Production of steviol glycosides in recombinant hosts

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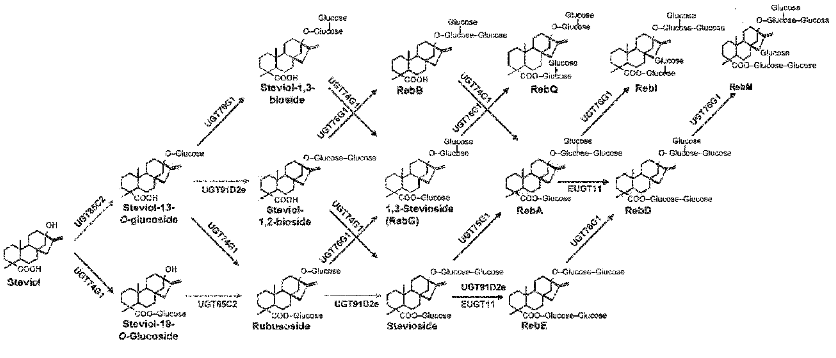
(54) **Title:** PRODUCTION OF STEVIOL GLYCOSIDES IN RECOMBINANT HOSTS

Figure 1



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

PRODUCTION OF STEVSOL GLYCOSIDES IN RECOMBINANT HOSTS

BACKGROUND OF THE INVENTION

Field of the Invention

[0001] 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.

Description of Related Art

[0002] 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.

[0003] Chemical structures for several steviol glycosides are shown in Figure 1, including the diterpene steviol and various steviol glycosides. Extracts of the Stevia plant generally comprise 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.

[0004] 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

[0005] It is against the above background that the present invention provides certain advantages and advancements over the prior art.

[0006] 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.

[0007] In some aspects of the recombinant host disclosed herein, the gene encoding the transporter polypeptide is an endogenous gene.

[0008] 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.

[0009] In some aspects of the recombinant host disclosed herein, the modified expression comprises 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.

[0010] 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.

[0011] 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.

[0012] 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.

[0013] 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.

[0014] In some aspects, the recombinant host further comprises:

(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;

(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.

[0015] In some aspects of the recombinant host disclosed herein, at least one of the genes is codon optimized for expression in the host.

[0016] In some aspects of the recombinant host disclosed herein, at least one of the genes is codon optimized for expression in *Saccharomyces cerevisiae.*

[0017] In some aspects of the recombinant host disclosed herein,

(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 EUGT1 1 polypeptide comprises a polypeptide having at least 65% identity to an amino acid sequence set forth in SEQ ID NO: 148.

[0018] 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.

[0019] 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.

[0020] In some aspects, the fungal cell is a yeast cell.

[0021] 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.

[0022] In some aspects, the yeast cell is a *Saccharomycete.*

[0023] In some aspects, the yeast cell is a ceil from the *Saccharomyces cerevisiae* species.

[0024] The invention further provides a method of producing a steviol glycoside, comprising:

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

wherein the steviol glycoside is synthesized by the host; and

(b) optionally isolating the steviol glycoside.

[0025] In some aspects of the methods disclosed herein, the steviol glycoside is RebA, RebB, RebD, and/or RebM, and wherein:

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

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

(c) RebD is capable of being synthesized in the recombinant host disclosed herein expressing UGT85C2, UGT76G1, UGT74G1, and UGT91D2 and/or EUGT1 1; and

(d) RebM is capable of being synthesized in the recombinant host disclosed herein expressing UGT85C2, UGT76G1, UGT74G1, and UGT91D2 and/or EUGT1 1.

[0026] 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.

[0027] 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.

[0028] The invention further provides a method of increasing production or transport of a steviol glycoside into a culture medium, comprising:

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

wherein the steviol glycoside is synthesized by the host; and

(b) optionally isolating the steviol glycoside.

[0029] In some aspects of the methods disclosed herein, the steviol glycoside is RebA, RebB, RebD, and/or RebM.

[0030] 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.

[0031] 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

[0032] Figure 1 shows the chemical structures and synthesis pathways for various steviol glycosides.

[0033] Figure 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.

[0034] Figure 3A and Figure 3B are bar graphs of the amount (mg/L) of RebA, RebD, or RebM in the supernatant (Figure 3A) or total culture (Figure 3B) of a YGR181W (SEQ ID NO:38) or YDR061W (SEQ ID NO:26) overexpressing strain, compared to a control steviol glycoside-producing strain. *See* Example 4.

[0035] Figure 4A shows levels of 13-SMG (total levels and supernatant levels; µM/Oü 60o), Figure 4B shows levels of RebA (total levels and supernatant levels; µM/OD$_{60}$o), Figure 4C shows levels of RebB (total levels and supernatant levels; µM/OD$_{600}$), Figure 4D shows levels of RebD (total levels and supernatant levels; µM/OD$_{600}$), and Figure 4E shows levels of RebM (total levels and supernatant levels; µM/00 $_{60}$o) in a steviol glycoside-producing S. *cerevisiae* strain with a genomically integrated transporter gene. The genomically integrated transporter genes of Figures 4A-E are YBR043C (SEQ ID NO:88), YEL027W (SEQ ID NO:102), YJL093C (SEQ ID NO:44), YJR106W (SEQ ID NO:48), YMR166C (SEQ ID NO: 132), YIL166C (SEQ ID NO: 121), YKL120W (SEQ ID NO: 126), YDL054C (SEQ ID NO:94), YDL128W (SEQ ID NO:22), YDR536W (SEQ ID NO:30), YGL167C (SEQ ID NO:1 12), YKL146W (SEQ ID NO:127), YKR039W (SEQ ID NO: 129), YOL122C (SEQ ID NO:68), and YPR01 1C (SEQ ID NO:82). *See* Example 6.

[0036] Figure 5A shows supernatant levels of RebA, RebB, RebD, and RebM (in µM/ODeoo) 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. Figure 5B shows total levels of RebA, RebB, RebD, and RebM (in µM/OD$_{60}$o) 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

[0037] All publications, patents and patent applications cited herein are hereby expressly incorporated by reference in their entirety for all purposes.

[0038] 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.

[0039] 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.

[0040] 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.

[0001] 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 (PGR) 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 PGR Protocols: A Guide to Methods and Applications (Innis *et al.,* 1990, Academic Press, San Diego, CA).

[0041] 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.

[0042] 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.

[0043] 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.

[0044] 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.

[0045] 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.

[0046] 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.

[0047] 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, PGR 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* a/., 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.

[0048] 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.

[0049] 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.

[0050] 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), Duicoside 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.

[0051] 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.

[0052] 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.

[0053] 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.

[0054] 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* Figure 1, Example 2).

[0055] 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.*

[0056] 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.

[0057] 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, carophyllenes and derivatives, beta-pinene, beta-sitosterol, and gibberellin.

[0058] As used herein, the terms "detectable amount," "detectable concentration," "measurable amount," and "measurable concentration" refer to a level of steviol glycosides measured in AUC, μM/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).

[0059] 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

[0060] 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.

[0061] 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.

[0062] 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 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.

[0063] 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 a UGT91D2 functional homolog; and/or a gene encoding a EUGT11 polypeptide; wherein experession of one or more of these genes results in production of steviol steviol glycosides such as RebA, RebB, RebD, and/or RebM.

[0064] 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.

[0065] 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.

[0066] 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.

[0067] 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. Biotechnoi. 1:257-279 (1999). In some aspects, MDR transporters transport steviol glycosides.

[0068] 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, SE01, 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 , TP04 and FLR1 (or a functional homolog thereof). In some aspects, MFS transporters transport steviol glycosides.

[0069] 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.

[0070] 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 a/.*, 2001, Plant Cell. 13(7): 1625-8. The MATE family members are sodium or proton antiporters. In some aspects, MATE transporters transport steviol glycosides.

[0071] Additional transporter families include the amino acid/auxin permease (AAAP) family (for example, YKL146W/AVT3, YBL089W/AVT5, YER1 19C/AVT6 and YIL088C/AVT7), the ATPase family (for example, YBL099W/ATP1, YDL185W/VMA1 , YLR447C/VMA6, YOL077W/ATP19, YPL078C/ATP4, YEL027W/VMA3, YKL016C/ATP7, and YOR332W7VMA4), 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/oligosaccharidyi-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 YGL1 14W), 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, YPR01 1C, 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 nucieobasexation symporter-1 (NCS1) family (for example, YBR021W/FUR4), the inorganic phosphate transporter (PiT) family (for example, YBR296C/PH089), the arsenite-antimonite (ArsAB) efflux family (for example, YDL100C/GET3), the MSP 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, YLR41 1W/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.

[0072] 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.

[0073] 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 microorganims 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.

[0074] 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 repiacing 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 microorganim. 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.

[0075] In certain other embodiments, modified expression of a target gene in a recombinant mircroorganism 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.

[0076] 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.

[0077] 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.

[0078] 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), Y1L088C (SEQ ID NO:43), YJL094C (SEQ ID NO:45), YJR106W (SEQ ID NO:48), YKR050W (SEQ ID N0:51), YNL065W (SEQ ID NO:59), YNL083W (SEQ ID N0:61), 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), YPR01 1C (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.

[0079] 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), YFL01 1W (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), YML1 16W (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), YPR01 1C (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.

[0080] 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, Figure 2, and Figure 3.

[0081] 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.

[0082] 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.

[0083] 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.

[0084] 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

[0085] 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.

[0086] 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.

[0087] 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.

[0088] 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.

[0089] 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.

[0090] 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

[0091] 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).

[0092] 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.

[0093] 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.

[0094] 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.

[0095] 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.

[0096] 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.

[0097] 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, Physcomitreila, Rhodoturula, Saccharomyces, Schizosaccharomyces, Sphaceloma, Xanthophyilomyces* or *Yarrowia.* Exemplary species from such genera include *Lentinus tigrinus, Laetiporus sulphureus, Phanerochaete chrysosporium, Pichia pastoris, Cyberlindnera jadinii, Physcomitreila patens, Rhodoturula giutinis, Rhodoturula mucilaginosa, Phaffia rhodozyma, Xanthophyilomyces dendrorhous, Fusarium fujikuroi/Gibberella fujikuroi, Candida utilis, Candida glabrata, Candida albicans,* and *Yarrowia lipolytica.*

[0098] In some embodiments, a microorganism can be a prokaryote such as *Escherichia coli.*

[0099] In some embodiments, a microorganism can be an Ascomycete such as *Gibberella fujikuroi, Kluyveromyces lactis, Schizosaccharomyces pombe, Aspergillus niger, Yarrowia lipolytica, Ashbya gossypii,* or S. *cerevisiae.*

[00100] 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.

[00101] 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.***

[00102] *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.***

[00103] *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

[00104] *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.

[00105] *Agaricus, Gibberella. and Phanerochaete spp.*

[00106] *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 (Blastobotrvs adeninivorans)

[00107] *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 lipolvtica

[00108] *Yarrowia lipolytica* is dimorphic yeast *(see Arxula adeninivorans)* and belongs to the family Hemiascomycetes. The entire genome of *Yarrowia lipolytica* is known. *Yarrowia* species is aerobic and considered to be non-pathogenic. *Yarrowia* is efficient in using hydrophobic substrates *(e.g.* alkanes, fatty acids, oils) and can grow on sugars. It has a high potential for industrial applications and is an oleaginous microorgamism. *Yarrowia lipolyptica* can accumulate lipid content to approximately 40% of its dry cell weight and is a model organism for lipid accumulation and remobilization. *See e.g.,* Nicaud, 2012, *Yeast* 29(10):409-18; Beopoulos *et al.,* 2009, *Biohimie* 91(6):692-6; Bankar *et al.,* 2009, *Appl Microbiol Biotechnol.* 84(5):847-65.

Rhodotorula sp.

[00109] *Rhodotorula* is unicellular, pigmented yeast. The oleaginous red yeast, *Rhodotorula glutinis,* has been shown to produce lipids and carotenoids from crude glycerol (Saenge *et al.,* 2011, *Process Biochemistry* 46(1):210-8). *Rhodotorula toruloides* strains have been shown to be an efficient fed-batch fermentation system for improved biomass and lipid productivity (Li *et al.,* 2007, *Enzyme and Microbial Technology* 41:312-7).

Rhodosporidium toruloides

[00110] *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

[00111] *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)

[00112] *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

[00113] *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

[00114] *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.

[00115] *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

[00116] 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.

[00117] 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.

[00118] 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 stevioi and/or stevioi glycosides. For example, a first microorganism can comprise one or more biosynthesis genes for producing stevioi and null mutations in a first group of endogenous transporters, while a second microorganism comprises stevioi 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.

[00119] 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., stevioi, 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.

[00120] Stevioi glycosides do not necessarily have equivalent performance in different food systems. It is therefore desirable to have the ability to direct the synthesis to stevioi glycoside compositions of choice. Recombinant hosts described herein can produce compositions that are selectively enriched for specific stevioi 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 stevioi glycoside that is consistent from batch to batch. Microorganisms described herein do not produce the undesired plant byproducts found in Stevia extracts. Thus, stevioi glycoside compositions produced by the recombinant microorganisms described herein are distinguishable from compositions derived from *Stevia* plants.

[00121] Stevioi 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 201 1/153378, WO 2013/022989, WO 2014/122227, and WO 2014/122328, each of which has been incorporated by reference in its entirety.

[00122] 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.

[00123] 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. 2007/01 2831 1. In some embodiments, the steviol or steviol glycoside may be provided with a flavor (***e.g.,*** citrus) as a flavor modulator.

[00124] 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.

[00125] 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.

[00126] 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.

[00127] 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.

[00128] 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.

[00129] 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.

[00130] 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.

[00131] The invention will be further described in the following examples, which do not limit the scope of the invention described in the claims.

EXAMPLES

[00132] 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

[00133] 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) sytem. Specific methods used for each system are described below.

[00134] Method A: LC-MS analyses were performed using an UltiMate® 3000 UPLC system (Dionex) fitted with a waters ACQUITY UPLC® BEH shield RP18 column (2.1 x 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)

[00135] 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.

[00136] Method B: A second analytical method was performed on the Agilent system 1290 Infinity fitted with a waters ACQUiTY UPLC® BEH shield RP18 column (2.1 x 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	0.0-1.51min	1289.5	[M-H]$^-$	Steviol	RebM (0.91)

			1289.5281	+ 6 Glucose	
	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)

[00137] 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.

[00138] Method C: A third analytical method used was LC-MS analyses performed using a Waters ACQUITY UPLC (Waters Corporation, Miiford, MA) with Waters ACQUITY UPLC® BEH C18 column (2.1 x 50 mm, 1.7 µm particles, 130 A pore size) coupled to a Waters ACQUITY **TQD** triple quadropoie 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

[00139] 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* K01 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* EUGT1 1 polypeptide (SEQ ID NO: 12; SEQ ID NO: 148), a recombinant gene encoding an SrKAHel 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:1 1, 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/mLJODeoo 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, SrKAHel, 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**

[00140] 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.

[00141] 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 pg/mL or 4-6 µg/mLJOD$_{6}$oo 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, SrKAHe-l, 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

[00142] 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 PGR. 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).

[00143] 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.

[00144] 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 pL of the 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 1.

[00145] 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).

[00146] 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 5A. Transport related genes with over a 40% decrease in Reb A, RebB, RebD or RebM levels compared to a control steviol glycoside-producing strain.

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
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-ATPase	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

Table 5B. Continued list of Transport related genes **with over a 40% decrease in Reb A, RebB, RebD or RebM levels compared to a control steviol glycoside-producing strain.**

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
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 6A. Transport related genes with a 20-40% decrease in Reb A, RebB, RebD or RebM levels compared to a control steviol glycoside-producing strain.

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

Table 6B. Continued list of Transport related genes with a 20-40% decrease in Reb A, RebB, RebD or RebM levels compared to a control steviol glycoside-producing strain.

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
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

[00147] Steviol glycoside exporter candidates were selected from the data based on two selection criteria for each steviol glycoside measured (*i.e.,* two methods of normalizing expression).

[00148] 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.

[00149] 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.

[00150] 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.

[00151] 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), YFL01 1W (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 YPR01 1C (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).

[00152] 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).

[00153] Table 7 represents the calculated ratio, normalized to a steviol glycoside-producing strain comprising genes encoding GGPPS, truncated CDPS, KS, KO, ATR2, EUGT11, SrKAHel, 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, SrKAHel, 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, SrKAHel, 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
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

	Transports cal 1; total vs sup				Transports cal 2; ratio sup/total vs total			
	RebA	RebB	RebD	RebM	RebA	RebB	RebD	RebM
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
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

[00154] 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, SrKAHef , 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, indiciating 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).

[00155] 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).

[00156] 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, SrKAHel, 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, SrKAHel, 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		
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		0.449				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	

	Transporter selection criterion 1 total vs sup				**Transporter selection criterion 2 ratio sup/total vs total**			
	RebA	RebB	RebD	RebM	RebA	RebB	RebD	RebM
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, SrKAHel, 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
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			
YMR166C		0.924						
YNL003C		0.814						
YOR153W	0.801							
YOR316C					0.640			
YOR332W	0.700				0.700			

[00157] 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, SrKAHel, 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, SrKAHel, 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

[00158] 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 experiements. 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 Figure 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.

[00159] 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 Figure 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* Figure 3A. The ratio of transported RebD as compared to the total RebD increased from 0.158 in the control strain to 0.21-0.25 with the candidate genes overexpressed. RebM transport into the culture medium was also simultaneously improved. *See* Figure 3.

Example 5. Overexpression of Selected Yeast Endogenous Transport Genes

[00160] 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 stevtol 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			

	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 stevioi 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

	Increases in Production			
	RebB	RebA	RebD	RebM
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

[00161] 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 PGR 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-Eidin *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. (Figure 4A). YBR043C (SEQ ID NO:88), YEL027W (SEQ ID NO.102), and YMR166C (SEQ ID NO:132) showed improved excretion of RebA (Figure 4B). YBR043C (SEQ ID NO:88), YEL027W (SEQ ID NO:102), and YMR166C (SEQ ID NO:132) showed improved excretion of RebB (Figure 4C). YBR043C of SEQ ID NO:88, YEL027W of SEQ ID NO:102, YJL093C of SEQ ID NO:44, YJR106W of SEQ ID NO:48, and YMR166C of SEQ ID NO:132 showed improved production of RebD, and YBR043C of SEQ ID NO:88, YEL027W of SEQ ID NO:102, YIL166C (SEQ ID NO:121), YJL093C of SEQ ID NO:44, YJR106W of SEQ ID NO:48, and YMR166C of SEQ ID NO:132 showed improved production of RebM, as measured by an increase in RebD and RebM levels in the supernatant compared to a control steviol glycoside-producing strain. *See* Figures 4D and 4E. Controls with a URA marker are also shown in Figure 4.

[00162] Figure 5A shows supernatant levels of RebA, RebB, RebD, and RebM of an additional steviol glycoside-producing strain overexpressing YMR166C (SEQ ID NO:132), YEL027W (SEQ ID NO:102), YKL120W (SEQ ID NO:126), YJR106W (SEQ ID NO:48), YJL093C (SEQ ID NO:44), and YBR043C (SEQ ID NO:88) by the USER cloning system. The strain of Figure 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* K01 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* EUGT1 1 polypeptide (SEQ ID NO:12; SEQ ID NO:148), a recombinant gene encoding an SrKAHel 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:1 1, SEQ ID NO:159) polypeptide. Figure 5B shows total levels of RebA, RebB, RebD, and RebM of the above described steviol glycoside-producing strain overexpressing YMR166C (SEQ ID NO:132), YEL027W (SEQ ID NO:102), YKL120W (SEQ ID NO:126), YIL166C (SEQ ID NO:132), YJR106W (SEQ ID NO:48), YJL093C (SEQ ID NO:44), and YBR043C (SEQ ID NO:88) by the USER cloning system.

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

[00163] 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
gcacacgata 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 gagcagcgac ggaagttttt tgttctcacc agctgccact 720
gcatatgctt **taatgaatac** cggagatgac aggtgtttta gctacatcga. tagaacagta 780
aagaaattca acggcggcgt ccctaatgtt tatccagtgg atctatttga acatatttgg 840
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tgcatggatt atgtaaacag gcattggact gaggacggta tttgttgggc **aaggaactct** 960
gatgtcaaag aggtggacga cacagctatg gcctttagac ttcttaggtt gcacggctac 1020
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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

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 aggaatgatt 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
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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 gaaaagtggg **atcttaatgg** agttcctgaa 1680
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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 KOI (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 730
aagttcgaaa atactattca acaaatgtac atcagaagag aagctgttat gaaatcttta 840
atcaaagagc acaaaaagag aatagcgtca ggcgaaaagc taaatagtta tatcgattac 900
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SEQ ID NO: 5
A. thaliana ATR2 (codon optimized)
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gaattgtctt caatgttgat cgaaaacaga caattcgcca tgatcgtaac tacatcaatc 180
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SEQ ID NO: 6

Stevia rebaudiana KAHel (codon-optimized)

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aagtacggac caatactgca attacaactc ggctacagac gtgttctggt gatttcctca 240
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taa 1503

SEQ ID NO: 7

Stevia rebaudiana CPR8

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SEQ ID NO: 8

Stevia rebaudiana UGT85C2 (codon optimized)

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tactggactc ttgctgcatg cggtttcatg ggtttctatc acatccattc tcttatcgaa     480
aagggttttg ctccactgaa agatgcatca tacttaacca acggctacct ggatactgtt     540
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aactaa 1446

SEQ ID NO: 9
S, rebaudiana UGT74G1 {GenBank AAR06920.1)
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acaacacttg ttaccaccat ccacacctta aactcaaccc taaaccacag taacaccacc 180
accacctcca tcgaaatcca agcaatttcc gatggttgtg atgaaggcgg ttttatgagt 240
gcaggagaat catatttgga aacattcaaa caagttgggt ctaaatcact agctgactta 300
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SEQ ID NO: 10
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SEQ ID NO: 11
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SEQ ID NO: 12
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aaagactaa 1389

SEQ ID NO: 13
YBR180W
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PDSSPSLSAQKAKTKEEEVAVKSSNSQSRDPSPDTQAHIPYTYFSKDQRLI IFGII IFIG
FLGPMSGNIYIPALPLLQREYDVSATTINATVSVFMAVFSVGPLFWGALADFGGRKFLYM
VSLSLMLIVNILLAAVPVNIAAL FVLRIFQAFASSSVISLGAGTVTDVVPPKHRGKAIAY
FMMGPNMGPI IAPIVAGLILMKGNYWRWLFGFTSIMTGIALILVTALLPETLRCIVGNGD
PKWGDKKDERENNESPFFEGNKISHRRLFPDIGIRKPVNNDAFFQENFPKPPKAGLTLYW
KMIKCPPI I ITSVSTALLFSSYYAFSVTFSYYLEHDYRFTMLEIGAAYVCPGVAMLLGSQ
SGGHLSDYLRSRWIKSHPKKKFPAEFRLLLNLIGILLTICGTIGYGWAIFFHYHFVVLLV
FSALTAFGMTWCSNTSMTYLTELFPKRAAGTVAVSSFFRNVGAAISSAI ILQLCNAMGIG
WCFTGLGLCSSISLIGILYLLI FQRKYTAKE F

SEQ ID NO: 14
YAL067C
>sp|P39709|**SE01_YEAST** Probable transporter SEOl OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SE01 PE=1 SV=1
MYSIVKEIIVDPYKRLKWGFIPVKRQVEDLPDDLNSTEIVTISNSIQSHETAENFITTTS
EKDQLHFETSSYSEHKDNVNVTRSYEYRDEADRPWWRFFDEQEYRINEKERSHNKWYSWF
KQGTSFKEKKLLIKLDVLLAFYSCIAYWVKYLDTVNINNAYVSGMKEDLGFQGNDLVHTQ
VMYTVGNI IFQLPFLI YLNKLPLNYVLPSLDLCWSLLTVGAAYVNSVPHLKAIRFFIGAF
EAPSYLAYQYLFGSFYKHDEMVRRSAFYYLGQYIGILSAGGIQSAVYSSLNGVNGLEGWR
WNFI IDAIVSVVVGLIGFYSLPGDPYNCYSIFLTDDEIRLARKRLKENQTGKSDFETKVF
DIKLWKTIFSDWKIYILTLWNIFCWNDSNVSSGAYLLWLKSLKRYSIPKLNQLSMITPGL
GMVYLMLTGI IADKLHSRWFAI IFTQVFNI IGNS ILAAWDVAEGAKWFAFMLQCFGWAMA
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
VPKSENASFAKLTQLINPSISVVFDFAIAVKCFGVGVSYLIIVGDLVPQI VQSIFYRNDD
NMSGSQEHHMFLDRRLYITLI IVFVISPLCFKRSLNSLRYASMIAIVSVAYLSGLIIYHF
VNRHQLERGQVYFMVPHGDSQSHSPLTTLPI FVFAYTCHHNMFSVINEQVDKSFKVIRRI
PIFAIVLAYFLYI IIGGTGYMTFGENIVGNILTLYPNSISTTIGRLAMLLLVMLAFPLQC
HPCRSSVKNII IFIENFRKGKLYDNRASFIPLDNFNSEDPQEAPTQQNNEEPNLRSESLR

HINIITLCILLFSYLLAISITSLAKVLAIVGATGSTSISFTLPGLFGYKLIGSEFTGTNE
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
NLNETGRVLAVGDGIARVFGLNNIQAEELVE FSSGVKGMALNLE PGQVGIVLFGS DRLVK
EGELVKRTGNIVDVPVGPGLLGRVVDALGNPIDGKGPIDAAGRSRAQVKAPGILPRRSVH
EPVQTGLKAVDALVP IGRGQRELI IGDRQTGKTAVALDT ILNQKRWNNGS DESKKLYCVY
VAVGQKRSTVAQLVQTLEQHDAMKYSIIVAATASEAAPLQYLAPFTAASIGEWFRDNGKH
ALIVYDDLSKQAVAYRQLSLLLRRPPGREAYPGDVFYLHSRLLERAAKLSEKEGSGSLTA
LPVIETQGGDVSAYIPTNVISITDGQIFLEAELFYKGIRPAINVGLSVSRVGSAAQVKAL
KQVAGSLKLFLAQYREVAAFAQFGSDLDASTKQTLVRGERLTQLLKQNQYSPLATEEQVP
LIYAGVNGHLDGIELSRIGEFESSFLSYLKSNHNELLTEIREKGELSKELLASLKSATES
FVATF

SEQ ID NO: 17
YBR241C
>sp| P38142|**YB91_YEAST** Probable metabolite transport protein YBR241C OS=Saccharomyces cerevisiae (strain ATCC 204508 / 5288c) GN=YBR241C PE=1 SV=1
MAETERLMPNGGSRETKPLITGHLILGTIVACLGSIQYGYHIAELNAPQEFLSCSRFEAP
DENISYDDTWVGQHGLKQCIALTDSQYGAITSIFSIGGLFGSYYAGNWANRYGRKYVSMG
ASAMCMVSSLLLFFSNSYLQLLFGRFLVGMSCGTAIVITPLFINEIAPVEWRGAMGSMNQ
VSINLGILLTQTLALKYADSYNWRWLLFSGSVIAVANILAWLKVDESPRWLVSHGFVSEA
ETAL FKLRPGTYQQAKQEIQDWQRSHGHNRDPESSEETHSGPTLWQYVTDPSYKKPRTVI
LAILSCQQFCGINSI IFYGVKVIGKILPDYSIQVNFAISILNVVVTLAASAI IDHVGRRP
LLLASTTVMTAMSLLISVGLTLSVSFLLVTAT FVYIAAFAIGLGPIPFLI IGELSYPQDA
ATAQSFGTVCNWLATFIVGYLFPIGHGLMGGYVFAIFAAIAAMFATYVYKRVPETKGKTT
YSEVWAGY

SEQ ID NO: 18
YBR2 94W
>sp|P38359|**SUL1_YEAST** Sulfate permease 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SUL1 PE=1 SV=2
MSRKSSTEYVHNQEDADIEVFESEYRTYRESEAAENRDGLHNGDEENWKVNSSKQKFGVT
KNELSDVLYDS IPAYEESTVTLKEYYDHS IKNNLTAKSAGS YLVSLFPI IKWFPHYNFTW
GYADLVAGITVGCVLVPQSMSYAQIASLSPEYGLYSSFIGAFIYSLFATSKDVCIGPVAV
MSLQTAKVIAEVLKKYPEDQTEVTAPIIATTLCLLCGIVATGLGILRLGFLVELISLNAV
AGFMTGSAFNI IWGQIPALMGYNSLVNTREATYKVVINTLKHLPNTKLDAVFGLI PLVIL
YVWKWWCGTFGITLADRYYRNQPKVANRLKSFYFYAQAMRNAVVIVVFTAISWSITRNKS
SKDRPISILGTVPSGLNEVGVMKIPDGLLSNMSSEIPASI IVLVLEHIAISKSFGRINDY
KVVPDQELIAIGVTNLIGTFFHSYPATGSFSRSALKAKCNVRTPFSGVFTGGCVLLALYC
LTDAFFFIPKATLSAVIIHAVSDLLTSYKTTWTFWKTNPLDCISFIVTVFITVFSSIENG
IYFAMCWSCAMLLLKQAFPAGKFLGRVEVAEVLNPTVQEDIDAVISSNELPNELNKQVKS
TVEVLPAPEYKFS VKWVPFDHGYSRELNINTTVRPPPPGVIVYRLGDSFTYVNCSRHYDI
IFDRIKEETRRGQLITLRKKSDRPWNDPGEWKMPDSLKSLFKFKRHSATTNSDLPISNGS
SNGETYEKPLLKVVCLDFSQVAQVDSTAVQSLVDLRKAVNRYADRQVEFHFAGIISPWIK

RSLL5VKFGTTNEEYSDDSIIAGH5SFHVAKYLKDDYDYIDED5RISTSYSNYETLCAAT
GTNLPFFHIDIPDFSKWDV

SEQ ID NO: 19
YCL069W
>sp|P25594 |¥BA3_YEAST Vacuolar basic amino acid transporter 3
OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YBA3
PE=1 SV=1
MNMLIVGRVVASVGGSGLQTLCFVIGCTMVGERSRPLVISILSCAFAVAAIVGPI IGGAF
TTHVTWRWCFYINLPIGGLAI IMFLLTYKAENKGILQQIKDAIGTISSFTFSKFRHQVNF
KRLMNGII FKFDFFGFALCSAGLVLFLLGLTFGGNKYSWNSGQVIAYLVLGVLLFIFSLV
YDFFLFDKFNPEPDNISYRPLLLRRLVAKPAI IIINMVTFLLCTGYNGQMIYSVQFFQLI
FASSAWKAGLHLIPIVITNVIAAIASGVITKKLGLVKPLLIFGGVLGVIGAGLMTLMTNT
STKSTQIGVLLLPGFSLGFALQASLMSAQLQITKDRPEAAMDFIEVTAFNTFMKSLGTTL
GGVLSTTVFSASFHNKVSRAHLEPYEGKTVDDMILYRLQNYDGSHSTIGNILSDSIKNVF
WMDLGFYALGFLFCSFSSNKKLI IPKKDETPEDNLEDK

