphs of the amount (mg/L) of RebA, RebD, or RebM in the supernatant (FIG. **3**A) or total culture (FIG. **3**B) 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. **4**A shows levels of 13-SMG (total levels and supernatant levels; μM/OD_{600}), FIG. **4**B shows levels of RebA (total levels and supernatant levels; μM/OD_{600}), FIG. **4**C shows levels of RebB (total levels and supernatant levels; μM/OD_{600}), FIG. **4**D shows levels of RebD (total levels and supernatant levels; μM/OD_{600}), and FIG. **4**E shows levels of RebM (total levels and supernatant levels; μM/OD_{600}) in a steviol glycoside-producing *S. cerevisiae* strain with a genomically integrated transporter gene. The genomically integrated transporter genes of FIGS. **4**A-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. **5**A shows supernatant levels of RebA, RebB, RebD, and RebM (in μM/OD_{600}) of a steviol glycoside-producing strain overexpressing YMR166C (SEQ ID NO:132), YEL027W (SEQ ID NO:102), YKL120W (SEQ ID NO:126), YIL166C (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. **5**B shows total levels of RebA, RebB, RebD, and RebM (in μM/OD_{600}) of a steviol glycoside-producing strain overexpressing YMR166C (SEQ ID NO:132), YEL027W (SEQ ID NO:102), YKL120W (SEQ ID NO:126), YIL166C (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-glycosylated 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 EUGT11 polypeptides. In yet another particular embodiment, a steviol-producing recombinant microorganism comprises the exogenous nucleic acids encoding UGT85C2, UGT76G1, UGT74G1, 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-amryin acetate, pentacyclic triterpenes, centauredin, quercitin, epi-alpha-cadinol, carophylienes 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, $\mu M/OD_{600}$, mg/L, μM, or mM. Steviol glycoside production (i.e., total, supernatant, and/or intracellular steviol glycoside levels) can be detected and/or analyzed by techniques generally available to one skilled in the art, for example, but not limited to, liquid chromatography-mass spectrometry (LC-MS), thin layer chromatography (TLC), high-performance liquid chromatography (HPLC), ultraviolet-visible spectroscopy/spectrophotometry (UV-Vis), mass spectrometry (MS), and 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 (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 (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 electrochemical 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 (AAAP) 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 (SulP) 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 (Mn^{2+}-iron) transporter (Nramp) family (for example, YOL122C/SMF1), the transient receptor potential Ca^{2+} 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 microorganisms 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 transcriptions 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 transformed exogenous nucleic acids typically are integrated at positions other than the position where the native sequence is found. "Regulatory region" refers to a nucleic acid having nucleotide sequences that influence transcription or translation initiation and rate, and stability and/or mobility of a transcription or translation product. Regulatory regions include, without limitation, promoter sequences, enhancer sequences, response elements, protein recognition sites, inducible elements, protein binding sequences, 5' and 3' untranslated regions (UTRs), transcriptional start sites, termination sequences, polyadenylation sequences, introns, and combinations thereof. A regulatory region typically comprises at least a core (basal) promoter. A regulatory region also may include at least one control element, such as an enhancer sequence, an upstream element or an upstream activation region (UAR). A regulatory region is operably linked to a coding sequence by positioning the regulatory region and the coding sequence so that the regulatory region is effective for regulating transcription or translation of the sequence. For example, to operably link a coding sequence and a promoter sequence, the translation initiation site of the translational reading frame of the coding sequence is typically positioned between one and about fifty nucleotides downstream of the promoter. A regulatory region can, however, be positioned as much as about 5,000 nucleotides upstream of the translation initiation site, or about 2,000 nucleotides upstream of the transcription start site.

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

[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 gossypil*, 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 lipolyptica* can accumulate lipid content to approximately 40% of its dry cell weight and is a model organism for lipid accumulation and remobilization. See e.g., Nicaud, 2012, *Yeast* 29(10):409-18; Beopoulos et al., 2009, *Biohimie* 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] *Rhodosporidium toruloides*

[0150] *Rhodosporidium toruloides* is oleaginous yeast and useful for engineering lipid-production pathways (See e.g. Zhu et al., 2013, *Nature Commun.* 3:1112; Ageitos et al., 2011, *Applied Microbiology and Biotechnology* 90(4):1219-27).

Candida boidinii

[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, *Virol 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 at least 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 Infitity—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 quadropole 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	$[M + H]^+$ 481.2796 $[M + Na]^+$ 503.2615	481.2 ± 0.5 503.1 ± 0.5	19-SMG (2.29), 13-SMG (3.5)
Steviol + 2 Glucose	$[M + Na]^+$ 665.3149	665 ± 0.5	Rubusoside (2.52) Steviol-1,2-bioside (2.92) Steviol-1,3-bioside (2.28)
Steviol + 3 Glucose	$[M + Na]^+$ 827.3677	827.4 ± 0.5	1,2-Stevioside (2.01) 1,3-Stevioside (2.39) RebB (2.88)
Steviol + 4 Glucose	$[M + Na]^+$ 989.4200	989.4 ± 0.5	RebA (2.0)
Steviol + 5 Glucose	$[M + Na]^+$ 1151.4728	1151.4 ± 0.5	RebD (1.1)
Steviol + 6 Glucose	$[M + Na]^+$ 1313.5257	1313.5 ± 0.5	RebM (1.3)

[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 quadrupol 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 μM 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 μm particles, 130 Å pore size) coupled to a Waters ACQUITY TQD triple quadropole 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), redaudioside 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 μg/mL or 1-1.5 μg/mL/OD$_{600}$ 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 *S. cerevisiae* strain comprising genes encoding GGPPS, truncated CDPS, KS, KO, ATR2, EUGT11, SrKAHe1, CPR8, UGT85C2, UGT74G1, UGT76G1, and EUGT11 polypeptides.

RebB (μg/mL/ OD$_{600}$)	RebA (μg/mL/ OD$_{600}$)	RebD (μg/mL/ OD$_{600}$)	RebM (μg/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 (μg/mL)	RebA (μg/mL)	RebD (μg/mL)	RebM (μg/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 μg/mL or 4-6 μg/mL/OD$_{600}$ 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 *S. cerevisiae* strain comprising additional copies of genes encoding GGPPS, truncated CDPS, KS, KO, ATR2, EUGT11, SrKAHe1, CPR8, UGT85C2, UGT74G1, UGT76G1, and EUGT11 polypeptides.

RebA (μg/mL/ OD_{600})	RebB (μg/mL/ OD_{600})	RebD (μg/mL/ OD_{600})	RebM (μg/mL/ 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 (μg/mL)	RebB (μg/mL)	RebD (μg/mL)	RebM (μg/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	P0CE00
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.

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	0.790		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					
YJL212C			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	0.608			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 supernatant, 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.

	Transports 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 intergration 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. **3**A. 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 OD_{600} 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. **4**A). YBR043C (SEQ ID NO:88), YEL027W (SEQ ID NO:102), and YMR166C (SEQ ID NO:132) showed improved excretion of RebA (FIG. **4**B). YBR043C (SEQ ID NO:88), YEL027W (SEQ ID NO:102), and YMR166C (SEQ ID NO:132) showed improved excretion of RebB (FIG. **4**C). 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. **4**D and **4**E. Controls with a URA marker are also shown in FIG. **4**.

[0205] FIG. **5**A 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. **5**B 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 RebD+RebM, as compared to a control steviol glycoside-producing strain.

TABLE 13

Production of RebD and RebM in *S. cerevisiae* 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

Synechococcus sp. GGPPS (GenBank ABC98596.1)

```
atggtcgcac 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
ttagcttacg cttttgaaca tattgcttct caaacaagag gagtaccacc tcaattggtg      420
ctacaagtta ttgctagaat cggacacgcc gttgctgcaa caggcctcgt tggaggccaa      480
gtcgtagacc ttgaatctga aggtaaagct atttccttag aaacattgga gtatattcac      540
tcacataaga ctggagcctt gctggaagca tcagttgtct caggcggtat tctcgcaggg      600
gcagatgaag agcttttggc cagattgtct cattacgcta gagatatagg cttggctttt      660
caaatcgtcg atgatatcct ggatgttact gctacatctg aacagttggg gaaaaccgct      720
ggtaaagacc aggcagccgc aaaggcaact tatccaagtc tattgggttt agaagcctct      780
agacagaaag cggaagagtt gattcaatct gctaaggaag ccttaagacc ttacggttca      840
caagcagagc cactcctagc gctggcagac ttcatcacac gtcgtcagca ttaa            894
```

SEQ ID NO: 2

Zea mays truncated CDPS

```
atggcacagcaca catcagaatc cgcagctgtc gcaaagggca gcagtttgac ccctatagtg    60
agaactgacg ctgagtcaag gagaacaaga tggccaaccg atgacgatga cgccgaacct      120
ttagtggatg agatcagggc aatgcttact tccatgtctg atggtgacat ttccgtgagc      180
gcatacgata cagcctgggt cggattggtt ccaagattag acggcggtga aggtcctcaa      240
tttccagcag ctgtgagatg gataagaaat aaccagttgc ctgacggaag ttggggcgat      300
gccgcattat tctctgccta tgacaggctt atcaataccc ttgcctgcgt tgtaactttg      360
acaaggtggt ccctagaacc agagatgaga ggtagaggac tatctttttt gggtaggaac      420
atgtggaaat tagcaactga agatgaagag tcaatgccta ttggcttcga attagcattt      480
ccatctttga tagagcttgc taagagccta ggtgtccatg acttccctta tgatcaccag      540
gccctacaag gaatctactc ttcaagagag atcaaaatga agaggattcc aaaagaagtg      600
atgcataccg ttccaacatc aatattgcac agtttggagg gtatgcctgg cctagattgg      660
gctaaactac ttaaactaca gaggagcgac ggaagttttt tgttctcacc agctgccact      720
gcatatgctt taatgaatac cggagatgac aggtgtttta gctacatcga tagaacagta      780
aagaaattca acggcggcgt ccctaatgtt tatccagtgg atctatttga acatatttgg      840
gccgttgata gacttgaaag attaggaatc tccaggtact tccaaaagga gatcgaacaa      900
tgcatggatt atgtaaacag gcattggact gaggacggta tttgttgggc aaggaactct      960
gatgtcaaag aggtggacga cacagctatg gcctttagac ttcttaggtt gcacggctac     1020
agcgtcagtc ctgatgtgtt taaaaacttc gaaaaggacg gtgaattttt cgcatttgtc     1080
ggacagtcta atcaagctgt taccggtatg tacaacttaa acagagcaag ccagatatcc     1140
ttcccaggcg aggatgtgct tcatagagct ggtgccttct catatgagtt cttgaggaga     1200
aaagaagcag agggagcttt gagggacaag tggatcattt ctaaagatct acctggtgaa     1260
gttgtgtata ctttggattt tccatggtac ggcaacttac ctagagtcga ggccagagac     1320
tacctagagc aatacggagg tggtgatgac gtttggattg gcaagacatt gtataggatg     1380
ccacttgtaa acaatgatgt atatttggaa ttggcaagaa tggatttcaa ccactgccag     1440
gctttgcatc agttagagtg gcaaggacta aaaagatggt atactgaaaa taggttgatg     1500
gactttggtg tcgcccaaga agatgccctt agagcttatt ttcttgcagc cgcatctgtt     1560
tacgagcctt gtagagctgc cgagaggctt gcatgggcta gagccgcaat actagctaac     1620
gccgtgagca cccacttaag aaatagccca tcattcagag aaaggttaga gcattctctt     1680
aggtgtagac ctagtgaaga gacagatggc tcctggttta actcctcaag tggctctgat     1740
gcagttttag taaaggctgt cttaagactt actgattcat tagccaggga agcacagcca     1800
atccatggag gtgacccaga agatattata cacaagttgt taagatctgc ttgggccgag     1860
tgggttaggg aaaaggcaga cgctgccgat agcgtgtgca atggtagttc tgcagtagaa     1920
caagagggat caagaatggt ccatgataaa cagacctgtc tattattggc tagaatgatc     1980
gaaatttctg ccggtagggc agctggtgaa gcagccagtg aggacggcga tagaagaata     2040
attcaattaa caggctccat ctgcgacagt cttaagcaaa aaatgctagt ttcacaggac     2100
cctgaaaaaa atgaagagat gatgtctcac gtggatgacg aattgaagtt gaggattaga     2160
gagttcgttc aatatttgct tagactaggt gaaaaaaaga ctggatctag cgaaaccagg     2220
caaacatttt taagtatagt gaaatcatgt tactatgctg ctcattgccc acctcatgtc     2280
gttgatagac acattagtag agtgattttc gagccagtaa gtgccgcaaa gtaaccgcgg     2340
```

TABLE 14-continued

Sequences disclosed herein.	
SEQ ID NO: 3	
Arabidopsis thaliana KS (similar to GenBank AEE36246.1)	
atgtctatta atttgagatc ttccggttgt agctccccaa taagcgcaac tttggaaagg	60
ggtctagact ctgaagttca aacaagagca aacaatgtat cttttgagca gaccaaagag	120
aagatcagga aaatgcttga gaaggtcgag ttgagcgtga gtgcctatga cactagttgg	180
gtagctatgg tcccatcacc atccagtcaa aacgcacctc ttttcccaca gtgcgtcaaa	240
tggctacttg ataatcaaca tgaggacggc tcttggggat tggataacca cgaccatcag	300
agcttaaaga aagatgtgtt gtcatccaca ttagcctcta tcctagctct taagaaatgg	360
ggaataggcg aaagacagat caataagggt ctacagttca ttgaattaaa ctctgcacta	420
gttaccgatg aaactataca aaaacctaca ggtttcgaca tcatttttcc aggaatgalt	480
aagtacgcca gggaccttaa tttgaccata cctcttggct cagaagtagt cgacgatatg	540
atcaggaaaa gagatctaga cttaaagtgt gatagcgaga aattcagcaa aggtagagag	600
gcttatcttg cctatgttct tgaaggaact aggaacttga aggactggga cttaattgtg	660
aaatatcaga gaaagaacgg tagtctattt gatagtccag ctacaaccgc cgcagctttc	720
actcaatttg gcaatgacgg ttgcttgagg tacttatgtt cacttttaca gaaattcgag	780
gccgcagtgc ctagtgtata tccatttgat caatacgcta gattaagcat aatcgtcact	840
ttagaatcat tgggaattga cagagatttc aagactgaga taaaaagcat attggatgag	900
acctataggt actggcttag aggtgacgaa gaaatttgcc tagatttggc cacatgtgca	960
cttgctttta ggttgctttt agcccacggc tatgacgtgt catacgatcc tctaaagcca	1020
tttgcagagg aatctggttt cagcgatacc cttgagggat atgttaaaaa caccttttcc	1080
gtattagagc ttttcaaggc tgcccaaagt taccctcatg agagtgcttt gaaaaagcag	1140
tgttgctgga caaaacaata tctagaaatg gaactaagtt catgggttaa aacaagcgtt	1200
agggacaagt acttgaaaaa ggaagtggag gatgctttgg catttccatc atatgcctct	1260
ttaaaaagaa gtgaccacag aaggaaaatt cttaatggct cagcagttga aaacacaaga	1320
gtaaccaaga cctcttacag gttgcataat atatgtacat cagatatctt aaaacttgct	1380
gtcgacgatt tcaacttttg ccaatctatt catagagagg aaatggaaag attggataga	1440
tggatagtgg agaatagact acaggaatta aagttcgcca gacaaaaatt ggcttactgt	1500
tactttagtg gcgctgccac actattctct ccagaattgt ctgacgcaag gatctcatgg	1560
gctaagggag gtgttctaac cacagtagtc gatgactttt ttgatgttgg cggtagtaaa	1620
gaagagcttg agaacttaat tcacttggtg caaaagtggg atcttaatgg agttcctgaa	1680
tactcttcag agcatgtaga aataattttc tctgtcctaa gagacactat cttagaaacc	1740
ggtgataaag cctttacata tcagggcaga aacgttactc accatattgt gaaaatatgg	1800
ttggacttac ttaagagcat gctaagggag gctgaatggt ccagtgacaa atcaacccca	1860
tctttggaag attacatgga gaatgcctat atcagcttcg cattaggtcc tattgtattg	1920
ccagctacat accttatagg acctccacta cctgaaaaga ctgtcgactc ccaccaatat	1980
aatcaattat acaaattggt tagtaccatg ggtagactat taaacgatat ccagggcttt	2040
aagagggaat cagccgaggg aaaacttaat gcagtgtctc tacatatgaa gcatgaaaga	2100
gacaacagaa gcaaagaggt tattatagaa tccatgaaag gattggctga aaggaaaaga	2160
gaggaattac acaaacttgt actagaagag aaaggtagtg 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 KO1 (codon optimized)	
atggatgctg tgacgggttt gttaactgtc ccagcaaccg ctataactat tggtggaact	60
gctgtagcat tggcggtagc gctaatcttt tggtacctga aatcctacac atcagctaga	120
agatcccaat caaatcatct tccaagagtg cctgaagtcc caggtgttcc attgttagga	180
aatctgttac aattgaagga gaaaaagcca tacatgactt ttacgagatg ggcagcgaca	240
tatggaccta tctatagtat caaaactggg gctacaagta tggttgtggt atcatctaat	300
gagatagcca aggaggcatt ggtgaccaga ttccaatcca tatctacaag gaacttatct	360
aaagccctga aagtacttac agcagataag acaatggtcg caatgtcaga ttatgatgat	420
tatcataaaa cagttaagag acacatactg accgccgtct tgggtcctaa tgcacagaaa	480
aagcatagaa ttcacagaga tatcatgatg gataacatat ctactcaact tcatgaattc	540
gtgaaaaaca acccagaaca ggaagaggta gaccttagaa aaatctttca atctgagtta	600
ttcggcttag ctatgagaca agccttagga aaggatgttg aaagtttgta cgttgaagac	660
ctgaaaatca ctatgaatag agacgaaatc tttcaagtcc ttgttgttga tccaatgatg	720
ggagcaatcg atgttgattg gagagacttc tttccatacc taaagtgggt cccaaacaaa	780
aagttcgaaa atactattca acaaatgtac atcagaagag aagctgttat gaaatcttta	840
atcaaagagc acaaaaagag aatagcgtca ggcgaaaagc taaatagtta tatcgattac	900
cttttatctg aagctcaaac tttaaccgat cagcaactat tgatgtcctt gtgggaacca	960
atcattgaat cttcagatac aacaatggtc acaacagaat gggcaatgta cgaattagct	1020
aaaaacccta aattgcaaga taggttgtac agagacatta agtccgtctg tggatctgaa	1080
aagataaccg aagagcatct atcacagctg ccttacatta cagctatttt ccacgaaaca	1140
ctgagaagac actcaccagt tcctatcatt cctctaagac atgtacatga agataccgtt	1200
ctaggcggct accatgttcc tgctggcaca gaacttgccg ttaacatcta cggttgcaac	1260
atggacaaaa acgtttggga aaatccagag gaatggaacc cagaaagatt catgaaagag	1320
aatgagacaa ttgattttca aaagacgatg gccttcggtg gtggtaagag agtttgtgct	1380
ggttccttgc aagccctttt aactgcatct attgggattg ggagaatggt tcaagagttc	1440
gaatggaaac tgaaggatat gactcaagag gaagtgaaca cgataggcct aactacacaa	1500
atgttaagac cattgagagc tattatcaaa cctaggatct aa	1542

TABLE 14-continued

Sequences disclosed herein.

SEQ ID NO: 5
A. thaliana ATR2 (codon optimized)
atgtcttcct cttcctcttc cagtacctct atgattgatt tgatggctgc tattattaaa 60
ggtgaaccag ttatcgtctc cgacccagca aatgcctctg cttatgaatc agttgctgca 120
gaattgtctt caatgttgat cgaaaacaga caattcgcca tgatcgtaac tacatcaatc 180
gctgttttga tcggttgtat tgtcatgttg gtatggagaa gatccggtag tggtaattct 240
aaaagagtcg aacctttgaa accattagta attaagccaa gagaagaaga aatagatgac 300
ggtagaaaga aagttacaat atttttcggt acccaaactg gtacagctga aggttttgca 360
aaagccttag gtgaagaagc taaggcaaga tacgaaaaga ctagattcaa gatagtcgat 420
ttggatgact atgccgctga tgacgatgaa tacgaagaaa agttgaagaa agaagatgtt 480
gcatttttct tttggcaac ctatggtgac ggtgaaccaa ctgacaatgc agccagattc 540
tacaaatggt ttacagaggg taatgatcgt ggtgaatggt tgaaaaactt aaagtacggt 600
gttttcggtt tgggtaacag acaatacgaa catttcaaca aagttgcaaa ggttgtcgac 660
gatattttgg tcgaacaagg tgctcaaaga ttagtccaag taggtttggg tgacgatgac 720
caatgtatag aagatgactt tactgcctgg agagaagctt tgtggcctga attagacaca 780
atcttgagag aagaaggtga caccgccgtt gctaccccat atactgctgc agtattagaa 840
tacagagttt ccatccatga tagtgaagac gcaaagttta atgatatcac tttggccaat 900
ggtaacggtt atacagtttt cgatgcacaa caccсttaca aagctaacgt tgcagtcaag 960
agagaattac atacaccaga atccgacaga agttgtatac acttggaatt tgatatcgct 1020
ggttccggtt taaccatgaa gttgggtgac catgtaggtg ttttatgcga caatttgtct 1080
gaaactgttg atgaagcatt gagattgttg gatatgtccc ctgacactta ttttagtttg 1140
cacgctgaaa aagaagatgg tacaccaatt tccagttctt taccacctcc attccctcca 1200
tgtaacttaa gaacagcctt gaccagatac gcttgcttgt tatcatcccc taaaaagtcc 1260
gccttggttg ctttagccgc tcatgctagt gatcctactg aagcagaaag attgaaacac 1320
ttagcatctc cagccggtaa agatgaatat tcaaagtggg tagttgaatc tcaaagatca 1380
ttgttagaag ttatggcaga atttccatct gccaagcctc cattaggtgt cttctttgct 1440
ggtgtagcac ctagattgca accaagattc tactcaatca gttcttcacc taagatcgct 1500
gaaactagaa ttcatgttac atgtgcatta gtctacgaaa agatgccaac cggtagaatt 1560
cacaagggtg tatgctctac ttggatgaaa aatgctgttc cttacgaaaa atcagaaaag 1620
ttgttcttag gtagaccaat cttcgtaaga caatcaaact tcaagttgcc ttctgattca 1680
aaggttccaa taatcatgat aggtcctggt acaggtttag ccccattcag aggtttcttg 1740
caagaaagat tggctttagt tgaatctggt gtcgaattag gtccttcagt tttgttcttt 1800
ggttgtagaa acagaagaat ggatttcatc tatgaagaag aattgcaaag attcgtcgaa 1860
tctggtgcat tggccgaatt atctgtagct tttcaagag aaggtccaac taaggaatac 1920
gttcaacata agatgatgga taaggcatcc gacatatgga acatgatcag tcaaggtgct 1980
tatttgtacg tttgcggtga cgcaaagggt atggccagag atgtccatag atctttgcac 2040
acaattgctc aagaacaagg ttccatggat agtaccaaag ctgaaggttt cgtaaagaac 2100
ttacaaactt ccggtagata cttgagagat gtctggtga 2139

SEQ ID NO: 6
Stevia rebaudiana KAHe1 (codon-optimized)
atggaagcct cttacctata catttctatt ttgcttttac tggcatcata cctgttcacc 60
actcaactta gaaggaagag cgctaatcta ccaccaaccg tgtttccatc aataccaatc 120
attggacact tatacttact caaaaagcct ctttatagaa ctttagcaaa aattgccgct 180
aagtacggac caatactgca attacaactc ggctacagac gtgttctggt gatttcctca 240
ccatcagcag cagaagagtg ctttaccaat aacgatgtaa tcttcgcaaa tagacctaag 300
acattgtttg gcaaaatagt gggtggaaca tcccttggca gtttatccta cggcgatcaa 360
tggcgtaatc taaggagagt agcttctatc gaaatcctat cagttcatag gttgaacgaa 420
tttcatgata tcagagtgga tgagaacaga ttgttaatta gaaaacttag aagttcatct 480
tctcctgtta ctcttataac agtcttttat gctctaacat tgaacgtcat tatgagaatg 540
atctctggca aaagatattt cgacagtggg gatagagaat tggaggagga aggtaagaga 600
tttcgagaaa tcttagacga aacgttgctt ctagccggtg cttctaatgt tggcgactac 660
ttaccaatat tgaactggtt gggagttaag tctcttgaaa agaaattgat cgctttgcag 720
aaaaagagag atgacttttt ccagggtttg attgaacagg ttagaaaatc tcgtggtgct 780
aaagtaggca aaggtagaaa aacgatgatc gaactcttat tatctttgca agagtcagaa 840
cctgagtact atacagatgc tatgataaga tcttttgtcc taggtctgct ggctgcaggt 900
agtgatactt cagcgggcac tatggaatgg gccatgagct tactggtcaa tcacccacat 960
gtattgaaga aagctcaagc tgaaatcgat agagttatcg gtaataacag attgattgac 1020
gagtcagaca ttggaaatat cccttacatc gggtgtatta tcaatgaaac tctaagactc 1080
tatccagcag ggccattgtt gttcccacat gaaagttctg ccgactgcgt tatttccggt 1140
tacaatatac ctagaggtac aatgttaatc gtaaaccaat gggcgattca tcacgatcct 1200
aaagtctygg atgatcctga aacctttaaa cctgaaagat ttcaaggatt agaaggaact 1260
agagatggtt tcaaacttat gccattcggt tctgggagaa gaggatgtcc aggtgaaggt 1320
ttggcaataa ggctgttagg gatgacacta ggctcagtga tccaatgttt tgattgggag 1380
agagtaggag atgagatggt tgacatgaca gaaggtttgg gtgtcacact tcctaaggcc 1440
gttccattag ttgccaaatg taagccacgt tccgaaatga ctaatctcct atccgaactt 1500
taa 1503

SEQ ID NO: 7
Stevia rebaudiana CPR8
ATGCAATCTAACTCCGTGAAGATTTCGCCGCTTGATCTGGTAACTGCGCTGTTTAGCGGCAAGGTTTT
GGACACATCGAACGCATCGGAATCGGGAGAATCTGCTATGCTGCCGACTATAGCGATGATTATGGAGA
ATCGTGAGCTGTTGATGATACTCACAACGTCGGTTGCTGTATTGATCGGATGCGTTGTCGTTTTGGTG
TGGCGGAGATCGTCTACGAAGAAGTCGGCGTTCGAGCCACCGGTGATTGTGGTTCCGAAGAGAGTGCA

TABLE 14-continued

Sequences disclosed herein.

```
AGAGGAGGAAGTTGATGATGGTAAGAAGAAAGTTACGGTTTTCTTCGGCACCCAAACTGGAACAGCTG
AAGGCTTCGCTAAGGCACTTGTTGAGGAAGCTAAAGCTCGATATGAAAAGGCTGTCTTTAAAGTAATT
GATTTGCATGATTATGCTGCTGATGACDATGAGTATGAGGAGAAACTAAAGAAAGAATCTTTGGCCTT
TTTCTTTTTGGCTACGTATGGAGATGGTGAGCCAACAGATAATGCTGCCAGATTTTATAAATGGTTTA
CTGAGGGAGATGCGAAAGGAGAATGGCTTAATAAGCTTCAATATGGAGTATTTGGTTTGGGTAACAGA
CAATATGAACATTTTAACAAGATCGCAAAAGTGGTTGATGATGGTCTTGTAGAACAGGGTGCAAAGCG
TCTTGTTCCTGTTGGACTTGGAGATGATGATCAATGTATTGAAGATGACTTCACCGCATGGAAAGAGT
TAGTATGGCCGGAGTTGGATCAATTACTTCGTGATGAGGATGACACAACTGTTGCTACTCCATACACA
GCTGCTGTTGCAGAATATCGCGTTGTTTTTCATGAAAAACCAGACGCGGTTTCTGAAGATTATAGTTA
TACAAATGGCCATGCTGTTCATGATGCTCAACATCCATGCAGATCCAACGTGGCTGTCAAAAAGGAAC
TTCATAGTCCTGAATCTGACCGGTCTTGCACTCATCTTGAATTTGACATCTCGAACACCGGACTATCA
TATGAAACTGGGGACCATGTTGGAGTTTACTGTGAAAACTTGAGTGAAGTTGTGAATGATGCTGAAAG
ATTAGTAGGATTACCACCAGACACTTACTCCTCCATCCACACTGATAGTGAAGACGGGTCGCCACTTG
GCGGAGCCTCATTGCCGCCTCCTTTCCCGCCATGCACTTTAAGGAAAGCATTGACGTGTTATGCTGAT
GTTTTGAGTTCTCCCAAGAAGTCGGCTTTGCTTGCACTAGCTGCTCATGCCACCGATCCCAGTGAAGC
TGATAGATTGAAATTTCTTGCATCCCCCGCCGGAAAGGATGAATATTCTCAATGGATAGTTGCAAGCC
AAAGAAGTCTCCTTGAAGTCATGGAAGCATTCCCGTCAGCTAAGCCTTCACTTGGTGTTTTCTTTGCA
TCTGTTGCCCCGCGCTTACAACCAAGATACTACTCTATTTCTTCCTCACCCAAGATGGCACCGGATAG
GATTCATGTTACATGTGCATTAGTCTATGAGAAAACACCTGCAGGCCGCATCCACAAAGGAGTTTGTT
CAACTTGGATGAAGAACGCAGTGCCTATGACCGAGAGTCAAGATTGCAGTTGGGCCCCAATATACGTC
CGAACATCCAATTTCAGACTACCATCTGACCCTAAGGTCCCGGTTATCATGATTGGACCTGGCACTGG
TTTGGCTCCTTTTAGAGGTTTCCTTCAAGAGCGGTTAGCTTTAAAGGAAGCCGGAACTGACCTCGGTT
TATCCATTTTATTCTTCGGATGTAGGAATCGCAAAGTGGATTTCATATATGAAAACGAGCTTAACAAC
TTTGTGGAGACTGGTGCTCTTTCTGAGCTTATTGTTGCTTTCTCCCGTGAAGGCCCGACTAAGGAATA
TGTGCAACACAAGATGAGTGAGAAGGCTTCGGATATCTGGAACTTGCTTTCTGAAGGAGCATATTTAT
ACGTATGTGGTGATGCCAAAGGCATGGCCAAAGATGTACATCGAACCCTCCACACAATTGTGCAAGAA
CAGGGATCTCTTGACTCGTCAAAGGCAGAACTCTACGTGAAGAATCTACAAATGTCAGGAAGATACCT
CCGTGACGTTTGGTAA
```

SEQ ID NO: 8

Stevia rebaudiana UGT85C2 (codon optimized)

```
atggatgcaa tggcaactac tgagaaaaag cctcatgtga tcttcattcc atttcctgca      60
caatctcaca taaaggcaat gctaaagtta gcacaactat tacaccataa gggattacag     120
ataactttcg tgaataccga cttcatccat aatcaatttc tggaatctag tggccctcat     180
tgtttggacg gagccccagg gtttagattc gaaacaattc ctgacggtgt ttcacattcc     240
ccagaggcct ccatcccaat aagagagagt ttactgaggt caatagaaac caactttttg     300
gatcgtttca ttgacttggt cacaaaactt ccagacccac caacttgcat aatctctgat     360
ggctttctgt cagtgtttac tatcgacgct gccaaaaagt tgggtatccc agttatgatg     420
tactggactc ttgctgcatg cggtttcatg ggtttctatc acatccattc tcttatcgaa     480
aagggttttg ctccactgaa agatgcatca tacttaacca acggctacct ggatactgtt     540
attgactggg taccaggtat ggaaggtata agacttaaag attttccttt ggattggtct     600
acagacctta atgataaagt attgatgttt actacagaag ctccacaaag atctcataag     660
gtttcacatc atatctttca cacctttgat gaattggaac catcaatcat caaaaccttg     720
tctctaagat acaatcatat ctacactatt ggtccattac aattacttct agatcaaatt     780
cctgaagaga aaaagcaaac tggtattaca tccttacacg gctactcttt agtgaaagag     840
gaaccagaat gttttcaatg gctacaaagt aaagagccta attctgtggt ctacgtcaac     900
ttcggaagta caacagtcat gtccttggaa gatatgactg aatttggttg gggccttgct     960
aattcaaatc attactttct atggattatc aggtccaatt tggtaatagg ggaaaacgcc    1020
gtattacctc cagaattgga ggaacacatc aaaaagagag gtttcattgc ttcctggtgt    1080
tctcaggaaa aggtattgaa acatccttct gttggtggtt tccttactca ttgcggttgg    1140
ggctctacaa tcgaatcact aagtgcagga gttccaatga tttgttggcc atattcatgg    1200
gaccaactta caaattgtag gtatatctgt aaagagtggg aagttggatt agaaatggga    1260
acaaaggtta aacgtgatga agtgaaaaga ttggttcagg agttgatggg ggaaggtggc    1320
cacaagatga gaaacaaggc caaagattgg aaggaaaaag ccagaattgc tattgctcct    1380
aacgggtcat cctctctaaa cattgataag atggtcaaag agattacagt cttagccaga    1440
aactaa                                                               1446
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SEQ ID NO: 9

S. rebaudiana UGT74G1 (GenBank AAR06920.1)

