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(71) Applicant *(for all designated States except US)*: **MICROBIA PRECISION ENGINEERING** [US/US]; 320 Bent Street, Cambridge, MA 02141 (US).

(72) Inventors; and
(75) Inventors/Applicants *(for US only)*: **BAILEY, Richard, B.** [US/US]; 23 Algonquian Drive, South Natick, MA 01760 (US). **MADDEN, Kevin, T.** [US/US]; 137 Sunset Road, Arlington, MA 02474 (US). **TRUEHEART, Joshua** [US/US]; 172 Annursnac Hill Road, Concord, MA 01742 (US).

(74) Agent: **LUITJENS, Cameron, M.**; Choate Hall & Stewart LLP, Two International Place, Boston, MA 02110 (US).

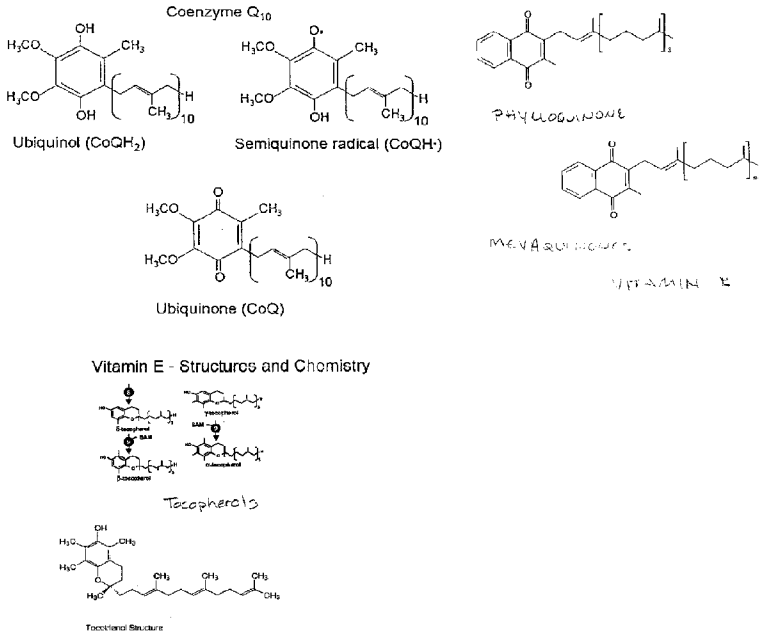
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(54) **Title:** PRODUCTION OF QUINONE DERIVED COMPOUNDS IN OLEAGINOUS YEAST FUNGI



(57) **Abstract:** The present invention provides systems for producing engineered oleaginous yeast or fungi that express quinone derived compounds.

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PRODUCTION OF QUINONE DERIVED COMPOUNDS IN OLEAGINOUS YEAST AND FUNGI

Cross Reference To Related Applications

[0001] The present application is copending with, shares at least one common inventor with and claims priority to US provisional patent application serial number 60/784,499, filed March 20, 2006, the entire contents of which are incorporated herein by reference. The present application is also copending with, shares at least one common inventor with and claims priority to US provisional patent application serial number 60/848,064, filed September 28, 2006, the entire contents of which are incorporated herein by reference.

Background of the Invention

[0002] Compounds containing or derived from quinone structures (i.e., "quinone derived compounds") play a variety of important roles in biological systems. Certain vitamins, for example, have quinone moieties (e.g., vitamin K) or are derived from such structures (e.g., vitamin E). Ubiquinones also represent an important class of quinone derived compounds. Ubiquinones play a critical function in the production of cellular ATP, serving as electron carriers in the respiratory chain. Furthermore, ubiquinones are lipophilic antioxidants that are capable of regenerating other antioxidants such as ascorbate and tocopherols.

[0003] Although many quinone derived compounds are naturally produced by the human body, they are often produced at levels lower than are required for optimal cell function. Accordingly, they must be obtained through the diet or by other means. There is a rapidly growing market for nutritional supplements and other products containing quinone derived compounds. Improved systems for enabling cost effective production, isolation, and/or formulation of such compounds are needed to effectively meet the growing demand.

Summary of the Invention

[0004] The present invention provides improved systems for the biological production of quinone derived compounds. In particular, the present invention provides improved systems for the biological production of ubiquinone(s) (e.g., CoQ10 and/or C_{5-9} quinone compounds), vitamin K compounds, and vitamin E compounds.

[0005] In one aspect, the invention encompasses the discovery that it is desirable to produce such quinone derived compounds in oleaginous organisms. The present invention thus provides biological systems able to accumulate one or more quinone derived compounds (e.g., ubiquinones, vitamin K compounds, and/or vitamin E compounds) in lipid bodies. In some

embodiments, the biological systems may produce higher levels of quinone derived compounds when the compound(s) is/are sequestered in lipid bodies. Regardless of whether absolute levels are higher; however, compounds that are accumulated within lipid bodies in oleaginous organisms are readily isolatable through isolation of the lipid bodies.

[0006] The present invention therefore provides oleaginous fungi (including, for example, yeast or other unicellular fungi) that produce one or more quinone derived compounds (e.g., ubiquinones, vitamin K compounds, and/or vitamin E compounds). The present invention also provides methods of constructing such yeast and fungi and methods of using such yeast and fungi to produce the quinone derived compounds. The present invention further provides methods of preparing quinone derived compounds, as well as compositions containing them, such as food or feed additives, nutritional supplements, or compositions for nutraceutical, pharmaceutical and/or cosmetic applications. In particular, the present invention provides systems and methods for generating yeast and fungi containing one or more oleaginic and/or quinonogenic modifications that increase the oleaginicity and/or alter their ability to produce one or more quinone derived compounds as compared with otherwise identical organisms that lack the modification(s). In some embodiments, the present invention provides a recombinant fungus. In certain embodiments, the recombinant fungus is oleaginous in that it can accumulate lipid to at least about 20% of its dry cell weight; and produces at least one quinone derived compound, and can accumulate the produced quinone derived compound to at least about 1% of its dry cell weight; wherein the recombinant fungus comprises at least one modification as compared with a parental fungus, which parental fungus both is not oleaginous and does not accumulate the quinone derived compound to at least about 1% of its dry cell weight, the at least one modification being selected from the group consisting of quinonogenic modifications, oleaginic modifications, and combinations thereof, and wherein the at least one modification alters oleaginicity of the recombinant fungus, confers to the recombinant fungus oleaginy, confers to the recombinant fungus the ability to produce the at least one quinone derived compound to a level at least about 1% of its dry cell weight, or confers to the recombinant fungus the ability to produce at least one quinone derived compound which the parental fungus does not produce.

[0007] In other embodiments, the recombinant fungus is oleaginous in that it can accumulate lipid to at least about 20% of its dry cell weight; and the recombinant fungus produces at least one quinone derived compound selected from the group consisting of: a ubiquinone (including, but not limited to, coenzyme Q10 and/or a C_{5-9} quinone compound), a vitamin K compound, a vitamin E compound, and combinations thereof, and can accumulate the produced quinone derived compound to at least about 1% of its dry cell weight; wherein the recombinant fungus comprises at least one modification as compared with a parental fungus, the at least one modification being selected from the group consisting of quinonogenic modifications, oleaginic modifications, and combinations thereof, and wherein the at least one modification alters

oleaginicity of the recombinant fungus, confers to the recombinant fungus oleaginy, confers to the recombinant fungus the ability to produce the at least one quinone derived compound to a level at least about 1% of its dry cell weight, or confers to the recombinant fungus the ability to produce at least one quinone derived compound which the parental fungus does not naturally produce.

[0008] In some embodiments, the recombinant fungus is oleaginous in that it can accumulate lipid to at least about 20% of its dry cell weight; and the recombinant fungus produces at least one quinone derived compound, and can accumulate the produced quinone derived compound to at least about 1% of its dry cell weight; wherein the recombinant fungus is a member of a genus selected from the group consisting of : *Aspergillus, Blakeslea, Botrytis, Candida, Cercospora, Cryptococcus, Cunninghamella, Fusarium (Gibberella), Kluyveromyces, Lipomyces, Mortierella, Mucor, Neurospora, Penicillium, Phycomyces, Pichia (Hansenula), Puccinia, Pythium, Rhodosporidium, Rhodotorula, Saccharomyces, Sclerotium, Trichoderma, Trichosporon, Xanthophyllomyces (Phaffia)*, and *Yarrowia*; or is a species selected from the group consisting of: *Aspergillus terreus, Aspergillus nidulans, Aspergillus niger, Blakeslea trispora, Botrytis cinerea, Candida japonica, Candida pulcherrima, Candida revkaufi, Candida tropicalis, Candida utilis, Cercospora nicotianae, Cryptococcus curvatus, Cunninghamella echinulata, Cunninghamella elegans, Fusarium fujikuroi (Gibberella zeae), Kluyveromyces lactis, Lipomyces starkeyi, Lipomyces lipoferus, Mortierella alpina, Mortierella ramanniana, Mortierella isabellina, Mortierella vinacea, Mucor circinelloides, Neurospora crassa, Phycomyces blakesleanus, Pichia pastoris, Puccinia distincta, Pythium irregulare, Rhodosporidium toruloides, Rhodotorula glutinis, Rhodotorula graminis, Rhodotorula mucilaginosa, Rhodotorula pinicola, Rhodotorula gracilis, Saccharomyces cerevisiae, Sclerotium rolfsii, Trichoderma reesei, Trichosporon cutaneum, Trichosporon pullans, Xanthophyllomyces dendrorhous (Phaffia rhodozyma)*, and *Yarrowia lipolytica*; wherein the recombinant fungus comprises at least one modification as compared with a parental fungus, the at least one modification being selected from the group consisting of quinonogenic modifications, oleaginic modifications, and combinations thereof, and wherein the at least one modification alters oleaginicity of the recombinant fungus, confers to the recombinant fungus oleaginy, confers to the recombinant fungus the ability to produce the at least one quinone derived compound to a level at least about 1% of its dry cell weight, or confers to the recombinant fungus the ability to produce at least one quinone derived compound which the parental fungus does not naturally produce.

[0009] In some embodiments, the recombinant fungus is oleaginous in that it can accumulate lipid to at least about 20% of its dry cell weight; and the recombinant fungus produces at least one quinone derived compound selected from the group consisting of: a ubiquinone (including, but not limited to, coenzyme Q10 and/or a C_{5-9} quinone compound), a vitamin K compound, a vitamin E compound, and combinations thereof, and can accumulate the produced quinone derived compound to at least about 1% of its dry cell weight; wherein the recombinant

fungus is a member of a genus selected from the group consisting of : *Aspergillus, Blakeslea, Botrytis, Candida, Cercospora, Cryptococcus, Cunninghamella, Fusarium (Gibberella), Kluyveromyces, Lipomyces, Mortierella, Mucor, Neurospora, Penicillium, Phycomyces, Pichia (Hansenula), Puccinia, Pythium, Rhodosporidium, Rhodotorula, Saccharomyces, Sclerotium, Trichoderma, Trichosporon, Xanthophyllomyces (Phaffia)*, and *Yarrowia*; or is of a species selected from the group consisting of: *Aspergillus terreus, Aspergillus nidulans, Aspergillus niger, Blakeslea trispora, Botrytis cinerea, Candida japonica, Candida pulcherrima, Candida revkaufi, Candida tropicalis, Candida utilis, Cercospora nicotianae, Cryptococcus curvatus, Cunninghamella echinulata, Cunninghamella elegans, Fusarium fujikuroi (Gibberella zeae), Kluyveromyces lactis, Lipomyces starkeyi, Lipomyces lipoferus, Mortierella alpina, Mortierella ramanniana, Mortierella isabellina, Mortierella vinacea, Mucor circinelloides, Neurospora crassa, Phycomyces blakesleanus, Pichia pastoris, Puccinia distincta, Pythium irregulare, Rhodosporidium toruloides, Rhodotorula glutinis, Rhodotorula graminis, Rhodotorula mucilaginosa, Rhodotorula pinicola, Rhodotorula gracilis, Saccharomyces cerevisiae, Sclerotium rolfsii, Trichoderma reesei, Trichosporon cutaneum, Trichosporon pullans, Xanthophyllomyces dendrorhous (Phaffia rhodozyma)*, and *Yarrowia lipolytica*; wherein the recombinant fungus comprises at least one modification as compared with a parental fungus, the at least one modification being selected from the group consisting of quinonogenic modifications, oleaginic modifications, and combinations thereof, and wherein the at least one modification alters oleaginicity of the recombinant fungus, confers to the recombinant fungus oleaginy, confers to the recombinant fungus the ability to produce the at least one quinone derived compound to a level at least about 1% of its dry cell weight, or confers to the recombinant fungus the ability to produce at least one quinone derived compound which the parental fungus does not naturally produce.

[0010] In some embodiments, the recombinant fungus accumulates the produced at least one quinone derived compound to a level selected from the group consisting of: above about 1%, above about 2%, above about 3%, above about 5%, and above about 10% of the fungus' dry cell weight.

[0011] In some embodiments, the present invention provides an engineered *S. cerevisiae* strain, comprising one or more quinonogenic modifications, wherein the one or more quinonogenic modifications are selected from the group consisting of: increased expression or activity of a decaprenyl diphosphate synthase polypeptide; increased expression or activity of an 4-hydroxybenzoate polyprenyl polypeptide; increased expression or activity of a GGPP synthase polypeptide; increased expression or activity of an FPP synthase polypeptide; increased expression or activity of an HMG CoA reductase polypeptide; decreased expression or activity of a squalene synthase polypeptide; decreased expression of activity of a prenyldiphosphate synthase polypeptide; increased expression or activity of a DAHP synthase polypeptide; increased expression or activity of a chorismate lyase polypeptide; increased expression or activity of a

chorismate synthase polypeptide; increased expression or activity of an ATP-citrate lyase polypeptide; increased expression or activity of an AMP deaminase polypeptide; increased expression or activity of a cytosolic malic enzyme polypeptide; and combinations thereof.

[0012] In some embodiments, the present invention provides an engineered *Y. lipolytica* strain containing a truncated HMG CoA reductase polypeptide.

[0013] In some embodiments, the present invention provides an engineered *Y. lipolytica* strain having increased expression or activity of a decaprenyl diphosphate synthase gene. In some embodiments, the present invention provides an engineered *Y. lipolytica* strain having decreased expression or activity of a squalene synthase polypeptide. In some embodiments, the present invention provides an engineered *Y. lipolytica* strain having decreased expression or activity of a squalene synthase polypeptide. In some embodiments, the present invention provides an engineered *Y. lipolytica* strain having increased expression or activity of a 4-hydroxybenzoate polyprenyl polypeptide. In some embodiments, the present invention provides an engineered *Y. lipolytica* strain having increased expression or activity of a DAHP synthase polypeptide. In some embodiments, the present invention provides an engineered *Y. lipolytica* strain having increased expression or activity of a chorismate lyase polypeptide. In some embodiments, the present invention provides an engineered *Y. lipolytica* strain having increased expression or activity of an ATP-citrate lyase polypeptide. In some embodiments, the present invention provides an engineered *Y. lipolytica* strain having increased expression or activity of a AMP deaminase polypeptide. In some embodiments, the present invention provides an engineered *Y. lipolytica* strain having increased expression or activity of a cytosolic malic polypeptide. In some embodiments, the present invention provides an engineered *Y. lipolytica* strain having increased expression or activity of a GGPP synthase polypeptide. In some embodiments, the present invention provides an engineered *Y. lipolytica* strain having increased expression or activity of an FPP synthase polypeptide. In some embodiments, the present invention provides an engineered *Y. lipolytica* strain having increased expression or activity of a chorismate synthase polypeptide.

[0014] In some embodiments, the present invention provides a strain of *Y. lipolytica* comprising one or more modifications selected from the group consisting of an oleaginic modification, a quinonogenic modification, and combinations thereof, such that the strain accumulates from 1% to 15% of its dry cell weight as at least one quinone derived compound.

[0015] In certain embodiments, the present invention provides an engineered *Y. lipolytica* strain that produces a ubiquinone, the strain containing one or more quinonogenic modifications selected from the group consisting of: increased expression or activity of a *Y. lipolytica* GGPP synthase polypeptide; expression or activity of a truncated HMG CoA reductase polypeptide; increased expression or activity of a 4-hydroxybenzoate polyprenyl transferase polypeptide; increased expression or activity of a decaprenyl diphosphate synthase polypeptide; increased

expression or activity of a DAHP synthase polypeptide; increased expression or activity of a chorismate lyase polypeptide; increased expression or activity of a shikimate pathway polypeptide; increased expression or activity of a chorismate mutase polypeptide; increased expression or activity of a transketolase polypeptide; increased expression or activity of an FPP synthase polypeptide; increased expression or activity of an IPP isomerase polypeptide; increased expression or activity of an HMG-CoA synthase polypeptide; increased expression or activity of a mevalonate kinase polypeptide; increased expression or activity of a phosphomevalonate kinase polypeptide; increased expression or activity of a mevalonate pyrophosphate decarboxylate polypeptide; increased expression or activity of a cytosolic malic enzyme polypeptide; increased expression or activity of a malate dehydrogenase polypeptide; increased expression or activity of an AMP deaminase polypeptide; increased expression or activity of a glucose 6 phosphate dehydrogenase polypeptide; increased expression or activity of a malate dehydrogenase homolog 2 polypeptide; increased expression or activity of a GND1-6-phosphogluconate dehydrogenase polypeptide; increased expression or activity of a isocitrate dehydrogenase polypeptide; increased expression or activity of a IDH2-isocitrate dehydrogenase polypeptide; increased expression or activity of a fructose 1,6 bisphosphatase polypeptide; increased expression or activity of a Erg10-acetoacetyl CoA thiolase polypeptide; increased expression or activity of a ATP citrate lyase subunit 2 polypeptide; increased expression or activity of a ATP citrate lyase subunit 1 polypeptide; decreased expression or activity of a squalene synthase polypeptide; decreased expression or activity of a prenyldiphosphate synthase polypeptide; or decreased expression or activity of a PHB polyprenyltransferase polypeptide; and combinations thereof.

[0016] In certain embodiments, the present invention provides a recombinant fungus characterized in that the fungus accumulates lipid in the form of cytoplasmic oil bodies.

[0017] In some embodiments, the present invention provides a composition comprising: lipid bodies; at least one quinone derived compound; and intact fungal cells.

[0018] In some embodiments, the present invention provides a method of producing a quinone derived compound, the method comprising steps of cultivating a fungus under conditions that allow production of the quinone derived compound; and isolating the produced quinone derived compound.

[0019] In some embodiments, the present invention provides a composition comprising: an oil suspension comprising: lipid bodies; at least one quinone derived compound; and intact fungal cells; and a binder or filler.

[0020] In some embodiments, the present invention provides a composition comprising: an oil suspension comprising: lipid bodies; at least one quinone derived compound; and intact fungal cells; and one or more other agents selected from the group consisting of chelating agents,

pigments, salts, surfactants, moisturizers, viscosity modifiers, thickeners, emollients, fragrances, preservatives, and combinations thereof.

[0021] In some embodiments, the present invention provides an isolated quinone derived compound composition, prepared by a method comprising steps of cultivating a fungus under conditions that allow production of a quinone derived compound; and isolating the produced quinone derived compound.

[0022] In some embodiments, the present invention provides a quinone derived compound composition comprising a *Y. lipolytica* cell containing at least 1% quinone derived compounds by weight.

[0023] In some embodiments, the present invention provides a quinone derived compound comprising *Y lipolytica* lipid bodies; and at least one quinone derived compound, wherein the at least one quinone derived compound is present at a level that is at least 1% by weight of the lipid bodies. In some embodiments, the present invention provides a composition comprising a quinone derived compound and one or more additional compounds (e.g., binders, fillers, chelating agents, pigments, salts, surfactants, moisturizers, viscosity modifiers, thickeners, emollients, fragrances, preservatives, etc. and combinations thereof).

[0024] In some embodiments, the present invention provides a feedstuff comprising a quinone derived compound in lipid bodies.

[0025] In some embodiments, the present invention provides methods comprising steps of cultivating the recombinant fungus under conditions that allow production of a quinone derived compound (e.g., ubiquinones, vitamin K compounds, and/or vitamin E compounds) and isolating the produced quinone derived compound (e.g., extracting with an organic or non-organic solvent). In certain embodiments, the recombinant fungus is cultured by growing under conditions of limiting nutrient (e.g., one or more of carbon, nitrogen, phosphate, magnesium, etc.) and/or by controlling at least one environmental parameter (e.g. one or more of nutrients, pH, temperature, pressure, oxygen concentration, timing of feeds, content of feeds, etc.) for at least a portion of the cultivation. In certain embodiments, the recombinant fungus is cultivated at a temperature of 20, 20.5, 21, 21.5, 22, 22.5, 23, 23.5, 24, 24.5, 25, 25.5, 26, 26.5, 27, 27.5, 28, 28.5, 29, 29.5, 30 °C or above, and/or at one or more ranges within these temperatures. In certain embodiments, the recombinant fungus is cultivated at a pH of 4.0, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5.0, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6.0, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7.0, 7.1, 7.2, 7.3, 7.4, 7.5 or above, and/or at one or more ranges within these pH's. In certain embodiments, the temperature, the pH, or both is varied during the culture period. In certain embodiments, the recombinant fungus is cultivated at an oxygen concentration

within the rage of about 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, or more, and/or at one or more ranges within these concentrations. In certain embodiments, the produced quinone derived compound is isolated by crystallization.

[0026] Additional aspects of the present invention will be apparent to those of ordinary skill in the art from the present description, including the appended claims. Various polypeptides are listed in Tables 1-101; as one of ordinary skill in the art will understand, the order in which these polypeptides are listed is not indicative of their importance to the present invention. Various patent and non-patent publications are referenced throughout the present application. Unless otherwise indicated, each of these references is hereby incorporated by reference in its entirety.

Brief Description of the Drawing

[0027] *Figure 1* depicts various quinone derived compounds including ubiquinone/Coenzyme Q10 in its various oxidated forms (Panel A); vitamin K (Panel B); and vitamin E (Panel C).

[0028] *Figure 2* depicts how sufficient levels of acetyl-CoA and NADPH may be accumulated in the cytosol of oleaginous organisms to allow for production of significant levels of cytosolic lipids. Enzymes: 1, pyruvate decarboxylase; 2, malate dehydrogenase; 3, malic enzyme; 4, pyruvate dehydrogenase; 5, citrate synthase; 6, ATP-citrate lyase; 7, citrate/malate translocase.

[0029] *Figure 3* illustrates biosynthetic pathways of aromatic amino acids, and the shikimate pathway for production of chorismate. A depiction of how these pathways feed into ubiquinone biosynthesis is depicted. Boxed numerical references are IUBMB Enzyme Nomenclature EC numbers for enzymes catalyzing the relevant reaction.

[0030] *Figure 4* depicts ubiquinone biosynthesis pathways. *Fig. 4A* shows the mevalonate isoprenoid biosynthesis pathway, which typically operates in eukaryotes, including fungi; as well as the mevalonate-independent isoprenoid biosynthesis pathway, also known as the DXP pathway, which typically operates in bacteria and in the plastids of plants and production of isoprenoid precursors; *Fig 4B* depicts production of *para*-hydroxybenzoate (23) from precursor chorismate or tyrosine, and condensation with isoprene, resulting in formation of polyprenylhydroxybenzoate (24), followed by subsequent oxygenation, decarboxylation, and methylation reactions involved in production of quinine compound, polyprenyl-6-methoxy-1,4-benzoquinol (30). *Fig 4C* depicts the final steps of methylation and oxygenation for generation of the ubiquinone CoQ10.

[0031] *Figure 5*, illustrates how intermediates in the isoprenoid biosynthesis pathway can be processed into biomolecules, including ubiquinones, carotenoids, sterols, steroids, and vitamins, such as vitamin E or vitamin K.

[0032] *Figure 6* illustrates how intermediates in ubiquinone biosynthesis feed into the biosynthetic pathway, and how some intermediates can be processed into other molecules.

[0033] *Figures 7A-7C* show an alignment of certain representative fungal HMG-CoA reductase polypeptides. As can be seen, these polypeptides show very high identity across the catalytic region, and also have complex membrane spanning domains. In some embodiments of the invention, these membrane-spanning domains are disrupted or are removed, so that, for example, a hyperactive version of the polypeptide may be produced.

[0034] *Figure 8* depicts the steroid biosynthesis pathways, including the isoprenoid biosynthesis pathway, it indicates where certain quinone derived compounds (e.g., a ubiquinone, vitamin E and vitamin K) are produced via geranylgeranyl pyrophosphate.

[0035] *Figure 9* depicts ubiquinone and vitamin K biosynthesis pathways.

[0036] *Figure 10*, Panels A-C, depict vitamin E biosynthesis pathways. Panel A shows synthesis of γ- and α- tocopherols from isopentenyl pyrophosphate and *p*-hydroxyphenpyruvate through action of geranylgeranylpyrophosphate synthse, geranylgeranyl reductase, *p*-hydroxyphenpyruvate dioxygenase, prenyl transferase, methyltransferase I, cyclase, and γ-methyltransferase enzyme activities. Panel B depicts the tocopherol biosynthetic pathway in plants. Dashed arrows represent multiple steps. Enzymes are indicated by circled numbers as follows: 1) HGA phytyltransferase; 2) *p*-hydroxyphenyl pyruvate dioxygenase; 3) HGA dioxygenase; 4) geranylgeranyl diphosphate reductase, 5) geranylgeranyl diphsophate synthase; 6) 1-deoxy-D-xylulose-5-phosphate sunthase; 7) 2-methyl-6-phytyl-1,4-benzoquinol methyltransferase; 8) tocopherol cyclase; and 9) γ-tocopherol methyltransferase. Panel C depicts synthesis of α, β, γ, and δ tocopherols.

[0037] *Figure 11* is a Table listing certain *Y. lipolytica* genes representing various polypeptides useful in engineering cells in accordance with the present invention.

[0038] *Figures 12*, Panels A-M depict schematic representations of plasmids generated and described in detail in the exemplification

Definitions

[0039] *Aromatic amino acid biosynthesis polypeptide*: The term "aromatic amino acid biosynthesis polypeptide" refers to any polypeptide that is involved in the synthesis of aromatic amino acids in yeast and/or bacteria through chorismate and the shikimate pathway. For example, as discussed herein, anthranilate synthase, enzymes of the shikimate pathway, chorismate mutase, chorismate synthase, DAHP synthase, and transketolase are all aromatic amino acid biosynthesis

polypeptides. Each of these polypeptides is also a ubiquinone biosynthesis polypeptide or a ubiquinone biosynthesis competitor for purposes of the present invention, as production of chorismate is a precursor in the synthesis of *para*-hydroxybenzoate for the biosynthesis of a ubiquinone. Representative examples of some of these enzymes are provided in Tables 32-37.

[0040] *Aromatic amino acid pathway*: The "aromatic amino acid pathway" is understood in the art to refer to a metabolic pathway that produces or utilizes shikimate pathway enzymes and chorismate in the production of phenylalanine, tryptophan or tyrosine. As discussed herein, two different pathways can produce the ubiquinoid precursor *para*-hydroxybenzoate —the first, the "shikimate pathway" is utilized in prokaryotes and induces conversion of chorismate to *para*-hydroxybenzoate through the action of chorismate pyruvate lyase; the second is utilized in mammalian systems and induces induction of *para*-hydroxybenzoate by derivation of tyrosine or phenylalanine. The term "aromatic amino acid pathway" encompasses both of these pathways. Lower eukaryotes such as yeast can utilize either method for production of *para*-hydroxybenzoate.