SEQ ID NO: 20
YCR028C
>sp|P25621|FEN2__YEAST Pantothenate transporter FEN2 OS=Saccharomyces
cerevisiae (strain ATCC 204508 / 5288c) GN=FEN2 PE=1 SV=1
MMKESKSITQHEVERESVSSKRAIKKRLLLFKIDLFVLSFVCLQYWINYVDRVGFTNAYI
SGMKEDLKMVGNDLTVSNTVFMIGYIVGMVPNNLMLLCVPPRIWLSFCTFAWGLLTLGMY
KVTSFKHICAIRFFQALFESCTFSGTHFVLGSWYKEDELPIRSAIFTGSGLVGSMFSGFM
QTSIFTHLNGRNGLAGWRWLFIIDFCITLPIAI YGFIFFPGLPDQTSAVSKFSMTRYIFN
EQELHYARRRLPARDESTRLDWSTIPRVLKRWHWWMFSLVWVLGGENLGFASNSTFALWL
QNQKYTLAQRNNYPSGIFAVGIVSTLCSAVYMSKI PRARHWHVSVFISLVMVIVAVLIRA
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
MVSLDDILGIVYYVTSWSISMYPPIITNWRHKSASAISMDFVMLNTAGYSYLVISIFLQLY
CWKMTGDESDLGRPKLTQFDFWYCLHGCLMNVVLLTQVVAGARIWRFPGKGHRKMNPWYL
RILLASLAIFSLLTVQFMYSNYWYDWHNSRTLAYCNNLFLLKISMSLIKYIPQVTHNSTR
KSMDCFPIQGVFLDVTGGIASLLQLIWQLSNDQGFSLDTFVTNFGKVGLSMVTLIFNFIF
IMQWFVYRSRGHDLASEYPL

SEQ ID NO:22
YDL128W
>sp|Q99385|VCX1__YEAST Vacuolar calcium ion transporter
OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VCX1
PE=1 SV=1
MDATTPLLTVANSHPARNPKHTAWRAAVYDLQYILKASPLNFLLVFVPLGLIWGHFQLSH
TLTFLFNFLAI IPLAAILANATEELADKAGNTIGGLLNATFGNAVELIVSI IALKKGQVR
IVQASMLGSLLSNLLLVLGLCFI FGGYNRVQQTFNQTAAQTMSSLLAIACASLLI PAAFR

ATLPHGKEDHFIDGKILELSRGTSIVILIVY¥LFLYFQLGSHHALFEQQEEETDE¥MSTI
SRNPHHSLSVKSSLVILLGTTVIISFCADFL¥GTIDN¥VESTGLSKTFIGLI¥IPI¥GNA
AEH¥TS¥LVAMKDKMDLALG¥AIGSSLQ¥AL FVTPFMVLVGWM IDVPMTLNFSTFETATL
FIAVFLSNYLILDGESNWLEGVMSLAMYILIAMAFFYYPDEKTLDSIGNSL

SEQ ID NO:23
YDL185W
>sp|P17255|¥ATA_YEAST V-type proton ATPase catalytic subunit A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=¥MA1 PE=1 S¥=3
MAGAIENARKEIKRISLEDHAESEYGAIYS¥SGP¥¥IAENMIGCAMYEL¥KVGHDNLVGE
VIRIDGDKATIQVYEETAGLTVGDPVLRTGKPLSVELGPGLMETI YDGIQRPLKAIKEES
QSIYIPRGIDTPALDRTIKWQFTPGKFQ¥GDHISGGDIYGS¥FENSLISSHKILLPPRSR
GTITWIAPAGEYTLDEKILEVEFDGKKSDFTLYHTWPVRVPRPVTEKLSADYPLLTGQRV
LDALFPC¥QGGTTCIPGAFGCGKTVISQSLSKYSNSDAII YVGCFAKGTNVLMADGSIEC
IENIE¥GNKVMGKDGRPRE¥IKLPRGRETMYS¥¥QKSQHRAHKSDSSREVPELLKFTCNA
THEL¥¥RTPRS¥RRLSRTIKGVEYFEVITFEMGQKKAPDGRIVEL¥KEVSKSYPISEGPE
RANELVESYRKASNKAYFEWTIEARDLSLLGSHVRKATYQTYAPILYENDHFFDYMQKSK
FHLTIEGPKVLAYLLGLWIGDGLSDRATFSVDSRDTSLMER¥TEYAEKLNLCAEYKDRKE
PQ¥AKT¥NLYSK¥¥RGNGIRNNLNTENPLWDAI¥GLGFLKDG¥KNI PSFLSTDNIGTRET
FLAGLIDSDGYVTDEHGIKATIKTIHTSVRDGLVSLARSLGL¥VSVNAEPAKVDMNGTKH
KISYAIYMSGGDVLLNVLSKCAGSKKFRPAPAAAFARECRGFYFELQELKEDDYYGITLS
DDSDHQFLLANQ¥VVHNCGERGNEMAEVLMEFPELYTEMSGTKEPIMKRTTL¥ANTSNMP
¥AAREASIYTGITLAEYFRDQGKN¥SMIADSSSRWAEALREISGRLGEMPADQGFPAYLG
AKLAS FYERAGKAVALGS PDRTGSVS I¥AA¥S PAGGDFS DP¥TTATLGI TQVFWGLDKKL
AQRKHFPSINTS¥SYSKYTN¥LNKFYDSNYPEFPVLRDRMKEILSNAEELEQ¥VQLVGKS
ALSDSDKITLDVATLIKEDFLQQNGYSTYDAFCPIWKTFDMMRAFISYHDEAQKA¥ANGA
NWSKLADSTGDVKHA¥SSSKFFEPSRGEKEVHGEFEKLLSTMQERFAESTD

SEQ ID NO:24
YDL194W
>sp|P10870|SNF3__YEAST High-affinity glucose transporter SNF3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / 5288c) GN=SNF3 PE=1 SV=3
MDPNSNSSSETLRQEKQGFLDKALQRVKGIALRRNNSNKDHTTDDTTGSIRTPTSLQRQN
SDRQSNMTSVFTDDISTIDDNSILFSEPPQKQSMMMSIC¥G¥FVA¥GGFLFGYDTGLINS
ITSMNYVKSHVAPNHDSFTAQQMSILVSFLSLGTFFGALTAPFISDSYGRKPTI IFSTIF
IFSIGNSLQVGAGGITLLIVGR¥ISGIGIGAISAVVPLYQAEATHKSLRGAI ISTYQWAI
TWGLLVSSAVSQGTHARNDASSYRIPIGLQY¥WSSFLAIGMFFLPESPRYY¥LKDKLDEA
AKSLSFLRGVPVHDSGLLEELVEIKATYDYEASFGSSNFIDCFISSKSRPKQTLRMFTGI
ALQAFQQFSGINFIFYYGVNFFNKTGVSNSYLVSFITYAVNVVFNVPGLFFVEFFGRRKV
LVVGGVIMTIANFIVAI¥GCSLKT¥AAAK¥MIAFICLFIAAFSATWGGV¥W¥ISAELYPL
GVRSKCTAICAAANWLVNFICALITPYI¥DTGSHTSSLGAKI FFIWGSLNAMG¥I VVYLT
¥YETKGLTLEEIDELYIKSSTGV¥SPKFNKDIRERALKFQYDPLQRLEDGKNTFVAKRNN
FDDETPRNDFRNTISGEIDHSPNQKE¥HSIPER¥DIPTSTEILESPNKSSGMT¥P¥SPSL
QDVPIPQTTEPAEIRTKY¥DLGNGLGLNTYNRGPPSLSSDSSEDYTEDEIGGPSSQGDQS
NRSTMNDINDYMARLIHSTSTASNTTDKFSGNQSTLRYHTASSHSDTTEEDSNLMDLGNG
LALNAYNRGPPSILMNSSDEEANGGETSDNLNTAQDLAGMKERMAQFAQSYIDKRGGLEP
ETQSNILSTSLSVMADTNEHNNEILHSSEENATNQPVNENNDLK

SEQ ID NO: 25

YDL210W

>sp|P32837 |UGA4_YEAST GABA-specific permease OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=UGA4 PE=1 SV=1

MSMSSKNENKISVEQRISTDIGQAYQLQGLGSNLRSIRSKTGAGEVNYIDAAKSVNDNQL
LAEIGYKQELKRQFSTLQVFGIAFSIMGLLPSIASVMGGGLGGGPATLVWGWFVAAFFIL
LVGITMAEHASSIPTAGGLYYWTYYYAPEGYKEI ISFI IGCSNSLALAAGVCSIDYGLAE
EIAAAVTLTKDGNFEVTSGKLYGIFAGAVVVMCICTCVASGAIARLQTLSIFANLFIIVL
LFIALPIGTKHRMGGFNDGDFIFGKYENLSDWNNGWQFCLAGFMPAVWTIGSFDSCVHQS
EEAKDAKKSVPIGI ISSIAVCWILGWLI IICLMACINPDIDSVLDSKYGFALAQI IYDSL
GKKWAIAFMSLIAFCQFLMGASITTAVSRQVWAFSRDNGLPLSKYIKRVDSKYSVPFFAI
LAACVGSLILGLLCLIDDAATDALFSLAVAGNNLAWSTPTVFRLTSGRDLFRPGPFYLGK
IWSPIVAWTGVAFQLFII ILVMFPSQQHGITKSTMNYACVIGPGIWILAGI YYKVYKKKY
YHGPATNLSDDDYTEAVGADVIDTIMSKQEP

SEQ ID NO: 26

YDR061W

>sp| Q12298 |YD061__YEAST Uncharacterized ABC transporter ATP-binding protein YDR061W OS=Saccharomyces cerevisiae (strain ATCC 204508 / 5288c) GN=YDR061W PE=1 SV=1

MSTNKFVVRITNALFKSSLASNSPPVYPKRIRHFEILPNEKWVIWGPGKGKFLDVLNNKY
ICEPPLSLRFGFLKESSNILPRIEQVAFKGVMPTAHLSARYEYFKDDYDQTCKQFIFDKA
SGSNAVSYKVETNNRQINMELYNALVENLNLSSLQDRWVMGLSNGQMRRARLARSILKEP
DLLLIDDPFLGLDPAAIATISQFLAKYDSIEVSGGCPIVIGLRYQDTIPAWCTHICCVDE
KNGILFEGPIEKLQSKMDETRSRALKELEQLKKASNSKEDISINDLICIHPMYGKKEHEI
IKMPHLIELDGLSVSYKGEAVLENLHWKVQPGSKWHIRGDNGSGKSTLLSLLTAEHPQSW
NSRVIDNGVPRRTGKTNYFDLNSKIGMSSPELHAI FLKNAGGRLNIRESVATGYHEASSN
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
PLTFFPKNILFQFHNFANIYFLILLILGAFQIFGVTNPGFASVPLIVIVI ITAIKDGIED
SRRTVLDLEVNNTRTHILSGVKNENVAVDNVSLWRRFKKANTRALIKIFEYFSENLTAAG
REKKLQKKREELRRKRNSRSFGPRGSLDSIGSYRMSADFGRPSLDYENLNQTMSQANRYN
DGENLVDRTLQPNPECRFAKDYWKNVKVGDIVRVHNNDEIPADMILLSTSDVDGACYVET
KNLDGETNLKVRQSLKCSKIIKSSRDITRTKFWVESEGPHANLYSYQGNFKWQDTQNGNI
RNEPVNINNLLLRGCTLRNTKWAMGMVIFTGDDTKIMINAGVTPTKKSRISRELNFSVIL
NFVLLFILCFTAGIVNGVYYKQKPRSRDYFEFGTIGGSASTNGFVSFWVAVILYQSLVPI
SLYISVEI IKTAQAIFIYTDVLLYNAKLDYPCTPKSWNISDDLGQIEYIFSDKTGTLTQN
VMEFKKCTINGVSYGRAYTEALAGLRKRQGVDVESEGRREKEEIAKDRETMIDELRSMSD
NTQFCPEDLTFVSKEIVEDLKGSSGDHQQKCCEHFLLALALCHSVLVEPNKDDPKKLDIK
AQSPDESALVSTARQLGYSFVGSSKSGLIVEIQGVQKEFQVLNVLEFNSSRKRMSCI IKI
PGSTPKDEPKALLICKGADSVIYSRLDRTQNDATLLEKTALHLEEYATEGLRTLCLAQRE
LTWSEYERWVKTYDVAAASVTNREEELDKVTDVIERELILLGGTAIEDRLQDGVPDSIAL

LAEAGIKLWVLTGDKVETAINIGFSCNVLNNDMELLVVKASGEDVEEFGSDPIQVVNNLV
TKYLREKFGMSGSEEELKEAKREHGLPQGNFAVI IDGDALKVALNGEEMRRKFLLLCKNC
KAVLCCRVSPAQKAAVVKLVKKTLDVMTLAIGDGSNDVAMIQSADVGVGIAGEEGRQAVM
CSDYAIGQFRYVTRLVLVHGKWCYKRLAEMI PQFFYKNVI FTLSLFWYGI YNNFDGSYLF
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=YDR338C
PE=1 SV=1
MAGILSKTLSEVHPSLRTNGMGIGNTHRRISLGFLPPNKKNPLVRKFRARTRNIDQRSFR
SLTDDFGSNVHEPNPYLGNIDEEPDLYYHDEEDGELSRTISLPSRVSETPELSPQDVDWI
LHEHERRYSSVCNSDNEEASQSNTPDRIQEYSGRELEYDEFMNRLQAQKQKLTRSAVTDA
KGTSHHRRPSFVSVTSRGSVPTIYQEIDENDSEALAELAHSHVTFKSEARVLASYSFPLI
FTFLLEQIFPMVCSLTVGHLGKNELAAVSLASMTSNITLAIFEGIATSLDTLCPQAYGSG
RFYSVGVHLQRCIAFSLVI YIPFAVMWWYSEPLLSYI IPEKELINLTSRFLRVLILGAPA
YIFFENLKRFLQAQGIFDAGI YVLTICAPLNVLVSYTLVWNKYIGVGFIGAAIAVVLNFW
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
IRKHYRGEVVYNAESDIHLPHLTVYQTLFTVARMKTPQNRIKGVDREAYANHVTEVAMAT
YGLSHTRDTKVGNDLVRGVSGGERKRVSIAEVAICGARFQCWDNATRGLDSATALEFIRA
LKTQADIGKTAATVAIYQCSQDAYDLFDKVCVLDDGYQLYFGPAKDAKKYFQDMGYYCPP
RQTTADFLTSITSPTERI ISKEFIEKGTRVPQTPKDMAEYWLQSESYKNLIKDIDSTLEK
NTDEARNI1RDAHHAKQAKRAPPS SPYVVNYGMQVKYLL IRNFWRMKQSASVTLWQVI GN
SVMAFILGSMFYKVMKKNDTSTFYFRGAAMFFAILFNAFSCLLEI FSLYETRPITEKHRT
YSLYHPSADAFASVLSEMPPKLITAVCFNIIFYFLVDFRRNGGVFFFYFLINVIATFTLS
HLFRCVGSLTKTLQEAMVPASMLLLAISMYTGFAIPKTKILGWSIWIWYINPLAYLFESL
MINEFHDRRFPCAQYI PAGPAYQNITGTQRVCSAVGAYPGNDYVLGDDFLKESYDYEHKH
KWRGFGIGMAYVVFFFFVYLILCEYNEGAKQKGEMVVFLRSKIKQLKKEGKLQEKHRPGD
IENNAGSSPDSATTEKKILDDSSEGSDSSSDNAGLGLSKSEAIFHWRDLCYDVPIKGGQR
RILNNVDGWVKPGTLTALMGASGAGKTTLLDCLAERVTMGVITGNI FVDGRLRDESFPRS
IGYCQQQDLHLKTATVRESLRFSAYLRQPSSVSIEEKNRYVEEVIKILEMQQYSDAVVGV
AGEGLNVEQRKRLTIGVELAARPKLLVFLDEPTSGLDSQTAWDTCQLMRKLATHGQAILC
TIHQPSAILMQQFDRLLFLQKGGQTVYFGDLGEGCKTMIDYFESKGAHKCPPDANPAEWM

LEVVGAAPGSHATQDYNEVWRNSDEYKAVQEELDWMEKNLPGRSKEPTAEEHKPFAASLY
YQFKMVTIRLFQQYWRSPDYLWSKFILTIFNQVFIGFTFFKADRSLQGLQNQMLSIFMYT
V IFNPILQQYLPSFVQQRDLYEARERPSRTFSWLAFFLSQI IVEI PWNILAGTIAYCI YY
YAVGFYANASAAGQLHERGALFWLFSIAFYVYIGSMGLLMISFNEVAETAAHMGTLLFTM
ALSFCGVMATPKVMPRFWIFMYRVSPLTYMI DALLALGVANVDVKCSNYEMVKFTPPSGT
TCGDYMASYIKLAGTGYLSDPSATDICSFCAVSTTNAFLATFSSHYYRRWRNYGIFICYI
AFDYIAATFLYWLSRVPKKNGKISEKPKK

SEQ ID NO: 30
YDR536W
>sp|P39932 |STL1_YEAST Sugar transporter STLl OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=STL1 PE=1 SV=2
MKDLKLSNFKGKFISRTSHWGLTGKKLRYFITIASMTGFSLFGYDQGLMASLITGKQFNY
EFPATKENGDHDRHATVVQGATTSCYELGCFAGSLFVMFCGERIGRKPLILMGSVITIIG
AVISTCAFRGYWALGQFI IGRVVTGVGTGLNTSTI PVWQSEMSKAENRGLLVNLEGSTIA
FGTMIAYWIDFGLSYTNSSVQWRFPVSMQIVFALFLLAFMIKLPESPRWLISQSRTEEAR
YLVGTLDDADPNDEEVITEVAMLHDAVNRTKHEKHSLSSLFSRGRSQNLQRALIAASTQF
FQQFTGCNAAIYYSTVLFNKTIKLDYRLSMIIGGVFATIYALSTIGSFFLIEKLGRRKLF
LLGATGQAVSFTITFACLVKENKENARGAAVGLFLFITFFGLSLLSLPWIYPPEIASMKV
RASTNAFSTCTNWLCNFAVVMFTPIFIGQSGWGCYLFFAVMNYLYIPVIFFFYPETAGRS
LEEIDI IFAKAYEDGTQPWRVANHLPKLSLQEVEDHANALGSYDDEMEKEDFGEDRVEDT
YNQINGDNSSSSSNIKNEDTVNDKANFEG

SEQ ID NO: 31
YEL031W
>sp|P3998 6|ATC6_YEAST Manganese-transporting ATPase 1 OS=Saccharomyces cerevisiae {strain ATCC 204508 / S288c) GN=SPF1 PE=1 SV=1
MTKKSFVSSPIVRDSTLLVPKSLIAKPYVLPFFPLYATFAQLYFQQYDRYIKGPEWTFVY
LGTLVSLNILVMLMPAWNVKIKAKFNYSTTKNVNEATHILIYTTPNNGSDGIVEIQRVTE
AGSLQTFFQFQKKRFLWHENEQVFSSPKFLVDESPKIGDFQKCKGHSGDLTHLKRLYGEN
SFDIPIPTFMELFKEHAVAPLFVFQVFCVALWLLDEFWYYSLFNLFMIISMEAAAVFQRL
TALKEFRTMGIKPYTINVFRNKKWVALQTNELLPMDLVSITRTAEESAIPCDLILLDGSA
IVNEAMLSGESTPLLKESIKLRPSEDNLQLDGVDKIAVLHGGTKALQVTPPEHKSDI PPP
PDGGALAI VTKTGFETSQGSLVRVMI YSAERVSVDNKEALMFILFLLIFAVIASWYVWVE
GTKMGRIQSKLILDCILI ITSVVPPELPMELTMAVNSSLAALAKFYVYCTEPFRI PFAGR
IDVCCFDKTGTLTGEDLVFEGLAGISADSENIRHLYSAAEAPESTILVIGAAHALVKLED
GDIVGDPMEKATLKAVGWAVERKNSNYREGTGKLDIIRRFQFSSALKRSASIASHNDALF
AAVKGAPETIRERLSDIPKNYDEIYKSFTRSGSRVLALASKSLPKMSQSKIDDLNRDDVE
SELTFNGFLIFHCPLKDDAIETIKMLNESSHRSIMITGDNPLTAVHVAKEVGIVFGETLI
LDRAGKSDDNQLLFRDVEETVS IPFDPSKDTFDHSKLFDRYDIAVTGYALNALEGHSQLR
DLLRHTWVYARVSPSQKEFLLNTLKDMGYQTLMCGDGTNDVGALKQAHVGIALLNGTEEG
LKKLGEQRRLEGMKMMYIKQTEFMARWNQPQPPVPEPIAHLFPPGPKNPHYLKALESKGT
VITPEIRKAVEEANSKPVEVIKPNGLSEKKPADLASLLLNSAGDAQGDEAPALKLGDASC
AAPFTSKLANVSAVTNI IRQGRCALVNTIQMYKILALNCLISAYSLSI IYMAGVKFGDGQ
ATVSGLLLSVCFLSISRGKPLEKLSKQRPQSGIFNVYIMGSILSQFAVHIATLVYITTEI
YKLEPREPQVDLEKEFAPSLLNTGIFIIQLVQQVSTFAVNYQGEPFRENIRSNKGMYYGL
LGVTGLALASATEFLPELNEAMKFVPMTDDFKIKLTLTLLLDFFGSWGVEHFFKFFFMDD
KPSDISVQQVKIASK

SEQ ID NO: 32

YER166W
>spi P32660 !A?C5_YEAST Phospholipid- transporting ATPase DNF1
OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=DNF1
PE=1 SV=2
MSGTFHGDGHAPMSPFEDTFQFEDNSSNEDTHIAPTHFDDGATSNKYSRPQVSFNDETPK
NKRE DAEEFTFNDDTEYDNHSFQPTPKLNNGSGTFDDVELDNDSGEPHTNYDGMKRFRMG
TKRNKKGNPIMGRSKTLKWARKNIPNPFEDFTKDDIDPGAINRAQELRTVYYNMPLPKDM
IDEEGNPIMQYPRNKIRTTKYTPLTFLPKNILFQFHNFANVYFLVLIILGAFQIFGVTNP
GLSAVPLVVIVI ITAIKDAIEDSRRTVLDLEVNNTKTHILEGVENENVSTDNISLWRRFK
KANSRLLFKFIQYCKEHLTEEGKKKRMQRKRHELRVQKTVGTSGPRSSLDSIDSYRVSAD
YGRPSLDYDNLEQGAGEANIVDRSLPPRTDCKFAKNYWKGVKVGDIVRIHNNDEI PADII
LLSTSDTDGACYVETKNLDGETNLKVRQSLKCTNTIRTSKDIARTKFWIESEGPHSNLYT
YQGNMKWRNLADGEIRNEPITINNVLLRGCTLRNTKWAMGVVMFTGGDTKIMLNSGITPT
KKSRISRELNFSVVINFVLLFILCFVSGIANGVYYDKKGRSRFSYEFGTIAGSAATNGFV
SFWVAVILYQSLVPISLYISVEIIKTAQAAFIYGDVLLYNAKLDYPCTPKSWNISDDLGQ
VEYIFSDKTGTLTQNVMEFKKCTINGVSYGRAYTEALAGLRKRQGIDVETEGRREKAEIA
KDRDTMIDELRALSGNSQFYPEEVTFVSKEFVRDLKGASGEVQQRCCEHFMLALALCHSV
LVEANPDNPKKLDLKAQSPDEAALVATARDVGFSFVGKTKKGLIIEMQGIQKEFEILNIL
EFNSSRKRMSCIVKI PGLNPGDEPRALLICKGADS IIYSRLSRQSGSNSEAILEKTALHL
EQYATEGLRTLCIAQRELSWSEYEKWNEKYDIAAASLANREDELEVVADSIERELILLGG
TAIEDRLQDGVPDCIELLAEAGIKLWVLTGDKVETAINIGFSCNLLNNEMELLVIKTTGD
DVKEFGSEPSEIVDALLSKYLKEYFNLTGSEEEIFEAKKDHEFPKGNYAIVIDGDALKLA
LYGEDIRRKFLLLCKNCRAVLCCRVSPSQKAAVVKLVKDSLDVMTLAIGDGSNDVAMIQS
ADVGIGIAGEEGRQAVMCSDYAIGQFRYLARLVLVHGRWSYKRLAEMIPEFFYKNMIFAL
ALFWYGIYNDFDGSYLYEYTYMMFYNLAFTSLPVI FLGILDQDVNDTISLVVPQLYRVGI
LRKEWNQRKFLWYMLDGLYQSIICFFFPYLVYHKNMIVTSNGLGLDHRYFVGVYVTTIAV
ISCNTYVLLHQYRWDWFSGLFIALSCLVVFAWTGIWSSAIASREFFKAAARI YGAPSFWA
VFFVAVLFCLLPRFTYDSFQKFFYPTDVEIVREMWQHGHFDHYPPGYDPTDPNRPKVTKA
GQHGEKI IEGIALSDNLGGSNYSRDSVVTEEIPMTFMHGEDGSPSGYQKQETWMTSPKET
QDLLQSPQFQQAQTFGRGPSTNVRSSLDRTREQMIATNQLDNRYSVERARTSLDLPGVTN
AASLIGTQQNN

SEQ ID NO: 33
YFL011W
>sp| P43581 IHXT10JYEAST Kexcse transporter HXT10 OS=Saccharomyces
cerevisiae (strain ATCC 204508 / S288c) GN=HXT10 PE=1 SV=1
MVSSSVSILGTSAKASTSLSRKDEIKLTPETREASLDIPYKPIIAYWTVMGLCLMIAFGG
FIFGWDTGTISGFINQTDFKRRFGELQRDGSFQLSDVRTGLIVGI FNIGCALGGLTLGRL
GDIYGRKIGLMCVILVYWGIVIQIASSDKWYQYFIGRIVSGMGVGGVAVLSPTLISEIS
PKHLRGTCVSFYQLMITLGIFLGYCTNYGTKKYSNSIQWRVPLGLCFAWAIFMVIGMVMV
PESPRYLVEKGKYEEARRSLAKSNKVTVTDPGVVFEFDTIVANMELERAVGNASWHELFS
NKGAILPRVIMGIVIQSLQQLTGCNYFFYYGTTIFNAVGMQDSFETSIVLGAVNFASTFV
ALYIVDKFGRRKCLLWGSASMAICFVIFATVGVTRLWPQGKDQPSSQSAGNVMIVFTCFF
IFSFAITWAPIAYVIVAETYPLRVKNRAMAIAVGANWMWGFLIGFFTPFITRSIGFSYGY
VFMGCLI FSYFYVFFFVCETKGLTLEEVNEMYEERIKPWKSGGWI PSSRRTPQPTSSTPL
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

SLFKYLKT DKNAGISLPEISNYRKTNRYKNYGDNS LPERI PKSFLQLVWAAFNDKTMQLL
TVAAVVSFVLGLYELWMQPPQYDPEGNKIKQVDWIEGVAIMIAVFVVVLVSAANDYQKEL
QFAKLNKKKENRKIIVIRNDQEILISIHHVLVGDVISLQTGDVVPADCVMISGKCEADES
SITGESNTIQKFPVDNSLRDFKKFNSIDSHNHSKPLDIGDVNEDGNKIADCMLISGSRIL
SGLGRGVITSVGINSVYGQTMTSLNAEPESTPLQLHLSQLADNISVYGCVSAI ILFLVLF
TRYLFYII PEDGRFHDLDPAQKGSKFMNIFITSITVI VVAVPEGLPLAVTLALAFATTRM
TKDGNLVRVLRSCETMGSATAVCSDKTGTLTENVMTVVRGFPGNSKFDDSKSLPVSEQRK
LNSKKVFEENCSSSLRNDLLANIVLNSTAFENRDYKKNDKNTNGSKNMSKNLSFLDKCKS
RLSFFKKGNREDDEDQLFKNVNKGRQEPFIGSKTETALLSLARLSLGLQPGELQYLRDQP
MEKFNIEKVVQTIPFESSRKWAGLVVKYKEGKNKKPFYRFFIKGAAEIVSKNCSYKRNSD
DTLEEINEDNKKETDDEIKNLASDALRAISVAHKDFCECDSWPPEQLRDKDSPNIAALDL
LFNSQKGLILDGLLGIQDPLRAGVRESVQQCQRAGVTVRMVTGDNILTAKAIARNCAILS
TDISSEAYSAMEGTEFRKLTKNERIRILPNLRVLARSSPEDKRLLVETLKGMGDVVAVTG
DGTNDAPALKLADVGFSMGISGTEVAREASDIILMTDDFSAIVNAIKWGRCVSVSIKKFI
QFQLIVNITAVILTFVSSVASSDETSVLTAVQLLWINLIMDTLAALALATDKPDPNIMDR
KPRGRSTSLISVSTWKMILSQATLQLIVTFILHFYGPELFFKKHEDEITSHQQQLNAMT
FNTFVWLQFFTMLVSRKLDEGDGISNWRGRISAANLNFFQDLGRNYYFLTIMAIIGSCQV
LIMFFGGAPFSIARQTKSMWITAVLCGMLSLIMGVLVRICPDEVAVKVFPAAFVQRFKYV
FGLEFLRKNHTGKHDDEEALLEESDSPESTAFY

SEQ ID NO: 35
YGL013C
>sp|P12383|PDR1___YEAST Transcription factor PDRl OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PDR1 PE=1 SV=2
MRGLTPKNGVHIETGPDTESSADSSNFSTGFSGKIRKPRSKVSKACDNCRKRKIKCNGKF
PCASCEIYSCECTFSTRQGGARIKNLHKTSLEGTTVQVKEETDSSSTSFSNPQRCTDGPC
AVEQPTKFFENFKLGGRSSGDNSGSDGKNDDDVNRNGFYEDDSESQATLTSLQTTLKNLK
EMAHLGTHVTSAIESIELQISDLLKRWEPKVRTKELATTKFYPNKSIETQLMKNKYCDVV
HLTRYAAWSNNKKDQDTSSQPLIDEIFGLYSPFQFLSLQGIGKCFQNYRSKSKCEIFPRT
AKETIYIMLRFFDVCFHHINQGCVSIANPLENYLQKMNLLPSTPSSISSAGSPNTAHTKS
HVALVINHLPQPFVRNITGISNSELLSEMNNDISMFGILLKMLDMHKNSYQNFLMEITSN
PSVAKNTQSIDVLQEFIHYCQAGEALIALCYSYYNSTLYNYVDFTCDITHLEQLLYFLDL
LFWLSEIYGFEKVLNVAVHFVSRVGLSRWEFYVGLDENFAERRRNLWWKAFYFEKTLASK
LGYPSNIDDSKINCLLPKNFRDVGFLDNRDFIENVHLVRRSEAFDNMCISDLKYYGELAV
LQIVSHFSSSVLFNEKFTSIRNTSKPSVVREKLLFEVLEIFNETEMKYDAIKEQTGKLFD
IAFSKDSTELKVSREDKIMASKFVLFYEHHFCRMVNESDNIVARLCVHRRPSILIENLKI
YLHKIYKSWTDMNKILLDFDNDYSVYRSFAHYSISCIILVSQAFSVAEFIKVNDVVNMIR
VFKRFLDIKIFSENETNEHVFNSQSFKDYTRAFSFLTIVTRIMLLAYGESSSTNLDVISK
YIDENAPDLKGI IELVLDTNSCAYRFLLEPVQKSGFHLTVSQMLKNRKFQEPLMSNEDNK
QMKHNSGKNLNPDLPSLKTGTSCLLNGIESPQLPFNGRSAPSPVRNNSLPEFAQLPSFRS
LSVSDMINPDYAQPTNGQNNTQVQSNKPINAQQQIPTSVQVPFMNTNEINNNNNNNNNNK
NNINNINNNNSNNFSATSFNLGTLDEFVNNGDLEDLYSILWSDVYPDS