```
atggcggaac aacaaaagat caagaaatca ccacacgttc tactcatccc attcccttta      60
caaggccata taaacccttt catccagttt ggcaaacgat taatctccaa aggtgtcaaa     120
acaacacttg ttaccaccat ccacacctta aactcaaccc taaaccacag taacaccacc     180
accacctcca tcgaaatcca agcaatttcc gatggttgtg atgaaggcgg ttttatgagt     240
gcaggagaat catatttgga aacattcaaa caagttgggt ctaaatcact agctgactta     300
atcaagaagc ttcaaagtga aggaaccaca attgatgcaa tcatttatga ttctatgact     360
gaatgggttt tagatgttgc aattgagttt ggaatcgatg gtggttcgtt tttcactcaa     420
gcttgtgttg taaacagctt atattatcat gttcataagg gtttgatttc tttgccattg     480
ggtgaaactg tttcggttcc tggatttcca gtgcttcaac ggtyggagac accgttaatt     540
ttgcagaatc atgagcaaat acagagccct tggtctcaga tgttgtttgg tcagtttgct     600
aatattgatc aagcacgttg ggtcttcaca aatagttttt acaagctcga ggaagaggta     660
atagagtgga cgagaaagat atggaacttg aaggtaatcg ggccaacact tccatccatg     720
taccttgaca aacgacttga tgatgataaa gataacggat ttaatctcta caaagcaaac     780
catcatgagt gcatgaactg gttagacgat aagccaaagg aatcagttgt ttacgtagca     840
tttggtagcc tggtgaaaca tggacccgaa caagtggaag aaatcacacg ggctttaata     900
gatagtgatg tcaacttctt gtgggttatc aaacataaag aagagggaaa gctcccagaa     960
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TABLE 14-continued

Sequences disclosed herein.

aatctttcgg aagtaataaa aaccggaaag ggtttgattg tagcatggtg caaacaattg 1020
gatgtgttag cacacgaatc agtaggatgc tttgttacac attgtgggtt caactcaact 1080
cttgaagcaa taagtcttgg agtccccgtt gttgcaatgc ctcaattttc ggatcaaact 1140
acaaatgcca agcttctaga tgaaattttg ggtgttggag ttagagttaa ggctgatgag 1200
aatgggatag tgagaagagg aaatcttgcg tcatgtatta agatgattat ggaggaggaa 1260
agaggagtaa taatccgaaa gaatgcggta aaatggaagg atttggctaa agtagccgtt 1320
catgaaggtg gtagctcaga caatgatatt gtcgaatttg taagtgagct aattaaggct 1380
taaatttttg ttgctttgta ttttatgtgt tatggttttt tgatttagat gtattcaatt 1440
aatattgaat 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 ctctaaaggt 120
ttttctatta caatctttca caccaatttc aacaaaccaa aaacatccaa ttacccacat 180
ttcacattca gattcatact tgataatgat ccacaagatg aacgtatttc aaacttacct 240
acccacggtc ctttagctgg aatgagaatt ccaatcatca atgaacatgg tgccgatgag 300
cttagaagag aattagagtt acttatgttg gcatccgaag aggacgagga agtctcttgt 360
ctgattactg acgctctatg gtactttgcc caatctgtgg ctgatagttt gaatttgagg 420
agattggtac taatgacatc cagtctgttt aactttcacg ctcatgttag tttaccacaa 480
tttgacgaat tgggatactt ggaccctgat gacaagacta ggttagagga acaggcctct 540
ggttttccta tgttgaaagt caaagatatc aagtctgcct attctaattg gcaaatcttg 600
aaagagatct taggaaagat gatcaaacag acaaaggctt catctggagt gatttggaac 660
agtttcaaag agttagaaga gtctgaattg gagactgtaa tcagagaaat tccagcacct 720
tcattcctga taccattacc aaaacatttg actgcttcct cttcctcttt gttggatcat 780
gacagaacag tttttcaatg gttggaccaa caaccaccta gttctgtttt gtacgtgtca 840
tttggtagta cttctgaagt cgatgaaaag gacttccttg aaatcgcaag aggcttagtc 900
gatagtaagc agtcattcct ttgggtcgtg cgtccaggtt tcgtgaaagg ctcaacatgg 960
gtcgaaccac ttccagatgg ttttctaggc gaaagaggta gaatagtcaa atgggttcct 1020
caacaggaag ttttagctca tggcgctatt ggggcattct ggactcattc cggatggaat 1080
tcaactttag aatcagtatg cgaaggggta cctatgatct tttcagattt tggtcttgat 1140
caaccactga acgcaagata catgtctgat gttttgaaag tgggtgtata tctagaaaat 1200
ggctgggaaa ggggtgaaat agctaatgca ataagacgtg ttatggttga tgaagagggg 1260
gagtatatca gacaaaacgc aagagtgctg aagcaaaagg ccgacgtttc tctaatgaag 1320
ggaggctctt catacgaatc cttagaatct cttgtttcct acatttcatc actgtaa 1377

SEQ ID NO: 11
S. rebaudiana UGT91D2e-b (codon optimized)
atggctactt ctgattccat cgttgacgat agaaagcaat tgcatgttgc tacttttcca 60
tggttggctt tcggtcatat tttgccatac ttgcaattgt ccaagttgat tgctgaaaag 120
ggtcacaagg tttcattctt gtctaccacc agaaacatcc aaagattgtc ctctcatatc 180
tccccattga tcaacgttgt tcaattgact ttgccaagag tccaagaatt gccagaagat 240
gctgaagcta ctactgatgt tcatccagaa gatatccctt acttgaaaaa ggcttccgat 300
ggtttacaac cagaagttac tagattcttg gaacaacatt ccccagattg gatcatctac 360
gattatactc attactggtt gccatccatt gctgcttcat tgggtatttc tagagcccat 420
ttctctgtta ctactccatg ggctattgct tatatgggtc catctgctga tgctatgatt 480
aacggttctg atggtagaac taccgttgaa gatttgacta ctccaccaaa gtggtttcca 540
tttccaacaa aagtctgttg gagaaaacac gatttggcta gattggttcc atacaaagct 600
ccaggtattt ctgatggtta cagaatgggt atggttttga aggttccga ttgcttgttg 660
tctaagtgct atcatgaatt cggtactcaa tggttgcctt tgttggaaac attgcatcaa 720
gttccagttg ttccagtagg tttgttgcca ccagaaattc caggtgacga aaaagacgaa 780
acttgggttt ccatcaaaaa gtggttggat ggtaagcaaa agggttctgt tgtttatgtt 840
gctttgggtt ccgaagcttt ggtttctcaa accgaagttg ttgaattggc tttgggtttg 900
gaattgtctg gtttgccatt tgtttgggct tacagaaaac ctaaaggtcc agctaagtct 960
gattctgttg aattgccaga tggtttcgtt gaaagaacta gagatagagg tttggtttgg 1020
acttcttggg ctccacaatt gagaattttg tctcatgaat ccgtctgtgg tttcttgact 1080
cattgtggtt ctggttctat cgttgaaggt ttgatgtttg gtcacccatt gattatgttg 1140
ccaatctttg gtgaccaacc attgaacgct agattattgg aagataagca agtcggtatc 1200
gaaatcccaa gaaatgaaga agatggttgc ttgaccaaag aatctgttgc tagatctttg 1260
agatccgttg tcgttgaaaa agaaggtgaa atctacaagg ctaacgctag agaattgtcc 1320
aagatctaca acgataccaa ggtcgaaaaa gaatacgttt cccaattcgt tgactacttg 1380
gaaaagaatg ctagagctgt tgccattgat catgaatctt ga 1422

SEQ ID NO: 12
Oryza sativa sequence encoding EUGT11 (codon optimized)
atggatagtg gctactcctc atcttatgct gctgccgctg gtatgcacgt tgtgatctgc 60
ccttggttgg cctttggtca cctgttacca tgtctggatt tagcccaaag actggcctca 120
agaggccata gagtatcatt tgtgtctact cctagaaata tctctcgttt accaccagtc 180
agacctgctc tagctcctct agttgcattc gttgctcttc cacttccaag agtagaagga 240
ttgccagacg gcgctgaatc tactaatgac gtaccacatg atagacctga catggtcgaa 300
ttgcatagaa gagcctttga tggattggca gctccatttt ctgagttcct gggcacagca 360
tgtgcagact gggttatagt cgatgtattt catcactggg ctgctgcagc cgcattggaa 420
cataaggtgc cttgtgctat gatgttgtta gggtcagcac acatgatcgc atccatagct 480
gatagaagat tggaaagagc tgaaacagaa tccccagccg cagcaggaca aggtaggcca 540

TABLE 14-continued

Sequences disclosed herein.

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gctgccgccc caacctttga agtggctaga atgaaattga ttcgtactaa aggtagttca      600
gggatgagtc ttgctgaaag gttttctctg acattatcta gatcatcatt agttgtaggt      660
agatcctgcg tcgagttcga acctgaaaca gtacctttac tatctacttt gagaggcaaa      720
cctattactt tccttggtct aatgcctcca ttacatgaag gaaggagaga agatggtgaa      780
gatgctactg ttaggtggtt agatgcccaa cctgctaagt ctgttgttta cgttgcattg      840
ggttctgagg taccactagg ggtggaaaag gtgcatgaat tagcattagg acttgagctg      900
gccggaacaa gattcctttg ggctttgaga aaaccaaccg gtgtttctga cgccgacttg      960
ctaccagctg ggttcgaaga gagaacaaga ggccgtggtg tcgttgctac tagatgggtc     1020
ccacaaatga gtattctagc tcatgcagct gtaggggcct ttctaaccca ttgcggttgg     1080
aactcaacaa tagaaggact gatgtttggt catccactta ttatgttacc aatctttggc     1140
gatcagggac ctaacgcaag attgattgag gcaaagaacg caggtctgca ggttgcacgt     1200
aatgatggtg atggttcctt tgatagagaa ggcgttgcag ctgccatcag agcagtcgcc     1260
gttgaggaag agtcatctaa agttttccaa gctaaggcca aaaaattaca agagattgtg     1320
gctgacatgg cttgtcacga aagatacatc gatggtttca tccaacaatt gagaagttat     1380
aaagactaa                                                             1389
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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
MGSEPFQKKNLGLQINSQESGTTRSTFHSLEDLGDDVINESWDQVNQKRANIDHDVFHEH
PDSSPSLSAQKAKTKEEEVAVKSSNSQSRDPSPDTQAHIPYTYFSKDQRLIIFGIIIFIG
FLGPMSGNIYIPALPLLQREYDVSATTINATVSVFMAVFSVGPLFWGALADFGGRKFLYM
VSLSLMLIVNILLAAVPVNIAALFVLRIFQAFASSSVISLGAGTVTDVVPPKHRGKAIAY
FMMGPNMGPIIAPIVAGLILMKGNYWRWLFGFTSIMTGIALILVTALLPETLRCIVGNGD
PKWGDKKDERENNESPFFEGNKISHRRLFPDIGIRKPVNNDAFFQENFPKPPKAGLTLYW
KMIKCPPIIITSVSTALLFSSYYAFSVTFSYYLEHDYRFTMLEIGAAYVCPGVAMLLGSQ
SGGHLSDYLRSRWIKSHPKKKFPAEFRLLLNLIGILLTICGTIGYGWAIFFHYHFVVLLV
FSALTAFGMTWCSNTSMTYLTELFPKRAAGTVAVSSFFRNVGAAISSAIILQLCNAMGIG
WCFTGLGLCSSISLIGILYLLIFQRKYTAKEF

SEQ ID NO: 14
YAL067C
>sp|P39709|SEO1_YEAST Probable transporter SEO1 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / *S288c*) GN = SEO1 PE = 1 *SV* = 1
MYSIVKEIIVDPYKRLKWGFIPVKRQVEDLPDDLNSTEIVTISNSIQSHETAENFITTTS
EKDQLHFETSSYSEHKDNVNVTRSYEYRDEADRPWWRFFDEQEYRINEKERSHNKWYSWF
KQGTSFKEKKLLIKLDVLLAFYSCIAYWVKYLDTVNINNAYVSGMKEDLGFQGNDLVHTQ
VMYTVGNIIFQLPFLIYLNKLPLNYVLPSLDLDWSLLTVGAAYVNSVPHLKAIRFFIGAF
EAPSYLAYQYLFGSFYKHDEMVRRSAFYYLGQYIGILSAGGIQSAVYSSLNGVNGLEGWR
WNFIIDAIVSVVVGLIGFYSLPGDPYNCYSIFLTDDEIRLARKRLKENQTGKSDFETKVF
DIKLWKTIFSDWKIYILTLWNIFCWNDSNVSSGAYLLWLKSLKRYSIPKLNQLSMITPGL
GMVYLMLTGIIADKLHSRWFAIIFTQVFNIIGNSILAAWDVAEGAKWFAFMLQCFGWAMA
PVLYSWQNDICRRDAQTRAITLVTMNIMAQSSTAWISVLVWKTEEAPRYLKGFTFTACSA
FCLSIWTFVVLYFYKRDERNNAKKNGIVLYNSKHGVEKPTSKDVETLSVSDEK

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
MPSNVRSGVLTLLHTACGAGVLAMPFAFKPFGLMPGLITLTFCGICSLCGLLLQTRIAKY
VPKSENASFAKLTQLINPSISVVFDFAIAVKCFGVGVSYLIIVGDLVPQIVQSIFYRNDD
NMSGSQEHHMFLDRRLYITLIIVFVISPLCFKRSLNSLRYASMIAIVSVAYLSGLIIYHF
VNRHQLERGQVYFMVPHGDSQSHSPLTTLPIFVFAYTCHHNMFSVINEQVDKSFKVIRRI
PIFAIVLAYFLYIIIGGTGYMTFGENIVGNILTLYPNSISTTIGRLAMLLLVMLAFPLQC
HPCRSSVKNIIIFIENFRKGKLYDNRASFIPLDNFNSEDPQEAPTQQNNEEPNLRSESLR
HINIITLCILLFSYLLAISITSLAKVLAIVGATGSTSISFILPGLFGYKLIGSEFTGTNE
RVPTSIKIFKYLSLSLFIWGIAVMVASLSAIVFLGTSSH

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
MLARTAAIRSLSRTLINSTKAARPAAAALASTRRLASTKAQPTEVSSILEERIKGVSDEA
NLNETGRVLAVGDGIARVFGLNNIQAEELVEFSSGVKGMALNLEPGQVGIVLFGSDRLVK
EGELVKRTGNIVDVPVGPGLLGRVVDALGNPIDGKGPIDAAGRSRAQVKAPGILPRRSVH
EPVQTGLKAVDALVPIGRGQRELIIGDRQTGKTAVALDTILNQKRWNNGSDESKKLYCVY
VAVGQKRSTVAQLVQTLEQHDAMKYSIIVAATASEAAPLQYLAPFTAASIGEWFRDNGKH
ALIVYDDLSKQAVAYRQLSLLLRRPPGREAYPGDVFYLHSRLLERAAKLSEKEGSGSLTA
LPVIETQGGDVSAYIPTNVISITDGQIFLEAELFYKGIRPAINVGLSVSRVGSAAQVKAL
KQVAGSLKLFLAQYREVAAFAQFGSDLDASTKQTLVRGERLTQLLKQNQYSPLATEEQVP
LIYAGVNGHLDGIELSRIGEFESSFLSYLKSNHNELLTEIREKGELSKELLASLKSATES
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
DENISYDDTWVGQHGLKQCIALTDSQYGAITSIFSIGGLFGSYYAGNWANRYGRKYVSMG
ASAMCMVSSLLLFFSNSYLQLLFGRFLVGMSCGTAIVITPLFINEIAPVEWRGAMGSMNQ
VSINLGILLTQTLALKYADSYNWRWLLFSGSVIAVANILAWLKVDESPRWLVSHGFVSEA
ETALFKLRPGTYQQAKQEIQDWQRSHGHNRDPESSEETHSGPTLWQYVTDPSYKKPRTVI
LAILSCQQFCGINSIIFYGVKVIGKILPDYSIQVNFAISILNVVVTLAASAIIDHVGRRP
LLLASTTVMTAMSLLISVGLTLSVSFLLVTATFVYIAAFAIGLGPIPFLIIGELSYPQDA
ATAQSFGTVCNWLATFIVGYLFPIGHGLMGGYVFAIFAAIAAMFATYVYKRVPETKGKTT
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
MSRKSSTEYVHNQEDADIEVFESEYRTYRESEAAENRDGLHNGDEENWKVNSSKQKFGVT
KNELSDVLYDSIPAYEESTVTLKEYYDHSIKNNLTAKSAGSYLVSLFPIIKWFPHYNFTW
GYADLVAGITVGCVLVPQSMSYAQIASLSPEYGLYSSFIGAFIYSLFATSKDVCIGPVAV
MSLQTAKVIAEVLKKYPEDQTEVTAPIIATTLCLLCGIVATGLGILRLGFLVELISLNAV
AGFMTGSAFNIIWGQIPALMGYNSLVNTREATYKVVINTLKHLPNTKLDAVFGLIPLVIL
YVWKWWCGTFGITLADRYYRNQPKVANRLKSFYFYAQAMRNAVVIVVFTAISWSITRNKS
SKDRPISILGTVPSGLNEVGVMKIPDGLLSNMSSEIPASIIVLVLEHIAISKSFGRINDY
KVVPDQELIAIGVTNLIGTFFHSYPATGSFSRSALKAKCNVRTPFSGVFTGGCVLLALYC
LTDAFFFIPKATLSAVIIHAVSDLLTSYKTTWTFWKTNPLDCISFIVTVFITVFSSIENG
IYFAMCWSCAMLLLKQAFPAGKFLGRVEVAEVLNPTVQEDIDAVISSNELPNELNKQVKS
TVEVLPAPEYKFSVKWVPFDHGYSRELNINTTVRPPPPGVIVYRLGDSFTYVNCSRHYDI
IFDRIKEETRRGQLITLRKKSDRPWNDPGEWKMPDSLKSLFKFKRHSATTNSDLPISNGS
SNGETYEKPLLKVVCLDFSQVAQVDSTAVQSLVDLRKAVNRYADRQVEFHFAGIISPWIK
RSLLSVKFGTTNEEYSDDSIIAGHSSFHVAKVLKDDVDYTDEDSRISTSYSNYETLCAAT
GTNLPFFHIDIPDFSKWDV

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
MNMLIVGRVVASVGGSGLQTLCFVIGCTMVGERSRPLVISILSCAFAVAAIVGPIIGGAF
TTHVTWRWCFYINLPIGGLAIIMFLLTYKAENKGILQQIKDAIGTISSFTFSKFRHQVNF
KRLMNGIIFKFDFFGFALCSAGLVLFLLGLTFGGNKYSWNSGQVIAYLVLGVLLFIFSLV
YDFFLFDKFNPEPDNISYRPLLLRRLVAKPAIIIINMVTFLLCTGYNGQMIYSVQFFQLI
FASSAWKAGLHLIPIVITNVIAAIASGVITKKLGLVKPLLIFGGVLGVIGAGLMTLMTNT
STKSTQIGVLLLPGFSLGFALQASLMSAQLQITKDRPEAAMDFIEVTAFNTFMKSLGTTL
GGVLSTTVFSASFHNKVSRAHLEPYEGKTVDDMILYRLQNYDGSHSTIGNILSDSIKNVF
WMDLGFYALGFLFCSFSSNKKLIIPKKDETPEDNLEDK

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
MMKESKSITQHEVERESVSSKRAIKKRLLLFKIDLFVLSFVCLQYWINYVDRVGFTNAYI
SGMKEDLKMVGNDLTVSNTVFMIGYIVGMVPNNLMLLCVPPRIWLSFCTFAWGLLTLGMY
KVTSFKHICAIRFFQALFESCTFSGTHFVLGSWYKEDELPIRSAIFTGSGLVGSMFSGFM
QTSIFTHLNGRNGLAGWRWLFIIDFCITLPIAIYGFIFFPGLPDQTSAVSKFSMTRYIFN
EQELHYARRRLPARDESTRLDWSTIPRVLKRWHWWMFSLVWVLGGENLGFASNSTFALWL
QNQKYTLAQRNNYPSGIFAVGIVSTLCSAVYMSKIPRARHWHVSVFISLVMVIVAVLIRA
DPLNPKVVFSAQYLGGVAYAGQAVFFSWANIICHADLQERAIVLASMNMFSGAVNAWWSI
LFFASDMVPKFERGCYALLATAISSGIVSVVIRSLQIKENLSKKQVPYIDANDMPGEDDD
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
MVSLDDILGIVYVTSWSISMYPPIITNWRHKSASAISMDFVMLNTAGYSYLVISIFLQLY
CWKMTGDESDLGRPKLTQFDFWYCLHGCLMNVVLLTQVVAGARIWRFPGKGHRKMNPWYL
RILLASLAIFSLLTVQFMYSNYWYDWHNSRTLAYCNNLFLLKISMSLIKYIPQVTHNSTR
KSMDCFPIQGVFLDVTGGIASLLQLIWQLSNDQGFSLDTFVTNFGKVGLSMVTLIFNFIF
IMQWFVYRSRGHDLASEYPL

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 / *S*288c) GN = VCX1
PE = 1 *SV* = 1
MDATTPLLTVANSHPARNPKHTAWRAAVYDLQYILKASPLNFLLVFVPLGLIWGHFQLSH
TLTFLFNFLAIIPLAAILANATEELADKAGNTIGGLLNATFGNAVELIVSIIALKKGQVR
IVQASMLGSLLSNLLLVLGLCFIFGGYNRVQQTFNQTAAQTMSSLLAIACASLLIPAAFR
ATLPHGKEDHFIDGKILELSRGTSIVILIVYVLFLYFQLGSHHALFEQQEEETDEVMSTI
SRNPHHSLSVKSSLVILLGTTVIISFCADFLVGTIDNVVESTGLSKTFIGLIVIPIVGNA
AEHVTSVLVAMKDKMDLALGVAIGSSLQVALFVTPFMVLVGWMIDVPMTLNFSTFETATL
FIAVFLSNYLILDGESNWLEGVMSLAMYILIAMAFFYYPDEKTLDSIGNSL

SEQ ID NO: 23
YDL185W
>sp|P17255|VATA_YEAST V-type proton ATPase catalytic subunit A
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / *S*288c) GN = VMA1
PE = 1 *SV* = 3
MAGAIENARKEIKRISLEDHAESEYGAIYSVSGPVVIAENMIGCAMYELVKVGHDNLVGE
VIRIDGDKATIQVYEETAGLTVGDPVLRTGKPLSVELGPGLMETIYDGIQRPLKAIKEES
QSIYIPRGIDTPALDRTIKWQFTPGKFQVGDHISGGDIYGSVFENSLISSHKILLPPRSR
GTITWIAPAGEYTLDEKILEVEFDGKKSDFTLYHTWPVRVPRPVTEKLSADYPLLTGQRV
LDALFPCVQGGTTCIPGAFGCGKTVISQSLSKYSNSDAIIYVGCFAKGTNVLMADGSIEC
IENIEVGNKVMGKDGRPREVIKLPRGRETMYSVVQKSQHRAHKSDSSREVPELLKFTCNA
THELVVRTPRSVRRLSRTIKGVEYFEVITFEMGQKKAPDGRIVELVKEVSKSYPISEGPE
RANELVESYRKASNKAYFEWTIEARDLSLLGSHVRKATYQTYAPILYENDHFFDYMQKSK
FHLTIEGPKVLAYLLGLWIGDGLSDRATFSVDSRDTSLMERVTEYAEKLNLCAEYKDRKE
PQVAKTVNLYSKVVRGNGIRNNLNTENPLWDAIVGLGFLKDGVKNIPSFLSTDNIGTRET
FLAGLIDSDGYVTDEHGIKATIKTIHTSVRDGLVSLARSLGLVVSVNAEPAKVDMNGTKH
KISYAIYMSGGDVLLNVLSKCAGSKKFRPAPAAAFARECRGFYFELQELKEDDYYGITLS
DDSDHQFLLANQVVVHNCGERGNEMAEVLMEEPELYTEMSGTKEPIMKRTTLVANTSNMP
VAAREASIYTGITLAEYFRDQGKNVSMIADSSSRWAEALREISGRLGEMPADQGFPAYLG
AKLASFYERAGKAVALGSPDRTGSVSIVAAVSPAGGDFSDPVTTATLGITQVFWGLDKKL
AQRKHFPSINTSVSYSKYTNVLNKFYDSNYPEFPVLRDRMKEILSNAEELEQVVQLVGKS
ALSDSDKITLDVATLIKEDFLQQNGYSTYDAFCPIWKTFDMMRAFISYHDEAQKAVANGA
NWSKLADSTGDVKHAVSSSKFFEPSRGEKEVHGEFEKLLSTMQERFAESTD

SEQ ID NO: 24
YDL194W
>sp|P10870|SNF3_YEAST High-affinity glucose transporter SNF3
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / *S*288c) GN = SNF3
PE = 1 *SV* = 3
MDPNSNSSSETLRQEKQGFLDKALQRVKGIALRRNNSNKDHTTDDTTGSIRTPTSLQRQN
SDRQSNMTSVFTDDISTIDDNSILFSEPPQKQSMMMSICVGVFVAVGGFLFGYDTGLINS
ITSMNYVKSHVAPNHDSFTAQQMSILVSFLSLGTFFGALTAPFISDSYGRKPTIIFSTIF
IFSIGNSLQVGAGGITLLIVGRVISGIGIGAISAVVPLYQAEATHKSLRGAIISTYQWAI
TWGLLVSSAVSQGTHARNDASSYRIPIGLQYVWSSFLAIGMFFLPESPRYYVLKDKLDEA
AKSLSFLRGVPVHDSGLLEELVEIKATYDYEASEGSSNFIDCFISSKSRPKQTLRMFTGI
ALQAFQQFSGINFIFYYGVNFFNKTGVSNSYLVSFITYAVNVVFNVPGLFFVEFFGRRKV
LVVGGVIMTIANFIVAIVGCSLKTVAAAKVMIAFICLFIAAFSATWGGVVWVISAELYPL
GVRSKCTAICAAANWLVNFICALITPYIVDTGSHTSSLGAKIFFIWGSLNAMGVIVVYLT
VYETKGLTLEEIDELYIKSSTGVVSPKFNKDIRERALKFQYDPLQRLEDGKNTFVAKRNN
FDDETPRNDFRNTISGEIDHSPNQKEVHSIPERVDIPTSTEILESPNKSSGMTVPVSPSL
QDVPIPQTTEPAEIRTKYVDLGNGLGLNTYNRGPPSLSSDSSEDYTEDEIGGPSSQGDQS
NRSTMNDINDYMARLIHSTSTASNTTDKFSGNQSTLRYHTASSHSDTTEEDSNLMDLGNG
LALNAYNRGPPSILMNSSDEEANGGETSDNLNTAQDLAGMKERMAQFAQSYIDKRGGLEP
ETQSNILSTSLSVMADTNEHNNEILHSSEENATNQPVNENNDLK

SEQ ID NO: 25
YDL210W
>sp1P32837|UGA4_YEAST GABA-specific permease 0S = *Saccharomyces*
cerevisiae (strain ATCC 204508 / *S*288c) GN = UGA4 PE = 1 *SV* = 1
MSMSSKNENKISVEQRISTDIGQAYQLQGLGSNLRSIRSKTGAGEVNYIDAAKSVNDNQL
LAEIGYKQELKRQFSTLQVFGIAFSIMGLLPSIASVMGGGLGGGPATLVWGWFVAAFFIL
LVGITMAEHASSIPTAGGLYYWTYYYAPEGYKEIISFIIGCSNSLALAAGVCSIDYGLAE
EIAAAVTLTKDGNFEVTSGKLYGIFAGAVVVMCICTCVASGAIARLQTLSIFANLFIIVL
LFIALPIGTKHRMGGFNDGDFIFGKYENLSDWNNGWQFCLAGEMPAVWTIGSFDSCVHQS
EEAKDAKKSVPIGIISSIAVCWILGWLIIICLMACINPDIDSVLDSKYGFALAQIIYDSL
GKKWAIAFMSLIAFCQFLMGASITTAVSRQVWAFSRDNGLPLSKYIKRVDSKYSVPFFAI
LAACVGSLILGLLCLIDDAATDALFSLAVAGNNLAWSTPTVFRLTSGRDLFRPGPFYLGK
IWSPIVAWTGVAFQLFIIILVMFPSQQHGITKSTMNYACVIGPGIWILAGIYYKVYKKKY
YHGPATNLSDDDYTEAVGADVIDTIMSKQEP

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
MSTNKFVVRITNALFKSSLASNSPPVYPKRIRHFEILPNEKWVIWGPGKGKFLDVLNNKY
ICEPPLSLRFGFLKESSNILPRIEQVAFKGVMPTAHLSARYEYFKDDYDQTCKQFIFDKA
SGSNAVSYKVETNNRQINMELYNALVENLNLSSLQDRWVMGLSNGQMRRARLARSILKEP
DLLLIDDPFLGLDPAAIATISQFLAKYDSIEVSGGCPIVIGLRYQDTIPAWCTHICCVDE
KNGILFEGPIEKLQSKMDETRSRALKELEQLKKASNSKEDISINDLICIHPMYGKKEHEI
IKMPHLIELDGLSVSYKGEAVLENLHWKVQPGSKWHIRGDNGSGKSTLLSLLTAEHPQSW
NSRVIDNGVPRRTGKTNYFDLNSKIGMSSPELHAIFLKNAGGRLNIRESVATGYHEASSN
NYLPIWKRLDKNSQEIVNMYLKYFGLDKDADSVLFEQLSVSDQKLVLFVRSLIKMPQILI
LDEAFSGMEVEPMMRCHEFLEEWPGTVLVVAHVAEETPKCAHYLRLISPGEYEIGDMEN

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
MSSPSKPTSPFVDDIEHESGSASNGLSSMSPFDDSFQFEKPSSAHGNIEVAKTGGSVLKR
QSKPMKDISTPDLSKVTFDGIDDYSNDNDINDDDELNGKKTEIHEHENEVDDDLHSFQAT
PMPNTGGFEDVELDNNEGSNNDSQADHKLKRVRFGTRRNKSGRIDINRSKTLKWAKKNFH
NAIDEFSTKEDSLENSALQNRSDELRTVYYNLPLPEDMLDEDGLPLAVYPRNKIRTTKYT
PLTFFPKNILFQFHNFANIYFLILLILGAFQIFGVTNPGFASVPLIVIVIITAIKDGIED
SRRTVLDLEVNNTRTHILSGVKNENVAVDNVSLWRRFKKANTRALIKIFEYFSENLTAAG
REKKLQKKREELRRKRNSRSFGPRGSLDSIGSYRMSADFGRPSLDYENLNQTMSQANRYN
DGENLVDRTLQPNPECRFAKDYWKNVKVGDIVRVHNNDEIPADMILLSTSDVDGACYVET
KNLDGETNLKVRQSLKCSKIIKSSRDITRTKFWVESEGPHANLYSYQGNFKWQDTQNGNI
RNEPVNINNLLLRGCTLRNTKWAMGMVIFTGDDTKIMINAGVTPTKKSRISRELNFSVIL
NFVLLFILCFTAGIVNGVYYKQKPRSRDYFEFGTIGGSASTNGFVSFWVAVILYQSLVPI
SLYISVEIIKTAQAIFIYTDVLLYNAKLDYPCTPKSWNISDDLGQIEYIFSDKTGTLTQN
VMEFKKCTINGVSYGRAYTEALAGLRKRQGVDVESEGRREKEEIAKDRETMIDELRSMSD
NTQFCPEDLTFVSKEIVEDLKGSSGDHQQKCCEHFLLALALCHSVLVEPNKDDPKKLDIK
AQSPDESALVSTARQLGYSFVGSSKSGLIVEIQGVQKEFQVLNVLEFNSSRKRMSCIIKI
PGSTPKDEPKALLICKGADSVIYSRLDRTQNDATLLEKTALHLEEYATEGLRTLCLAQRE
LTWSEYERWVKTYDVAAASVTNREEELDKVTDVIERELILLGGTAIEDRLQDGVPDSIAL
LAEAGIKLWVLTGDKVETAINIGFSCNVLNNDMELLVVKASGEDVEEFGSDPIQVVNNLV
TKYLREKFGMSGSEEELKEAKREHGLPQGNFAVIIDGDALKVALNGEEMRRKFLLLCKNC
KAVLCCRVSPAQKAAVVKLVKKTLDVMTLAIGDGSNDVAMIQSADVGVGIAGEEGRQAVM
CSDYAIGQFRYVTRLVLVHGKWCYKRLAEMIPQFFYKNVIFTLSLFWYGIYNNFDGSYLF
EYTYLTFYNLAFTSVPVILLAVLDQDVSDTVSMLVPQLYRVGILRKEWNQTKFLWYMLDG
VYQSVICFFFPYLAYHKNMVVTENGLGLDHRYFVGVFVTAIAVTSCNFYVFMEQYRWDWF
CGLFICLSLAVFYGWTGIWTSSSSSNEFYKGAARVFAQPAYWAVLFVGVLFCLLPRFTID
CIRKIFYPKDIEIVREMWLRGDFDLYPQGYDPTDPSRPRINEIRPLTDFKEPISLDTHFD
GVSHSQETIVTEEIPMSILNGEQGSRKGYRVSTTLERRDQLSPVTTTNNLPRRSMASARG
NKLRTSLDRTREEMLANHQLDTRYSVERARASLDLPGINHAETLLSQRSRDR

SEQ ID NO: 28
YDR338C
>sp|Q05497|YD338_YEAST Uncharacterized transporter YDR338C
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YDR3380
PE = 1 SV = 1
MAGILSKTLSEVHPSLRTNGMGIGNTHRRISLGFLPPNKKNPLVRKFRARTRNIDQRSFR
SLTDDFGSNVHEPNPYLGNIDEEPDLYYHDEEDGELSRTISLPSRVSETPELSPQDVDWI
LHEHERRYSSVCNSDNEEASQSNTPDRIQEYSGRELEYDEFMNRLQAQKQKLTRSAVTDA
KGTSHHRRPSFVSVTSRGSVPTIYQEIDENDSEALAELAHSHVTFKSEARVLASYSFPLI
FTFLLEQIFPMVCSLTVGHLGKNELAAVSLASMTSNITLAIFEGIATSLDTLCPQAYGSG
RFYSVGVHLQRCIAFSLVIYIPFAVMWWYSEPLLSYIIPEKELINLTSRFLRVLILGAPA
YIFFENLKRFLQAQGIFDAGIYVLTICAPLNVLVSYTLVWNKYIGVGFIGAAIAVVLNFW
LMFFLLLFYALYIDGRKCWGGFSRKAFTHWNDLGHLAFSGIIMLEAEELSYELLTLFSAY
YGVSYLAAQSAVSTMAALLYMIPFAIGISTSTRIANFIGAKRTDFAHISSQVGLSFSFIA
GFINCCILVFGRNLIANIYSKDPEVIKLIAQVLPLVGIVQNFDSLNAVAGSCLRGQGMQS
LGSIVNLMAYYLFGIPLALILSWFFDMKLYGLWIGIGSAMLLIGLVEAYYVLFPDWDKIM
TYAEILKETEDDEVDSDEYLTDSDDPDENTALLGA

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
MSSDIRDVEERNSRSSSSSSSSNSAAQSIGQHPYRGFDSEAAERVHELARTLTSQSLLYT
ANSNNSSSSNHNAHNADSRSVFSTDMEGVNPVFTNPDTPGYNPKLDPNSDQFSSTAWVQN
MANICTSDPDFYKPYSLGCVWKNLSASGDSADVSYQSTFANIVPKLLTKGLRLLKPSKEE
DTFQILKPMDGCLNPGELLVVLGRPGSGCTTLLKSISSNSHGFKIAKDSIVSYNGLSSSD

TABLE 14-continued

Sequences disclosed herein.