[0041] *Biosynthesis polypeptide*: The term "biosynthesis polypeptide" as used herein (typically in reference to a particular compound or class of compounds), refers to polypeptides involved in the production of the compound or class of compounds. In some embodiments of the invention, biosynthesis polypeptides are synthetic enzymes that catalyze particular steps in a synthesis pathway that ultimately produces a relevant compound. In some embodiments, the term "biosynthesis polypeptide" may also encompass polypeptides that do not themselves catalyze synthetic reactions, but that regulate expression and/or activity of other polypeptides that do so.

[0042] *C_{5-9} quinone biosynthesis polypeptide*: The term "C_{5-9} quinone biosynthesis polypeptide" refers to any polypeptide that is involved in the synthesis of a C_{5-9} quinone, for example a polyprenyldiphosphate synthase polypeptide. To mention but a few, these include, for example, pentaprenyl, hexaprenyl, heptaprenyl, octaprenyl, and/or solanesyl(nonaprenyl) diphosphate synthase polypeptides (i.e., polypeptides that perform the chemical reactions performed by the pentaprenyl, hexaprenyl, heptaprenyl, octaprenyl, and solanesyl(nonaprenyl) polypeptides, respectively, listed in Tables 61-65 (see also Okada et al., *Biochim. Biophys. Acta* 1302:217, 1996; Okada et al., *J. Bacteriol.* 179:5992, 1997). As will be appreciated by those of ordinary skill in the art, in some embodiments of the invention, C_{5-9} quinone biosynthesis polypeptides include polypeptides that affect the expression and/or activity of one or more other C_{5-9} quinone biosynthesis polypeptides.

[0043] *C_{5-9} quinone compound*: The term "C_{5-9} quinone compound", as used herein, refers to a family of ubiquinone compounds having 5-9 isoprenoid units in the side chain.

[0044] *C_{5-9} quinone production modification*: The term "C_{5-9} quinone production modification", as used herein, refers to a modification of a host organism that adjusts production of one or more C_{5-9} quinones, as described herein. For example, a C_{5-9} quinone production

modification may increase the production level of one or more C_{5-9} quinones, and/or may alter relative production levels of different C_{5-9} quinones. In principle, an inventive C_{5-9} quinone production modification may be any chemical, physiological, genetic, or other modification that appropriately alters production of one or more C_{5-9} quinones in a host organism produced by that organism as compared with the level produced in an otherwise identical organism not subject to the same modification. In most embodiments, however, the C_{5-9} quinone production modification will comprise a genetic modification, typically resulting in increased production of one or more selected C_{5-9} quinones. In some embodiments, the C_{5-9} quinone production modification comprises at least one chemical, physiological, genetic, or other modification; in other embodiments, the C_{5-9} quinone production modification comprises more than one chemical, physiological, genetic, or other modification. In certain aspects where more than one modification is utilized, such modifications can comprise any combination of chemical, physiological, genetic, or other modification (e.g., one or more genetic, chemical and/or physiological modification(s)).

[0045] *Carotenogenic modification*: The term "carotenogenic modification", as used herein, refers to a modification of a host organism that adjusts production of one or more carotenoids, as described herein. For example, a carotenogenic modification may increase the production level of one or more carotenoids, and/or may alter relative production levels of different carotenoids. In principle, an inventive carotenogenic modification may be any chemical, physiological, genetic, or other modification that appropriately alters production of one or more carotenoids in a host organism produced by that organism as compared with the level produced in an otherwise identical organism not subject to the same modification. In most embodiments, however, the carotenogenic modification will comprise a genetic modification, typically resulting in increased production of one or more selected carotenoids. In some embodiments, the carotenogenic modification comprises at least one chemical, physiological, genetic, or other modification; in other embodiments, the carotenogenic modification comprises more than one chemical, physiological, genetic, or other modification. In certain aspects where more than one modification is utilized, such modifications can comprise any combination of chemical, physiological, genetic, or other modification (e.g., one or more genetic, chemical and/or physiological modification(s)). In some embodiments, the selected carotenoid is one or more of astaxanthin, β-carotene, canthaxanthin, lutein, lycopene, phytoene, zeaxanthin, and/or modifications of zeaxanthin or astaxanthin (e. g., glucoside, or other ester of zeaxanthin or astaxanthin). In some embodiments, the selected carotenoid is astaxanthin. In some embodiments, the selected carotenoid is other than β-carotene.

[0046] *Carotenogenic polypeptide*: The term "carotenogenic polypeptide", as used herein, refers to any polypeptide that is involved in the process of producing carotenoids in a cell, and may include polypeptides that are involved in processes other than carotenoid production but

whose activities affect the extent or level of production of one or more carotenoids, for example by scavenging a substrate or reactant utilized by a carotenoid polypeptide that is directly involved in carotenoid production. Carotenogenic polypeptides include isoprenoid biosynthesis polypeptides, carotenoid biosynthesis polypeptides, and isoprenoid biosynthesis competitor polypeptides, as those terms are defined herein. The term also encompasses polypeptides that may affect the extent to which carotenoids are accumulated in lipid bodies.

[0047] *Carotenoid*: The term "carotenoid" is understood in the art to refer to a structurally diverse class of pigments derived from isoprenoid pathway intermediates. The commitment step in carotenoid biosynthesis is the formation of phytoene from geranylgeranyl pyrophosphate. Carotenoids can be acyclic or cyclic, and may or may not contain oxygen, so that the term carotenoids include both carotenes and xanthophylls. In general, carotenoids are hydrocarbon compounds having a conjugated polyene carbon skeleton formally derived from the five-carbon compound IPP, including triterpenes (C_{30} diapocarotenoids) and tetraterpenes (C_{40} carotenoids) as well as their oxygenated derivatives and other compounds that are, for example, C_{35}, C_{50}, C_{60}, C_{70}, C_{80} in length or other lengths. Many carotenoids have strong light absorbing properties and may range in length in excess of C_{200}. C_{30} diapocarotenoids typically consist of six isoprenoid units joined in such a manner that the arrangement of isoprenoid units is reversed at the center of the molecule so that the two central methyl groups are in a 1,6-positional relationship and the remaining non-terminal methyl groups are in a 1,5-positional relationship. Such C_{30} carotenoids may be formally derived from the acyclic $C_{30}H_{42}$ structure, having a long central chain of conjugated double bonds, by: (i) hydrogenation (ii) dehydrogenation, (iii) cyclization, (iv) oxidation, (v) esterification/glycosylation, or any combination of these processes. C_{40} carotenoids typically consist of eight isoprenoid units joined in such a manner that the arrangement of isoprenoid units is reversed at the center of the molecule so that the two central methyl groups are in a 1,6-positional relationship and the remaining non-terminal methyl groups are in a 1,5-positional relationship. Such C_{40} carotenoids may be formally derived from the acyclic $C_{40}H_{56}$ structure, having a long central chain of conjugated double bonds, by (i) hydrogenation, (ii) dehydrogenation, (iii) cyclization, (iv) oxidation, (v) esterification/glycosylation, or any combination of these processes. The class of C_{40} carotenoids also includes certain compounds that arise from rearrangements of the carbon skeleton, or by the (formal) removal of part of this structure. More than 600 different carotenoids have been identified in nature; carotenoids include but are not limited to: antheraxanthin, adonirubin, adonixanthin, astaxanthin, canthaxanthin, capsorubrin, β-cryptoxanthin, α-carotene, β-carotene, β,ψ-carotene, δ-carotene, ε-carotene, echinenone, 3-hydroxyechinenone, 3'-hydroxyechinenone, γ-carotene, ψ-carotene, 4-keto- γ-carotene, ζ-carotene, α-cryptoxanthin, deoxyflexixanthin, diatoxanthin, 7,8-didehydroastaxanthin, didehydrolycopene, fucoxanthin, fucoxanthinol, isorenieratene, β-isorenieratene, lactucaxanthin, lutein, lycopene, myxobactone, neoxanthin, neurosporene, hydroxyneurosporene, peridinin,

phytoene, rhodopin, rhodopin glucoside, 4-keto-rubixanthin, siphonaxanthin, spheroidene, spheroidenone, spirilloxanthin, torulene, 4-keto-torulene, 3-hydroxy-4-keto-torulene, uriolide, uriolide acetate, violaxanthin, zeaxanthin-β-diglucoside, zeaxanthin, and C30 carotenoids. Additionally, carotenoid compounds include derivatives of these molecules, which may include hydroxy-, methoxy-, oxo-, epoxy-, carboxy-, or aldehydic functional groups. Further, included carotenoid compounds include ester (e. g., glycoside ester, fatty acid ester) and sulfate derivatives (e. g., esterified xanthophylls).

[0048] *Carotenoid biosynthesis polypeptide*: The term "carotenoid biosynthesis polypeptide" refers to any polypeptide that is involved in the synthesis of one or more carotenoids. To mention but a few, these carotenoid biosynthesis polypeptides include, for example, polypeptides of phytoene synthase, phytoene dehydrogenase (or desaturase), lycopene cyclase, carotenoid ketolase, carotenoid hydroxylase, astaxanthin synthase, carotenoid epsilon hydroxylase, lycopene cyclase (beta and epsilon subunits), carotenoid glucosyltransferase, and Acyl CoA:diacyglycerol acyltransferase. In some instances, a single gene may encode a protein with multiple carotenoid biosynthesis polypeptide activities. Representative examples of carotenoid biosynthesis polypeptide sequences are presented in Tables 17-21 and Tables 38-41. As will be appreciated by those of ordinary skill in the art, in some embodiments of the invention, carotenoid biosynthesis polypeptides include polypeptides that affect the expression and/or activity of one or more other carotenoid biosynthesis polypeptides.

[0049] *Effective amount.* The term "effective amount" is used herein to describe concentrations or amounts of compounds and/or compositions that, when administered to a subject, achieve a desired therapeutic or physiological effect.

[0050] *FPP biosynthesis polypeptides*: The term "FPP biosynthesis polypeptide" refers to any polypeptide that is involved in the synthesis of farnesyl pyrophosphate. As discussed herein, farnesyl pyrophosphate represents the branchpoint between the sterol biosynthesis pathway and the carotenoid and other biosynthesis pathways. One specific example of an FPP biosynthesis polypeptide is FPP synthase. Representative examples of FPP synthase polypeptide sequences are presented in Table 14. As will be appreciated by those of ordinary skill in the art, in some embodiments of the invention, FPP biosynthesis polypeptides include polypeptides that affect the expression and/or activity of one or more other FPP biosynthesis polypeptides.

[0051] *Gene*: The term "gene", as used herein, generally refers to a nucleic acid encoding a polypeptide, optionally including certain regulatory elements that may affect expression of one or more gene products (i. e., RNA or protein).

[0052] *Heterologous*: The term "heterologous", as used herein to refer to genes or polypeptides, refers to a gene or polypeptide that does not naturally occur in the organism in which it is being expressed. It will be understood that, in general, when a heterologous gene or

polypeptide is selected for introduction into and/or expression by a host cell, the particular source organism from which the heterologous gene or polypeptide may be selected is not essential to the practice of the present invention. Relevant considerations may include, for example, how closely related the potential source and host organisms are in evolution, or how related the source organism is with other source organisms from which sequences of other relevant polypeptides have been selected. Where a plurality of different heterologous polypeptides are to be introduced into and/or expressed by a host cell, different polypeptides may be from different source organisms, or from the same source organism. To give but one example, in some cases, individual polypeptides may represent individual subunits of a complex protein activity and/or may be required to work in concert with other polypeptides in order to achieve the goals of the present invention. In some embodiments, it will often be desirable for such polypeptides to be from the same source organism, and/or to be sufficiently related to function appropriately when expressed together in a host cell. In some embodiments, such polypeptides may be from different, even unrelated source organisms. It will further be understood that, where a heterologous polypeptide is to be expressed in a host cell, it will often be desirable to utilize nucleic acid sequences encoding the polypeptide that have been adjusted to accommodate codon preferences of the host cell and/or to link the encoding sequences with regulatory elements active in the host cell.

[0053] *Host cell*: As used herein, the "host cell" is a fungal cell or yeast cell that is manipulated according to the present invention to accumulate lipid and/or to express one or more quinone derived compounds as described herein. A "modified host cell", as used herein, is any host cell which has been modified, engineered, or manipulated in accordance with the present invention as compared with a parental cell. In some embodiments, the modified host cell has at least one quinonogenic and/or at least one oleagenic modification. In some embodiments, the modified host cell containing at least one oleaginic modification and/or one quinonogenic modification further has at least one sterologenic modification and/or or at least one carotenogenic modification. In some embodiments, the parental cell is a naturally occurring parental cell.

[0054] *Isolated*: The term "isolated", as used herein, means that the isolated entity has been separated from at least one component with which it was previously associated. When most other components have been removed, the isolated entity is "purified" or "concentrated". Isolation and/or purification and/or concentration may be performed using any techniques known in the art including, for example, fractionation, extraction, precipitation, or other separation.

[0055] *Isoprenoid biosynthesis polypeptide*: The term "isoprenoid biosynthesis polypeptide" refers to any polypeptide that is involved in the synthesis of isoprenoids. For example, as discussed herein, acetoacetyl-CoA thiolase, HMG-CoA synthase, HMG-CoA reductase, mevalonate kinase, phosphomevalonate kinase, mevalonate pyrophosphate decarboxylase, IPP isomerase, FPP synthase, and GGPP synthase, are all involved in the

mevalonate pathway for isoprenoid biosynthesis. Each of these proteins is also an isoprenoid biosynthesis polypeptide for purposes of the present invention, and sequences of representative examples of these enzymes are provided in Tables 7-15. As will be appreciated by those of ordinary skill in the art, in some embodiments of the invention, isoprenoid biosynthesis polypeptides include polypeptides that affect the expression and/or activity of one or more other isoprenoid biosynthesis polypeptides (e.g., of one or more enzymes that participate(s) in isoprenoid synthesis). Thus, for instance, transcription factors that regulate expression of isoprenoid biosynthesis enzymes can be isoprenoid biosynthesis polypeptides for purposes of the present invention. To give but a couple of examples, the *S. cerevisiae* Upc2 and YLR228c genes, and the *Y. lipolytica* YALI0B00660g gene encode transcription factors that are isoprenoid biosynthesis polypeptides according to certain embodiments of the present invention. For instance, the semidominant upc2-1 point mutation (G888D) exhibits increased sterol levels (Crowley et al., *J. Bacteriol* 180:4177-4183, 1998). Corresponding YLR228c mutants have been made and tested (Shianna et al., *J Bacteriol* 183:830, 2001); such mutants may be useful in accordance with the present invention, as may be YALI0B00660g derivatives with corresponding upc2-1 mutation(s).

[0056] *Isoprenoid pathway*: The "isoprenoid pathway" is understood in the art to refer to a metabolic pathway that either produces or utilizes the five-carbon metabolite isopentyl pyrophosphate (IPP). As discussed herein, two different pathways can produce the common isoprenoid precursor IPP —the "mevalonate pathway" and the "non-mevalonate pathway". The term "isoprenoid pathway" is sufficiently general to encompass both of these types of pathway. Biosynthesis of isoprenoids from IPP occurs by polymerization of several five-carbon isoprene subunits. Isoprenoid metabolites derived from IPP are of varying size and chemical structure, including both cyclic and acyclic molecules. Isoprenoid metabolites include, but are not limited to, monoterpenes, sesquiterpenes, diterpenes, sterols, and polyprenols such as carotenoids.

[0057] *Oleaginic modification*: The term "oleaginic modification", as used herein, refers to a modification of a host organism that adjusts the desirable oleaginy of that host organism, as described herein. In some cases, the host organism will already be oleaginous in that it will have the ability to accumulate lipid to at least about 20% of its dry cell weight. It may nonetheless be desirable to apply an oleaginic modification to such an organism, in accordance with the present invention, for example to increase (or, in some cases, possibly to decrease) its total lipid accumulation, or to adjust the types or amounts of one or more particular lipids it accumulates (e. g., to increase relative accumulation of triacylglycerol). In other cases, the host organism, may be non-oleaginous (though may contain some enzymatic and/or regulatory components used in other organisms to accumulate lipid), and may require oleaginic modification in order to become oleaginous in accordance with the present invention. The present invention also contemplates application of oleaginic modification to non-oleaginous host strains such that their oleaginicity is

increased even though, even after being modified, they may not be oleaginous as defined herein. In principle, the oleaginic modification may be any chemical, physiological, genetic, or other modification that appropriately alters oleaginy of a host organism as compared with an otherwise identical organism not subjected to the oleaginic modification. In most embodiments, however, the oleaginic modification will comprise a genetic modification, typically resulting in increased production and/or activity of one or more oleaginic polypeptides. In some embodiments, the oleaginic modification comprises at least one chemical, physiological, genetic, or other modification; in other embodiments, the oleaginic modification comprises more than one chemical, physiological, genetic, or other modification. In certain aspects where more than one modification is utilized, such modifications can comprise any combination of chemical, physiological, genetic, or other modification (e.g., one or more genetic, chemical and/or physiological modification(s)).

[0058] *Oleaginic polypeptide*: The term "oleaginic polypeptide", as used herein, refers to any polypeptide that is involved in the process of lipid accumulation in a cell and may include polypeptides that are involved in processes other than lipid biosynthesis but whose activities affect the extent or level of accumulation of one or more lipids, for example by scavenging a substrate or reactant utilized by an oleaginic polypeptide that is directly involved in lipid accumulation. For example, as discussed herein, acetyl-CoA carboxylase, pyruvate decarboxylase, isocitrate dehydrogenase, ATP-citrate lyase, malic enzyme, malate dehydrogenase, and AMP deaminase, among other proteins, are all involved in lipid accumulation in cells. In general, reducing the activity of pyruvate decarboxylase or isocitrate dehydrogenase, and/or increasing the activity of acetyl CoA carboxylase, ATP-citrate lyase, malic enzyme, malate dehydrogenase, and/or AMP deaminase is expected to promote oleaginy. Each of these proteins is an oleaginic peptide for the purposes of the present invention, and sequences of representative examples of these enzymes are provided in Tables 1-6, 69. Other peptides that can be involved in regenerating NADPH may include, for example, 6-phosphogluconate dehydrogenase (gnd); Fructose 1,6 bisphosphatase (fbp); Glucose 6 phosphate dehydrogenase (g6pd); NADH kinase (EC 2.7.1.86); and/or transhydrogenase (EC 1.6.1.1 and 1.6.1.2). Alternative or additional strategies to promote oleaginy may include one or more of the following: (1) increased or heterologous expression of one or more of acyl-CoA:diacylglycerol acyltransferase (e.g., DGA1; YALI0E32769g); phospholipid:diacylglycerol acyltransferase (e.g., LRO1; YALI0E16797g); and acyl-CoA:cholesterol acyltransferase (e.g., ARE genes such as ARE1, ARE2, YALI0F06578g), which are involved in triglyceride synthesis (Kalscheuer et al. *Appl Environ Microbiol* p.7119–7125, 2004; Oelkers et al. *J Biol Chem* 277:8877–8881, 2002; and Sorger et al. *J Biol Chem* 279:31190–31196, 2004), (2) decreased expression of triglyceride lipases (e.g., TGL3 and/or TGL4; YALI0D17534g and/or YALI0F10010g (Kurat et al. *J Biol Chem* 281:491–500, 2006); and (3) decreased expression of one or more acyl-coenzyme A oxidase activities, for example encoded by

POX genes (e.g. POX1, POX2, POX3, POX4, POX5; YALI0C23859g , YALI0D24750g, YALI0E06567g, YALI0E27654g, YALI0E32835g, YALI0F10857g; see, for example, Mlíckova et al. *Appl Environ Microbiol* 70: 3918–3924, 2004; Binns et al. *J Cell Biol* 173:719, 2006). Each of these proteins is an oleaginic peptide for the purposes of the present invention, and sequences of representative examples of these enzymes are provided in Tables 70-85 and Tables 100-101.

[0059] *Oleaginous*: The term "oleaginous", as used herein, refers to ability of an organism to accumulate lipid to at least about 20% of its dry cell weight. In certain embodiments of the invention, oleaginous yeast or fungi accumulate lipid to at least about 25% of their dry cell weight. In other embodiments, inventive oleaginous yeast or fungi accumulate lipid within the range of about 20-45% (e.g., about 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, or more) of their dry cell weight. In some embodiments, oleaginous organisms may accumulate lipid to as much as about 70% of their dry cell weight. In some embodiments of the invention, oleaginous organisms may accumulate a large fraction of total lipid accumulation in the form of triacylglycerol. In certain embodiments, the majority of the accumulated lipid is in the form of triacylglycerol. Alternatively or additionally, the lipid may accumulate in the form of intracellular lipid bodies, or oil bodies. In certain embodiments, the present invention utilizes yeast or fungi that are naturally oleaginous. In some aspects, naturally oleaginous organisms are manipulated (e. g., genetically, chemically, or otherwise) so as to further increase the level of accumulated lipid in the organism. For example, for the purposes of the present invention, *Yarrowia lipolytica* is a naturally oleaginous fungi. In other embodiments, yeast or fungi that are not naturally oleaginous are manipulated (e. g., genetically, chemically, or otherwise) to accumulate lipid as described herein. For example, for the purposes of the present invention, *Saccharomyces cerevisiae*, *Xanthophyllomyces dendrorhous* (*Phaffia rhodozyma*), and *Candida utilis* are not naturally oleaginous fungi.

[0060] *PHB polypeptide or PHB biosynthesis polypeptide*: The terms "PHB polypeptide" or "PHB biosynthesis polypeptide" as used herein refers to a polypeptide that is involved in the synthesis of *para*-hydroxybenzoate from chorismate. In prokaryotes and lower eukaryotes, synthesis of *para*-hydroxybenzoate occurs by the action of chorismate pyruvate lyase. Biosynthesis of *para*-hydroxybenzoate from tyrosine or phenylalanine occurs through a five-step process in mammalian cells. Lower eukaryotes such as yeast can utilize either method for production of *para*-hydroxybenzoate. For example, enzymes of the shikimate pathway, chorismate synthase, DAHP synthase, and transketolase are all PHB biosynthesis polypeptides. Each of these polypeptides is also a ubiquinone biosynthesis polypeptide or a ubiquinone biosynthesis competitor polypeptide for purposes of the present invention. Exemplary PHB polypeptides are provided in Tables 33 and 35-37.

[0061] *Polypeptide*: The term "polypeptide", as used herein, generally has its art-recognized meaning of a polymer of at least three amino acids. However, the term is also used to refer to specific functional classes of polypeptides, such as, for example, aromatic amino acid biosynthesis polypeptides, biosynthesis polypeptides, C_{5-9} quinone biosynthesis polypeptides, carotenogenic polypeptides, carotenoid biosynthesis polypeptides, isoprenoid biosynthesis polypeptides, oleaginic polypeptides, PHB polypeptides, PHB biosynthesis polypeptides, quinone biosynthesis polypeptides, quinonogenic polypeptides, ubiquinone biosynthesis polypeptides, ubiquinone biosynthesis competitor polypeptides, ubiquinogenic polypeptides, Vitamin E biosynthesis polypeptides, Vitamin K biosynthesis polypeptides, etc. For each such class, the present specification provides several examples of known sequences of such polypeptides. Those of ordinary skill in the art will appreciate, however, that the term "polypeptide" is intended to be sufficiently general as to encompass not only polypeptides having the complete sequence recited herein (or in a reference or database specifically mentioned herein), but also to encompass polypeptides that represent functional fragments (i. e., fragments retaining at least one activity) of such complete polypeptides. Moreover, those of ordinary skill in the art understand that protein sequences generally tolerate some substitution without destroying activity. Thus, any polypeptide that retains activity and shares at least about 30-40% overall sequence identity, often greater than about 50%, 60%, 70%, or 80%, and further usually including at least one region of much higher identity, often greater than 90% or even 95%, 96%, 97%, 98%, or 99% in one or more highly conserved regions (e.g., isocitrate dehydrogenase polypeptides often share a conserved AMP-binding motif; HMG-CoA reductase polypeptides typically include a highly conserved catalytic domain [see, for example, Figure 7] ; acetyl coA carboxylase typically has a carboxyl transferase domain; see, for example, Downing et al., *Chem. Abs.* 93:484, 1980; Gil et al., *Cell* 41:249, 1985; Jitrapakdee *et al. Curr Protein Pept Sci.* 4:217, 2003; U.S. Patent Number 5,349,126, each of which is incorporated herein by reference in its entirety), usually encompassing at least 3-4 and often up to 20 or more amino acids, with another polypeptide of the same class, is encompassed within the relevant term "polypeptide" as used herein. Other regions of similarity and/or identity can be determined by those of ordinary skill in the art by analysis of the sequences of various polypeptides presented in the Tables herein.

[0062] *Quinone biosynthesis polypeptide*: A "quinone biosynthesis polypeptide", as that term is used herein, refers to any polypeptide involved in the synthesis of one or more quinone derived compound, as described herein. In particular, quinone biosynthesis polypeptides include ubiquinone biosynthesis polypeptides (e.g., biosynthesis polypeptides involved in production of coenzyme Q10 and/or a C_{5-9} quinone compound), vitamin K biosynthesis polypeptides, and vitamin E biosynthesis polypeptides.

[0063] *Quinone derived compounds*: The term "quinone derived compounds" is used herein to refer to certain compounds that either contain a quinone moiety or are derived from a precursor that contains a quinone moiety. In particular, quinone derived compounds according to the present invention are ubiquinones (e.g., coenzyme Q10, C_{5-9} quinone compounds, etc.), vitamin E compounds, and/or vitamin K compounds. Structures of representative quinone derived compounds are presented in Figure 1.

[0064] *Quinonogenic modification*: The term "quinonogenic modification", as used herein, refers to refers to a modification of a host organism that adjusts production of one or more quinone derived compounds (*e.g.*, ubiquinones, vitamin K compounds, vitamin E compounds, etc.), as described herein. For example, a quinonogenic modification may increase the production level of a particular quinone derived compound, or of a variety of different quinone derived compounds. In some embodiments of the invention, production of a particular quinone derived compound may be increased while production of other quinone derived compounds is decreased. In some embodiments of the invention, production of a plurality of different quinone derived compounds is increased. In principle, an inventive quinonogenic modification may be any chemical, physiological, genetic, or other modification that appropriately alters production of one or more quinone derived compounds in a host organism produced by that organism as compared with the level produced in an otherwise identical organism not subject to the same modification. In most embodiments, however, the quinonogenic modification will comprise a genetic modification, typically resulting in increased production of one or more quinone derived compounds (*e.g.*, ubiquinones, vitamin K compounds, vitamin E compounds). In some embodiments, the quinonogenic modification comprises at least one chemical, physiological, genetic, or other modification; in other embodiments, the quinonogenic modification comprises more than one chemical, physiological, genetic, or other modification. In certain aspects where more than one modification is utilized, such modifications can comprise any combination of chemical, physiological, genetic, or other modification (e.g., one or more genetic, chemical and/or physiological modification(s)).