SEQ ID NO: 36
YGL255W
>sp|P32804|ZRT1__YEAST Zinc-regulated transporter 1 0S=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ZRT1 PE=1 SV=1
MSNVTTPWWKQWDPSEVTLADKTPDDVWKTCVLQGVYFGGNEYNGNLGARISSVFVILFV
STFFTMFPLISTKVKRLRIPLYVYLFAKYFGSGVIVATAFIHLMDPAYGAIGGTTCVGQT
GNWGLYSWCPAIMLTSLTFTFLTDLFSSVWVERKYGLSHDHTHDEIKDTVVRNTAAVSSE
NDNENGTANGSHDTKNGVEYYEDSDATSMDVVQSFQAQFYAFLILEFGVIFHSVMIGLNL
GSVGDEFSSLYPVLVFHQSFEGLGIGARLSAIEFPRSKRWWPWALCVAYGLTTPICVAIG

LG¥RTRY¥5G5YTAL¥I5G¥LDAI5AGILLYTGL¥ELLARDFIFNPQRIKDLRELSFN¥I
CTLFGAG IMALIGKWA

SEQ ID NO: 37
YGR125W
>sp|P53273|YG35__YEAST Uncharacterized vacuolar membrane protein YGR125W OS=Saccharomyces cerevisiae (strain ATCC 204508 / 5288c) GN=YGR125W PE-1 S¥=l
MGRTIRRRRSNSSLSEAIS¥SLGINQDSS¥NKMHRAS¥SAMSPPLCRSYMSGFFTGGNSP
MINNLSDSKLPISNKQHPK¥IHGSENLHRQTAQLSNEFCSSS¥EENSPTIKDYMDI IGNG
DRKDDQSMRTIEENIDEEYSDEYSRLLLSPASSN¥DDDRNRGLQNSSLPELEDGYAGGYQ
SLRPSHNLRFRPRNLWHMCTSFPSKFAHYLPAA¥LGLLLNILDALSYGMIIFPITEPVFS
HLGPTGISMFYISTI ISQA¥YSGGWSSFPSGIGSEMIEITPFYHTMALAIKEALAGNDDE
IITTTIFCY¥ISSMLTG¥¥FYALGKLRLGKI¥GFFPRHILIGCIGG¥GYFLI ITGIEVTT
R¥AKFEYSWPFFSGLFTDYDTLAKWLLPVLLT¥¥LIGTQRYFKNSL¥LPSFYILTLVLFH
FIVAIIPTLSLDALRQAGWI FPIANS DSKWYDHYRLFN¥HK¥HWSL¥LQQI PTMMALTFF
GILH¥PIN¥PALAMSLQMDKYDVDRELIAHGYSNFFSGLLGS¥QNYL¥YTNS¥LFIRAGA
DSPFAGFLLIALTICIMI IGP¥I ISFIPICI¥GSLIFLLGYELL¥EAL¥DTWNKLNRFEY
LTV¥II¥FTMGIFDF¥LGII¥GILIACFSFL¥DSTKLQTINGEYNGN¥ARST¥YRDYVQT
KFLDGIGEQI Y¥LKLQNLLFFGTIISIEEKIERLLQISNKDATKRRIKYLILDFKNINAD
NIDYSAAEGFNRIKRFTETKRIKLI ISSIKERDRIYNAFNN¥GLLND¥ELFADLNSALEW
CENEFLFQYKQLRKKAKERLEEGKQNN¥¥SA¥IAATKNKKIDTIGNGLNRGSNGDTARNL
MSLPTNTPRNYQILS¥AQNVF¥NDEQA¥KNFKKEYKDDEP¥LPILLFALKQYRPDIISE¥
QKVREKEIKFWAQLCPYFTRRRLASQSHLLHADNIFFL¥ETGMLKATYELPQGTLYEIFS
NGTCFGKIIAPGNAMPREQKLTIETETDS¥LW¥IDSSSLNKLKEDNLALYVE¥ALM¥MCI
KDTRFKELLGYTL¥SA

SEQ ID NO: 38
YGR181W
>sp|P53299|TIM13__YEAST Mitochondrial import inner membrane translocase subunit TIM13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / 5288c) GN=TIM13 PE=1 S¥=l
MGLSSI FGGGAPSQQKEAATTAKTTPNPIAKELKNQIAQELA¥ANATEL¥NKISENCFEK
CLTSPYATRNDACIDQCLAKYMRSWN¥ISKAYISRIQNASASGEI

SEQ ID NO: 39
YGR217W
>sp|P50077|CCH1___YEAST Calcium-channel protein CCHl OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CCH1 PE=1 S¥=l
MQGRKRTLTEPFEPNTNPFGDNAAVMTEN¥EDNSETDGNRLESKPQAL¥PPALNIVPPES
SIHSTEEKKGDEYNGNDKDSSLISNIFRTRVGRSSHENLSRPKLSLKTASFGAAESSRRN
¥SPSTKSAKSSSQYIDLNDERLRRRSFSSYSRSSSRRVSNSPSSTDRPPRSAK¥LSLIAA
DDMDDFEDLQKGFKSAIDEEGLTWLPQLKSEKSRP¥SD¥GEDRGEGEQESIPD¥HTPN¥G
ASATPGSIHLTPEPAQNGSVSEGLEGSINNSRKKPSPKFFHHLSPQKEDKDQTE¥IEYAE
DILDFETLQRKLESRPFVLYGHSLGVFSPTNPLRIKIARFLLHRRYSLLYNTLLTFYAIL
LAIRTYNPHN¥¥FLYRFSNWTDYFIFILSACFTGNDIAKIIAFGFWDDSEMFKAYGREYK
SILQRSGIMKLYIYLREKYGRKLIDFII PFRIISPGEETKYQRSSLSTSLTKPYGAKENQ
RPFGTPRAFARSSWNRIDL¥SS¥SFWLGMFLSIKSYDTKTGIRIFKPLAILRILRLVN¥D
TGMPSILRGLKYGI PQL¥NVSSML¥YFWIFFGILG¥QIFQGSFRRQCVWFNPEDPTDTYQ

YDMQFCGGYLDP¥TKRKQNYIYEDGSEGSY5KGFLCPQY5KC¥5NANPYNGRI5FDNI¥N
SMELVFVIMSANTFTDLMYYTMDSDEMAACLFFIVCIFVLTIWLLNLLIAVLVSSFEIAN
EEYKKKKFIYGSRKTGYVARIVTGYWKYFKLKANQTKFPNWSQKGLAIYSHVEFIFVILI
ICDIGMRASVKVSTSANCNNILLKTDRGISIVLFIESLARLVLYLPNMWKFLTKPSYVYD
FIISII TLVI SCLAVEGVLGHMYAWLS IFHI SRFYRVI ISFNLTKKLWKQI LSNGVMI WN
LSSFYFFFTFLVAIIMAVYFEGVIPPEEMADQPFGMYSLPNSFLSLFIIGSTENWTDILY
ALQKHSPNISSTFFCSVFFI IWFLLSNSVILNIFIALISESMEVKEEEKRPQQIKHYLKF
VYPQKIQEYTHASLVARIRKKFFGGHRNEDTRDFKQFLMRGTAIMNIAQNMGELADEFKE
PPSENLFKKGLSKLTIGVPSLKRLRMFANNPFYKNSDVVFTETNDINGRTYILELNEYED
EKLDYLKKYPLFNYSYYFFSPQHRFRRFCQRLVPPSTGKRTDGSRFFEDSTDLYNKRSYF
HHIERDVFVFIFALATILLIVCSCYVTPLYRMHHKMGTWNWSSALDCAFIGAFSIEFIVK
TVADGFIYSPNAYLRNPWNFIDFCVLISMWINLIAYLKNNGNLSRIFKGLTALRALRCLT
ISNTARQTFNLVMFDGLNKIFEAGLISLSLLFPFTVWGLSIFKGRLGTCNDGSLGRADCY
NEYSNSVFQWDIMSPRVYQQPYLHLDSFASAFSSLYQIISLEGWVDLLENMMNSSGIGTP
ATVMGSAGNALFLVLFNFLSMVFILNLFVSFIVNNQARTTGSAYFTIEEKAWLESQKLLS
QAKPKAI PNL IELSRVRQ FFYQLAVEKKN FYYAS FLQVVL YLHI IMLL3RSYN PGNLIGY
QGVYFMFSTSVFLIQEALHMCGEGPRLYFRQKWNSIRLSIII IAFIMNAVAFHVPASHYW
FHNIKGFFLLVIFLFI IPQNDTLTELLETAMASLPPILSLTYTWGVLFLVYAIALNQIFG
LTRLGSNTTDNINFRTVIKSMIVLFRCSFGEGWNYIMADLTVSEPYCSSDDNSTYTDCGS
ETYAYLLLMSWNIISMYIFVNMFVSLI IGNFSYVYRSGGSRSGINRSEIKKYIEAWSKFD
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
FYNPGLSTFQETMDNIRKFPSQFIEIVRNVAYHLLKIKGFSKLNGWRKPFMELI FMYDII
EFVFCSAGFTCILLAFTFGGNRYAWNSASI I ILFIIGIVLWLAGIYDFLVFPKFNIVKA
TPHYQPLMSWTNIKKPGIFTVNIALFLTCAGYISQFTYIVQYFQLIYNDSAWRAAVHLVA
CIISTVVTAILCGAITDKTRQIKPIIVISSIFGVVGAGILTLLNNNANNSAHIGLLILPG
VAFGGLAQSSMLASQIQLDKKSPTFRSDFVSITTFNTFCKNLGQALGGVISNTVFSAAAI
KKLTKANIQLPDGTTVDNLVIYRQTNFDGSHSKLGNIISESLTDVFYMALGFYALSLIFA
VFASNKKVTASLR

SEQ ID NO: 41
YGR281W
>sp|P53049 ɪYORl__YEAST Oligomycin resistance ATP-dependent permease YORl OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YORl PE=1 SV=1
MTITVGDAVSETELENKSQNVVLSPKASASSDISTDVDKDTSSSWDDKSLLPTGEYIVDR
NKPQTYLNSDDIEKVTESDIFPQKRLFSFLHSKKIPEVPQTDDERKIYPLFHTNI ISNMF
FWWVLPILRVGYKRTIQPNDLFKMDPRMSIETLYDDFEKNMIYYFEKTRKKYRKRHPEAT
EEEVMENAKLPKHTVLRALLFTFKKQYFMSIVFAILANCTSGFNPMITKRLIEFVEEKAI
FHSMHVNKGIGYAIGACLMMFVNGLTFNHFFHTSQLTGVQAKSILTKAAMKKMFNASNYA

RHCFPNGKVISFVTTDLARIEFALSFQPFLAGFPAILAICIVLLIVNLGPIALYGIGIFF
GGFFISLFAFKLILGFRIAANIFTDARVTMMREVLNNIKMIKYYTWEDAYEKNIQDIRTK
EISKVRKMQLSRNFLIAMAMSLPSIASLVTFLAMYKVNKGGRQPGNIFASLSLFQVLSLQ
MFFLPIAIGTGIDMIIGLGRLQSLLEAPEDDPNQMIEMKPSPGFDPKLALKMTHCSFEWE
DYELNDAIEEAKGEAKDEGKKNKKKRKDTWGKPSASTNKAKRLDNMLKDRDGPEDLEKTS
FRGFKDLNFDIKKGEFIMITGPIGTGKSSLLNAMAGSMRKTDGKVEVNGDLLMCGYPWIQ
NASVRDNI IFGSPFNKEKYDEVVRVCSLKADLDILPAGDMTEIGERGITLSGGQKARINL
ARSVYKKKDI YLFDDVLSAVDSRVGKHIMDECLTGMLANKTRILATHQLSLIERASRVIV
LGTDGQVDIGTVDELKARNQTLINLLQFSSQNSEKEDEEQEAVVAGELGQLKYESEVKEL
TELKKKATEMSQTANSGKIVADGHTSSKEERAVNSISLKIYREYIKAAVGKWGFIALPLY
AILVVGTTFCSLFSSVWLSYWTENKFKNRPPSFYMGLYSFFVFAAFIFMNGQFTILCAMG
IMASKWLNLRAVKRILHTPMSYIDTTPLGRILNRFTKDTDSLDNELTESLRLMTSQFANI
VGVCVMCIVYLPWFAIAI PFLLVI FVLIADHYQS SGRE IKRLEAVQRS FVYNNLNEVLGG
MDTIKAYRSQERFLAKSDFLINKMNEAGYLVVVLQRWVGIFLDMVAIAFALIITLLCVTR
AFPISAASVGVLLTYVLQLPGLLNTILRAJMTQTENDMNSAERLVTYATELPLEASYRKPE
MTPPESWPSMGEI IFENVDFAYRPGLPI VLKNLNLNIKSGEKIGICGRTGAGKSTIMSAL
YRLNELTAGKILIDNVDISQLGLFDLRRKLAIIPQDPVLFRGTIRKNLDPFNERTDDELW
DALVRGGAIAKDDLPEVKLQKPDENGTHGKMHKFHLDQAVEEEGSNFSLGERQLLALTRA
LVRQSKILILDEATSSVDYETDGKIQTRIVEEFGDCTILCIAHRLKTIVNYDRILVLEKG
EVAEFDTPWTLFSQEDSIFRSMCSRSGIVENDFENRS

SEQ ID NO: 42

YHL016C

>sp|P33413|DUR3_YEAST Urea active transporter OS=Saccharomyces cerevisiae (strain ATCC 204508 / 5288c) GN=DUR3 PE=1 S¥=2
MGEFKPPLPQGAGYAIVLGLGAVFAGMMVLTTYLLKRYQKEIITAEEFTTAGRSVKTGLV
AAAVVSSWIWCSTLLTSSTKEYADGIFGGYAYAAGACFQIIAFAILAIKTKQMAPNAHTY
LELVRTRYGKIGHGCYLFYAIATNILVTSMLLTSGSAVFSDLTGMNTIASCFLLPVGVVV
YTLFGGIKATFLTDYMHTCVIII IVLVFAFKVYATSDVLGSPGKVYDLVREAAKRHPVDG
NYQGEYMTMTSKSAGILLIINLIGNFGTVFLDNGYWNKAISASPAASLKAYAIGGLAWFA
VPSLISLTMGLACLAVETSPNFPTYPDPLTSFQANSGLVLPAAAIAIMGKGGAVASLLMI
FMAVTSAMSAELIAVSSVFTYDIYREYIDPRASGKKLI YTSHVACI FFGLAMSGFSVGLY
YGGISMGYIYEMMGI IISSAVLPVVLTLCSKDMNLVAAVVSPILGTGLAIMSWLVCTKSL
YKELTVDTTFMDYPMLTGNLVALLSPAIFIPILTYVFKPQNFDWEKMKDITRVDETAELV
QADPDIQLYDAEANDKEQEEETNSLVSDSEKNDVRVNNEKLIEPNLGVVISNAIFQEDDT
QLQNELDEEQRELARGLKIAYFLCVFFALAFLVVWPMPMYGSKYI FSKKFFTGWVVVMI I
WLFFSAFAVCIYPLWEGRHGIYTTLRGLYWDLSGQTYKLREWQNSNPQDLHVVTSQISAR
AHRQSSHFGQVDEII

SEQ ID NO: 43

YIL088C

>sp|P40501|AVT7__YEAST Vacuolar amino acid transporter 7 0S=Saccharomyces cerevisiae (strain ATCC 204508 / 5288c) GN=AVT7 PE=1 SV=1
MEATSSALSSTANLVKTIVGAGTLAIPYSFKSDGVLVGVILTLLAAVTSGLGLFVLSKCS
KTLINPRNSSFFTLCMLTYPTLAPIFDLAMIVQCFGVGLSYLVLIGDLFPGLFGGERNYW
IIASAVIIIPLCLVKKLDQLKYSSILGLFALAYISILVFSHFVFELGKGELTNILRNDIC
WWKIHDFKGLLSTFSI IIFAFTGSMNLFPMINELKDNSMENITFVINNSISLSTALFLIV
GLSGYLTFGNETLGNLMLNYDPNSIWIVIGKFCLGSMLILSFPLLFHPLRIAVNNVIIWI
EITYGGANPEEDPQVSEYTRASNLRPISMTVEDPAQPSDALDATSYNEQECLLPNGNFDN
GSIESQENNNDERGTMAVAGDNEHHAPFVKSRFYWITALLLISMYTLALSVQSFALVLSF

VGATGSTSISIFTLPGLLGYKLIGLDSLAIGKMI PPKDRFYKRCSLLLVFYGLSVMFLSLY
VTVFNRSDEA

SEQ ID NO: 44
YJL093C
>sp| P40310 IT0K1__YEAST Outward-rectifier potassium channel TOKl
OS=Saccharomyces cerevisiae (strain ATCC 204508 / 5288c) GN=TOKl
PE=1 SV=1
MTRFMNSFAKQTLGYGNMATVEQESSAQAVDSHSNNTPKQAKGVLAEELKDALRFRDERV
SIINAEPSSTLFVFWFVVSCYFPVITACLGPVANTISIACWEKWRSLKNNSVVTNPRSN
DTDVLMNQVKTVFDPPGI FAVNIISLVLGFTSNI ILMLHFSKKLTYLKSQLINITGWTIA
GGMLLVDVIVCSLNDMPSIYSKTIGFWFACISSGLYLVCTI ILTIHFIGYKLGKYPPTFN
LLPNERSIMAYTVLLSLWLIWGAGMFSGLLHITYGNALYFCTVSLLTVGLGDILPKSVGA
KIMVLI FSLSGVVLMGLIVFMTRS IIQKSSGPI FFFHRVEKGRSKSWKHYMDSSKNLSER
EAFDLMKCIRQTASRKQHWFSLSVTIAIFMAFWLLGALVFKFAENWSYFNCI YFCFLCLL
TIGYGDYAPRTGAGRAFFVIWALGAVPLMGAILSTVGDLLFDISTSLDIKIGESFNNKVK
SIVFNGRQRALSFMVNTGEIFEESDTADGDLEENTTSSQSSQISEFNDNNSEENDSGVTS
PPASLQESFSSLSKASSPEGI LPLEYVSSAEYALQDSGTCNLRNLQELLKAVKKLHRICL
ADKDYTLSFSDWSYIHKLHLRNITDIEEYTRGPEFWISPDTPLKFPLNEPHFAFMMLFKN
IEELVGNLVEDEELYKVISKRKFLGEHRKTL

SEQ ID NO: 45
YJL094C
>sp IP40309 IKHA1_YEAST K(+)/H(+} an.tiporter 1 OS=Saccharcmyces
cerevisiae (strain ATCC 204508 / S288c) GN=KHA1 PE=1 SV=1
MANTVGGILSGVNPFHYNSSSPLTLFLFQACLILLVCNLIHIPFSMMRQPKVISEVISGV
ILGPTIFGQIPNYTNTIFPTSSI PGLNLVANLGI ILFMFFLGLEVDIAFIKKHLKKALVI
GIVTLAVPFGFGCLLAIPLFHTYANKTEGERHIKFSVFMVFIAVSISVTAFPVLCRILNE
LRLIKDRAGIVVLAAGIINDIMGWILLALSIILSSAEGSPVNTVYILLITFAWFLIYFFP
LKYLLRWVLIRTHELDRSKPS PLATMCILFIMFISAYFTDIIGVHPIFGAFIAGLVVPRD
DHYVVKLTERMEDI PNIVFIPI YFAVAGLNVDLTLLNEGRDWGYVFATIGIAIFTKI ISG
TLTAKLTGLFWREATAAGVLMSCKGIVEI VVLTVGLNAGI ISRKIFGMFVLMALVSTFVT
TPLTQLVYPDSYRDGVRKSLSTPAEDDGAADGLDSEGVDKTEINTQLNSLADVSKYRIGE
LTTVINTTEAISPSLKLLNYLSLGVSPKPKNNKHKNETSLSRMTTATDSTLKSNTFKIKK
MVHIWSKSVDDVDTNLSVIDEKLTPFEGVGALRAIHLRLLTERTTDLLQSSSLYNDDPHF
TANTDSLLQIFDIFSNLSKIPFSSEVIFSTMREKAANIATMKMDSTDLILLPLKGASYEY
RGSPVFIDEKYANFDHIYSHLLGLNELSSTFFKSIFQSLKANFAVQISNTYGRLNADRFK
RKRFNLLLPKPYLTQSDYLGLYLLLLICYRDGYNNDNASCSIFINSKNIDFAKDLSTAFA
EHDWLNESTIKIVDIPFETKVPEEAIEKPSFIETVLDVGLSDTALADIEETTFI IGEDLP
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
ISASI WSFCGRAFGSIPRSHICFGAVTQGSLALILPGYIILCGALELQSRSLVAGAVRM
FYAIIYSLFLGFGITLGSALFGWMYHNATNEISCPQLI SPWFRFLFVPAFTISISLLNQA

HISQLPVMVFTSCTGYVVTYWAGKHFANSTEFTAALAAFVIGVLGNLYSRIWKGLAVSAM
LPAIFVQVPSGIASQNSLLSGLQSANTI VNANETITTSTSDPSSSMSFGMTMIQVCVGIS
VGLFASSLFVYPFGKKKTGLFSL

SEQ ID NO:47
YJL212C
>sp|P40897|0PT1__YEAST Oligopeptide transporter 1 OS=Saccharoir.yces cerevisiae (strain ATCC 204508 / S288c) GN=OPTl PE=1 SV=1
MSTIYRESDSLESEPSPTPTTIPIQINMEEEKKDAFVKNIDEDVNNLTATTDEEDRDPES
QKFDRHSIQEEGLVWKGDPTYLPNSPYPEVRSAVSIEDDPTIRLNHWRTWFLTTVFVVVF
AGVNQFFSLRYPSLEINFLVAQVVCYPIGRILALLPDWKCSKVPFFDLNPGPFTKKEHAV
VTIA¥ALTSSTAYAMYILNAQGSFYNMKLN¥GYQFLL¥WTSQMIGYGAAGLTRRW¥¥NPA
SSIWPQTLIS¥SLFDSLHSRK¥EKT¥ANGWTMPRYRFFLI¥LIGSFIWYW¥PGFLFTGLS
YFN¥ILWGSKTRHNFIANTIFGTQSGLGALPITFDYTQ¥SQAMSGSVFATPFY¥SANTYA
S¥LIFFVI¥LPCLYFTNTWYAKYMPVISGSTYDNTQNKYNVTKILNEDYSINLEKYKEYS
P¥FVPFSYLLSYALNFAA¥IA¥F¥HCILYHGKDI¥AKFKDRKNGGTDIHMRI YSKNYKDC
PDWWYLLLQI¥MIGLGF¥A¥CCFDTKFPAWAF¥IAILISLVNFIPQGILEAMTNQH¥GLN
IITELICGYMLPLRPMANLLFKLYGFI¥MRQGLNLSRDLKLAMYMK¥SPRLIFA¥QIYAT
IISGM¥N¥GVQEWMMHNIDGLCTTDQPNGFTCANGRTVFNASIIWSLPKYLFSSGRI YNP
LMWFFLIGLLFPLAVYAVQWKFPKFKFAKHIHTPVFFTGPGNIPPSTPYNYSLFFAMSFC
LNLIRKRWRAWFNKYNF¥MGAGVEAG¥AISV¥IIFLC¥QYPGGKLSWWGNNVWKRTYDND
YKKFYTLKKGETFGYDKWW

SEQ ID NO:48
YJR106W
>sp|P47144|ECM27_YEAST Protein ECM27 OS=Saccharomyces cerevisiae (strain ATCC 204508 / 5288c) GN=ECM27 PE=1 SV=2
MDWAINVAHPRLLYKDPKLS¥TFI¥PSLFHIIIAF¥LLGICASDFLCPNVAHISDPNSLR
SNGSL¥SKTASHASHTGALMA¥LLSWCNSSPDLFSNLMSWATSTRETRSTS¥SLSIGE¥L
GACGIILCI¥EGSI FI IMSRTHIEI SQIQKLS IMRDLLFSLAAMC¥MSY¥SLMNQVTVLN
CLLMAFLYAFYL¥VKLTFKLNHSAETPDETAADTSLRENS¥SPFLDDSLMASGLLPPIQP
GFDISNSITHGIKPSLLSAMDFNSFLSMLENSSLEEDDSRNEMAELNTLRSMTPGQHWSA
SATVAGEATSAGRPFSEPTNAFTEYRDSERAINSSPA¥FAPYRDNPDDEESQEQ¥LLETT
THGHFGAQEMRRFSKRSLGWI IKI FIPHLSNFSQKSISDAI FSI IT¥PFFI IFKLSCPQP
PSDILSYDPTLNRYSLTTLPI ILLFIQS ITAPFLLCS ILSVLLTYHLGYLVYLFPLILAM
ALILLLTAFITK¥NLHNKFTLSLDSSNILQEKLQKRKLLERLNTSIQIIFLAIGIINII I
WISLLANSLIEMMEIYQKILGLSKAILGLTIFAWGNSVGDLISNISMCRLYKTQTHYQDR
¥RLATKFFMISCASCLGG¥MLNSMGGIGFSGL¥SMLFIGAFNDNEWWFLRK¥KLQETSQL
DNTLNYKFI¥SC¥FI ILQI ILLLLFFGGPNNIKRRLTKEMKL¥GISMCGLWALATLINIL
LELFS

SEQ ID NO:49
YJR160C
>sp|POCEOO|MPH3_YEAST Alpha-giucosides permease MPH3 OS=Saccharorayces cerevisiae (strain ATCC 204508 / S288c) GN=MPH3 PE=1 SV=1
MKNLSFLINRRKENTSDSN¥YPGKAKSHEPSWIEMDDQTKKDGLDI¥H¥EFSPDTRAPSD
SNKVITEI FDATEDAKEADESERGMPLATALNTYPKAAAWSLL¥STTLIMEGYDTAILGA
FYALPIFQRKFGSQNDKTGEWEISASWQIGLTLCYMAGEI¥GLQLTGPS¥DLVGNRYTLI
IALFF'LAAFTFILYFCNSLGMI AV'GQALCGMPWGCFQCLT¥S YASEICPLALRYYLTTYS

NLCWLFGQLFAAGIMKNSQKKYADSELGYKLPFALQWILPVPLALGIFFAPESPWWLVKK
GRFDEARRSLRRTLSGKGPEKEILVTLEVDKIKVTIDKEKRLTSKEGSYSDCFEDKINRR
RTRITCLCWAGQATCGSILIGYSTYFYEKAGVSTEMSFTFSI IQYCLGICATFLSWWASK
YFGRYDLYAFGLAFQTIVFFIIGGLGCSSTHGSKMGSGSLLMAVAFFYNLGIAPVVFCLV
SEMPSSRLRTKTIILARNTYNVVSI ICSVLILYQLNSKKWNWGAKSGFFWGVLCFCTLIW
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
EAFHFQYDEDEEDGTSNEDGILFSKPIVTNIDVPELGNRRVNETENLKNGRLRPKRIAPW
HLIQRPMVLGSNSTKDSKSRIQSGLQDNLLVGRNIQYPPHI ISNNPEHFRFTYFRVDLDS
TVHSPTISGLLQPGQKFQDLFVASIYSQDNSAGHIKTHPNSPTPGIKAETVSQLQGLTAK
NPSTLSSMSVANIEDVPPFWLDVSNPTEEEMKILSKAFGIHPLTTEDI FLGEVREKVELF
RDYYLICFRSFDIVAEKHVRRRRKEKQESATLDHESISRRKSQAYGATMSNESNANNNNS
TSNASRSKWLPSILRARRRSSANRTTNTSSSSYKRRVKSEKKKMEENEKFKRKSGDRHKP
REGELEPLNVYI IVFRTGVLTFHFAPTPHPINVRRRARLLKDYLNVTSDWIAYALIDDIT
DAFAPMIELIEDEVYEIEDAILKMHQSDDSSDSDSSDSDSDSGASDEDAFPFDVYSKKTS
YSSAKSSVSSRSMSTSEAS FNANLIGWKRKGDMLRRIGECRKRVMS ILRLLGSKADVIKG
FAKRYNEQWEASPQSEIAMYLGDIQDHIVTMVSSLNHYEKLLSRSHSNYLAQINIDMTKV
NNDMNDVLGKITILGTI VLPMNVITGLWGMNVI VPGQYRDSLTWFIGIVLFMCMLACSAY
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
SDVDPRDI YKSIMMLQKQQEKSNANSTDSFSSETNGPAFIVQERHERRAPHCSLKRHSVL
PSSQELNKLAQTKSFQKLLGLRRDEGDHDYFDGAPHKYMVTKKKKISRTQSCNIPTYTAS
PSPKTSGQVVENHRNLAKSAPSSFVDEEMSFSPQESLNLQFQAHPPKPKRREGDIGHPFT
RTMSTNYLSWQPTFGRNSVFIGLTKQQKEELGGVEYRALRLLCCILMVYYIGFNILAFVT
IVPWACTRHHYSEIIRRNGVSPTWWGFFTAMSAFSNLGLSLTADSMVSFDTAPYPLIFMM
FFI IIGNTGFPIMLRFIIWIMFKTSRDLSQFKESLGFLLDHPRRCFTLLFPSGPTWWLFT
TLVVLNATDWILFI ILDFNSAVVRQVAKGYRALMGLFQSVCTRTAGFNVVDLSKLHPSIQ
VSYMLMMYVSVLPLAISIRRTNVYEEQSLGLYDSGQDDENITHEDDIKETDHDGESEERD
TVSTKSKPKKQSPKSFVGAHLRRQLSFDLWYLFLGLFI ICICEGRKIEDVNKPDFNVFAI
LFEVVSAYGTVGLSLGYPNTNTSLSAQFTVLSKLVI IAMLIRGRNRGLPYTLDRAIMLPS
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
MEETKYSSQQEIEGACGSDASLNARGSNDSPMGLSLYLCLASLTLVLFITALDILIVGTI
IDVVAEQFGNYSKTGWLVTGYSLPNAILSLIWGRFASI IGFQHSLILAILIFEAGSLIAA
LASSMNMLIFGRVVAGVGGSGLQTLCFVIGCTMVGERSRPLVISILSCAFAVAAIVGPII
GGAFTTHVTWRWCFYINLPIGGLAI IMFLLTYKAENKGILQQIKDAIGTISSFTFSKFRH
QVNFKRLMNGI IFKFDFFGFALCSAGLVLFLLGLTFGGNKYSWNSGQVITYLVLGVLLFI
FSLVYDFFLFDKFNPEPDNISYRPLLLRRLVAKPAI IIVNMVTFLLCTGYNGQMI YSVQF
FQLI FASSAWKAGLHLIPIVITNVIAAIASGVITKKLGLVKPLLIFGGVLGVIGAGLMTL
MTNTSTKSTQIGVLLLPGFSLGFALQASLMSAQLQITKDRPEAAMDFIEVTAFNTFMKSL
GTTLGGVLSTTVFSASFHNKVSRAHLEPYEGKTVDDMILYRLQNYDGSHSTIGNILSDSI
KNVFWMDLGFYALGFLFCSFSSNKKLI IPKKDDTPEDNLEDK