IRKHYRGEVVYNAESDIHLPHLTVYQTLFTVARMKTPQNRIKGVDREAYANHVTEVAMAT
YGLSHTRDTKVGNDLVRGVSGGERKRVSIAEVAICGARFQCWDNATRGLDSATALEFIRA
LKTQADIGKTAATVAIYQCSQDAYDLFDKVCVLDDGYQLYFGPAKDAKKYFQDMGYYCPP
RQTTADFLTSITSPTERIISKEFIEKGTRVPQTPKDMAEYWLQSESYKNLIKDIDSTLEK
NTDEARNIIRDAHHAKQAKRAPPSSPYVVNYGMQVKYLLIRNFWRMKQSASVTLWQVIGN
SVMAFILGSMFYKVMKKNDTSTFYFRGAAMFFAILFNAFSCLLEIFSLYETRPITEKHRT
YSLYHPSADAFASVLSEMPPKLITAVCFNIIFYFLVDFRRNGGVFFFYFLINVIATFTLS
HLFRCVGSLTKTLQEAMVPASMLLLAISMYTGFAIPKTKILGWSIWIWYINPLAYLFESL
MINEFHDRRFPCAQYIPAGPAYQNITGTQRVCSAVGAYPGNDYVLGDDFLKESYDYEHKH
KWRGFGIGMAYVVFFFFVYLILCEYNEGAKQKGEMVVFLRSKIKQLKKEGKLQEKHRPGD
IENNAGSSPDSATTEKKILDDSSEGSDSSSDNAGLGLSKSEAIFHWRDLCYDVPIKGGQR
RILNNVDGWVKPGTLTALMGASGAGKTTLLDCLAERVTMGVITGNIFVDGRLRDESFPRS
IGYCQQQDLHLKTATVRESLRFSAYLRQPSSVSIEEKNRYVEEVIKILEMQQYSDAVVGV
AGEGLNVEQRKRLTIGVELAARPKLLVFLDEPTSGLDSQTAWDTCQLMRKLATHGQAILC
TIHQPSAILMQQFDRLLFLQKGGQTVYFGDLGEGCKTMIDYFESKGAHKCPPDANPAEWM
LEVVGAAPGSHATQDYNEVWRNSDEYKAVQEELDWMEKNLPGRSKEPTAEEHKPFAASLY
YQFKMVTIRLFQQYWRSPDYLWSKFILTIFNQVFIGFTFFKADRSLQGLQNQMLSIFMYT
VIFNPILQQYLPSFVQQRDLYEARERPSRTFSWLAFFLSQIIVEIPWNILAGTIAYCIYY
YAVGFYANASAAGQLHERGALFWLFSIAFYVYIGSMGLLMISFNEVAETAAHMGTLLFTM
ALSFCGVMATPKVMPRFWIFMYRVSPLTYMIDALLALGVANVDVKCSNYEMVKFTPPSGT
TCGDYMASYIKLAGTGYLSDPSATDICSFCAVSTTNAFLATFSSHYYRRWRNYGIFICYI
AFDYIAATFLYWLSRVPKKNGKISEKPKK

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
MKDLKLSNFKGKFISRTSHWGLTGKKLRYFITIASMTGFSLFGYDQGLMASLITGKQFNY
EFPATKENGDHDRHATVVQGATTSCYELGCFAGSLFVMFCGERIGRKPLILMGSVITIIG
AVISTCAFRGYWALGQFIIGRVVTGVGTGLNTSTIPVWQSEMSKAENRGLLVNLEGSTIA
FGTMIAYWIDFGLSYTNSSVQWRFPVSMQIVFALFLLAFMIKLPESPRWLISQSRTEEAR
YLVGTLDDADPNDEEVITEVAMLHDAVNRTKHEKHSLSSLFSRGRSQNLQRALIAASTQF
FQQFTGCNAAIYYSTVLFNKTIKLDYRLSMIIGGVFATIYALSTIGSFFLIEKLGRRKLF
LLGATGQAVSFTITFACLVKENKENARGAAVGLFLFITFFGLSLLSLPWIYPPEIASMKV
RASTNAFSTCTNWLCNFAVVMFTPIFIGQSGWGCYLFFAVMNYLYIPVIFFFYPETAGRS
LEEIDIIFAKAYEDGTQPWRVANHLPKLSLQEVEDHANALGSYDDEMEKEDFGEDRVEDT
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
MTKKSFVSSPIVRDSTLLVPKSLIAKPYVLPFFPLYATFAQLYFQQYDRYIKGPEWTFVY
LGTLVSLNILVMLMPAWNVKIKAKFNYSTTKNVNEATHILIYTTPNNGSDGIVEIQRVTE
AGSLQTFFQFQKKRFLWHENEQVFSSPKFLVDESPKIGDFQKCKGHSGDLTHLKRLYGEN
SFDIPIPTFMELFKEHAVAPLFVFQVFCVALWLLDEFWYYSLFNLFMIISMEAAAVFQRL
TALKEFRTMGIKPYTINVFRNKKWVALQTNELLPMDLVSITRTAEESAIPCDLILLDGSA
IVNEAMLSGESTPLLKESIKLRPSEDNLQLDGVDKIAVLUGGTKALQVTPPEHKSDIPPP
PDGGALAIVTKTGFETSQGSLVRVMIYSAERVSVDNKEALMFILFLLIFAVIASWYVWVE
GTKMGRIQSKLILDCILIITSVVPPELPMELTMAVNSSLAALAKFYVYCTEPFRIPFAGR
IDVCCFDKTGTLTGEDLVFEGLAGISADSENIRHLYSAAEAPESTILVIGAAHALVKLED
GDIVGDPMEKATLKAVGWAVERKNSNYREGTGKLDIIRRFQFSSALKRSASIASHNDALF
AAVKGAPETIRERLSDIPKNYDEIYKSFTRSGSRVLALASKSLPKMSQSKIDDLNRDDVE
SELTFNGFLIFHCPLKDDAIETIKMLNESSHRSIMITGDNPLTAVHVAKEVGIVFGETLI
LDRAGKSDDNQLLFRDVEETVSIPFDPSKDTFDHSKLFDRYDIAVTGYALNALEGHSQLR
DLLRHTWVYARVSPSQKEFLLNTLKDMGYQTLMCGDGTNDVGALKQAHVGIALLNGTEEG
LKKLGEQRRLEGMKMMYIKQTEFMARWNQPQPPVPEPIAHLFPPGPKNPHYLKALESKGT
VITPEIRKAVEEANSKPVEVIKPNGLSEKKPADLASLLLNSAGDAQGDEAPALKLGDASC
AAPFTSKLANVSAVTNIIRQGRCALVNTIQMYKILALNCLISAYSLSIIYMAGVKFGDGQ
ATVSGLLLSVCFLSISRGKPLEKLSKQRPQSGIFNVYIMGSILSQFAVHIATLVYITTEI
YKLEPREPQVDLEKEFAPSLLNTGIFIIQLVQQVSTFAVNYQGEPFRENIRSNKGMYYGL
LGVTGLALASATEFLPELNEAMKFVPMTDDFKIKLTLTLLLDFFGSWGVEHFFKFFFMDD
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
MSGTFHGDGHAPMSPFEDTFQFEDNSSNEDTHIAPTHFDDGATSNKYSRPQVSFNDETPK
NKREDAEEFTFNDDTEYDNHSFQPTPKLNNGSGTFDDVELDNDSGEPHTNYDGMKRFRMG
TKRNKKGNPIMGRSKTLKWARKNIPNPFEDFTKDDIDPGAINRAQELRTVYYNMPLPKDM
IDEEGNPIMQYPRNKIRTTKYTPLIFLPKNILFQFHNFANVYFLVLIILGAFQIFGVTNP
GLSAVPLVVIVIITAIKDAIEDSRRTVLDLEVNNTKTHILEGVENENVSTDNISLWRRFK

TABLE 14-continued

Sequences disclosed herein.

KANSRLLFKFIQYCKEHLTEEGKKKRMQRKRHELRVQKTVGTSGPRSSLDSIDSYRVSAD
YGRPSLDYDNLEQGAGEANIVDRSLPPRTDCKFAKNYWKGVKVGDIVRIHNNDEIPADII
LLSTSDTDGACYVETKNLDGETNLKVRQSLKCTNTIRTSKDIARTKFWIESEGPHSNLYT
YQGNMKWRNLADGEIRNEPITINNVLLRGCTLRNTKWAMGVVMFTGGDTKIMLNSGITPT
KKSRISRELNFSVVINFVLLFILCFVSGIANGVYYDKKGRSRFSYEFGTIAGSAATNGFV
SFWVAVILYQSLVPISLYISVEIIKTAQAAFIYGDVLLYNAKLDYPCTPKSWNISDDLGQ
VEYIFSDKTGTLTQNVMEFKKCTINGVSYGRAYTEALAGLRKRQGIDVETEGRREKAEIA
KDRDTMIDELRALSGNSQFYPEEVTFVSKEFVRDLKGASGEVQQRCCEHFMLALALCHSV
LVEANPDNPKKLDLKAQSPDEAALVATARDVGFSFVGKTKKGLIIEMQGIQKEFEILNIL
EFNSSRKRMSCIVKIPGLNPGDEPRALLICKGADSIIYSRLSRQSGSNSEAILEKTALHL
EQYATEGLRTLCIAQRELSWSEYEKWNEKYDIAAASLANREDELEVVADSIERELILLGG
TAIEDRLQDGVPDCIELLAEAGIKLWVLTGDKVETAINIGFSCNLLNNEMELLVIKTTGD
DVKEFGSEPSEIVDALLSKYLKEYFNLTGSEEEIFEAKKDHEFPKGNYAIVIDGDALKLA
LYGEDIRRKFLLLCKNCRAVLCCRVSPSQKAAVVKLVKDSLDVMTLAIGDGSNDVAMIQS
ADVGIGIAGEEGRQAVMCSDYAIGQFRYLARLVLVHGRWSYKRLAEMIPEFFYKNMIFAL
ALFWYGIYNDFDGSYLYEYTYMMFYNLAFTSLPVIFLGILDQDVNDTISLVVPQLYRVGI
LRKEWNQRKFLWYMLDGLYQSIICFFFPYLVYMKNMIVISNGLGLDHRYFVGVYVTTIAV
ISCNTYVLLHQYRWDWFSGLFIALSCLVVFAWTGIWSSAIASREFFKAAARIYGAPSFWA
VFFVAVLFCLLPRFTYDSFQKFFYPTDVEIVREMWQMGHFDHYPPGYDPIDPNRPKVTKA
GQHGEKIIEGIALSDNLGGSNYSRDSVVTEEIPMTFMHGEDGSPSGYQKQETWMTSPKET
QDLLQSPQFQQAQTFGRGPSINVRSSLDRTREQMIATNQLDNRYSVERARTSLDLPGVIN
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
MVSSSVSILGTSAKASTSLSRKDEIKLTPETREASLDIPYKPIIAYWTVMGLCLMIAFGG
FIFGWDTGTISGFINQTDFKRRFGELQRDGSFQLSDVRTGLIVGIFNIGCALGGLTLGRL
GDIYGRKIGLMCVILVYVVGIVIQIASSDKWYQYFIGRIVSGMGVGGVAVLSPTLISEIS
PKHLRGTCVSFYQLMITLGIFLGYCTNYGTKKYSNSIQWRVPLGLCFAWAIFMVIGMVMV
PESPRYLVEKGKYEEARRSLAKSNKVTVTDPGVVFEFDTIVANMELERAVGNASWHELFS
NKGAILPRVIMGIVIQSLQQLTGCNYFFYYGTTIFNAVGMQDSFETSIVLGAVNFASTFV
ALYIVDKFGRRKCLLWGSASMAICFVIFATVGVTRLWPQGKDQPSSQSAGNVMIVFTCFF
IFSFAITWAPIAYVIVAETYPLRVKNRAMAIAVGANWMWGFLIGFFTPFITRSIGFSYGY
VFMGCLIFSYFYVFFFVCETKGLTLEEVNEMYEERIKPWKSGGWIPSSRRTPQPTSSTPL
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
MSRQDENSALLANNENNKPSYTGNENGVYDNFKLSKSQLSDLHNPKSIRSFVRLFGYESN
SLFKYLKTDKNAGISLPEISNYRKTNRYKNYGDNSLPERIPKSFLQLVWAAFNDKTMQLL
TVAAVVSFVLGLYELWMQPPQYDPEGNKIKQVDWIEGVAIMIAVFVVVLVSAANDYQKEL
QFAKLNKKKENRKIIVIRNDQEILISIHHVLVGDVISLQTGDVVPADCVMISGKCEADES
SITGESNTIQKFPVDNSLRDFKKFNSIDSHNHSKPLDIGDVNEDGNKIADCMLISGSRIL
SGLGRGVITSVGINSVYGQTMTSLNAEPESTPLQLHLSQLADNISVYGCVSAIILFLVLF
TRYLFYIIPEDGRFHDLDPAQKGSKFMNIFITSITVIVVAVPEGLPLAVTLALAFATTRM
TKDGNLVRVLRSCETMGSATAVCSDKTGTLTENVMTVVRGFPGNSKFDDSKSLPVSEQRK
LNSKKVFEENCSSSLRNDLLANIVLNSTAFENRDYKKNDKNTNGSKNMSKNLSFLDKCKS
RLSFFKKGNREDDEDQLFKNVNKGRQEPFIGSKTETALLSLARLSLGLQPGELQYLRDQP
MEKFNIEKVVQTIPFESSRKWAGLVVKYKEGKNKKPFYRFFIKGAAEIVSKNCSYKRNSD
DTLEEINEDNKKETDDEIKNLASDALRAISVAHKDFCECDSWPPEQLRDKDSPNIAALDL
LFNSQKGLILDGLLGIQDPLRAGVRESVQQCQRAGVTVRMVTGDNILTAKAIARNCAILS
TDISSEAYSAMEGTEFRKLTKNERIRILPNLRVLARSSPEDKRLLVETLKGMGDVVAVTG
DGTNDAPALKLADVGFSMGISGTEVAREASDIILMTDDFSAIVNAIKWGRCVSVSIKKFI
QFQLIVNITAVILTFVSSVASSDETSVLTAVQLLWINLIMDTLAALALATDKPDPNIMDR
KPRGRSTSLISVSTWKMILSQATLQLIVTFILHFYGPELFFKKHEDEITSHQQQQLNAMT
FNTFVWLQFFTMLVSRKLDEGDGISNWRGRISAANLNFFQDLGRNYYFLTIMAIIGSCQV
LIMFFGGAPFSIARQTKSMWITAVLCGMLSLIMGVLVRICPDEVAVKVFPAAFVQRFKYV
FGLEFLRKNHTGKHDDEEALLEESDSPESTAFY

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
MRGLTPKNGVHIETGPDTESSADSSNFSTGFSGKIRKPRSKVSKACDNCRKRKIKCNGKF
PCASCEIYSCECTFSTRQGGARIKNLHKTSLEGTTVQVKEETDSSSTSFSNPQRCTDGPC
AVEQPTKFFENFKLGGRSSGDNSGSDGKNDDDVNRNGFYEDDSESQATLTSLQTTLKNLK
EMAHLGTHVTSAIESIELQISDLLKRWEPKVRTKELATTKFYPNKSIETQLMKNKYCDVV
HLTRYAAWSNNKKDQDTSSQPLIDEIFGLYSPFQFLSLQGIGKCFQNYRSKSKCEIFPRT
AKETIYIMLRFFDVCFHHINQGCVSIANPLENYLQKMNLLPSTPSSISSAGSPNTAHTKS
HVALVINHLPQPFVRNITGISNSELLSEMNNDISMFGILLKMLDMHKNSYQNFLMEITSN
PSVAKNTQSIDVLQEFIHYCQAGEALIALCYSYYNSTLYNYVDFTCDITHLEQLLYFLDL

TABLE 14-continued

Sequences disclosed herein.

LFWLSEIYGFEKVLNVAVHFVSRVGLSRWEFYVGLDENFAERRRNLWWKAFYFEKTLASK
LGYPSNIDDSKINCLLPKNFRDVGFLDNRDFIENVHLVRRSEAFDNMCISDLKYYGELAV
LQIVSHFSSSVLFNEKFTSIRNTSKPSVVREKLLFEVLEIFNETEMKYDAIKEQTGKLFD
IAFSKDSTELKVSREDKIMASKFVLFYEHHFCRMVNESDNIVARLCVHRRPSILIENLKI
YLHKIYKSWTDMNKILLDFDNDYSVYRSFAHYSISCIILVSQAFSVAEFIKVNDVVNMIR
VFKRFLDIKIFSENETNEHVFNSQSFKDYTRAFSFLTIVTRIMLLAYGESSSTNLDVISK
YIDENAPDLKGIIELVLDTNSCAYRFLLEPVQKSGFHLTVSQMLKNRKFQEPLMSNEDNK
QMKHNSGKNLNPDLPSLKTGTSCLLNGIESPQLPFNGRSAPSPVRNNSLPEFAQLPSFRS
LSVSDMINPDYAQPTNGQNNTQVQSNKPINAQQQIPTSVQVPFMNTNEINNNNNNNNNNK
NNINNINNNNSNNFSATSFNLGTLDEFVNNGDLEDLYSILWSDVYPDS

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
MSNVTTPWWKQWDPSEVTLADKTPDDVWKTCVLQGVYFGGNEYNGNLGARISSVFVILFV
STFFTMFPLISTKVKRLRIPLYVYLFAKYFGSGVIVATAFIHLMDPAYGAIGGTTCVGQT
GNWGLYSWCPAIMLTSLTFTFLTDLFSSVWVERKYGLSHDHTHDEIKDTVVRNTAAVSSE
NDNENGTANGSHDTKNGVEYYEDSDATSMDVVQSFQAQFYAFLILEFGVIFHSVMIGLNL
GSVGDEFSSLYPVLVFHQSFEGLGIGARLSAIEFPRSKRWWPWALCVAYGLTTPICVAIG
LGVRTRYVSGSYTALVISGVLDAISAGILLYTGLVELLARDFIFNPQRTKDLRELSFNVI
CTLFGAGIMALIGKWA

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
MGRTIRRRRSNSSLSEAISVSLGINQDSSVNKMHRASVSAMSPPLCRSYMSGFFTGGNSP
MINNLSDSKLPISNKQHPKVIHGSENLHRQTAQLSNEFCSSSVEENSPTIKDYMDIIGNG
DRKDDQSMRTIEENIDEEYSDEYSRLLLSPASSNVDDDRNRGLQNSSLPELEDGYAGGYQ
SLRPSHNLRFRPRNLWHMCTSFPSKFAHYLPAAVLGLLLNILDALSYGMIIFPITEPVFS
HLGPTGISMFYISTIISQAVYSGGWSSFPSGIGSEMIEITPFYHTMALAIKEALAGNDDE
IITTTIFCYVISSMLTGVVFYALGKLRLGKIVGFFPRHILIGCIGGVGYFLIITGIEVTT
RVAKFEYSWPFFSGLFTDYDTLAKWLLPVLLTVVLIGTQRYFKNSLVLPSFYILTLVLFH
FIVAIIPTLSLDALRQAGWIFPIANSDSKWYDHYRLFNVHKVHWSLVLQQIPTMMALTFF
GILHVPINVPALAMSLQMDKYDVDRELIAHGYSNFFSGLLGSVQNYLVYTNSVLFIRAGA
DSPFAGFLLIALTICIMIIGPVIISFIPICIVGSLIFLLGYELLVEALVDTWNKLNRFEY
LTVVIIVFTMGIFDFVLGIIVGILIACFSFLVDSTKLQTINGEYNGNVARSTVYRDYVQT
KFLDGIGEQIYVLKLQNLLFFGTIISIEEKIERLLQISNKDATKRRIKYLILDFKNINAD
NIDYSAAEGFNRIKRFTETKRIKLIISSIKERDRIYNAFNNVGLLNDVELFADLNSALEW
CENEFLFQYKQLRKKAKERLEEGKQNNVVSAVIAATKNKKIDTIGNGLNRGSNGDTARNL
MSLPTNTPRNYQILSVAQNVFVNDEQAVKNFKKEYKDDEPVLPILLFALKQYRPDIISEV
QKVREKEIKFWAQLCPYFTRRRLASQSHLLHADNIFFLVETGMLKATYELPQGTLYEIFS
NGTCFGKIIAPGNAMPREQKLTIETETDSVLWVIDSSSLNKLKEDNLALYVEVALMVMCI
KDTRFKELLGYTLVSA

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
MGLSSIFGGGAPSQQKEAATTAKTTPNPIAKELKNQIAQELAVANATELVNKISENCFEK
CLTSPYATRNDACIDQCLAKYMRSWNVISKAYISRIQNASASGEI

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
MQGRKRTLTEPFEPNTNPFGDNAAVMTENVEDNSETDGNRLESKPQALVPPALNIVPPES
SIHSTEEKKGDEYNGNDKDSSLISNIFRTRVGRSSHENLSRPKLSLKTASFGAAESSRRN
VSPSTKSAKSSSQYIDLNDERLRRRSFSSYSRSSSRRVSNSPSSTDRPPRSAKVLSLIAA
DDMDDFEDLQKGFKSAIDEEGLTWLPQLKSEKSRPVSDVGEDRGEGEQESIPDVHTPNVG
ASATPGSIHLTPEPAQNGSVSEGLEGSINNSRKKPSPKFFHHLSPQKEDKDQTEVIEYAE
DILDFETLQRKLESRPFVLYGHSLGVFSPTNPLRIKIARFLLHRRYSLLYNTLLTFYAIL
LAIRTYNPHNVVFLYRFSNWTDYFIFILSACFTGNDIAKIIAFGFWDDSEMFKAYGREYK
SILQRSGIMKLYIYLREKYGRKLIDFIIPFRIISPGEETKYQRSSLSTSLTKPYGAKENQ
RPFGTPRAFARSSWNRIDLVSSVSFWLGMFLSIKSYDTKTGIRIFKPLAILRILRLVNVD
TGMPSILRGLKYGIPQLVNVSSMLVYFWIFFGILGVQIFQGSFRRQCVWFNPEDPTDTYQ
YDMQFCGGYLDPVTKRKQNYIYEDGSEGSVSKGFLCPQYSKCVSNANPYNGRISFDNIVN
SMELVFVIMSANTFTDLMYYTMDSDEMAACLFFIVCIFVLTIWLLNLLIAVLVSSFEIAN
EEYKKKKFIYGSRKTGYVARIVTGYWKYFKLKANQTKFPNWSQKGLAIYSHVEFIFVILI
ICDIGMRASVKVSTSANCNNILLKTDRGISIVLFIESLARLVLYLPNMWKFLTKPSYVYD
FIISIITLVISCLAVEGVLGHMYAWLSIFHISRFYRVIISFNLTKKLWKQILSNGVMIWN
LSSFYFFFTFLVAIIMAVYFEGVIPPEEMADQPFGMYSLPNSFLSLFIIGSTENWTDILY

TABLE 14-continued

Sequences disclosed herein.
ALQKHSPNISSTFFCSVFFIIWFLLSNSVILNIFIALISESMEVKEEEKRPQQIKHYLKF VYPQKIQEYTHASLVARIRKKFFGGHRNEDTRDFKQFLMRGTAIMNIAQNMGELADEFKE PPSENLFKKGLSKLTIGVPSLKRLRMFANNPFYKNSDVVFTETNDINGRTYILELNEYED EKLDYLKKYPLFNYSYYFFSPQHRFRRFCQRLVPPSTGKRTDGSRFFEDSTDLYNKRSYF HHIERDVFVFIFALATILLIVCSCYVTPLYRMHHKMGTWNWSSALDCAFIGAFSIEFIVK TVADGFIYSPNAYLRNPWNFIDFCVLISMWINLIAYLKNNGNLSRIFKGLTALRALRCLT ISNTARQTFNLVMFDGLNKIFEAGLISLSLLFPFTVWGLSIFKGRLGTCNDGSLGRADCY NEYSNSVFQWDIMSPRVYQQPYLHLDSFASAFSSLYQIISLEGWVDLLENMMNSSGIGTP ATVMGSAGNALFLVLFNFLSMVFILNLFVSFIVNNQARTTGSAYFTIEEKAWLESQKLLS QAKPKAIPNLIELSRVRQFFYQLAVEKKNFYYASFLQVVLYLHIIMLLSRSYNPGNLIGY QGVYFMFSTSVFLIQEALHMCGEGPRLYFRQKWNSIRLSIIIIAFIMNAVAFHVPASHYW FHNIKGFFLLVIFLFIIPQNDTLTELLETAMASLPPILSLTYTWGVLFLVYAIALNQIFG LTRLGSNTTDNINFRTVIKSMIVLFRCSFGEGWNYIMADLTVSEPYCSSDDNSTYTDCGS ETYAYLLLMSWNIISMYIFVNMFVSLIIGNFSYVYRSGGSRSGINRSEIKKYIEAWSKFD TDGTGELELSYLPRIMHSFDGPLSFKIWEGRLTIKSLVENYMEVNPDDPYDVKIDLIGLN KELNTIDKAKIIQRKLQYRRFVQSIHYTNAYNGCIRFSDLLLQIPLYTAYSARECLGIDQ YVHHLYILGKVDKYLENQRNFDVLEMVVTRWKFHCRMKRTIEPEWDVKDPTVSSHISNIN VNLEPAPGILEREPIATPRMDYGVNNFMWSPRMNQDSTMEPPEEPIDNNDDSANDLIDR
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 MKGEPKTYSMSDLSYYGEKAQQQNEKQQKQYVVRRNSTQSTSKQNVSVVLEDNASESNEL PKGFILYASLIALALSLFLAALDIMIVSTIIEEVAKQFGSYSEIGWLFTGYSLPNALLAL IWGRIATPIGFKETMLFAIVIFEIGSLISALANSMSMLIGGRVIAGVGGCGIQSLSFVIG STLVEESQRGILIAVLSCSFAIASVVGPFLGGVFTSSVTWRWCFYVNLPIGGLAFFLFLF FYNPGLSTFQETMDNIRKFPSQFIEIVRNVAYHLLKIKGFSKLNGWRKPFMELIFMYDII EFVFCSAGFTCILLAFTFGGNRYAWNSASIIILFIIGIVLVVLAGIYDFLVFPKFNIVKA TPHYQPLMSWTNIKKPGIFTVNIALFLTCAGYISQFTYIVQYFQLIYNDSAWRAAVHLVA CIISTVVTAILCGAITDKTRQIKPIIVISSIFGVVGAGILTLLNNNANNSAHIGLLILPG VAFGGLAQSSMLASQIQLDKKSPTFRSDFVSITTFNTFCKNLGQALGGVISNTVFSAAAI KKLTKANIQLPDGTTVDNLVIYRQTNFDGSHSKLGNIISESLTDVFYMALGFYALSLIFA 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 MTITVGDAVSETELENKSQNVVLSPKASASSDISTDVDKDTSSSWDDKSLLPTGEYIVDR NKPQTYLNSDDIEKVTESDIFPQKRLFSFLHSKKIPEVPQTDDERKIYPLFHTNIISNMF FWWVLPILRVGYKRTIQPNDLFKMDPRMSIETLYDDFEKNMIYYFEKTRKKYRKRHPEAT EEEVMENAKLPKHTVLRALLFTFKKQYFMSIVFAILANCTSGFNPMITKRLIEFVEEKAI FHSMHVNKGIGYAIGACLMMFVNGLTFNHFFHTSQLTGVQAKSILTKAAMKKMFNASNYA RHCFPNGKVTSFVTTDLARIEFALSFQPFLAGFPAILAICIVLLIVNLGPIALVGIGIFF GGFFISLFAFKLILGFRIAANIFTDARVTMMREVLNNIKMIKYYTWEDAYEKNIQDIRTK EISKVRKMQLSRNFLIAMAMSLPSIASLVTFLAMYKVNKGGRQPGNIFASLSLFQVLSLQ MFFLPIAIGTGIDMIIGLGRLQSLLEAPEDDPNQMIEMKPSPGFDPKLALKMTHCSFEWE DYELNDAIEEAKGEAKDEGKKNKKKRKDTWGKPSASTNKAKRLDNMLKDRDGPEDLEKTS FRGFKDLNFDIKKGEFIMITGPIGTGKSSLLNAMAGSMRKTDGKVEVNGDLLMCGYPWIQ NASVRDNIIFGSPFNKEKYDEVVRVCSLKADLDILPAGDMTEIGERGITLSGGQKARINL ARSVYKKKDIYLFDDVLSAVDSRVGKHIMDECLTGMLANKTRILATHQLSLIERASRVIV LGTDGQVDIGTVDELKARNQTLINLLQFSSQNSEKEDEEQEAVVAGELGQLKYESEVKEL TELKKKATEMSQTANSGKIVADGHTSSKEERAVNSISLKIYREYIKAAVGKWGFIALPLY AILVVGTTFCSLFSSVWLSYWTENKFKNRPPSFYMGLYSFFVFAAFIFMNGQFTILCAMG IMASKWLNLRAVKRILHTPMSYIDTTPLGRILNRFTKDTDSLDNELTESLRLMTSQFANI VGVCVMCIVYLPWFAIAIPFLLVIFVLIADHYQSSGREIKRLEAVQRSFVYNNLNEVLGG MDTIKAYRSQERFLAKSDFLINKMNEAGYLVVVLQRWVGIFLDMVAIAFALIITLLCVTR AFPISAASVGVLLTYVLQLPGLLNTILRAMTQTENDMNSAERLVTYATELPLEASYRKPE MTPPESWPSMGEIIFENVDFAYRPGLPIVLKNLNLNIKSGEKIGICGRTGAGKSTIMSAL YRLNELTAGKILIDNVDISQLGLFDLRRKLAIIPQDPVLFRGTIRKNLDPFNERTDDELW DALVRGGAIAKDDLPEVKLQKPDENGTHGKMHKFHLDQAVEEEGSNFSLGERQLLALTRA LVRQSKILILDEATSSVDYETDGKIQTRIVEEFGDCTILCIAHRLKTIVNYDRILVLEKG EVAEFDTPWTLFSQEDSIFRSMCSRSGIVENDFENRS
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 MGEFKPPLPQGAGYAIVLGLGAVFAGMMVLTTYLLKRYQKEIITAEEFTTAGRSVKTGLV AAAVVSSWIWCSTLLTSSTKEYADGIFGGYAYAAGACFQIIAFAILAIKTKQMAPNAHTY LELVRTRYGKIGHGCYLFYAIATNILVTSMLLTSGSAVFSDLTGMNTIASCFLLPVGVVV YTLFGGIKATFLTDYMHTCVIIIIVLVFAFKVYATSDVLGSPGKVYDLVREAAKRHPVDG NYQGEYMTMTSKSAGILLIINLIGNFGTVFLDNGYWNKAISASPAASLKAYAIGGLAWFA

TABLE 14-continued

Sequences disclosed herein.