[0065] *Quinonogenic polypeptide*: The term "quinonogenic polypeptide", as used herein, refers to any polypeptide whose activity in a cell increases production of one or more quinone derived compounds (*e.g.*, ubiquinones, vitamin K compounds, vitamin E compounds) in that cell. The term encompasses both polypeptides that are directly involved in quinone derived compound synthesis and those whose expression or activity affects the extent or level of production of one or more quinone derived compounds, for example by scavenging a substrate or reactant utilized by a quinone biosynthetic polypeptide that is directly involved in quinone derived compound production. Quinonogenic polypeptides include isoprenoid biosynthesis polypeptides, ubiquinone biosynthesis polypeptides (e.g., polypeptides involved in production of coenzyme Q10 and/or a

C5-9 quinone compound), vitamin E biosynthesis polypeptides, and vitamin K biosynthesis polypeptides. Quinonogenic polypeptides may also include ubiquinogenic polypeptides, etc. The term also encompasses polypeptides that may affect the extent to which one or more quinone derived compounds is accumulated in lipid bodies.

[0066] *Small Molecule:* In general, a small molecule is understood in the art to be an organic molecule that is less than about 5 kilodaltons (Kd) in size. In some embodiments, the small molecule is less than about 3 Kd, 2 Kd, or 1 Kd. In some embodiments, the small molecule is less than about 800 daltons (D), 600 D, 500 D, 400 D, 300 D, 200 D, or 100 D. In some embodiments, small molecules are non-polymeric. In some embodiments, small molecules are not proteins, peptides, or amino acids. In some embodiments, small molecules are not nucleic acids or nucleotides. In some embodiments, small molecules are not saccharides or polysaccharides.

[0067] *Source organism*: The term "source organism", as used herein, refers to the organism in which a particular polypeptide sequence can be found in nature. Thus, for example, if one or more heterologous polypeptides is/are being expressed in a host organism, the organism in which the polypeptides are expressed in nature (and/or from which their genes were originally cloned) is referred to as the "source organism". Where multiple heterologous polypeptides are being expressed in a host organism, one or more source organism(s) may be utilized for independent selection of each of the heterologous polypeptide(s). It will be appreciated that any and all organisms that naturally contain relevant polypeptide sequences may be used as source organisms in accordance with the present invention. Representative source organisms include, for example, animal, mammalian, insect, plant, fungal, yeast, algal, bacterial, archaebacterial, cyanobacterial, and protozoal source organisms.

[0068] *Sterol biosynthesis polypeptide*: The term "sterol biosynthesis polypeptide", as used herein, refers to any polypeptide that is involved in the synthesis of one or more sterol compounds. Thus, sterol biosynthesis polypeptides can include isoprenoid biosynthesis polypeptides to the extent that they are involved in production of isopentyl pyrophosphate. Moreover, the term refers to any polypeptide that acts downstream of farnesyl pyrophosphate and in involved in the production of one or more sterol compounds. For example, sterol biosynthesis polypeptides include squalene synthase, which catalyses conversion of farnesyl pyrophosphate to presqualene pyrophosphate, and further catalyzes conversion of presqualene pyrophosphate to squalene (*i.e.*, enzyme 2.5.1.21 in Figure 8). In some embodiments of the invention, sterol biosynthesis polypeptides further include one or more polypeptides involved in metabolizing squalene into a vitamin D compound. Thus, sterol biosynthesis polypeptides can include one or more of the 1.14.99.7, 5.4.99.7, 5.4.99.8, 5.3.3.5, 1.14.21.6, 1.14.15.-, 1.14.13.13 enzyme polypeptides depicted in Figure 8, as well as other enzyme polypeptides involved in the illustrated pathways. Furthermore, sterol biosynthesis polypeptides can include one or more enzyme

polypeptides including, for example, C-14 demethylase (ERG9), squalene monooxygenase (ERG1), 2,3-oxidosqualene-lanosterol synthase (ERG7), C-1 demethylase (ERG11), C-14 reductase (ERG24), C-4 methyloxidase (ERG25), C-4 decarboxylase (ERG26), 3-ketoreductase (ERG27), C-24 methyltransferase (ERG6), Δ8-7 isomerase (ERG2), C-5 desaturase (ERG3), C-22 desaturase (ERG5)and/or C-24 reductase (ERG4) polypeptides, and/or other polypeptides involved in producing one or more vitamin D compounds (*e.g.*, vitamin D2, vitamin D3, or a precursor thereof). As will be appreciated by those of ordinary skill in the art, in some embodiments of the invention, sterol biosynthesis polypeptides include polypeptides that affect the expression and/or activity of one or more other sterol biosynthesis polypeptides. Thus, for instance, transcription factors that regulate expression of sterol biosynthesis enzymes can be sterol biosynthesis polypeptides for purposes of the present invention. To give but a couple of examples, the *S .cerevisiae* Upc2 and YLR228c genes, and the *Y. lipolytica* YALI0B00660g gene encode transcription factors that are sterol biosynthesis polypeptides according to certain embodiments of the present invention. For instance, the semidominant upc2-1 point mutation (G888D) exhibits increased sterol levels (Crowley et al., *J. Bacteriol* 180:4177-4183, 1998). Corresponding YLR228c mutants have been made and tested (Shianna et al., *J Bacteriol* 183:830, 2001); such mutants may be useful in accordance with the present invention, as may be YALI0B00660g derivatives with corresponding upc2-1 mutation(s). Representative examples of certain sterol biosynthesis polypeptide sequences are presented in Table 16 and 86-99.

[0069] *Sterologenic modification*: The term "sterologenic modification", as used herein, refers to a modification of a host organism that adjusts production of one or more sterol compounds (e.g., squalene, lanosterol, zymosterol, ergosterol, 7-dehydrocholesterol (provitamin D3), vitamin D compound(s), etc.), as described herein. For example, a sterologenic modification may increase the production level of a particular sterol compound, or of a variety of different sterol compounds. In some embodiments of the invention, production of a particular sterol compound may be increased while production of other sterol compounds is decreased. In some embodiments of the invention, production of a plurality of different sterol compounds is increased. In principle, an inventive sterologenic modification may be any chemical, physiological, genetic, or other modification that appropriately alters production of one or more sterol compounds in a host organism produced by that organism as compared with the level produced in an otherwise identical organism not subject to the same modification. In most embodiments, however, the sterologenic modification will comprise a genetic modification, typically resulting in increased production of one or more sterol compounds (e.g., squalene, lanosterol, zymosterol, ergosterol, 7-dehydrocholesterol (provitamin D3) or vitamin D compound(s)). In certain aspects where more than one modification is utilized, such modifications can comprise any combination of chemical,

physiological, genetic, or other modification (e.g., one or more genetic modification and chemical or physiological modification).

[0070] *Subject*: The term "subject" is used throughout the present specification to describe an animal, in most instances a human, to whom inventive compositions are administered.

[0071] *Ubiquinone*: The term "ubiquinone" is understood in the art to refer to a structural class of quinone derivatives with or without isoprenoid side chains. Ubiquinones are described in the Merck Index, 11th Edition, Merck & Co., Inc. Rahway, N. Y., USA, Abstr. 9751 (1989), which is incorporated herein by reference. A dual nomenclature exists for these compounds and is based upon the length of the terpenoid side chain. Those which contain an isoprene side chain are also referred to by the term coenzymes Q. A benzoquinone of this family is therefore properly referred to as either "Coenzyme Qn," where n is an integer from one to twelve and designates the number of isoprenoid units in the side chain, or alternatively, "ubiquinone (x)" where x designates the total number of carbon atoms in the side chain and is a multiple of five. Typically, n is an integer ranging from 0 to 12, in particular from 1 to 12, and more particularly 6, 7, 8, 9, or 10. For example, the most common ubiquinone in animals has a ten isoprenoid side chain and is referred to as either Coenzyme Q10, ubiquinone, or ubidecarenone. In other organisms (e.g. fungi, bacteria), other ubiquinones, for example C_5 (CoQ5), C_6 (CoQ6), C_7 (CoQ7), C_8 (CoQ8), or C_9 (CoQ9) (collectively C_{5-9}) quinones are more prevalent than Coenzyme Q10 (CoQ10). As mentioned, ubiquinones may lack an isoprene side chain, and may be selected from alkylubiquinones in which the alkyl group may contain from 1 to 20 and preferably from 1 to 12 carbon atoms, such as, for example, decylubiquinones such as 6-decylubiquinone or 2,3-dimethoxy-5-decyl-1,4-ubiquinone, derivatives thereof, and mixtures thereof. Ubiquinones may exist in reduced (ubiquinol), oxidized or superoxidized states. For example, the oxidation states of the ubiquinone coenzyme Q10 are depicted in Figure 1A.

[0072] *Ubiquinone biosynthesis competitor*: The term "ubiquinone biosynthesis competitor", as used herein, refers to an agent whose presence or activity in a cell reduces the level of farnesyl pyrophosphate (FPP), geranylgeranyl diphosphate (GGPP), chorismate, or any combination thereof that is available to enter the ubiquinogenic biosynthesis pathway. The term "ubiquinone biosynthesis competitor" encompasses both polypeptide (e.g. ubiquinone biosynthesis competitor polypeptides) and non-polypeptide (*e.g.*, small molecule) inhibitor agents. Those of ordinary skill in the art will appreciate that certain competitor agents that do not act as inhibitors of ubiquinone biosynthesis generally can nonetheless act as inhibitors of biosynthesis of a particular ubiquinone compound (e.g. CoQ10 or a C_{5-9} quinone compound). Particular examples of ubiquinone biosynthesis competitor agents act on isoprenoid intermediates prior to FPP or GGPP, such that less FPP or GGPP is generated (see, for example, Figure 5, Figure 6). Squalene synthase (also called squalene synthetase) is a ubiquinone biosynthesis competitor according to the present

invention; representative squalene synthase sequences are presented in Table 16. In another example, ubiquinone biosynthesis competitors include aromatic amino acid polypeptide enzymes that act on PHB precursors at or prior to chorismate, such that less chorismate is available for synthesis of *para*-hydroxybenzoate (see, for example Figure 3). Anthranilate synthase is one ubiquinone biosynthesis competitor according to the present invention, and chorismate mutase another; representative anthranilate synthase and chorismate mutase polypeptides are presented in Table 32, 32B and Table 34, respectively. Those of ordinary skill in the art, considering the known metabolic pathways relating to ubiquinone production and/or metabolism (see, for example, Figure 1 and other Figures and references herein) will readily appreciate a variety of other particular ubiquinone biosynthesis competitors, including ubiquinone biosynthesis polypeptides.

[0073] *Ubiquinone biosynthesis polypeptide*: The term "ubiquinone biosynthesis polypeptide" refers to any polypeptide that is involved in the synthesis of a ubiquinone (e. g., CoQ10 or a C_{5-9} quinone compound). To mention but a few, these ubiquinone biosynthesis polypeptides include, for example, polypeptides of polyprenyldiphosphate synthase (e.g. penta-, hexa-, hepta, octa-, nona-, deca- prenyldiphosphate synthase, PHB-polyprenyltransferase, and O-methyltransferase. Representative examples of ubiquinone biosynthesis polypeptide sequences are presented in Tables 23 (including 23b and 23c), 24-31, Table 33 as well as 35-37 (see also above PHB biosynthesis, C_{5-9} quinone biosynthesis polypeptides (e.g., Tables 61-65), and isoprenoid biosynthesis polypeptides which are ubiquinone biosynthesis polypeptides).

[0074] *Ubiquinogenic modification*: The term "ubiquinogenic modification", as used herein, refers to a modification of a host organism that adjusts production of a ubiquinone (e. g., CoQ10), as described herein. For example, a ubiquinogenic modification may increase the production level of a ubiquinone (e.g., CoQ10 and/or a C_{5-9} quinone compound), and/or may alter relative levels of a ubiquinone and/or a ubiquinol. In principle, an inventive ubiquinogenic modification may be any chemical, physiological, genetic, or other modification that appropriately alters production of a ubiquinone (e.g., CoQ10 and/or a C_{5-9} quinone compound) in a host organism produced by that organism as compared with the level produced in an otherwise identical organism not subject to the same modification. In most embodiments, however, the ubiquinogenic modification will comprise a genetic modification, typically resulting in increased production of a ubiquinone (e.g., CoQ10 and/or a C_{5-9} quinone compound). In some embodiments, the ubiquinogenic modification comprises at least one chemical, physiological, genetic, or other modification; in other embodiments, the ubiquinogenic modification comprises more than one chemical, physiological, genetic, or other modification. In certain aspects where more than one modification is utilized, such modifications can comprise any combination of chemical, physiological, genetic, or other modification (e.g., one or more genetic, chemical and/or physiological modification(s)).

[0075] *Ubiquinogenic polypeptide*: The term "ubiquinogenic polypeptide," as used herein, refers to any polypeptide that is involved in the process of producing a ubiquinone (e.g., CoQ10 and/or a C_{5-9} quinone compound) in a cell, and may include polypeptides that are involved in processes other than ubiquinone production but whose expression or activity affects the extent or level of production of a ubiquinone and/or a ubiquinol, for example by scavenging a substrate or reactant utilized by a ubiquinone biosynthetic polypeptide that is directly involved in ubiquinone production. Ubiquinogenic polypeptides include isoprenoid biosynthesis polypeptides, ubiquinone biosynthesis polypeptides, and ubiquinone biosynthesis competitor polypeptides, as those terms are defined herein. The term also encompasses polypeptides that may affect the extent to which a given ubiquinone is accumulated in lipid bodies.

[0076] *Vitamin D biosynthesis polypeptide*: The term "vitamin D biosynthesis polypeptide" refers to any polypeptide that is involved in the synthesis of one or more vitamin D compounds. To mention but a few, these include, for example, the 1.14.99.7, 5.4.99.7, 5.4.99.8, 5.3.3.5, and/or 1.14.21.6, polypeptides depicted in Figure 8. They further can include the hydroxylases that convert vitamin D_3 to calcitriol (*e.g.*, the 1.14.15.- and 1.14.13.13 polypeptides depicted in Figure 8). As will be appreciated by those of ordinary skill in the art, in some embodiments of the invention, vitamin D biosynthesis polypeptides include polypeptides that affect the expression and/or activity of one or more other vitamin D biosynthesis polypeptides. Particular examples of certain vitamin D biosynthesis polypeptides are presented in Tables 86-99.

[0077] *Vitamin E biosynthesis polypeptide:* The term "vitamin E biosynthesis polypeptide" refers to any polypeptide that is involved in the synthesis of vitamin K. To mention but a few, these include, for example, tyrA, pds1(hppd), VTE1, HPT1(VTE2), VTE3, VTE4, and/or GGH polypeptides (i.e., polypeptides that perform the chemical reactions performed by tyrA, pds1(hppd), VTE1, HPT1(VTE2), VTE3, VTE4, and/or GGH, respectively). Particular examples of such vitamin E biosynthesis polypeptides are presented in Tables 54-60.

[0078] *Vitamin E compound*: The term "vitamin E compound", as used herein, refers to members of a family of structurally related compounds that have a 6-chromanol ring, an isoprenoid side chain, and the biologic activity of α-tocopherol. The term encompasses the eight known naturally occurring vitamin E compounds, the four tocopherols (α, β, γ, δ) and four tocotrienols (α, β, γ, δ), which all contain a hydrophilic chromanol ring and a hydrophobic side chain. The α, β, γ, and δ forms differ from one another in the number of methyl groups on the chromanol ring. Several synthetic vitamin E compounds have also been prepared, and still others are possible (see, for example, Bramley et al., *J. Sci Food Agric* 80:913, 2000). α-tocopherol is a potent antioxidant, and is generally considered to be the most active vitamin E compound in humans.

[0079] *Vitamin E production modification:* The term "Vitamin E production modification", as used herein, refers to a modification of a host organism that adjusts production of Vitamin E. For example, a Vitamin E production modification may increase the production level of one or more vitamin E compounds, and/or may alter relative production levels of different vitamin E compounds. In principle, an inventive vitamin E production modification may be any chemical, physiological, genetic, or other modification that appropriately alters production of one or more vitamin E compounds in a host organism produced by that organism as compared with the level produced in an otherwise identical organism not subject to the same modification. In most embodiments, however, the vitamin E production modification will comprise a genetic modification, typically resulting in increased production of one or more selected vitamin E compounds. In some embodiments, the vitamin E production modification comprises at least one chemical, physiological, genetic, or other modification; in other embodiments, the vitamin E production modification comprises more than one chemical, physiological, genetic, or other modification. In certain aspects where more than one modification is utilized, such modifications can comprise any combination of chemical, physiological, genetic, or other modification (e.g., one or more genetic, chemical and/or physiological modification(s)).

[0080] *Vitamin K biosynthesis polypeptide*: The term "vitamin K biosynthesis polypeptide" refers to any polypeptide that is involved in the synthesis of vitamin K. To mention but a few, these include, for example, MenF, MenD, MenC, MenE, MenB, MenA, UbiE, and/or MenG polypeptides (i.e., polypeptides that perform the chemical reactions performed by MenF, MenD, MenC, MenE, MenB, MenA, UbiE, and/or MenG, respectively). Particular examples of such vitamin K biosynthesis polypeptides are presented in Tables 46-53.

[0081] *Vitamin K compounds*: The term "vitamin K compounds", as used herein, refers to members of a family of structurally related compounds that share a common biologic activity. In particular, vitamin K compounds are derivatives of 2-methyl-1,4-naphthoquinone that have coagulation activity. The two natural forms of vitamin K differ in the identity of their side chains at position 3. Vitamin K_1, also known as phylloquinone (based on its presence in plants), has a phytyl side chain in position 3; vitamin K2, also known as menaquinone, has an isoprenyl side chain at position 3. Different forms of menaquinone, having side chains with different numbers of isoprene units (typically 4-13) are found in different types of cells.

[0082] *Vitamin K production modification:* The term "Vitamin K production modification", as used herein, refers to a modification of a host organism that adjusts production of Vitamin K. For example, a Vitamin K production modification may increase the production level of one or more vitamin K compounds, and/or may alter relative production levels of different vitamin K compounds. In principle, an inventive vitamin K production modification may be any chemical, physiological, genetic, or other modification that appropriately alters production of one

or more vitamin K compounds in a host organism produced by that organism as compared with the level produced in an otherwise identical organism not subject to the same modification. In most embodiments, however, the vitamin K production modification will comprise a genetic modification, typically resulting in increased production of one or more selected vitamin K compounds. In some embodiments, the vitamin K production modification comprises at least one chemical, physiological, genetic, or other modification; in other embodiments, the vitamin K production modification comprises more than one chemical, physiological, genetic, or other modification. In certain aspects where more than one modification is utilized, such modifications can comprise any combination of chemical, physiological, genetic, or other modification (e.g., one or more genetic, chemical and/or physiological modification(s)).

Detailed Description of Certain Preferred Embodiments of the Invention

[0083] The present invention embraces the reasoning that quinone derived compound(s) (e.g., ubiquinones, vitamin K compounds, and vitamin E compounds) can effectively be produced in oleaginous yeast and fungi. According to the present invention, strains that both (i) accumulate lipid, often in the form of cytoplasmic oil bodies; and (ii) produce one or more quinone derived compound(s) at a level at least about 1%, of their dry cell weight, are generated through manipulation of host cells (i.e., strains, including, e.g., naturally-occurring strains and strains which have been previously modified). In certain embodiments, strains can accumulate lipid typically to at least about 20% of their dry cell weight. In some embodiments quinone derived compound(s) can be produced in the strains to at least about 2%, at least about 3%, at least about 4%, at least about 5%, at least about 6%, at least about 7%, at least about 8%, at least about 9%, at least about 10%, at least about 11%, at least about 12%, at least about 13%, at least about 14%, at least about 15%, at least about 16%, at least about 17%, at least about 18%, at least about 19%, or at least about 20% of fungus' dry cell weight. Thus, the provided manipulated strains can then be used to produce the quinone derived compound(s). In some embodiments, the compound(s) that partition(s) into the lipid bodies can readily be isolated. In some embodiments the quinone derived compound is Coenzyme Q10 (CoQ10; Ubiquinone 10; Ubiquinone 50). In some embodiments, the quinone derived compound is C_5 (CoQ5), C_6 (CoQ6), C_7 (CoQ7), C_8 (CoQ8), or C_9 (CoQ9) quinone. In some embodiments, the quinone derived compound is a tocopherol or a tocotrienols. In some embodiments, the quinone derived compound is phylloquinone (vitamin K_1), or menaquinone (vitamin K_2).

[0084] In some embodiments, it will be desirable to balance oleaginy and production of quinone derived compound(s) in cells such that, as soon as a minimum desirable level of oleaginy is achieved, substantially all further carbon is diverted into a metabolic pathway that results in production of one or more quinone derived compounds. In some embodiments of the invention,

this strategy involves engineering cells to be oleaginous; in other embodiments, it involves engineering cells to accumulate a higher level of lipid, particularly cytoplasmic lipid, than they would do in the absence of such engineering even though the engineered cells may not become "oleaginous" as defined herein. In other embodiments, the extent to which an oleaginous host cell accumulates lipid is actually reduced so that remaining carbon can be utilized in ubiquinone production.

[0085] To give but one example of adjustments that could be made to achieve a desired balance between oleaginy and production of quinone derived compound(s), we note that, while increasing acetyl CoA carboxylase expression (and/or activity) promotes oleaginy, decreasing its expression and/or activity may promote production of quinone derived compound(s). Those of ordinary skill in the art will appreciate that the expression and/or activity of acetyl CoA carboxylase, or of other polypeptides, may be adjusted up or down as desired according to the characteristics of a particular host cell of interest.

[0086] We note that engineered cells and processes of using them as described herein may provide one or more advantages as compared with unmodified cells. Such advantages may include, but are not limited to: increased yield (e.g., quinone derived compound expressed as either % dry cell weight (mg/mg) or parts per million), titer (g quinone derived compound/L), specific productivity (mg quinone derived compound g^{-1} biomass $hour^{-1}$), and/or volumetric productivity (g quinone derived compound $liter^{-1}$ $hour^{-1}$)) of the desired quinone derived compound (and/or intermediates thereof), and/or decreased formation of undesirable side products (for example, undesirable intermediates).

[0087] Thus, for example, the specific productivity for one or more quinone derived compounds (e.g., ubiquinones, vitamin K compounds, and/or vitamin E compounds) or total quinone derived compounds may be at or about 0.1, at or about 0.11, at or about 0.12, at or about 0.13, at or about 0.14, at or about 0.15, at or about 0.16, at or about 0.17, at or about 0.18, at or about 0.19, at or about 0.2, at or about 0.21, at or about 0.22, at or about 0.23, at or about 0.24, at or about 0.25, at or about 0.26, at or about 0.27, at or about 0.28, at or about 0.29, at or about 0.3, at or about 0.31, at or about 0.32, at or about 0.33, at or about 0.34, at or about 0.35, at or about 0.36, at or about 0.37, at or about 0.38, at or about 0.39, at or about 0.4, at or about 0.41, at or about 0.42, at or about 0.43, at or about 0.44, at or about 0.45, at or about 0.46, at or about 0.47, at or about 0.48, at or about 0.49, at or about 0.5, at or about 0.51, at or about 0.52, at or about 0.53, at or about 0.54, at or about 0.55, at or about 0.56, at or about 0.57, at or about 0.58, at or about 0.59, at or about 0.6, at or about 0.61, at or about 0.62, at or about 0.63, at or about 0.64, at or about 0.65, at or about 0.66, at or about 0.67, at or about 0.68, at or about 0.69, at or about 0.7, at or about 0.71, at or about 0.72, at or about 0.73, at or about 0.74, at or about 0.75, at or about 0.76, at or about 0.77, at or about 0.78, at or about 0.79, at or about 0.8, at or about 0.81, at or about

0.82, at or about 0.83, at or about 0.84, at or about 0.85, at or about 0.86, at or about 0.87, at or about 0.88, at or about 0.89, at or about 0.9, at or about 0.91, at or about 0.92, at or about 0.93, at or about 0.94, at or about 0.95, at or about 0.96, at or about 0.97, at or about 0.98, at or about 0.99, at or about 1, 1.05, at or about 1.1, at or about 1.15, at or about 1.2, at or about 1.25, at or about 1.3, at or about 1.35, at or about 1.4, at or about 1.45, at or about 1.5, at or about 1.55, at or about 1.6, at or about 1.65, at or about 1.7, at or about 1.75, at or about 1.8, at or about 1.85, at or about 1.9, at or about 1.95, at or about 2 mg g^{-1} $hour^{-1}$ or more.

[0088] Thus, for example, the volumetric productivity for one or more quinone derived compounds (e.g., ubiquinones, vitamin K compounds, and/or vitamin E compounds) or total quinone derived compounds may be at or about 0.01, at or about 0.011, at or about 0.012, at or about 0.013, at or about 0.014, at or about 0.015, at or about 0.016, at or about 0.017, at or about 0.018, at or about 0.019, at or about 0.02, at or about 0.021, at or about 0.022, at or about 0.023, at or about 0.024, at or about 0.025, at or about 0.026, at or about 0.027, at or about 0.028, at or about 0.029, at or about 0.03, at or about 0.031, at or about 0.032, at or about 0.033, at or about 0.034, at or about 0.035, at or about 0.036, at or about 0.037, at or about 0.038, at or about 0.039, at or about 0.04, at or about 0.041, at or about 0.042, at or about 0.043, at or about 0.044, at or about 0.045, at or about 0.046, at or about 0.047, at or about 0.048, at or about 0.049, at or about 0.05, at or about 0.051, at or about 0.052, at or about 0.053, at or about 0.054, at or about 0.055, at or about 0.056, at or about 0.057, at or about 0.058, at or about 0.059, at or about 0.06, at or about 0.061, at or about 0.062, at or about 0.063, at or about 0.064, at or about 0.065, at or about 0.066, at or about 0.067, at or about 0.068, at or about 0.069, at or about 0.07, at or about 0.071, at or about 0.072, at or about 0.073, at or about 0.074, at or about 0.075, at or about 0.076, at or about 0.077, at or about 0.078, at or about 0.079, at or about 0.08, at or about 0.081, at or about 0.082, at or about 0.083, at or about 0.084, at or about 0.085, at or about 0.086, at or about 0.087, at or about 0.088, at or about 0.089, at or about 0.09, at or about 0.091, at or about 0.092, at or about 0.093, at or about 0.094, at or about 0.095, at or about 0.096, at or about 0.097, at or about 0.098, at or about 0.099, at or about 0.1, 0.105, at or about .110, at or about .115, at or about .120, at or about .125, at or about .130, at or about .135, at or about .14, at or about .145, at or about .15, at or about .155, at or about .16, at or about .165, at or about .17, at or about .175, at or about .18, at or about .185, at or about .19, at or about .195, at or about .20 grams $liter^{-1}$ $hour^{-1}$ or more.

Host Cells

[0089] Those of ordinary skill in the art will readily appreciate that a variety of yeast and fungal strains exist that are naturally oleaginous or that naturally produce one or more quinone derived compounds (e.g., a ubiquinone, a vitamin K compound and/or a vitamin E compound). Any of such strains may be utilized as host strains according to the present invention, and may be engineered or otherwise manipulated to generate inventive oleaginous, quinone derived-compound-producing strains. Alternatively, strains that naturally are neither oleaginous nor

quinone derived-compound-producing may be employed. Furthermore, even when a particular strain has a natural capacity for oleaginy or for production of one or more quinone derived compounds, its natural capabilities may be adjusted as described herein for optimal production of one or more particular desired compounds.

[0090] In certain embodiments, engineering or manipulation of a strain results in modification of a type of lipid and/or quinone derived compound produced. For example, a strain may be naturally oleaginous and/or may naturally produce one or more quinone derived compounds (e.g., a ubiquinone, including, e.g., CoQ5, CoQ6, CoQ8, CoQ9, CoQ10; vitamin K, including phylloquinone and/or one or more menaquinones; and/or vitamin E, including one or more tocopherols and/or one or more tocotrienols). However, engineering or modification of the strain may be employed so as to change the type or amount of lipid that is accumulated and/or to adjust production of one or more quinone derived compounds (including, for example, modulating relative amounts of particular quinone derived compounds). In some embodiments, production of CoQ10; phylloquinone; menaquinone; and/or α-tocopherol production will be optimized.