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
WRMFYQYASYWPYII IPWISGNI ITAANPQKNWSWNIAMWAFI YPLSTLPIIFLILYMKY
KSSKTAEWRSLKEQARKERTGGLFENLVFLFWKLDIVGILLITVSLGCILVPLTLANETS
QKWHNSKI IATLVSGGCLFFI FLYWEAKFAKSPLLPFKLLSDRGIWAPLGVTFFNFFTFF
ISCDYLYPVLLVSMKESSTSAARIVNLPDFVAATASPFYSLLVAKTRKLKLSVIGGCAAW
MVCMGLFYKYRGGSGSHEGVIAASVIMGLSGLLCSNSVIVILQAMTTHSRMAVITGIQYT
FSKLGAAIGASVSGAIWTQTMPNQLYKNLGNDTLAEIAYASPYTFISDYPWGSPERDAVV
ESYRYVQRIIMTVGLACTVPFFTFTMFMRNPELIDKATHEEFTEDGLVVLPDEENIFSQI
KALFRHNRSNKKSGC

SEQ ID NO: 54
YLR447C
>sp|P32366|VA0DJYEAST V-type proton ATPase subunit d OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VMA6 PE=1 SV=2
MEGVYFNIDNGFIEGVVRGYRNGLLSNNQYINLTQCDTLEDLKLQLSSTDYGNFLSSVSS
ESLTTSLIQEYASSKLYHEFNYIRDQSSGSTRKFMDYITYGYMIDNVALMITGTIHDRDK
GEILQRCHPLGWFDTLPTLS VATDLESLYETVLVDTPLAPYFKNCFDTAEELDDMNIEII
RNKLYKAYLEDFYNFVTEEIPEPAKECMQTLLGFEADRRSINIALNSLQSSDIDPDLKSD
LLPNIGKLYPLATFHLAQAQDFEGVRAALANVYEYRGFLETGNLEDHFYQLEMELCRDAF
TQQFAISTVWAWMKSKEQEVRNITWIAECIAQNQRERINNYISVY

SEQ ID NO: 55
YML116W
>sp|P13090|ATR1_YEAST Aminotriazole resistance protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / 5288c) GN=ATR1 PE=1 SV=2

MGNQSLVVLTESKGEYENETELPVKKSSRDNNIGESLTATAFTQSEDEMVDSNQKWQNPN
YFKYAWQEYLFIFTCMISQLLNQAGTTQTLSIMNILSDSFGSEGNSKSWLMASFPLVSGS
FILISGRLGDI YGLKKMLLVGYVLVIIWSLICGITKYSGSDTFFI ISRAFQGLGIAFVLP
NVLGI IGNIYVGGTFRKNIVISFVGAMAPIGATLGCLFAGLIGTEDPKQWPWAFYAYSIA
AFINFVLSIYAIPSTIPTNIHHFSMDWIGSVLGVIGLILLNFVWNQAPISGWNQAYIIVI
LIISVIFLVVFI IYEIRFAKTPLLPRAVIKDRHMIQIMLALFFGWGSFGIFTFYYFQFQL
NIRQYTALWAGGTYFMFLIWGI IAALLVGFTIKNVSPSVFLFFSMVAFNVGSIMASVTPV
HETYFRTQLGTMIILSFGMDLSFPASSI IFSDNLPMEYQGMAGSLVNTVVNYSMSLCLGM
GATVETQVNS DGKHLLKGYRGAQYLGI GLASLACMISGLYMVES FIKGRRARAAAE YDCT
VA

SEQ ID NO: 56

YMR034C

>sp IQ05131 IYMS4___YEAST Uncharacterized membrane protein YMR034C
OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YMR034C
PE=1 SV=1
MKTQYSLIRKIWAHSVTEFLKSQWFFICLAILIVIARFAPNFARDGGLIKGQYSIGYGCV
AWIFLQSGLGMKSRSLMANMLNWRAHATILVLSFLITSSIVYGFCCAVKAANDPKIDDWV
LIGLILTATCPTTVASNVIMTTNAGGNSLLCVCEVFIGNLLGAFITPALVQMFTNRAPFA
YGNPATGNGIGALYGRVMKQVGLSVFVPLFVGQVIQNCFPKGTAYYLGFLKKYHIKIGSY
MLLLIMFSSFSTAFYQDAFTSVSHVCIIFLCFFNLGI YIFFTGLSYLCARPWFILKLFPH
EPIEGKSTRLYRYSYNIFRPFYYSKEDAICIMFCGPAKTAALGVSLITSQYGDKKEHLGK
LLVPLVLYQVEQVMTANFFVSLFKRWIQKDAQADGSESSCANENEEVDLEKI ISIGTGEN
QSVLSNNVPYTQPR

SEQ ID NO: 57

YMR056C

>sp 1P04710 |ADT1__YEAST ADP, ATP carrier protein 1 OS=Saccharomyces
cerevisiae (strain ATCC 204508 / S288c) GN=AAC1 PE=1 SV=1
MSHTETQTQQSHFGVDFLMGGVSAAIAKTGAAPIERVKLLMQNQEEMLKQGSLDTRYKGI
LDCFKRTATHEGIVSFWRGNTANVLRYFPTQALNFAFKDKIKSLLSYDRERDGYAKWFAG
NLFSGGAAGGLSLLFVYSLDYARTRLAADARGSKSTSQRQFNGLLDVYKKTLKTDGLLGL
YRGFVPSVLGI IVYRGLYFGLYDSFKPVLLTGALEGSFVASFLLGWVITMGASTASYPLD
TVRRRMMMTSGQTIKYDGALDCLRKIVQKEGAYSLFKGCGANI FRGVAAAGVISLYDQLQ
LIMFGKKFK

SEQ ID NO: 58

YMR253C

>sp| Q04835 |YM87_YEAST Oncharacterized membrane protein YMR2 53C
OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YMR2 53C
PE=1 SV=1
MNPSVPKVMKRENNTHLLVSKEMNDTSLQLPSTTRSLSPKESNSNEDFNVDGNETTLQRI
SKDYLKPNIGLVLLTVSYFFNSAMVVSTKVLENDPDDIANDRQIKPLQILLVRMVITYIG
TLIYMYINKST ISDVP FGKPE VRKWLVLRGCTG FFGVFGMYYS LMYLT ISDAVL ITFLAP
SLTIFLSWVILRERFTKVEALGSLISLLGVVLIVRPSFLFGTPELTDSSSQIVESSDPKS
RLIATLVGLWGVLGMSCVYII IRYIGKRAHAIMSVSYFSLITAIVSFIGINTIPSMKFQI
PHSKKQWILFGNLGVSGFI FQLLLTMGIQRERAGRGSLMTYTQLLYAVFWDVALYKHWPN
IWSWIGMI II ISATLWVIRIRAANNETTAKDLTPIIDDEENSIPLTEFDLSDSK

SEQ ID NO: 59
YNL065W
>sp|P53943|AQR1_YEAST Probable transporter AQRl OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN-AQR1 PE=1 SV=1
MSRSNSIYTEDIEMYPTHNEQHLTREYTKPDGQTKSEKLNFEGAYINSHGTLSKTTTREI
EGDLDSETSSHSSDDKVDPTQQITAETKAPYTLLSYGQKWGMVAILTMCGFWSSLGSPIY
YPALRQLEKQFNVDENMVNVTVVVYLLFQGISPTVSGGLADCFGRRPIILAGMLIYVIAS
IGLACAPSYGVIIFLRCIQSIGISPTIAISSGVVGDFTLKHERGTFVGATSGFVLLGQCF
GSLIGAVLTARWDWRAIFWFLTIGCGSCFLIAFLILPETKRTIAGNLSIKPKRFINRAPI
FLLGPVRRRFKYDNPDYETLDPTIPKLDLSSAGKILVLPEIILSLFPSGLLFAMWTLMLS
SISSGLSVAPYNYHLVIIGVCYLPGGIGGLMGSFFTGRIIDMYFKRKIKKFEQDKANGLI
PQDAEINMFKVRLVCLLPQNFLAVVAYLLFGWSIDKGWRIESILITSFVCSYCAMSTLST
STTLLVDL YPTKS STAS SCFN FVRCS LSTI FMGC FAKMKAAMT VGGTFT FLCALVFFFN F
LMFI PMKYGMKWREDRLLKQQRQSWLNTLAVKAKKGTKRDQNDNHN

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 SALl-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / 5288c) GN=SAL1 PE=1 SV=2
MLLKNCETDKQRDIRYACLFKELDVKGNGQVTLDNLISAFEKNDHPLKGNDEAIKMLFTA
MDVNKDSVVDLSDFKKYASNAESQIWNGFQRIDLDHDGKIGINEINRYLSDLDNQSICNN
ELNHELSNEKVNKFSRFFEWAFPKRKANIALRGQASHKKNTDNDRSKKTTDSDLYVTYDQ
WRDFLLLVPRKQGSRLHTAYSYFYLFNEDVDLSSEGDVTLINDFIRGFGFFIAGGISGVI
SRTCTAPFDRLKVFLIARTDLSSILLNSKTDLLAKNPNADINKISSPLAKAVKSLYRQGG
IKAFYVGNGLNVIKVFPESSIKFGSFEVTKKIMTKLEGCRDTKDLSKFSTYIAGGLAGMA
AQFSVYPIDTLKFRVQCAPLDTKLKGNNLLFQTAKDMFREGGGQI ILQRCHSRYSGHISL
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
MVHITLGQAIWVSVKPI IKIYLIIGVGFLMAKMGILTVEATRI ISDIVLTVLLPSLSFNK
IVANIEDKDIKSVGIICLSALLIFGSGFFFAYVVRLFLPVPKQWYGGILAGGMFPNISDL
PIAYLQSMDQGLVFSEEEGNKGVANVIIFLTMFLICIFNLGGFRLIESDFEYNDDESAVR
VSETTKTQPAVSANTTNTDTSERFFSNEQQLFNNKYTARDSLTEAIGTKGENADVPPISR
RSTNSIAPLSLPDTSSNSKITKPVQVKARNTIACTQSEESQATRGSNPLDSQSSASTIHS
YNTSESYESSIDTMRARRTASQPRAYNTTTLLEENCLDEKCPKNMSMAALEPIRSIDMRA

LPSQNIHHLIREYSNVDQYGHQRRNSSLRGADMNDVHSISSNSTLQTIKTANLTRILTSD
ATVSKKDIETSGESLPQWMRKFSLTPLLVFFLKNCLRPCSMAVIIALTVAFI PWVKALFV
TTANTPHISQAPDNAPPLSFFMDFTGYVGAACVPFGLILLGATLGRLKIGNLYPGFWKAA
VTLVILRQCVMPI FGVLWCDRLVKAGWVNWQDDRMLLFVIAISWNLPTMTTLIYFTASFT
PPETTAPIQMECVSFFLMLQYPLMVVSLPFLVSYFLKVQMNL

SEQ ID NO: 63
YNL121C
>sp|P07213|TOM70__YEAST Mitochondrial import receptor subunit TOM70 OS=Saccharomyces cerevisiae (strain ATCC 204508 / 5288c) GN=TOM70 PE=1 SV=2
MKSFITRNKTAILATVAATGTAIGAYYYYNQLQQQQRGKKNTINKDEKKDTKDSQKETE
GAKKSTAPSNPPIYPVSSNGEPDFSNKANFTAEEKDKYALALKDKGNQFFRNKKYDDAIK
YYNWALELKEDPVFYSNLSACYVSVGDLKKVVEMSTKALELKPDYSKVLLRRASANEGLG
KFADAMFDLSVLSLNGDFN DASIEPMLERNLNKQAMSKLKEKFGDIDTATATPTELSTQP
AKERKDKQENLPSVTSMASFFGI FKPELTFANYDESNEADKELMNGLSNLYKRSPESYDK
ADESFTKAARLFEEQLDKNNEDEKLKEKLAISLEHTGIFKFLKNDPLGAHEDIKKAIELF
PRVNSYI YMALIMADRNDSTEYYNYFDKALKLDSNNSSVYYHRGQMNFILQNYDQAGKDF
DKAKELDPENI FPYIQLACLAYRENKFDDCETLFSEAKRKFPEAPEVPNFFAEILTDKND
FDKALKQYDLAIELENKLDGI YVGIAPLVGKATLLTRNPTVENFIEATNLLEKASKLDPR
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
PDIL FAVYQGM FAAVT GALML GGACE RARL FPMMVFL FLWMTIVYC PIACWVWNAEGWLV
KLGSLDYAGGLCVHLTSGHGGLVYALILGKRNDPVTRKGMPKYKPHSVTSVVLGTVFLWF
GWMFFNGGSAGNATIRAWYSIMSTNLAAACGGLTWMVIDYFRCGRKWTTVGLCSGIIAGL
VGITPAAGFVPIWSAVVIGVVTGAGCNLAVDLKSLLRIDDGLDCYSIHGVGGCIGS VLTG
IFAADYVNATAGSYISPIDGGWINHHYKQVGYQLAGICAALAWTVTVTSILLLTMNAIPF
LKLRLSADEEELGTDAAQIGEFTYEESTAYIPEPIRSKTSAQMPPPHENIDDKIVGNTDA
EKNSTPSDASSTKNTDHIV

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
AIAGSQI IGTIHGLGEITVRFPVVGAFANYGTRFLDPSISFVVSTIYVLQWFFVLPLEI I
AAAMTVQYWNSSIDPVIWVAIFYAVIVSINLFGVRGFGEAEFAFSTIKAITVCGFIILCV
VLICGGGPDHEFIGAKYWHDPGCLANGFPGVLSVLVVASYSLGGIEMTCLASGETDPKGL
PSAIKQVFWRILFFFLISLTLVGFLVPYTNQNLLGGSSVDNSPFVIAIKLHHIKALPSIV
NAVILISVLSVGNSCIFASSRTLCSMAHQGLIPWWFGYIDRAGRPLVGIMANSLFGLLAF
LVKSGSMSEVFNWLMAIAGLATCIVWLSINLSHIRFRLAMKAQGKSLDELEFVSAVGIWG
SAYSALINCLILIAQFYCSLWPIGGWTSGKERAKIFFQNYLCALIMLFIFIVHKIYYKCQ

TGKWWGVKALKDI DLETDRKDIDIEIVKQEIAEKKMYLDSRPWYVRQFHFWC

SEQ ID NO: 66

YOL075C

>sp|Q08234 |YO075___YEAST Uncharacteri zed ABC transporter **ATP-binding** protein/permease YOL075C OS=Saccharomyces **cerevisiae** (strain ATCC 204508 / S288c) GN=YOL075C PE=1 SV=3
MSQQENGDVATELIENRLSFSRIPRISLHVRDLSI VASKTNTTLVNTFSMDLPSGSVMAV
MGGSGSGKTTLLNVLASKISGGLTHNGSIRYVLEDTGSEPNETEPKRAHLDGQDHPIQKH
VIMAYLPQQDVLSPRLTCRETLKFAADLKLNSSERTKKLMVEQLIEELGLKDCADTLVGD
NSHRGLSGGEKRRLSIGTQMISNPSIMFLDEPTTGLDAYSAFLVIKTLKKLAKEDGRTFI
MSIHQPRSDILFLLDQVCILSKGNVVYCDKMDNTIPYFESIGYHVPQLVNPADYFIDLSS
VDS RSDKE EAATQS RLN SLIDHWHDYERTHLQLQAE SYISNAT EIQIQNMTTRLP FWXQ V
TVLTRRNFKLNFSDYVTLISTFAEPLI IGTVCGWI YYKPDKSS IGGLRTTTACLYASTIL
QCYLYLLFDTYRLCEQDIALYDRERAEGSVTPLAFIVARKISLFLSDDFAMTMIFVSITY
FMFGLEADARKFFYQFAVVFLCQLSCSGLSMLSVAVSRDFSKASLVGNMTFTVLSMGCGF
FVNAKVMPVYYVRWIKYIAFTWYSFGTLMSSTFTNSYCTTDNLDECLGNQILEVYGFPRNW
ITVPAVVLLCWSVGYFVVGAI ILYLHKIDITLQNEVKSKQKKIKKKSPTGMKPEIQLLDD
VYHQKDLEAEKGKNIHITIKLEDIDLRVI FSAPFSNWKEGNFHHETKEILQSVNAI FKPG
MINA IMGPSGSGKSSLLNLISGRLKSSVFAKFDTSGSIMFNDIQVSELMFKNVCSYVSQD
DDHLLAALTVKETLKYAAALRLHHLTEAERMERTDNLIRSLGLKHCENNI IGNEFVKGIS
GGEKRRVTMGVQLLNDPPILLLDEPTSGLDSFTSATILEILEKLCREQGKTI IITIHQPR
SELFKRFGNVLLLAKSGRTAFNGSPDEMIAYFTELGYNCPSFTNVADFFLDLISVNTQNE
QNEISSRARVEKILSAWKANMDNESLSPTPISEKQQYSQESFFTEYSEFVRKPANLVLAY
IVNVKRQFTTTRRSFDSLMARIAQIPGLGVIFALFFAPVKHNYTSISNRLGLAQESTALY
FVGMLGNLACYPTERDYFYEEYNDNVYGIAPFFLAYMTLELPLSALASVLYAVFTVLACG
LPRTAGNFFATVYCSFIVTCCGEALGIMTNTFFERPGFVVNCISI ILSIGTQMSGLMSLG
MSRVLKGFNYLNPVGYTSMI IINFAFPGNLKLTCEDGGKNSDGTCEFANGHDVLVSYGLV
RNTQKYLGI IVCVAIIYRLIAFFILKAKLEWIKW

SEQ ID NO: 67

YOL077W-A

>sp[P814 51|ATP19_YEAST ATP synthase subunit κ, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ATP19 PE=1 SV=1
MGAAYHFMGKAIPPHQLAIGTLGLLGLLVVPNPFKSAKPKTVDIKTDNKDEEKFIENYLK
KHSEKQDA

SEQ ID NO: 68

YOL122C

>sp|P38925 iSMF1__YEAST Manganese transporter SMFl 05=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SMF1 PE=1 SV=2
MVNVGPSHAAVAVDASEARKRNISEEVFELRDKKDSTVVIEGEAPVRTFTSSSSNHERED
TYVSKRQVMRDIFAKYLKFIGPGLMVSVAYI DPGNYSTAVDAGASNQFSLLCI ILLSNFI
AIFLQCLCIKLGSVTGLDLSRACREYLPRWLNWTLYFFAECAVIATDIAEVIGTAIALNI
LIKVPLPAGVAITVVDVFLIMFTYKPGASSIRFIRIFECFVAVLVVGVCICFAIELAYIP
KSTSVKQVFRGFVPSAQMFDHNGIYTAISILGATVMPHSLFLGSALVQPRLLDYDVKHGN
YTVSEEQDKVKKSKSTEEIMEEKYFNYRPTNAAIKYCMKYSMVELSITLFTLALFVNCAI
LVVAGSTLYNSPEADGADLFTIHELLSRNLAPAAGTI FMLALLLSGQSAGVVCTMSGQIV
SEGH INWKLQPWQRRLATRC IS1IPCLVISIC IGREALS KALNASQVVLS IVLPFLVAPL
IFFTCKKSIMKTEITVDHTEEDSHNHQNNNDRSAGSVIEQDGSSGMEIENGKDVKIVYMA
NNWIITVIA IIVWLFLSLLNVYAIVQLGMSHGDIS

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
MKFLGVILLASFLLIATFLIGLIPLYYIDKQKSSIVTNQEGADSISDFTTNADTQTINDD
VSSYRVKIAVLSQFGIGMLLGTSFMLVI PEGIKACVEHDGNVGVNLLIGFLGVYVLDRLV
TLWVSRKQTVYTHDAVKFQSWKDIINHPRQIWMNLIQNNVVFALFIHGLSDGIALGTTTN
NDSLLIVVLIAIVIHKIPAVLSLTSLMVSRQNLMKWEVICNVFLFASSTPIGYIVLSLLN
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
CDHSEILSPKVVKLAYEACGGNPKDKANKRKYQSVII FSLLKVCEWYSILATMEVHNAKL
YETRNLASQQLCKLLIEREETRDLQFLFMQLLLRRYVINENDEDQEPLNALELAT DMHCT
TVIGSSGFQRCLKWIWRGWIVQNGLDPTTFIKDDSLAEVSLISHFNPVRLKAPVYQNYLQ
MIFSFLFLGLYTLVVNGKDSERVQSFDLLESIFYVFNTGFILDELTKLYYIGYAHLSFWN
LFNDTTYLIITFAMGFRAMSVTPLNAKYSSEDWDKISYRVLSCAAPFVWSRLLLYLESQR
FIGIMLVILKHMMKESIVFFFLLFLIMIGFTQGFLGLDSADGKRDITGPILGNLTITVLG
LGSFDVFEEFAPPYAAILYYGYYFIVSVILLNILIALYSTAYQKVIDNADDEYMALMSQK
TLRYIRAPDEDVYVSPLNLIEVFMTPI FRILPPKRAKDLSYTVMTIVYSPFLLLI SVKET
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
IVANIEDNDIKDVGI ICLTSVILFATGLGFAFIVRSVLPVPKRWRGGILAGGMFPNISDL
PIAYLQSMDQGFIFTEAEGEKGVANVI IFLAMFLICVFNLGGFRLIENDFHYKGDDDEEN
TLTNDDSAQQPTQPIEGNSSSSSNQDILKEPNESTVPNSSQASYISEKNKKEKTELSVPK
PTHTAPPAIDDRSSNSSAVVSIDSITHSLRTNHVDAQSVSELNDPTYRTRSQPIAYTTES
RTSHVHNNRRNSITGSLRSIDMRELPAEGMSDLIREYSNVDQYGRRRKSSISSQGAPSVL
QADGTISPNLTRTSTLQRVKTSNLTRI ITSDATVSKKDIETSGSSLPKWLQKFPLTKFFV
FFLKNCLRPCSMAVILALI IAFIPWVKALFVTTSNTPKIKQAPDNAPALTFIMDFTSYVG
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 S¥=2
MEDSKKKGLIEGAILDI INGSIAGACGKVIEFPFDTVKVRLQTQASNVFPTTWSCIKFTY
QNEGIARGFFQGIASPLVGACLENATLFVSYNQCSKFLEKHTNVSPLGQILISGGVAGSC
ASLVLTPVELVKCKLQVANLQVASAKTKHTKVLPTIKAI ITERGLAGLWQGQSGTFIRES
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
SVDAVSSAVKKYNWCLPSLLVI YREEGFRALYKGFVPKVCRLAPGGSLMLWFTGMMNFF
RDLKYGH

SEQ ID NO; 74
YOR2 91W
>sp|Q12697 |YPK9_YEAST Vacuolar cation-transporting ATPase YPK9
OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YPK9
PE=1 SV=1
MDIPSSNQIQHGQRSERNRRMPRASFSSTATTSTAATLTSAMVLDQNNSEPYAGATFEAV
PSSIVSFHHPHSFQSSNLPSPHSSGNLEQRGRRLTESEPLVLSSAEQSRSSSRNPSHFRF
FTQEQISNAEGASTLENTDYDMAWDATPAYEQDRI YGTGLSSRRSS IRS FSRASSLSNAK
SYGSFSKRGRSGSRAPQRLGENSDTGFVYHSATHSSSSLSRYTTRERIPIELESQTDEIL
EDESSTHSLESSDSRRSASENNRGSFSGHDDVHNQHSEYLKPDYHEKFYPQYAPNLHYQR
FYIAEEDLVIGIAAYQTSKFWYI IYNLCCFLTFGLVYLLTRWLPHLKVKLYGVKVPLAKA
EWVVIENEFGEFVIQPI DRQWYNRPLSTVLPFENYPNPSYEPNDINLSHHHANEINPNVP
ILITFEYRYIKFI YSPLDDLFKTNNNWIDPDWVDLSTVSNGLTKGVQEDRELAFGKNQIN
LRMKTTSEILFNEVLHPFYVFQVFSI ILWGIDEYYYYAACI FLISVLSIFDSLNEQKKVS
RNLAEMSHFHCDVRVLRDKFWTTISSSELVPGDI YEVSDPNITILPCDSILLSSDCIVNE
SMLTGESVPVSKFPATEETMYQLCDDFQSTQISSFVSKSFLYNGTNI IRARIAPGQTAAL
AMVVRTGFSTTKGSLVRSMVFPKPTGFKFYRDSFKYIGFMSLIAIFGFCVSCVQFIKLGL
DKKTMILRALDIITI VVPPALPATLTIGTNFALSRLKEKGIFCISPTRLNISGKIDVMCF
DKTGTLTEDGLDVLGVQISEPNGVRGQKFGELLSDIRQVFPKFSLNDCSSPLDFKSRNFF
MSLLTCHSLRSVDGNLLGDPLDFKMFQFTGWSFEEDFQKRAFHSLYEGRHEDDVFPENSE
IIPAVVHPDSNNRENTFTDNDPHNFLGVVRSFEFLSELRRMSVIVKTNNDDVYWSFTKGA
PEVISEICNKSTLPADFEEVLRCYTHNGYRVIACAGKTLPKRTWLYSQKVSREEVESNLE
FLGFI IFQNKLKKETSETLKSLQDANIRTIMCTGDNILTAI SVGREAGLIQCSRVYVPS I
NDTPLHGEPVIVWRDVNEPDKILDTKTLKPVKLGNNSVESLRECNYTLAVSGDVFRLLFR
DENEIPEEYLNEILLNSSIYARMSPDEKHELMIQLQKLDYTVGFCGDGANDCGALKAADV
GISLSEAEASVAAPFTSKI FNISCVLDVIREGRAALVTSFACFQYMSLYSAIQFITITIL
YSRGSNLGDFQFLYIDLLLIVPIAICMSWSKSYEKIDKKRPSANLVSPKILVPLLISVFL
VFLFQFIPWI IVQKMSWYIKPIVGGDDAVQSSDNTVLFFVSNFQYILTAIVLSVGPPYRE
PMSKNFEFIVDITVSIGASLLLMTLDTESYLGKMLQLTPISNSFTMFI IVWVILNYYAQL
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
FGLLNSTGVIESHLQDNQLSSESVSTIGWLFSLFLFVCSASCI ISGTYFDRNGFRTIMIV
GTVFHVAGLFATANSTKYWHFILSFAIVCGFGNGIVLSPLVSVPAHYFFKRRGTALAMAT
IGGSVGGVVFPIMLRSFFSMKSDTDPTYGFVWGIRTLGFLDLALLTLS IILVKERLPHVI
ENSKDGESRWRYILRVYILQCFDAKAFLDMKYLFCVLGTVFSELSINSALTYYGSYATSH
GISANDAYTLIMI INVCGIPGRWVPGYLSDKFGRFNVAIATLLTLFIVMFVGWLPFGTNL
TNMYVISALYGFCSGSVFSLLPVCCGQISKTEEFGKRYSTMYFVVGFGTLVGIPITGAI I
SIKTTADYQHYI IFCGLATFVSAVCYI ISRAYCVGFKWVRF

SEQ ID NO: 76
YOR316C
>sp| P32798 |COTl__YEAST Cobalt **uptake** protein COTl OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=COTl PE=1 SV=2
MKLGSKQVKI ISLLLLDTVFFGIEITTGYLSHSLALIADSFHMLNDIISLVVALWAVNVA
KNRNPDSTYTYGWKRAEILGALINAVFLIALCVSILIEALQRIIAPPVIENPKFVLYVGV
AGLISNTVGLFLFHDNDQEHGHGHGHSHGGIFADHEMHMPSSHTHTHAHVDGIENTTPMD
STDNISEIMPNAIVDSFMNENTRLLTPENASKTPSYSTSSHTIASGGNYTEHNKRKRSLN
MHGVFLHVLGDALGNIGVMLSAFFIWKTDYSWKYYTDPLVSLI ITGI IFSSALPLSCKAS
KILLQATPSTLSGDQVEGDLLKI PGI IAIHDFHIWNLTESIFIASLHIQLDISPEQFTDL
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
SLFISCTVFNSKGNI ISMSEKFPKWSFLTEHSLFPRDLRKIDNSSIDI IPTIMCKPNCI V
INLLHIKALIERDKVYVFDTTNPSAAAKLSVLMYDLESKLSSTKNNSQFYEHRALESIFI
NVMSALETDFKLHSQICIQILNDLENEVNRLKLRHLLIKSKDLTLFYQKTLLIRDLLDEL
LENDDDLANMYLTVKKSPKDNFSDLEMLIETYYTQCDEYVQQSESLIQDIKSTEEIVNI I
LDANRNSLMLLELKVTIYTLGFTVASVLPAFYGMNLKNFIEESEWGFTSVAVFSIVSALY
ITKKNFNSLRSVTKMTMYPNSPANSSVYPKTSASIALTNKLKRRRKWWKSTKQRLGVLLY
GSSYTNKANLSNNKINKGFSKVKKFNMENDIKNKQNRDMIWKWLIEDKKN

SEQ ID NO: 78
YPL078C
>sp|P05626 IATPF_YEAST ATP synthase subunit 4, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ATP4 PE=1 SV=2
MSMSMGVRGLALRSVSKTLFSQGVRCPSMVIGARYMSSTPEKQTDPKAKANSIINAIPGN
NI LTKTGVLGT SAAAVI YAI SNELYVINDESILLLTFLGFTGLVAKYLAPAYKDFADARM
KKVSDVLNASRNKHVEAVKDRIDSVSQLQNVAETTKVLFDVSKETVELESEAFELKQKVE
LAHEAKAVLDSWVRYEASLRQLEQRQLAKSVISRVQSELGNPKFQEKVLQQSISEIEQLL
SKLK

SEQ ID NO: 79

YPL270W

>sp|P33311 |MDL2_YEAST ATP-dependent permease MDL2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / 5288c) GN=MDL2 **PE=1** SV=3

MLNGRLPLLRLGICRNMLSRPRLAKLPS IRFRSLVTPSSSQLI PLSRLCLRSPAVGKSLI
LQSFRCNSSKTVPETSLPSASPISKGSARSAHAKEQSKTDDYKDIIRLFMLAKRDWKLLL
TAILLLTISCSIGMSIPKVIGIVLDTLKTSSGSDFFDLKIPIFSLPLYEFLSFFTVALLI
GCAANFGRFILLRILSERVVARLRANVIKKTLHQDAEFFDNHKVGDLISRLGSDAYVVSR
SMTQKVSDGVKALICGVVGVGMMCSLSPQLSILLLFFTPPVLFSASVFGKQIRNTSKDLQ
EATGQLTRVAEEQLSGIKTVQSFVAEGNELSRYNVAIRDI FQVGKTAAFTNAKFFTTTSL
LGDLSFLTVLAYGSYLVLQSQLSIGDLTAFMLYTEYTGNAVFGLSTFYSEIMQGAGAASR
LFELTDRKPSISPTVGHKYKPDRGVIEFKDVSFSYPTRPSVQIFKNLNFKIAPGSSVCIV
GPSGRGKSTIALLLLRYYNPTTGTITIDNQDISKLNCKSLRRHIGIVQQEPVLMSGTIRD
NITYGLTYTPTKEEIRSVAKQCFCHNFITKFPNTYDTVIGPHGTLLSGGQKQRIAIARAL
IKKPTILILDEATSAL DVESEGAINYTFGQLMKS KSMT IVSIAHRLST IRRSENVI VLGH
DGSVVEMGKFKELYANPTSALSQLLNEKAAPGPSDQQLQIEKVIEKEDLNESKEHDDQKK
DDNDDNDNNHDNDSNNQSPETKDNNSDDIEKSVEHLLKDAAKEANPIKITPQP