VPSLISLTMGLACLAVETSPNFPTYPDPLTSFQANSGLVLPAAAIAIMGKGGAVASLLMI
FMAVTSAMSAELIAVSSVFTYDIYREYIDPRASGKKLIYTSHVACIFFGLAMSGFSVGLY
YGGISMGYIYEMMGIIISSAVLPVVLTLCSKDMNLVAAVVSPILGTGLAIMSWLVCTESL
YKELTVDTTFMDYPMLTGNLVALLSPAIFIPILTYVFKPQNFDWEKMKDITRVDETAELV
QADPDIQLYDAEANDKEQEEETNSLVSDSEKNDVRVNNEKLIEPNLGVVISNAIFQEDDT
QLQNELDEEQRELARGLKIAYFLCVFFALAFLVVWPMPMYGSKYIFSKKFFTGWVVVMII
WLFFSAFAVCIYPLWEGRHGIYTTLRGLYWDLSGQTYKLREWQNSNPQDLHVVTSQISAR
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
MEATSSALSSTANLVKTIVGAGTLAIPYSFKSDGVLVGVILTLLAAVTSGLGLFVLSKCS
KTLINPRNSSFFTLCMLTYPTLAPIFDLAMIVQCFGVGLSYLVLIGDLFPGLFGGERNYW
IIASAVIIIPLCLVKKLDQLKYSSILGLFALAYISILVFSHFVFELGKGELTNILRNDIC
WWKIHDFKGLLSTFSIIIFAFTGSMNLFPMINELKDNSMENITFVINNSISLSTALFLIV
GLSGYLTFGNETLGNLMLNYDPNSIWIVIGKFCLGSMLILSFPLLFHPLRIAVNNVIIWI
EITYGGANPEEDPQVSEYTRASNLRPISMTVEDPAQPSDALDATSYNEQECLLPNGNFDN
GSIESQENNNDERGTMAVAGDNEHHAPFVKSRFYWITALLLISMYTLALSVQSFALVLSF
VGATGSTSISFTLPGLLGYKLIGLDSLAIGKMIPPKDRFYKRCSLLLVFYGLSVMFLSLY
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
MTRFMNSFAKQTLGYGNMATVEQESSAQAVDSHSNNTPKQAKGVLAEELKDALRFRDERV
SIINAEPSSTLFVFWFVVSCYFPVITACLGPVANTISIACVVEKWRSLKNNSVVTNPRSN
DTDVLMNQVKTVFDPPGIFAVNIISLVLGFTSNIILMLHFSKKLTYLKSQLINITGWTIA
GGMLLVDVIVCSLNDMPSIYSKTIGFWFACISSGLYLVCTIILTIHFIGYKLGKYPPTFN
LLPNERSIMAYTVLLSLWLIWGAGMFSGLLHITYGNALYFCTVSLLTVGLGDILPKSVGA
KIMVLIFSLSGVVLMGLIVFMTRSIIQKSSGPIFFFHRVEKGRSKSWKHYMDSSKNLSER
EAFDLMKCIRQTASRKQHWFSLSVTIAIFMAFWLLGALVFKFAENWSYFNCIYFCFLCLL
TIGYGDYAPRTGAGRAFFVIWALGAVPLMGAILSTVGDLLFDISTSLDIKIGESFNNKVK
SIVFNGRQRALSFMVNTGEIFEESDTADGDLEENTTSSQSSQISEFNDNNSEENDSGVTS
PPASLQESFSSLSKASSPEGILPLEYVSSAEYALQDSGTCNLRNLQELLKAVKKLHRICL
ADKDYTLSFSDWSYIHKLHLRNITDIEEYTRGPEFWISPDTPLKFPLNEPHFAFMMLFKN
IEELVGNLVEDEELYKVISKRKFLGEHRKTL

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
MANTVGGILSGVNPFHYNSSSPLTLFLFQACLILLVCNLIHIPFSMMRQPKVISEVISGV
ILGPTIFGQIPNYTNTIFPTSSIPGLNLVANLGIILFMFFLGLEVDIAFIKKHLKKALVI
GIVTLAVPFGFGCLLAIPLFHTYANKTEGERHIKFSVFMVFIAVSISVTAFPVLCRILNE
LRLIKDRAGIVVLAAGIINDIMGWILLALSIILSSAEGSPVNTVYILLITFAWFLIYFFP
LKYLLRWVLIRTHELDRSKPSPLATMCILFIMFISAYFTDIIGVHPIFGAFIAGLVVPRD
DHYVVKLTERMEDIPNIVFIPIYFAVAGLNVDLTLLNEGRDWGYVFATIGIAIFTKIISG
TLTAKLTGLFWREATAAGVLMSCKGIVEIVVLTVGLNAGIISRKIFGMFVLMALVSTFVT
TPLTQLVYPDSYRDGVRKSLSTPAEDDGAADGLDSEGVDKTEINTQLNSLADVSKYRIGE
LTTVINTTEAISPSLKLLNYLSLGVSPKPKNNKHKNETSLSRMTTATDSTLKSNTFKIKK
MVHIWSKSVDDVDTNLSVIDEKLTPFEGVGALRAIHLRLLTERTTDLLQSSSLYNDDPHF
TANTDSLLQIFDIFSNLSKIPFSSEVIFSTMREKAANIATMKMDSTDLILLPLKGASYEY
RGSPVFIDEKYANFDHIYSHLLGLNELSSTFFKSIFQSLKANFAVQISNTYGRLNADRFK
RKRFNLLLPKPYLTQSDYLGLYLLLLICYRDGYNNDNASCSIFINSKNIDFAKDLSTAFA
EHDWLNESTIKIVDIPFETKVPEEAIEKPSFIETVLDVGLSDTALADIEETTFIIGEDLP
DESEPFSEEVRTVIFEGSNRRFDTLIVHHFSSE

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
MIVSFGDATTRTSEVQLVRCTQGLNLWKLHQVHAVYKRVVHDTLGADEGNALLDQILADT
NLYPPWMCVLLYAFCSAMVTPYAFGGDWVNLAISFFMGLCVGSLQFILSQKSYMYSNVFE
ISASIVVSFCGRAFGSIPRSHICFGAVTQGSLALILPGYIILCGALELQSRSLVAGAVRM
FYAIIYSLFLGFGITLGSALFGWMYHNATNEISCPQLISPWFRFLFVPAFTISISLLNQA
HISQLPVMVFISCTGYVVTYWAGKHFANSTEFTAALAAFVIGVLGNLYSRIWKGLAVSAM
LPAIFVQVPSGIASQNSLLSGLQSANTIVNANETITTSTSDPSSSMSFGMTMIQVCVGIS
VGLFASSLFVYPFGKKKTGLFSL

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
MSTIYRESDSLESEPSPTPTTIPIQINMEEEKKDAFVKNIDEDVNNLTATTDEEDRDPES
QKFDRHSIQEEGLVWKGDPTYLPNSPYPEVRSAVSIEDDPTIRLNHWRTWFLTTVFVVVF
AGVNQFFSLRYPSLEINFLVAQVVCYPIGRILALLPDWKCSKVPFFDLNPGPFTKKEHAV
VTIAVALTSSTAYAMYILNAQGSFYNMKLNVGYQFLLVWTSQMIGYGAAGLIRRWVVNPA
SSIWPQTLISVSLFDSLHSRKVEKTVANGWTMPRYRFFLIVLIGSFIWYWVPGFLFTGLS
YFNVILWGSKTRHNFIANTIFGTQSGLGALPITFDYTQVSQAMSGSVFATPFYVSANTYA
SVLIFFVIVLPCLYFTNTWYAKYMPVISGSTYDNTQNKYNVTKILNEDYSINLEKYKEYS
PVFVPFSYLLSYALNFAAVIAVFVHCILYHGKDIVAKFKDRKNGGTDIHMRIYSKNYKDC
PDWWYLLLQIVMIGLGFVAVCCFDTKFPAWAFVIAILISLVNFIPQGILEAMTNQHVGLN
IITELICGYMLPLRPMANLLFKLYGFIVMRQGLNLSRDLKLAMYMKVSPRLIFAVQIYAT
IISGMVNVGVQEWMMHNIDGLCTTDQPNGFTCANGRTVFNASIIWSLPKYLFSSGRIYNP
LMWFFLIGLLFPLAVYAVQWKFPKFKFAKHIHTPVFFTGPGNIPPSTPYNYSLFFAMSFC
LNLIRKRWRAWFNKYNFVMGAGVEAGVAISVVIIFLCVQYPGGKLSWWGNNVWKRTYDND
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
MDWAINVAHPRLLYKDPKLSVTFIVPSLFHIIIAFVLLGICASDFLCPNVAHISDPNSLR
SNGSLVSKTASHASHTGALMAVLLSWCNSSPDLFSNLMSWATSTRETRSTSVSLSIGEVL
GACGIILCIVEGSIFIIMSRTHIEISQIQKLSIMRDLLFSLAAMCVMSYVSLMNQVTVLN
CLLMAFLYAFYLVVKLTFKLNHSAETPDETAADTSLRENSVSPFLDDSLMASGLLPPIQP
GFDISNSITHGIKPSLLSAMDFNSFLSMLENSSLEEDDSRNEMAELNTLRSMTPGQHWSA
SATVAGEATSAGRPFSEPTNAFTEYRDSERAINSSPAVFAPYRDNPDDEESQEQVLLETT
THGHFGAQEMRRFSKRSLGWIIKIFIPHLSNFSQKSISDAIFSIITVPFFIIFKLSCPQP
PSDILSYDPILNRYSLTTLPIILLFIQSITAPFLLCSILSVLLTYHLGYLVYLFPLILAM
ALILLLTAFITKVNLHNKFTLSLDSSNILQEKLQKRKLLERLNTSIQIIFLAIGIINIII
WISLLANSLIEMMEIYQKILGLSKAILGLTIFAWGNSVGDLISNISMCRLYKTQTHYQDR
VRLATKFFMISCASCLGGVMLNSMGGIGFSGLVSMLFIGAFNDNEWWFLRKVKLQETSQL
DNILNYKFIVSCVFIILQIILLLLFFGGPNNIKRRLTKEMKLVGISMCGLWALATLINIL
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
MKNLSFLINRRKENTSDSNVYPGKAKSHEPSWIEMDDQTKKDGLDIVHVEFSPDTRAPSD
SNKVITEIEDATEDAKEADESERGMPLATALNTYPKAAAWSLLVSTTLIMEGYDTAILGA
FYALPIFQRKFGSQNDKTGEWEISASWQIGLTLCYMAGEIVGLQLTGPSVDLVGNRYTLI
IALFFLAAFTFILYFCNSLGMIAVGQALCGMPWGCFQCLTVSYASEICPLALRYYLTTYS
NLCWLFGQLFAAGIMKNSQKKYADSELGYKLPFALQWILPVPLALGIFFAPESPWWLVKK
GRFDEARRSLRRTLSGKGPEKEILVTLEVDKIKVTIDKEKRLTSKEGSYSDCFEDKINRR
RTRITCLCWAGQATCGSILIGYSTYFYEKAGVSTEMSFTFSIIQYCLGICATFLSWWASK
YFGRYDLYAFGLAFQTIVFFIIGGLGCSSTHGSKMGSGSLLMAVAFFYNLGIAPVVFCLV
SEMPSSRLRTKTIILARNTYNVVSIICSVLILYQLNSKKWNWGAKSGFFWGVLCFCTLIW
AVVDLPETAGKTFVEINELFKLGVSARKFKSTKVDPFVVKTPPKDVSHNDPKGDIEASIA
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
MSTDNSQKDEGVPLLSPYSSSPQLRKKKRNQKRRKDKFVGHLKSDSRRPTQLLHDNLQHN
HGQITDFDQIDSWGMLHESDSTSNDIIKSEDPSLKGAFIDHRPSMSQPREGPQSVSSTVQ
PQPIMKFSTPSYKKPAGLRPSDQNRSLVSDLSPSELESWLKRRKSVHKSFVDENSPTDRR
QSNANNDVVIDVDALMNHVNNNASTGVNDNSKRRKKKRGSDDSSNKNSKSTSSDSNDEED
EYNSRPSSSLSSNNSSLDDVCLVLDDEGSEVPKAWPDCTVLEEFSKEETERLRSQAIQDA
EAFHFQYDEDEEDGTSNEDGILFSKPIVINIDVPELGNRRVNETENLKNGRLRPKRIAPW
HLIQRPMVLGSNSTKDSKSRIQSGLQDNLLVGRNIQYPPHIISNNPEHFRFTYFRVDLDS
TVHSPTISGLLQPGQKFQDLFVASIYSQDNSAGHIKTHPNSPTPGIKAETVSQLQGLTAK
NPSTLSSMSVANIEDVPPFWLDVSNPTEEEMKILSKAFGIHPLTTEDIFLGEVREKVELF
RDYYLICFRSFDIVAEKHVRRRRKEKQESAILDHESISRRKSQAYGATMSNESNANNNNS
TSNASRSKWLPSILRARRRSSANRTTNTSSSSYKRRVKSEKKKMEENEKFKRKSGDRHKP
REGELEPLNVYIIVFRTGVLTFHFAPTPHPINVRRRARLLKDYLNVTSDWIAYALIDDIT
DAFAPMIELIEDEVYEIEDAILKMHQSDDSSDSDSSDSDSDSGASDEDAFPFDVYSKKTS

TABLE 14-continued

Sequences disclosed herein.

YSSAKSSVSSRSMSTSEASFNANLIGWKRKGDMLRRIGECRKRVMSILRLLGSKADVIKG
FAKRYNEQWEASPQSEIAMYLGDIQDHIVTMVSSLNHYEKLLSRSHSNYLAQINIDMTKV
NNDMNDVLGKITILGTIVLPMNVITGLWGMNVIVPGQYRDSLTWFIGIVLFMCMLACSAY
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
MPTAKRTSSRASLALPFQLRLVHKKSWGHRLRDFISGFLKSCRPIAKYVFPNFIVVHYIY
LITLSIIGSILLYPCKNTAFIDVLFLAAGASTQGGLATKSTNDFNLYQQIVVYVITLLST
PILIHGFLAFVRLYWFERYFDNIRDISKQNFKLRRTMTLQQRELSGSSGNAARSRSFKDN
LFRGKFVSREDPRQSASDVPMDSPDTSALSSISPLNVSSSKEESSDTQSSPPNFSSKRQP
SDVDPRDIYKSIMMLQKQQEKSNANSTDSFSSETNGPAFIVQERHERRAPHCSLKRHSVL
PSSQELNKLAQTKSFQKLLGLRRDEGDHDYFDGAPHKYMVTKKKKISRTQSCNIPTYTAS
PSPKTSGQVVENHRNLAKSAPSSFVDEEMSFSPQESLNLQFQAHPPKPKRREGDIGHPFT
RTMSTNYLSWQPTFGRNSVFIGLTKQQKEELGGVEYRALRLLCCILMVYYIGFNILAFVT
IVPWACTRHHYSEIIRRNGVSPTWWGFFTAMSAFSNLGLSLTADSMVSFDTAPYPLIFMM
FFIIIGNTGFPIMLRFIIWIMFKTSRDLSQFKESLGFLLDHPRRCFTLLFPSGPTWWLFT
TLVVLNATDWILFIILDFNSAVVRQVAKGYRALMGLFQSVCTRTAGFNVVDLSKLHPSIQ
VSYMLMMYVSVLPLAISIRRTNVYEEQSLGLYDSGQDDENITHEDDIKETDHDGESEERD
TVSTKSKPKKQSPKSFVGAHLRRQLSFDLWYLFLGLFIICICEGRKIEDVNKPDFNVFAI
LFEVVSAYGTVGLSLGYPNTNTSLSAQFTVLSKLVIIAMLIRGRNRGLPYTLDRAIMLPS
DKLEQIDRLQDMKAKGKLLAKVGEDPMTTYVKKRSHKLKKIATKFWGKH

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
MEETKYSSQQEIEGACGSDASLNARGSNDSPMGLSLYLCLASLILVLFITALDILIVGTI
IDVVAEQFGNYSKTGWLVTGYSLPNAILSLIWGRFASIIGFQHSLILAILIFEAGSLIAA
LASSMNMLIFGRVVAGVGGSGLQTLCFVIGCTMVGERSRPLVISILSCAFAVAAIVGPII
GGAFTTHVTWRWCFYINLPIGGLAIIMFLLTYKAENKGILQQIKDAIGTISSFTFSKFRH
QVNFKRLMNGIIFKFDFFGFALCSAGLVLFLLGLTFGGNKYSWNSGQVITYLVLGVLLFI
FSLVYDFFLFDKFNPEPDNISYRPLLLRRLVAKPAIIIVNMVTFLLCTGYNGQMIYSVQF
FQLIFASSAWKAGLHLIPIVITNVIAAIASGVITKKLGLVKPLLIFGGVLGVIGAGLMTL
MTNTSTKSTQIGVLLLPGFSLGFALQASLMSAQLQITKDRPEAAMDFIEVTAFNTFMKSL
GTTLGGVLSTTVFSASFHNKVSRAHLEPYEGKTVDDMILYRLQNYDGSHSTIGNILSDSI
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
MSSSVVGASSNKKSGIRQSCEIIERERHSNDDTYSMTSTFFKLKENEIMSAQFDSLKYKI
LLISTAFVCGFGISLDYTLRSTYTGYATNSYSEHSLLSTVQVINAVVSVGSQVVYSRLSD
HFGRLRLFLVATIFYIMGTIIQSQATRLTMYAAGSVFYNCGYVGTNLLLTLILSDFSSLK
WRMFYQYASYWPYIIIPWISGNIITAANPQKNWSWNIAMWAFIYPLSTLPIIFLILYMKY
KSSKTAEWRSLKEQARKERTGGLFENLVFLFWKLDIVGILLITVSLGCILVPLTLANETS
QKWHNSKIIATLVSGGCLFFIFLYWEAKFAKSPLLPFKLLSDRGIWAPLGVTFFNFFTFF
ISCDYLYPVLLVSMKESSTSAARIVNLPDFVAATASPFYSLLVAKTRKLKLSVIGGCAAW
MVCMGLFYKYRGGSGSHEGVIAASVIMGLSGLLCSNSVIVILQAMTTHSRMAVITGIQYT
FSKLGAAIGASVSGAIWTQTMPNQLYKNLGNDTLAEIAYASPYTFISDYPWGSPERDAVV
ESYRYVQRIIMTVGLACTVPFFTFTMFMRNPELIDKATHEEFTEDGLVVLPDEENIFSQI
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
MEGVYFNIDNGFIEGVVRGYRNGLLSNNQYINLTQCDTLEDLKLQLSSTDYGNFLSSVSS
ESLTTSLIQEYASSKLYHEFNYIRDQSSGSTRKFMDYITYGYMIDNVALMITGTIHDRDK
GEILQRCHPLGWFDTLPTLSVATDLESLYETVLVDTPLAPYFKNCFDTAEELDDMNIEII
RNKLYKAYLEDFYNFVTEEIPEPAKECMQTLLGFEADRRSINIALNSLQSSDIDPDLKSD
LLPNIGKLYPLATFHLAQAQDFEGVRAALANVYEYRGFLETGNLEDHFYQLEMELCRDAF
TQQFAISTVWAWMKSKEQEVRNITWIAECIAQNQRERINNYISVY

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
MGNQSLVVLTESKGEYENETELPVKKSSRDNNIGESLTATAFTQSEDEMVDSNQKWQNPN
YFKYAWQEYLFIFTCMISQLLNQAGTTQTLSIMNILSDSFGSEGNSKSWLMASFPLVSGS
FILISGRLGDIYGLKKMLLVGYVLVIIWSLICGITKYSGSDIFFIISRAFQGLGIAFVLP
NVLGIIGNIYVGGTFRKNIVISFVGAMAPIGATLGCLFAGLIGTEDPKQWPWAFYAYSIA
AFINFVLSIYAIPSTIPTNIHHFSMDWIGSVLGVIGLILLNFVWNQAPISGWNQAYIIVI
LIISVIFLVVFIIYEIRFAKTPLLPRAVIKDRHMIQIMLALFFGWGSFGIFTFYYTQFQL
NIRQYTALWAGGTYFMFLIWGIIAALLVGFTIKNVSPSVFLFFSMVAFNVGSIMASVTPV
HETYFRTQLGTMIILSFGMDLSFPASSIIFSDNLPMEYQGMAGSLVNTVVNYSMSLCLGM
GATVETQVNSDGKHLLKGYRGAQYLGIGLASLACMISGLYMVESFIKGRRARAAAEYDCT
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
MKTQYSLIRKIWAHSVTEFLKSQWFFICLAILIVIARFAPNFARDGGLIKGQYSIGYGCV
AWIFLQSGLGMKSRSLMANMLNWRAHATILVLSFLITSSIVYGFCCAVKAANDPKIDDWV
LIGLILTATCPTTVASNVIMTTNAGGNSLLCVCEVFIGNLLGAFITPALVQMFTNRAPFA
YGNPATGNGIGALYGRVMKQVGLSVFVPLFVGQVIQNCFPKGTAYYLGFLKKYHIKIGSY
MLLLIMFSSFSTAFYQDAFTSVSHVCIIFLCFFNLGIYIFFTGLSYLCARPWFILKLFPH
EPIEGKSTRLYRYSYNIFRPFYYSKEDAICIMFCGPAKTAALGVSLITSQYGDKKEHLGK
LLVPLVLYQVEQVMTANFFVSLFKRWIQKDAQADGSESSCANENEEVDLEKIISIGTGEN
QSVLSNNVPYTQPR

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
MSHTETQTQQSHFGVDFLMGGVSAAIAKTGAAPIERVKLLMQNQEEMLKQGSLDTRYKGI
LDCFKRTATHEGIVSFWRGNTANVLRYFPTQALNFAFKDKIKSLLSYDRERDGYAKWFAG
NLFSGGAAGGLSLLFVYSLDYARTRLAADARGSKSTSQRQFNGLLDVYKKTLKTDGLLGL
YRGFVPSVLGIIVYRGLYFGLYDSFKPVLLTGALEGSFVASFLLGWVITMGASTASYPLD
TVRRRMMMTSGQTIKYDGALDCLRKIVQKEGAYSLFKGCGANIFRGVAAAGVISLYDQLQ
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
MNPSVPKVMKRENNTHLLVSKEMNDTSLQLPSTTRSLSPKESNSNEDFNVDGNETTLQRI
SKDYLKPNIGLVLLTVSYFFNSAMVVSTKVLENDPDDIANDRQIKPLQILLVRMVITYIG
TLIYMYINKSTISDVPFGKPEVRKWLVLRGCTGFFGVFGMYYSLMYLTISDAVLITFLAP
SLTIFLSWVILRERFTKVEALGSLISLLGVVLIVRPSFLFGTPELTDSSSQIVESSDPKS
RLIATLVGLWGVLGMSCVYIIIRYIGKRAHAIMSVSYFSLITAIVSFIGINTIPSMKFQI
PHSKKQWILFGNLGVSGFIFQLLLTMGIQRERAGRGSLMTYTQLLYAVFWDVALYKHWPN
IWSWIGMIIIISATLWVIRAANNETTAKDLTPIIDDEENSIPLTEFDLSDSK

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
MSRSNSIYTEDIEMYPTHNEQHLTREYTKPDGQTKSEKLNFEGAYINSHGTLSKTTTREI
EGDLDSETSSHSSDDKVDPTQQITAETKAPYTLLSYGQKWGMVAILTMCGFWSSLGSPIY
YPALRQLEKQFNVDENMVNVTVVVYLLFQGISPTVSGGLADCFGRRPIILAGMLIYVIAS
IGLACAPSYGVIIFLRCIQSIGISPTIAISSGVVGDFTLKHERGTFVGATSGFVLLGQCF
GSLIGAVLTARWDWRAIFWFLTIGCGSCFLIAFLILPETKRTIAGNLSIKPKRFINRAPI
FLLGPVRRRFKYDNPDYETLDPTIPKLDLSSAGKILVLPEIILSLFPSGLLFAMWTLMLS
SISSGLSVAPYNYHLVIIGVCYLPGGIGGLMGSFFTGRIIDMYFKRKIKKFEQDKANGLI
PQDAEINMFKVRLVCLLPQNFLAVVAYLLFGWSIDKGWRIESILITSFVCSYCAMSTLST
STTLLVDLYPTKSSTASSCFNFVRCSLSTIFMGCFAKMKAAMTVGGTFTFLCALVFFFNF
LMFIPMKYGMKWREDRLLKQQRQSWLNTLAVKAKKGTKRDQNDNHN

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
MLLKNCETDKQRDIRYACLFKELDVKGNGQVTLDNLISAFEKNDHPLKGNDEAIKMLFTA
MDVNKDSVVDLSDFKKYASNAESQIWNGFQRIDLDHDGKIGINEINRYLSDLDNQSICNN
ELNHELSNEKVNKFSRFFEWAFPKRKANIALRGQASHKKNTDNDRSKKTTDSDLYVTYDQ
WRDFLLLVPRKQGSRLHTAYSYFYLFNEDVDLSSEGDVTLINDFIRGFGFFIAGGISGVI
SRTCTAPFDRLKVFLIARTDLSSILLNSKTDLLAKNPNADINKISSPLAKAVKSLYRQGG
IKAFYVGNGLNVIKVFPESSIKFGSFEVTKKIMTKLEGCRDTKDLSKFSTYIAGGLAGMA
AQFSVYPIDTLKFRVQCAPLDTKLKGNNLLFQTAKDMFREGGGQIILQRCHSRYSGHISL
CCIRFGDFFCLKKMVYCQTGKDPEPTTRSGHSKQPGCTSNGCIQWNCRSFCCLSNQSFKN
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
IVANIEDKDIKSVGIICLSALLIFGSGFFFAYVVRLFLPVPKQWYGGILAGGMFPNISDL
PIAYLQSMDQGLVFSEEEGNKGVANVIIFLTMFLICIFNLGGFRLIESDFEYNDDESAVR
VSETTKTQPAVSANTTNTDTSERFFSNEQQLFNNKYTARDSLTEAIGTKGENADVPPISR
RSTNSIAPLSLPDTSSNSKITKPVQVKARNTIACTQSEESQATRGSNPLDSQSSASTIHS
YNTSESYESSIDTMRARRTASQPRAYNTTTLLEENCLDEKCPKNMSMAALEPIRSIDMRA
LPSQNIHHLIREYSNVDQYGHQRRNSSLRGADMNDVHSISSNSTLQTIKTANLTRILTSD
ATVSKKDIETSGESLPQWMRKFSLTPLLVFFLKNCLRPCSMAVIIALTVAFIPWVKALFV
TTANTPHISQAPDNAPPLSFFMDFTGYVGAACVPFGLILLGATLGRLKIGNLYPGFWKAA
VTLVILRQCVMPIFGVLWCDRLVKAGWVNWQDDRMLLFVIAISWNLPTMTTLIYFTASFT
PPETTAPIQMECVSFFLMLQYPLMVVSLPFLVSYFLKVQMNL

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
MKSFITRNKTAILATVAATGTAIGAYYYYNQLQQQQRGKKNTINKDEKKDTKDSQKETE
GAKKSTAPSNPPIYPVSSNGEPDFSNKANFTAEEKDKYALALKDKGNQFFRNKKYDDAIK
YYNWALELKEDPVFYSNLSACYVSVGDLKKVVEMSTKALELKPDYSKVLLRRASANEGLG
KFADAMFDLSVLSLNGDFNDASIEPMLERNLNKQAMSKLKEKFGDIDTATATPTELSTQP
AKERKDKQENLPSVTSMASFFGIFKPELTFANYDESNEADKELMNGLSNLYKRSPESYDK
ADESFTKAARLFEEQLDKNNEDEKLKEKLAISLEHTGIFKFLKNDPLGAHEDIKKAIELF
PRVNSYIYMALIMADRNDSTEYYNYFDKALKLDSNNSSVYYHRGQMNFILQNYDQAGKDF
DKAKELDPENIFPYIQLACLAYRENKFDDCETLFSEAKRKFPEAPEVPNFFAEILTDKND
FDKALKQYDLAIELENKLDGIYVGIAPLVGKATLLTRNPTVENFIEATNLLEKASKLDPR
SEQAKIGLAQMKLQQEDIDEAITLFEESADLARTMEEKLQAITFAEAAKVQQRIRSDPVL
AKKIQETLAKLREQGLM