[0091] When selecting a particular yeast or fungal strain for use in accordance with the present invention, it will generally be desirable to select one whose cultivation characteristics are amenable to commercial scale production. For example, it will generally (though not necessarily always) be desirable to avoid filamentous organisms, or organisms with particularly unusual or stringent requirements for growth conditions. In some embodiments of the invention, it will be desirable to utilize edible organisms as host cells, as they may optionally be formulated directly into pharmaceutical compositions, food or feed additives, or into nutritional supplements, as desired. Some embodiments of the invention utilize host cells that are genetically tractable, amenable to molecular genetics (e.g., can be efficiently transformed, especially with established or available vectors; optionally can incorporate and/or integrate multiple genes, for example sequentially; and/or have known genetic sequence; etc), devoid of complex growth requirements (e.g., a necessity for light), mesophilic (e.g., prefer growth temperatures within the range of about 20-32 °C) (e.g., 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32 °C), able to assimilate a variety of carbon and nitrogen sources and/or capable of growing to high cell density. Alternatively or additionally, various embodiments of the invention utilize host cells that grow as single cells rather than, for example, as mycelia.

[0092] In general, when it is desirable to utilize a naturally oleaginous organism in accordance with the present invention, any modifiable and cultivatable oleaginous organism may be employed. In certain embodiments of the invention, yeast or fungi of genera including, but not limited to, *Blakeslea*, *Candida*, *Cryptococcus*, *Cunninghamella*, *Lipomyces*, *Mortierella*, *Mucor*, *Phycomyces*, *Pythium*, *Rhodosporidium*, *Rhodotorula*, *Thraustochytrium*, *Trichosporon*, and *Yarrowia* are employed. In certain particular embodiments, organisms of species that include, but

are not limited to, *Blakeslea trispora*, *Candida pulcherrima*, *C. revkaufi*, *C. tropicalis*, *Cryptococcus curvatus*, *Cunninghamella echinulata*, *C. elegans*, *C. japonica*, *Lipomyces starkeyi*, *L. lipoferus*, *Mortierella alpina*, *M. isabellina*, *M. ramanniana*, *M. vinacea*, *Mucor circinelloides*, *Phycomyces blakesleanus*, *Pythium irregulare*, *Rhodosporidium toruloides*, *Rhodotorula glutinis*, *R. gracilis*, *R. graminis*, *R. mucilaginosa*, *R. pinicola*, *Thraustochytrium* sp, *Trichosporon pullans*, *T. cutaneum*, and *Yarrowia lipolytica* are used.

[0093] Of these naturally oleaginous strains, some also naturally produce one or more quinone derived compounds and some do not. In most cases, only low levels (less than about 0.05% dry cell weight) of quinone derived compounds are produced by naturally-occurring oleaginous yeast or fungi.

[0094] In general, any organism that is naturally oleaginous but does not naturally produce one or more particular quinone derived compounds of interest (e.g., does not produce a ubiquinone such as CoQ10, vitamin K compounds, vitamin E compounds be utilized as a host cell in accordance with the present invention. In some embodiments, the organism is a yeast or fungus from a genus such as, but not limited to, *Candida*, *Mortierella*, and *Yarrowia*; in some embodiments, the organism is of a species including, but not limited to, *Mortierella alpina* and *Yarrowia lipolytica*. At least some fungal strains are known not to produce vitamin K.

[0095] Comparably, the present invention may utilize any naturally oleaginous organism that does naturally produce one or more quinone derived compounds as a host cell. In general, the present invention may be utilized to increase carbon flow into the isoprenoid pathway organisms that naturally produce a particular quinone derived compounds of interest and/or to shift production of one or more different quinone derived compounds. For example, the present invention may be utilized to shift production from one ubiquinone (e.g., CoQ5, CoQ6, CoQ8, CoQ9) to another (e.g., CoQ10). Introduction of one or more quinonogenic modifications (e.g., one or more ubiquinogenic modifications), such as but not limited to increased expression of one or more endogenous or heterologous quinonogenic polypeptides), in accordance with the present invention, can achieve these goals.

[0096] In certain embodiments of the invention, the utilized oleaginous, quinone derived compound-producing organism is a yeast or fungus, for example of a genus such as, but not limited to, *Rhodotorula*; in some embodiments, the organism is of a species such as *Rhodotorula glutinis*.

[0097] When it is desirable to utilize strains that are naturally non-oleaginous as host cells in accordance with the present invention, genera of non-oleaginous yeast or fungi include, but are not limited to, *Aspergillus*, *Botrytis*, *Cercospora*, *Fusarium* (*Gibberella*), *Kluyveromyces*, *Neurospora*, *Penicillium*, *Pichia* (*Hansenula*), *Puccinia*, *Saccharomyces*, *Schizosaccharomyces*, *Sclerotium*, *Trichoderma*, and *Xanthophyllomyces* (*Phaffia*); in some embodiments, the organism

is of a species including, but not limited to, *Candida utilis, Aspergillus nidulans, A. niger, A. terreus, Botrytis cinerea, Cercospora nicotianae, Fusarium fujikuroi* (*Gibberella zeae*), *Kluyveromyces lactis, K. lactis, Neurospora crassa, Pichia pastoris, Puccinia distincta, Saccharomyces cerevisiae, Schizosaccharomyces pombe, Sclerotium rolfsii, Trichoderma reesei,* and *Xanthophyllomyces dendrorhous* (*Phaffia rhodozyma*).

[0098] It will be appreciated that the term "non-oleaginous", as used herein, encompasses both strains that naturally have some ability to accumulate lipid, especially cytoplasmically, but do not do so to a level sufficient to qualify as "oleaginous" as defined herein, as well as strains that do not naturally have any ability to accumulate extra lipid, e.g., extra-membranous lipid. It will further be appreciated that, in some embodiments of the invention, it will be sufficient to increase the natural level of oleaginy of a particular host cell, even if the modified cell does not qualify as oleaginous as defined herein. In some embodiments, the cell will be modified to accumulate at least about 19%, 18%, 17%, 16%, 15%, 14%, 13%, 12%, 11%, 10%, 9%, 8%, 7%, 6%, or 5% dry cell weight as lipid, so long as the accumulation level is more than that observed in the unmodified parental cell.

[0099] As with the naturally oleaginous organisms, some of the naturally non-oleaginous fungi naturally produce one or more quinone derived compounds, whereas others do not. Genera of naturally non-oleaginous fungi that do not naturally produce quinone derived compounds (such as CoQ10 or other ubiquinone, vitamin K compounds, vitamin E compounds) for instance, but that may desirably be used as host cells in accordance with the present invention include, but are not limited to, *Aspergillus*, *Kluyveromyces*, *Penicillium*, *Saccharomyces*, and *Pichia*; species include, but are not limited to, *Candida utilis, Aspergillus niger, Xanthophyllomyces dendrorhous* (*Phaffia rhodozyma)* and *Saccharomyces cerevisiae. Saccharomyces cerevisiae*, in particular, is known not to produce vitamin E or vitamin K compounds; other fungi likely also do not produce these compounds. Genera of naturally non-oleaginous fungi that do naturally produce one or more quinone derived compounds (e.g., CoQ10) and that may desirably be used as host cells in accordance with the present invention include, but are not limited to, yeasts of such genera as *Schizosaccharomyces* and *Basidiomycetes*; fungi of such genera as *Tremella* are capable of producing certain quinone derived compounds, and in particular are capable of producing CoQ10.

[00100] As discussed above, any of a variety of organisms may be employed as host cells in accordance with the present invention. In certain embodiments of the invention, host cells will be *Y. lipolytica* cells. Advantages of *Y. lipolytica* include, for example, tractable genetics and molecular biology, availability of genomic sequence (see, for example, Sherman et al. *Nucleic Acids Res.* 32(Database issue):D315-8, 2004), suitability to various cost-effective growth conditions, ability to grow to high cell density. In addition, *Y. lipolytica* is naturally oleaginous, such that fewer manipulations may be required to generate an oleaginous, ubiquinone-producing

(e. g., CoQ10) *Y. lipolytica* strain than might be required for other organisms. Furthermore, there is already extensive commercial experience with *Y. lipolytica.*

[00101] *Saccharomyces cerevisiae* is also a useful host cell in accordance with the present invention, particularly due to its experimental tractability and the extensive experience that researchers have accumulated with the organism. Although cultivation of *Saccharomyces* under high carbon conditions may result in increased ethanol production, this can generally be managed by process and/or genetic alterations.

[00102] The edible fungus, *Candida utilis* is also a useful host cell in accordance with the present invention. Molecular biology tools and techniques are available in *C. utilis* (for example, see Iwakiri et al. (2006) Yeast 23:23-34, Iwakiri et al. (2005) Yeast 2005 22:1079-87, Iwakiri et al. (2005) Yeast 22:1049-60, Rodriquez et al. (1998) Yeast 14:1399-406, Rodriquez et al. (1998) FEMS Microbiol Lett. 165:335-40, and Kondo et al. (1995) J Bacteriol. 177:7171-7).

[00103] Additional useful hosts include *Xanthophyllomyces dendrorhous (Phaffia rhodozyma)*, which is experimentally tractable and naturally produces isoprenoid compounds.

[00104] *Aspergillus niger* and *Mortierella alpina* accumulate large amounts of citric acid and fatty acid, respectively; *Mortierella alpina* is also oleaginous.

[00105] *Neurospora* or *Gibberella* are also useful. They are not naturally oleaginous and may require extensive modification to be used in accordance with the present invention. *Neurospora* and *Gibberella* are considered relatively tractable from an experimental standpoint. Both are filamentous fungi, such that production at commercial scales can be a challenge necessary to overcome in utilization of such strains.

[00106] *Mucor circinelloides* is another available useful species. While its molecular genetics are generally less accessible than are those of some other organisms, it naturally produces isoprenoids and may require less modification than other species available.

[00107] Molecular genetics can be performed in *Blakeslea*, though significant effort may be required. Furthermore, cost-effective fermentation conditions can be challenging, as, for example, it may be required that the two mating types are mixed. Fungi of the genus *Phycomyces* are also possible sources which have the potential to pose fermentation process challenges, and these fungi may be less amenable to manipulate than several other potential host organisms.

[00108] Additional useful hosts include strains, such as *Schizosaccharomyces pombe*, *Saitoella complicata*, and *Sporidiobolus ruineniae*, which can produce certain quinone derived compounds including, for example, CoQ10.

[00109] Those of ordinary skill in the art will appreciate that the selection of a particular host cell for use in accordance with the present invention will also affect, for example, the selection of expression sequences utilized with any heterologous polypeptide to be introduced into the cell, and will also influence various aspects of culture conditions, etc. Much is known about

the different gene regulatory requirements, protein targeting sequence requirements, and cultivation requirements, of different host cells to be utilized in accordance with the present invention (see, for example, with respect to *Yarrowia*, Barth et al. *FEMS Microbiol Rev.* 19:219, 1997; Madzak et al. *J Biotechnol.* 109:63, 2004; see, for example, with respect to *Xanthophyllomyces*, Verdoes et al. *Appl Environ Microbiol* 69: 3728-38, 2003; Visser et al. FEMS Yeast Res 4: 221-31, 2003; Martinez et al. Antonie Van Leeuwenhoek. 73(2):147-53, 1998; Kim et al. Appl Environ Microbiol. 64(5):1947-9, 1998; Wery et al. Gene. 184(1):89-97, 1997; see, for example, with respect to *Saccharomyces*, Guthrie and Fink *Methods in Enzymology* 194:1-933, 1991). In certain aspects, for example, targeting sequences of the host cell (or closely related analogs) may be useful to include for directing heterologous proteins to subcellular localization. Thus, such useful targeting sequences can be added to heterologous sequence for proper intracellular localization of activity. In other aspects (e.g., addition of mitochondrial targeting sequences), heterologous targeting sequences may be eliminated or altered in the selected heterologous sequence (e.g., alteration or removal of source organism plant chloroplast targeting sequences).

[00110] To give but a few specific examples, of promoters and/or regulatory sequences that may be employed in expression of polypeptides according to the present invention, useful promoters include, but are not limited to, the Leu2 promoter and variants thereof (see, for example, see US patent number 5,786,212); the EF1alpha protein and ribosomal protein S7 gene promoters (see, for example, PCT Application WO 97/44470); the Gpm (see US20050014270), Xpr2 (see US4937189), Tef1, Gpd1 (see, for example, US Application 2005-0014270A1), Cam1 (YALI0C24420g), YALI0D16467g, Tef4 (YALI0B12562g), Yef3 (YALI0E13277g), Pox2, Yat1(see, for example US Application 2005-0130280; PCT Application WO 06/052754), Fba1 (see, for example WO05049805), and/or Gpat (see WO06031937) promoters; the sequences represented by SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, and SEQ ID NO: 12, subsequences thereof, and hybrid and tandem derivatives thereof (e.g., as disclosed in US Application 2004-0146975); the sequences represented by SEQ ID NO: 1, 2, or 3 including fragments (e.g. bp 462-1016 and bp 197-1016 of SEQ ID NO: 1; bp 5-523 of SEQ ID NO:3) and complements thereof (e.g., as disclosed in US patent number 5,952,195); CYP52A2A (see, for example, US Application 2002-0034788); promoter sequences from fungal (e.g., *C. tropicalis*) catalase, citrate synthase, 3-ketoacyl-CoA thiolase A, citrate synthase, O-acetylhomserine sulphydrylase, protease, carnitine O-acetyltransferase, hydratase-dehydrogenase, epimerase genes; promoter sequences from Pox4 genes (see, for example, US application 2004-0265980); and/or promoter sequences from Met2, Met3, Met6, Met25 and YALI0D12903g genes. Any such promoters can be used in conjunction with endogenous genes and/or heterologous genes for

modification of expression patterns of endogenous polypeptides and/or heterologous polypeptides in accordance with the present invejtion.

[00111] Alternatively or additionally, regulatory sequences useful in accordance with the present invention may include one or more Xpr2 promoter fragments, for example as described in US patent 6,083,717 (e.g. SEQ ID NOS: 1-4 also including sequences with 80% or more identity to these SEQ ID NOs) in one or more copies either in single or in tandem. Similarly, exemplary terminator sequences include, but are not limited to, *Y. lipolytica* Xpr2 (see US4937189) and Pox2 (YALI0F10857g) terminator sequences and those listed in example 11 herein.

Engineering Oleaginy

[00112] All living organisms synthesize lipids for use in their membranes and various other structures. However, most organisms do not accumulate in excess of about 10% of their dry cell weight as total lipid, and most of this lipid generally resides within cellular membranes.

[00113] Significant biochemical work has been done to define the metabolic enzymes necessary to confer oleaginy on microorganisms (primarily for the purpose of engineering single cell oils as commercial sources of arachidonic acid and docosahexaenoic acid; see for example Ratledge *Biochimie* 86:807, 2004, the entire contents of which are incorporated herein by reference). Although this biochemical work is compelling, there only have been a limited number of reports of *de novo* oleaginy being established through genetic engineering with the genes encoding the key metabolic enzymes. It should be noted that oleaginous organisms typically accumulate lipid only when grown under conditions of carbon excess and nitrogen limitation. The present invention further establishes that the limitation of other nutrients (e.g. phosphate or magnesium) can also induce lipid accumulation. The present invention establishes, for example, that limitation of nutrients such as phosphate and/or magnesium can induce lipid accumulation, much as is observed under conditions of nitrogen limitation. Under these conditions, the organism readily depletes the limiting nutrient but continues to assimilate the carbon source. The "excess" carbon is channeled into lipid biosynthesis so that lipids (usually triacylglycerols) accumulate in the cytosol, typically in the form of bodies.

[00114] In general, it is thought that, in order to be oleaginous, an organism must produce both acetyl-CoA and NADPH in the cytosol, which can then be utilized by the fatty acid synthase machinery to generate lipids. In at least some oleaginous organisms, acetyl-CoA is generated in the cytosol through the action of ATP-citrate lyase, which catalyzes the reaction:

(1) **citrate + CoA + ATP → acetyl-CoA + oxaloacetate + ADP + P_i.**

[00115] Of course, in order for ATP-citrate lyase to generate appropriate levels of acetyl-CoA in the cytosol, it must first have an available pool of its substrate citric acid. Citric acid is

generated in the mitochondria of all eukaryotic cells through the tricarboxylic acid (TCA) cycle, and can be moved into the cytosol (in exchange for malate) by citrate/malate translocase.

[00116] In most oleaginous organisms, and in some non-oleaginous organisms, the enzyme isocitrate dehydrogenase, which operates as part of the TCA cycle in the mitochondria, is strongly AMP-dependent. Thus, when AMP is depleted from the mitochondria, this enzyme is inactivated. When isocitrate dehydrogenase is inactive, isocitrate accumulates in the mitochondria. This accumulated isocitrate is then equilibrated with citric acid, presumably through the action of aconitase. Therefore, under conditions of low AMP, citrate accumulates in the mitochondria. As noted above, mitochondrial citrate is readily transported into the cytosol.

[00117] AMP depletion, which in oleaginous organisms is believed to initiate the cascade leading to accumulation of citrate (and therefore acetyl-CoA) in the cytoplasm, occurs as a result of the nutrient depletion mentioned above. When oleaginous cells are grown in the presence of excess carbon source but the absence of nitrogen or other nutrient (e.g., phosphate or magnesium), the activity of AMP deaminase, which catalyzes the reaction:

(2) **AMP → inosine 5'-monophosphate + NH_3**

is strongly induced. The increased activity of this enzyme depletes cellular AMP in both the cytosol and the mitochondria. Depletion of AMP from the mitochondria is thought to inactivate the AMP-dependent isocitrate dehydrogenase, resulting in accumulation of citrate in the mitochondria and, therefore, the cytosol. This series of events is depicted diagrammatically in Figure 2.

[00118] As noted above, oleaginy requires *both* cytosolic acetyl-CoA *and* cytosolic NADPH. It is believed that, in many oleaginous organisms, appropriate levels of cytosolic NADPH are provided through the action of malic enzyme (Enzyme 3 in Figure 2). Some oleaginous organisms (e.g., *Lipomyces* and some *Candida*) do not appear to have malic enzymes, however, so apparently other enzymes can provide comparable activity, although it is expected that a dedicated source of NADPH is probably required for fatty acid synthesis (see, for example, Wynn et al., *Microbiol* 145:1911, 1999; Ratledge *Adv. Appl. Microbiol.* 51:1, 2002, each of which is incorporated herein by reference in its entirety).

[00119] Other activities which can be involved in regenerating NADPH include, for example, 6-phosphogluconate dehydrogenase (gnd); Fructose 1,6 bisphosphatase (fbp); Glucose 6 phosphate dehydrogenase (g6pd); NADH kinase (EC 2.7.1.86); and/or transhydrogenase (EC 1.6.1.1 and 1.6.1.2).

[00120] Gnd is part of the pentose phosphate pathway and catalyses the reaction:

6-phospho-D-gluconate + NADP+ → D-ribulose 5-phosphate + CO_2 + NADPH

[00121] Fbp is a hydrolase that catalyses the gluconeogenic reaction:

D-fructose 1,6-bisphosphate + H_2O → D-fructose 6-phosphate +phosphate

Fbp redirects carbon flow from glycolysis towards the pentose phosphate pathway. The oxidative portion of the pentose phosphate pathway, which includes glucose 6 phosphate dehydrogenase and 6-phosphogluconate dehydrogenase, enables the regeneration of NADPH.

[00122] G6pd is part of the pentose phosphate pathway and catalyses the reaction:

D-glucose 6-phosphate + $NADP^+$ → D-glucono-1,5-lactone 6-phosphate + NADPH + H^+

[00123] NADH kinase catalyzes the reaction:

ATP + NADH → ADP + NADPH

[00124] Transhydrogenase catalyzes the reaction:

NADPH + NAD^+ ↔ $NADP^+$ + NADH

[00125] Thus, enhancing the expression and/or activity of any of these enzymes can increase NADPH levels and promote anabolic pathways requiring NADPH.

[00126] Alternative or additional strategies to promote oleaginy may include one or more of the following: (1) increased or heterologous expression of one or more of acyl-CoA:diacylglycerol acyltransferase (e.g., DGA1; YALI0E32769g); phospholipid:diacylglycerol acyltransferase (e.g., LRO1; YALI0E16797g); and acyl-CoA:cholesterol acyltransferase (e.g., ARE genes such as ARE1, ARE2, YALI0F06578g), which are involved in triglyceride synthesis (Kalscheuer et al. *Appl Environ Microbiol* p.7119–7125, 2004; Oelkers et al. *J Biol Chem* 277:8877–8881, 2002; and Sorger et al. *J Biol Chem* 279:31190–31196, 2004), (2) decreased expression of triglyceride lipases (e.g., TGL3 and/or TGL4; YALI0D17534g and/or YALI0F10010g (Kurat et al. *J Biol Chem* 281:491–500, 2006); and (3) decreased expression of one or more acyl-coenzyme A oxidase activities, for example encoded by POX genes (e.g. POX1, POX2, POX3, POX4, POX5; YALI0C23859g , YALI0D24750g, YALI0E06567g, YALI0E27654g, YALI0E32835g, YALI0F10857g; see for example Mlíckova et al. *Appl Environ Microbiol* 70: 3918–3924, 2004; Binns et al. *J Cell Biol* 173:719, 2006).

[00127] Thus, according to the present invention, the oleaginy of a host organism may be enhanced by modifying the expression or activity of one or more polypeptides involved in generating cytosolic acetyl-CoA and/or NADPH and/or altering lipid levels through other mechanisms. For example, modification of the expression or activity of one or more of acetyl-CoA carboxylase, pyruvate decarboxylase, isocitrate dehydrogenase, ATP-citrate lyase, malic enzyme, AMP-deaminase, glucose-6-phosphate dehydrogenase, 6-phosphogluconate dehydrogenase, fructose 1, 6 bisphosphatase, NADH kinase, transhydrogenase, acyl-CoA:diacylglycerol acyltransferase, phospholipid:diacylglycerol acyltransferase, acyl-CoA:cholesterol acyltransferase, triglyceride lipase, acyl-coenzyme A oxidase can enhance oleaginy in accordance with the present invention. Exemplary polypeptides which can be utilized or derived so as to enhance oleaginy in accordance with the present invention include, but are not limited to those acetyl-CoA carboxylase, pyruvate decarboxylase, isocitrate dehydrogenase, ATP-

citrate lyase, malic enzyme, AMP-deaminase, glucose-6-phosphate dehydrogenase, 6-phosphogluconate dehydrogenase, fructose 1, 6 bisphosphatase, NADH kinase, transhydrogenase, acyl-CoA:diacylglycerol acyltransferase, phospholipid:diacylglycerol acyltransferase, acyl-CoA:cholesterol acyltransferase, triglyceride lipase, acyl-coenzyme A oxidase polypeptides provided in Tables 1-6 and Tables 69-85 respectively.

[00128] In some embodiments of the invention, where an oleaginous host cell is employed, enzymes and regulatory components relevant to oleaginy are already in place but could be modified, if desired, by for example altering expression or activity of one or more oleaginic polypeptides and/or by introducing one or more heterologous oleaginic polypeptides. In those embodiments of the invention where a non-oleaginous host cell is employed, it is generally expected that at least one or more heterologous oleaginic polypeptides will be introduced.

[00129] The present invention contemplates not only introduction of heterologous oleaginous polypeptides, but also adjustment of expression or activity levels of heterologous or endogenous oleaginic polypeptides, including, for example, alteration of constitutive or inducible expression patterns. In some embodiments of the invention, expression patterns are adjusted such that growth in nutrient-limiting conditions is not required to induce oleaginy. For example, genetic modifications comprising alteration and/or addition of regulatory sequences (e.g., promoter elements, terminator elements) and/or regulatory factors (e.g., polypeptides that modulate transcription, splicing, translation, modification, etc.) may be utilized to confer particular regulation of expression patterns. Such genetic modifications may be utilized in conjunction with endogenous genes (e.g., for regulation of endogenous oleagenic polypeptide(s)); alternatively, such genetic modifications may be included so as to confer regulation of expression of at least one heterologous polypeptide (e.g., oleagenic polypeptide(s)).

[00130] In some embodiments, at least one oleaginic polypeptide is introduced into a host cell. In some embodiments of the invention, a plurality (e.g., two or more) of different oleaginic polypeptides is introduced into the same host cell. In some embodiments, the plurality of oleaginic polypeptides contains polypeptides from the same source organism; in other embodiments, the plurality includes polypeptides independently selected from different source organisms.

[00131] Representative examples of a variety of oleaginic polypeptides that may be introduced into or modified within host cells according to the present invention, include, but are not limited to, those provided in Tables 1-6, and Tables 69-85. As noted above, it is expected that at least some of these polypeptides (e.g., malic enzyme and ATP-citrate lyase) should desirably act in concert, and possibly together with one or more components of fatty acid synthase, such that, in some embodiments of the invention, it will be desirable to utilize two or more oleaginic polypeptides from the same source organism.

[00132] In general, source organisms for oleaginic polypeptides to be used in accordance with the present invention include, but are not limited to, *Blakeslea, Candida, Cryptococcus, Cunninghamella, Lipomyces, Mortierella, Mucor,* Phycomyces, *Pythium, Rhodosporidium, Rhodotorula, Trichosporon, Yarrowia, Aspergillus, Botrytis, Cercospora, Fusarium (Gibberella), Kluyveromyces, Neurospora, Penicillium, Pichia (Hansenula), Puccinia, Saccharomyces, Sclerotium, Trichoderma, and Xanthophyllomyces (Phaffia).* In some embodiments, the source species for acetyl CoA carboxylase, ATP-citrate lyase, malic enzyme and/or AMP deaminase polypeptides include, but are not limited to, *Aspergillus nidulans, Cryptococcus neoformans, Fusarium fujikuroi, Kluyveromyces lactis, Neurospora crassa, Saccharomyces cerevisiae, Schizosaccharomyces pombe, Ustilago maydis*, and *Yarrowia lipolytica*; in some embodiments, source species for pyruvate decarboxylase or isocitrate dehydrogenase polypeptides include, but are not limited to *Neurospora crassa, Xanthophyllomyces dendrorhous (Phaffia rhodozyma), Aspergillus niger, Saccharomyces cerevisiae, Mucor circinelloides, Rhodotorula glutinis, Candida utilis, Mortierella alpina,* and *Yarrowia lipolytica.*

[00133] *Aspergillus niger* accumulates large amounts of citric acid, whereas *Mortierella alpina* and *Thraustochytrium* sp. accumulate large amounts of fatty acid, respectively; *Mortierella alpina* and *Thraustochytrium* are also oleaginous. To give but one particular example of a host cell engineered to be oleaginous (or at least to accumulate increased levels of lipid) in accordance with the present invention, *S. cerevisiae* can be engineered to express one or more oleaginic polypeptides, e.g., from heterologous source organisms.

[00134] In some embodiments, a plurality of different oleaginic polypeptides are expressed, optionally from different source organisms. For instance, in some embodiments, *S. cerevisiae* cells are engineered to express (and/or to increase expression of) ATP-citrate lyase (e.g., from *N. crassa*), AMP deaminase (e.g., from *S. cerevisiae*), and/or malic enzyme (e.g., from *M. circinelloides*). In other embodiments, *Candida utilis* and *Phaffia rhodozyma* can be similarly modified. Modified *S. cerevisiae*, *C. utilis*, and *P. rhodozyma* strains can be further modified as described herein to increase production of one or more quinone derived compounds.