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
QEKIQWKLASQPYQKVLSQRHLTMI AIGGTLGTGLFIGLGYSLASGPAALLIGFLLVGTS
MFCVVQSAAELSCQFPVSGSYATHVSRFIDESVGFTVATNYALAWLISFPSELIGCALTI
SYWNQTVNPAVWVAIFYVFIMVLNLFGVRGFAETEFALSI IKVIAIFIFIIIGIVLIAGG
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 / 5288c) GN=YPR003C PE=1 SV=1

MTSNNSLLGRGRMSYSSTAPPRFKRSVDQRDTFSDNFDYDKDSSNRGRTYIAASNSTTGV
PPPNNSRSGCTNNTNNTNNTSNTSNTNNNDSVDENTVFETLPYYLPCFSWLPEYTFNKLW
GDVIAGISVASFQIPLALSYTTSIAHVPPLCGLYSLAISPFVYGILGSVPQMIVGPESAI
SLVVGQAVESITLHKENVSLIDISTVITFVSGTILLFSGISRFGFLGNVLSKALLRGFIS
SVGLVMI INSLISELKLDKFLVSLPQHYHTPFEKILFLIDYAPAQYHIPTAIFSGCCLIV
LFLTRLLKRKLMKYHKSAIFFPDILLVVIVTILISMKFNLKHRYGISI IGDFSMDNFDEL
KNPLTRPRRKLI PDLFSASLIVAMLGFFESTTASKSLGTTYNLTVSSNRELVALGFMNIV
ISLFGALPAFGGYGRSKINALSGAQSVMSGVFMGVITLITMNLLLQFVHYIPNCVLSVIT
TIIGISLLEEVPGDIKFHLRCGGFSELFVFAVTFCTTIFYSIEAGICIGCVYSI INI IKH
SAKSRIQILARVAGTSNFTNLDDYMMNMKRNSLDVEGTEEIEGCMIVRIPEPLTFTNSED
LKQRLDRIERYGSSKIHPGRKSLRSKDSIKYVIFDLGGMTSIDSSAAQVLEEI ITSYKRR
NVFI YLVNVSINDKVRRRLFKAGVAASVERAQANNNENNTSNTFSDAGETYSPYFDSIDA
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 / 5288c) GN=YMCl PE=1 SV=2
MSEEFPSPQLIDDLEEHPQHDNARVVKDLLAGTAGGIAQVLVGQPFDTTKVRLQTSSTPT
TAMEVVRKLLANEGPRGFYKGTLTPLIGVGACVSLQFGVNEAMKRFFHHRNADMSSTLSL
PQYYACGVTGGIVNSFLASPIEHVRIRLQTQTGSGTNAEFKGPLECIKKLRHNKALLRGL
TPTILREGHGCGTYFLVYEALIANQMNKRRGLERKDIPAWKLCI FGALSGTALWLMVYPL
DVIKSVMQTDNLQKPKFGNSISSVAKTLYANGGIGAFFKGFGPTMLRAAPANGATFATFE
LAMRLLG

SEQ ID NO: 84
YPR128C
>sp|Q06497|ANT1_YEAST Peroxisomal adenine nucleotide transporter 1 O5=5accharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ANTl PE=1 SV=1
MLTLESALTGAVASAMANI AVYPLDLSKTI IQSQVSPSSSEDSNEGKVLPNRRYKNVVDC
MINIFKEKGILGLYQGMTVTT VATFVQNFVYFFWYTFIRKSYMKHKLLGLQSLKNRDGPI
TPSTIEELVLGVAAASISQLFTSPMAVVATRQQTVHSAESAKFTNVIKDIYRENNGDITA
FWKGLRTGLALTINPSITYASFQRLKEVFFHDHSNDAGSLSAVQNFILGVLSKMISTLVT
QPLIVAKAMLQSAGSKFTTFQEALLYLYKNEGLKSLWKGVLPQLTKGVIVQGLLFAFRGE
LTKSLKRLI FLYSSFFLKHNGQRKLAST

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
MSEDQKSENSVPSKVNMVNRTDILTTIKSLSWLDLMLPFTI ILSII IAVI ISVYVPSSRH
TFDAEGHPNLMGVSIPLTVGMIVMMIPPICKVSWESIHKYFYRSYIRKQLALSLFLNWVI
GPLLMTALAWMALFDYKEYRQGIIMIGVARCIAMVLIWNQIAGGDNDLCVVLVITNSLLQ
MVLYAPLQIFYCYVISHDHLNTSNRVLFEEVAKSVGVFLGIPLGIGIIIRLGSLTIAGKS
NYEKYILRFISPWAMIGFHYTLFVI FISRGYQFIHEIGSAILCFVPLVLYFFIAWFLTFA
LMRYLSI SRSDTQRECSCDQELLLKRVWGRKSCEASFSITMTQCFTMASNNFELSLAIAI
SLYGNNSKQAIAATFGPLLEVPILLILAIVARILKPYYIWNNRN

SEQ ID NO: 86
YBR008C
>sp| P38124|FLR1_YEAST Fluconazole resistance protein 1
0S=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=FLR1
PE=1 SV=1
MVYTSTYRHTIVVDLLEYLGIVSNLETLQSAREDETRKPENTDKKECKPDYDIECGPNRS
CSESSTDSDSSGSQIEKNDPFRVDWNGPSDPENPQNWPLLKKSLVVFQIMLLTCVTYMGS
SIYTPGQEYIQEEFHVGHVVATLNLSLYVLGYGLGPI IFSPLSETARYGRLNLYMVTLFF
FMIFQVGCATVHNIGGLIVMRFISGILCSPSLATGGGTVADI ISPEMVPLVLGMWSAGAV
AAPVLAPLLGAAMVDAKNWRFIFWLLMWLSAATFILLAFFFPETQHHNILYRRALKLRKE
TGDDRYYTEQDKLDREVDARTFLINTLYRPLKMI IKEPAILAFDLYIAVAYGCFYLFFEA
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
VSSEKPQYSSFWKKI YYEYVWDKSILGVSILDSFMYNQDLKPVEKERRVWSWYNYCYFW
LAECFNINTWQIAATGLQLGLNWWQCWITIWIGYGFVGAFVVLASRVGSAYHLSFPISSR
ASFGIFFSLWPVINRVVMAIVWYSVQAYIAATPVSLMLKSIFGKDLQDKI PDHFGSPNAT
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 S¥=2
MQAQGSQSNVGSLRSNCSDNSLPNNHVMMHCDESSGSPHSEHNDYSYEKTNLESTASNSR
EHRDNQLSRLKSEEYVVPKNQRRGLLPQLAIIPEFKDARDYPPMMKKMIVFLIAFSSMMG
PMGTSI IFPA INSITTEFKTSVIMVNVS IGVYLLSLGVFPLWWSSLSELEGRRTTYITSF
ALLFAFNIGSALAPDINSFIALRMLCGAASASVQSVGAGTVADLYISEDRGKNLSYYYLG
PLLAPLLSPIFGSLLVNRWPWRSTQWFMVILSGCNVILLTVLLPETLRKQDSKGAIAQIL
AERRIQVDNNERGEIQEDYQRGEDETDRIENQVATLSTEKHNYVGEVRDQDSLDLESHSS
PNTYDGRAGETQLQRI YTEASRSLYEYQLDDSGIDATTAQVTRIRSTDPKLARSIRENSL
RKLQTNLEEQVKKVLSSNGGEIAPKQVSAVRKVWDTFFVYFIKPLKSLHFLEYPPVALAI
TFSAISFSTVYFVNMTVEYKYSRPPYNFKPLYIGLLYIPNSVTYFFASI YGGRWVDMLLK
RYKEKYGILAPEARISWNVVTSVISFPIALLIFGWCLDKKCHWVTPLIGTALFGYAAMMT
IGATLSYLVDSLPGKGATGVALNNLIRQILAATAVFVTTPMLNGMGTGWAFTMLAFIVLG
ASSVLIILKKHGDYWRENYDLQKLYDKID

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
MVETFSFAHLAYLVFESVLQVVIIALAGFWSASSGLLPKQSQKI ISLLNVDLFTPCLIFS
KLAKSLSMAKIFEIAI IPIFFGLTTGISFISGKIMSRILDLDKDETNFVVANSVFGNSNS
LPVSLTLSLAYTLPNLTWDQIPNDNRDNVASRGILYLLI FQQIGQMLRWSWGYNKLMKWS
GENTQHMPPSQVQSLLERTPNIDNEELVNEEQEEQELLEEENNRMNSSFLSSSSIGDKIW
QKSCTVFERIRANLNPPLYSMIFAVVVAAIGPLQRELFMEDGFINNTFAEAVTQLGSVSI
PLILVVLGSNLYPSAEVFPKTVHHSKLLIGSI IGRMILPSCFLLPIIAIAVKYINVSILD
DPIFLVVGFLLTVSPPAIQLTQITQLNEFFEAEMADILFWGYAVLSLPVSI IVVSGA IYV
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
NHGSTIDVVVPYAAKDFINEEWPQGVTELKIVERNIIRI YFDPKVIGARDLVNEGWSVPV
SIAPFSCHPTIEVGRKHLVRVGCTTALSIILTIPILVMAWAPQLREKISTISASMVLATI
IQFVIAGPFYLNALKSLI FSRLIEMDLLIVLSTSAAYIFSIVSFGYFVVGRPLSTEQFFE
TSSLLVTLIMVGRFVSELARHRAVKSISVRSLQASSAILVDKTGKETEINIRLLQYGDIF
KVLPDSRIPTDGTVISGSSEVDEALITGESMPVPKKCQSI VVAGSVNGTGTLFVKLSKLP
GNNTISTIATMVDEAKLTKPKIQNIADKIASYFVPTIIGITVVTFCVWIAVGIRVEKQSR
SDAVIQAIIYAITVLIVSCPCVIGLAVPIVFVIASGVAAKRGVIFKSAESIEVAHNTSHV
VFDKTGTLTEGKLTVVHETVRGDRHNSQSLLLGLTEGIKHPVSMAIASYLKEKGVSAQNV
SNTKAVTGKRVEGTSYSGLKLQGGNCRWLGHNNDPDVRKALEQGYSVFCFSVNGSVTAVY
ALEDSLRADAVSTINLLRQRGISLHILSGDDDGAVRSMAARLGIESSNIRSHATPAEKSE
YIKDIVEGRNCDSSSQSKRPVVVFCGDGTNDAIGLTQATIGVHINEGSEVAKLAADVVML
KPKLNNILTMITVSQKAMFRVKLNFLWSFTYNLFAILLAAGAFVDFHI PPEYAGLGELVS
ILPVIFVAILLRYAKI

SEQ ID NO: 91
YBR296C
>sp|P38361 |PH089_YEAST Phosphate permease PH089 OS=Saccharomyces
cerevisiae (strain ATCC 204508 / S288c) GN=PH089 PE=1 SV=1
MALHQFDYIFAIAMLFAFLDAFNIGANDVANSFASSISSRSLKYWQAMVLAGLCEFLGAV
LAGARVSGTIKNNI IDSSIFTNDPAVLMLTMTSALIGSSCWLTFATAIGMPVSTTHSIVG
GTIGAGIAAGGANGVVWGWSGVSQI IASWFIAPILAGAIAAIVFSISRFSVLEVKSLERS
IKNALLLVGVLVFATFS ILTMLIVWKGSPNLHLDDLSETETAVSIVLTGAIASIVYFIFF
YPFYRRKVLDQDWTLKLIDIFRGPSFYFKSTDDIPPMPEGHQLTIDYYEGRRNLGTTVSV
EDEENKAASNSNDSVKNKEDIQEVDLVRTETEPETKLSTKQYWWSLLKQGPKKWPLLFWL

VISHGWTQDVIHAQVNDRDMLSGDLKGMYERSKFYDNRVEYIYSVLQAITAATMSFAHGA
NDVANATGPLSAVYVIWKTNTIGAKSEVPVWVLAYGGVALVIGCWTYGYNIIKNLGNKMI
LQSPSRGFSIELAVAITTVMATQLGIPTSTTQIAVGGIVAVGLCNKDLKSVNWRMVAWCY
SGWFLTLPIAGLIAGI INGI ILNAPRFGVEYQMT

SEQ ID NO: 92
YCL038C
>sp|P25568 |ATG22_YEAST Autophagy-related protein 22 OS=Saccharomyces cerevisiae (strain ATCC 204508 / 5288c) GN=ATG22 PE=1 SV=1
MSYGTINDMNESVTNYRIKKAQNNIKGWYAYSFSSEPFVVSAVSTYIPLLLQQFASINGV
KVHDHSIPCLSETGSDSDKCVLGLFNNRI FVDTSSFALYVFSLSVLFQTI IVISVSGIVD
LWGSVKFKGRILVWFGIVGALSTVAISKLNDTQI YSLAGLYIVANGCFGVINVVGNSLLP
IFVKDSLKCQSQGAYEPDKVDSLTTVISGRGASLGYSSALIVQIVSMFLVASKKGSKQDV
QVAVLFVGIWWFVWQLPMIWLIDDVTIPIRVDDSTLASARSPYPGEQDALGQLNWKNYLS
YGWVSLFESFKHARLLKDVMIFLIAWFIISDSITTINSTAVLFSKAELHMSTLNLIMISV
LTVVNAMLGAFMI PQFLATKFRWTSSQTLMYI IIWASFIPFYGILGFFFNAFGLKHKFEM
FLLAIWYGLSLGGLSAVSRSVFSLIVPPGKESTFFSMFSITDKGSSILGPFLVGLLTDKT
HNIRYSFYFFFLLLMLSLPVLNCLDVKRGRREAEELSQVLPESERRLD

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
LEAGTDTNDIDNTIHQTTFTSSDGTTQREWAHLAAHRDEIRSLLRDEEDVEGTDGRRGAT
EIDLNTKLLHDKYKDSVYYAELSQEIEEVLSEGDEESNVLNGDLPTGQQSAGFLQQLSIL
NSRSFKNMYRNPKLLLGNYLLTILLSLFLGTLYYNVSNDISGFQNRMGLFFFILTYFGFV
TFTGLSSFALERIIFIKERSNNYYSPLAYYISKIMSEVVPLRVVPPILLSLIVYPMTGLN
MKDNAFFKCIGILILFNLGISLEILTIGIIFEDLNNSI ILSVLVLLGSLLFSGLFINTKN
ITNVAFKYLKNFSVFYYAYESLLINEVKTLMLKERKYGLNIEVPGATILSTFGFVVQNLV
FDIKILALFNVVFLIMGYLALKWIVVEQK

SEQ ID NO: 94
YDL054C
>sp|Q07376|**MCH1_YEAST** Probable transporter MCHl OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MCH1 PE=1 SV=1
MPLSKVEHYLSYHTRLLLPHVLSLQSSHRVAYIFSLLSAVSTGFITLISLYSQPWQKHLN
YSSWQINTIASMTNLGMYLTPPILGMIADSHGPITLSLLAIIGFI PSYSYLAYVFNHPEL
SLGGNGDSSFNLSIICFVFIGISTSALYFSALLTCTKLYPHTKLLSISLPTTCYGISSVV
GSQLLRIKWFWSSNASSSSSNSDLNLGRVFQTFALVYVVIGLLAWIATSVVSLLHFNEEQ

DNQKRLDDQTDVEQS PLLERSNHVQEKFTQTMLRI FSDPVTYI LAVSILLSLGPLEMFI A
NMGSLTNLLVQLDAPTLSTKLLSTYALSSTFTRLLTGIVADFFAKKKISIKWILLTFLSL
GVCAQLFLLKMTSSASPWGLVPTGSLVGIVYGGLFTVYPTLVLLVWGERSFGTVYGSLLI
APAIGSMI FCMLYAKFYDSRCMSGGGDLRNPSCISAVYKYSSIAFVVSAVLSAVVFWKLK
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
LQGGALADLTGS IPGI DEALS FMEVMKHIKRQEQGEGETFDTVI FDTAPTGHTLRFLQLP
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
MASEQSSPEINADNLNSSAADVHVQPPGEKEWSDGFYDKEVINGNTPDAPKRGFLGYLI I
YLLCYPVSFGGFLPGWDSGITAGFINMDNFKMNFGSYKHSTGEYYLSNVRMGLLVAMFSV
GCSIGGVAFARLADTLGRRLAIVIVVLVYMVGAIIQISSNHKWYQYFVGKI IYGLGAGGC
SVLCPMLLSEIAPTDLRGGLVSLYQLNMTFGIFLGYCSVYGTRKYSNTAQWRIPVGLCFL
WALIIIVGMLLVPESPRYLIECERHEEACVSIAKINKVSPEDPWVLKQADEINAGVLAQR
ELGEASWKELFSVKTKVLQRLITGILVQTFLQLTGENYFFFYGTTI FKSVGLTDGFETSI
VLGTVNFFSTIIAVMVVDKIGRRKCLLFGAASMMACMVIFASIGVKCLYPHGQDGPSSKG
AGNAMIVFTCFYIFCFATTWAPVAYIVVAESFPSKVKSKAMSISTAFNWLWQFLIGFFTP
FITGSIHFYYGYVFVGCLVAMFLYVFFFLPETIGLSLEEIQLLYEEGIKPWKSASWVPPS
RRGASSRETEAKKKSWKEVLKFPKSFN

SEQ ID NO:97
YDL247W
>sp|P0CD99|MPH2__YEAST Alpha-glucosides permease MPH2
OS=Saccharomyces cerevisiae (strain ATCC 204508 / 5288c) GN=MPH2
PE=2 SV=1
MKNLSFLINRRKENTSDSNVYPGKAKSHEPSWIEMDDQTKKDGLDIVHVEFSPDTRAPSD
SNKVITEIFDATEDAKEADESERGMPLATALNTYPKAAAWSLLVSTTLIMEGYDTAILGA
FYALPIFQRKFGSQNDKTGEWEISASWQIGLTLCYMAGEIVGLQLTGPSVDLVGNRYTLI
IALFFLAAFTFILYFCNSLGMIAVGQALCGMPWGCFQCLTVSYASEICPLALRYYLTTYS
NLCWLFGQLFAAGIMKNSQKKYADSELGYKLPFALQWILPVPLALGIFFAPESPWWLVKK
GRFDEARRSLRRTLSGKGPEKEILVTLEVDKIKVTIDKEKRLTSKEGSYSDCFEDKINRR
RTRITCLCWAGQATCGSILIGYSTYFYEKAGVSTEMSFTFSI IQYCLGICATFLSWWASK
YFGRYDLYAFGLAFQTIVFFI IGGLGCSSTHGSKMGSGSLLMAVAFFYNLGIAPVVFCLV
SEMPSSRLRTKTI ILARNTYNVVSI ICSVLILYQLNSKKWNWGAKSGFFWGVLCFCTLIW
AVVDLPETAGKTFVEINELFKLGVSARKFKSTKVDPFVVKTPLKTSLITTPREISKLPLQ
RNSNVSHHL

SEQ ID NO: 98
YDR011W
>sp IP32568 |SNQ2_YEAST Protein SNQ2 0S=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SNQ2 PE=1 SV=2
MSNIKSTQDSSHNAVARSSSASFAASEESFTGITHDKDEQSDTPADKLTKMLTGPARDTA
SQISATVSEMAPDVVSKVESFADALSRHTTRSGAFNMDSDSDDGFDAHAIFESFVRDADE
QGIHIRKAGVT IEDV'SAKG VDAS ALEGAT FGNILCLPLTIFKGIKAKRHQKMRQ1ISNVN
ALAEAGEMILVLGRPGAGCSSFLKVTAGEIDQFAGGVSGEVAYDGIPQEEMMKRYKADVI
YNGELDVHFPYLTVKQTLDFAIACKTPALRVNNVSKKEYIASRRDLYATIFGLRHTYNTK
VGNDFVRGVSGGERKRVSIAEALAAKGSIYCWDNATRGLDASTALEYAKAIRIMTNLLKS
TAFVTIYQASENI YETFDKVTVLYSGKQI YFGLIHEAKPYFAKMGYLCPPRQATAEFLTA
LTDPNGFHLIKPGYENKVPRTAEEFETYWLNSPEFAQMKKDIAAYKEKVNTEKTKEVYDE
SMAQEKSKYTRKKSYYTVSYwEQVKLCTQRGFQRI YGNKSYTVINVCSAIIQSFITGSLF
YNTPSSTSGAFSRGGVLYFALLYYSLMGLANISFEHRPILQKHKGYSLYHPSAEAIGSTL
ASFPFRMIGLTCFFIILFFLSGLHRTAGSFFTIYLFLTMCSEAINGLFEMVSSVCDTLSQ
ANSISGILMMSISMYSTYMIQLPSMHPWFKWISYVLPIRYAFESMLNAEFHGRHMDCANT
LVPSGGDYDNLSDDYKVCAFVGSKPGQSYVLGDDYLKNQFQYVYKHTWRNFGILWCFLLG
YVVLKVIFTEYKRPVKGGGDALIFKKGSKRFIAHADEESPDNVNDIDAKEQFSSESSGAN
DEVFDDLEAKGVFIWKDVCTTI PYEGGKRMLLDNVSGYCI PGTMTALMGESGAGKTTLLN
TLAQRNVGI ITGDMLVNGRPIDASFERRTGYVQQQDIHIAELTVRESLQFSARMRRPQHL
PDSEKMDYVEKI IRVLGMEEYAEALVGEVGCGLNVEQRKKLS IGV'ELVAKPDLLLFLDEP
TSGLDSQSSWAI IQLLRKLSKAGQSILCTIHQPSATLFEEFDRLLLLRKGGQTVYFGDIG
KNSATILNYFERNGARKCDSSENPAEYILEA IGAGATASVKEDWKEKWLNSVEFEQTKEK
VQDLINDLSKQETKSEVGDKPSKYATSYAYQFRYVLIRTSTSFWRSLNYIMSKMMLMLVG
GLYIGFTFFNVGKSYVGLQNAMFAAFISIILSAPAMNQIQGRAIASRELFEVRESQSNMF
HWSLVLITQYLSELPYHLFFSTIFFVSSYFPLRIFFEASRSAVYFLNYCIMFQLYYVGLG
LMILYMSPNLPSANVILGLCLSFMLSFCGVTQPVSLMPGFWTFMWKASPYTYFVQNLVGI
MLHKKPVVCKKKELNYFNPPNGSTCGEYMKPFLEKATGYIENPDATSDCAYCIYEVGDNY
LTH ISSKYSYLWRNFGIFWIYIFFN1IAMVCVYYLFHVRQ3 SFLSPVS ILNKIKNIRKKK
Q

SEQ ID NO: 99
YDR2 92C
>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
GEALVGTDSVQQAKN FNDAFGKGRNL DFFI ISKC DTVGEMLGTMVNMVYATGI PILFVGV
GQTYTDLRTLSVKWAVNTLMS

SEQ ID NO: 100
YDR497C
>sp IP30605 |ITRl__YEAST Myo-inositol transporter 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ITR1 PE=1 SV=2

MGIHI PYLTSKTSQSNVGDAVGNADSVEFNSEHDSPSKRGKITLESHEIQRAPASDDEDR
IQIKPVNDEDDTSVMITFNQSLSPFI ITLTFVASISGFMFGYDTGYISSALISIGTDLDH
KVLTYGEKEIVTAATSLGALITSIFAGTAADI FGRKRCLMGSNLMFVIGAI LQVSAHTFW
QMAVGRLIMGFGVGIGSLIAPLFISEIAPKMIRGRLTVINSLWLTGGQLVAYGCGAGLNY
VNNGWRILVGLSLIPTAVQFTCLCFLPDTPRYYVMKGDLARATEVLKRSYTDTSEEIIER
KVEELVTLNQSIPGKNVPEKVWNTIKELHTVPSNLRALIIGCGLQAIQQFTGWNSLMYFS
GTIFETVGFKNSSAVSIIVSGTNFIFTLVAFFSIDKIGRRTILLIGLPGMTMALVVCSIA
FHFLGIKFDGAVAVVVSSGFSSWGIVIIVFI IVFAAFYALGIGTVPWQQSELFPQNVRGI
GTSYATATNWAGSLVIASTFLTMLQNITPAGTFAFFAGLSCLSTIFCYFCYPELSGLELE
EVQTILKDGFNI KAS KALAKKRKQQVARVHELKYE PTQEIIEDI

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
MNNGDNKTTLENSKNASLANGNYAIPTKLNRLKKNADPRVAAIS GALS GALS AMLVCPFD
VAKTRLQAQGLQNMTHQSQHYKGFFGTFATI FKDEGAAGLYKGLQPTVLGYI PTLMIYFS
VYDFCRKYSVDIFPHSPFLSNASSAITAGAISTVATNPIWVVKTRLMLQTGIGKYSTHYK
GTIDTFRKI IQQEGAKALYAGLVPALLGMLNVAIQFPLYENLKIRFGYSESTDVSTDVTS
SNFQKLILASMLSKMVASTVTYPHEILRTRMQLKSDLPNTVQRHLLPLIKITYRQEGFAG
FYSGFATNLVRTVPAAVVTLVSFEYSKKYLTTFFQ

SEQ ID NO: 102
YEL027W
>sp|P2551 5|VATL1_YEAST V-type proton ATPase subunit c OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VMA3 PE=1 SV=1
MTELCPVYAPFFGAIGCASAIIFTSLGAAYGTAKSGVGICATCVLRPDLLFKNIVPVIMA
G I IAIYGLVVSVLVCYSLGQKQALYTGFIQLGAGLSVGLSGLAAGFAIGIVGDAGVRGSS
QQPRLFVGMILILIFAEVLGLYGLIVALLLNSRATQDVVC

SEQ ID NO: 103
YEL065W
>sp IP39980 ISIT1JYEAST Siderophore iron transporter 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SIT1 PE=3 SV=1
MDPGIANHTLPEEFEEVVVPEMLEKEVGAKVDVKPTLTTSSPAPSYIELIDPGVHNIEIY
AEMYNRPI YRVALFFSLFLIAYAYGLDGNIRYTFQAYATSSYSQHSLLSTVNCIKTVIAA
VGQIFFARLSDI FGRFSIMIVSI IFYSMGTI IESQAVNITRFAVGGCFYQLGLTGIILIL
EVIASDFSNLNWRLLALFIPALPFIINTWISGNVTSAIDANWKWGIGMWAFILPLACIPL
GICMLHMRYLARKHAKDRLKPEFEALNKLKWKSFCIDIAFWKLDIIGMLLITVFFGCVLV
P FTLAGGLKEEWKTAH I 1V PEV IGWVVVLPLYM LWE IKYSRHPLT PWDL IQDRGI FFALL
IAFFINFNWYMQGDYMYTVLVVAVHESIKSATRITSLYSFVSVIVGTILGFILIKVRRTK
PFIIFGISCWIVSFGLLVHYRGDSGAHSGI IGSLCLLGFGAGSFTYVTQASIQASAKTHA
RMAVVTSLYLATYNIGSAFGSSVSGAVWTNILPKEISKRISDPTLAAQAYGSPFTFITTY
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=i
MESNKQPRKIQLYTKEFYATCTLGGI IACGPTHSSITPLDLVKCRLQVNPKLYTSNLQGF
RKIIANEGWKKVYTGFGATFVGYSLQGAGKYGGYEYFKHLYSSWLSPGVTVYLMASATAE
FLADIMLCPFEAIKVKQQTTMPPFCNNVVDGWKKMYAESGGMKAFYKGIVPLWCRQIPYT
MCKFTSFEKIVQKIYSVLPKKKEEMNALQQISVSFVGGYLAGILCAAVSHPADVMVSKIN
SERKANESMSVASKRIYQKIGFTGLWNGLMVRIVMIGTLTSFQWLIYDSFKAYVGLPTTG

SEQ ID NO: 106

YER119C

>sp|P40074 IAVT6_YEAST Vacuolar amino acid **transporter** 6 OS=Saccharomyces **cerevisiae (strain** ATCC 204508 / S288c) GN=AVT6 PE=1 SV=1
MVASIRSGVLTLLHTACGAGILAMPYAFKPFGLIPGVIMIVLCGACAMQSLFIQARVAKY
VPQGRASFSALTRLINPNLGIVFDLAIAIKCFGVGVSYMIVVGDLMPQIMSVWTRNAWLL
NRNVQISLIMLFFVAPLSFLKKLNSLRYASMVAI SSVAYLCVLVLLHYVAPS DEILRLKG
RISYLLPPQSHDLNVLNTLPIFVFAYTCHHNMFS IINEQRSSRFEHVMKIPLIAISLALI
LYIAIGCAGYLTFGDNI IGNI IMLYPQAVSSTIGRIAIVLLVMLAFPLQCHPARASIHQI
LQHFAEENVSISATSADEPTVATESSPLIRDSSLDLNEVIEEESI YQPKETPLRGKSFIV
ITCSILVASYLVAISVSSLARVLAIVGATGSTSISFILPGLFGYKLIGTEHKTAVPLTTK
I FKYTGLLLFIWGLIIMITCLTAALKLN

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
LDGKILVNGLDPFSPLSMNQVDDDESVEDSTNYQTTTYLGTEWCHMSI INRDIGVLELLK
SIGFDHFRERGERLVRILDIDVRWRMHRLSDGQKRRVQLAMGLLKPWRVLLLDEVTVDLD
VIARARLLEFLKWETETRRCS VVYATHIFDGLAKWPNQVYHMKSGKI VDNLDYQKDVEFS
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
ALNVAAFGKTILRFVTFDKLCHSLNNNIDNNDNFQRLTGYNLLIAGTLTGIVESLFI IPF
ENIKTTLIQSAMIDHKKLEKNQPVVNAKATFHKVATKSTPVARIEKLLPAVKHMYQTRGP

AAFVQG7TATTFRQ IANTSIQ FTAYTAFKRL LQARN DKAS SV ITGLATSFTLVAMTQPID
VVKTRMMSQNAKTEYKNTLNCMYRI FVQE GMATFWKGSIFRFMKVGI SGGLTFTVYEQVS
LLLGFSSRS

SEQ ID NO: 109

YGL084C

>sp|P53154|GUP1___YEAST Glycerol uptake protein 1 OS=Saccharomyces cerevisiae {strain ATCC 204508 / 5288c) GN=GUP1 PE=1 SV=1
MSLISILSPLITSEGLDSRIKPSPKKDASTTTKPSLWKTTEFKFYYIAFLVVVPLMFYAG
LQASSPENPNYARYERLLSQGWLFGRKVDNSDSQYRFFRDNFALLSVLMLVHTSIKRIVL
YSTNITKLRFDLIFGLIFLVAAHGVNSIRILAHMLILYAIAHVLKNFRRIATISIWIYGI
STLFINDNFRAYPFGNICSFLSPLDHWYRGI IPRWDVFFNFTLLRVLSYNLDFLERWENL
QKKKSPSYESKEAKSAILLNERARLTAAHPIQDYSLMNYIAYVTYTPLFIAGPI ITFNDY
VYQSKHTLPSINFKFIFYYAVRFVIALLSMEFILHFLHVVAISKTKAWENDTPFQISMIG
LFNLNI IWLKLLI PWRLFRLWALLDGI DTPENMIRCVDNNYSSLAFWRAWHRS YNKWVVR
Y IYIPLGGSKNRVLTSLAVFSFVAIWHDIELKLLLWGWLI VLFLLPEIFATQIFSHYTDA
VWYRHVCAVGAVFNIWVMMIANLFGFCLGSDGTKKLLSDMFCTVSGFKFVILASVSLFIA
VQIMFEIREEEKRHGI YLKC