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
MSYNFTGTPTGEGTGGNSLTTDLNTQFDLANMGWIGVASAGVWIMVPGIGLLYSGLSRKK
HALSLLWASMMASAVCIFQWFFWGYSLAFSHNTRGNGFIGTLEFFGFRNVLGAPSSVSSL
PDILFAVYQGMFAAVTGALMLGGACERARLFPMMVFLFLWMTIVYCPIACWVWNAEGWLV
KLGSLDYAGGLCVHLTSGHGGLVYALILGKRNDPVTRKGMPKYKPHSVTSVVLGTVFLWF
GWMFFNGGSAGNATIRAWYSIMSTNLAAACGGLTWMVIDYFRCGRKWTTVGLCSGIIAGL
VGITPAAGFVPIWSAVVIGVVTGAGCNLAVDLKSLLRIDDGLDCYSIHGVGGCIGSVLTG
IFAADYVNATAGSYISPIDGGWINHHYKQVGYQLAGICAALAWTVTVTSILLLTMNAIPF
LKLRLSADEEELGTDAAQIGEFTYEESTAYIPEPIRSKTSAQMPPPHENIDDKIVGNTDA
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
MTEDFISSVKRSNEELKERKSNFGFVEYKSKQLTSSSSHNSNSSHHDDDNQHGKRNIFQR
CVDSFKSPLDGSFDTSNLKRTLKPRHLIMIAIGGSIGTGLFVGSGKAIAEGGPLGVVIGW
AIAGSQIIGTIHGLGEITVRFPVVGAFANYGTRFLDPSISFVVSTIYVLQWFFVLPLEII
AAAMTVQYWNSSIDPVIWVAIFYAVIVSINLFGVRGFGEAEFAFSTIKAITVCGFIILCV
VLICGGGPDHEFIGAKYWHDPGCLANGFPGVLSVLVVASYSLGGIEMTCLASGETDPKGL
PSAIKQVFWRILFFFLISLTLVGFLVPYTNQNLLGGSSVDNSPFVIAIKLHHIKALPSIV
NAVILISVLSVGNSCIFASSRTLCSMAHQGLIPWWFGYIDRAGRPLVGIMANSLFGLLAF
LVKSGSMSEVFNWLMAIAGLATCIVWLSINLSHIRFRLAMKAQGKSLDELEFVSAVGIWG
SAYSALINCLILIAQFYCSLWPIGGWTSGKERAKIFFQNYLCALIMLFIFIVHKIYYKCQ
TGKWWGVKALKDIDLETDRKDIDIEIVKQEIAEKKMYLDSRPWYVRQFHFWC

SEQ ID NO: 66
YOL075C
>sp|Q08234|YO075_YEAST Uncharacterized ABC transporter ATP-binding
protein/permease YOL075C OS = *Saccharomyces cerevisiae* (strain ATCC
204508 / S288c) GN = YOL075C PE = 1 SV = 3
MSQQENGDVATELIENRLSFSRIPRISLHVRDLSIVASKTNTTLVNTFSMDLPSGSVMAV
MGGSGSGKTTLLNVLASKISGGLTHNGSIRYVLEDTGSEPNETEPKRAHLDGQDHPIQKH
VIMAYLPQQDVLSPRLTCRETLKFAADLKLNSSERTKKLMVEQLIEELGLKDCADTLVGD
NSHRGLSGGEKRRLSIGTQMISNPSIMFLDEPTTGLDAYSAFLVIKTLKKLAKEDGRTFI
MSIHQPRSDILFLLDQVCILSKGNVVYCDKMDNTIPYFESIGYHVPQLVNPADYFIDLSS
VDSRSDKEEAATQSRLNSLIDHWHDYERTHLQLQAESYISNATEIQIQNMTTRLPFWKQV
TVLTRRNFKLNFSDYVTLISTFAEPLIIGTVCGWIYYKPDKSSIGGLRTTTACLYASTIL
QCYLYLLFDTYRLCEQDIALYDRERAEGSVTPLAFIVARKISLFLSDDFAMTMIFVSITY
FMFGLEADARKFFYQFAVVFLCQLSCSGLSMLSVAVSRDFSKASLVGNMTFTVLSMGCGF
FVNAKVMPVYVRWIKYIAFTWYSFGTLMSSTFTNSYCTTDNLDECLGNQILEVYGFPRNW
ITVPAVVLLCWSVGYFVVGAIILYLHKIDITLQNEVKSKQKKIKKKSPTGMKPEIQLLDD
VYHQKDLEAEKGKNIHITIKLEDIDLRVIFSAPFSNWKEGNFHHETKEILQSVNAIFKpG
MINAIMGPSGSGKSSLLNLISGRLKSSVFAKFDTSGSIMFNDIQVSELMFKNVCSYVSQD
DDHLLAALTVKETLKYAAALRLHHLTEAERMERTDNLIRSLGLKHCENNIIGNEFVKGIS
GGEKRRVTMGVQLLNDPPILLLDEPTSGLDSFTSATILEILEKLCREQGKTIIITIHQpR
SELFKRFGNVLLLAKSGRTAFNGSPDEMIAYFTELGYNCPSFTNVADFFLDLISVNTQNE
QNEISSRARVEKILSAWKANMDNESLSPTPISEKQQYSQESFFTEYSEFVRKPANLVLAy
IVNVKRQFTTTRRSFDSLMARIAQIPGLGVIFALFFAPVKHNTISISNRLGLAQESTALY
FVGMLGNLACYPTERDYFYEEYNDNVYGIAPFFLAYMTLELPLSALASVLYAVETVLACG
LPRTAGNFFATVYCSFIVTCCGEALGIMTNTFFERPGFVVNCISIILSIGTQMSGLMSLG
MSRVLKGFNYLNPVGYTSMIIINFAFPGNLKLTCEDGGKNSDGTCEFANGHDVLVSYGLV
RNTQKYLGIIVCVAIIYRLIAFFILKAKLEWIKW

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
MGAAYHFMGKAIPPHQLAIGTLGLLGLLVVPNPFKSAKPKTVDIKTDNKDEEKFIENYLK
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
MVNVGPSHAAVAVDASEARKRNISEEVFELRDKKDSTVVIEGEAPVRTFTSSSSNHERED
TYVSKRQVMRDIFAKYLKFIGPGLMVSVAYIDPGNYSTAVDAGASNQFSLLCIILLSNFI
AIFLQCLCIKLGSVTGLDLSRACREYLPRWLNWTLYFFAECAVIATDIAEVIGTAIALNI
LIKVPLPAGVAITVVDVFLIMFTYKPGASSIRFIRIFECFVAVLVVGVCICFAIELAYIP
KSTSVKQVFRGFVPSAQMFDHNGIYTAISILGATVMPHSLFLGSALVQPRLLDYDVKHGN
YTVSEEQDKVKKSKSTEEIMEEKYFNYRPTNAAIKYCMKYSMVELSITLFTLALFVNCAI
LVVAGSTLYNSPEADGADLFTIHELLSRNLAPAAGTIFMLALLLSGQSAGVVCTMSGQIV
SEGHINWKLQPWQRRLATRCISIIPCLVISICIGREALSKALNASQVVLSIVLPFLVAPL
IFFTCKKSIMKTEITVDHTEEDSHNHQNNNDRSAGSVIEQDGSSGMEIENGKDVKIVYMA
NNWIITVIAIIVWLFLSLLNVYAIVQLGMSHGDIS

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
MKFLGVILLASELLIATFLIGLIPLYYIDKQKSSIVTNQEGADSISDFTTNADTQTINDD
VSSYRVKIAVLSQFGIGMLLGTSFMLVIPEGIKACVEHDGNVGVNLLIGFLGINVLDRLV
TLWVSRKQTVYTHDAVKFQSWKDIINHPRQIWMNLIQNNVVFALFIHGLSDGIALGTTTN
NDSLLIVVLIAIVIHKIPAVLSLTSLMVSRQNLMKWEVICNVELFASSTPIGYIVLSLLN

TABLE 14-continued

Sequences disclosed herein.

LSHSPTMDWISGNLLLMSGGSLLYASFTAFVGGDSHDHDLSVEQEVVLPHDESVYVLIGV
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
MVSANGDLHLPISNEQCMPENNGSLGFEAPTPRQILRVTLNLKYLIDKVVPIVYDPNDIV
CDHSEILSPKVVKLAYEACGGNPKDKANKRKYQSVIIFSLLKVCEWYSILATMEVHNAKL
YETRNLASQQLCKLLIEREETRDLQFLFMQLLLRRYVINENDEDQEPLNALELATDMHCT
TVIGSSGFQRCLKWIWRGWIVQNGLDPTTFIKDDSLAEVSLISHFNPVRLKAPVYQNYLQ
MIFSFLFLGLYTLVVNGKDSERVQSFDLLESIFYVFNTGFILDELTKLYYIGYAHLSFWN
LFNDTTYLIITFAMGFRAMSVTPLNAKYSSEDWDKISYRVLSCAAPFVWSRLLLYLESQR
FIGIMLVILKHMMKESIVFFFLLFLIMIGFTQGFLGLDSADGKRDITGPILGNLTITVLG
LGSFDVFEEFAPPYAAILYYGYYFIVSVILLNILIALYSTAYQKVIDNADDEYMALMSQK
TLRYIRAPDEDVYVSPLNLIEVFMTPIFRILPPKRAKDLSYTVMTIVYSPFLLLISVKET
REARRIKYNRMKRLNDDANEYDTPWDLTDGYLDDDDGLFSDNRNSGMRATQLKNSRSLKL
QRTAEQEDVHFKVPKKWYKNVKKCSPSFEQYDNDDTEDDAGEDKDEVKELTKKVENLTAV
ITDLLEKLDIKDKKE

SEQ ID NO: 71
YOR092W
>sp|Q99252|ECM3_YEAST Protein ECM3 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = ECM3 PE = 1 SV = 1
MTHITLGQAIWASVRPIIKIYLIIGVGFGLCKMNILTVQATRSISDIVLTILLPCLSFNK
IVANIEDNDIKDVGIICLTSVILFATGLGFAFIVRSVLPVPKRWRGGILAGGMFPNISDL
PIAYLQSMDQGFIFTEAEGEKGVANVIIFLAMFLICVFNLGGFRLIENDFHYKGDDDEEN
TLTNDDSAQQPTQPIEGNSSSSSNQDILKEPNESTVPNSSQASYISEKNKKEKTELSVPK
PTHTAPPAIDDRSSNSSAVVSIDSITHSLRTNHVDAQSVSELNDPTYRTRSQPIAYTTES
RTSHVHNNRRNSITGSLRSIDMRELPAEGMSDLIREYSNVDQYGRRRKSSISSQGAPSVL
QADGTISPNLTRTSTLQRVKTSNLTRIITSDATVSKKDIETSGSSLPKWLQKFPLTKFFV
FFLKNCLRPCSMAVILALIIAFIPWVKALFVTTSNTPKIKQAPDNAPALTFIMDFTSYVG
AASVPFGLILLGATLGRLKIGKLYPGFWKSAVVLVFLRQCIMPIFGVLWCDRLVKAGWLN
WENDKMLLFVTAITWNLPTMTTLIYFTASYTPEDETEPVQMECTSFFLMLQYPLMVVSLP
FLVSYFIKVQMKL

SEQ ID NO: 72
YOR130C
>sp|Q12375|ORTl_YEAST Mitochondrial ornithine transporter 1 OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = ORT1 PE = 1 SV = 2
MEDSKKKGLIEGAILDIINGSIAGACGKVIEFPFDTVKVRLQTQASNVFPTTWSCIKFTY
QNEGIARGFFQGIASPLVGACLENATLFVSYNQCSKFLEKHINVSPLGQILISGGVAGSC
ASLVLTPVELVKCKLQVANLQVASAKTKHTKVLPTIKAIITERGLAGLWQGQSGTFIRES
FGGVAWFATYEIVKKSLKDRHSLDDPKRDESKIWELLISGGSAGLAFNASIFPADTVKSV
MQTEHISLTNAVKKIFGKFGLKGFYRGLGITLFRAVPANAAVFYIFETLSAL

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
SIAAGASAGMTEAAVIVPFELIKIRMQDVKSSYLGPMDCLKKTIKNEGIMGLYKGIESTM
WRNALWNGGYFGVIYQVRNSMPVAKTKGQKTRNDLIAGAIGGTVGTMLNTPFDVVKSRIQ
SVDAVSSAVKKYNWCLPSLLVIYREEGFRALYKGFVPKVCRLAPGGSLMLVVFTGMMNFF
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
MDIPSSNQIQHGQRSERNRRMPRASFSSTATTSTAATLTSAMVLDQNNSEPYAGATFEAV
PSSIVSFHHPHSFQSSNLPSPHSSGNLEQRGRRLTESEPLVLSSAEQSRSSSRNPSHFRF
FTQEQISNAEGASTLENTDYDMAWDATPAYEQDRIYGTGLSSRRSSIRSFSRASSLSNAK
SYGSFSKRGRSGSRAPQRLGENSDTGFVYHSATHSSSSLSRYTTRERIPIELESQTDEIL
EDESSTHSLESSDSRRSASENNRGSFSGHDDVHNQHSEYLKPDYHEKFYPQYAPNLHYQR
FYIAEEDLVIGIAAYQTSKFWYIIYNLCCFLTFGLVYLLTRWLPHLKVKLYGVKVPLAKA
EWVVIENEFGEFVIQPIDRQWYNRPLSTVLPFENYPNPSYEPNDINLSHHHANEINPNVP
ILITFEYRYIKFIYSPLDDLFKTNNNWIDPDWVDLSTVSNGLTKGVQEDRELAFGKNQIN
LRMKTTSEILFNEVLHPFYVFQVFSIILWGIDEYYYYAACIFLISVLSIFDSLNEQKKVS
RNLAEMSHFHCDVRVLRDKFWTTISSSELVPGDIYEVSDPNITILPCDSILLSSDCIVNE
SMLTGESVPVSKFPATEETMYQLCDDFQSTQISSFVSKSFLYNGTNIIRARIAPGQTAAL

TABLE 14-continued

Sequences disclosed herein.
AMVVRTGFSTTKGSLVRSMVFPKPTGFKFYRDSFKYIGFMSLIAIFGFCVSCVQFIKLGL DKKTMILRALDIITIVVPPALPATLTIGTNFALSRLKEKGIFCISPTRLNISGKIDVMCF DKTGTLTEDGLDVLGVQISEPNGVRGQKFGELLSDIRQVFPKFSLNDCSSPLDFKSRNFF MSLLTCHSLRSVDGNLLGDPLDFKMFQFTGWSFEEDFQKRAFHSLYEGRHEDDVFPENSE IIPAVVHPDSNNRENTFTDNDPHNFLGVVRSFEFLSELRRMSVIVKTNNDDVYWSFTKGA PEVISEICNKSTLPADFEEVLRCYTHNGYRVIACAGKTLPKRTWLYSQKVSREEVESNLE FLGFIIFQNKLKKETSETLKSLQDANIRTIMCTGDNILTAISVGREAGLIQCSRVYVPSI NDTPLHGEPVIVWRDVNEPDKILDTKTLKPVKLGNNSVESLRECNYTLAVSGDVFRLLFR DENEIPEEYLNEILLNSSIYARMSPDEKHELMIQLQKLDYTVGFCGDGANDCGALKAADV GISLSEAEASVAAPFTSKIFNISCVLDVIREGRAALVISFACFQYMSLYSAIQFITITIL YSRGSNLGDFQFLYIDLLLIVPIAICMSWSKSYEKIDKKRPSANLVSPKILVPLLISVFL VFLFQFIPWIIVQKMSWYIKPIVGGDDAVQSSDNTVLFFVSNFQYILTAIVLSVGPPYRE PMSKNFEFIVDITVSIGASLLLMTLDTESYLGKMLQLTPISNSFTMFIIVWVILNYYAQL YIPPSIKGWLKKKKSSKKYKLLIQEEMKLKEV
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 MSSDSLTPKDTIVPEEQTNQLRQPDLDEDSIHYDPEADDLESLETTASYASTSVSAKVYT KKEVNKGTDIESQPHWGENTSSTHDSDKEEDSNEEIESFPEGGFKAWVVTFGCFLGLIAC FGLLNSTGVIESHLQDNQLSSESVSTIGWLFSLFLFVCSASCIISGTYFDRNGFRTIMIV GTVFHVAGLFATANSTKYWHFILSFAIVCGFGNGIVLSPLVSVPAHYFFKRRGTALAMAT IGGSVGGVVFPIMLRSFFSMKSDTDPTYGFVWGIRTLGFLDLALLTLSIILVKERLPHVI ENSKDGESRWRYILRVYILQCFDAKAFLDMKYLFCVLGTVFSELSINSALTYYGSYATSH GISANDAYTLIMIINVCGIPGRWVPGYLSDKFGRFNVAIATLLTLFIVMFVGWLPFGTNL TNMYVISALYGFCSGSVFSLLPVCCGQISKTEEFGKRYSTMYFVVGFGTLVGIPITGAII SIKTTADYQHYIIFCGLATFVSAVCYIISRAYCVGFKWVRF
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 MKLGSKQVKIISLLLLDTVFFGIEITTGYLSHSLALIADSFHMLNDIISLVVALWAVNVA KNRNPDSTYTYGWKRAEILGALINAVFLIALCVSILIEALQRIIAPPVIENPKFVLYVGV AGLISNTVGLFLFHDNDQEHGHGHGHSHGGIFADHEMHMPSSHTHTHAHVDGIENTTPMD STDNISEIMPNAIVDSFMNENTRLLTPENASKTPSYSTSSHTIASGGNYTEHNKRKRSLN MHGVFLHVLGDALGNIGVMLSAFFIWKTDYSWKYYTDPLVSLIITGIIFSSALPLSCKAS KILLQATPSTLSGDQVEGDLLKIPGIIAIHDFHIWNLTESIFIASLHIQLDISPEQFTDL 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 MNRRLLVRSISCFQPLSRITFGRPNTPFLRKYADTSTAANTNSTILRKQLLSLKPISASD SLFISCTVFNSKGNIISMSEKFPKWSFLTEHSLFPRDLRKIDNSSIDIIPTIMCKPNCIV INLLHIKALIERDKVYVFDTTNPSAAAKLSVLMYDLESKLSSTKNNSQFYEHRALESIFI NVMSALETDFKLHSQICIQILNDLENEVNRLKLRHLLIKSKDLTLFYQKTLLIRDLLDEL LENDDDLANMYLTVKKSPKDNFSDLEMLIETYYTQCDEYVQQSESLIQDIKSTEEIVNII LDANRNSLMLLELKVTIYTLGFTVASVLPAFYGMNLKNFIEESEWGFTSVAVFSIVSALY ITKKNFNSLRSVTKMTMYPNSPANSSVYPKTSASIALTNKLKRRRKWWKSTKQRLGVLLY GSSYTNKANLSNNKINKGFSKVKKFNMENDIKNKQNRDMIWKWLIEDKKN
SEQ ID NO: 78 YPL078C >sp|P05626|ATPF_YEAST ATP synthase subunit 4, mitochondrial OS = *Saccharomyces cerevisiae* (strain ATCC 204508 S288c) GN = ATP4 PE = 1 SV = 2 MSMSMGVRGLALRSVSKTLFSQGVRCPSMVIGARYMSSTPEKQTDPKAKANSIINAIPGN NILTKTGVLGTSAAAVIYAISNELYVINDESILLLTFLGFTGLVAKYLAPAYKDFADARM KKVSDVLNASRNKHVEAVKDRIDSVSQLQNVAETTKVLFDVSKETVELESEAFELKQKVE LAHEAKAVLDSWVRYEASLRQLEQRQLAKSVISRVQSELGNPKFQEKVLQQSISEIEQLL 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 MLNGRLPLLRLGICRNMLSRPRLAKLPSIRFRSLVTPSSSQLIPLSRLCLRSPAVGKSLI LQSFRCNSSKTVPETSLPSASPISKGSARSAHAKEQSKTDDYKDIIRLFMLAKRDWKLLL TAILLLTISCSIGMSIPKVIGIVLDTLKTSSGSDFFDLKIPIFSLPLYEFLSFFTVALLI

TABLE 14-continued

Sequences disclosed herein.

GCAANFGRFILLRILSERVVARLRANVIKKTLHQDAEFFDNHKVGDLISRLGSDAYVVSR
SMTQKVSDGVKALICGVVGVGMMCSLSPQLSILLLFFTPEWLFSASVFGKQIRNTSKDLQ
EATGQLTRVAEEQLSGIKTVQSFVAEGNELSRYNVAIRDIFQVGKTAAFTNAKFFTTTSL
LGDLSFLTVLAYGSYLVLQSQLSIGDLTAFMLYTEYTGNAVFGLSTFYSEIMQGAGAASR
LFELTDRKPSISPTVGHKYKPDRGVIEFKDVSFSYPTRPSVQIFKNLNFKIAPGSSVCIV
GPSGRGKSTIALLLLRYYNPTTGTITIDNQDISKLNCKSLRRHIGIVQQEPVLMSGTIRD
NITYGLTYTPTKEEIRSVAKQCFCHNFITKFPNTYDTVIGPHGTLLSGGQKQRIAIARAL
IKKPTILILDEATSALDVESEGAINYTFGQLMKSKSMTIVSIAHRLSTIRRSENVIVLGH
DGSVVEMGKFKELYANPTSALSQLLNEKAAPGPSDQQLQIEKVIEKEDLNESKEHDDQKK
DDNDDNDNNHDNDSNNQSPETKONNSDDIEKSVEHLLKDAAKEANPIKITPQP

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
MDILKRGNESDKFTKIETESTTIPNDSDRSGSLIRRMKDSFKQSNLHVIPEDLENSEQTE
QEKIQWKLASQPYQKVLSQRHLTMIAIGGTLGTGLFIGLGYSLASGPAALLIGFLLVGTS
MFCVVQSAAELSCQFPVSGSYATHVSRFIDESVGFTVATNYALAWLISFPSELIGCALTI
SYWNQTVNPAVWVAIFYVFIMVLNLFGVRGFAETEFALSIIKVIAIFIFIIIGIVLIAGG
GPNSTGYIGAKYWHDPGAFAKPVFKNLCNTFVSAAFSFGGSELVLLTSTESKNISAISRA
AKGTFWRIAIFYITTVVIIGCLVPYNDPRLLSGSNSEDVSASPFVIALSNTGSMGAKVSN
FMNVVILVAVVSVCNSCVYASSRLIQALGASGQLPSVCSYMDRKGRPLVGIGISGAFGLL
GFLVASKKEDEVFTWLFALCSISSFFTWFCICMSQIRFRMALKAQGRSNDEIAYKSILGV
YGGILGCVLNALLIAGEIYVSAAPVGSPSSAEAFFEYCLSIPIMIVVYFAHRFYRRDWKH
FYIKRSEIDLDTGCSVENLELFKAQKEAEEQLIASKPFYYKIYRFWC

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
MTSNNSLLGRGRMSYSSTAPPRFKRSVDQRDTFSDNFDYDKDSSNRGRTYIAASNSTTGV
PPPNNSRSGCTNNTNNTNNTSNTSNTNNNDSVDENTVFETLPYYLPCFSWLPEYTFNKLW
GDVIAGISVASFQIPLALSYTTSIAHVPPLCGLYSLAISPFVYGILGSVPQMIVGPESAI
SLVVGQAVESITLHKENVSLIDISTVITFVSGTILLFSGISRFGFLGNVLSKALLRGFIS
SVGLVMIINSLISELKLDKFLVSLPQHYHTPFEKILFLIDYAPAQYHIPTAIFSGCCLIV
LFLTRLLKRKLMKYHKSAIFFPDILLVVIVTILISMKFNLKHRYGISIIGDFSMDNFDEL
KNPLTRPRRKLIPDLFSASLIVAMLGFFESTTASKSLGTTYNLTVSSNRELVALGFMNIV
ISLFGALPAFGGYGRSKINALSGAQSVMSGVFMGVITLITMNLLLQFVHYIPNCVLSVIT
TIIGISLLEEVPGDIKFHLRCGGFSELFVFAVTFCTTIFYSIEAGICIGCNNSIINIIKH
SAKSRIQILARVAGTSNFTNLDDYMMNMKRNSLDVEGTEEIEGCMIVRIPEPLTFTNSED
LKQRLDRIERYGSSKIHPGRKSLRSKDSIKYVIFDLGGMTSIDSSAAQVLEEIITSYKRR
NVFIYLVNVSINDKVRRRLFKAGVAASVERAQANNNENNTSNTFSDAGETYSPYTDSIDA
ALYEIEKMKIKGNNVPNNDSESFMSNTLFNSSLV

SEQ ID NO: 82
YPR011C
>sp|Q12251|YP011_YEAST Uncharacterized mitochondrial carrier YPR011C
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = YPR011C
PE = 1 SV = 1
MAEVLTVLEQPNSIKDFLKQDSNIAFLAGGVAGAVSRTVVSPFERVKILLQVQSSTTSYN
RGIFSSIRQVYHEEGTKGLFRGNGLNCIRIFPYSAVQFVVYEACKKKLFHVNGNNGQEQL
TNTQRLFSGALCGGCSVVATYPLDLIKTRLSIQTANLSSLNRSKAKSISKPPGIWQLLSE
TYRLEGGLRGLYRGVWPTSLGVVPYVALNFAVYEQLREFGVNSSDAQPSWKSNLYKLTIG
AISGGVAQTITYPFDLLRRRFQVLAMGGNELGFRYTSVWDALVTIGRAEGVSGYYKGLAA
NLFKVVPSTAVSWLVYEVVCDSVRNW

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
MSEEFPSPQLIDDLEEHPQHDNARVVKDLLAGTAGGIAQVLVGQPFDTTKVRLQTSSTPT
TAMEVVRKLLANEGPRGFYKGTLTPLIGVGACVSLQFGVNEAMKRFFHHRNADMSSTLSL
PQYYACGVTGGIVNSFLASPIEHVRIRLQTQTGSGTNAEFKGPLECIKKLRHNKALLRGL
TPTILREGHGCGTYFLVYEALIANQMNKRRGLERKDIPAWKLCIFGALSGTALWLMVYPL
DVIKSVMQTDNLQKPKFGNSISSVAKTLYANGGIGAFFKGFGPTMLRAAPANGATFATFE
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
MLTLESALTGAVASAMANIAVYPLDLSKTIIQSQVSPSSSEDSNEGKVLPNRRYKNVVDC
MINIFKEKGILGLYQGMTVTTVATFVQNFVYFFWYTFIRKSYMKHKLLGLQSLKNRDGPI
TPSTIEELVLGVAAASISQLFTSPMAVVATRQQTVHSAESAKFTNVIKDIYRENNGDITA
FWKGLRTGLALTINPSITYASFQRLKEVFFHDHSNDAGSLSAVQNFILGVLSKMISTLVT
QPLIVAKAMLQSAGSKFTTFQEALLYLYKNEGLKSLWKGVLPQLTKGVIVQGLLFAFRGE
LTKSLKRLIFLYSSFFLKHNGQRKLAST

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
MSEDQKSENSVPSKVNMVNRTDILTTIKSLSWLDLMLPFTIILSIIIAVIISVYVPSSRH
TFDAEGHPNLMGVSIPLTVGMIVMMIPPICKVSWESIHKYFYRSYIRKQLALSLFLNWVI
GPLLMTALAWMALFDYKEYRQGIIMIGVARCIAMVLIWNQIAGGDNDLCVVLVITNSLLQ
MVLYAPLQIFYCYVISHDHLNTSNRVLFEEVAKSVGVFLGIPLGIGIIIRLGSLTIAGKS
NYEKYILRFISPWAMIGFHYTLFVIFISRGYQFIHEIGSAILCFVPLVLYFFIAWFLTFA
LMRYLSISRSDTQRECSCDQELLLKRVWGRKSCEASFSITMTQCFTMASNNFELSLAIAI
SLYGNNSKQAIAATFGPLLEVPILLILAIVARILKPYYIWNNRN

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
MVYTSTYRHTIVVDLLEYLGIVSNLETLQSAREDETRKPENTDKKECKPDYDIECGPNRS
CSESSTDSDSSGSQIEKNDPFRVDWNGPSDPENPQNWPLLKKSLVVFQIMLLTCVTYMGS
SIYTPGQEYIQEEFHVGHVVATLNLSLYVLGYGLGPIIFSPLSETARYGRLNLYMVTLFF
FMIFQVGCATVHNIGGLIVMRFISGILCSPSLATGGGTVADIISPEMVPLVLGMWSAGAV
AAPVLAPLLGAAMVDAKNWRFIFWLLMWLSAATFILLAFFFPETQHHNILYRRALKLRKE
TGDDRYYTEQDKLDREVDARTFLINTLYRPLKMIIKEPAILAFDLYIAVAYGCFYLFFEA
FPIVFVGIYHFSLVEVGLAYMGFCVGCVLAYGLFGILNMRIIVPRFRNGTFTPEAFLIVA
MCVCWCLPLSLFLFGWTARVHWILPVISEVFFVLAVFNIFQATFAYLATCYPKYVASVFA
GNGFCRASFACAFPLFGRAMYDNLATKNYPVAWGSSLVGFLTLGLAIIPFILYKYGPSLR
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
MPDNLSLHLSGSSKRLNSRQLMESSNETFAPNNVDLEKEYKSSQSNITTEVYEASSFEEK
VSSEKPQYSSFWKKIYYEYVVVDKSILGVSILDSFMYNQDLKPVEKERRVWSWYNYCYFW
LAECFNINTWQIAATGLQLGLNWWQCWITIWIGYGFVGAFVVLASRVGSAYHLSFPISSR
ASFGIFFSLWPVINRVVMAIVWYSVQAYIAATPVSLMLKSIFGKDLQDKIPDHFGSPNAT
TYEFMCFFIFWAASLPFLLVPPHKIRHLFTVKAVLVPFASFGFLIWAIRRAHGRIALGSL
TDVQPHGSAFSWAFLRSLMGCMANFSTMVINAPDFSRFSKNPNSALWSQLVCIPFLFSIT
CLIGILVTAAGYEIYGINYWSPLDVLEKFLQTTYNKGTRAGVFLISFVFAVAQLGTNISA
NSLSCGTDMSAIFPKFINIKRGSLFCAAMALCICPWNLMATSSKFTMALSAYAIFLSSIA
GVVCSDYFVVRRGYIKLTHIYSHQKGSFYMYGNRFGINWRALAAYLCGVAPCLPGFIAEV
GAPAIKVSDGAMKLYYLSYWVGYGLSFSSYTALCYFFPVPGCPVNNIIKDKGWFQRWANV
DDFEEEWKDTIERDDLVDDNISVYEHEHEKTFI

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
MQAQGSQSNVGSLRSNCSDNSLPNNHVMMHCDESSGSPHSEHNDYSYEKTNLESTASNSR
EHRDNQLSRLKSEEYVVPKNQRRGLLPQLAIIPEFKDARDYPPMMKKMIVFLIAFSSMMG
PMGTSIIFPAINSITTEFKTSVIMVNVSIGVYLLSLGVFPLWWSSLSELEGRRTTYITSF
ALLFAFNIGSALAPDINSFIALRMLCGAASASVQSVGAGTVADLYISEDRGKNLSYYYLG
PLLAPLLSPIFGSLLVNRWPWRSTQWFMVILSGCNVILLTVLLPETLRKQDSKGAIAQIL
AERRIQVDNNERGEIQEDYQRGEDETDRIENQVATLSTEKHNYVGEVRDQDSLDLESHSS
PNTYDGRAGETQLQRIYTEASRSLYEYQLDDSGIDATTAQVTRIRSTDPKLARSIRENSL
RKLQTNLEEQVKKVLSSNGGEIAPKQVSAVRKVWDTFFVYFIKPLKSLHFLEYPPVALAI
TFSAISFSTVYFVNMTVEYKYSRPPYNFKPLYIGLLYIPNSVTYFFASIYGGRWVDMLLK
RYKEKYGILAPEARISWNVVTSVISFPIALLIFGWCLDKKCHWVTPLIGTALFGYAAMMT
IGATLSYLVDSLPGKGATGVALNNLIRQILAATAVFVTTPMLNGMGTGWAFTMLAFIVLG
ASSVLIILKKHGDYWRENYDLQKLYDKID