Engineering Production of Quinone Derived Compounds

[00135] The present invention encompasses the recognition that lipid-accumulating systems are useful for the production and/or isolation of certain quinone derived compounds, and particularly of a ubiquinone (e.g., CoQ10 and/or one or more C_{5-9} quinone compounds such as CoQ5, CoQ6, CoQ7, CoQ8, CoQ9), one or more vitamin K compounds (e.g., phylloquinone and/or one or more menaquinones), and/or one or more vitamin E compounds (e.g., one or more tocopherols and/or tocotrienols). Without wishing to be bound by theory, the present inventors propose that the higher intracellular membrane content may facilitate increased quinone derived

compound production and/or accumulation. The present invention therefore encompasses the discovery that certain quinone derived compounds can desirably be produced in oleaginous yeast and fungi.

[00136] According to the present invention, strains that both (i) accumulate lipid, often in the form of cytoplasmic lipid bodies and typically to at least about 20% of their dry cell weight; and (ii) produce one or more quinone derived compounds at a level at least about 1%, and in some embodiments at least about 3-20%, of their dry cell weight, are generated through manipulation of generally available strains (*e.g.*, naturally-occurring strains and strains which have been previously genetically modified, whether via recombinant DNA techniques or mutagenesis directed modification). These manipulated strains are then used to produce one or more quinone derived compounds, so that compound(s) that partitions into the lipid bodies can readily be isolated.

[00137] In certain embodiments of the invention, host cells are *Yarrowia lipolytica* cells. Advantages of *Y. lipolytica* include, for example, tractable genetics and molecular biology, availability of genomic sequence, suitability to various cost-effective growth conditions, and ability to grow to high cell density. In addition, *Y. lipolytica* is naturally oleaginous, such that fewer manipulations may be required to generate an oleaginous, quinone derived compound-producing *Y. lipolytica* strain than might be required for other organisms. Furthermore, there is already extensive commercial experience with *Y. lipolytica.* In certain embodiments, host cells are *Saccharomyces cerevisiae* cells. In other embodiments, host cells are *Candida utilis* cells.

[00138] As mentioned, quinone derived compounds are produced from the isoprenoid compound isopentyl pyrophosphate (IPP), via geranylgeranyl pyrophosphate (see, for example, Figure 8. IPP can be generated through one of two different isoprenoid biosynthesis pathways. The most common isoprenoid biosynthesis pathway, sometimes referred to as the "mevalonate pathway", is generally depicted in Figure 4A. As shown, acetyl-CoA is converted, via hydroxymethylglutaryl-CoA (HMG-CoA), into mevalonate. Mevalonate is then phosphorylated and converted into the five-carbon compound isopentenyl pyrophosphate (IPP).

[00139] An alternative isoprenoid biosynthesis pathway, that is utilized by some organisms (particularly bacteria) and is sometimes called the "mevalonate-independent pathway", is also depicted in Figure 4A. This pathway is initiated by the synthesis of 1-deoxy-D-xyloglucose-5-phosphate (DOXP) from pyruvate and glyceraldehyde-3-phosphate. DOXP is then converted, via a series of reactions shown in Figure 4B, into IPP.

[00140] Various proteins involved in isoprenoid biosynthesis have been identified and characterized in a number of organisms. Moreover, isoprenoids are synthesized in many, if not most, organisms. Thus, various aspects of the isoprenoid biosynthesis pathway are conserved throughout the fungal, bacterial, plant and animal kingdoms. For example, polypeptides corresponding to the acetoacetyl-CoA thiolase, HMG-CoA synthase, HMG-CoA reductase,

mevalonate kinase, phosphomevalonate kinase, mevalonate pyrophosphate decarboxylase, IPP isomerase, FPP synthase, and GGPP synthase shown in Figures 4-6 and 8 have been identified in and isolated from a wide variety of organisms and cells; representative examples of a wide variety of such polypeptides are provided in Tables 7-15. One or more of the polypeptides selected from those provided in any one of Tables 7-15 may be utilized or derived for use in the methods and compositions in accordance with the present invention.

[00141] Alternatively or additionally, modified mevalonate kinase polypeptides that exhibit decreased feedback inhibition properties (*e.g.*, to farnesyl pyrophosphate (FPP)) may be utilized in accordance with the present invention. Such modified mevalonate kinase polypeptides may be of eukaryotic or prokaryotic origin. For example, modified versions of mevalonate kinase polypeptides from animals (including humans), plants, algae, fungi (including yeast), and/or bacteria may be employed; for instance, modified versions of mevalonate kinase polypeptides disclosed in Table 10 herein may be utilized.

[00142] Particular examples of modified mevalonate kinase polypeptides include "feedback-resistant mevalonate kinases" disclosed in PCT Application WO 06/063,752. Thus, for example, a modified mevalonate kinase polypeptide may include one or more mutation(s) at one or more amino acid position(s) selected from the group consisting of amino acid positions corresponding to positions 17, 47, 93, 94, 132, 167, 169, 204, and 266 of the amino acid sequence of *Paracoccus zeaxanthinifaciens* mevalonate kinase as shown in SEQ ID NO:1 of PCT Application WO 04/111,214. For example, the modified mevalonate kinase polypeptide may contain one or more substitutions at positions corresponding to one or more of I17T, G47D, K93E, V94I, R204H and C266S.

[00143] To give but a few specific examples, when a modified mevalonate kinase polypeptide comprises 2 amino acid changes as compared with a parent mevalonate kinase polypeptide, it may comprise changes at positions corresponding to the following positions 132/375,167/169, 17/47 and/or 17/93 of SEQ ID NO:1 of WO 04/111,214 (*e.g.* P132A/P375R, R167W/K169Q, I17T/G47D or I17T/K93E); when a modified mevalonate kinase polypeptide comprises 3 amino acid changes as compared with a parent mevalonate kinase, it may comprise changes at positions corresponding to the following positions 17/167/169, 17/132/375, 93/132/375, and/or 17/47/93 of SEQ ID NO : 1 of WO/2004/111214 (*e.g.*, I17T/R167W/K169Q, I17T/P132A/P375R, K93E/P132A/P375R, I17T/R167W/K169H, I17T/R167T/K169M, I17T/R167T/K169Y, I17T/R167F/K169Q, I17T/R167I/K169N, I17T/R167H/K169Y, I17T/G47D/K93E or I17T/G47D/K93Q).

[00144] Thus, for example, a modified mevalonate kinase polypeptide may include one or more mutation(s) (particularly substitutions), as compared with a parent mevalonate kinase polypeptide, at one or more amino acid position(s) selected from the group consisting of amino

acid positions corresponding to positions 55, 59, 66, 83, 106, 111, 117, 142, 152, 158, 218, 231, 249, 367 and 375 of the amino acid sequence of *Saccharomyces cerevisiae* mevalonate kinase as shown in SEQ ID NO:1 of PCT application WO 06/063,752. For example, such corresponding substitutions may comprise one or more of P55L, F59S, N66K, C117S, or I152M. A modified mevalonate kinase may comprise a substitution corresponding to F59S substitution. A modified mevalonate kinase polypeptide comprising 2 amino acid changes as compared with its parent mevalonate kinase polypeptide may, for example, comprise changes at positions corresponding to the following positions 55/117, 66/152, 83/249, 111/375 or 106/218 of to SEQ ID NO : 1 of WO 06/063,752 (*e.g.* P55L/C117S, N66K/I152M, K83E/S249P, H111N/K375N or L106P/S218P). A modified mevalonate kinase may comprise a substitution corresponding to N66K/I152M. A modified mevalonate kinase polypeptide comprising 4 amino acid changes as compared with its parent mevalonate kinase polypeptide may have changes at positions corresponding to one or more of the following positions 42/158/231/367 of SEQ ID NO:1 of WO 06/063,752 (*e.g.*, I142N/L158S/L231I/T367S).

[00145] According to the present invention, quinone derived compound production in a host organism may be adjusted by modifying the expression or activity of one or more proteins involved in isoprenoid biosynthesis. In some embodiments, such modification involves introduction of one or more heterologous isoprenoid biosynthesis polypeptides into the host cell; alternatively or additionally, modifications may be made to the expression or activity of one or more endogenous or heterologous isoprenoid biosynthesis polypeptides. Given the considerable conservation of components of the isoprenoid biosynthesis polypeptides, it is expected that heterologous isoprenoid biosynthesis polypeptides will often function well even in significantly divergent organisms. Furthermore, should it be desirable to introduce more than one heterologous isoprenoid biosynthesis polypeptide (*e.g.*, more than one version of the same polypeptide and/or more than one different polypeptides), in many cases polypeptides from different source organisms may function well together. In some embodiments of the invention, a plurality of different heterologous isoprenoid biosynthesis polypeptides is introduced into the same host cell. In some embodiments, this plurality contains only polypeptides from the same source organism; in other embodiments the plurality includes polypeptides from different source organisms.

[00146] In certain embodiments of the present invention that utilize heterologous isoprenoid biosynthesis polypeptides, the source organisms include, but are not limited to, fungi of the genera *Blakeslea, Candida, Cryptococcus, Cunninghamella, Lipomyces, Mortierella, Mucor, Phycomyces, Pythium, Rhodosporidium, Rhodotorula, Trichosporon, Yarrowia, Aspergillus, Botrytis, Cercospora, Fusarium (Gibberella), Kluyveromyces, Neurospora, Penicillium, Pichia (Hansenula), Puccinia, Saccharomyces, Schizosaccharomyces, Sclerotium, TrichodermsUstilago, and Xanthophyllomyces (Phaffia).* In certain embodiments, the source organisms are of a species including, but not limited to, *Cryptococcus neoformans, Fusarium fujikuroi, Kluyverimyces lactis,*

Neurospora crassa, Saccharomyces cerevisiae, Schizosaccharomyces pombe, Ustilago maydis, and Yarrowia lipolytica.

Ubiquinone-10/Coenzyme Q10

[00147] Ubiquinone-10, or coenzyme Q10 (CoQ10), is synthesized *de novo* in all mammalian tissues, and serves a critical function in mediating electron transport in the mitochondrial respiratory chain. The reduced form of CoQ10 is also thought to function as an antioxidant and to protect against lipid peroxidation as well as against other free radical-induced oxidative damage. Recent studies have confirmed the role of CoQ10 in certain disease states, and additional roles in certain disorders continue to be elucidated. For example, administration of cholesterol lowering drugs, including HMG-CoA reductase inhibitors (e.g., the statins) to patients can result in diminished CoQ10 levels since cholesterol biosynthesis and CoQ10 biosynthesis share many of the same biosynthetic steps. Additionally, several clinical studies have been conducted to examine whether supplemental CoQ10 administration provides protection against, for example, deterioration in cardiac function (e.g., congestive heart failure), slows deterioration in Parkinson's patients, or protects the heart from damage caused by certain chemotherapeutic drugs.

[00148] While cells are capable of endogenously producing CoQ10, only about half of the levels required for optimum human cell function are produced in the body; the other half is acquired through dietary sources. Also, cellular levels of CoQ10 decrease under stress, with increasing age, and after certain pharmacological treatments, further increasing the need for exogenous CoQ10 to maintain optimum cell function.

[00149] CoQ10 has been used commercially in dietary and nutritional supplements as well as in functional foods, cosmetics and in personal care items. A rapidly growing market exists for CoQ10. The 2005 market for CoQ10 as an ingredient is estimated to be approximate $500 million, which represented approximately 250 metric tonnes of CoQ10. Further market expansion for CoQ10 is expected. Improved systems for enabling cost effective production, isolation, and/or formulation of CoQ10 are needed to effectively meet the growing demand for CoQ10.

[00150] The commitment step in ubiquinone biosynthesis is the formation of *para*-hydroxybenzoate (PHB) from tyrosine or phenylalanine in mammals or chorismate in bacteria, followed by condensation of PHB and isoprene precursor, resulting in addition of the prenyl group (see Figure 9). Lower eukaryotes, such as yeast, can synthesize PHB from either tyrosine or chorismate. The 3-decaprenyl-4-hydroxybenzoic acid resulting from the condensation reaction undergoes further modifications, which include hydroxylation, methylation and decarboxylation, in order to form ubiquinone. Ubiquinone biosynthetic enzymes and genes encoding these proteins have been characterized in several organisms. The most extensive analysis has been performed in bacterial systems such as *Escherichia coli* and *Rhodobacter sphaeroides* as well as the yeast,

Saccharomyces cerevisiae. At least 8 enzymes are required for the synthesis of CoQ10 from PHB and the isoprene precursors.

[00151] Biomanufacturing processes for CoQ10 have been developed or attempted using several genera of bacteria and yeast. Bacterial hosts have included *R. sphaeroides*, *Agrobacterium tumefaciens*, *Paracoccus denitrificans*, *Rhodopseudomonas spheroides*, and recombinant strains of *E. coli*, which naturally produces CoQ8. Yeast hosts have included *Saitoella complicata*, *Sporidiobolus ruineniae*, *Schizosaccharomyces pombe*, and several species of Rhodotorula and Candida. In addition, a semi-synthetic process for producing CoQ10 has been developed using solanesol extracted from tobacco leaves as a starting material; this process has economic and environmental disadvantages.

[00152] Despite the early identification of several microorganisms as potential hosts for CoQ10 production, only limited progress has been made towards the development of a cost-effective CoQ10 process using fermentation. Without wishing to be bound by any particular theory, the present inventors note that the hydrophobic isoprenoid side chain on CoQ10 causes it to localize to cell membranes, and offer that enhanced CoQ10 concentrations in the membranes might be detrimental to cell growth or viability. Efforts to engineer strains with increased production of CoQ10 have focused primarily in prokaryotes such as *E. coli*. While *E. coli* is a host with facile molecular genetic tools, this organism's fundamental physiology, may limit its ultimate utility as a CoQ10 production system.

[00153] The present invention encompasses the recognition that lipid-accumulating systems are useful for the production and/or isolation of ubiquinone(s). Indeed, several of the more productive natural CoQ10 strains (e.g., *P. denitrificans, R. sphaeroides*) display a relatively high intracellular membrane content. Without wishing to be bound by theory, the present inventors propose that the higher intracellular membrane content may facilitate increased CoQ10 production and/or accumulation. The present invention therefore encompasses the discovery that CoQ10 can desirably be produced in oleaginous yeast and fungi. According to the present invention, strains that both (i) accumulate lipid, often in the form of cytoplasmic lipid bodies and typically to at least about 20% of their dry cell weight; and (ii) produce CoQ10 at a level at least about 1%, and in some embodiments at least about 3-20%, of their dry cell weight, are generated through manipulation of generally available strains (e.g., naturally-occurring strains and strains which have been previously genetically modified, whether via recombinant DNA techniques or mutagenesis directed modification). These manipulated strains are then used to produce CoQ10, so that the CoQ10 that partitions into the lipid bodies can readily be isolated.

[00154] In certain embodiments of the invention, host cells are *Yarrowia lipolytica* cells. Advantages of *Y. lipolytica* include, for example, tractable genetics and molecular biology, availability of genomic sequence, suitability to various cost-effective growth conditions, and

ability to grow to high cell density. In addition, *Y. lipolytica* is naturally oleaginous, such that fewer manipulations may be required to generate an oleaginous, CoQ10-producing *Y. lipolytica* strain than might be required for other organisms. Furthermore, there is already extensive commercial experience with *Y. lipolytica.*

[00155] As mentioned, ubiquinone is formed by the combination of *para*-hydroxybenzoate and isoprenoid chains produced, for example, via the isoprenoid biosynthesis pathways discussed above. Once IPP is formed according to that pathway, it isomerizes into dimethylallyl pyrophophate (DMAPP). Three sequential condensation reactions with additional molecules of IPP generate the ten-carbon molecule geranyl pyrophosphate (GPP), followed by the fifteen-carbon molecule farnesyl pyrophosphate (FPP), which can be used to form the twenty-carbon compound geranylgeranyl pyrophosphate (GGPP). In many instances, FPP appears to be the predominant substrate used by polyprenyldiphosphate synthases (e.g., Coq1 polypeptides) during ubiquinone biosynthesis. According to the present invention, ubiquinone production in a host organism may be adjusted by modifying the expression or activity of one or more proteins involved in isoprenoid biosynthesis as discussed above.

[00156] As discussed herein, two different pathways can produce the ubiquinoid precursor *para*-hydroxybenzoate —the first, the "shikimate pathway" is utilized in prokaryotes and yeast, involves synthesis of *para*-hydroxybenzoate (PHB) through chorismate. Biosynthesis of *para*-hydroxybenzoate from chorismate occurs by the action of chorismate pyruvate lyase. For example, as discussed herein, enzymes of the shikimate pathway, chorismate synthase, DAHP synthase, and transketolase are involved in this process. Representative examples of these enzymes are provided in Table 33 and Tables 35 through 37. In the second possible pathway, *para*-hydroxybenzoate is produced by derivation of tyrosine or phenylalanine. Biosynthesis of para-hydroxybenzate from tyrosine or phenylalanine occurs through a five step process in mammalian cells (see, for example Figure 3).

[00157] Accordingly, ubiquinone (e.g., CoQ10 and/or C_{5-9} quinone compounds) production in a host organism may be adjusted by modifying the expression or activity of one or more proteins involved in PHB biosynthesis. In some embodiments, such modification involves introduction of one or more heterologous PHB polypeptides into the host cell; alternatively or additionally, modifications may be made to the expression or activity of one or more endogenous or heterologous additional PHB polypeptide, and/or isoprenoid biosynthesis polypeptides. Given the considerable conservation of components of the PHB biosynthesis polypeptides, it is expected that heterologous PHB biosynthesis polypeptides will often function well even in significantly divergent organisms. Further, given the conservation of the pathways among organism, it is anticipated that heterologous polypeptides throughout the ubiquinone biosynthetic pathway will function together effectively. Furthermore, should it be desirable to introduce more than one

heterologous PHB polypeptide and/or isoprenoid biosynthesis polypeptide, in many cases polypeptides from different source organisms will function well together. In some embodiments of the invention, a plurality of different heterologous PHB and/or isoprenoid biosynthesis polypeptides is introduced into the same host cell. In some embodiments, this plurality contains only polypeptides from the same source organism; in other embodiments the plurality includes polypeptides from different source organisms. In still other embodiments, modification of endogenous PHB and/or isoprenoid biosynthesis polypeptides are also utilized, either alone or in combination with heterologous polypeptides as discussed herein.

[00158] As noted herein, the isoprenoid biosynthesis pathway is also involved in the production of non-ubiquinone compounds, such as carotenoids, sterols, steroids, and vitamins, such as vitamin K or vitamin E. Proteins that act on isoprenoid biosynthesis pathway intermediates, and divert them into biosynthesis of non-ubiquinone compounds are therefore indirect inhibitors of ubiquinone biosynthesis (see, for example, Figure 5, which illustrates points at which isoprenoid intermediates are channeled into other biosynthesis pathways). Such proteins are therefore considered ubiquinone biosynthesis competitor polypeptides. Reductions of the level or activity of such ubiquinone biosynthesis competitor polypeptides are expected to increase ubiquinone (e.g., CoQ10 and/or C_{5-9} quinone compounds) production in host cells according to the present invention.

[00159] In some embodiments of the present invention, production or activity of endogenous ubiquinone biosynthesis competitor polypeptides may be reduced or eliminated in host cells. In some embodiments, this reduction or elimination of the activity of a ubiquinone biosynthesis competitor polypeptide can be achieved by treatment of the host organism with small molecule inhibitors of enzymes of the ergosterol biosynthetic pathway. Enzymes of the ergosterol biosynthetic pathway include, for example, squalene synthase (Erg9), squalene epoxidase (Erg1), 2,3-oxidosqualene-lanosterol cyclase (Erg7), cytochrome P450 lanosterol 14α-demethylase (Erg11), C-14 sterol reductase (Erg24), C-4 sterol methyl oxidase (Erg25), SAM:C-24 sterol methyltransferase (Erg6), C-8 sterol isomerase (Erg2), C-5 sterol desaturase (Erg3), C-22 sterol desaturase (Erg5), and C-24 sterol reductase (Erg4) polypeptides. Each of these enzymes is considered a ubiquinone biosynthesis competitor polypeptide. Regulators of these enzymes may also be considered ubiquinone biosynthesis competitor polypeptides (e.g., the yeast proteins Sut1 (Genbank Accession JC4374 GI:2133159) and Mot3 (Genbank Accession NP_013786 GI:6323715), which may or may not have homologs in other organisms.

In some embodiments of the invention, production or activity of endogenous ubiquinone biosynthesis competitor polypeptides may be reduced or eliminated in host cells. In some embodiments, this reduction or elimination of the activity of a ubiquinone biosynthesis competitor polypeptide can be achieved by treatment of the host organism with small molecule inhibitors of

enzymes of the ergosterol biosynthetic pathway. Enzymes of the ergosterol biosynthetic pathway include, for example, squalene synthase, squalene epoxidase, 2,3-oxidosqualene-lanosterol cyclase, cytochrome P450 lanosterol 14α-demethylase, C-14 sterol reductase, C-4 sterol methyl oxidase, SAM:C-24 sterol methyltransferase, C-8 sterol isomerase, C-5 sterol desaturase, C-22 sterol desaturase, and C-24 sterol reductase. Each of these enzymes is considered a ubiquinone biosynthesis competitor polypeptide. Regulators of these enzymes may also be considered ubiquinone biosynthesis competitor polypeptides (e.g., the yeast proteins Sut1 (Genbank Accession JC4374 GI:2133159) and Mot3 (Genbank Accession NP_013786 GI:6323715), which may or may not have homologs in other organisms).

[00160] Known small molecule inhibitors of some ubiquinone biosynthesis competitor enzymes include, but are not limited to, zaragosic acid (including analogs thereof such as TAN1607A (Biochem Biophys Res Commun 1996 Feb 15;219(2):515-520)), RPR 107393 (3-hydroxy-3-[4-(quinolin-6-yl)phenyl]-1-azabicyclo[2-2-2]octane dihydrochloride; J Pharmacol Exp Ther. 1997 May;281(2):746-52), ER-28448 (5-{N-[2-butenyl-3-(2-methoxyphenyl)]-N-methylamino}-1,1-penthylidenebis(phosphonic acid) trisodium salt; Journal of Lipid Research, Vol. 41, 1136-1144, July 2000), BMS-188494 (The Journal of Clinical Pharmacology, 1998; 38:1116-1121), TAK-475 (1-[2-[(3R,5S)-1-(3-acetoxy-2,2-dimethylpropyl)-7-chloro-1,2,3,5-tetrahydro-2-oxo-5-(2,3-dimethoxyphenyl)-4,1-benzoxazepine-3-yl] acetyl] piperidin-4-acetic acid; Eur J Pharmacol. 2003 Apr 11;466(1-2):155-61), YM-53601 ((E)-2-[2-fluoro-2-(quinuclidin-3-ylidene) ethoxy]-9H-carbazole monohydrochloride; Br J Pharmacol. 2000 Sep;131(1):63-70), or squalestatin I that inhibit squalene synthase; terbinafine (*e.g.*, LAMISIL®), naftifine (NAFTIN®), S-allylcysteine, garlic, resveratrol, NB-598 (*e.g.*, from Banyu Pharmaceutical Co), and/or green tea phenols that inhibit squalene epoxidase (see, for example, *J. Biol Chem* 265:18075, 1990; *Biochem. Biophys. Res. Commun.* 268:767, 2000); various azoles that inhibit cytochrome P450 lanosterol 14α-demethylase; and fenpropimorph that inhibits the C-14 sterol reductase and the C-8 sterol isomerase. In other embodiments, heterologous ubiquinone biosynthesis competitor polypeptides may be utilized (whether functional or non-functional; in some embodiments, dominant negative mutants are employed).

[00161] One ubiquinone biosynthesis competitor polypeptide useful according to the present invention is squalene synthase which has been identified and characterized from a variety of organisms; representative examples of squalene synthase polypeptide sequences are included in Table 16. In some embodiments of the invention that utilize squalene synthase (or modifications of squalene synthase) source organisms include, but are not limited to, *Neurospora crassa, Xanthophyllomyces dendrorhous (Phaffia rhodozyma), Aspergillus niger, Saccharomyces cerevisiae, Mucor circinelloides, Rhotorula glutinis, Candida utilis, Mortierella alpina,* and *Yarrowia lipolytica.*

[00162] Another ubiquinone biosynthesis competitor polypeptide useful according to the present invention is anthranilate synthase, which has also been identified in a variety of organisms; representative anthranilate synthase polypeptides are provided in Table 32 and 32B. In some embodiments of the invention, anthranilate synthase polypeptide, or modifications thereof are utilized and adapted from source organisms including, but not limited to: *Kluyveromyces lactis, Candida glabrata, Saccharomyces cerevisiae, Yarrowia lipolytica, Debaryomyces hansenii, Candida albicans, Aspergillus fumigatus, Aspergillus oryzae, Aspergillus nidulans, Ustilago maydis, Neurospora crassa, Schizosaccharomyces pombe, Gibberella zeae,* and *Cryptococcus neoformans var.*

[00163] Similarly, yet another ubiquinone biosynthesis competitor polypeptide useful according to the invention is chorismate mutase, which has also been identified in a variety of organisms; representative chorismate mutase polypeptides are provided in Table 34. In some embodiments of the invention, chorismate mutase polypeptide, or modifications thereof are utilized and adapted from source organimsms including, but not limited to: *Kluyveromyces lactis, Candida glabrata, Arabidopsis thaliana, Yarrowia lipolytica, Candida albicans, Aspergillus fumigatus, Aspergillus oryzae, Aspergillus nidulans, Ustilago maydis, Neurospora crassa, Schizosaccharomyces pombe, Gibberella zeae,* and *Pichia pastoris.*

[00164] Particularly for embodiments of the present invention directed toward production of CoQ10, it will often be desirable to utilize one or more genes from a natural CoQ10-producing organism. In general, where multiple heterologous polypeptides are to be expressed, it may be desirable to utilize the same source organism for all, or to utilize closely related source organisms.

[00165] Bacterial ubiquinogenic genes have already been demonstrated to be transferable to other organisms, and are therefore useful in accordance with the present invention (see, for example, Okada et al., *FEMS Lett.* 431:241-244 (1998)). In some embodiments of this invention, it may be desirable to fused sequences encoding specific targeting signals to bacterial ubiquinogenic genes. For example, in certain embodiments mitochondrial signal sequences are useful in conjunction with, e.g., bacterial ubiquinogenic polypeptides for effective targeting of polypeptides for proper functioning. Mitochondrial signal sequences are known in the art, and include, but are not limited to example, mitochondrial signal sequences provided in Table 22. In other embodiments, it may be desirable to utilize genes from other source organisms such as animals, plants, alga, or microalgae, fungi, yeast, insect, protozoa, and mammals.

[00166] The present invention contemplates not only introduction of heterologous ubiquinogenic polypeptides, but also adjustment of expression or activity levels of heterologous or endogenous ubiquinogenic polypeptides, including, for example, alteration of constitutive or inducible expression patterns so as to increase activity of ubiquinogenic polypeptides. For example, genetic modifications comprising alteration and/or addition of regulatory sequences (e.g.,

promoter elements, terminator elements) may be utilized to confer particular regulation of expression patterns. Such genetic modifications may be utilized in conjunction with endogenous genes (e.g., for regulation of endogenous ubiquinogenic polypeptide(s)); alternatively, such genetic modifications may be included so as to confer regulation of expression of heterologous polypeptides (e.g., ubiquinogenic polypeptide(s)).