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
MNRILSSASLLSNVSMPRQNKHKITKALCYAI IVASIGSIQFGYHLSELNAPQQVLSCSE
FDIPMEGYPYDRTWLGKRGYKQCI PLNDEQIGIVTSVFCIGGILGSYFATSLANI YGRKF
SSLINCTLNIVGSLII FNSNSYRGLI IGRILVGISCGSLIVI IPLFIKEVAPSGWEGLLG
SMTQICIRLGVLLTQGIALPLTDSYRWRWILFGSFLIAVLNFFMWFIVDESPKWLLAHGR
VTDAKLSLCKLRGVTFDEAAQEIQDWQLQIESGDPLIEPTTTNSISGSNSLWKYLRDRTN
VKSRHVITVLLFGQQFCGINSIVLYGTKI ISQLYPQHAIRINFFISMVNVLVTILVSLLI
HSLPRKPLLMTSTVLVSVTAFIMGIAMNHNKMNLLIVFSFI YMGVFTMGLNPLPFIIMRE
VSKPQDMVLAQRYGTICNWVGTFI IAYTFPI IHDVLSGYVFI IFAI IACSISAFIWKKVP
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
SILSTGSENYRANI IILLKTFVVSSLYTMVSYFVPVIRSIPVFGKYLSNNYLWNFQPSPA
YIGQGI IMGLPTVSYMLIGCFLGWGVLAPLARYKRWVPPDADVHDWEEGVQGWILWSSLS
IMVADSVVAFI VVTVKSIVKFILI DDKAALLNNIIDDTFQSMLLEEERAINSSRRNTYVD
GRQDTVRLVSRDNEIEVDSKHLVRYTTVISGCLVSSIICIVSII YLFGIQVIPLYAI ITA
LILALFLSILGIRALGETDLNPVSGIGKISQLIFAFI IPRDRPGSVLMNVVSGGIAEASA
QQAGDLMQDLKTGHLLGAS PRAQFCAQLI GACWS 11LSSFMYLC YNKVYS IPSEQFRI PT
AVVWIDCARLVTGKGLPDKALECSMILGVIFAVLSLIRNTYRDYGYGWILYIPSGVAVGV
GIFNSPSFTIARFIGGWASHFWLKNHRGDLNAKTKMIVFSSGLVLGEGIFSVINMLFICL
NVPHY

SEQ ID NO: 112
YGL167C
>sp| P13586 |ATC1_YEAST Calcium-transporting ATPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / 5288c) GN=PMR1 PE=1 SV=1
MSDNPFNASLLDEDSNREREILDATAEALSKPSPSLEYCTLSVDEALEKLDTDKNGGLRS
SNEANNRRSLYGPNEITVEDDESLFKKFLSNFIEDRMILLLIGSAVVSLFMGNI DDAVSI
TLAIFI VVTVGFVQEYRSEKSLEALNKLVPAECHLMRCGQESHVLASTLVPGDLVHFRIG
DRIPADIRI IEAIDLSIDESNLTGENEPVHKTSQTIEKSSFNDQPNSIVPISERSCIAYM
GTLVKEGHGKGIVVGTGTNTSFGAVFEMMNNIEKPKTPLQLTMDKLGKDLSLVSFIVIGM
ICLVGI IQGRSWLEMFQISVSLAVAAI PEGLPI IVTVTLALGVLRMAKRKAI VRRLPSVE
TLGSVNVICSDKTGTLTSNHMTVSKLWCLDSMSNKLNVLSLDKNKKTKNSNGNLKNYLTE
DVRETLTIGNLCNNASFSQEHAIFLGNPTDVALLEQLANFEMPDIRNTVQKVQELPFNSK
RKLMATKILNPVDNKCTVYVKGAFERILEYSTSYLKSKGKKTEKLTEAQKATINECANSM
ASEGLRVFGFAKLTLSDSSTPLTEDLIKDLTFTGLIGMNDPPRPNVKFAIEQLLQGGVHI
IMITGDSENTAVNIAKQIGIPVI DPKLSVLSGDKLDEMSDDQLANVI DHVNIFARATPEH
KLNIVRALRKRGDVVAMTGDGVN DAPALKLSDIGVSMGRIGTDVAKEASDMVLTDDDFST
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
LVKTKLQSI PRSSKSTKTWMMVKDLLNETRQEMKMVGPSRALFKGLEITLWRDVPFSAI Y
WSSYELCKERLWLDSTRFASKDANWVHFINSFASGCISGMIAAICTHPFDVGKTRWQISM
MNNSDPKGGNRSRNMFKFLETIWRTEGLAALYTGLAARVIKIRPSCAIMISSYEISKKVF
GNKLHQ

SEQ ID NO: 114
YHL035C
>sp|P38735|VMR1__YEAST ABC transporter ATP-binding protein/permease VMRl OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=VMR1 PE=2 SV=1
MGTDPLI IRNNGSFWEVDDFTRLGRTQLLSYYLPLAIIASIGI FALCRSGLSRYVRSAEC
DLVNEYLFGAQEERKEDNSIERLLRNSNTQANYVNVKKQGRILKLRHFDITTIDVKQIDA
KNHGGLTFSRPSTSDHLRKSSEIVLMSLQI IGLSFLRVTKINIELTNRDVTTLLLFWLIL
LSLSILRVYKRSTNLWAICFTAHTTIWISTWI PIRSVYIGNIDDVPSQI FYI FEFVITST
LQPIKLTSPIKDNSSII YVRDDHTSPSREHISSILSCITWSWITNFIWEAQKNTIKLKDI
WGLSMEDYSIFILKGFTRRNKHINNLTLALFESFKTYLLIGMLWVLVNSIVNLLPTILMK
RFLEIVDNPNRSSSCMNLAWLYI IGMFICRLTLAICNSQGQFVSDKICLRIRAILIGEI Y
AKGLRRRLFTSPKTSSDSDSISANLGTIINLISIDSFKVSELANYLYVTVQAVIMIIVVV
GLLFNFLGVSAFAGISIILVMFPLNFLLANLLGKFQKQTLKCTDQRISKLNECLQNIRI V
KYFAWERNIINEIKSIRQKELRSLLKKSLVWSVTSFLWFVTPTLVTGVTFAICTFVQHED
LNAPLAFTTLSLFTLLKTPLDQLSNMLSFINQSKVSLKRISDFLRMDDTEKYNQLTISPD
KNKIEFKNATLTWNENDSDMNAFKLCGLNIKFQIGKLNLILGSTGSGKSALLLGLLGELN

LISGSIIVPSLEPKHDLIPDCEGLTNSFAYCSQSAWLLNDTVKNNI IFDNFYNEDRYNKV
IDACGLKRDLEILPAGDLTEIGEKGITLSGGQKQRISLARAVYSSAKHVLLDDCLSAVDS
HTAVWIYENCITGPLMKNRTCILVTHNVSLTLRNAHFAIVLENGKVKNQGTITELQSKGL
FKEKYVQLSSRDSINEKNANRLKAPRKNDSQKIEPVTENINFDANFVNDGQLIEEEEKSN
GAISPDVYKWYLKFFGGFKALTALFALYITAQILFISQSWWIRHWVNDTNVRINAPGFAM
DTLPLKGMTDSSKNKHNAFYYLTVYFLIGI IQAMLGGFKTMMTFLSGMRASRKI FNNLLD
LVLHAQIRFFDVTPVGRIMNRFSKDIEGVDQELI PYLEVTIFCLIQCASI IFLITVITPR
FLTVAVIVFVLYFFVGKWYLTASRELKRLDSITKSPIFQHFSETLVGVCTIRAFGDERRF
ILENMNKIDQNNRAFFYLSVTVKWFSFRVDMIGAFIVLASGSFILLNIANIDSGLAGISL
TYAILFTDGALWLVRLYSTFEMNMNSVERLKEYSSIEQENYLGHDEGRILLLNEPSWPKD
GEIEIENLSLRYAPNLPPVIRNVSFKVDPQSKIGIVGRTGAGKSTI ITALFRLLEPITGC
IKIDGQDISKIDLVTLRRSITI IPQDPILFAGTIKSNVDPYDEYDEKKI FKALSQVNLIS
SHEFEEVLNSEERFNSTHNKFLNLHTEIAEGGLNLSQGERQLLFIARSLLREPKI ILLDE
ATSSIDYDSDHLIQGI IRSEFNKSTILTIAHRLRSVIDYDRIIVMDAGEVKEYDRPSELL
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
QGRHLGVFSTVVLFVSRIMGSGIFAVPSVILLNTGGNKLIYFAIWVFSAAIAFAGLYLFL
EFGSWIPKSGGRKNFLERSFERPRLLIS VVFSCYSVLTGYALTGSIVFGKYVLSAFGVTD
DSWSKYVSISFIIFAVLIHGVSVRHGVFIQNALGGLKLIMIVLMCFAGLYTLFFYKSTGQ
VAWDLPVTQVEKDSLLSVSSIATAFISSFFCFSGWDTVHTVTSEIKNPVKTLKVSGPLSL
IICFVCYTMMNVAYLKVLTYEEIVSAGPLVGSVLFTKLFGPRVGGKFIAFSIAISAASNI
LVVI YSISRVNQEIFKEGYLPFSIHMSKNWPFDAPLPSISLCGFITIAWILILPKEGESF
NYLVSMDGYGNQFFLLLVAIGLFIWRFKHKNEVPEIRASTFGVLAI ITLSLYMLMAPFFA
DPSLNRVGFLPPYQIMSLLVIVACFFFWLVKFVLLPKFFHYKLLPKITYLHDGLI VTEWV
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
NTLIPSKEFESHWRRLVSGSLAGLCSVFITYPLDLVRVRLAYETEHKRVKLGRI IKKI YK
EPASATLIKNDYIPNWFCHWCNFYRGYVPTVLGMIPYAGVSFFAHDLLHDVLKSPFFAPY
SVLELSEDDELERVQKKQRRPLRTWAELISGGLAGMASQTAAYPFEI IRRRLQVSALSPK
TMYDHKFQS ISEIAH 11FKERGVRGFFVGLSI GY IKVTPMVACS FFVYERMKWNFGI

SEQ ID NO: 117
YHR096C
>sp IP38 695|HXT5_YEAST Probable glucose transporter HXT5
OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HXT5
PE=1 SV=1
MSELENAHQGPLEGSATVSTNSNSYNEKSGNSTAPGTAGYNDNLAQAKPVSSYISHEGPP

KDELEELQKEVDKQLEKKSKSDLLFVSVCCLMVAFGGFVFGWDTGTISGFVRQTDFIRRF
GSTRANGTTYLSDVRTGLMVSIFNIGCAIGGIVLSKLGDMYGRKIGLMTVVVIYSIGIII
QIASIDKWYQYFIGRIISGLGVGGITVLAPMLISEVSPKQLRGTLVSCYQLMITFGIFLG
YCTNFGTKNYSNSVQWRVPLGLCFAWSIFMIVGMTFVPESPRYLVEVGKIEEAKRSLARA
NKTTEDSPLVTLEMENYQSS IEAERLAGSASWGELVTGKPQMFRRTLMGMMIQSLQQLTG
DNYFFYYGTTIFQAVGLEDSFETAIVLGVVNFVSTFFSLYTVDRFGRRNCLLWGCVGMIC
CYVVYAS VGVTRLWPNGQDQPSSKGAGNCMIVFACFYIFCFATTWAPVAYVLI SESYPLR
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
MTQTDNPVPNCGLLPEQQYCSADHEEPLLLHEEQLIFPDHSSQLSSADI   IEPIKMNSSTE
SIIGTTLRKKWVPLSSTQITALSGAFAGFLSGVAVCPLDVAKTRLQAQGLQTRFENPYYR
GIMGTLSTIVRDEGPRGLYKGLVPIVLGYFPTWMI   YFSVYEFSKKFFHGIFPQFDFVAQS
CAAITAGAASTTLTNPIWVVKTRLMLQSNLGEHPTHYKGTFDAFRKLFYQEGFKALYAGL
VPSLLGLFHVAIHFPIYEDLKVRFHCYSRENNTNSINLQRLIMASSVSKMIASAVTYPHE
ILRTRMQLKS DIPDS IQRRLFPLI KATYAQEGLKGFYSGFTTNLVRT IPASAITLVS FEY
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
SRFSHKQKMLLVVQCAFTGFFSTVAGSIYYPVLTIIERKFNITEELANVTI   VVYFIFQGV
APS IMGGLADTFGRRPI VLWAILAYFCAC IGLACAHNYAQI LALRCLQAAGI SPVIAINS
GIMGDVTTKVERGGYVGLVAGFQVVGTAFGALIGAGLSSKWGWRAIFWFLAIGSGICLVF
STLLMPETKRTLVGNGSVTPRSFLNRSLILHVGSVKKTLHLDDPDPETLEPRTSVDFLAP
LKILHIREI DILLS IAGLQFSTWTTHQTALTIVLSKKYNLSVAKIGLCFLPAGISTLTSI
ISAGRYLNWSYRTRKVKYNRWIKEQELQLMEKYKGDKNKVAELIHSNSHYAFNLVEARLH
PAFVTLLLSSIGFTAFGWCISVKTPLAAVLCTSAFASLFSNCILTFSTTLIVDLFPSKAS
TATGCLNLFRCLLSAIFIAALTKMVEKMRYGGVFTFLSAITSSSSLLLFYLLKNGKQLSF
DRIRANDKSAGRSVGKNSEKVST

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
TVLIAQCAFTGFFSTIAGAIYYPVLS VIERKFDIDEELVNVTVVVYFVFQGLAPTFMGGF
ADSLGRRPVVLVAIVI YFGACIGLACAQTYAQI IVLRCLQAAGI SPVIAINSG1MGDVTT
RAERGGYVGYVAGFQVLGSAFGALIGAGLSSRWGWRAI   FWFLAIGSGICFLASFLILPET
KRNISGNGSVTPKSYLNRAPILVLPTVRKSLHLDNPDYETLELPTQLNLLAPFKILKAYE
ICILMLVAGLQFAMYTTHLTALSTALSKQYHLTVAKVGLCYLPSGICTLCSI   VIAGRYLN
WNYRRRLKYYQNWLGKKRSKLLEEHDNDLNLVQRIIENDPKYTFNIFKARLQPAFVTLLL

SSSGFCAYGWCITVKAPLAAVLCMSGFASLFSNCILTFSTTLI VDLFPTKTSTATGCLNL
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
PEFTWTKDEEKKLVRKMDLKIFLWVFIMFAFLDLIRKNIARAVSDNFIVDLKMNTNDYNL
GQTVYLVIFLASELPGNLLSKRFGPERVIPVQIVLWSVICITQAGLKNRGQFIATRCLLG
MVQGGFIPDNILYLSYYYTGAELTFRLSFFWCAIPLFQILGSLLASGI IEMRGIHNLAGW
QYLFIIEGFLSLSVGVASFYLMRRGPTQTGESAFHKGKSLFTEYEEKIMVNRILRDDPSK
GDMSNRQPVTFKEILYTLTEFDLWPLFIQGITAFISLQTVGSYLSLILKSLNYSTFLSNI
LAIPGQALLLINLPLAALLSRKLKEKSLCVGIANVWVLPFIVSLVALPTDTNPWIKYILL
TGILGLPYTHSILAGWVSEISNSVRSRTVGTALYNMSAQVGAIIASNMYRNDDKPYYTRG
NKILLGFTCFNICMAVATKFYYISRNKYKDRKWNSMTKEEQINYLDTTKDKGMKRLDYRF
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
AFYYSYPTTLVMNI PFAAFNFVIYESSTKFLNPSNEYNPLIHCLCGSISGSTCAAITTPL
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
VAILCLMIAFGGFI FGWDTGTISGFVNLSDFIRRFGQKNDKGTYYLSKVRMGLI VSIFNI
GCAIGGIVLSKVGDIYGRRIGLITVTAI YVVGILIQITSINKWYQYFIGRIISGLGVGGI
AVLSPMLISEVAPKQIRGTLVQLYQLMCTMGI FLGYCTNYGTKNYHNATQWRVGLGLCFA
WTTFMVSGMMFVPESPRYLIE VGKDEEAKRSLSKSNKVSVDDPALLAEYDTIKAGIELEK
LAGNASWSELLSTKTKVFQRVLMGVMIQSLQQLTGDNYFFYYGTTI FKSVGLKDSFQTSI
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
YKL0 50C
>sp|P35736|YKF0_YEAST Uncharacterized protein YKL050C
OS=Saccharomyces cerevisiae (strain ATCC 204508 / 5288c) GN=YKL050C
PE=1 SV=1
MSLISALQTTDVESVQTSPEQITERKAVRVSTLQESLHSSEMHRAAPETPRSI SNSVHKL
KTIYSTYQQSGQPLSKEAIFRAKQKYGILNTPANYKTLGLGDSKSESVDLAARLASKRTK
VSPDDCVETAIEQKARGEAFKVTFSKIPLTPPEDVPITVNLGLKGRRDFLTRLAAQKALA
FSPSLDNSMKGTSDSSSVKKKRFSGAPIGNEFDANLVNPQHPAGFKSLDLSKVLDGAERR
AISRVNDRLYPQKVNFKNGLQSSDQSGVSKANKEVFKKGTLEKLEHSAEQFLESHAGNER
QRLSDQQYMCAKGAADAVKDLDPKTLEDPDFAAREAQKKLYIKQVASPVVLNEAQKLANR
KLQDIDSRDTYMLLFGNQAYNKLAVNIALQHYSVKQEEKKKIYLGGGLWMTPEEVNAVAK
KLISPVVNEIDERASRQRDVDKDIERRSRVLDQEYEDGNSMERAKEQNDGQLLLAMASKQ
QQEKEAKKAEEGQRYDQFVQKMNIKLQQKEKELENARENRENLRNELQERLSKNLSGEND
ELNDWNDACERDLKNSSIEHYYAVRSHFDNLGNSERGYDELLEERSKIQVEIERLVASIA
EHKTAIHGFGETADAGGAIPAVQKQKI PTRKDLLDATVNDPLVISAEMAKEEAEMATEEC
MLKELQVDEMI IIRNIMLRECEKKLEEEKETAKRSRRGTEESKNNSNFSRDVIMSTPDNN
EKVTPIGKSASPKDVVKSRFLSTYNTGKDIDSSASARSITGVSGVLDDGPKTPTSNKENE
LIDDEVKSYKVHQAVDGTGEDSIANKRDKSSRPAANSGGSITIEQFLFNKNADKQGLSKT
ESVTMKREPVVDQMDSKKGHDFTHCNDNGRRSFSGFSQGSIENDYSNEVTDDQDDQEGSE
IRVRDSNDSNTSPKESFFKEVI

SEQ ID NO: 126
YKL120W
>sp|P32332|OACl_YEAST Mitochondrial oxaloacetate transport protein
OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=OACl
PE=1 SV=1
MSSDNSKQDKQIEKTAAQKISKFGSFVAGGLAACIAVTVTNPIELIKIRMQLQGEMSASA
AKVYKNPIQGMAVIFKNEGIKGLQKGLNAAYIYQIGLNGSRLGFYEPIRSSLNQLFFPDQ
EPHKVQSVGVNVFSGAASGI IGAVIGSPLFLVKTRLQSYSEFIKIGEQTHYTGVWNGLVT
IFKTEGVKGLFRGIDAAILRTGAGSSVQLPIYNTAKNILVKNDLMKDGPALHLTASTISG
LGVAVVMNPWDVILTRI YNQKGDLYKGPIDCLVKTVRIEGVTALYKGFAAQVFRIAPHTI
MCLTFMEQTMKLVYSIESRVLGHN

SEQ ID NO: 127
YKL14 6W
>sp|P36062[AVT3__YEAST Vacuolar amino acid transporter 3
OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=AVT3
PE=1 SV=1
MNGKEVSSGSGRTQSNNNKKNNNGGSTGISHASGSPLTDGNGGNSNGNSRSRSRSRKSSG
TTGGLLKKPPLLVNNEAVHASVPDASHTSCNNGTLEVSINNPEPHVVDAVARHLIRNPSN
SLQLQGGDITRDLYKWTNDHPSSPSQYQYPSQPALSTSI PSQAPSFSNRKRSMSFSAASI
ASSSHLNNNSEANGNPLAAIGLAPAPMTHEEIRAPGGFRRSFI IQKRRKHNVDAPI PNFF
TRNFIEFLTLYGHFAGEDLSEEEEEEETEEEPEEEALETESTQLVSREHGRHPHKSSTV

KAVLLLLKSFVGTGVLFLPKAFHNGGWGFSALCLLSCALI SYGCFVSLITTKDKVGVDGY
GDMGRILYGPKMKFAILSSIALSQIGFSAAYTVFTATNLQVFSENFFHLKPGSISLATYI
FAQVLIFVPLSLTRNIAKLSGTALIADLFILLGLVYVYVYSI YYIAVNGVASDTMLMFNK
ADWSLFIGTAIFTFEGIGLLIPIQESMKHPKHFRPSLSAVMCI VAVIFISCGLLCYAAFG
SDVKTVVLLNFPQDTSYTLTVQLLYALAILLSTPLQLFPAIRILENWTFPSNASGKYNPK
VKWLKNYFRCAIVVLTSILAWVGANDLDKFVSLVGSFACIPLI YIYPPLLHYKASILSGT
SRARLLLDLI VIVFGVAVMAYTSWQT IKMWSQ

SEQ ID NO: 128

YKL209C

>sp| P12866 ISTE6___YEAST Alpha-factor-transporting ATPase
OS=Saccharomyces cerevisiae (strain ATCC 204508 / 5288c) GN=STE6
PE=1 SV=1
MNFLSFKTTKHYHIFRYVNIRNDYRLLMIMI IGTVATGLVPAITSILTGRVFDLLSVFVA
NGSHQGLYSQLVQRSMAVMALGAASVPVMWLSLTSWMHIGERQGFRIRSQILEAYLEEKP
MEWYDNNEKLLGDFTQINRCVEELRSSSAEASAITFQNLVAICALLGTSFYYSWSLTLII
LCSSP1ITFFAVVFSRMIHVVYSEKENSETSKAAQLLTWSMNAAQLVRLYCTQRLERKKFK
EIILNCNTFFIKSCFFVAANAGILRFLTLTMFVQGFWFGSAMIKKGKLNINDVITCFHSC
IMLGSTLNNTLHQIVVLQKGGVAMEKIMTLLKDGSKRNPLNKTVAHQFPLDYATSDLTFA
NVSFSYPSRPSEAVLKNVSLNFSAGQFTFIVGKSGSGKSTLSNLLLRFYDGYNGSISING
HNIQTIDQKLLIENITVVEQRCTLFNDTLRKNILLGSTDSVRNADCSTNENRHLIKDACQ
MALLDRFILDLPDGLETLIGTGGVTLSGGQQQRVAIARAFIRDTPILFLDEAVSALDIVH
RNLLMKAIRHWRKGKTTIILTHELSQIESDDYLYLMKEGEVVESGTQSELLADPTTTFST
WYHLQNDYSDAKTIVDTETEEKSIHTVESFNSQLETPKLGSCLSNLGYDETDQLSFYEAI
YQKRSNVRTRRVKVEEENIGYALKQQKNTESSTGPQLLSIIQI IKRMIKSIRYKKILILG
LLCSLIAGATNPVFSYTFSFLLEGIVPSTDGKTGSSHYLAKWSLLVLGVAAADGI FNFAK
GFLLDCCSEYWVMDLRNEVMEKLTRKNMDWFSGENNKASEISALVLNDLRDLRSLVSEFL
SAMTSFVTVSTIGLIWALVSGWKLSLVCISMFPLI IIFSAIYGGILQKCETDYKTSVAQL
ENCLYQIVTNIKTIKCLQAEFHFQLTYHDLKIKMQQIASKRAIATGFGISMTNMIVMCIQ
AIIYYYGLKLVMIHEYTSKEMFTTFTLLLFTIMSCTSLVSQI PDISRGQRAASWI YRILD
EKHNTLEVENNNARTVGIAGHTYHGKEKKPIVSIQNLTFAYPSAPTAFVYKNMNFDMFCG
QTLGIIGESGTGKSTLVLLLTKLYNCEVGKIKIDGTDVNDWNLTSLRKEISVVEQKPLLF
NGTIRDNLTYGLQDEILEIEMYDALKYVGIHDFVISSPQGLDTRIDTTLLSGGQAQRLCI
ARALLRKSKILILDECTSALDSVSSSIINEIVKKGPPALLTMVITHSEQMMRSCNSIAVL
KDGKVVERGNFDTLYNNRGELFQIVSNQSS

SEQ ID NO: 129

YKR039W

>sp| PI9145|GAP1__YEAST General amino-acid permease GAP1
OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=GAP1
PE=1 SV=2
MSNTSSYEKNNPDNLKHNGITIDSEFLTQEPITI PSNGSAVSIDETGSGSKWQDFKDSFK
RVKPIEVDPNLSEAEKVAI ITAQTPLKHHLKNRHLQMIAIGGAIGTGLLVGSGTALRTGG
PASLLIGWGSTGTMI YAMVMALGELAVI FPISGGFTTYATRFIDESFGYANNFNYMLQWL
VVLPLEIVSASITVNFWGTDPKYRDGFVALFWLAIVI INMFGVKGYGEAEFVFSFIKVIT
VVGFIILGI ILNCGGGPTGGYIGGKYWHDPGAFAGDTPGAKFKGVCSVFVTAAFSFAGSE
LVGLAASESVEPRKSVPKAAKQVFWRITLFYILSLLMIGLLVPYNDKSLIGASSVDAAAS
PFVIAIKTHGIKGLPSVVNVVILIAVLSVGNSAIYACSRTMVALAEQRFLPEIFSYVDRK
GRPLVGIAVTSAFGLIAFVAASKKEGEVFNWLLALSGLSSLFTWGGICICHIRFRKALAA
QGRGLDELSFKSPTGVWGSYWGLFMVIIMFIAQFYVAVFPVGDSPSAEGFFEAYLSFPL¥
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
LQKSFI YSFYVWGPRRLNEPEDDLLKKVLSCCTLITPVDLYPTFLDHMIRVTI FVLQWGL
SYIIMLLFMYYNGYI II SCLIGAI VGRFI FCYEPLGSLGANGSAQGTVSYDKESDDRKCC
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
RHKPVKNVLRKNNGFNWSFFLKFLLPTAVASAGDIGLSNVSFQYVPLTIYTI IKSSSIAF
VLLFGCIFKLEKFHWKLALSVI IMFVGVALMVFKPSDSTSTKNDQALVIFGSFLVLASSC
LSGLRWVYTQLMLRNNPIQTNTAAAVEESDGALFTENEDNVDNEPVVNLANNKMLENFGE
SKPHPIHTIHQLAPIMGITLLLTSLLVEKPFPGI FSSSIFRLDTSNGGVGTETTVLSIVR
GIVLLILPGFAVFLLTICEFSILEQTPVLTVSI VGIVKELLTVIFGI IILSERLSGFYNW
LGMLI IMADVCYYNYFRYKQDLLQKYHSVSTQDNRNELKGFQDFEQLGSKKIAPYSISVD
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
MNSWNLSSSIPI IHTPHDHPPTSEGTPDQPNNNRKDDKLHKKRGDSDEDLSPIWHCVVSG
GIGGKIGDSAMHSLDTVKTRQQGAPNVKKYRNMISAYRTIWLEEGVRRGLYGGYMAAMLG
SFPSAAI FFGTYEYTKRTMIEDWQINDTITHLSAGFLGDFISSFVYVPSEVLKTRLQLQG
RFNNPFFQSGYNYSNLRNAIKTVIKEEGFRSLFFGYKATLARDLPFSALQFAFYEKFRQL
AFKIEQKDGRDGELSIPNEILTGACAGGLAGIITTPMDVVKTRVQTQQPPSQSNKSYSVT
HPHVTNGRPAALSNSISLSLRTVYQSEGVLGFFSGVGPRFVWTSVQSSIMLLLYQMTLRG
LSNAFPTD

SEQ ID NO: 133
YMR27 9C
>sp|Q03263 **I**YM8M__YEAST Uncharacterized transporter YMR279C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YMR27 9C PE=1 SV=1
MFSIFKKKTSVQGTDSEIDEKITVKAKDKVVVSTEDEEVTTIVSSTKSTQVTNDSPWQDP
TYFSSFGKELMFIATCMLAQLLNQAGQTHALCIMNVLSKSFNSEANNQAWLMASFPLAAG
SFILISGRLGDIYGLKKMLIVGYVIVIVWSIISGLSKYSNSDAFFITSRAFQGVGIAFIL
PNIMGLVGHVYKVGSFRKNIVISFIGACAPTGGMFGGLFGGLIVTEDPNQWPWVFYAFGI
ATFLSLLMAWYSI PNNVPTNIHGLSMDWTGSALAIIGLILFNFVWNQAPIVGWDKPYIIV
LLIISVI FLVAFFVYESKYAEVPLLPRAMTKNRHMIMILLAVFLGWGSFGIWTFYYVSFQ
LNLRHYSPVWTGGTYFVFVIFGSMAAFFVAFSIKRLGPALLLCFSLMAFDAGSIMFSVLP
VEQSYWKLNFAMQAILCFGMDLSFPASSIILSDGLPMQYQGMAGSLVNTVINYSASLCLG
MGGTVEHQINKSGNDLLKGYRAAVYLGVGLASLGVVISVTYMLENLWNRHRKSEDRSLEA

SEQ ID NO: 134
YNL003C
>sp! P38 921 | PET8_YEAST Putative mitochondrial carrier protein PETS
OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PET8
PE=1 SV=1
MNTFFLSLLSGAAAGTSTDLVFFPIDTIKTRLQAKGGFFANGGYKGIYRGLGSAVVASAP
GASLFFISYDYMKVKSRPYISKLYSQGSEQLIDTTTHMLSSSIGEICACLVRVPAEVVKQ
RTQVHSTNSSWQTLQSILRNDNKEGLRKNLYRGWSTTIMREIPFTCIQFPLYEYLKKTWA
KANGQSQVEPWKGAICGSIAGGIAAATTTPLDFLKTRLMLNKTTASLGSVI IRIYREEGP
AVFFSGVGPRTMWISAGGAI FLGMYETVKSLLSKSFPTAGEMRA