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
MVETFSFAHLAYLVFESVLQVVIIALAGFWSASSGLLPKQSQKIISLLNVDLFTPCLIFS
KLAKSLSMAKIFEIAIIPIFFGLTTGISFISGKIMSRILDLDKDETNFVVANSVFGNSNS
LPVSLTLSLAYTLPNLTWDQIPNDNRDNVASRGILYLLIFQQIGQMLRWSWGYNKLMKWS
GENTQHMPPSQVQSLLERTPNIDNEELVNEEQEEQELLEEENNRMNSSFLSSSSIGDKIW
QKSCTVFERIRANLNPPLYSMIFAVVVAAIGPLQRELFMEDGFINNTFAEAVTQLGSVSI
PLILVVLGSNLYPSAEVFPKTVHHSKLLIGSIIGRMILPSCFLLPIIAIAVKYINVSILD
DPIFLVVGFLLTVSPPAIQLTQITQLNEFFEAEMADILFWGYAVLSLPVSIIVVSGAIYV
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
MKPEKLFSGLGTSDGEYGVVNSENISIDAMQDNRGECHRRSIEMHANDNLGLVSQRDCTN
RPKITPQECLSETEQICHHGENRTKAGLDVDDAETGGDHTNESRVDECCAEKVNDTETGL
DVDSCCGDAQTGGDHTNESCVDGCCVRDSSVMVEEVTGSCEAVSSKEQLLTSFEVVPSKS
EGLQSIHDIRETTRCNTNSNQHTGKGRLCIESSDSTLKKRSCKVSRQKIEVSSKPECCNI
SCVERIASRSCEKRTFKGSTNVGISGSSSTDSLSEKFFSEQYSRMYNRYSSILKNLGCIC
NYLRTLGKESCCLPKVRFCSGEGASKKTKYSYRNSSGCLTKKKTHGDKERLSNDNGHADF
VCSKSCCTKMKDCAVTSTISGHSSSEISRIVSMEPIENHLNLEAGSTGTEHIVLSVSGMS
CTGCESKLKKSFGALKCVHGLKTSLILSQAEFNLDLAQGSVKDVIKHLSKTTEFKYEQIS
NHGSTIDVVVPYAAKDFINEEWPQGVTELKIVERNIIRIYFDPKVIGARDLVNEGWSVPV
SIAPFSCHPTIEVGRKHLVRVGCTTALSIILTIPILVMAWAPQLREKISTISASMVLATI
IQFVIAGPFYLNALKSLIFSRLIEMDLLIVLSTSAAYIFSIVSFGYFVVGRPLSTEQFFE
TSSLLVTLIMVGRFVSELARHRAVKSISVRSLQASSAILVDKTGKETEINIRLLQYGDIF
KVLPDSRIPTDGTVISGSSEVDEALITGESMPVPKKCQSIVVAGSVNGTGTLFVKLSKLP
GNNTISTIATMVDEAKLTKPKIQNIADKIASYFVPTIIGITVVTFCVWIAVGIRVEKQSR
SDAVIQAIIYAITVLIVSCPCVIGLAVPIVFVIASGVAAKRGVIFKSAESIEVAHNTSHV
VFDKTGTLTEGKLTVVHETVRGDRHNSQSLLLGLTEGIKHPVSMAIASYLKEKGVSAQNV
SNTKAVTGKRVEGTSYSGLKLQGGNCRWLGHNNDPDVRKALEQGYSVFCFSVNGSVTAVy
ALEDSLRADAVSTINLLRQRGISLHILSGDDDGAVRSMAARLGIESSNIRSHATPAEKSE
YIKDIVEGRNCDSSSQSKRPVVVFCGDGTNDAIGLTQATIGVHINEGSEVAKLAADVVML
KPKLNNILTMITVSQKAMFRVKLNFLWSFTYNLFAILLAAGAFVDFHIPPEYAGLGELVS
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
MALHQFDYIFAIAMLFAFLDAFNIGANDVANSFASSISSRSLKYWQAMVLAGLCEFLGAV
LAGARVSGTIKNNIIDSSIFTNDPAVLMLTMTSALIGSSCWLTFATAIGMPVSTTHSIVG
GTIGAGIAAGGANGVVWGWSGVSQIIASWFIAPILAGAIAAIVFSISRFSVLEVKSLERS
IKNALLLVGVLVFATFSILTMLIVWKGSPNLHLDDLSETETAVSIVLTGAIASIVYFIFF
YPFYRRKVLDQDWTLKLIDIFRGPSFYFKSTDDIPPMPEGHQLTIDYYEGRRNLGTTVSV
EDEENKAASNSNDSVKNKEDIQEVDLVRTETEPETKLSTKQYWWSLLKQGPKKWPLLFWL
VISHGWTQDVIHAQVNDRDMLSGDLKGMYERSKFYDNRVEYIYSVLQAITAATMSFAHGA
NDVANATGPLSAVYVIWKTNTIGAKSEVPVWVLAYGGVALVIGCWTYGYNIIKNLGNKMI
LQSPSRGFSIELAVAITTVMATQLGIPTSTTQIAVGGIVAVGLCNKDLKSVNWRMVAWCY
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
MSYGTINDMNESVTNYRIKKAQNNIKGWYAYSFSSEPFVVSAVSTYIPLLLQQFASINGV
KVHDHSIPCLSETGSDSDKCVLGLFNNRIFVDTSSFALYVFSLSVLFQTIIVISVSGIVD
LWGSVKFKGRILVWFGIVGALSTVAISKLNDTQIYSLAGLYIVANGCFGVINVVGNSLLP
IFVKDSLKCQSQGAYEPDKVDSLTTVISGRGASLGYSSALIVQIVSMFLVASKKGSKQDV
QVAVLFVGIWWFVWQLPMIWLIDDVTIPIRVDDSTLASARSPYPGEQDALGQLNWKNYLS
YGWVSLFESFKHARLLKDVMIFLIAWFIISDSITTINSTAVLFSKAELHMSTLNLIMISV
LIVVNAMLGAFM1PQFLATKFRWTSSQTLMYIIIWASFIPFYGILGFFFNAFGLKHKFEM
FLLAIWYGLSLGGLSAVSRSVFSLIVPPGKESTFFSMFSITDKGSSILGPFLVGLLTDKT
HNIRYSFYFFFLLLMLSLPVLNCLDVKRGRREAEELSQVLPESERRLD

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
MGSHRRYLYYSILSFLLLSCSVVLAKQDKTPFFEGTSSKNSRLTAQDKGNDTCPPCFNCM
LPIFECKQFSECNSYTGRCECIEGFAGDDCSLPLCGGLSPDESGNKDRPIRAQNDTCHCD
NGWGGINCDVCQEDFVCDAFMPDPSIKGTCYKNGMIVDKVFSGCNVTNEKILQILNGKIP
QITFACDKPNQECNFQFWIDQLESFYCGLSDCAFEYDLEQNTSHYKCNDVQCKCVPDTVL
CGAKGSIDISDFLTETIKGPGDFSCDLETRQCKFSEPSMNDLILTVFGDPYITLKCESGE
CVHYSEIPGYKSPSKDPTVSWQGKLVLALTAVMVLALFTFATFYISKSPLFRNGLGSSKS
PIRLPDEDAVNNFLQNEDDTLATLSFENITYSVPSINSDGVEETVLNEISGIVKPGQILA
IMGGSGAGKTTLLDILAMKRKTGHVSGSIKVNGISMDRKSFSKIIGFVDQDDFLLPTLTV
FETVLNSALLRLPKALSFEAKKARVYKVLEELRIIDIKDRIIGNEFDRGISGGEKRRVSI
ACELVTSPLVLFLDEPTSGLDASNANNVIECLVRLSSDYNRTLVLSIHQPRSNIFYLFDK
LVLLSKGEMVYSGNAKKVSEFLRNEGYICPDNYNIADYLIDITFEAGPQGKRRRIRNISD
LEAGTDTNDIDNTIHQTTFTSSDGTTQREWAHLAAHRDEIRSLLRDEEDVEGTDGRAGAT
EIDLNTKLLHDKYKDSVYYAELSQEIEEVLSEGDEESNVLNGDLPTGQQSAGFLQQLSIL
NSRSFKNMYRNPKLLLGNYLLTILLSLFLGTLYYNVSNDISGFQNRMGLFFFILTYFGFV
TFTGLSSFALERIIFIKERSNNYYSPLAYYISKIMSEVVPLRVVPPILLSLIVYPMTGLN
MKDNAFFKCIGILILFNLGISLEILTIGIIFEDLNNSIILSVLVLLGSLLFSGLFINTKN
ITNVAFKYLKNFSVFYYAYESLLINEVKTLMLKERKYGLNIEVPGATILSTFGFVVQNLV
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
MPLSKVEHYLSYHTRLLLPHVLSLQSSHRVAYIFSLLSAVSTGFITLISLYSQPWQKHLN
YSSWQINTIASMTNLGMYLTPPILGMIADSHGPITLSLLAIIGFIPSYSYLAYVFNHPEL
SLGGNGDSSFNLSIICFVFIGISTSALYFSALLTCTKLYPHTKLLSISLPITCYGISSVV
GSQLLRIKWFWSSNASSSSSNSDLNLGRVFQTFALVYVVIGLLAWIATSVVSLLHFNEEQ
DNQKRLDDQTDVEQSPLLERSNHVQEKFTQTMLRIFSDPVIYILAVSILLSLGPLEMFIA
NMGSLINLLVQLDAPTLSTKLLSTYALSSTFTRLLTGIVADFFAKKKISIKWILLTFLSL
GVCAQLFLLKMTSSASPWGLVPTGSLVGIVYGGLFTVYPTLVLLVWGERSFGTVYGSLLI
APAIGSMIFCMLYAKFYDSRCMSGGGDLRNPSCISAVYKYSSIAFVVSAVLSAVVFWKLK
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
MDLTVEPNLHSLITSTTHKWIFVGGKGGVGKTTSSCSIAIQMALSQPNKQFLLISTDPAH
NLSDAFGEKFGKDARKVTGMNNLSCMEIDPSAALKDMNDMAVSRANNNGSDGQGDDLGSL
LQGGALADLTGSIPGIDEALSFMEVMKHIKRQEQGEGETFDTVIFDTAPTGHTLRFLQLP
NTLSKLLEKFGEITNKLGPMLNSFMGAGNVDISGKLNELKANVETIRQQFTDPDLTTFVC
VCISEFLSLYETERLIQELISYDMDVNSIIVNQLLFAENDQEHNCKRCQARWKMQKKYLD
QIDELYEDFHVVKMPLCAGEIRGLNNLTKFSQFLNKEYNPITDGKVIYELEDKE

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
MASEQSSPEINADNLNSSAADVHVQPPGEKEWSDGFYDKEVINGNTPDAPKRGFLGYLII
YLLCYPVSFGGFLPGWDSGITAGFINMDNFKMNFGSYKHSTGEYYLSNVRMGLLVAMFSV
GCSIGGVAFARLADTLGRRLAIVIVVLVYMVGAIIQISSNHKWYQYFVGKIIYGLGAGGC
SVLCPMLLSEIAPTDLRGGLVSLYQLNMTFGIFLGYCSVYGTRKYSNTAQWRIPVGLCFL
WALIIIVGMLLVPESPRYLIECERHEEACVSIAKINKVSPEDPWVLKQADEINAGVLAQR
ELGEASWKELFSVKTKVLQRLITGILVQTFLQLTGENYFFFYGTTIFKSVGLTDGFETSI
VLGTVNFFSTIIAVMVVDKIGRRKCLLFGAASMMACMVIFASIGVKCLYPHGQDGPSSKG
AGNAMIVFTCFYIFCFATTWAPVAYIVVAESFPSKVKSKAMSISTAFNWLWQFLIGFFTP
FITGSIHFYYGYVFVGCLVAMFLYVFFFLPETIGLSLEEIQLLYEEGIKPWKSASWVPPS
RRGASSRETEAKKKSWKEVLKFPKSFN

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
MKNLSFLINRRKENTSDSNVYPGKAKSHEPSWIEMDDQTKKDGLDIVHVEFSPDTRAPSD
SNKVITEIFDATEDAKEADESERGMPLATALNTYPKAAAWSLLVSTTLIMEGYDTAILGA
FYALPIFQRKEGSQNDKTGEWEISASWQIGLTLCYMAGEIVGLQLTGPSVDLVGNRYTLI
IALFFLAAFTFILYFCNSLGMIAVGQALCGMPWGCFQCLTVSYASEICPLALRYYLTTYS
NLCWLFGQLFAAGIMKNSQKKYADSELGYKLPFALQWILPVPLALGIFFAPESPWWLVKK

TABLE 14-continued

Sequences disclosed herein.
GRFDEARRSLRRTLSGKGPEKEILVTLEVDKIKVTIDKEKRLTSKEGSYSDCFEDKINRR RTRITCLCWAGQATCGSILIGYSTYFYEKAGVSTEMSFTFSIIQYCLGICATFLSWWASK YFGRYDLYAFGLAFQTIVFFIIGGLGCSSTHGSKMGSGSLLMAVAFFYNLGIAPVVFCLV SEMPSSRLRTKTIILARNTYNVVSIICSVLILYQLNSKKWNWGAKSGFFWGVLCFCTLIW AVVDLPETAGKTFVEINELFKLGVSARKFKSTKVDPFVVKTPLKTSLITTPREISKLPLQ 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 MSNIKSTQDSSHNAVARSSSASFAASEESFTGITHDKDEQSDTPADKLTKMLTGPARDTA SQISATVSEMAPDVVSKVESFADALSRHTTRSGAFNMDSDSDDGFDAHAIFESFVRDADE QGIHIRKAGVTIEDVSAKGVDASALEGATFGNILCLPLTIFKGIKAKRHQKMRQIISNVN ALAEAGEMILVLGRPGAGCSSFLKVTAGEIDQFAGGVSGEVAYDGIPQEEMMKRYKADVI YNGELDVHFPYLTVKQTLDFAIACKTPALRVNNVSKKEYIASRRDLYATIFGLRHTYNTK VGNDFVRGVSGGERKRVSIAEALAAKGSIYCWDNATRGLDASTALEYAKAIRIMTNLLKS TAFVTIYQASENIYETFDKVTVLYSGKQIYFGLIHEAKPYFAKMGYLCPPRQATAEFLTA LTDPNGFHLIKPGYENKVPRTAEEFETYWLNSPEFAQMKKDIAAYKEKVNTEKTKEVYDE SMAQEKSKYTRKKSYYTVSYWEQVKLCTQRGFQRIYGNKSYTVINVCSAIIQSFITGSLF YNTPSSTSGAFSRGGVLYFALLYYSLMGLANISFEHRPILQKHKGYSLYHPSAEAIGSTL ASFPFRMIGLTCFFIILFFLSGLHRTAGSFFTIYLFLTMCSEAINGLFEMVSSVCDTLSQ ANSISGILMMSISMYSTYMIQLPSMHPWFKWISYVLPIRYAFESMLNAEFHGRHMDCANT LVPSGGDYDNLSDDYKVCAFVGSKPGQSYVLGDDYLKNQFQYVYKHTWRNFGILWCFLLG YVVLKVIFTEYKRPVKGGGDALIFKKGSKRFIAHADEESPDNVNDIDAKEQFSSESSGAN DEVFDDLEAKGVFIWKDVCFTIPYEGGKRMLLDNVSGYCIPGTMTALMGESGAGKTTLLN TLAQRNVGIITGDMLVNGRPIDASFERRTGYVQQQDIHIAELTVRESLQFSARMRRPQHL PDSEKMDYVEKIIRVLGMEEYAEALVGEVGCGLNVEQRKKLSIGVELVAKPDLLLFLDEP TSGLDSQSSWAIIQLLRKLSKAGQSILCTIHQPSATLFEEFDRLLLLRKGGQTVYFGDIG KNSATILNYFERNGARKCDSSENPAEYILEAIGAGATASVKEDWHEKWLNSVEFEQTKEK VQDLINDLSKQETKSEVGDKPSKYATSYAYQFRYVLIRTSTSFWRSLNYIMSKMMLMLVG GLYIGFTFFNVGKSYVGLQNAMFAAFISIILSAPAMNQIQGRAIASRELFEVRESQSNMF HWSLVLITQYLSELPYHLFFSTIFFVSSYFPLRIFFEASRSAVYFLNYCIMFQLYYVGLG LMILYMSPNLPSANVILGLCLSFMLSFCGVTQPVSLMPGFWTFMWKASPYTYFVQNLVGI MLHKKPVVCKKKELNYFNPPNGSTCGEYMKPFLEKATGYIENPDATSDCAYCIYEVGDNY LTHISSKYSYLWRNFGIFWIYIFFNIIAMVCVYYLFHVRQSSFLSPVSILNKIKNIRKKK 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 MFDQLAVFTPQGQVLYQYNCLGKKFSEIQINSFISQLITSPVTRKESVANANTDGFDFNL LTINSEHKNSPSFNALFYLNKQPELYFVVTFAEQTLELNQETQQTLALVLKLWNSLHLSE SILKNRQGQNEKNKHNYVDILQGIEDDLKKFEQYFRIKYEESIKQDHINPDNFTKNGSVP QSHNKNTKKKLRDTKGKKQSTGNVGSGRKWGRDGGMLDEMNHEDAAKLDFSSSNSHNSSQ VALDSTINKDSFGDRTEGGDFLIKEIDDLLSSHKDEITSGNEAKNSGYVSTAFGFLQKHV LGNKTINESDLKSVLEKLTQQLITKNVAPEAADYLTQQVSHDLVGSKTANWTSVENTARE SLTKALTQILTPGVSVDLLREIQSKRSKKDEEGKCDPYVFSIVGVNGVGKSTNLSKLAFW LLQNNFKVLIVACDTFRSGAVEQLRVHVENLAQLMDDSHVRGSKNKRGKTGNDYVELFEA GYGGSDLVTKIAKQAIKYSRDQNFDIVLMDTAGRRHNDPTLMSPLKSFADQAKPDKIIMV GEALVGTDSVQQAKNFNDAFGKGRNLDFFIISKCDTVGEMLGTMVNMVYATGIPILFVGV GQTYTDLRTLSVKWAVNTLMS
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 MGIHIPYLTSKTSQSNVGDAVGNADSVEFNSEHDSPSKRGKITLESHEIQRAPASDDEDR IQIKPVNDEDDTSVMITFNQSLSPFIITLTFVASISGFMFGYDTGYISSALISIGTDLDH KVLTYGEKEIVTAATSLGALITSIFAGTAADIFGRKRCLMGSNLMFVIGAILQVSAHTFW QMAVGRLIMGFGVGIGSLIAPLFISEIAPKMIRGRLTVINSLWLTGGQLVAYGCGAGLNy VNNGWRILVGLSLIPTAVQFTCLCFLPDTPRYYVMKGDLARATEVLKRSYTDTSEEIIER KVEELVTLNQSIPGKNVPEKVWNTIKELHTVPSNLRALIIGCGLQAIQQFTGWNSLMYFS GTIFETVGFKNSSAVSIIVSGTNFIFTLVAFFSIDKIGRRTILLIGLPGMTMALVVCSIA FHFLGIKFDGAVAVVVSSGFSSWGIVIIVFIIVFAAFYALGIGTVPWQQSELFPQNVRGI GTSYATATNWAGSLVIASTFLTMLQNITPAGTFAFFAGLSCLSTIFCYFCYPELSGLELE EVQTILKDGFNIKASKALAKKRKQQVARVHELKYEPTQEIIEDI

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
MNNGDNKTTLENSKNASLANGNYAIPTKLNRLKKNADPRVAAISGALSGALSAMLVCPFD
VAKTRLQAQGLQNMTHQSQHYKGFFGTFATIFKDEGAAGLYKGLQPTVLGYIPTLMIYFS
VYDFCRKYSVDIFPHSPFLSNASSAITAGAISTVATNPIWVVKTRLMLQTGIGKYSTHYK
GTIDTFRKIIQQEGAKALYAGLVPALLGMLNVAIQFPLYENLKIRFGYSESTDVSTDVTS
SNFQKLILASMLSKMVASTVTYPHEILRTRMQLKSDLPNTVQRHLLPLIKITYRQEGFAG
FYSGFATNLVRTVPAAVVTLVSFEYSKKYLTTFFQ

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
GIIAIYGLVVSVLVCYSLGQKQALYTGFIQLGAGLSVGLSGLAAGFAIGIVGDAGVRGSS
QQPRLFVGMILILIFAEVLGLYGLIVALLLNSRATQDVVC

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
MDPGIANHTLPEEFEEVVVPEMLEKEVGAKVDVKPTLTTSSPAPSYIELIDPGVHNIEIY
AEMYNRPIYRVALFFSLFLIAYAYGLDGNIRYTFQAYATSSYSQHSLLSTVNCIKTVIAA
VGQIFFARLSDIFGRFSIMIVSIIFYSMGTIIESQAVNITRFAVGGCFYQLGLTGIILIL
EVIASDFSNLNWRLLALFIPALPFIINTWISGNVTSAIDANWKWGIGMWAFILPLACIPL
GICMLHMRYLARKHAKDRLKPEFEALNKLKWKSFCIDIAFWKLDIIGMLLITVFFGCVLV
PFTLAGGLKEEWKTAHIIVPEVIGWVVVLPLYMLWEIKYSRHPLTPWDLIQDRGIFFALL
IAFFINFNWYMQGDYMYTVLVVAVHESIKSATRITSLYSFVSVIVGTILGFILIKVRATK
PFIIFGISCWIVSFGLLVHYRGDSGAHSGIIGSLCLLGFGAGSFTYVTQASIQASAKTHA
RMAVVTSLYLATYNIGSAFGSSVSGAVWTNILPKEISKRISDPTLAAQAYGSETTFITTY
TWGTPERIALVMSYRYVQKILCIIGLVFCFPLLGCAFMLRNHKLTDSIALEGNDHLESKN
TFEIEEKEESFLKNKFFTHFTSSKDRKD

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
MAASVPPGGQRILQKRRQAQSIKEKQAKQTPTSTRQAGYGGSSSSILKLYTDEANGFRVD
SLVVLFLSVGFIFSVIALHLLTKFTHII

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
MESNKQPRKIQLYTKEFYATCTLGGIIACGPTHSSITPLDLVKCRLQVNPKLYTSNLQGF
RKIIANEGWKKVYTGFGATFVGYSLQGAGKYGGYEYFKHLYSSWLSPGVTVYLMASATAE
FLADIMLCPFEAIKVKQQTTMPPFCNNVVDGWKKMYAESGGMKAFYKGIVPLWCRQIPYT
MCKFTSFEKIVQKIYSVLPKKKEEMNALQQISVSFVGGYLAGILCAAVSHPADVMVSKIN
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
VPQGRASFSALTRLINPNLGIVFDLAIAIKCFGVGVSYMIVVGDLMPQIMSVWTRNAWLL
NRNVQISLIMLFFVAPLSFLKKLNSLRYASMVAISSVAYLCVLVLLHYVAPSDEILRLKG
RISYLLPPQSHDLNVLNTLPIFVFAYTCHHNMFSIINEQRSSRFEHVMKIPLIAISLALI
LYIAIGCAGYLTFGDNIIGNIIMLYPQAVSSTIGRIAIVLLVMLAFPLQCHPARASIHQI
LQHFAEENVSISATSADEPTVATESSPLIRDSSLDLNEVIEEESIYQPKETPLRGKSFIV
ITCSILVASYLVAISVSSLARVLAIVGATGSTSISFILPGLFGYKLIGTEHKTAVPLTTK
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
MVSQFAIEVRNLTYKFKESSDPSVVDINLQIPWNTRSLVVGANGAGKSTLLKLLSGKHLC
LDGKILVNGLDPFSPLSMNQVDDDESVEDSTNYQTTTYLGTEWCHMSIINRDIGVLELLK
SIGFDHFRERGERLVRILDIDVRWRMHRLSDGQKRRVQLAMGLLKPWRVLLLDEVTVDLD
VIARARLLEFLKWETETRRCSVVYATHIFDGLAKWPNQVYHMKSGKIVDNLDYQKDVEFS
EVVNAKVNGQVAFENDNNKVVISKVNSLHPLALEWLKRDNQIPDKEIGI

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
MANQNSDLYKQITAGSVAAVFQTTMTYPFEYLKTGLQLQPKGTAFEIILPQIKSYFVGCS
ALNVAAFGKTILRFVTFDKLCHSLNNNIDNNDNFQRLTGYNLLIAGTLTGIVESLFIIPF
ENIKTTLIQSAMIDHKKLEKNQPVVNAKATFHKVATKSTPVARIEKLLPAVKHMYQTRGP
AAFVQGTTATIFRQIANTSIQFTAYTAFKRLLQARNDKASSVITGLATSFTLVAMTQPID
VVKTRMMSQNAKTEYKNTLNCMYRIFVQEGMATFWKGSIFRFMKVGISGGLTFTVYEQVS
LLLGFSSRS

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
MSLISILSPLITSEGLDSRIKPSPKKDASTTTKPSLWKTTEFKFYYIAFLVVVPLMFYAG
LQASSPENPNYARYERLLSQGWLFGRKVDNSDSQYRFFRDNFALLSVLMLVHTSIKRIVL
YSTNITKLRFDLIFGLIFLVAAHGVNSIRILAHMLILYAIAHVLKNFRRIATISIWIYGI
STLFINDNFRAYPFGNICSFLSPLDHWYRGIIPRWDVFFNFTLLRVLSYNLDFLERWENL
QKKKSPSYESKEAKSAILLNERARLTAAHPIQDYSLMNYIAYVTYTPLFIAGPIITFNDY
VYQSKHTLPSINFKFIFYYAVRFVIALLSMEFILHFLHVVAISKTKAWENDTPFQISMIG
LFNLNIIWLKLLIPWRLFRLWALLDGIDTPENMIRCVDNNYSSLAFWRAWHRSYNKWVVR
YIYIPLGGSKNRVLTSLAVFSFVAIWHDIELKLLLWGWLIVLFLLPEIFATQIFSHYTDA
VWYRHVCAVGAVFNIWVMMIANLFGFCLGSDGTKKLLSDMFCTVSGFKFVILASVSLFIA
VQIMFEIREEEKRHGIYLKC

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
MNRILSSASLLSNVSMPRQNKHKITKALCYAIIVASIGSIQFGYHLSELNAPQQVLSCSE
FDIPMEGYPYDRTWLGKRGYKQCIPLNDEQIGIVTSVFCIGGILGSYFATSLANIYGRKF
SSLINCTLNIVGSLIIFNSNSYRGLIIGRILVGISCGSLIVIIPLFIKEVAPSGWEGLLG
SMTQICIRLGVLLTQGIALPLTDSYRWRWILFGSFLIAVLNFFMWFIVDESPKWLLAHGR
VTDAKLSLCKLRGVTFDEAAQEIQDWQLQIESGDPLIEPTTTNSISGSNSLWKYLRDRTN
VKSRHVITVLLFGQQFCGINSIVLYGTKIISQLYPQHAIRINFFISMVNVLVTILVSLLI
HSLPRKPLLMTSTVLVSVTAFIMGIAMNHNKMNLLIVFSFIYMGVFTMGLNPLPFIIMRE
VSKPQDMVLAQRYGTICNWVGTFIIAYTFPIIHDVLSGYVFIIFAIIACSISAFIWKKVP
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
MPQSTPSQEVQRVPWDNKPALKQITLRATIAGIAIGSLVLTSNFQFGLQTGWVSMMSLPS
ALLACAFFKNIWPLIFPNDRPFSDVENVYVQSMAVAVGTGPLAFGFVGVIPAIEKFLTND
ESGGLREQGQSFTFRELLIWSTALAFFGIFFAVPLRKQVIVREKLPFPSGSATATLISVL
NGTEILQEVSKSELLEMRQRRLNECPEVLQPNRDPEEADYLMNSSHSELGDYTATSQDGS
SILSTGSENYRANIIILLKTFVVSSLYTMVSYFVPVIRSIPVFGKYLSNNYLWNFQPSPA
YIGQGIIMGLPTVSYMLIGCFLGWGVLAPLARYKRWVPPDADVHDWEEGVQGWILWSSLS
IMVADSVVAFIVVTVKSIVKFILIDDKAALLNNIIDDTFQSMLLEEERAINSSRRNTYVD
GRQDTVRLVSRDNEIEVDSKHLVRYTTVISGCLVSSIICIVSIIYLFGIQVIPLYAIITA
LILALFLSILGIRALGETDLNPVSGIGKISQLIFAFIIPRDRPGSVLMNVVSGGIAEASA
QQAGDLMQDLKTGHLLGASPRAQFCAQLIGACWSIILSSFMYLCYNKVYSIPSEQFRIPT
AVVWIDCARLVTGKGLPDKALECSMILGVIFAVLSLIRNTYRDYGYGWILYIPSGVAVGV
GIFNSPSFTIARFIGGWASHFWLKNHRGDLNAKTKMIVFSSGLVLGEGIFSVINMLFICL
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
MSDNPFNASLLDEDSNREREILDATAEALSKPSPSLEYCTLSVDEALEKLDTDKNGGLRS
SNEANNRRSLYGPNEITVEDDESLFKKFLSNFIEDRMILLLIGSAVVSLFMGNIDDAVSI
TLAIFIVVTVGFVQEYRSEKSLEALNKLVPAECHLMRCGQESHVLASTLVPGDLVHFRIG
DRIPADIRIIEAIDLSIDESNLTGENEPVHKTSQTIEKSSFNDQPNSIVPISERSCIAYM
GTLVKEGHGKGIVVGTGTNTSFGAVFEMMNNIEKPKTPLQLTMDKLGKDLSLVSFIVIGM
ICLVGIIQGRSWLEMFQISVSLAVAAIPEGLPIIVTVTLALGVLRMAKRKAIVRRLPSVE
TLGSVNVICSDKTGTLTSNHMTVSKLWCLDSMSNKLNVLSLDKNKKTKNSNGNLKNYLTE
DVRETLTIGNLCNNASFSQEHAIFLGNPTDVALLEQLANFEMPDIRNTVQKVQELPFNSK
RKLMATKILNPVDNKCTVYVKGAFERILEYSTSYLKSKGKKTEKLTEAQKATINECANSM
ASEGLRVFGFAKLTLSDSSTPLTEDLIKDLTFTGLIGMNDPPRPNVKFAIEQLLQGGVHI
IMITGDSENTAVNIAKQIGIPVIDPKLSVLSGDKLDEMSDDQLANVIDHVNIFARATPEH
KLNIVRALRKRGDVVAMTGDGVNDAPALKLSDIGVSMGRIGTDVAKEASDMVLTDDDFST
ILTAIEEGKGIFNNIQNFLTFQLSTSVAALSLVALSTAFKLPNPLNAMQILWINILMDGP
PAQSLGVEPVDHEVMKKPPRKRTDKILTHDVMKRLLTTAACIIVGTVYIFVKEMAEDGKV
TARDTTMTFTCFVFFDMFNALACRHNTKSIFEIGFFTNKMFNYAVGLSLLGQMCAIYIPF
FQSIFKTEKLGISDILLLLLISSSVFIVDELRKLWTRKKNEEDSTYFSNV

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
MSDRNTSNSLTLKERMLSAGAGSVLTSLILTPMDVVRIRLQQQQMIPDCSCDGAAEVPNA
VSSGSKMKTFTNVGGQNLNNAKIFWESACFQELHCKNSSLKFNGTLEAFTKIASVEGITS
LWRGISLTLLMAIPANMVYFSGYEYIRDVSPIASTYPTLNPLFCGAIARVFAATSIAPLE
LVKTKLQSIPRSSKSTKTWMMVKDLLNETRQEMKMVGPSRALFKGLEITLWRDVPFSAIY
WSSYELCKERLWLDSTRFASKDANWVHFINSFASGCISGMIAAICTHPFDVGKTRWQISM
MNNSDPKGGNRSRNMFKFLETIWRTEGLAALYTGLAARVIKIRPSCAIMISSYEISKKVF
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
MGTDPLIIRNNGSFWEVDDFTRLGRTQLLSYYLPLAIIASIGIFALCRSGLSRYVRSAEC
DLVNEYLFGAQEERKEDNSIERLLRNSNTQANYVNVKKQGRILKLRHFDITTIDVKQIDA
KNHGGLTFSRPSTSDHLRKSSEIVLMSLQIIGLSFLRVTKINIELTNRDVTTLLLFWLIL
LSLSILRVYKRSTNLWAICFTAHTTIWISTWIPIRSVYIGNIDDVPSQIFYIFEFVITST
LQPIKLTSPIKDNSSIIYVRDDHTSPSREHISSILSCITWSWITNFIWEAQKNTIKLKDI
WGLSMEDYSIFILKGFTRRNKHINNLTLALFESFKTYLLIGMLWVLVNSIVNLLPTILMK
RFLEIVDNPNRSSSCMNLAWLYIIGMFICRLTLAICNSQGQFVSDKICLRIRAILIGEIY
AKGLRRRLFTSPKTSSDSDSISANLGTIINLISIDSFKVSELANYLYVTVQAVIMIIVVV
GLLFNFLGVSAFAGISIILVMFPLNFLLANLLGKFQKQTLKCTDQRISKLNECLQNIRIV
KYFAWERNIINEIKSIRQKELRSLLKKSLVWSVTSFLWFVTPTLVTGVTFAICTFVQHED
LNAPLAFTTLSLFTLLKTPLDQLSNMLSFINQSKVSLKRISDFLRMDDTEKYNQLTISPD
KNKIEFKNATLTWNENDSDMNAFKLCGLNIKFQIGKLNLILGSTGSGKSALLLGLLGELN
LISGSIIVPSLEPKHDLIPDCEGLTNSFAYCSQSAWLLNDTVKNNIIFDNFYNEDRYNKV
IDACGLKRDLEILPAGDLTEIGEKGITLSGGQKQRISLARAVYSSAKHVLLDDCLSAVDS
HTAVWIYENCITGPLMKNRTCILVTHNVSLTLRNAHFAIVLENGKVKNQGTITELQSKGL
FKEKYVQLSSRDSINEKNANRLKAPRKNDSQKIEPVTENINFDANFVNDGQLIEEEEKSN
GAISPDVYKWYLKFFGGFKALTALFALYITAQILFISQSWWIRHWVNDTNVRINAPGFAM
DTLPLKGMTDSSKNKHNAFYYLTVYFLIGIIQAMLGGFKTMMTFLSGMRASRKIFNNLLD
LVLHAQIRFFDVTPVGRIMNRFSKDIEGVDQELIPYLEVTIFCLIQCASIIFLITVITPR
FLTVAVIVFVLYFFVGKWYLTASRELKRLDSITKSPIFQHFSETLVGVCTIRAFGDERRF
ILENMNKIDQNNRAFFYLSVTVKWFSFRVDMIGAFIVLASGSFILLNIANIDSGLAGISL
TYAILFTDGALWLVRLYSTFEMNMNSVERLKEYSSIEQENYLGHDEGRILLLNEPSWPKD
GEIEIENLSLRYAPNLPPVIRNVSFKVDPQSKIGIVGRTGAGKSTIITALFRLLEPITGC
IKIDGQDISKIDLVTLRRSITIIPQDPILFAGTIKSNVDPYDEYDEKKIFKALSQVNLIS
SHEFEEVLNSEERFNSTHNKFLNLHTEIAEGGLNLSQGERQLLFIARSLLREPKIILLDE
ATSSIDYDSDHLIQGIIRSEFNKSTILTIAHRLRSVIDYDRIIVMDAGEVKEYDRPSELL
KDERGIFYSMCRDSGGLELLKQIAKQSSKMMK

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
MEPLLFNSGKANPSQDVFIDVEVGDITTKYGSTNTGSFSSMDTVEAQAIKAETARFMEVP
QGRHLGVFSTVVLFVSRIMGSGIFAVPSVILLNTGGNKLIYFAIWVFSAAIAFAGLYIFL

TABLE 14-continued

Sequences disclosed herein.