[00167] To give but a few specific examples of strains engineered to produce CoQ10 (and optionally to be oleaginic) according to the present invention, in some embodiments, *Yarrowia lipolytica* cells are engineered to express a decaprenyl diphosphate synthase polypeptide(s) from a source organism. In some embodiments, the source organism is selected from the group consisting of *Silibacter pomeroyi* and *Loktanella vestfoldensis*. As is discussed herein, where the source organism is other than *Y. lipolytica*, nucleic acid sequences encoding the polypeptide(s) can be established with *Y. lipolytica* codon preferences and/or targeting sequences (e.g., mitochondrial targeting sequences). In some embodiments, one or more endogenous polyprenyl synthase genes (e.g., nonaprenyl diphosphate synthase) is/are disrupted or inactivated, and a decaprenyl diphosphate synthase gene from a different source organism is introduced. In some embodiments, the different source organism is selected from the group consisting of *Silibacter pomeroyi* and *Loktanella vestfoldensis*.

[00168] Alternatively or additionally, in some embodiments of the invention, host cells are engineered to produce CoQ10 by introducing or increasing expression or activity of one or more ubiquinone biosynthesis polypeptides, and in particular of one or more polypeptides involved in converting *para*-hydroxybenzoic acid to CoQ10 (e.g., via a ubiquinol pathway). To give but one specific example, *Yarrowia lipolytica* cells are engineered to express a 4-hydroxybenzoate polyprenyltransferase polypeptide from source organism, for example selected from the group consisting of *Silibacter pomeroyi* and *Bos taurus*. Sequences encoding the polypeptide(s) can optionally be established with *Y. lipolytica* codon preferences and/or targeting sequences (e.g., mitochondrial targeting sequences).

[00169] In some embodiments, CoQ10 production in cells, e.g., in *Yarrowia lipolytica* cells is enhanced by engineering the cells to increase production of *para*-hydroxybenzoic acid (PHB), for example by increasing expression or activity of one or more PHB polypeptides. In some embodiments, *Y. lipolytica* cells are engineered to express one or more of 3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP) and chorismate lyase polypeptides from a source organism. Where the source organism is other than *Y. lipolytica*, nucleic acid sequences encoding the polypeptide(s) can be established with *Y. lipolytica* codon preferences and/or targeting sequences (e.g., mitochondrial targeting sequences). In some embodiments, one or both of the DAHP and chorismate lyase polypeptides are from heterologous source organisms, which may be the same or different. In some embodiments, at least one source organism is *Erwinia carotovora*.

[00170] In some embodiments, host cells (e.g., *Yarrowia lipolytica*) engineered to increase production of *para*-hydroxybenzoic acid are further engineered to increase expression and/or activity of one or more ubiquinone biosynthesis polypeptides involved in converting *para*-hydroxybenzoic acid to a ubiquinone (e.g., via a ubiquinol pathway), and/or of one or more decaprenyl diphosphate synthase. To give but a couple of particular examples, such strains may be engineered to express a 4-hydroxybenzoate polyprenyltransferase polypeptide from source organism, for example selected from the group consisting of *Silibacter pomeroyi* and *Bos taurus* and/or to express a decaprenyl diphosphate synthase polypeptide(s) from a source organism, for example selected from the group consisting of *Silibacter pomeroyi* and *Loktanella vestfoldensis*.

[00171] Alternatively or additionally, in some specific embodiments, CoQ10 production is enhanced by engineering cells to reduce carbon flow into competing metabolic pathways such as, for example, the sterol pathway. To give but one specific example, in some embodiments of the invention, *Yarrowia lipolytica* cells are engineered to inactivate (e.g., partially) an endogenous gene (e.g., *ERG9)* encoding a squalene synthase polypeptide.

[00172] Yet further, in some particular embodiments, CoQ10 production is enhanced by engineering cells by expression of a truncated HMG CoA reductase polypeptide (e.g., from a source organism such as *Y. lipolytica*).

[00173] In some embodiments of the present invention, host cells are engineered to produce one or more ubiquinones other than CoQ10 in addition or as an alternative to CoQ10. Specifically, in some embodiments of the invention, host cells are engineered to produce one or more C_{5-9} quinones.

[00174] That is, the present invention provides engineered host cells, e.g., fungal cells, that produce C_{5-9} quinones as a result of the engineering. The present invention therefore provides engineered host cells containing a C_{5-9} quinones production modification. Such a modification may comprise, for instance, introduction or activation of one or more C_{5-9} quinones biosynthetic polypeptides within a host cell. Exemplary such polypeptides include, for example, pentaprenyl, hexaprenyl, heptaprenyl, octaprenyl, and/or solanesyl(nonaprenyl) biosynthesis polypeptides. Specific examples of each of these can be found, for example, in Tables 61-65.

[00175] To give but a few specific examples, in some embodiments of the present invention, *Yarrowia lipolytica* cells are engineered to express one or more polyprenyl diphosphate synthase genes (e.g., nonaprenyl diphosphate synthase, octaprenyl diphosphate synthase, heptaprenyl diphosphate synthase, hexaprenyl diphosphate synthase, pentaprenyl disphosphate synthase, etc.). In some embodiments, one or more endogenous polyprenyl synthase genes (e.g., nonaprenyl diphosphate synthase) is/are disrupted or inactivated, and a polyprenyl synthase gene from a different source organism is introduced. In some embodiments, the different source

organism is selected from the group consisting of *Silibacter pomeroyi* and *Loktanella vestfoldensis.*

Vitamin K

[00176] Vitamin K is a generic term that refers to derivatives of 2-methyl-1,4-naphthoquinone that have coagulation activity. The two natural forms of vitamin K differ in the identity of their side chains at position 3. Vitamin K_1, also known as phylloquinone (based on its presence in plants), has a phytyl side chain in position 3; vitamin K_2, also known as menaquinone, has an isoprenyl side chain at position 3. Different forms of menaquinone, having side chains with different numbers of isoprene units (typically 4-13) are found in different types of cells.

[00177] Vitamin K has been found to be an important vitamin involved in the blood coagulation system, and is utilized as a hemostatic agent. Recently it has been suggested that vitamin K is involved in osteo-metabolism, and vitamin K is expected to be applied to the treatment of osteoporosis. Both phylloquinone and menaquinone have been approved as pharmaceuticals.

[00178] The daily requirement for vitamin K is about 1 ug/kg; an average diet typically contains about 75-150 ug/day. Vitamin K deficiency results in hypoprothrombinemia and defective coagulation. Primary vitamin K deficiency is uncommon in adults because of its general availability in the food chain, and potentially also because it can be produced by microbes inhabiting the human gastrointestinal tract. Vitamin K deficiency is observed in newborns, as breast milk contains very little and the newborn gut is sterile (i.e., not inhabited by vitamin K-producing organisms) for the first several days of life.

[00179] Vitamin K is considered an essential nutrient since mammals do not produce it and it is a dietary requirement. As depicted for example in Figure 9, vitamin K is produced through precursor molecules chorismate and isoprenoids, similar to ubiquinone production, though biosynthesis proceeds through production of isochorismate, and prenyl addition does not occur until the final or next to last step in synthesis. Details of production of vitamin K, and the relevant enzymes involved are known in the art and can be adapted for use in combination with the provided methods and compositions. See, e.g., Meganathan, *Vitamins and Hormones* 61: 173-219, 2001.

[00180] The present invention provides engineered host cells, e.g., fungal cells, that produce vitamin K as a result of the engineering. That is, the present invention provides engineered host cells containing a Vitamin K production modification. Such a modification may comprise, for instance, introduction or activation of one or more Vitamin K biosynthetic polypeptides within a host cell. Exemplary such polypeptides include, for example, MenF, MenD,

MenC, MenE, MenB, MenA, UbiE, and/or MenG polypeptides. Specific examples of each of these can be found, for example, in Tables 46-53.

Vitamin E

[00181] Vitamin E is a generic term for a family of structurally related compounds that have a 6-chromanol ring, an isoprenoid side chain, and the biologic activity of α-tocopherol. The term encompasses the eight known naturally occurring vitamin E compounds, the four tocopherols (α, β, γ, δ) and four tocotrienols (α, β, γ, δ), which all contain a hydrophilic chromanol ring and a hydrophobic side chain. .The α, β, γ, and δ forms differ from one another in the number of methyl groups on the chromanol ring. Several synthetic vitamin E compounds have also been prepared, and still others are possible (see, for example, Bramley et al., *J. Sci Food Agric* 80:913, 2000). α-tocopherol is a potent antioxidant, and is generally considered to be the most active vitamin E compound in humans.

[00182] Vitamin E is commonly included in nutritional supplements and also in skin creams and lotions (based on a reported role in wound healing). Vitamin E deficiency is manifested differently in different species and in different individual cases, but can include reproductive disorders; abnormalities of muscle, liver, bone marrow, and/or brain function; red blood cell hemolysis; defective embryogenesis; exudative diathesis, a disorder of capillary permeability; and/or skeletal muscular dystrophy (with or without cardiomyopathy). Vitamin E is used to treat vitamin E deficiency, and is also suspected to be useful in the treatment of cancer (thanks to its antioxidant properties), cataracts and macular degeneration (particularly age-related), heart disease, neurological disorders (e.g., Alzheimer's Disease, Parkinson's Disease, etc.), immune disorders, inflammatory diseases, among other things.

[00183] The U.S. Dietary Reference Intake (DRI) Recommended Daily Amount (RDA) for a 25-year old male for Vitamin E is 15 mg/day. This is approximately 15 IU/day. Specifically, The natural form of alpha-tocopherol: RRR-alpha-tocopherol maintain 1.5 IU/mg.

[00184] Vitamin E compounds are synthesized by higher plants and cyanobacteria by two pathways: the isoprenoid pathway and the homogentisic acid formation pathway. The overall synthsis is depicted in Figure 10, Panels A-C. As can be seen, the first step is formation of the homogentisic head group (HGA), which is produced from *p*-hydroxyphenylpyruvic acid (HPP) by the enzyme *p*-hydroxyphenylpyruvic acid dioxygenase (HPPDase). This is a complex reaction involving the addition of two oxygen atoms as well as the decarboxylation and rearrangement of the HPP side chain.

[00185] In the next step, HGS is prenylated and decarboxylated to form 2-methyl-6-phytylplastoquinol. This step also represents the commitment step for production of tocopherols and/or tocotrienols, as 2-methyl-6-phytylplastoquinol represents the common intermediate in the

synthesis of all tocopherols. The present invention provides host cells that have been engineered to accumulate 2-methyl-6-phytlplastoquinol. In some embodiments, the host cells are (or have been engineered to be) oleaginous or lipid-accumulating. In some embodiments, produced 2-methyl-6-phytylplastoquinol accumulates in lipid bodies within the engineered host cells.

[00186] In the final steps of tocopherol synthesis, methylation and ring cyclization reactions convert the 2-methyl-6-phytylplastoquinol into various tocopherols.

[00187] It is expected in accordance with the present invention that availability of tocopherol precursors and/or intermediates may well affect the rate and/or extent of tocopherol (or other vitamin E compound) production and/or accumulation by and/or within cells. The present invention therefore encompasses engineering host cells to adjust the rate or amount of one or more tocopherol precursors and/or intermediates.

[00188] The present invention provides engineered host cells, e.g., fungal cells, that produce vitamin E as a result of the engineering. The present invention specifically provides engineered host cells, e.g., fungal cells, that produce larger amounts of vitamin E that an otherwise identical non-engineered host cell. That is, the present invention provides engineered host cells containing a Vitamin E production modification. Such a modification may comprise, for instance, introduction or activation of one or more Vitamin E biosynthetic polypeptides within a host cell. Exemplary such polypeptides include, for example, tyrA, pds1(hppd), VTE1, HPT1(VTE2), VTE3, VTE4, and/or GGH polypeptides. Specific examples of each of these can be found, for example, in Tables 54-60.

Production and Isolation of Quinone Derived Compounds

[00189] Accumulation of lipid bodies in oleaginous organisms is generally induced by growing the relevant organism under conditions of carbon excess and nitrogen or other nutrient (e.g., phosphate and/or magnesium) limitation. Specific conditions for inducing such accumulation have previously been established for a number of different oleaginous organisms (see, for example, Wolf (ed.) *Nonconventional yeasts in biotechnology* Vol. 1, Springer-Verlag, Berlin, Germany, pp. 313-338; *Lipids* 18(9):623, 1983; *Indian J. Exp. Biol.* 35(3):313, 1997; *J. Ind. Microbiol. Biotechnol.* 30(1):75, 2003; *Bioresour Technol.* 95(3):287, 2004, each of which is incorporated herein by reference in its entirety).

[00190] In general, it will be desirable to cultivate inventive modified host cells under conditions that allow accumulation of at least about 20% of their dry cell weight as lipid. In other embodiments, the inventive modified host cells are grown under conditions that permit accumulation of at least about 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, or even 80% of their dry cell weight as lipid. In certain embodiments, the host cells utilized are cells which are naturally oleaginous and

induced to produce lipid to the desired levels. In other embodiments, the host cells are cells which naturally produce lipid, but have been engineered to increase production of lipid such that desired levels of lipid production and accumulation are achieved.

[00191] In certain embodiments, the host cells of the invention are not naturally oleaginous, but have been engineered to produce lipid such that desired levels of lipid production are obtained. Those of ordinary skill in the art will appreciate that, in general, growth conditions that are effective for inducing lipid accumulation in a source organism may also be useful for inducing lipid accumulation in a host cell into which a source organism's oleaginic polypeptides have been introduced. Of course, modifications may be required in light of characteristics of the host cell, which modifications are within the skill of those of ordinary skill in the art.

[00192] It will also be appreciated by those of ordinary skill in the art that it will often be desirable to ensure that production of a desired quinone derived compound by an inventive modified host cell occurs at an appropriate time in relation to the induction of oleaginy such that the compound(s) accumulate(s) in the lipid bodies. In some embodiments, it will be desirable to induce production of a particular quinone derived compound (e.g., a ubiquinone, α-tocopherol, phylloquinone and/or menaquinone) in a host cell which does not naturally the particular compound, such that detectable levels of the compound are produced. In certain embodiments, host cells that do not naturally produce a particular quinone derived compound are capable of producing one or more other quinone derived compounds (e.g., cells that do not produce CoQ10 may produce one or more of CoQ5, CoQ6, CoQ7, CoQ8, CoQ9, etc). In additional embodiments, it will be desirable to increase production levels of a particular quinone derived compound in a host cell which does naturally produce low levels of that compound, such that increased detectable levels of the compound are produced. In certain aspects, the host cells which do naturally produce a particular compound (e.g., CoQ10) also produce additional quinone derived compound(s) (e.g., CoQ6, CoQ8); in other aspects, the cells which naturally produce the particular compound do not produce additional quinone derived compound(s).

[00193] In certain embodiments of the invention, it will be desirable to accumulate one or more quinone derived compounds (i. e., considering the total amount of all produced quinone derived compounds together or considering a particular quinone derived compound) to levels that are greater than at least about 1% of the dry weight of the cells. In some embodiments, the total quinone derived compound accumulation will be to a level at least about 1.5%, at least about 2%, at least about 2.5 %, at least about 3%, at least about 3.5 %, at least about 4%, at least about 4.5 %, at least about 5%, at least about 5.5 %,at least about 6%, at least about 6.5 %,at least about 7%, at least about 7.5 %,at least about 8%, at least about 8.5 %,at least about 9%, at least about 9.5 %,at least about 10%, at least about 10.5 %,at least about 11%, at least about 11.5 %,at least about 12%, at least about 12.5 %,at least about 13%, at least about 13.5 %, at least about 14%, at least about

14.5 %, at least about 15%, at least about 15.5 %, at least about 16%, at least about 16.5 %, at least about 17%, at least about 17.5 %, at least about 18%, at least about 18.5 %, at least about 19%, at least about 19.5 %, at least about 20% or more of the total dry weight of the cells.

[00194] In some embodiments of the invention, a particular quinone derived compound may not accumulate to a level as high as 1% of the total dry weight of the cells; appropriately engineered cells according to the present invention, and any lipid bodies and/or quinone derived compound(s) they produce, remain within the scope of the present invention. Thus, in some embodiments, the cells accumulate a given quinone derived compound to a level below about 1% of the dry weight of the cells. In some embodiments, the quinone derived compound accumulates to a level below about 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, 0.1%, 0.05%, or lower, of the dry cell weight of the cells.

[00195] In some embodiments of the invention, one or more quinone derived compound(s) accumulate both within lipid bodies and elsewhere in the cells. In some embodiments, quinone derived compound (s) accumulate primarily within lipid bodies. In some embodiments, quinone derived compound (s) accumulate substantially exclusively within lipid bodies. In some embodiments, at least about 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more of a desired produced quinone derived compound (s) accumulates in lipid bodies.

[00196] In some embodiments of the invention, modified host cells are engineered to produce one or more quinone derived compound(s) characterized by negligible solubility in water (whether hot or cold) and detectable solubility in one or more oils. In some embodiments, such compounds have a solubility in oil below about 0.2%. In some embodiments, such compounds have a solubility in oil within the range of about <0.001% - 0.2%.

[00197] The present invention therefore provides engineered host cells (and methods of making and using them) that contain lipid bodies and that further contain one or more quinone derived compounds accumulated in the lipid bodies, where the compounds are characterized by a negligible solubility in water and a solubility in oil within the range of about <0.001% - 0.2%; 0.004%-0.15%; 0.005-0.1%; or 0.005-0.5%. For example, in some embodiments, such compounds have a solubility in oil below about 0.15%, 0.14%, 0.13%, 0.12%, 0.11%, 0.10%. 0.09, 0.08%, 0.07%, 0.06%, 0.05%, 0.04%, 0.03%, 0.02%, 0.01%, 0.05%, or less. In some embodiments, the compounds show such solubility in an oil selected from the group consisting of sesame; soybean; apricot kernel; palm; peanut; safflower; coconut; olive; cocoa butter; palm kernel; shea butter; sunflower; almond; avocado; borage; carnauba; hazel nut; castor; cotton seed; evening primrose; orange roughy; rapeseed; rice bran; walnut; wheat germ; peach kernel; babassu; mango seed; black current seed; jojoba; macadamia nut; sea buckthorn; sasquana; tsubaki; mallow; meadowfoam

seed; coffee; emu; mink; grape seed; thistle; tea tree; pumpkin seed; kukui nut; and mixtures thereof.

[00198] Also, it should be noted that, the absolute and/or relative amounts of quinone derived compounds produced in accordance with the present invention can sometimes be altered by adjustment of growth conditions, for example to modulate the isoprenoid biosynthesis pathway and/or one or more downstream pathways. For example, controlling the concentration of dissolved oxygen in a culture during cultivation may regulate relative production levels of CoQ10.

[00199] Inventive modified cells, that have been engineered to produce one or more quinone derived compounds and/or to accumulate lipid (including to be oleaginous), can be cultured under conditions that achieve ubiquinone (e.g. CoQ10 and/or C_5-C_9 quinone compounds) production and/or oleaginy.

[00200] In some embodiments, it will be desirable to control growth conditions in order to maximize production of a particular quinone derived compound or quinone derived compounds and/or to optimize accumulation of the particular quinone derived compound(s) in lipid bodies. In some embodiments it will be desirable to control growth conditions to adjust the relative amounts of different quinone derived compound products produced.

[00201] In some embodiments, it will be desirable to limit accumulation of a particular intermediate, for example ensuring that substantially all of a particular intermediate compound is converted so that accumulation is limited. For example, particularly in situations where a downstream enzyme may be less efficient than an upstream enzyme and it is desirable to limit accumulation of the product of the upstream enzyme (e.g., to avoid its being metabolized via a competitive pathway and/or converted into an undesirable product), it may be desirable to grow cells under conditions that control (e.g., slow) activity of the upstream enzyme so that the downstream enzyme can keep pace.

[00202] Those of ordinary skill in the art will appreciate that any of a variety of growth parameters, including for example amount of a particular nutrient, pH, temperature, pressure, oxygen concentration, timing of feeds, content of feeds, etc can be adjusted as is known in the art to control growth conditions as desired.

[00203] To give but a few examples, in some embodiments, growth and/or metabolism is/are limited by limiting the amount of biomass accumulation. For example, growth and/or metabolism can be limited by growing cells under conditions that are limiting for a selected nutrient. The selected limiting nutrient can then be added in a regulated fashion, as desired. In some embodiments, the limiting nutrient is carbon, nitrogen (e.g., via limiting ammonium or protein), phosphate, magnesium, or combinations thereof. In some embodiments, the limiting nutrient is carbon.

[00204] In some embodiments, use of a limiting nutrient can be utilized to control metabolism of a particular intermediate and/or to adjust relative production of particular quinone derived compounds. In some embodiments, this result can be achieved by controlling metabolism of a particular intermediate as discussed above; in some embodiments, it can be achieved, for example, by limiting progress through the quinone biosynthesis pathway so that a desired quinone derived compound product is not converted to a downstream compound. For example, nutrient limitation (e.g. phosphate limitation) may slow the overall rate of flux through the quinone derived compound biosynthesis pathway and may be utilized to change the ratio of one quinone derived compound versus another.

[00205] In some embodiments, cells are grown in the presence of excess carbon source and limiting nitrogen, phosphate, and/or magnesium to induce oleaginy. In some embodiments cells are grown in the presence of excess carbon source and limiting nitrogen. In some embodiments, the carbon:nitrogen ratio is within the range of about 200:1, 150:1, 125:1, 100:1, 95:1, 90:1, 85:1, 80:1, 75:1, 70:1, 65:1, 60:1, 55:1, 50:1, 45:1, 40:1, 35:1, 30:1, 25:1, 20:1, 15:1, 10:1, or less. Those of ordinary skill in the art are aware of a wide variety of carbon sources, including, for example, glycerol, glucose, galactose, dextrose, any of a variety of oils (e.g., olive, canola, corn, sunflower, soybean, cottonseed, rapeseed, etc., and combinations thereof) that may be utilized in accordance with the present invention. Combinations of such may also be utilized. For example, common carbon source compositions contain oil:glucose in a ratios within the range of about 5:95 to 50:50 (e.g. about 5:95, about 10:90, about 15:85, about 20:80, about 25:75, about 30:70, about 35:65, about 40:60, about 45:55, about 50:50).

[00206] Those of ordinary skill in the art are also aware of a variety of different nitrogen sources (e.g., ammonium sulfate, proline, sodium glutamate, soy acid hydrolysate, yeast extract-peptone, yeast nitrogen base, corn steep liquor, etc, and combinations thereof) that can be utilized in accordance with the present invention.

[00207] In some embodiments, cultures are grown at a selected oxygen concentration (e.g., within a selected range of oxygen concentrations). In some embodiments, oxygen concentration may be varied during culture. In some embodiments, oxygen concentration may be controlled during some periods of culture and not controlled, or controlled at a different point, during others. In some embodiments, oxygen concentration is not controlled. In some embodiments, cultures are grown at an oxygen concentration within the rage of about 5-30%, 5-20%, 10-25%, 10-30%, 15-25%, 15-30%, including at about 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, or more. In some embodiments, oxygen concentration is maintained above about 20%, at least for some period of the culture.

[00208] In some embodiments, cells are grown via fed-batch fermentation. In some embodiments, feed is continued until feed exhaustion and/or the feed is controlled to initiate or increase once a certain level of dissolved oxygen is detected in the culture medium (e.g., about 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, or more dissolved oxygen). The feed rate can be modulated to maintain the dissolved oxygen at a specific level (e.g., about 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, or more dissolved oxygen).

[00209] In some embodiments, inventive modified cells are grown in a two-phase feeding protocol in which the first phase is designed to maintain conditions of excess carbon and limiting oxygen, and the second phase results in conditions of excess oxygen and limiting carbon.

[00210] In some embodiments, inventive modified cells are cultivated at constant temperature (e.g., between about 20-40, or 20-30 °C, including for example at about 20, 20.5, 21, 21.5, 22, 22.5, 23, 23.5, 24, 24.5, 25, 25.5, 26, 26.5, 27, 27.5, 28, 28.5, 29, 29.5, 30 °C or above) and/or pH (e.g., within a range of about 4-7.5, or 4-6.5, 3.5-7, 3.5-4, 4-4.5, 4.5-5, 5-5.5, 5.5-6, 6-6.5, 6.5-7, etc., including at about 4.0, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5.0, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6.0, 6.1, 6.2, 6.3, 6.4, or 6.5, 6.6, 6.7, 6.8, 6.9, 7.0, 7.1, 7.2, 7.3, 7.4, 7.5 or above); in other embodiments, temperature and/or pH may be varied during the culture period, either gradually or in a stepwise fashion.

[00211] In some embodiments, the temperature at which inventive cells are cultivated is selected so that production of one or more particular carotenoid compound(s) is adjusted (e.g., so that production of one or more particular compound(s) is increased and/or production of one or more other compound(s) is decreased). In some embodiments, the temperature at which inventive cells are cultivated is selected so that the ratio of one quinone derived compound to another, is adjusted. To give but one example, in some embodiments, a temperature is selected to be sufficiently low that levels of one quinone derived compound are reduced and the level of at least one other quinone derived compound(s) is increased.

[00212] In some embodiments, cultures are grown at about pH 5.5 and or at a temperature between about 28-30 °C. In some embodiments, it may be desirable to grow inventive modified cells under low pH conditions, in order to minimize growth of other cells. In some embodiments, it will be desirable to grow inventive modified cells under relatively higher temperature conditions in order to slow growth rate and/or increase the ultimate dry cell weight output of quinone derived compounds (e.g. CoQ10, C_5-C_9 quinones, vitamin K compounds, vitamin E compounds).

[00213] One advantage provided by the present invention is that, in addition to allowing the production of high levels of one or more quinone derived compounds, certain embodiments of

the present invention allow produced compounds to be readily isolated because they accumulate in the lipid bodies within oleaginous organisms. Methods and systems for isolating lipid bodies have been established for a wide variety of oleaginous organisms (see, for example, United States Patents 5,164,308; 5,374,657; 5,422,247; 5,550,156; 5,583,019; 6,166,231; 6,541,049; 6,727,373; 6,750,048; and 6,812,001, each of which is incorporated herein by reference in its entirety). In brief, cells are typically recovered from culture, often by spray drying, filtering or centrifugation.

[00214] Of course, it is not essential that lipid bodies be specifically isolated in order to collect quinone derived compounds produced according to the present invention. Any of a variety of approaches can be utilized to isolate and/or purify quinone derived compounds. Many useful extraction and/or purification procedures for lipophilic agents generally, are known in the art (see, for example, EP670306, EP719866, US4439629, US4680314, US5310554, US5328845, US5356810, US5422247, US5591343, US6166231, US6750048, US6812001, US6818239, US7015014, US2003/0054070, US2005/0266132, each of which is incorporated herein by reference).

[00215] In many typical isolation procedures, cells are disrupted (e.g., mechanically, chemically [e.g., by exposure to a mild caustic agent such as a detergent or 0.1 N NaOH, for example at room temperature or at elevated temperature], etc.) to allow access of intracellular quinone derived compound(s) to an extraction solvent, and are then extracted one or more times. Cells may optionally be concentrated (e.g., to at least about 100 g/L or more, including to at least about 120 g/l, 150 g/l, 175 g/L, 200 g/L or more) and/or dried (e.g., with a spray dryer, Blaw Knox double drum dryer, single drum vacuum dryer, etc.), prior to exposure to extraction solvent (and/or prior to disruption or homogenization). Disruption can, of course, be performed prior to and/or during exposure to extraction solvent. After extraction, solvent is typically removed (e.g., by evaporation, for example by application of vacuum, change of temperature, etc.).