SEQ ID NO: 135
YNL2 68W
>sp !P32487 jLYP1__YEAST Lysine -specific permease OS=Saccharomyces
cerevisiae (strain ATCC 204508 / S288c) GN=LYP1 PE=1 SV=2
MGRFSNI ITSNKWDEKQNNIGEQSMQELPEDQIEHEMEAIDPSNKTTPYSIDEKQYNTKK
KHGSLQGGAIADVNSITNSLTRLQVVSHETDINEDEEEAHYEDKHVKRALKQRHIGMIAL
GGTIGTGLFVGISTPLSNAGPVGSLIAYIFMGTIVYFVTQSLGEMATFIPVTSSITVFSK
RFLSPAFGVSNGYMYWFNWAITYAVEVSVIGQVIEYWTDKVPLAAWIAIFWVI ITLMNFF
PVKVYGEFEFWVASVKVLAIMGYLIYALIIVCGGSHQGPIGFRYWRNPGAWGPGIISSDK
SEGRFLGWVSSLINAAFTYQGTELVGITAGEAANPRKTVPRAINKVVFRIVLFYIMSLFF
IGLLVPYNDSRLSASSAVIASSPFVISIQNAGTYALPDIFNAVVLITVVSAANSNVYVGS
RVLYSLARTGNAPKQFGYVTRQGVPYLGVVCTAALGLLAFLVVNNNANTAFNWLINISTL
AGLCAWLFISLAHIRFMQALKHRGISRDDLPFKAKLMPYGAYYAAFFVTVIIFIQGFQAF
CPFKVSEFFTSYISLILLAVVFIGCQIYYKCRFIWKLEDIDIDSDRREIEAIIWEDDEPK
NLWEKFWAAVA

SEQ ID NO: 136
YNR055C
>sp| P53389 **IHOLl_YEAST** Protein HOL1 OS=Saccharomyces cerevisiae
(strain ATCC 204508 / S288c) GN=HOLl PE=1 SV=1
MDKYTNRDHPDYIPGTFNIYSSQNLENGI IYESKLKKTSSGVVLIPQPSYSPNDPLNWSS
WRKLAHFGLMAFI TAFTAATSNDAGAAQDSLNE IYGI SYDSMNTGAGVLFLG IGW5TLFL
APFANLYGRKITYI VCTTLGLFGALWFALAKRTSDTIWSQLFVGISESCAEAQVQLSLSD
IFFQHQLGSVLTVYIMCTSIGTFLGPLIAGYISAFTNFRWVGWVAVI ISGGLLITIIFGC
EETYFDRGQYMTPLTSCQSGYEDGTTLQNSDNTAVSRRKRHLDAKLSTPGAMGEKGVDLS
ETAEFEVNNEEEVTIPETRELIDGSKEHLKPYPKRVAILTKATNLKGYGFKQYFKYLKIN
LRMFLFPPVWLSGMFWGIQDVFLTFYLTTQESAYYEPPWNYSDFGVAIMNVPTLIGAVIG
CICAGIVSDYFVLWMARHNRGILEAEFRLYFSIATAI IGPAGLLMFGIGTARQWPWQAI Y
VGLGFVGFAWGCSGDIAMAYLMDCYPDMVLEGMVCTAI INNTISCI FTFTCSDWLAASGT
ENTYIALAVINFGITAFALPMYYYGKRIRLWTKRWYLQSVNLRDGV

SEQ ID NO: 137
YOL158C
>sp | Q08299 | **ENB1_YEAST** Siderophore iron transporter ENB1
OS=Saccharomyces cerevisiae (strain ATCC 204508 / 5288c) GN=ENB1
PE=1 SV=1
MLETDHSRNDNLDDKSTVCYSEKTDSNVEKSTTSGLRRIDAVNKVLSDYSSFTAFGVTFS

SLKTALLVALFLQGYCTGLGGQISQS IQTYAANSFGKHSQVGSINTVKS IVASVVAVPYA
RISDRFGRIECWIFALVLYTIGEIISAATPTFSGLFAGI VIQQFGYSGFRLLATALTGDL
SGLRDRTFAMNIFLIPVI INTWVSGNIVSSVAGNVAPYKWRWGYGIFCIIVPISTLILVL
PYVYAQYISWRSGKLPPLKLKEKGQTLRQTLWKFADDINLIGVILFTAFLVLVLLPLTIA
GGATSKWREGHIIAMI VVGGCLGFI FLIWELKFAKNPFI PRVYLGDPTI YVALLMEFVWR
LGLQIELEYLVTVLMVAFGESTLSAQRIAQLYNFLQSCTNIVVGIMLHFYPHPKVFVVAG
SLLGVIGMGLLYKYRVVYDGISGLIGAEIVVGIAGGMIRFPMWTLVHASTTHNEMATVTG
LLMSVYQ IGDAVGASI AGAIWTQRLAKELIQRLGSSLGMAI YKSPLNYLKKYPIGSEVRV
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
MSSDTSLSESSLLKEESGSLTKSRPPIKSNPVRENIKS FVAGGVGGVCAVFTGHPFDLI K
VRCQNGQANSTVHAITNIIKEAKTQVKGTLFTNSVKGFYKGVIPPLLGVTPIFAVSFWGY
DVGKKLVTFNNKQGGSNELTMGQMAAAGFISAIPTTLVTAPTERVKVVLQTSSKGSFIQA
AKTI VKEGGIASLFKGSLATLARDGPGSALYFASYEISKNYLNSRQPRQDAGKDEPVNIL
NVCLAGGIAGMSMWLAVFPIDTIKTKLQASSTRQNMLSATKEIYLQRGGIKGFFPGLGPA
LLRSFPANAATFLGVEMTHSLFKKYGI

SEQ ID NO: 139
YOR153W
>sp|P33302|PDR5_YEAST Pleiotropic ABC efflux transporter of multiple
drugs OS=Saccharomyces cerevisiae (strain ATCC 204508 / 5288c)
GN=PDR5 PE=1 SV=1
MPEAKLNNNVNDVTSYSSASSSTENAADLHNYNGFDEHTEARIQKLARTLTAQSMQNSTQ
SAPNKSDAQSIFSSGVEGVNPIFSDPEAPGYDPKLDPNSENFSSAAWVKNMAHLSAADPD
FYKPYSLGCAWKNLSASGASADVAYQSTVVNIPYKILKSGLRKFQRSKETNTFQILKPMD
GCLNPGELLVVLGRPGSGCTTLLKSISSNTHGFDLGADTKISYSGYSGDDIKKHFRGEVV
YNAEADVHLPHLTVFETLVTVARLKTPQNRIKGVDRESYANHLAEVAMATYGLSHTRNTK
VGNDIVRGVSGGERKRVSIAEVSICGSKFQCWDNATRGLDSATALEFIRALKTQADISNT
SATVAIYQCSQDAYDLFNKVCVLDDGYQIYYGPADKAKKYFEDMGYVCPSRQTTADFLTS
VTSPSERTLNKDMLKKGIHIPQTPKEMNDYWVKSPNYKELMKEVDQRLLNDDEASREAIK
EAHIAKQSKRARPSSPYTVSYMMQVKYLLIRNMWRLRNNIGFTLFMILGNCSMALILGSM
FFKIMKKGDTSTFYFRGSAMFFAILFNAFSSLLEIFSLYEARPITEKHRTYSLYHPSADA
FASVLSEIPSKLIIAVCFNI IFYFLVDFRRNGGVFFFYLLINIVAVFSMSHLFRCVGSLT
KTLSEAMVPASMLLLALSMYTGFAIPKKKILRWSKWIWYINPLAYLFESLLINEFHGIKF
PCAEYVPRGPAYANISSTESVCTVVGAVPGQDYVLGDDFIRGTYQYYHKDKWRGFGIGMA
YVVFFFFVYLFLCEYNEGAKQKGEILVFPRSI VKRMKKRGVLTEKNANDPENVGERSDLS
SDRKMLQESSEEESDTYGEIGLSKSEAI FHWRNLCYEVQIKAETRRI LNNVDGWVKPGTL
TALMGASGAGKTTLLDCLAERVTMGVITGDILVNGIPRDKSFPRSIGYCQQQDLHLKTAT
VRESLRFSAYLRQPAEVSIEEKNRYVEEVIKILEMEKYADAVVGVAGEGLNVEQRKRLTI
GVELTAKPKLLVFLDEPTSGLDSQTAWSICQLMKKLANHGQAILCTI HQPSAILMQEFDR
LLFMQRGGKTVYFGDLGEGCKTMIDYFESHGAHKCPADANPAEWMLEVVGAAPGSHANQD
YYEVWRNSEEYRAVQSELDWMERELPKKGSITAAEDKHEFSQSII YQTKLVSIRLFQQYW
RSPDYLWSKFILTI FNQLFIGFTFFiCAGTSLQGLQNQMLAVFMFTVIFNPILQQYLPSFV
QQRDLYEARERPSRTFSWISFI FAQIFVEVPWNI.LAGT IAYF.I YYYPIGFYSNASAAGQL
HERGALFWLFSCAFYVYVGSMGLLVISFNQVAESAANLASLLFTMSLSFCGVMTTPSAMP
RFWIFMYRVSPLTYFIQALLAVGVANVDVKCADYELLEFTPPSGMTCGQYMEPYLQLAKT

GYLIDENAIDTCSFCQISTINDYLANVNSFYSERWRNYGIFICYIAFNYIAGVFFYWLAR
VPKKNGKL5KK

SEQ ID NO: 140
YOR271C
>sp|Q12029|FSF1_YEAST Probable mitochondrial transport protein FSFl
OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN-FSF1
PE=1 SV=1
MASSVPGPIDLPESRYDLSTYWGRIRHCAEISDPTMLLTTEKDLAHAREI ISAYRHGELK
ETTPEFWRAKKQLDSTVHPDTGKTVLLPFRMSSNVLSNLVVTVGMLTPGLGTAGTVFWQW
ANQSLNVAVNSANANKSHPMSTSQLLTNYAAAVTASCGVALGLNNLVPRLKNISPHSKLI
LGRLVPFAAVVSAGIVNVFLMRGNEIRKGISVFDSNGDEVGKSKKAAFMAVGETALSRVI
NATPTMVIPPLILVRLQRGVLKGKSLGVQTLANLGLISVTMFSALPFALGIFPQRQAIHL
NKLEPELHGKKDKDGKPIEKVYFNRGI

SEQ ID NO: 141
YOR273C
>sp IQ12256 ITP04_YEAST Polyamine transporter 4 OS=Saccharomyces
cerevisiae (strain ATCC 204508 / 5288c) GN=TP04 PE=1 SV=1
MPSSLTKTESNSDPRTNIQQVPKALDKNVTNSGNLDSTSSSTGSITEDEKRSEPNADSNN
MTGGEPIDPRDLDWDGPDDPDNPHNWSSLKKWYTTMTSAFLCLVVTMGSSLYVSSVPELV
ERYHVSQTLALAGLTFYLLGLSTVIGAPLSEVFGRKPVYLFSLPVSMLFTMGVGLSNGHM
RIILPLRFLSGVFASPALSVGSGTILDI FDVDQVSVAMTYFVLSPFLGPVLSPIMAGFAT
EAKGWRWSEWIQLIAGGLILPFIALMPETHKGI ILRKRAKKRNIALKKFSREAQKEFLKT
TVTITILRPLKMLVVEPIVFVFSVYVAFIFAILFGFFEAYAVIYRGVYHMSMGISGLPFI
GIGVGLWIGAFFYLYIDRKYLFPKPPAGTQPLTEKERTSKRTTPYRGARDAETGELLPVV
PEKFLIACKFGSVALPIGLF¾ ʼQAWTARSDVHWMAPVAAGVPFGFGLILI FFSVLMYFSTC
YPPLTVASCLAANNLLRYVMSSVFPLFTIQMYTKMKIKWASTLFALVCVVMI PIPWVFEK
WGSKLRHKSQFGYAAMEKEAETEGGIDDVNAVDGELNLTRMTTLRTMETDPSTREKPGER
LSLRRTHTQPVPASFDREDGQHAQNRNEPISNSLYSAIKDNEDGYSYTEMATDASARMV

SEQ ID NO: 142
YOR307C
>sp|P22215|SLY41_YEAST Uncharacterized transporter SLY4I
OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SLY41
PE=1 SV=2
MIQTQSTAIKRRNSVHKNLFDPSLYQIPEPPRGGFQHQKKEYSKETFSNQVFGYDITSLK
KRFTQLFPSNIQGYLPEVDLRITI ICSIWYVTSSISSNLSKAILRTFNHPIALTELQFLV
SAVLCVGFASIVNLFRLPRLKHTKFSKALNSFPDGILPEYLDGNFRSSILHKFLVPSKLV
LMTTFPMGIFQFIGHITSHKAVSMIPVSLVHSVKALSPI ITVGYYKFFEHRYYNSMTYYT
LLLLI FGVMTTCWSTHGSKRASDNKSGSSLIGLLFAFISMI I FVAQNI FAKN ILTIRRKV
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
GGAIGTGLLVGTSSTLHTCGPAGLFISYIIISAVI YPIMCALGEMVCFLPGDGSDSAGST
ANLVTRYVDPSLGFATGWNYFYCYVILVAAECTAASGVVEYWTTAVPKGVWITIFLCVVV
ILNFSAVKVYGESEFWFASIKILCIVGLI ILSFILFWGGGPNHDRLGFRYWQHPGAFAHH
LTGGSLGNFTDI YTGI IKGAFAFILGPELVCMTSAECADQRRNI AKASRRFVWRLI FFYV
LGTLAISVIVPYNDPTLVNALAQGKPGAGSSPFVIGIQNAGIKVLPHI INGC ILTSAWSA
ANAFMFASTRSLLTMAQTGQAPKCLGRINKWGVPYVAVGVSFLCSCLAYLNVSSSTADVF
NWFSNISTISGFLGWMCGCIAYLRFRKAIFYNGLYDRLPFKTWGQPYTVWFSLIVIGIIT
ITNGYA IFIPKYWRVADFIAAYITLPIFLVLWFGHKLYTRTWRQWWLPVSEIDVTTGLVE
IEEKSREIEEMRLPPTGFKDKFLDALL

SEQ ID NO: 145
YPL036W
>sp| P19657 IPMA2_YEAST Plasma membrane ATPase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PMA2 PE=1 SV=3
MSSTEAKQYKEKPSKEYLHASDGDDPANNSAASSSSSSTSTSASSSAAAVPRKAAAASA
ADDSDSDEDIDQLIDELQSNYGEGDESGEEEVRTDGVHAGQRVVPEKDLSTDPAYGLTSD
EVARRRKKYGLNQMAEENESLIVKFLMFFVGPIQFVMEAAAILAAGLSDWVDVGVICALL
LLNASVGFIQEFQAGSIVDELKKTLANTATVIRDGQLIEIPANEVVPGEILQLESGTIAP
ADGRIVTEDCFLQIDQSAITGESLAAEKHYGDEVFSSSTVKTGEAFMVVTATGDNTFVGR
AAALVGQASGVEGHFTEVLNGIGIILLVLVIATLLLVWTACFYRTVGIVSILRYTLGITI
IGVPVGLPAVVTTTMAVGAAYLAKKQAIVQKLSAIESLAGVEILCSDKTGTLTKNKLSLH
EPYTVEGVSPDDLMLTACLAASRKKKGLDAI DKAFLKSLIEYPKAKDALTKYKVLEFHPF
DPVSKKVTAVVESPEGERIVCVKGAPLFVLKTVEEDHPIPEDVHENYENKVAELASRGFR
ALGVARKRGEGHWEILGVMPCMDPPRDDTAQTINEARNLGLRIKMLTGDAVGIAKETCRQ
LGLGTN IYNAERLGLGGGGDMPGSELADFVENADGFAEVFPQHKYRVVEILQNRGYLVAM
TGDGVNDAPSLKKADTGIAVEGATDAARSAADIVFLAPGLSAI IDALKTSRQIFHRMYSY
VVYRIALSLHLEIFLGLWIAILNNSLDINLIVFIAI FADVATLTIAYDNAPYAPEPVKWN
LPRLWGMSIILGIVLAIGSWITLTTMFLPNGGI IQNFGAMNGVMFLQISLTENWLIFVTR
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 GISGGH.TNPA 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
LAYAFEHI.A3 QTRGVPPQLV LQVIARIGHA VAATGLVGGQ VVDLESEGKA ISLETLEYIH
SHKTGALLEA SVVSGGILAG ADEELLARLS HYARDIGLAF QIVDDILDVT ATSEQLGKTA
GKDQAAAKAT YPSLLGLEAS RQKAEELIQS AKEALRPYGS QAEPLLALAD FITRRQH

SEQ ID NO: 150
Zea mays truncated CDPS
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
EVVYTLDFPW YGNLPRVEAR DYLEQYGGGD DVWIGKTLYR MPLVNNDVYL ELARMDFNHC
QALHQLEWQG LKRWYTENRL KDFGVAQEDA LRAYFLAAAS VYEPCRAAER LAWARAAILA
NAVSTHLRNS PSFRERLEHS LRCRPSEETD GSWFNSSSGS DAVLVKAVLR LTDSLAREAQ
PIHGGDPEDI IHKLLRSAWA EWVREKADAA DSVCNGSSAV EQEGSRMVHD KQTCLLLARM
lEISAGRAAG 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 KOI

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 NA5AYE5VAA 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** CPR8

MQSNSVKISP LDLVTALFSG KVLDTSNASE SGESAMLPTI AMIMENRELL MILTTSVAVL
IGCVVVLVWR RSSTKKSALE PPVIVVPKRV QEEEVDDGKK KVTVFFGTQT GTAEGFAKAL
VEEAKARYEK AVFKVIDLDD YAADDDEYEE KLKKESLAFF FLATYGDGEP TDNAARFYKW

FTEGCAKGEW 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
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 AALR06920.1)
MAEQQKIKKS PHVLLIPFPL QGHINPFIQF GKRLISKGVK TTLVTTIHTL NSTLNHSNTT
TTSIEIQAIS DGCDEGGFMS AGESYLETFK QVGSKSLADL IKKLQSEGTT IDAIIYDSMT
EWVLDVAIEF GIDGGSFFTQ ACVVNSLYYH VHKGLISLPL GETVSVPGFP VLQRWETPLI
LQNHEQIQSP WSQMLFGQFA NIDQARWVFT NSFYKLEEEV lEWTRKIWNL KVIGPTLPSM
YLDKRLDDDK DNGFNLYKAN HHECMNWLDD KPKESVVYVA FGSLVKHGPE QVEEITRALI
DSDVNFLWVI KHKEEGKLPE NLSEVIKTGK GLIVAWCKQL DVLAHESVGC FVTHCGFNST
LEAISLGVPV VAMPQFSDQT TNAKLLDEIL GVGVRVKADE NGIVRRGNLA SCIKMIMEEE
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 UGI91D2e-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 PIFGDQPLMA RLLEDKQVGI EIPRNEEDGC LTKESVARSL

RS¥WEKEGE IYKANARELS KIYNDTKVEK EYVSQFVDYL **EKNARAVAi**D 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

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

[00164] 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.

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 claims 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 (Ami) 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 MSP 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;

0) a gene encoding a UGT74G1 polypeptide;

(k) a gene encoding a UGT91D2 functional homolog; and/or

(I) a gene encoding a EUGT1 1 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 UGT91 D2 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 EUGT1 1 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 pastohs, 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 stevioi 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 UGT91 D2 and/or EUGT1 1; 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 EUGT1 1.

21. The method of claims 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:1 12, 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 YPR01 1C 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.

Figure 1

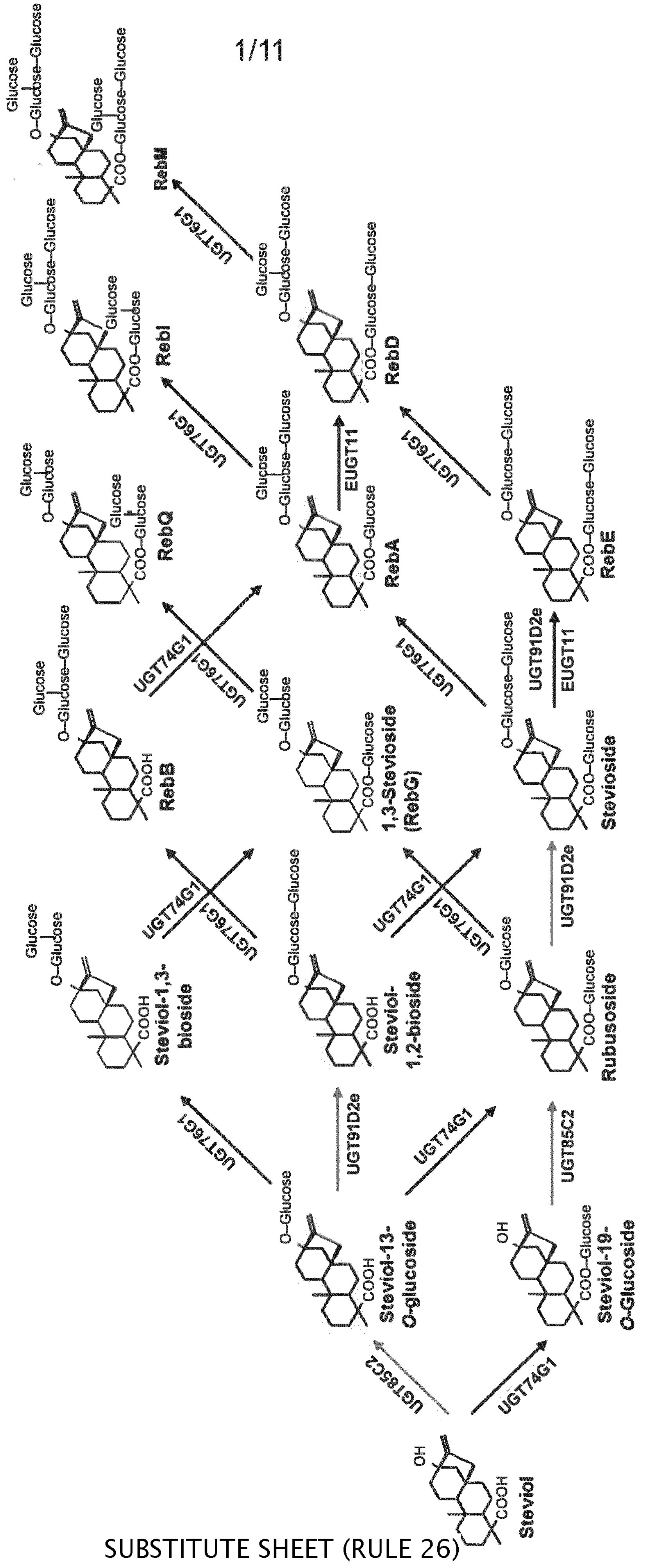

Steviol
COOH
OH
UGT85C2
UGT74G1
Steviol-13-O-glucoside
Steviol-19-O-Glucoside
O–Glucose
COO–Glucose
UGT76G1
UGT91D2e
UGT74G1
UGT85C2
Steviol-1,3-bioside
Steviol-1,2-bioside
Rubusoside
UGT74G1
UGT76G1
UGT91D2e
RebB
1,3-Stevioside (RebG)
Stevioside
UGT74G1
UGT76G1
UGT91D2e
EUGT11
RebQ
RebA
RebE
EUGT11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

Figure 2

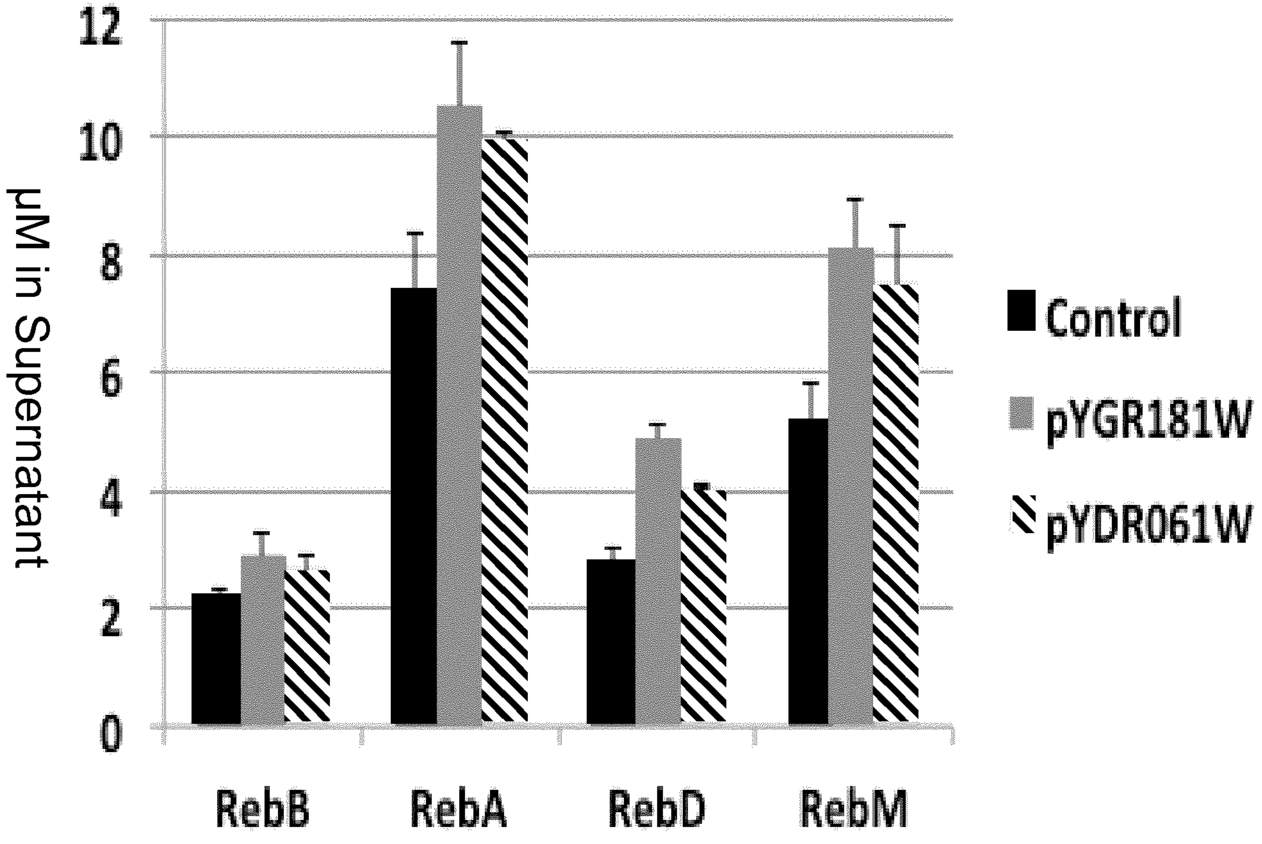

µM in Supernatant
12
10
8
6
4
2
0
RebB
RebA
RebD
RebM
Control
pYGR181W
pYDR061W

Figure 3A

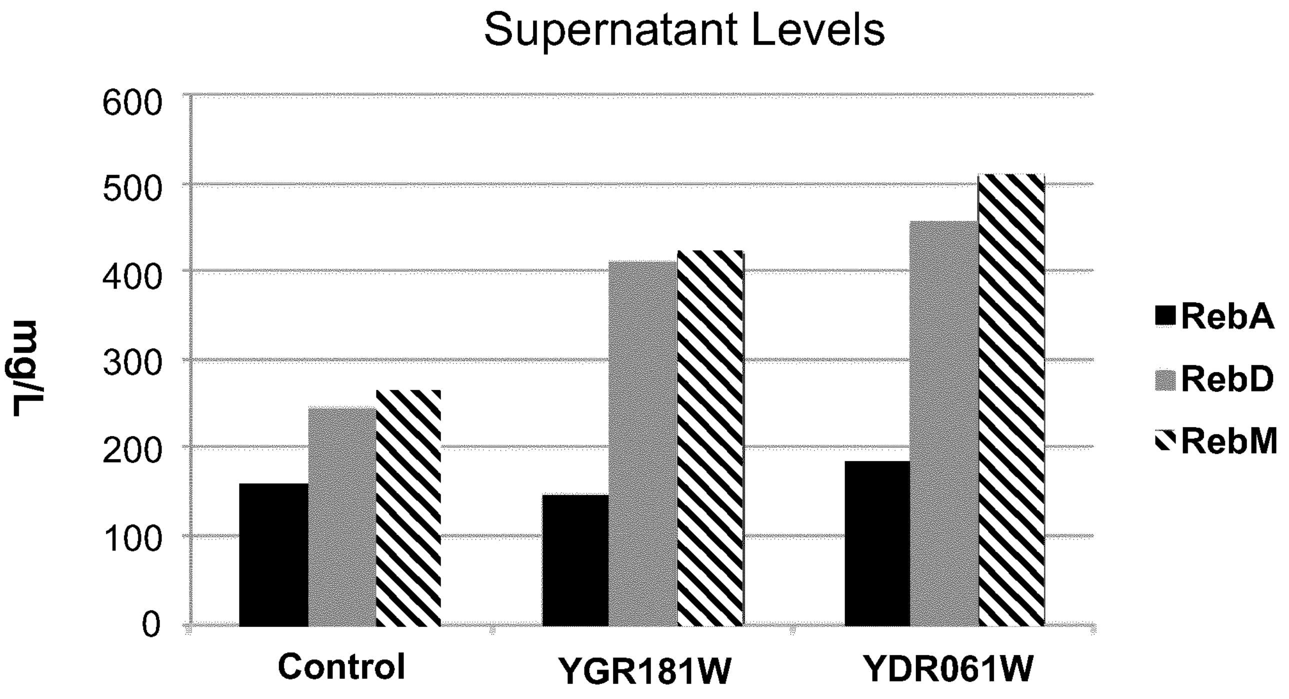
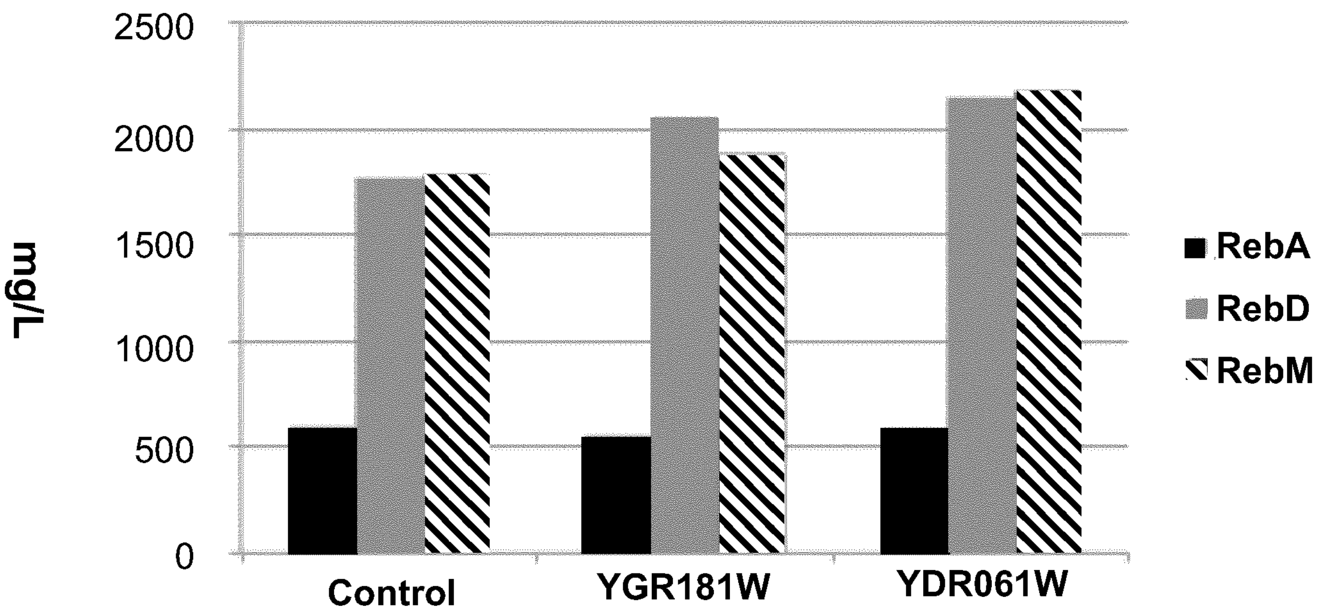