EFGSWIPKSGGRKNFLERSFERPRLLISVVFSCYSVLTGYALTGSIVFGKYVLSAFGVTD
DSWSKYVSISFIIFAVLIHGVSVRHGVFIQNALGGLKLIMIVLMCFAGLYTLFFYKSTGQ
VAWDLPVTQVEKDSLLSVSSIATAFISSFFCFSGWDTVHTVTSEIKNPVKTLKVSGPLSL
IICFVCYTMMNVAYLKVLTYEEIVSAGPLVGSVLFTKLFGPRVGGKFIAFSIAISAASNI
LVVIYSISRVNQEIFKEGYLPFSIHMSKNWPFDAPLPSISLCGFITIAWILILPKEGESF
NYLVSMDGYGNQFFLLLVAIGLFIWRFKHKNEVPEIRASTFGVLAITTLSLYMLMAPFFA
DPSLNRVGFLPPYQIMSLLVIVACFFFWLVKFVLLPKFFHYKLLPKITYLHDGLIVTEWV
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
MTRDSPDSNDSYKHINKNTTQKTSFDRNSFDYIVRSGLAGGISGSCAKTLIAPLDRIKIL
FQTSNPHYTKYTGSLIGLVEAAKHIWINDGVRGFFQGHSATLLRIFPYAAVKFVAYEQIR
NTLIPSKEFESHWRRLVSGSLAGLCSVFITYPLDLVRVRLAYETEHKRVKLGRIIKKIYK
EPASATLIKNDYIPNWFCHWCNFYRGYVPTVLGMIPYAGVSFFAHDLLHDVLKSPFFAPY
SVLELSEDDELERVQKKQRRPLRTWAELISGGLAGMASQTAAYPFEIIRRRLQVSALSPK
TMYDHKFQSISEIAHIIFKERGVRGFFVGLSIGYIKVTPMVACSFFNNERMKWNFGI

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
MSELENAHQGPLEGSATVSTNSNSYNEKSGNSTAPGTAGYNDNLAQAKPVSSYISHEGPP
KDELEELQKEVDKQLEKKSKSDLLFVSVCCLMVAFGGFVFGWDTGTISGFVRQTDFIRRF
GSTRANGTTYLSDVRTGLMVSIFNIGCAIGGIVLSKLGDMYGRKIGLMTVVVIYSIGIII
QIASIDKWYQYFIGRIISGLGVGGITVLAPMLISEVSPKQLRGTLVSCYQLMITFGIFLG
YCTNFGTKNYSNSVQWRVPLGLCFAWSIFMIVGMTFVPESPRYLVEVGKIEEAKRSLARA
NKTTEDSPLVTLEMENYQSSIEAERLAGSASWGELVTGKPQMFRRTLMGMMIQSLQQLTG
DNYFFYYGTTIFQAVGLEDSFETAIVLGVVNFVSTFFSLYTVDRFGRRNCLLWGCVGMIC
CYVVYASVGVTRLWPNGQDQPSSKGAGNCMIVFACFYIFCFATTWAPVAYVLISESYPLR
VRGKAMSIASACNWIWGFLISFFTPFITSAINFYYGYVFMGCMVFAYFYVFFFVPETKGL
TLEEVNEMYEENVLPWKSTKWIPPSRRTTDYDLDATRNDPRPFYKRMFTKEK

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
MTQTDNPVPNCGLLPEQQYCSADHEEPLLLHEEQLIFPDHSSQLSSADIIEPIKMNSSTE
SIIGTTLRKKWVPLSSTQITALSGAFAGFLSGVAVCPLDVAKTRLQAQGLQTRFENPYYR
GIMGTLSTIVRDEGPRGLYKGLVPIVLGYFPTWMIYFSVYEFSKKFFHGIFPQFDFVAQS
CAAITAGAASTTLTNPIWVVKTRLMLQSNLGEHPTHYKGTFDAFRKLFYQEGFKALYAGL
VPSLLGLFHVAIHFPIYEDLKVRFHCYSRENNTNSINLQRLIMASSVSKMIASAVTYPHE
ILRTRMQLKSDIPDSIQRRLFPLIKATYAQEGLKGFYSGFTTNLVRTIPASAITLVSFEY
FRNRLENISTMVI

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
MTKQQTSVMRNASIAKEEREGSDNNNVDRSSSDAISDNDAERSNSHSEIDNESNFDMVPY
SRFSHKQKMLLVVQCAFTGFFSTVAGSIYYPVLTIIERKFNITEELANVTIVVYFIFQGV
APSIMGGLADTFGRRPIVLWAILAYFCACIGLACAHNYAQILALRCLQAAGISPVIAINS
GIMGDVTTKVERGGYVGLVAGFQVVGTAFGALIGAGLSSKWGWRAIFWFLAIGSGICLVF
STLLMPETKRTLVGNGSVTPRSFLNRSLILHVGSVKKTLHLDDPDPETLEPRTSVDFLAP
LKILHIREIDILLSIAGLQFSTWTTHQTALTIVLSKKYNLSVAKIGLCFLPAGISTLTSI
ISAGRYLNWSYRTRKVKYNRWIKEQELQLMEKYKGDKNKVAELIHSNSHYAFNLVEARLH
PAFVTLLLSSIGFTAFGWCISVKTPLAAVLCTSAFASLFSNCILTFSTTLIVDLFPSKAS
TATGCLNLFRCLLSAIFIAALTKMVEKMRYGGVFTFLSAITSSSSLLLFYLLKNGKQLSF
DRI RANDKSAGRSVGKNSEKVST

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
MAGATSSIIRENDFEDELAESMQSYNRETADKLALTRTESVKPEPEITAPPHSRFSRSFK
TVLIAQCAFTGFFSTIAGAIYYPVLSVIERKFDIDEELVNVTVVVYFVFQGLAPTFMGGF
ADSLGRRPVVLVAIVIYFGACIGLACAQTYAQIIVLRCLQAAGISPVIAINSGIMGDVTT
RAERGGYVGYVAGFQVLGSAFGALIGAGLSSRWGWRAIFWFLAIGSGICFLASFLILPET

TABLE 14-continued

Sequences disclosed herein.

KRNISGNGSVTPKSYLNRAPILVLPTVRKSLHLDNPDYETLELPTQLNLLAPFKILKAYE
ICILMLVAGLQFAMYTTHLTALSTALSKQYHLTVAKVGLCYLPSGICTLCSIVIAGRYLN
WNYRRRLKYYQNWLGKKRSKLLEEHDNDLNLVQRIIENDPKYTFNIFKARLQPAFVTLLL
SSSGFCAYGWCITVKAPLAAVLCMSGFASLFSNCILTFSTTLIVDLFPTKTSTATGCLNL
FRCILSAVFIAALSKMVEKMKFGGVFTFLGALTSSSSILLFILLRKGKELAFKRKKQELG
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
MSVQKEEYDIVEKAQLSVSAESLTSDSESISHNPFDDFHKAERWRKVYESSGYEGLSKFD
PEFTWIKDEEKKLVRKMDLKIFLWVFIMFAFLDLIRKNIARAVSDNFIVDLKMNTNDYNL
GQTVYLVIFLASELPGNLLSKRFGPERVIPVQIVLWSVICITQAGLKNRGQFIATRCLLG
MVQGGFIPDNILYLSYYYTGAELTFRLSFFWCAIPLFQILGSLLASGIIEMRGIHNLAGW
QYLFIIEGFLSLSVGVASFYLMRRGPTQTGESAFHKGKSLFTEYEEKIMVNRILRDDPSK
GDMSNRQPVTFKEILYTLTEFDLWPLFIQGITAFISLQTVGSYLSLILKSLNYSTFLSNI
LAIPGQALLLINLPLAALLSRKLKEKSLCVGIANVWVLPFIVSLVALPTDINPWIKYILL
TGILGLPYTHSILAGWVSEISNSVRSRTVGTALYNMSAQVGAIIASNMYRNDDKPYYTRG
NKILLGFICFNICMAVATKFYYISRNKYKDRKWNSMTKEEQINYLDTTKDKGMKRLDYRF
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
MVENSSSNNSTRPIPAIPMDLPDYEALPTHAPLYHQLIAGAFAGIMEHSVMFPIDALKTR
IQSANAKSLSAKNMLSQISHISTSEGTLALWKGVQSVILGAGPAHAVYFGTYEFCKKNLI
DSSDTQTHHPFKTAISGACATTASDALMNPFDTIKQRIQLNTSASVWQTTKQIYQSEGLA
AFYYSYPTTLVMNIPFAAFNFVIYESSTKFLNPSNEYNPLIHCLCGSISGSTCAAITTPL
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
MSGVNNTSANDLSTTESNSNSVANAPSVKTEHNDSKNSLNLDATEPPIDLPQKPLSAYTT
VAILCLMIAFGGFIFGWDTGTISGFVNLSDFIRRFGQKNDKGTYYLSKVRMGLIVSIFNI
GCAIGGIVLSKVGDIYGRRIGLITVTAIYVVGILIQITSINKWYQYFIGRIISGLGVGGI
AVLSPMLISEVAPKQIRGTLVQLYQLMCTMGIFLGYCTNYGTKNYHNATQWRVGLGLCFA
WTTFMVSGMMFVPESPRYLIEVGKDEEAKRSLSKSNKVSVDDPALLAEYDTIKAGIELEK
LAGNASWSELLSTKTKVFQRVLMGVMIQSLQQLTGDNYFFYYGTTIFKSVGLKDSFQTSI
IIGVVNFFSSFIAVYTIERFGRRTCLLWGAASMLCCFAVFASVGVTKLWPQGSSHQDITS
QGAGNCMIVFTMFFIFSFATTWAGGCYVIVSETFPLRVKSRGMAIATAANWMWGFLISFF
TPFITGAINFYYGYVFLGCLVFAYFYVFFFVPETKGLTLEEVNTMWLEGVPAWKSASWVP
PERRTADYDADAIDHDDRPIYKRFFSS

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
MSLAKSAANKLDWAKVISSLRITGSTATQLSSFKKRNDEARRQLLELQSQPTEVDFSHYR
SVLKNTSVIDKIESYVKQYKPVKIDASKQLQVIESFEKHAMTNAKETESLVSKELKDLQS
TLDNIQSARPFDELTVDDLTKIKPEIDAKVEEMVKKGKWDVPGYKDRFGNLNVM

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
MSLISALQTTDVESVQTSPEQITERKAVRVSTLQESLHSSEMHRAAPETPRSISNSVHKL
KTIYSTYQQSGQPLSKEAIFRAKQKYGILNTPANYKTLGLGDSKSESVDLAARLASKRTK
VSPDDCVETAIEQKARGEAFKVTFSKIPLTPPEDVPITVNLGLKGRRDFLTRLAAQKALA
FSPSLDNSMKGTSDSSSVKKKRFSGAPIGNEFDANLVNPQHPAGFKSLDLSKVLDGAERR
AISRVNDRLYPQKVNFKNGLQSSDQSGVSKANKEVFKKGTLEKLEHSAEQFLESHAGNER
QRLSDQQYMCAKGAADAVKDLDPKTLEDPDFAAREAQKKLYIKQVASPVVLNEAQKLANR
KLQDIDSRDTYMLLFGNQAYNKLAVNIALQHYSVKQEEKKKIYLGGGLWMTPEEVNAVAK
KLISPVVNEIDERASRQRDVDKDIERRSRVLDQEYEDGNSMERAKEQNDGQLLLAMASKQ
QQEKEAKKAEEGQRYDQFVQKMNIKLQQKEKELENARENRENLRNELQERLSKNLSGEND
ELNDWNDACERDLKNSSIEHYYAVRSHFDNLGNSERGYDELLEERSKIQVEIERLVASIA
EHKTAIHGFGETADAGGAIPAVQKQKIPTRKDLLDATVNDPLVISAEMAKEEAEMATEEC

TABLE 14-continued

Sequences disclosed herein.

MLKELQVDEMIIIRNIMLRECEKKLEEEKETAKRSRRGTEESKNNSNFSRDVIMSTPDNN
EKVIPIGKSASPKDVVKSRFLSTYNTGKDIDSSASARSITGVSGVLDDGPKTPTSNKENE
LIDDEVKSYKVHQAVDGTGEDSIANKRDKSSRPAANSGGSITIEQFLFNKNADKQGLSKT
ESVTMKREPVVDQMDSKKGHDFTHCNDNGRRSFSGFSQGSIENDYSNEVIDDQDDQEGSE
IRVRDSNDSNTSPKESFFKEVI

SEQ ID NO: 126
YKL120W
>sp|P32332|OAC1_YEAST Mitochondrial oxaloacetate transport protein
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = OAC1
PE = 1 SV = 1
MSSDNSKQDKQIEKTAAQKISKFGSFVAGGLAACIAVTVTNPIELIKIRMQLQGEMSASA
AKVYKNPIQGMAVIFKNEGIKGLQKGLNAAYIYQIGLNGSRLGFYEPIRSSLNQLFFPDQ
EPHKVQSVGVNVFSGAASGIIGAVIGSPLFLVKTRLQSYSEFIKIGEQTHYTGVWNGLVT
IFKTEGVKGLFRGIDAAILRTGAGSSVQLPIYNTAKNILVKNDLMKDGPALHLTASTISG
LGVAVVMNPWDVILTRIYNQKGDLYKGPIDCLVKTVRIEGVTALYKGFAAQVFRIAPHTI
MCLTFMEQTMKLVYSIESRVLGHN

SEQ ID NO: 127
YKL146W
>sp|P36062|AVT3_YEAST Vacuolar amino acid transporter 3
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = AVT3
PE = 1 SV = 1
MNGKEVSSGSGRTQSNNNKKNNNGGSTGISHASGSPLTDGNGGNSNGNSRSRSRSRKSSG
TTGGLLKKPPLLVNNEAVHASVPDASHTSCNNGTLEVSINNPEPHVVDAVARHLIRNPSN
SLQLQGGDITRDLYKWTNDHPSSPSQYQYPSQPALSTSIPSQAPSFSNRKRSMSFSAASI
ASSSHLNNNSEANGNPLAAIGLAPAPMTHEEIRAPGGFRRSFIIQKRRKHNVDAPIPNFF
TRNFIEFLTLYGHFAGEDLSEEEEEEEETEEEPEEEALETESTQLVSREHGRHPHKSSTV
KAVLLLLKSFVGTGVLFLPKAFHNGGWGFSALCLLSCALISYGCFVSLITTKDKVGVDGY
GDMGRILYGPKMKFAILSSIALSQIGFSAAYTVFTATNLQVFSENFFHLKPGSISLATYI
FAQVLIFVPLSLTRNIAKLSGTALIADLFILLGLVYVYVYSIYYIAVNGVASDTMLMFNK
ADWSLFIGTAIFTFEGIGLLIPIQESMKHPKHFRPSLSAVMCIVAVIFISCGLLCYAAFG
SDVKTVVLLNFPQDTSYTLTVQLLYALAILLSTPLQLFPAIRILENWTFPSNASGKYNPK
VKWLKNYFRCAIVVLTSILAWVGANDLDKFVSLVGSFACIPLIYIYPPLLHYKASILSGT
SRARLLLDLIVIVFGVAVMAYTSWQTIKMWSQ

SEQ ID NO: 128
YKL209C
>sp|P12866|STE6_YEAST Alpha-factor-transporting ATPase
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = STE6
PE = 1 SV = 1
MNFLSFKTTKHYHIFRYVNIRNDYRLLMIMIIGTVATGLVPAITSILTGRVFDLLSVFVA
NGSHQGLYSQLVQRSMAVMALGAASVPVMWLSLTSWMHIGERQGFRIRSQILEAYLEEKP
MEWYDNNEKLLGDFTQINRCVEELRSSSAEASAITFQNLVAICALLGTSFYYSWSLTLII
LCSSPIITFFAVVFSRMIHVYSEKENSETSKAAQLLTWSMNAAQLVRLYCTQRLERKKFK
EIILNCNTFFIKSCFFVAANAGILRFLTLTMFVQGFWFGSAMIKKGKLNINDVITCFHSC
IMLGSTLNNTLHQIVVLQKGGVAMEKIMTLLKDGSKRNPLNKTVAHQFPLDYATSDLTFA
NVSFSYPSRPSEAVLKNVSLNFSAGQFTFIVGKSGSGKSTLSNLLLRFYDGYNGSISING
HNIQTIDQKLLIENITVVEQRCTLFNDTLRKNILLGSTDSVRNADCSTNENRHLIKDACQ
MALLDRFILDLPDGLETLIGTGGVTLSGGQQQRVAIARAFIRDTPILFLDEAVSALDIVH
RNLLMKAIRHWRKGKTTIILTHELSQIESDDYLYLMKEGEVVESGTQSELLADPTTTFST
WYHLQNDYSDAKTIVDTETEEKSIHTVESFNSQLETPKLGSCLSNLGYDETDQLSFYEAI
YQKRSNVRTRRVKVEEENIGYALKQQKNTESSTGPQLLSIIQIIKRMIKSIRYKKILILG
LLCSLIAGATNPVFSYTFSFLLEGIVPSTDGKTGSSHYLAKWSLLVLGVAAADGIFNFAK
GFLLDCCSEYWVMDLRNEVMEKLTRKNMDWFSGENNKASEISALVLNDLRDLRSLVSEFL
SAMTSFVTVSTIGLIWALVSGWKLSLVCISMFPLIIIFSAIYGGILQKCETDYKTSVAQL
ENCLYQIVTNIKTIKCLQAEFHFQLTYHDLKIKMQQIASKRAIATGFGISMTNMIVMCIQ
AIIYYYGLKLVMIHEYTSKEMFTTFTLLLFTIMSCTSLVSQIPDISRGQRAASWIYRILD
EKHNTLEVENNNARTVGIAGHTYHGKEKKPIVSIQNLTFAYPSAPTAFVYKNMNFDMFCG
QTLGIIGESGTGKSTLVLLLTKLYNCEVGKIKIDGTDVNDWNLTSLRKEISVVEQKPLLF
NGTIRDNLTYGLQDEILEIEMYDALKYVGIHDFVISSPQGLDTRIDTTLLSGGQAQRLCI
ARALLRKSKILILDECTSALDSVSSSIINEIVKKGPPALLTMVITHSEQMMRSCNSIAVL
KDGKVVERGNFDTLYNNRGELFQIVSNQSS

SEQ ID NO: 129
YKR039W
>sp|P19145|GAP1_YEAST General amino-acid permease GAP1
OS = *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) GN = GAP1
PE = 1 SV = 2
MSNTSSYEKNNPDNLKHNGITIDSEFLTQEPITIPSNGSAVSIDETGSGSKWQDFKDSFK
RVKPIEVDPNLSEAEKVAIITAQTPLKHHLKNRHLQMIAIGGAIGTGLLVGSGTALRTGG
PASLLIGWGSTGTMIYAMVMALGELAVIFPISGGFTTYATRFIDESFGYANNFNYMLQWL
VVLPLEIVSASITVNFWGTDPKYRDGFVALFWLAIVIINMFGVKGYGEAEFVFSFIKVIT
VVGFIILGIILNCGGGPTGGYIGGKYWHDPGAFAGDTPGAKFKGVCSVFVTAAFSFAGSE
LVGLAASESVEPRKSVPKAAKQVFWRITLFYILSLLMIGLLVPYNDKSLIGASSVDAAAS

TABLE 14-continued

Sequences disclosed herein.

PFVIAIKTHGIKGLPSVVNVVILIAVLSVGNSAIYACSRTMVALAEQRFLPEIFSYVDRK
GRPLVGIAVTSAFGLIAFVAASKKEGEVFNWLLALSGLSSLFTWGGICICHIRFRKALAA
QGRGLDELSFKSPTGVWGSYWGLFMVIIMFIAQFYVAVFPVGDSPSAEGFFEAYLSFPLV
MVMYIGHKIYKRNWKLFIPAEKMDIDTGRREVDLDLLKQEIAEEKAIMATKPRWYRIWNF
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
MNMGGSSSTAAKKATCKISMLWNWYTIDTCFIARSWRNDTKGKFAGSCIGCFALVVVAQW
LTRFSRQFDVELLKRQKIKHLASYSPEEYVVKCGEEDAKSDIEELQGFYNEPSWKTTLIS
LQKSFIYSFYVWGPRRLNEPEDDLLKKVLSCCTLITPVDLYPTFLDHMIRVTIFVLQWGL
SYIIMLLFMYYNGYIIISCLIGAIVGRFIFCYEPLGSLGANGSAQGTVSYDKESDDRKCC
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
MNRTVFLAFVFGWYFCSIALSIYNRWMFDPKDGLGIGYPVLVTTFHQATLWLLSGIYIKL
RHKPVKNVLRKNNGFNWSFFLKFLLPTAVASAGDIGLSNVSFQYVPLTIYTIIKSSSIAF
VLLFGCIFKLEKFHWKLALSVIIMFVGVALMVFKPSDSTSTKNDQALVIFGSFLVLASSC
LSGLRWVYTQLMLRNNPIQTNTAAAVEESDGALFTENEDNVDNEPVVNLANNKMLENFGE
SKPHPIHTIHQLAPIMGITLLLTSLLVEKPFPGIFSSSIFRLDTSNGGVGTETTVLSIVR
GIVLLILPGFAVFLLTICEFSILEQTPVLTVSIVGIVKELLTVIFGIIILSERLSGFYNW
LGMLIIMADVCYYNYFRYKQDLLQKYHSVSTQDNRNELKGFQDFEQLGSKKIAPYSISVD
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
MNSWNLSSSIPIIHTPHDHPPTSEGTPDQPNNNRKDDKLHKKRGDSDEDLSPIWHCVVSG
GIGGKIGDSAMHSLDTVKTRQQGAPNVKKYRNMISAYRTIWLEEGVRRGLYGGYMAAMLG
SFPSAAIFFGTYEYTKRTMIEDWQINDTITHLSAGFLGDFISSFVYVPSEVLKTRLQLQG
RFNNPFFQSGYNYSNLRNAIKTVIKEEGFRSLFFGYKATLARDLPFSALQFAFYEKFRQL
AFKIEQKDGRDGELSIPNEILTGACAGGLAGIITTPMDVVKTRVQTQQPPSQSNKSYSVT
HPHVTNGRPAALSNSISLSLRTVYQSEGVLGFFSGVGPRFVWTSVQSSIMLLLYQMTLRG
LSNAFPTD

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
MFSIFKKKTSVQGTDSEIDEKITVKAKDKVVVSTEDEEVTTIVSSTKSTQVTNDSPWQDP
TYFSSFGKELMFIATCMLAQLLNQAGQTHALCIMNVLSKSFNSEANNQAWLMASFPLAAG
SFILISGRLGDIYGLKKMLIVGYVIVIVWSIISGLSKYSNSDAFFITSRAFQGVGIAFIL
PNIMGLVGHVYKVGSFRKNIVISFIGACAPTGGMFGGLFGGLIVTEDPNQWPWVFYAFGI
ATFLSLLMAWYSIPNNVPTNIHGLSMDWTGSALAIIGLILFNFVWNQAPIVGWDKPYIIV
LLIISVIFLVAFFVYESKYAEVPLLPRAMTKNRHMIMILLAVFLGWGSFGIWTFYYVSFQ
LNLRHYSPVWTGGTYFVFVIFGSMAAFFVAFSIKRLGPALLLCFSLMAFDAGSIMFSVLP
VEQSYWKLNFAMQAILCFGMDLSFPASSIILSDGLPMQYQGMAGSLVNTVINYSASLCLG
MGGTVEHQINKSGNDLLKGYRAAVYLGVGLASLGVVISVTYMLENLWNRHRKSEDRSLEA

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
MNTFFLSLLSGAAAGTSTDLVFFPIDTIKTRLQAKGGFFANGGYKGIYRGLGSAVVASAP
GASLFFISYDYMKVKSRPYISKLYSQGSEQLIDTTTHMLSSSIGEICACLVRVPAEVVKQ
RTQVHSTNSSWQTLQSILRNDNKEGLRKNLYRGWSTTIMREIPFICIQFPLYEYLKKTWA
KANGQSQVEPWKGAICGSIAGGIAAATTTPLDFLKTRLMLNKTTASLGSVIIRIYREEGP
AVFFSGVGPRTMWISAGGAIFLGMYETVHSLLSKSFPTAGEMRA

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
KHGSLQGGAIADVNSITNSLTRLQVVSHETDINEDEEEAHYEDKHVKRALKQRHIGMIAL

TABLE 14-continued

Sequences disclosed herein.

GGTIGTGLFVGISTPLSNAGPVGSLIAYIFMGTIVYFVTQSLGEMATFIPVISSITVFSK
RFLSPAFGVSNGYMYWFNWAITYAVEVSVIGQVIEYWTDKVPLAAWIAIFWVIITLMNFF
PVKVYGEFEFWVASVKVLAIMGYLIYALIIVCGGSHQGPIGFRYWRNPGAWGPGIISSDK
SEGRFLGWVSSLINAAFTYQGTELVGITAGEAANPRKTVPRAINKVVFRIVLFYIMSLFF
IGLLVPYNDSRLSASSAVIASSPFVISIQNAGTYALPDIFNAVVLITVVSAANSNVYVGS
RVLYSLARTGNAPKQFGYVTRQGVPYLGVVCTAALGLLAFLVVNNNANTAFNWLINISTL
AGLCAWLFISLAHIRFMQALKHRGISRDDLPFKAKLMPYGAyyAAFFVTVIIFIQGFQAF
CPFKVSEFFTSYISLILLAVVFIGCQIYYKCRFIWKLEDIDIDSDRREIEAIIWEDDEPK
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
MDKYTNRDHPDYIPGTFNIYSSQNLENGIIYESKLKKTSSGVVLIPQPSYSPNDPLNWSS
WRKLAHFGLMAFITAFTAATSNDAGAAQDSLNEIYGISYDSMNTGAGVLFLGIGWSTLFL
APFANLYGRKITYIVCTTLGLFGALWFALAKRTSDTIWSQLFVGISESCAEAQVQLSLSD
IFFQHQLGSVLTVYIMCTSIGTFLGPLIAGYISAFTNFRWVGWVAVIISGGLLITIIFGC
EETYFDRGQYMTPLTSCQSGYEDGTTLQNSDNTAVSRRKRHLDAKLSTPGAMGEKGVDLS
ETAEFEVNNEEEVTIPETRELIDGSKEHLKPYPKRVAILTKATNLKGYGFKQYFKYLKIN
LRMFLFPPVWLSGMFWGIQDVFLTFYLTTQESAYYEPPWNYSDFGVAIMNVPTLIGAVIG
CICAGIVSDYFVLWMARHNRGILEAEFRLYFSIATAIIGPAGLLMFGIGTARQWPWQAIY
VGLGFVGFAWGCSGDIAMAYLMDCYPDMVLEGMVCTAIINNTISCIFTFTCSDWLAASGT
ENTYIALAVINFGITAFALPMYYYGKRIRLWTKRWYLQSVNLRDGV

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
MLETDHSRNDNLDDKSTVCYSEKTDSNVEKSTTSGLRRIDAVNKVLSDYSSFTAFGVTFS
SLKTALLVALFLQGYCTGLGGQISQSIQTYAANSFGKHSQVGSINTVKSIVASVVAVPYA
RISDRFGRIECWIFALVLYTIGEIISAATPTFSGLFAGIVIQQFGYSGFRLLATALTGDL
SGLADRTFAMNIFLIPVIINTWVSGNIVSSVAGNVAPYKWRWGYGIFCIIVPISTLILVL
PYVYAQYISWRSGKLPPLKLKEKGQTLRQTLWKFADDINLIGVILFTAFLVLVLLPLTIA
GGATSKWREGHIIAMIVVGGCLGFIFLIWELKFAKNPFIPRVYLGDPTIYVALLMEFVWR
LGLQIELEYLVTVLMVAFGESTLSAQRIAQLYNFLQSCTNIVVGIMLHFYPHPKVFVVAG
SLLGVIGMGLLYKYRVVYDGISGLIGAEIVVGIAGGMIRFPMWTLVHASTTHNEMATVTG
LLMSVYQIGDAVGASIAGAIWTQRLAKELIQRLGSSLGMAIYKSPLNYLKKYPIGSEVRV
QMIESYSKIQRLLIIVSISFAAFNAVLCFFLRGFTVNKKQSLSAEEREKEKLKIKQQSWL
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
MSSDTSLSESSLLKEESGSLTKSRPPIKSNPVRENIKSFVAGGVGGVCAVFTGHPFDLIK
VRCQNGQANSTVHAITNIIKEAKTQVKGTLFTNSVKGFYKGVIPPLLGVTPIFAVSFWGY
DVGKKLVTFNNKQGGSNELTMGQMAAAGFISAIPTTLVTAPTERVKVVLQTSSKGSFIQA
AKTIVKEGGIASLFKGSLATLARDGPGSALYFASYEISKNYLNSRQPRQDAGKDEPVNIL
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
SAPNKSDAQSIFSSGVEGVNPIFSDPEAPGYDPKLDPNSENFSSAAWVKNMAHLSAADPD
FYKPYSLGCAWKNLSASGASADVAYQSTVVNIPYKILKSGLRKFQRSKETNTFQILKPMD
GCLNPGELLVVLGRPGSGCTTLLKSISSNTHGFDLGADTKISYSGYSGDDIKKHFRGEVV
YNAEADVHLPHLTVFETLVTVARLKTPQNRIKGVDRESYANHLAEVAMATYGLSHTRNTK
VGNDIVRGVSGGERKRVSIAEVSICGSKFQCWDNATRGLDSATALEFIRALKTQADISNT
SATVAIYQCSQDAYDLFNKVCVLDDGYQIYYGPADKAKKYFEDMGYVCPSRQTTADFLTS
VTSPSERTLNKDMLKKGIHIPQTPKEMNDYWVKSPNYKELMKEVDQRLLNDDEASREAIK
EAHIAKQSKRARPSSPYTVSYMMQVKYLLIRNMWRLRNNIGFTLFMILGNCSMALILGSM
FFKIMKKGDTSTFYFRGSAMFFAILFNAFSSLLEIFSLYEARPITEKHRTYSLYHPSADA
FASVLSEIPSKLIIAVCFNIIFYFLVDFRRNGGVFFFYLLINIVAVFSMSHLFRCVGSLT
KTLSEAMVPASMLLLALSMYTGFAIPKKKILRWSKWIWYINPLAYLFESLLINEFHGIKF
PCAEYVPRGPAYANISSTESVCTVVGAVPGQDYVLGDDFIRGTYQYYHKDKWRGFGIGMA
YVVFFFFVYLFLCEYNEGAKQKGEILVFPRSIVKRMKKRGVLTEKNANDPENVGERSDLS
SDRKMLQESSEEESDTYGEIGLSKSEAIFHWRNLCYEVQIKAETRRILNNVDGWVKPGTL
TALMGASGAGKTTLLDCLAERVTMGVITGDILVNGIPRDKSFPRSIGYCQQQDLHLKTAT