[00216] In some instances, cells are homogenized and then subjected to supercritical liquid extraction or solvent extraction. Typical liquids or solvents utilized in such extractions include, for example, organic or non-organic liquids or solvents. To give but a few specific examples, such liquids or solvents may include acetone, carbon dioxide (e.g., supercritical carbon dioxide, acetone, heptane, octane, ethanol), chloroform, ethanol, ethyl acetate, heptane, hexane, hexane:ethyl acetate, isopropanol, methanol, methylene chloride, isopropanol, ethyl acetateoctane, tetrahydrofuran (THF), different types of oils (e.g., soybeen, rapeseed, etc.), and combinations thereof. Particular solvents may be selected, for example, based on their ability to solubilize particular quinone derived compounds or sets of quinone derived compounds (e.g., all quinone derived compounds), and/or based on regulatory or other considerations (e.g., toxicity, cost, ease of handling, ease of removal, ease of disposal, etc.). For example, more polar quinone derived compounds may be extracted more efficiently into extraction solvents with increased polarity. In

some embodiments, hexane is used as a solvent. In other embodiments, hexane:ethyl acetate is utilized.

[00217] In some embodiments, combinations of solvents may be utilized. In some embodiments, combinations of a relatively polar solvent (e.g., alcohols, acetone, chloroform, methylene chloride, ethyl acetate, etc.) and a relatively non-polar solvent (e.g., hexane, oils, etc.) are utilized for extraction. Those of ordinary skill in the art will readily appreciate that different ratios of polar to non-polar solvent may be employed as appropriate in a particular situation. Just to give a few examples, common ratios include 1:1, 2:1, 3:1, 3:2, 95:5, 90:10, 85:15, 80:20, 75:25, 70:30, 65:45, 60:40, 55:45, and 50:50. It will be appreciated that solvents or solvent mixtures of different polarities may be more effective at extracting particular quinone derived compounds (e.g., based on their polarities and/or as a function of other attributes of the host cell material from which they are being extracted). Those of ordinary skill in the art are well able to adjust the overall polarity of the extracting solvent, for instance by adjusting the relative amounts of polar and non-polar solvents in a solvent blend, in order to achieve more efficient extraction.

[00218] Extraction may be performed under any of a variety of environmental conditions, including any of a variety of temperatures. For example, extraction may be performed on ice, at room temperature, or at any of a variety of other temperatures. For example, a solvent may be maintained at a selected temperature (e.g., about 4, 25, 28, 30, 37, 68, 70, 75, 80, 85, 90, 95, or 100 °C) in order to improve or adjust extraction of a particular desired quinone derived compound.

[00219] Extraction typically yields a crude oil suspension. In some embodiments, the crude oil suspension contains some intact host cells but is at least about 95% free of intact host cells. In some embodiments, the crude oil suspension is at least about 96%, 97%, 98%, or 99% or more free of intact host cells. In some embodiments, the suspension is substantially free of water-soluble cell components (e.g., nucleic acids, cell wall or storage carbohydrates, etc.). In some embodiments, the suspension contains less than about 5%, 4%, 3%, 2%, or 1% or less water-soluble cell components.

[00220] Extraction conditions that yield a crude oil suspension will enrich for lipophilic components that accumulate in the lipid bodies within oleaginous organisms. In general, the major components of the lipid bodies consist of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and some proteins, which often function in the synthesis or regulation of the levels of other lipid body components. C16 and C18 (e.g. C16:0, C16:1, C18:0, C18:1, and C18:2) are generally the major fatty acids present in lipid bodies, mainly as components of triacylglycerol and steryl esters.

[00221] In some embodiments of the invention, the crude oil suspension contains at least about 2.5% by weight quinone derived compound(s); in some embodiments, the crude oil suspension contains at least about 5% by weight quinone derived compound(s), at least about 10%

by weight quinone derived compound(s), at least about 20% by weight quinone derived compound(s), at least about 30% by weight quinone derived compound(s), at least about 40% by weight quinone derived compound(s), or at least about 50% by weight quinone derived compound(s).

[00222] The crude oil suspension may optionally be refined as known in the art. Refined oils may be used directly as feed or food additives. Alternatively or additionally, quinone derived compounds (e.g. CoQ10) can be isolated from the oil using conventional techniques.

[00223] Given the sensitivity of quinones generally to oxidation, many embodiments of the invention employ oxidative stabilizers (e.g., tocopherols, vitamin C; ethoxyquin; vitamin E, BHT, BHA, TBHQ, etc., or combinations thereof) during and/or after quinone derived compound isolation. When the desired product is the reduced ubiquinol form, then it may be advantageous to further add conventional reducing agents (e.g. sodium dithionite, ascorbic acid). Alternatively or additionally, microencapsulation, for example with proteins, may be employed to add a physical barrier to oxidation and/or to improve handling (see, for example, U.S. Patent Application 2004/0191365).

[00224] Extracted quinone derived compounds may be further isolated and/or purified, for example, by crystallization, washing, recrystallization, and/or other purification strategies. In some embodiments, carotenoid crystals are collected by filtration and/or centrifugation. Isolated or purified quinone derived compounds may be dried and/or formulated for storage, transport, sale, and/or ultimate use. To give but a few specific examples, quinone derived compounds may be prepared as a cold-water dispersible powder, as a suspension of crystals in oil (e.g., vegetable oil, e.g., about 5%-30% w/w), etc.

Uses

[00225] Quinone derived compounds (e.g., ubiquinones, vitamin K compounds, and/or vitamin E compounds) produced according to the present invention can be utilized in any of a variety of applications, for example exploiting biological or nutritional (e.g., metabolic, anti-oxidant, anti-proliferative, etc.) properties.

[00226] For example, according to the present invention, one or more quinone derived compounds may be used in pharmaceutical and/or nutraceutical applications for treatment and/or prevention of disorders such as cardiovascular disorders (including, congestive heart failure, myocardial infarction and cardiac surgery patients, angina, hypertension, etc), metabolic disorders, diabetes, pain, aging, neurodegenerative disorders (e.g., Parkinson's and Huntington's disorders), inflammatory disorders and cancers. Additionally, supplements of certain quinone derived compounds (including, e.g., CoQ10) have been proposed to improve performance (e.g., athletic performance). See, for example, Choi, et al., *Appl. Microbiol, Biotechnol*, 68: 9-15, 2005;

Kawamukai, *J. Biosci. Bioeng* , 94:511-517, 2002; Ernster and Dallner, *Biochim. Biophys. Acta.*, 1271: 195-204, 1995; U. S. Patent No. 6806076; U. S. Patent No. 6867024; U.S. Patent No. 6686485; U.S. Patent No. 6417233; U.S. Patent Publication No. 2006/0010519; U.S. Patent Publication No. 2004/0034107; U.S. Patent Publication No. 2003/0236239; U.S. Patent Publication No. 2003/0167556; U.S. Patent Publication No. 2002/0058712), nutritional supplement (see for example, U.S. Patent No. 6686485; U.S. Patent No. 6080788, U.S. Patent Publication No. 2004/0082536) food supplements (see, for example, U.S. Patent Publication Nos. 2005/011226 and 2004/0115309, cosmetics (as anti-oxidants and/or as cosmetics, including fragrances; see for example U.S. Patent Publication No. 2005/0084505; U.S. Patent Publication No. 2003/0167556), etc. The contents of each of the foregoing journal and patent publications are hereby incorporated by reference. Quinone derived compound(s) produced herein can also be co-administered with an HMG CoA reductase inhibitor (e.g. a statin such as atorvastatin, simvastatin, rosuvastatin, etc.)

[00227] It will be appreciated that, in some embodiments of the invention, one or more quinone derived compound(s) produced by manipulated host cells as described herein are incorporated into a final product (e.g., food or feed supplement, pharmaceutical, cosmetic, etc.) in the context of the host cell. For example, host cells may be lyophilized, freeze dried, frozen or otherwise inactivated, and then whole cells may be incorporated into or used as the final product. The host cells may also be processed prior to incorporation in the product to, e.g., increase bioavailability (e.g., via lysis). Alternatively or additionally, a final product may incorporate only a portion of a host cell (e. g., fractionated by size, solubility), separated from the whole. For example, in some embodiments of the invention, lipid bodies are isolated from host cells and are incorporated into or used as the final product.

[00228] For instance, inventive compound-containing lipid bodies (e.g., from engineered cells, and particularly from engineered fungal cells) may be substituted for the plant oil bodies described in United States patent 6,599,513 (the entire contents of which are hereby incorporated by reference) and incorporated into emulsions or emulsion formulations, as described thereon. In other embodiments, a ubiquinone itself is isolated and reformulated into a final product.

[00229] Preparations of one or more quinone derived compounds, including formulations, dosing, supplements (e.g., dietary supplements), have been described and are known in the art. For example, see citations relating to pharmaceutical preparations, nutritional supplement, and food additives described above. Additionally, see, for example, U.S. Patent No. 6906106, U.S. Patent No. 6867024; U.S. Patent No. 6740338; U.S. Patent No. 6300377; U.S. Patent Publication No. 2003/0105168, U.S. Patent Publication No. 2004/0014817; U.S. Patent Publication No. 2005/0019268; U.S. Patent Publication No. 2004/0152612; U.S. Patent Publication No. 2003/0167556; U.S. Patent Publication No. 2005/0153406; U.S. Patent Publication No.

2005/0181109; U.S. Patent Publication No. 2006/0010519; International Patent Publication No. WO05069916A2, and International Patent Publication No. WO05092123A1, each of which is incorporated herein by reference.

[00230] The amount of any particular quinone derived compound incorporated into a given product may vary dramatically depending on the product, and the particular compound(s) involved. Amounts may range, for example, from less than 0.01% by weight of the product, to more than 1%, 10%, 20%, 30% or more; in some cases the compound may comprise 100% of the product. Thus, the amount of quinone derived compound incorporated into a given product may be, for example, 0.01%, 0.02%, 0.03%, 0.04%, 0.05%, 0.06%, 0.07%, 0.08%, 0.09%, 0.1%, 0.2%, 0.3%, 0.4%, 0.5%, 0.6%, 0.7%, 0.8%, 0.9%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100%.

[00231] In some embodiments of the invention, one or more produced quinone derived compound is incorporated into a component of food or feed (e. g., a food supplement, food additive). Types of food products into which quinone derived compound (s) can be incorporated according to the present invention are not particularly limited, and include beverages such as teas, juices, and liquors; confections such as jellies and biscuits; fat-containing foods and beverages such as dairy products; processed food products such as rice and soft rice (or porridge); infant formulas; or the like. In some embodiments of this aspect of the invention, it may be useful to incorporate the quinone derived compound within bodies of edible lipids as it may facilitate incorporation into certain fat-containing food products.

[00232] Examples of feedstuffs into which one or more quinone derived compounds produced in accordance with the present invention may be incorporated include, for instance, pet foods such as cat foods, dog foods and the like, feeds for aquarium fish or cultured fish, etc., feed for farm-raised animals (including livestock and further including fish raised in aquaculture). Food or feed material into which the quinone derived compound (s) produced in accordance with the present invention is incorporated is preferably palatable to the organism which is the intended recipient. This food or feed material may have any physical properties currently known for a food material (e. g., solid, liquid, soft).

[00233] In some embodiments of the invention, produced quinone derived compound is incorporated into a cosmetic product. Examples of such cosmetics include, for instance, skin cosmetics (e. g., lotions, emulsions, liquids, creams and the like), lipsticks, anti-sunburn cosmetics, makeup cosmetics, fragrances, products for daily use (e. g., toothpastes, mouthwashes, bad breath preventive agents, solid soaps, liquid soaps, shampoos, conditioners), etc.

[00234] In some embodiments, produced quinone derived compound is incorporated into a pharmaceutical. Examples of such pharmaceuticals include, for instance, various types of tablets,

capsules, drinkable agents, troches, gargles, etc. In some embodiments, the pharmaceutical is suitable for topical application. Dosage forms are not particularly limited, and include capsulae, oils, granula, granula subtilae, pulveres, tabellae, pilulae, trochisci, or the like. Oils and oil-filled capsules may provide additional advantages both because of their lack of ingredient decomposition during manufacturing, and because inventive compound-containing lipid droplets may be readily incorporated into oil-based formulations.

[00235] Pharmaceuticals according to the present invention may be prepared according to techniques established in the art including, for example, the common procedure as described in the United States Pharmacopoeia, for example.

[00236] In still other embodiments, produced quinone derived compound is incorporated into a nutritional supplement or nutraceutical. Examples of such nutraceuticals, include, for instance, various types of tablets, capsules, drinkable agents, troches, gargles, etc. In some embodiments, the nutraceutical is suitable for topical application. Dosage forms are, as in pharmaceutical products, not particularly limited and include any of the same types of dosages as pharmaceuticals.

[00237] Quinone derived compound(s) produced according to the present invention (whether isolated or in the context of lipid droplets or of cells, e.g., fungal cells) may be incorporated into products as described herein by combination with any of a variety of agents. For instance, such quinone derived compound (s) may be combined with one or more binders or fillers. In some embodiments, inventive products will include one or more chelating agents, pigments, salts, surfactants , moisturizers, viscosity modifiers, thickeners, emollients, fragrances, preservatives, etc., and combinations thereof.

[00238] Useful surfactants include, for example, anionic surfactants such as branched and unbranched alkyl and acyl hydrocarbon compounds, sodium dodecyl sulfate (SDS); sodium lauryl sulfate (SLS); sodium lauryl ether sulfate (SLES); sarconisate; fatty alcohol sulfates, including sodium, potassium, ammonium or triethanolamine salts of C_{10} to C_{18} saturated or unsaturated forms thereof; ethoxylated fatty alcohol sulfates, including alkyl ether sulfates; alkyl glyceryl ether sulfonate, alpha sulpho fatty acids and esters; fatty acid esters of isethionic acid, including Igepon A; acyl (fatty) N-methyltaurides, including Igepon T; dialkylsulfo succinate esters, including C_8, C_{10} and C_{12} forms thereof; Miranot BT also referred to as lauroamphocarboxyglycinate and sodium tridecath sulfate; N-acylated amino acids, such as sodium N-lauroyl sarconisate or gluconate; sodium coconut monoglyceride sulfonate; and fatty acid soaps, including sodium, potassium, DEA or TEA soaps.

[00239] Among the cationic surfactants that are useful are monoalkyl trimethyl quartenary salts; dialkyl dimethyl quartenary salts; ethoxylated or propoxylated alkyl quaternary amonium salts, also referred to in the art as ethoquats and propoquats; cetyl benzylmethylalkyl ammonium

chloride; quaternized imidazolines, which are generally prepared by reacting a fat or fatty acid with diethylenetriamine followed by quaternization, and non-fat derived cationic polymers such as the cellulosic polymer, Polymer JR (Union Carbide).

[00240] Further useful cationic surfactants include lauryl trimethyl ammonium chloride; cetyl pyridinium chloride; and alkyltrimethylammonium bromide. Cationic surfactants are particularly useful in the formulation of hair care products, such as shampoos, rinses and conditioners.

[00241] Useful nonionic surfactants include polyethoxylated compounds and polypropoxylated products. Examples of ethoxylated and propoxylated non-ionic surfactants include ethoxylated anhydrohexitol fatty esters, for example Tween 20; mono- and diethanolamides; Steareth-20, also known as Volpo20; polyethylene glycol fatty esters (PEGs), such as PEG-8-stearate, PEG-8 distearate; block co-polymers, which are essentially combinations of hydrophylic polyethoxy chains and lipophilic polypropoxy chains and generically known as Poloaxamers.

[00242] Still other useful non-ionic surfactants include fatty esters of polyglycols or polyhydric alcohols, such as mono and diglyceride esters; mono- and di-ethylene glycol esters; diethylene glycol esters; sorbitol esters also referred to as Spans; sucrose esters; glucose esters; sorbitan monooleate, also referred to as Span80; glyceryl monostearate; and sorbitan monolaurate, Span20 or Arlacel 20.

[00243] Yet other useful nonionic surfactants include polyethylene oxide condensates of alkyl phenols and polyhydroxy fatty acid amide surfactants which may be prepared as for example disclosed in U.S. Pat. No. 2,965,576.

[00244] Examples of amphoteric surfactants which can be used in accordance with the present invention include betaines, which can be prepared by reacting an alkyldimethyl tertiary amine, for example lauryl dimethylamine with chloroacetic acid. Betaines and betaine derivatives include higher alkyl betaine derivatives including coco dimethyl carboxymethyl betaine; sulfopropyl betaine; alkyl amido betaines; and cocoamido propyl betaine. Sulfosultaines which may be used include for example, cocoamidopropyl hydroxy sultaine. Still other amphoteric surfactants include imidazoline derivatives and include the products sold under the trade name "Miranol" described in U.S. Pat. No. 2,528,378 which is incorporated herein by reference in its entirety. Still other amphoterics include phosphates for example, cocamidopropyl PG-dimonium chloride phosphate and alkyldimethyl amine oxides.

[00245] Suitable moisturizers include, for example, polyhydroxy alcohols, including butylene glycol, hexylene glycol, propylene glycol, sorbitol and the like; lactic acid and lactate salts, such as sodium or ammonium salts; C_3 and C_6 diols and triols including hexylene glycol, 1,4 dihydroxyhexane, 1,2,6-hexane triol; aloe vera in any of its forms, for example aloe vera gel;

sugars and starches; sugar and starch derivatives, for example alkoxylated glucose; hyaluronic acid; lactamide monoethanolamine; acetamide monoethanolamine; glycolic acid; alpha and beta hydroxy acids (e.g. lactic, glycolic salicylic acid); glycerine; pantheol; urea; vaseline; natural oils; oils and waxes (see: the emollients section herein) and mixtures thereof.)

[00246] Viscosity modifiers that may be used in accordance with the present invention include, for example, cetyl alcohol; glycerol, polyethylene glycol (PEG); PEG-stearate; and/or Keltrol.

[00247] Appropriate thickeners for use in inventive products include, for example, gelling agents such as cellulose and derivatives; Carbopol and derivatives; carob; carregeenans and derivatives; xanthane gum; sclerane gum; long chain alkanolamides; bentone and derivatives; Kaolin USP; Veegum Ultra; Green Clay; Bentonite NFBC; etc.

[00248] Suitable emollients include, for example, natural oils, esters, silicone oils, polyunsaturated fatty acids (PUFAs), lanoline and its derivatives and petrochemicals.

[00249] Natural oils which may be used in accordance with the present invention may be obtained from sesame; soybean; apricot kernel; palm; peanut; safflower; coconut; olive; cocoa butter; palm kernel; shea butter; sunflower; almond; avocado; borage; carnauba; hazel nut; castor; cotton seed; evening primrose; orange roughy; rapeseed; rice bran; walnut; wheat germ; peach kernel; babassu; mango seed; black current seed; jojoba; macademia nut; sea buckthorn; sasquana; tsubaki; mallow; meadowfoam seed; coffee; emu; mink; grape seed; thistle; tea tree; pumpkin seed; kukui nut; and mixtures thereof.

[00250] Esters which may be used include, for example, C_8-C_{30} alklyl esters of C_8-C_{30} carboxylic acids; C_1–C_6 diol monoesters and diesters of C_8-C_{30} carboxylic acids; C_{10}–C_{20} alcohol monosorbitan esters, C_{10}–C_{20} alcohol sorbitan di- and tri-esters; C_{10}–C_{20} alcohol sucrose mono-, di-, and tri-esters and C_{10}–C_{20} fatty alcohol esters of C_2–C_6 2-hydroxy acids and mixtures thereof. Examples of these materials include isopropyl palmitate; isopropyl myristate; isopropyl isononate; C_{12} /C_{14} benzoate ester (also known as Finesolve); sorbitan palmitate, sorbitan oleate; sucrose palmitate; sucrose oleate; isostearyl lactate; sorbitan laurate; lauryl pyrrolidone carboxylic acid; panthenyl triacetate; and mixtures thereof.

[00251] Further useful emollients include silicone oils, including non-volatile and volatile silicones. Examples of silicone oils that may be used in the compositions of the present invention are dimethicone; cyclomethycone; dimethycone-copolyol; aminofunctional silicones; phenyl modified silicones; alkyl modified silicones; dimethyl and diethyl polysiloxane; mixed C_1 -C_{30} alkyl polysiloxane; and mixtures thereof. Additionally useful silicones are described in U.S. Pat. No. 5,011,681 to Ciotti et al., incorporated by reference herein.

[00252] A yet further useful group of emollients includes lanoline and lanoline derivatives, for example lanoline esters.

[00253] Petrochemicals which may be used as emollients in the compositions of the present invention include mineral oil; petrolatum; isohexdecane; permethyl 101; isododecanol; C_{11} -C_{12} Isoparrafin, also known as Isopar H.

[00254] Among the waxes which may be included in inventive products are animal waxes such as beeswax; plant waxes such as carnauba wax, candelilla wax, ouricurry wax, Japan wax or waxes from cork fibres or sugar cane. Mineral waxes, for example paraffin wax, lignite wax, microcrystalline waxes or ozokerites and synthetic waxes may also be included.

[00255] Exemplary fragrances for use in inventive products include, for instance, linear and cyclic alkenes (i.e. terpenes); primary, secondary and tertiary alcohols; ethers; esters; ketones; nitrites; and saturated and unsaturated aldehydes; etc.

[00256] Examples of synthetic fragrances that may be used in accordance with the present invention include without limitation acetanisole; acetophenone; acetyl cedrene; methyl nonyl acetaldehyde; musk anbrette; heliotropin; citronellol; sandella; methoxycitranellal; hydroxycitranellal; phenyl ethyl acetate; phenylethylisobutarate; gamma methyl ionone; geraniol; anethole; benzaldehyde; benzyl acetate; benzyl salicate; linalool; cinnamic alcohol; phenyl acetaldehyde; amyl cinnamic aldehyde; caphore; p-tertiairy butyl cyclohexyl acetate; citral; cinnamyl acetate; citral diethyl acetal; coumarin; ethylene brasslate; eugenol; l-menthol; vanillin; etc.

[00257] Examples of natural fragrances of use herein include without limitation lavandin; heliotropin; sandlewood oil; oak moss; pathouly; ambergris tincture; ambrette seed absolute; angelic root oil; bergamont oil; benzoin Siam resin; buchu leaf oil; cassia oil; cedarwood oil; cassia oil; castoreum; civet absolute; chamomile oil; geranium oil; lemon oil; lavender oil; Ylang Ylang oil; etc.

[00258] A list of generally used fragrance materials can be found in various reference sources, for example, "Perfume and Flavor Chemicals", Vols. I and II; Steffen Arctander Allured Pub. Co. (1994) and "Perfumes: Art, Science and Technology"; Muller, P. M. and Lamparsky, D., Blackie Academic and Professional (1994) both incorporated herein by reference.

[00259] Suitable preservatives include, among others, (e.g., sodium metabisulfite; Glydant Plus; Phenonip; methylparaben; Germall 115; Germaben II; phytic acid; sodium lauryl sulfate (SLS); sodium lauryl ether sulfate (SLES); Neolone; Kathon; Euxyl and combinations thereof), anti-oxidants (e.g., butylated hydroxytoluened (BHT); butylated hydroxyanisol (BHA); ascorbic acid (vitamin C); tocopherol; tocopherol acetate; phytic acid; citric acid; pro-vitamin A.

[00260] In some embodiments, inventive products will comprise an emulsion (e.g., containing inventive lipid bodies), and may include one or more emulsifying agents (e.g., Arlacel, such as Alacel 165; Glucamate; and combinations thereof) and/or emulsion stabilizing agents.

In some embodiments, inventive products will include one or more biologically active agents other than the ubiquinone(s). To give but a few examples, inventive cosmetic or pharmaceutical products may include one or more biologically active agents such as, for example, sunscreen actives, anti-wrinkle actives, anti-aging actives, whitening actives, bleaching actives, sunless tanning actives, anti-microbial actives, anti-acne actives, anti-psoriasis actices, anti-eczema actives, antioxidants, anesthetics, vitamins, protein actives, etc..

Engineering Production of Multiple Isoprenoid Compounds

[00261] In certain embodiments of the invention, it may be desirable to generate engineered organisms that accumulate one or more other compounds in addition to the quinone derived compound described herein, and further to accumulate such other compound(s), optionally together with the quinone derived compound(s), in lipid bodies. For example, certain inventive engineered organisms may accumulate quinone derived compound together with at least one other compound derived from an isoprenoid precursor. In some embodiments, the other compound derived from an isoprenoid precursor will be one or more quinone derived compound discussed herein (e.g., a ubiquinone, vitamin K, vitamin E). Alternatively or additionally, in some embodiments the other compound derived from an isoprenoid precursor will be one or more carotenoids. Production of carotenoids in oleaginous organisms is described in U. S. Provisional Application No. 60/663,621, filed March 18, 2005, and is also described in U.S. Patent Application No. 11/385,580, entitled Production of Carotenoids in Oleaginous Yeast and Fungi, filed March 20, 2006.

[00262] In some embodiments of the invention, host cells are engineered to produce at least two compounds selected from the group consisting of a ubiquinone (e.g. CoQ10, a C_{5-9} quinone), vitamin K, vitamin E, and carotenoids. In some such embodiments, host cells are engineered to produce a least one compound selected from the group consisting of a ubiquinone (e.g. CoQ10, a C_{5-9} quinone), vitamin K, vitamin E, and at least one other compound. Such host cells are particularly useful for producing mixtures or combination products that contain a ubiquinone and/or vitamin K. Such host cells are also useful for producing combination products including one or more carotenoids.

[00263] In some embodiments of the invention, host cells are engineered to produce at least one quinone derived compound and at least one carotenoid. Carotenoids, which have an isoprene backbone consisting of 40 carbon atoms, have antioxidant effects as well as use in coloring agents. Carotenoids such as β-carotene, astaxanthin, and cryptoxanthin are believed to possess cancer preventing and immunopotentiating activity.

[00264] The carotenoid biosynthesis pathway branches off from the isoprenoid biosynthesis pathway at the point where GGPP is formed. Up to and including formation of FPP,

and potentially GGPP, is as described above for production of a ubiquinone. The commitment step in carotenoid biosynthesis is the formation of phytoene by the head-to-head condensation of two molecules of GGPP, catalyzed by phytoene synthase (often called crtB). A series of dehydrogenation reactions, each of which increases the number of conjugated double bonds by two, converts phytoene into lycopene via neurosporene. The pathway branches at various points, both before and after lycopene production, so that a wide range of carotenoids can be generated. For example, action of a cyclase enzyme on lycopene generates γ-carotene; action of a desaturase instead produces 3,4-didehydrolycopene. γ-carotene is converted to β-carotene through the action of a cyclase. β-carotene can be processed into any of a number of products, including astaxanthin (via echinone, hydroxyechinone, and phoenicoxanthin).

[00265] Carotenoid production in a host organism may be adjusted by modifying the expression or activity of one or more proteins involved in carotenoid biosynthesis. In some embodiments of the invention, it will be desirable to utilize as host cells organisms that naturally produce one or more carotenoids. In some such cases, the focus will be on increasing production of a naturally-produced carotenoid, for example by increasing the level and/or activity of one or more proteins involved in the synthesis of that carotenoid and/or by decreasing the level or activity of one or more proteins involved in a competing biosynthetic pathway. Alternatively or additionally, in some embodiments it will be desirable to generate production of one or more carotenoids not naturally produced by the host cell.