Supernatant Levels
mg/L
600
500
400
300
200
100
0
Control
YGR181W
YDR061W
■RebA
▨RebD
▧RebM

Figure 3B



Total Levels

Figure 4A

13-SMG

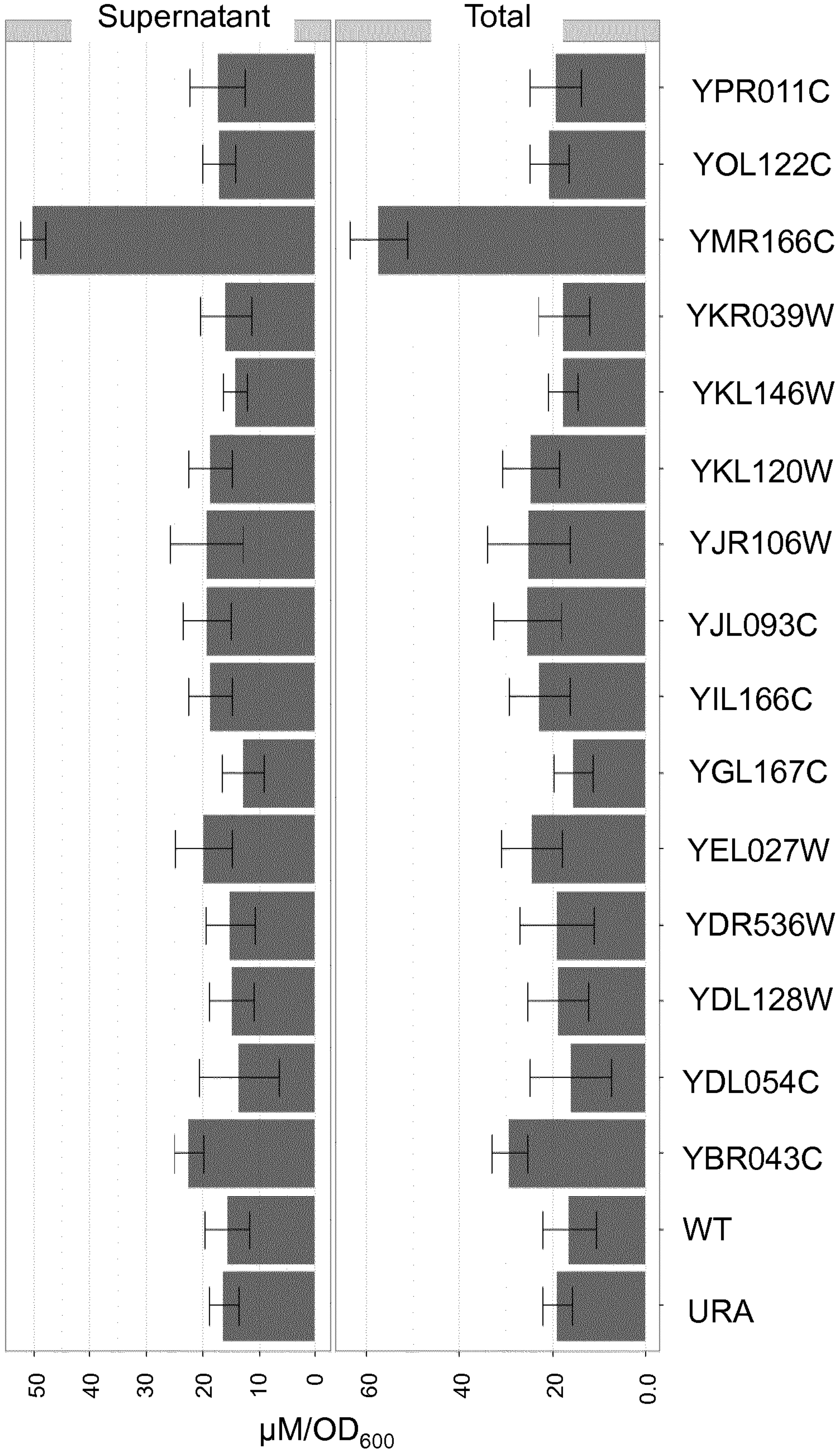


Figure 4B

RebA

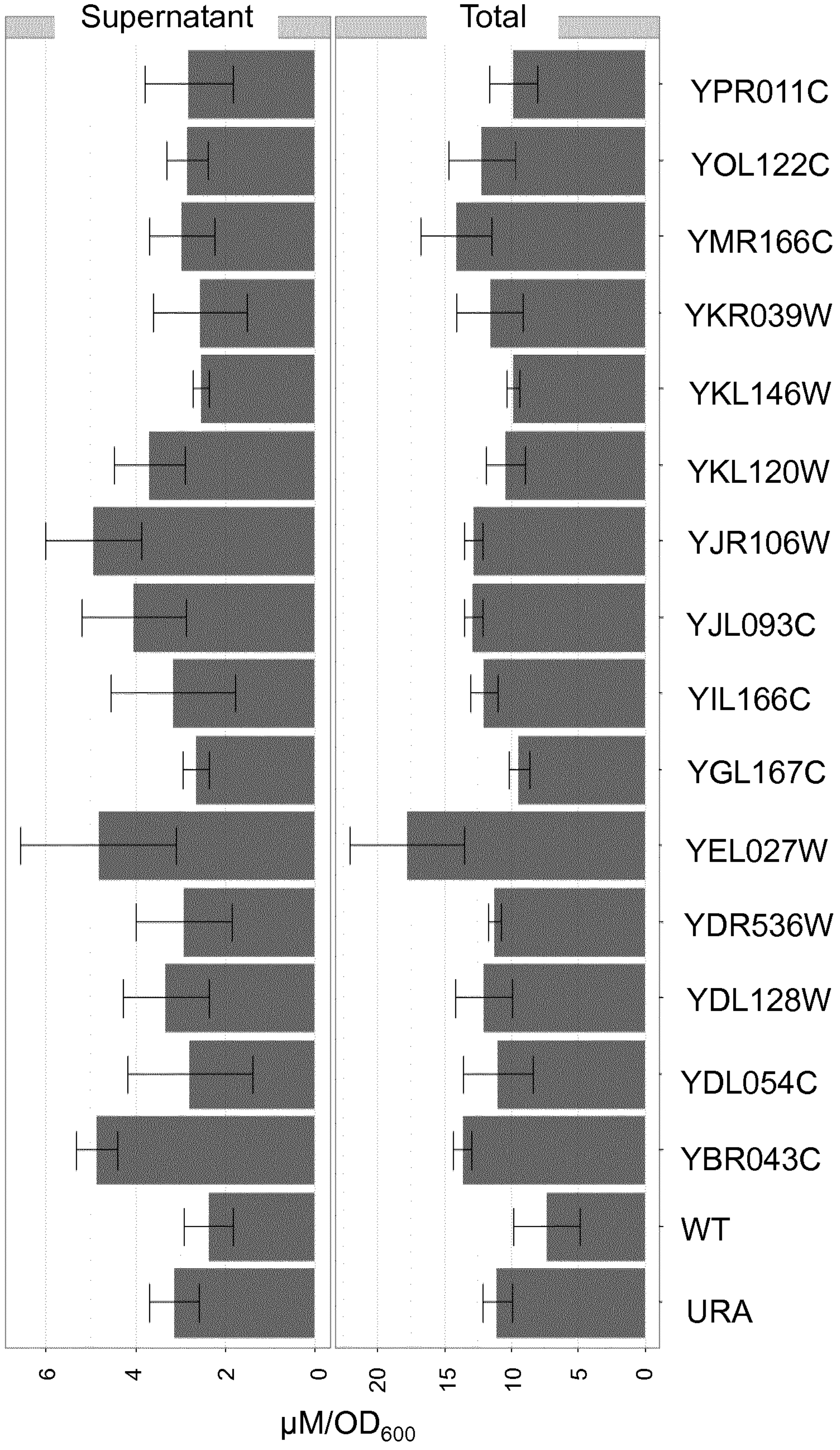


Figure 4C

RebB

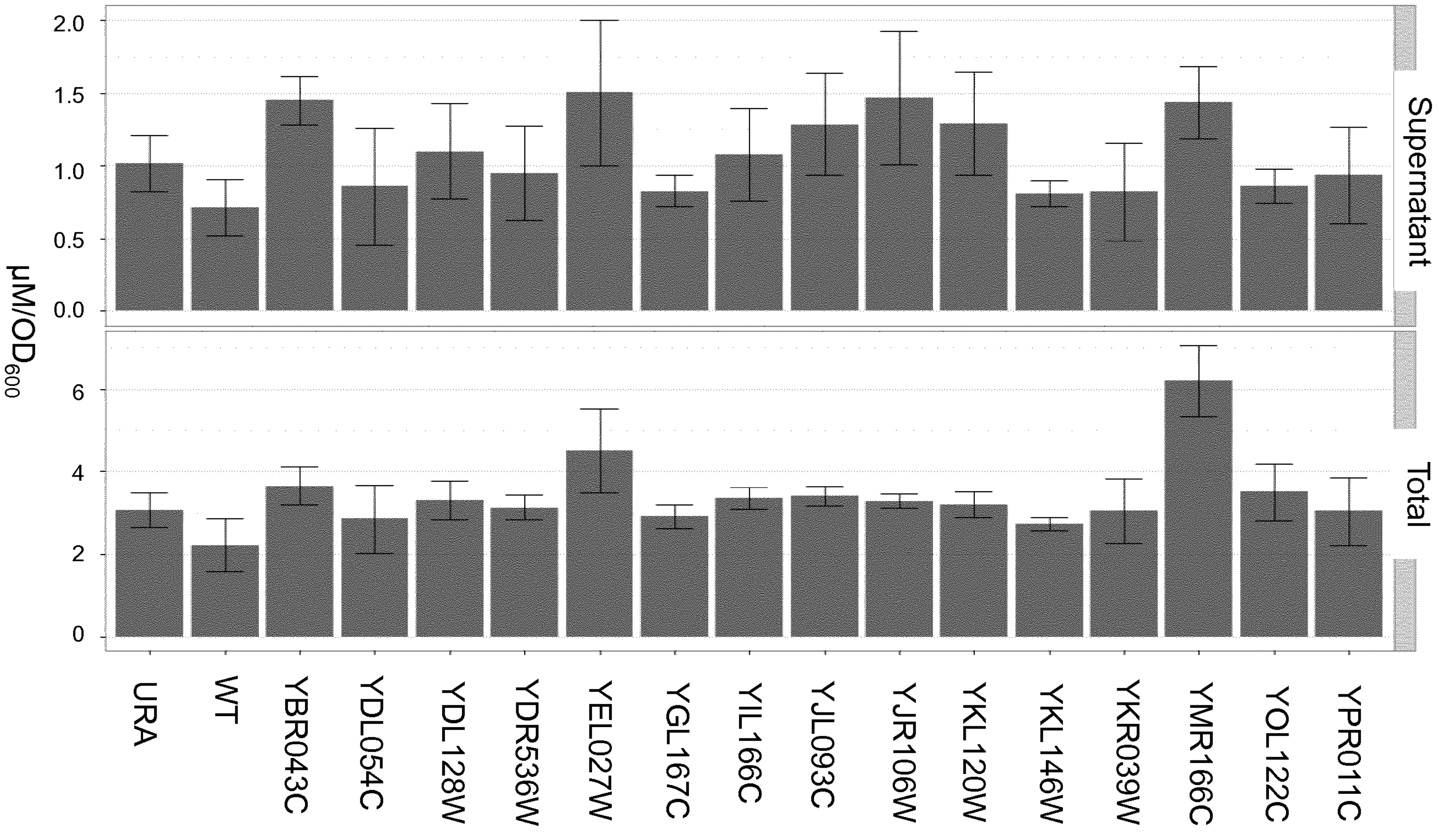


Figure 4D

RebD

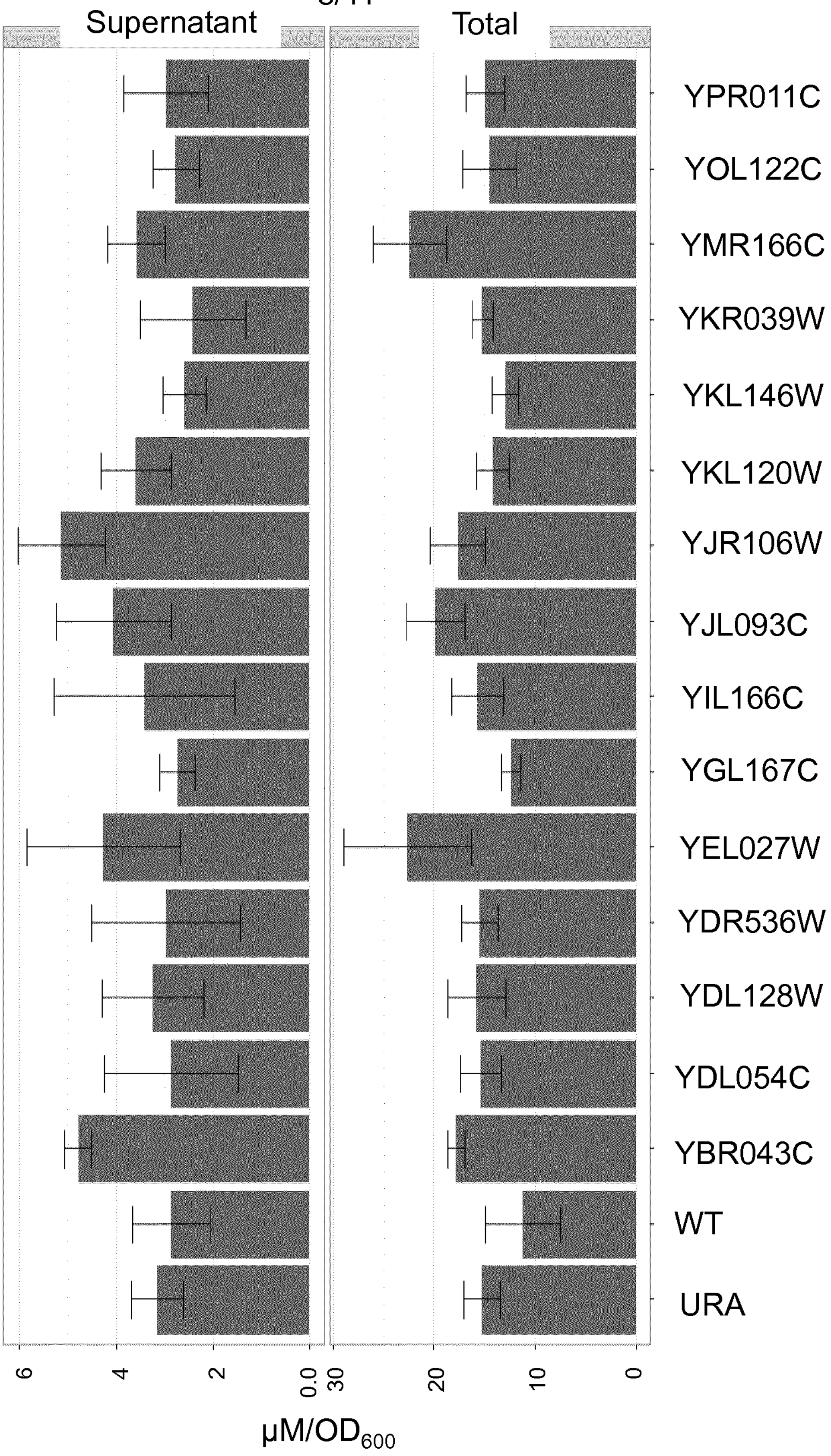


Figure 4E

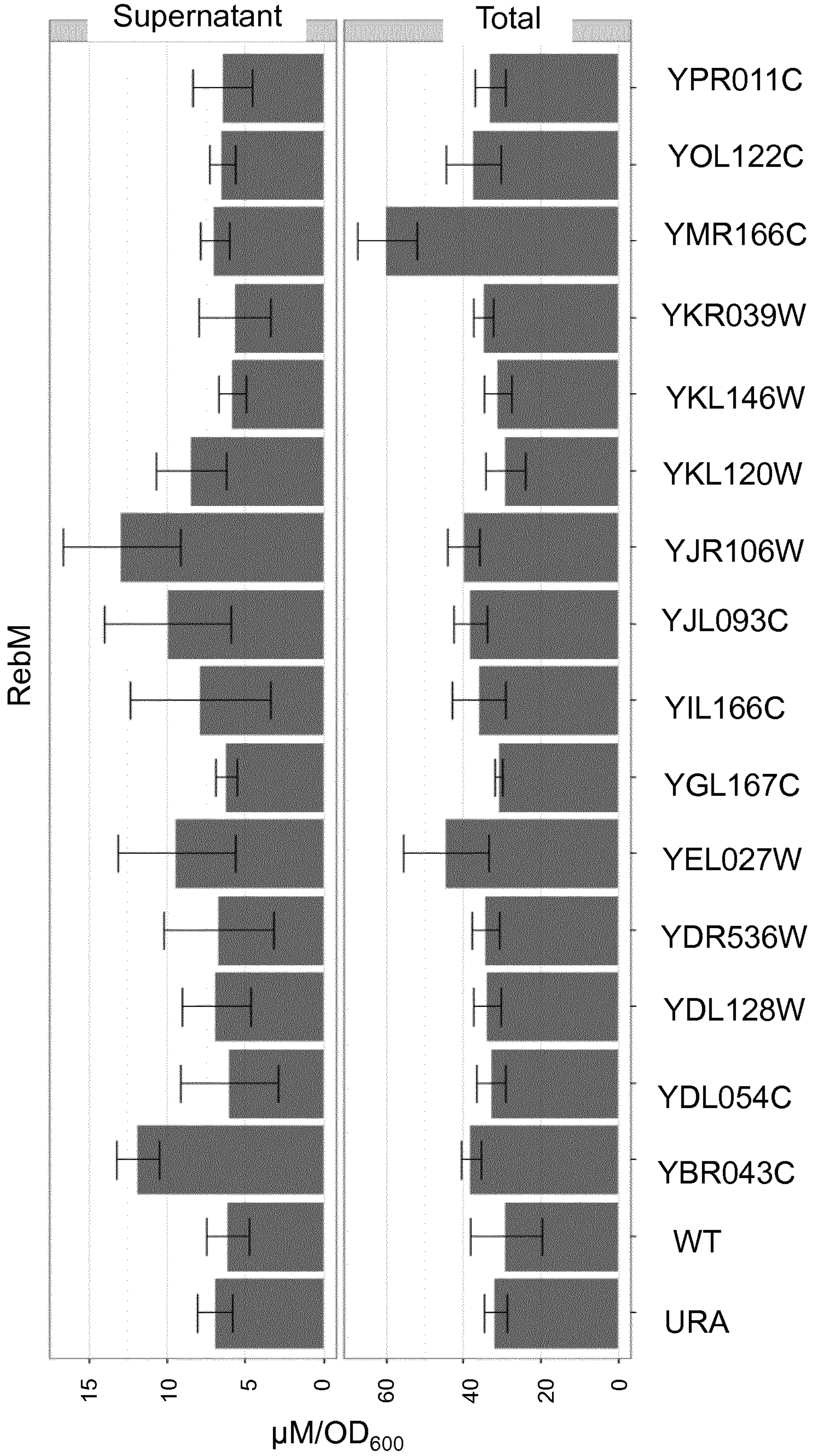

RebM
Supernatant
Total
YPR011C
YOL122C
YMR166C
YKR039W
YKL146W
YKL120W
YJR106W
YJL093C
YIL166C
YGL167C
YEL027W
YDR536W
YDL128W
YDL054C
YBR043C
WT
URA
15
10
5
0
60
40
20
0
µM/OD600

Figure 5A

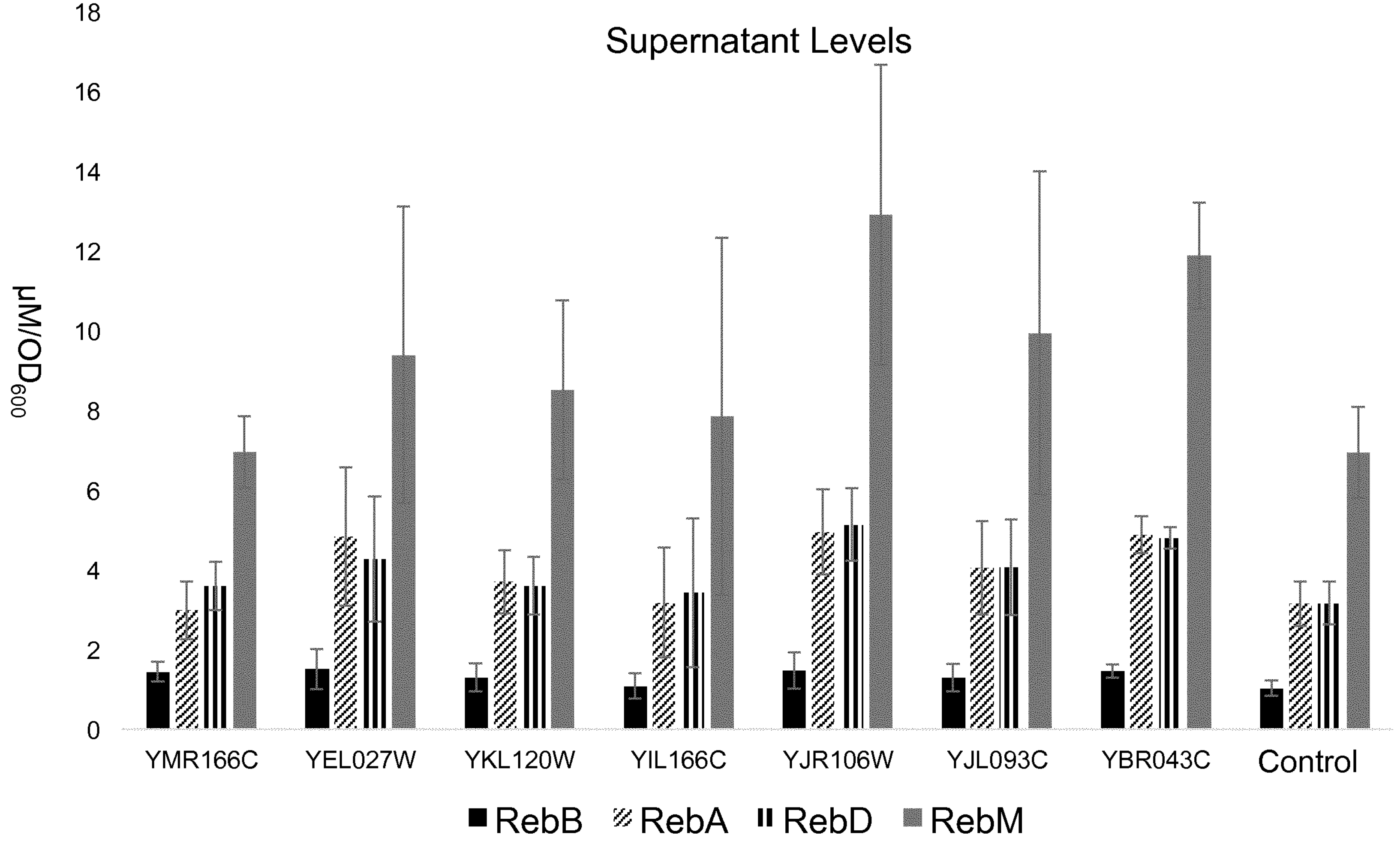
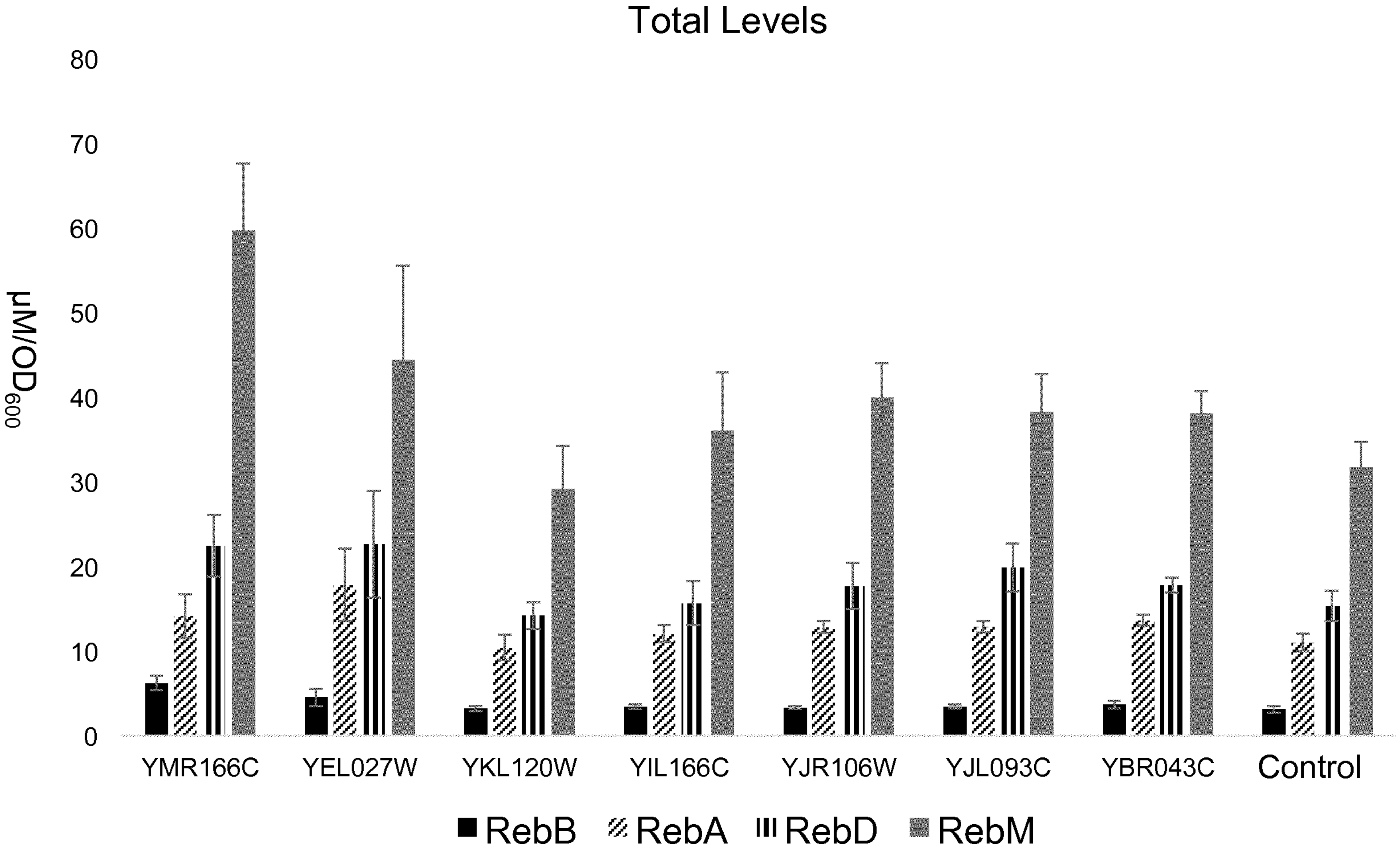

Supernatant Levels
µM/OD600
18
16
14
12
10
8
6
4
2
0
YMR166C
YEL027W
YKL120W
YIL166C
YJR106W
YJL093C
YBR043C
Control
■ RebB
▨ RebA
‖ RebD
■ RebM

Figure 5B


Total Levels
μM/OD600
0
10
20
30
40
50
60
70
80
YMR166C
YEL027W
YKL120W
YIL166C
YJR106W
YJL093C
YBR043C
Control
RebB
RebA
RebD
RebM

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2015/068314

A. CLASSIFICATION OF SUBJECT MATTER
INV. A23L1/236 C12N15/81 C07H1/08
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
A23L C12N C07H

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-Internal , EMBASE, WPI Data, Sequence Search

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2014/086890 A1 (EVOLVA SA [CH]) 12 June 2014 (2014-06-12) the whole document page 28 - page 39 -----	1-24
Y	BRANDLE ET AL: "Steviol glycoside biosynthesis", PHYTOCHEMISTRY, PERGAMON PRESS, GB, vol. 68, no. 14, 1 July 2007 (2007-07-01), pages 1855-1863, XP022145443, ISSN: 0031-9422, DOI: 10.1016/J.PHYTOCHEM.2007.02.010 page 1860, paragraph 2 - page 1861, paragraph 1 -----	1-24
	-/-	

☒ Further documents are listed in the continuation of Box C.

☒ See patent family annex.

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"A" document defining the general state of the art which is not considered to be of particular relevance

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"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search 15 October 2015	Date of mailing of the international search report 20/01/2016
Name and mailing address of the ISA/ European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Authorized officer Sprinks, Matthew

Form PCT/ISA/210 (second sheet) (April 2005)

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	YAZAKI ET AL: "ABC transporters involved in the transport of plant secondary metabolites" FEBS LETTERS, ELSEVIER, AMSTERDAM, NL, vol. 580, no. 4, 13 February 2006 (2006-02-13), pages 1183-1191, XP028030476, ISSN: 0014-5793, DOI: 10.1016/J.FEBSLET.2005.12.009 [retrieved on 2006-02-13] abstract page 1186, paragraph 4 -----	1-24
Y	WO 2011/151326 A2 (VIB VZW [BE]; UNIV LEUVEN KATH [BE]; THEVELEIN JOHAN [BE]; SAERENS SOF) 8 December 2011 (2011-12-08) abstract; sequence 38 page 2 - page 3; sequence 38 -----	1-24
Y	WO 2011/153144 A1 (GEVO INC [US]; VIB VZW [BE]; UNIV LEUVEN KATH [BE]; DUNDON CATHERINE A) 8 December 2011 (2011-12-08) abstract paragraph [0014]; table 1; sequence 38 -----	1-24

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-24(partially)

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-24(partially)

A recombinant host capable of synthesizing a steviol glycoside and transporting at least a portion of it into the culture medium, comprising a gene encoding a transporter polypeptide, the expression of which is modified, wherein the transporter polypeptide is an endogenous ABC transporter, and subject-matter relating thereto.

2-32. claims: 1-24(partially)

As subject 1 but wherein the transporter polypeptide is selected from the list in claim 3, starting with MFS transporter.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/EP2015/068314

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2014086890 A1	12-06-2014	EP 2928321 A1	14-10-2015
		US 2015342234 A1	03-12-2015
		WO 2014086890 A1	12-06-2014
WO 2011151326 A2	08-12-2011	EP 2575499 A2	10-04-2013
		US 2013302868 A1	14-11-2013
		WO 2011151326 A2	08-12-2011
		WO 2011153144 A1	08-12-2011
WO 2011153144 A1	08-12-2011	EP 2575499 A2	10-04-2013
		US 2013302868 A1	14-11-2013
		WO 2011151326 A2	08-12-2011
		WO 2011153144 A1	08-12-2011