TABLE 14-continued

Sequences disclosed herein.
VRESLRFSAYLRQPAEVSIEEKNRYVEEVIKILEMEKYADAVVGVAGEGLNVEQRKRLTI GVELTAKPKLLVFLDEPTSGLDSQTAWSICQLMKKLANHGQAILCTIHQPSAILMQEFDR LLFMQRGGKTVYFGDLGEGCKTMIDYFESHGAHKCPADANPAEWMLEVVGAAPGSHANQD YYEVWRNSEEYRAVQSELDWMERELPKKGSITAAEDKHEFSQSIIYQTKLVSIRLFQQYW RSPDYLWSKFILTIFNQLFIGFTFFKAGTSLQGLQNQMLAVFMFTVIFNPILQQYLPSFV QQRDLYEARERPSRTFSWISFIFAQIFVEVPWNILAGTIAYFIYYYPIGFYSNASAAGQL HERGALFWLFSCAFYVYVGSMGLLVISFNQVAESAANLASLLFTMSLSFCGVMTTPSAMP RFWIFMYRVSPLTYFIQALLAVGVANVDVKCADYELLEFTPPSGMTCGQYMEPYLQLAKT GYLTDENATDTCSFCQISTTNDYLANVNSFYSERWRNYGIFICYIAFNYIAGVFFYWLAR VPKKNGKLSKK
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 MASSVPGPIDLPESRYDLSTYWGRIRHCAEISDPTMLLTTEKDLAHAREIISAYRHGELK ETTPEFWRAKKQLDSTVHPDTGKTVLLPFRMSSNVLSNLVVTVGMLTPGLGTAGTVFWQW ANQSLNVAVNSANANKSHPMSTSQLLTNYAAAVTASCGVALGLNNLVPRLKNISPHSKLI LGRLVPFAAVVSAGIVNVFLMRGNEIRKGISVFDSNGDEVGKSKKAAFMAVGETALSRVI NATPTMVIPPLILVRLQRGVLKGKSLGVQTLANLGLISVTMFSALPFALGIFPQRQAIHL NKLEPELHGKKDKDGKPIEKVYFNRGI
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 MPSSLTKTESNSDPRTNIQQVPKALDKNVTNSGNLDSTSSSTGSITEDEKRSEPNADSNN MTGGEPIDPRDLDWDGPDDPDNPHNWSSLKKWYTTMTSAFLCLVVTMGSSLYVSSVPELV ERYHVSQTLALAGLTFYLLGLSTVIGAPLSEVFGRKPVYLFSLPVSMLFTMGVGLSNGHM RIILPLRFLSGVFASPALSVGSGTILDIFDVDQVSVAMTYFVLSPFLGPVLSPIMAGFAT EAKGWRWSEWIQLIAGGLILPFIALMPETHKGIILRKRAKKRNIALKKFSREAQKEFLKT TVTITILRPLKMLVVEPIVFVFSVYVAFIFAILFGFFEAYAVIYRGVYHMSMGISGLPFI GIGVGLWIGAFFYLYIDRKYLFPKPPAGTQPLTEKERTSKRTTPYRGARDAETGELLPVV PEKFLIACKFGSVALPIGLFWQAWTARSDVHWMAPVAAGVPFGFGLILIFFSVLMYFSTC YPPLTVASCLAANNLLRYVMSSVFPLFTIQMYTKMKIKWASTLFALVCVVMIPIPWVFEK WGSKLRHKSQFGYAAMEKEAETEGGIDDVNAVDGELNLTRMTTLRTMETDPSTREKPGER LSLRRTHTQPVPASFDREDGQHAQNRNEPISNSLYSAIKDNEDGYSYTEMATDASARMV
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 KRFTQLFPSNIQGYLPEVDLRITIICSIWYVTSSISSNLSKAILRTFNHPIALTELQFLV SAVLCVGFASIVNLFRLPRLKHTKFSKALNSFPDGILPEYLDGNFRSSILHKFLVPSKLV LMTTFPMGIFQFIGHITSHKAVSMIPVSLVHSVKALSPIITVGYYKFFEHRYYNSMTYYT LLLLIFGVMTTCWSTHGSKRASDNKSGSSLIGLLFAFISMIIFVAQNIFAKNILTIRRKV GILPSSSTDDVTSKEGQPSLDKTRFSPLQVDKITILFYCSCIGFSLTLLPFLTGELMHGG SVINDLTLETVALVAIHGIAHFFQAMLAFQLIGLLSSINYSVANIMKRIVVISVALFWET KLNFFQVFGVILTIAGLYGYDKWGLSKKDGRQA
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 MSSAITALTPNQVNDELNKMQAFIRKEAEEKAKEIQLKADQEYEIEKTNIVRNETNNIDG NFKSKLKKAMLSQQITKSTIANKMRLKVLSAREQSLDGIFEETKEKLSGIANNRDEYKPI LQSLIVEALLKLLEPKAIVKALERDVDLIESMKDDIMREYGEKAQRAPLEEIVISNDYLN KDLVSGGVVVSNASDKIEINNTLEERLKLLSEEALPAIRLELYGPSKTRKFFD
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 MVNILPFHKNNRHSAGVVTCADDVSGDGSGGDTKKEEDVVQVTESPSSGSRNNHRSDNEK DDAIRMEKISKNQSASSNGTIREDLIMDVDLEKSPSVDGDSEPHKLKQGLQSRHVQLIAL GGAIGTGLLVGTSSTLHTCGPAGLFISYIIISAVIYPIMCALGEMVCFLPGDGSDSAGST ANLVTRYVDPSLGFATGWNYFYCYVILVAAECTAASGVVEYWTTAVPKGVWITIFLCVVV ILNFSAVKVYGESEFWFASIKILCIVGLIILSFILFWGGGPNHDRLGFRYWQHPGAFAHH LTGGSLGNFTDIYTGIIKGAFAFILGPELVCMTSAECADQRRNIAKASRRFVWRLIFFYV LGTLAISVIVPYNDPTLVNALAQGKPGAGSSPFVIGIQNAGIKVLPHIINGCILTSAWSA ANAFMFASTRSLLTMAQTGQAPKCLGRINKWGVPYVAVGVSFLCSCLAYLNVSSSTADVF

TABLE 14-continued

Sequences disclosed herein.

NWFSNISTISGFLGWMCGCIAYLRFRKAIFYNGLYDRLPFKTWGQPYTVWFSLIVIGIIT
ITNGYAIFIPKYWRVADFIAAYITLPIFLVLWFGHKLYTRTWRQWWLPVSEIDVTTGLVE
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
MSSTEAKQYKEKPSKEYLHASDGDDPANNSAASSSSSSSTSTSASSSAAAVPRKAAAASA
ADDSDSDEDIDQLIDELQSNYGEGDESGEEEVRTDGVHAGQRVVPEKDLSTDPXYGLTSD
EVARRRKKYGLNQMAEENESLIVKFLMFFVGPIQFVMEAAAILAAGLSDWVDVGVICALL
LLNASVGFIQEFQAGSIVDELKKTLANTATVIRDGQLIEIPANEVVPGEILQLESGTIAP
ADGRIVTEDCFLQIDQSAITGESLAAEKHYGDEVFSSSTVKTGEAFMVVTATGDNTFVGR
AAALVGQASGVEGHFTEVLNGIGIILLVLVIATLLLVWTACFYRTVGIVSILRYTLGITI
IGVPVGLPAVVTTTMAVGAAYLAKKQAIVQKLSAIESLAGVEILCSDKTGTLTKNKLSLH
EPYTVEGVSPDDLMLTACLAASRKKKGLDAIDKAFLKSLIEYPKAKDALTKYKVLEFHPF
DPVSKKVTAVVESPEGERIVCVKGAPLFVLKTVEEDHPIPEDVHENYENKVAELASRGFR
ALGVARKRGEGHWEILGVMPCMDPPRDDTAQTINEARNLGLRIKMLTGDAVGIAKETCRQ
LGLGTNIYNAERLGLGGGGDMPGSELADFVENADGFAEVFPQHKYRVVEILQNRGYLVAM
TGDGVNDAPSLKKADTGIAVEGATDAARSAADIVFLAPGLSAIIDALKTSRQIFHRMYSY
VVYRIALSLHLEIFLGLWIAILNNSLDINLIVFIAIFADVATLTIAYDNAPYAPEPVKWN
LPRLWGMSIILGIVLAIGSWITLTTMFLPNGGIIQNFGAMNGVMFLQISLTENWLIFVTR
AAGPFWSSIPSWQLAGAVFAVDIIATMFTLFGWWSENWTDIVSVVRVWIWSIGIFCVLGG
FYYIMSTSQAFDRLMNGKSLKEKKSTRSVEDFMAAMQRVSTQHEKSS

SEQ ID NO: 146
YDL198C
MPHTDKKQSG LARLLGSASA GIMEIAVFHP VDTISKRLMS NHTKITSGQE LNRVIFRDHF
SEPLGKRLFT LFPGLGYAAS YKVLQRVYKY GGQPFANEFL NKHYKKDFDN LFGEKTGKAM
RSAAAGSLIG IGEIVLLPLD VLKIKRQTNP ESFKGRGFIK ILRDEGLFNL YRGWGWTAAR
NAPGSFALFG GNAFAKEYIL GLKDYSQATW SQNFISSIVG ACSSLIVSAP LDVIKTRIQN
RNFDNPESGL RIVKNTLKNE GVTAFFKGLT PKLLTTGPKL VFSFALAQSL IPRFDNLLSK

SEQ ID NO: 147
YFL054C
MSYESGRSSS SSESTRPPTL KEEPNGKIAW EESVKKSREN NENDSTLLRR KLGETRKAIE
TGGSSRNKLS ALTPLKKVVD ERKDSVQPQV PSMGFTYSLP NLKTLNSFSD AEQARIMQDY
LSRGVNQGNS NNYVDPLYRQ LNPTMGSSRN RPVWSLNQPL PHVLDRGLAA KMIQKNMDAR
SRASSRRGST DISRGGSTTS VKDWKRLLRG AAPGKKLGDI EAQTQRDNTV GADVKPTKLE
PENPQKPSNT HIENVSRKKK RTSHNVNFSL GDESYASSIA DAESRKLKNM QTLDGSTPVY
TKLPEELIEE ENKSTSALDG NEIGASEDED ADIMTFPNFW AKIRYHMREP FAEFLGTLVL
VIFGVGGNLQ ATVTKGSGGS YESLSFAWGF GCMLGVYVAG GISGGHINPA VTISMAIFRK
FPWKKVPVYI VAQIIGAYFG GAMAYGYFWS SITEFEGGPH IRTTATGACL FTDPKSYVTW
RNAFFDEFIG ASILVGCLMA LLDDSNAPPG NGMTALIIGF LVAAIGMALG YQTSFTINPA
RDLGPRIFAS MIGYGPHAFH LTHWWWTWGA WGGPIAGGIA GALIYDIFIF TGCESPVNYP
DNGYIENRVG KLLHAEFHQN DGTVSDESGV NSNSNTGSKK SVPTSS

SEQ ID NO: 148
Oryza sativa sequence encoding EUGT11
MDSGYSSSYA AAAGMHVVIC PWLAFGHLLP CLDLAQRLAS RGHRVSFVST PRNISRLPPV
RPALAPLVAF VALPLPRVEG LPDGAESTND VPHDRPDMVE LHRRAFDGLA APFSEFLGTA
CADWVIVDVF HHWAAAAALE HKVPCAMMLL GSAHMIASIA DRRLERAETE SPAAAGQGRP
AAAPTFEVAR MKLIRTKGSS GMSLAERFSL TLSRSSLVVG RSCVEFEPET VPLLSTLRGK
PITFLGLMPP LHEGRREDGE DATVRWLDAQ PAKSVVYVAL GSEVPLGVEK VHELALGLEL
AGTRFLWALR KPTGVSDADL LPAGFEERTR GRGVVATRWV PQMSILAHAA VGAFLTHCGW
NSTIEGLMFG HPLIMLPIFG DQGPNARLIE AKNAGLQVAR NDGDGSFDRE GVAAAIRAVA
VEEESSKVFQ AKAKKLQEIV ADMACHERYI DGFIQQLRSY KD

SEQ ID NO: 149
Synechococcus sp. GGPPS
MVAQTFNLDT YLSQRQQQVE EALSAALVPA YPERIYEAMR YSLLAGGKRL RPILCLAACE
LAGGSVEQAM PTACALEMIH TMSLIHDDLP AMDNDDFRRG KPTNHKVFGE DIAILAGDAL
LAYAFEHIAS QTRGVPPQLV LQVIARIGHA VAATGLVGGQ VVDLESEGKA ISLETLEYIH
SHKTGALLEA SVVSGGILAG ADEELLARLS HYARDIGLAF QIVDDILDVT ATSEQLGKTA
GKDQAAAKAT YPSLLGLEAS RQKAEELIQS AKEALRPYGS QAEPLLALAD FITRRQH

SEQ ID NO: 150
Zea mays truncated COPS
MAQHTSESAA VAKGSSLTPI VRTDAESRRT RWPTDDDDAE PLVDEIRAML TSMSDGDISV
SAYDTAWVGL VPRLDGGEGP QFPAAVRWIR NNQLPDGSWG DAALFSAYDR LINTLACVVT
LTRWSLEPEM RGRGLSFLGR NMWKLATEDE ESMPIGFELA FPSLIELAKS LGVHDFPYDH
QALQGIYSSR EIKMKRIPKE VMHTVPTSIL HSLEGMPGLD WAKLLKLQSS DGSFLFSPAA
TAYALMNTGD DRCFSYIDRT VKKFNGGVPN VYPVDLFEHI WAVDRLERLG ISRYFQKEIE
QCMDYVNRHW TEDGICWARN SDVKEVDDTA MAFRLLRLHG YSVSPDVFKN FEKDGEFFAF
VGQSNQAVTG MYNLNRASQI SFPGEDVLHR AGAFSYEFLR RKEAEGALRD KWIISKDLPG

TABLE 14-continued

Sequences disclosed herein.
EVVYTLDFPW YGNLPRVEAR DYLEQYGGGD DVWIGKTLYR MPLVNNDVYL ELARMDFNHC QALHQLEWQG LKRWYTENRL MDFGVAQEDA LRAYFLAAAS VYEPCRAAER LAWARAAILA NAVSTHLRNS PSFRERLEHS LRCRPSEETD GSWFNSSSGS DAVLVKAVLR LTDSLAREAQ PIHGGDPEDI IHKLLRSAWA EWVREKADAA DSVCNGSSAV EQEGSRMVHD KQTCLLLARM IEISAGRAAG EAASEDGDRR IIQLTGSICD SLKQKMLVSQ DPEKNEEMMS HVDDELKLRI REFVQYLLRL GEKKTGSSET RQTFLSIVKS CYYAAHCPPH VVDRHISRVI FEPVSAAK
SEQ ID NO: 151 *Arabidopsis thaliana* KS (similar to GenBank AEE36246.1) MSINLRSSGC SSPISATLER GLDSEVQTRA NNVSFEQTKE KIRKMLEKVE LSVSAYDTSW VAMVPSPSSQ NAPLFPQCVK WLLDNQHEDG SWGLDNHDHQ SLKKDVLSST LASILALKKW GIGERQINKG LQFIELNSAL VTDETIQKPT GFDIIFPGMI KYARDLNLTI PLGSEVVDDM IRKRDLDLKC DSEKFSKGRE AYLAYVLEGT RNLKDWDLIV KYQRKNGSLF DSPATTAAAF TQFGNDGCLR YLCSLLQKFE AAVPSVYPFD QYARLSIIVT LESLGIDRDF KTEIKSILDE TYRYWLRGDE EICLDLATCA LAFRLLLAHG YDVSYDPLKP FAEESGFSDT LEGYVKNTFS VLELFKAAQS YPHESALKKQ CCWTKQYLEM ELSSWVKTSV RDKYLKKEVE DALAFPSYAS LERSDHRRKI LNGSAVENTR VTKTSYRLHN ICTSDILKLA VDDFNFCQSI HREEMERLDR WIVENRLQEL KFARQKLAYC YFSGAATLFS PELSDARISW AKGGVLTTVV DDFFDVGGSK EELENLIHLV EKWDLNGVPE YSSEHVEIIF SVLRDTILET GDKAFTYQGR NVTHHIVKIW LDLLKSMLRE AEWSSDKSTP SLEDYMENAY ISFALGPIVL PATYLIGPPL PEKTVDSHQY NQLYKLVSTM GRLLNDIQGF KRESAEGKLN AVSLHMKHER DNRSKEVIIE SMKGLAERKR EELHKLVLEE KGSVVPRECK EAFLKMSKVL NLFYRKDDGF TSNDLMSLVK SVIYEPVSLQ KESLT
SEQ ID NO: 152 *S. rebaudiana* KO1 MDAVTGLLTV PATAITIGGT AVALAVALIF WYLKSYTSAR RSQSNHLPRV PEVPGVPLLG NLLQLKEKKP YMTFTRWAAT YGPIYSIKTG ATSMVVVSSN EIAKEALVTR FQSISTRNLS KALKVLTADK TMVAMSDYDD YHKTVKRHIL TAVLGPNAQK KHRIHRDIMM DNISTQLHEF VKNNPEQEEV DLRKIFQSEL FGLAMRQALG KDVESLYVED LKITMNRDEI FQVLVVDPMM GAIDVDWRDF FPYLKWVPNK KFENTIQQMY IRREAVMKSL IKEHKKRIAS GEKLNSYIDY LLSEAQTLTD QQLLMSLWEP IIESSDTTMV TTEWAMYELA KNPKLQDRLY RDIKSVCGSE KITEEHLSQL PYITAIFHET LRRHSPVPII PLRHVHEDTV LGGYHVPAGT ELAVNIYGCN MDKNVWENPE EWNPERFMKE NETIDFQKTM AFGGGKRVCA GSLQALLTAS IGIGRMVQEF EWKLKDMTQE EVNTIGLTTQ MLRPLRAIIK PRI
SEQ ID NO: 153 *A. thaliana* ATR2 MSSSSSSSTS MIDLMAAIIK GEPVIVSDPA NASAYESVAA ELSSMLIENR QFAMIVTTSI AVLIGCIVML VWRRSGSGNS KRVEPLKPLV IKPREEEIDD GRKKVTIFFG TQTGTAEGFA KALGEEAKAR YEKTRFKIVD LDDYAADDDE YEEKLKKEDV AFFFLATYGD GEPTDNAARF YKWFTEGNDR GEWLKNLKYG VFGLGNRQYE HFNKVAKVVD DILVEQGAQR LVQVGLGDDD QCIEDDFTAW REALWPELDT ILREEGDTAV ATPYTAAVLE YRVSIHDSED AKFNDITLAN GNGYTVFDAQ HPYKANVAVK RELHTPESDR SCIHLEFDIA GSGLTMKLGD HVGVLCDNLS ETVDEALRLL DMSPDTYFSL HAEKEDGTPI SSSLPPPFPP CNLRTALTRY ACLLSSPKKS ALVALAAHAS DPTEAERLKH LASPAGKDEY SKWVVESQRS LLEVMAEFPS AKPPLGVFFA GVAPRLQPRF YSISSSPKIA ETRIHVTCAL VYEKMPTGRI HKGVCSTWMK NAVPYEKSEK LFLGRPIFVR QSNFKLPSDS KVPIIMIGPG TGLAPFRGFL QERLALVESG VELGPSVLFF GCRNRRMDFI YEEELQRFVE SGALAELSVA FSREGPTKEY VQHKMMDKAS DIWNMISQGA YLYVCGDAKG MARDVHRSLH TIAQEQGSMD STKAEGFVKN LQTSGRYLRD VW
SEQ ID NO: 154 *Stevia rebaudiana* KAHel MEASYLYISI LLLLASYLFT TQLRRKSANL PPTVFPSIPI IGHLYLLKKP LYRTLAKIAA KYGPILQLQL GYRRVLVISS PSAAEECFTN NDVIFANRPK TLFGKIVGGT SLGSLSYGDQ WRNLRRVASI EILSVHRLNE FHDIRVDENR LLIRKLRSSS SPVTLITVFY ALTLNVIMRM ISGKRYFDSG DRELEEEGKR FREILDETLL LAGASNVGDY LPILNWLGVK SLEKKLIALQ KKRDDFFQGL IEQVRKSRGA KVGKGRKTMI ELLLSLQESE PEYYTDAMIR SFVLGLLAAG SDTSAGTMEW AMSLLVNHPH VLKKAQAEID RVIGNNRLID ESDIGNIPYI GCIINETLRL YPAGPLLFPH ESSADCVISG YNIPRGTMLI VNQWAIHHDP KVWDDPETFK PERFQGLEGT RDGFKLMPFG SGRRGCPGEG LAIRLLGMTL GSVIQCFDWE RVGDEMVDMT EGLGVTLPKA VPLVAKCKPR SEMTNLLSEL
SEQ ID NO: 155 *Stevia rebaudiana* CPRS MQSNSVKISP LDLVTALFSG KVLDTSNASE SGESAMLPTI AMIMENRELL MILTTSVAVL IGCVVVLVWR RSSTKKSALE PPVIVVPKRV QEEEVDDGKK KVTVFFGTQT GTAEGFAKAL VEEAKARYEK AVFKVIDLDD YAADDDEYEE KLKKESLAFF FLATYGDGEP TDNAARFYKW FTEGDAKGEW LNKLQYGVFG LGNRQYEHFN KIAKVVDDGL VEQGAKRLVP VGLGDDDQCI EDDFTAWKEL VWPELDQLLR DEDDTTVATP YTAAVAEYRV VFHEKPDALS EDYSYTNGHA VHDAQHPCRS NVAVKKELHS PESDRSCTHL EFDISNTGLS YETGDHVGVY CENLSEVVND AERLVGLPPD TYSSIHTDSE DGSPLGGASL PPPFPPCTLR KALTCYADVL SSPKKSALLA LAAHATDPSE ADRLKFLASP AGKDEYSQWI VASQRSLLEV MEAFPSAKPS LGVFFASVAP RLQPRYYSIS SSPKMAPDRI HVTCALVYEK TPAGRIHKGV CSTWMKNAVP MTESQDCSWA PIYVRTSNFR LPSDPKVPVI MIGPGTGLAP FRGFLQERLA LKEAGTDLGL SILFFGCRNR

TABLE 14-continued

Sequences disclosed herein.

KVDFIYENEL NNFVETGALS ELIVAFSREG PTKEYVQHKM SEKASDIWNL LSEGAYLYVC
GDAKGMAKDV HRTLHTIVQE QGSLDSSKAE LYVKNLQMSG RYLRDVW

SEQ ID NO: 156
Stevia rebaudiana UGT85C2
MDAMATTEKK PHVIFIPFPA QSHIKAMLKL AQLLHHKGLQ ITFVNTDFIH NQFLESSGPH
CLDGAPGFRF ETIPDGVSHS PEASIPIRES LLRSIETNFL DRFIDLVTKL PDPPTCIISD
GFLSVFTIDA AKKLGIPVMM YWTLAACGFM GFYHIHSLIE KGFAPLKDAS YLTNGYLDTV
IDWVPGMEGI RLKDFPLDWS TDLNDKVLMF TTEAPQRSHK VSHHIFHTFD ELEPSIIKTL
SLRYNHIYTI GPLQLLLDQI PEEKKQTGIT SLHGYSLVKE EPECFQWLQS KEPNSVVYVN
FGSTTVMSLE DMTEFGWGLA NSNHYFLWII RSNLVIGENA VLPPELEEHI KKRGFIASWC
SQEKVLKHPS VGGFLTHCGW GSTIESLSAG VPMICWPYSW DQLTNCRYIC KEWEVGLEMG
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 IDAIIYDSMT
EWVLDVAIEF GIDGGSFFTQ ACVVNSLYYH VHKGLISLPL GETVSVPGFP VLQRWETPLI
LQNHEQIQSP WSQMLFGQFA NIDQARWVFT NSFYKLEEEV IEWTRKIWNL KVIGPTLPSM
YLDKRLDDDK DNGFNLYKAN HHECMNWLDD KPKESVVYVA FGSLVKHGPE QVEEITRALI
DSDVNFLWVI KHKEEGKLPE NLSEVIKTGK GLIVAWCKQL DVLAHESVGC FVTHCGFNST
LEAISLGVPV VAMPQFSDQT TNAKLLDEIL GVGVRVKADE NGIVRRGNLA SC:KMIMEEE
RGVIIRKNAV KWKDLAKVAV HEGGSSDNDI VEFVSELIKA

SEQ ID NO: 158
S. rebaudiana UGT76G1
MENKTETTVR RRRRIILFPV PFQGHINPIL QLANVLYSKG FSITIFHTNF NKPKTSNYPH
FTFRFILDND PQDERISNLP THGPLAGMRI PIINEHGADE LRRELELLML ASEEDEEVSC
LITDALWYFA QSVADSLNLR RLVLMTSSLF NFHAHVSLPQ FDELGYLDPD DKTRLEEQAS
GFPMLKVKDI KSAYSNWQIL KEILGKMIKQ TKASSGVIWN SFKELEESEL ETVIREIPAP
SFLIPLPKHL TASSSSLLDH DRTVFQWLDQ QPPSSVLYVS FGSTSEVDEK DFLEIARGLV
DSKQSFLWVV RPGFVKGSTW VEPLPDGFLG ERGRIVKWVP QQEVLAHGAI GAFWTHSGWN
STLESVCEGV PMIFSDFGLD QPLNARYMSD VLKVGVYLEN GWERGEIANA IRRVMVDEEG
EYIRQNARVL KQKADVSLMK GGSSYESLES LVSYISSL

SEQ ID NO: 159
S. rebaudiana UGT91D2e-b
MATSDSIVDD RKQLHVATFP WLAFGHILPY LQLSKLIAEK GHKVSFLSTT RNIQRLSSHI
SPLINVVQLT LPRVQELPED AEATTDVHPE DIPYLKKASD GLQPEVTRFL EQHSPDWIIY
DYTHYWLPSI AASLGISRAH FSVTTPWAIA YMGPSADAMI NGSDGRTTVE DLTTPPKWFP
FPTKVCWRKH DLARLVPYKA PGISDGYRMG MVLKGSDCLL SKCYHEFGTQ WLPLLETLHQ
VPVVPVGLLP PEIPGDEKDE TWVSIKKWLD GKQKGSVVYV ALGSEALVSQ TEVVELALGL
ELSGLPFVWA YRKPKGPAKS DSVELPDGFV ERTRDRGLVW TSWAPQLRIL SHESVCGFLT
HCGSGSIVEG LMFGHPLIML PIFGDQPLNA RLLEDKQVGI EIPRNEEDGC LTKESVARSL
RSVVVEKEGE IYKANARELS KIYNDTKVEK EYVSQFVDYL EKNARAVAID HES

SEQ ID NO: 160
atggctacct tgttggaaca ttttcaagct atgccattcg ctattccaat tgctttggct
gctttgtctt ggttgttttt gttctacatc aaggtttctt tcttctccaa caaatccgct
caagctaaat tgccaccagt tccagttgtt ccaggtttgc cagttattgg taatttgttg
caattgaaag aaaagaagcc ataccaaacc ttcactagat gggctgaaga atatggtcca
atctactcta ttagaactgg tgcttctact atggttgtct tgaacactac tcaagttgcc
aaagaagcta tggttaccag atacttgtct atctctacca gaaagttgtc caacgccttg
aaaattttga ccgctgataa gtgcatggtt gccatttctg attacaacga tttccacaag
atgatcaaga gatatatctt gtctaacgtt ttgggtccat ctgcccaaaa aagacataga
tctaacagag ataccttgag agccaacgtt tgttctagat tgcattccca agttaagaac
tctccaagag aagctgtcaa ctttagaaga gttttcgaat gggaattatt cggtatcgct
ttgaaacaag ccttcggtaa ggatattgaa aagccaatct acgtcgaaga attgggtact
actttgtcca gagatgaaat cttcaaggtt ttggtcttgg acattatgga aggtgccatt
gaagttgatt ggagagattt tttcccatac ttgcgttgga ttccaaacac cagaatggaa
actaagatcc aaagattata ctttagaaga aaggccgtta tgaccgcctt gattaacgaa
caaaagaaaa gaattgcctc cggtgaagaa atcaactgct acatcgattt cttgttgaaa
gaaggtaaga ccttgaccat ggaccaaatc tctatgttgt tgtgggaaac cgttattgaa
actgctgata ccacaatggt tactactgaa tgggctatgt acgaagttgc taaggattct
aaaagacaag acagattata ccaagaaatc caaaaggtct gcggttctga aatggttaca
gaagaatact tgtcccaatt gccatacttg aatgctgttt tccacgaaac tttgagaaaa
cattctccag ctgctttggt tccattgaga tatgctcatg aagatactca attgggtggt
tattacattc cagccggtac tgaaattgcc attaacatct acggttgcaa catggacaaa
caccaatggg aatctccaga agaatggaag ccagaaagat tttggatcc taagtttgac
ccaatggact tgtacaaaac tatggctttt ggtgctggta aaagagtttg cgctggttct
ttacaagcta tgttgattgc ttgtccaacc atcggtagat tggttcaaga atttgaatgg
aagttgagag atggtgaaga agaaaacgtt gatactgttg gtttgaccac ccataagaga
tatccaatgc atgctatttt gaagccaaga tcttaa

TABLE 14-continued

Sequences disclosed herein.
SEQ ID NO: 161 MATLLEHFQA MPFAIPIALA ALSWLFLFYI KVSFFSNKSA QAKLPPVPVV PGLPVIGNLL QLKEKKPYQT FTRWAEEYGP IYSIRTGAST MVVLNTTQVA KEAMVTRYLS ISTRKLSNAL KILTADKCMV AISDYNDFHK MIKRYILSNV LGPSAQKRHR SNRDTLRANV CSRLHSQVKN SPREAVNFRR VFEWELFGIA LKQAFGKDIE KPIYVEELGT TLSRDEIFKV LVLDIMEGAI EVDWRDFFPY LRWIPNTRME TKIQRLYFRR KAVMTALINE QKKRIASGEE INCYIDFLLK EGKTLTMDQI SMLLWETVIE TADTTMVTTE WAMYEVAKDS KRQDRLYQEI QKVCGSEMVT EEYLSQLPYL NAVFHETLRK HSPAALVPLR YAHEDTQLGG YYIPAGTEIA INIYGCNMDK HQWESPEEWK PERFLDPKFD PMDLYKTMAF GAGKRVCAGS LQAMLIACPT IGRLVQEFEW KLRDGEEENV 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 (AAAP) 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 (Mn^{2+}-iron) transporter (Nramp) family transporter, a transient receptor potential Ca^{2+} 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 transporter, or a cation diffusion facilitator (CDF) family transporter.

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

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

(b) 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, 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.

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 adeninivorans, 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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