[00266] In some embodiments of the invention, it will be desirable to introduce one or more carotenogenic modifications into a host cell. In certain embodiments the carotenogenic modification may confer expression of one or more heterologous carotenogenic polypeptides into a host cell. As will be apparent to those of ordinary skill in the art, any of a variety of heterologous polypeptides may be employed; selection will consider, for instance, the particular carotenoid whose production is to be enhanced. Still further, selection will consider the complementation and/or ability of the selected polypeptide to function in conjunction with additional oleaginic and/or quinonogenic modifications of a cell such that each of oleaginy, ubiquinone biosynthesis and carotenoid biosynthesis are effectuated to the desired extent.

[00267] Proteins involved in carotenoid biosynthesis include, but are not limited to, phytoene synthase, phytoene dehydrogenase, lycopene cyclase, carotenoid ketolase, carotenoid hydroxylase, astaxanthin synthase (a single multifunctional enzyme found in some source organisms that typically has both ketolase and hydroxylase activities), carotenoid epsilon hydroxylase, lycopene cyclase (beta and epsilon subunits), carotenoid glucosyltransferase, and acyl CoA:diacyglycerol acyltransferase. Representative example sequences for carotenoid biosynthesis polypeptides are provided in Tables 17-21 and Tables 38-41.

[00268] Alternatively or additionally, modified carotenoid ketolase polypeptides that exhibit improved carotenoid production activity may be utilized in accordance with the present invention. For example, carotenoid ketolase polypeptides comprising one more mutations to corresponding to those identified Sphingomonassp. DC18 which exhibited improved astaxanthin production (Tao et al.2006 Metab Eng. 2006 Jun 27) and Paracoccus sp. strain N81106 which exhibited altered carotenoid production (Ye et al. *Appl Environ Microbiol* 72:5829, 2006).

[00269] In some embodiments of the invention, potential source organisms for carotenoid biosynthesis polypeptides include, but are not limited to, genera of naturally oleaginous or non-oleaginous fungi that naturally produce carotenoids. These include, but are not limited to, *Botrytis, Cercospora, Fusarium (Gibberella), Mucor, Neurospora, Phycomyces, Puccina, Rhodotorula, Sclerotium, Trichoderma,* and *Xanthophyllomyces*. Exemplary species include, but are not limited to, *Neurospora crassa, Xanthophyllomyces dendrorhous (Phaffia rhodozyma), Mucor circinelloides,* and *Rhodotorula glutinis*. Of course, carotenoids are produced by a wide range of diverse organisms such as plants, algae, yeast, fungi, bacteria, cyanobacteria, etc. Any such organisms may be source organisms for carotenoid biosynthesis polypeptides according to the present invention.

[00270] It will be appreciated that the particular carotenogenic modification to be applied to a host cell in accordance with the present invention will be influenced by which carotenoid(s) is desired to be produced. For example, isoprenoid biosynthesis polypeptides are relevant to the production of most carotenoids. Carotenoid biosynthesis polypeptides are also broadly relevant. Carotenoid ketolase activity is particularly relevant for production of canthaxanthin, as carotenoid hydroxylase activity is for production of lutein and zeaxanthin, among others. Both carotenoid hydroxylase and ketolase activities (and/oror astaxanthin synthase) are particularly useful for production of astaxanthin.

[00271] Bacterial carotenogenic genes have already been demonstrated to be transferable to other organisms, and are therefore particularly useful in accordance with the present invention (see, for example, Miura et al., *Appl. Environ. Microbiol.* 64:1226, 1998). In other embodiments, it may be desirable to utilize genes from other source organisms such as plant, alga, or microalgae; these organisms provide a variety of potential sources for ketolase and hydroxylase polypeptides. Still additional useful source organisms include fungal, yeast, insect, protozoal, and mammalian sources of polypeptides.

[00272] In certain embodiments of the present invention, cells are engineered to produce at least one sterol compound together with the at least one quinone derived compound. The commitment step in sterol biosynthesis is the conversion of farnesyl pyrophosphate into presqualene pyrophosphate. Farnesyl pyrophosphate (FPP) is produced from isopentenyl pyrophosphate (IPP), for example in a process that involves isomerization of IPP into

dimethylallyl pyrophosphate (DMAPP), followed by three sequential condensation reactions with additional molecules of IPP generate the ten-carbon molecule geranyl pyrophosphate (GPP), followed by the fifteen-carbon molecule farnesyl pyrophosphate (FPP). FPP can either enter the sterol biosynthesis pathway by conversion into presqualene puyrophosphate, or alternatively can be diverted toward biosynthesis of carotenoids and other compounds (*e.g.*, a ubiquinone, vitamin E, vitamin K, etc.) by conversion into the twenty-carbon compound geranylgeranyl pyrophosphate (GGPP). In many instances, FPP appears to be the predominant substrate used by polyprenyldiphosphate synthases (Coq1 polypeptides) during biosynthesis of ubiquinones.

[00273] Once the sterol biosynthesis pathway has been entered, presqualene pyrophosphate is then converted to squalene by the same enzyme that performed the farnesyl pyrophosphate → presqualene pyrophosphate conversion. Squalene is then converted into a variety of different sterol compounds, including, but not limited to, lanosterol, zymosterol, ergosterol, 7-dehydrocholesterol (provitamin D3), and vitamin D compounds. The vitamin D_2 biosynthetic pathway and the vitamin D_3 biosynthetic pathway share some common reactions, and there can be multiple points at which a vitamin D_2 intermediate can be converted into a vitamin D_3 intermediate (see, for example, Figure 1).

[00274] In some embodiments, the sterol compound whose production is engineered is selected from the group consisting of squalene, lanosterol, zymosterol, ergosterol, and vitamin D compounds (e.g., 7-dehydrocholesterol (provitamin D3)).

[00275] In some embodiments of the present invention, host cells are engineered to produce squalene in addition to one or more quinone derived compounds. In some embodiments, squalene production is enhanced in a cell by introduction of one or more sterologenic modifications that increases levels of IPP, FPP and/or squalene itself. In some embodiments, squalene production is enhanced in a cell by increasing the level and/or activity of one or more squalene biosynthesis polypeptides (e.g., one or more isoprenoid biosynthesis polypeptides, an FPP synthase polypeptide, and/or a squalene synthase polypeptide). Alternatively or additionally, in some embodiments, squalene production is enhanced in a cell by decreasing the level and/or activity of one or more sterol biosynthesis competitor polypeptides that diverts one or more intermediates away from squalene production and/or that metabolizes squalene itself.

[00276] For example, in some embodiments of the present invention, squalene production in a host cell is increased by introducing or increasing expression and/or activity of one or more squalene synthase polypeptides in the cell. Representative examples of squalene synthase polypeptide sequences are included in Table 16. In some embodiments of the invention that utilize squalene synthase (or modifications of squalene synthase) source organisms include, but are not limited to, *Neurospora crassa,, Aspergillus niger, Saccharomyces cerevisiae, Mucor circinelloides, Candida utilis, Mortierella alpina, Phaffia rhodozyma,* and *Yarrowia lipolytica.*

[00277] In some embodiments of the invention, squalene production in a host cell is increased by reducing the level or activity of one or more squalene biosynthesis competitor polypeptides, including for example one or more vitamin D biosynthesis polypeptides (*e.g.*, which act to metabolize squalene). For instance, in some embodiments, the level or activity of one or more polypeptides active in the ergosterol biosynthetic pathway (see below) is reduced or eliminated.

[00278] In some embodiments, the sterol compound produced in addition to one or more quinone derived compounds according to the present invention is lanosterol. In some embodiments, lanosterol production is enhanced in a cell by introduction of one or more sterologenic modifications that increases levels of IPP, FPP and/or lanosterol itself. In some embodiments, lanosterol production is enhanced in a cell by increasing the level and/or activity of one or more lanosterol biosynthesis polypeptides (e.g., one or more isoprenoid biosynthesis polypeptides, an FPP synthase polypeptide, squalene synthase polypeptide, squalene epoxidase polypeptide, or 2,3-oxidosqualene-lanosterol cyclase polypeptide). Alternatively or additionally, in some embodiments, lanosterol production is enhanced in a cell by decreasing the level and/or activity of one or more sterol biosynthesis competitor polypeptides that diverts one or more intermediates away from lanosterol production and/or that metabolizes lanosterol itself.

[00279] For example, in some embodiments of the present invention, lanosterol production in a host cell is increased by introducing or increasing expression and/or activity of one or more squalene synthase polypeptide, squalene epoxidase polypeptide, or 2,3-oxidosqualene-lanosterol cyclase polypeptide in the cell. Representative examples of squalene synthase polypeptide, squalene epoxidase polypeptide, and 2,3-oxidosqualene-lanosterol cyclase polypeptide sequences are included in Table 16, 83, and 85. . In some embodiments of the invention that utilize squalene synthase polypeptide, squalene epoxidase polypeptide, or 2,3-oxidosqualene-lanosterol cyclase polypeptide (or modifications of these polypeptides) source organisms include, but are not limited to, *Neurospora crassa, Aspergillus niger, Saccharomyces cerevisiae, Phaffia rhodozyma, Mucor circinelloides, Candida utilis, Mortierella alpina,* and *Yarrowia lipolytica.*

[00280] In some embodiments of the invention, lanosterol production in a host cell is increased by reducing the level or activity of one or more vitamin D biosynthesis polypeptides (e.g., which act to metabolize squalene). For instance, in some embodiments, the level or activity of one or more polypeptides active in the ergosterol biosynthetic pathway (see below).

[00281] In some embodiments of the present invention, host cells are engineered to produce zymosterol in addition to one or more quinone derived compounds. In some embodiments, zymosterol production is enhanced in a cell by introduction of one or more sterologenic modifications that increases levels of IPP, FPP and/or zymosterol itself. In some embodiments, zymosterol production is enhanced in a cell by increasing the level and/or activity of

one or more zymosterol biosynthesis polypeptides (e.g., one or more isoprenoid biosynthesis polypeptides, an FPP synthase polypeptide, squalene synthase polypeptide, squalene epoxidase polypeptide, 2,3-oxidosqualene-lanosterol cyclase polypeptide, cytochrome P450 lanosterol 14α-demethylase polypeptide, C-14 sterol reductase polypeptide, or C-4 sterol methyl oxidase polypeptide). Alternatively or additionally, in some embodiments, zymosterol production is enhanced in a cell by decreasing the level and/or activity of one or more sterol biosynthesis competitor polypeptides that diverts one or more intermediates away from lanosterol production and/or that metabolizes lanosterol itself.

[00282] For example, in some embodiments of the present invention, zymosterol production in a host cell is increased by introducing or increasing expression and/or activity of one or more squalene synthase polypeptide, squalene epoxidase polypeptide, 2,3-oxidosqualene-lanosterol cyclase polypeptide, cytochrome P450 lanosterol 14α-demethylase polypeptide, C-14 sterol reductase polypeptide, or C-4 sterol methyl oxidase polypeptide in the cell. Representative examples of squalene synthase polypeptide, squalene epoxidase polypeptide, 2,3-oxidosqualene-lanosterol cyclase polypeptide, cytochrome P450 lanosterol 14α-demethylase polypeptide, C-14 sterol reductase polypeptide, or C-4 sterol methyl oxidase polypeptide sequences are included in Tables 16, and tables 86-99. In some embodiments of the invention that utilize squalene synthase polypeptide, squalene epoxidase polypeptide, 2,3-oxidosqualene-lanosterol cyclase polypeptide, cytochrome P450 lanosterol 14α-demethylase polypeptide, C-14 sterol reductase polypeptide, or C-4 sterol methyl oxidase polypeptide (or modifications of these polypeptides) source organisms include, but are not limited to, *Neurospora crassa,*, *Aspergillus niger, Saccharomyces cerevisiae, Phaffia rhodozyma, Mucor circinelloides, Candida utilis, Mortierella alpina,* and *Yarrowia lipolytica.*

[00283] In some embodiments of the invention, zymosterol production in a host cell is increased by reducing the level or activity of one or more vitamin D biosynthesis polypeptides (e.g., which act to metabolize squalene). For instance, in some embodiments, the level or activity of one or more polypeptides active in the ergosterol biosynthetic pathway (see below).

[00284] In some embodiments of the present invention, host cells are engineered to produce ergosterol in addition to one or more quinone derived compounds. In some embodiments, ergosterol production is enhanced in a cell by introduction of one or more sterologenic modifications that increases levels of IPP, FPP and/or ergosterol itself. In some embodiments, ergosterol production is enhanced in a cell by increasing the level and/or activity of one or more ergosterol biosynthesis polypeptides (e.g., one or more isoprenoid biosynthesis polypeptides, an FPP synthase polypeptide, squalene synthase polypeptide, squalene epoxidase polypeptide, 2,3-oxidosqualene-lanosterol cyclase polypeptide, cytochrome P450 lanosterol 14α-demethylase polypeptide, C-14 sterol reductase polypeptide, C-4 sterol methyl oxidase polypeptide, SAM:C-24

sterol methyltransferase polypeptide, C-8 sterol isomerase polypeptide, C-5 sterol desaturase polypeptide, C-22 sterol desaturase polypeptide, or C-24 sterol reductase polypeptide. Alternatively or additionally, in some embodiments, ergosterol production is enhanced in a cell by decreasing the level and/or activity of one or more sterol biosynthesis competitor polypeptides that diverts one or more intermediates away from ergosterol production and/or that metabolizes ergosterol itself.

[00285] For example, in some embodiments of the present invention, ergosterol production in a host cell is increased by introducing or increasing expression and/or activity of one or more squalene synthase polypeptide, squalene epoxidase polypeptide, 2,3-oxidosqualene-lanosterol cyclase polypeptide, cytochrome P450 lanosterol 14α-demethylase polypeptide, C-14 sterol reductase polypeptide, C-4 sterol methyl oxidase polypeptide, SAM:C-24 sterol methyltransferase polypeptide, C-8 sterol isomerase polypeptide, C-5 sterol desaturase polypeptide, C-22 sterol desaturase polypeptide, or C-24 sterol reductase polypeptide in the cell. Representative examples of squalene synthase polypeptide, squalene epoxidase polypeptide, 2,3-oxidosqualene-lanosterol cyclase polypeptide, cytochrome P450 lanosterol 14α-demethylase polypeptide, C-14 sterol reductase polypeptide, C-4 sterol methyl oxidase polypeptide, SAM:C-24 sterol methyltransferase polypeptide, C-8 sterol isomerase polypeptide, C-5 sterol desaturase polypeptide, C-22 sterol desaturase polypeptide, or C-24 sterol reductase polypeptide sequences are included in Table 16, and tables 86-99. In some embodiments of the invention that utilize squalene synthase polypeptide, squalene epoxidase polypeptide, 2,3-oxidosqualene-lanosterol cyclase polypeptide, cytochrome P450 lanosterol 14α-demethylase polypeptide, C-14 sterol reductase polypeptide, C-4 sterol methyl oxidase polypeptide, SAM:C-24 sterol methyltransferase polypeptide, C-8 sterol isomerase polypeptide, C-5 sterol desaturase polypeptide, C-22 sterol desaturase polypeptide, or C-24 sterol reductase polypeptide (or modifications of these polypeptides) source organisms include, but are not limited to, *Neurospora crassa, Aspergillus niger, Saccharomyces cerevisiae, Mucor circinelloides, Candida utilis, Mortierella alpina,* and *Yarrowia lipolytica.*

[00286] In some embodiments of the invention, ergosterol production in a host cell is increased by reducing the level or activity of one or more vitamin D biosynthesis polypeptides (e.g., which act to metabolize squalene). For instance, in some embodiments, the level or activity of one or more polypeptides (see below).

[00287] In some embodiments, the sterol compound produced in addition to one or more quinone derived compounds in accordance with the present invention is a vitamin D compound. Vitamin D compounds are a group of steroid compounds including vitamin D_3 (cholecalciferol), vitamin D_2 (ergocalciferol), their provitamins, and certain metabolites (see, for example, Figure 10A-B). Vitamins D_3 and D_2 can be produced from their respective provitamins (*e.g.*, 7-dehydrocholesterol and ergosterol) by ultraviolet irradiation (*e.g.*, by the action of sunlight). The

most biologically active form of vitamin D is 1,25-dihydroxy vitamin D_3, which is also known as calcitriol. Calcitriol is produced by hydroxylation of vitamin D_3 at the 25 position, followed by hydroxylation to generate calcitriol.

[00288] In some embodiments, vitamin D production is enhanced in a cell by introduction of one or more sterologenic modifications that increases levels of IPP, FPP and/or squalene. In some embodiments, vitamin D production is enhanced in a cell by increasing the level and/or activity of one or more vitamin D biosynthesis polypeptides (e.g., one or more isoprenoid biosynthesis polypeptides, an FPP synthase polypeptide, a squalene synthase polypeptide, and/or one or more polypeptides involved in converting squalene into a particular vitamin D compound of interest [e.g., 7-dehydrocholesterol and/or calcitriol]). Alternatively or additionally, in some embodiments, vitamin D production is enhanced in a cell by decreasing the level and/or activity of one or more sterol biosynthesis competitor polypeptides that diverts one or more intermediates away from vitamin D production. In some embodiments of the invention, production of a particular vitamin D compound (e.g., 7-dehydrocholesterol and/or calcitriol) is enhanced by decreasing the level and/or activity of one or more polypeptides that diverts a relevant intermediate toward an alternative vitamin D compound (e.g., ergosterol, vitamin D_2).

[00289] To give but one particular example of a sterologenic modification that can be employed in accordance with the present invention to increase production of one or more vitamin D_3 compounds (*e.g.*, 7-dehydrocholesterol and/or calcitriol), in accordance with some embodiments of the present invention, the level and/or activity of one or more polypeptides that diverts a relevant intermediate toward a vitamin D_2 compound (*e.g.*, ergosterol, vitamin D_2), and away from vitamin D_3 compounds, can be inhibited or destroyed. In some embodiments of the invention, where multiple heterologous polypeptides are to be expressed (e.g., because one or more activities of interest require two or more polypeptide chains and/or because multiple activities of interest are being engineered), it may be desirable to utilize the same source organism for all, or to utilize closely related source organisms; in other embodiments, heterologous polypeptides may be from different source organisms. In some embodiments, two or more versions of a particular heterologous polypeptide, optionally from different source organisms, may be introduced into and/or engineered within, a single host cell.

[00290] Having now generally described the invention, the same will be more readily understood through reference to the following exemplification which is provided by way of illustration, and is not intended to be limiting of the present invention.

Exemplification

[00291] Table 42 describes the *Yarrowia lipolytica* strains used in the following exemplification:

Table 42. *Yarrowia lipolytica* strains.

NRRL Y-1095	Wild type diploid	Derived from strain
ATCC76861	*MATB ura2-21 lyc1-5 LYS1-5B*	
ATCC76982	*MATB ade1 leu2-35 lyc1-5 xpr2*	
ATCC201249	*MATA ura3-302 leu2-270 lys8-11 PEX17-HA*	
MF346	*MATA ura2-21*	ATCC76861 x ATCC201249
MF350	*MATB ura2-21 leu2-35 ade1*	ATCC76982 x MF346
MF358	*MATB ade1*	ATCC76982 x MF346
MF454	*MATB ura3-302 ade1 leu2-270*	ATCC201249 x MF358

[00292] (The genotypes at *LYC1*, *LYS1*, *XPR2*, and *PEX17* were not determined in crosses nor verified for ATCC strains.)

[00293] All basic molecular biology and DNA manipulation procedures described herein are generally performed according to Sambrook *et al.* or Ausubel *et al.* (Sambrook J, Fritsch EF, Maniatis T (eds). 1989. *Molecular Cloning: A Laboratory Manual.* Cold Spring Harbor Laboratory Press: New York; Ausubel FM, Brent R, Kingston RE, Moore DD, Seidman JG, Smith JA, Struhl K (eds). 1998. *Current Protocols in Molecular Biology.* Wiley: New York). The *GPD1* and *TEF1* promoters are from *Y. lipolytica* as is the *XPR2* terminator.

[00294] Plasmids were generated for construction of CoQ10 producing strains. The following subparts describe production of plasmids encoding ubiquinogenic polypeptides. General plasmid construction for expression vectors are described in Table 43, and further constructions in the text. All PCR amplifications used NRRL Y-1095 genomic DNA as template unless otherwise specified. The *URA5* gene described below is allelic with the *ura2-21* auxotrophy above in Table 42.

TABLE 43 Plasmids

Plasmid	Backbone	Insert	Oligos or source
pMB4529	pCR2.1	3.4 kb *ADE1* PCR product	MO4475 & MO4476
pMB4534	pCR2.1	2.1 kb *LEU2* PCR product	MO4477 & MO4478
pMB4535	pCR2.1	1.2 kb *URA5* PCR product	MO4471 & MO4472
pMB4589	pMB4535 (*Kpn*I + *Spe*I)	1.2 kb *GPD1* promoter (*Kpn*I + *Not*I); 0.14 kb *XPR2* terminator (*Not*I + *Spe*I)	MO4568 & MO4591; MO4566 & MO4593
pMB4590	pMB4535 (*Kpn*I + *Spe*I)	0.4 kb *TEF1* promoter (*Kpn*I + *Not*I); 0.14 kb *XPR2* terminator (*Not*I + *Spe*I)	MO4571 & MO4592; MO4566 & MO4593
pMB4597	pMB4534 (*Acc*65I + *Spe*I)	*GPD1* promoter & *XPR2*	From pMB4589

		terminator (*Acc*65I + *Spe*I)	
pMB4603	pMB4597 (*Rsr*II + *Mlu*I)	Residual backbone & *TEF1* promoter (*Rsr*II + *Mlu*I)	From pMB4590
pMB4616	pMB4529 (*Rsr*II + *Spe*I)	Residual backbone & *GPD1* promoter & *XPR2* terminator (*Rsr*II + *Spe*I)	From pMB4589
pMB4629	pMB4616 (*Rsr*II + *Mlu*I)	Residual backbone & *TEF1* promoter (*Rsr*II + *Mlu*I)	From pMB4590
pMB4631	pMB4603 (*Kpn*I + NheI)	1.2 kb *GPD1* promoter (*Kpn*I + NheI);	MO4568 & MO4659
pMB4637	pMB4629 (*Nhe*I + *Mlu*I)	1.5 kb *hmg1*^{trunc} ORF (XbaI + MluI)	MO4657 & MO4658
pMB4662	pMB4631 (*Spe*I + XhoI)	1.8 kb *URA3* fragment (*Spe*I + *Bsa*I	MO4684 & MO4685
pMB4691	pMB4662 (*Acc*65I + *Mlu*I)	0.4 kb *TEF1* promoter (*Acc*65I + *Mlu*I)	From pMB4629

TABLE 44: Oligonucleotides referenced in Table 43

MO4471	5'CTGGGTGACCTGGAAGCCTT
MO4472	5'AAGATCAATCCGTAGAAGTTCAG
MO4475	5'AAGCGATTACAATCTTCCTTTGG
MO4476	5'CCAGTCCATCAACTCAGTCTCA
MO4477	5'GCATTGCTTATTACGAAGACTAC
MO4478	5'CCACTGTCCTCCACTACAAACAC
MO4566	5'CACAAACTAGTTTGCCACCTACAAGCCAGAT
MO4568	5'CACAAGGTACCAATGTGAAAGTGCGCGTGAT
MO4571	5'CACAAGGTACCAGAGACCGGGTTGGCGG
MO4591	5'CACAAGCGGCCGCGCTAGCATGGGGATCGATCTCTTATAT
MO4592	5'CACAAGCGGCCGCGCTAGCGAATGATTCTTATACTCAGAAG
MO4593	5'CACAAGCGGCCGCACGCGTGCAATTAACAGATAGTTTGCC
MO4659	5'CACAAGCTAGCTGGGGATGCGATCTCTTATATC
MO4684	5' CATTCACTAGTGGTGTGTTCTGTGGAGCATTC
MO4685	5' CACACGGTCTCATCGAGGTGTAGTGGTAGTGCAGTG
MO4657	5'CACACTCTAGACACAAAAATGACCCAGTCTGTGAAGGTGG
MO4658	5'CACACACGCGTACACCTATGACCGTATGCAAAT

Example 1. Biosynthesis of CoQ10 in Yarrowia lipolytica.

[00295] Decaprenyl diphosphate synthases ("dpdpS") based on the amino acid sequence of those found in *Silicibacter pomeroyi* and in *Loktanella vestfoldensis* are expressed in *Yarrowia*

lipolytica, using nucleotide sequences with the appropriate *Yarrowia* codon bias, and with *Yarrowia* mitochondrial targeting sequences. Insertion of the expression cassette results in the disruption of the native *COQ1* gene, encoding nonaprenyl diphosphate synthase.

[00296] To construct the mitochondrial leader sequence encoding DNA of NADH:ubiquinone oxidoreductases (complex I) ["NUAM"], four oligos were annealed and treated sequentially with Klenow fragment and ligase:

MO4859: 5'-TCTAGACACAAAAATGCTCTCGAGAAACCTCAGCAAGTTTG
MO4860: 5'-GTGGTTGCTGGCCGGATGAGACCGGCTCGAGCAAACTTGCT
MO4861: 5'-CAGCAACCACATCCACACACACCCGACTATTCTCTGTCTCC
MO4862: 5'-GGATCCCGTCTCGGACAGACGTCGGGCGGAGACAGAG.

[00297] The resulting fragment was subsequently amplified with MO4859 and MO4862 using *Pfu* polymerase and the product was phosphorylated and ligated to pBluescriptSKII⁻ cut with *Eco*RV to create pMB4776. The mitochondrial leader sequence of NUAM is thereby encoded within the resultant *Xba*I-*Bsm*BI (underline) fragment:

(NUAMldr):
tctagacacaaaaatgctctcgagaaacctcagcaagtttgctcgagccggtctcatccggccagcaaccacatccacacacacccgactatt
ctctgtctccgcccgacgtctgtccgagacgggatcc

[00298] To construct the mitochondrial leader sequence encoding DNA of the native *Y. lipolytica* Coq1 protein, *Y. lipolytica* genomic DNA was amplified with MO4857 (5'-CGGATCCCGTCTCGGACATTTCTTGCGACACAATG) and MO4858 (5'-CTCTAGACACAAAAATGCTGAGAGTCGGACGAAT) and the 0.25 kb product was phosphorylated and ligated to pBluescriptSKII⁻ cut with *Eco*RV to create pMB4750. The mitochondrial leader sequence of Coq1 is thereby encoded within the resultant *Xba*I-*Bsm*BI (underline) fragment:

(Coq1ldr):
ctctagacacaaaaatgctgagagtcggacgaattggcaccaagaccctagccagcagcagcctgcgtttcgtggcaggtgctcggcccaa
atccacgctcaccgaggccgtgctggagaccacagggctgctgaaaaccacgccccaaaaccccgagtggtctggagccgtcaagcagg
catctcgtctggtggagaccgacactccgatccgagacccgttttccattgtgtcgcaagaaatgtcc**gagacg**ggatccg.

[00299] To construct a cassette encoding the decaprenyl diphosphate synthase (dpdpS) from *Silicibacter pomeroyi*, the following sequence was synthesized *de novo*:

(Sp-dpdpS):

GGATCCCGTCTCTTGTCTGATGCCAAAGTCTCTACAAAGCCTCACGAGATGCTCGCTG
CCACACTCTCTCAGGAAATGGCCGCTGTCAACGCCCTTATTCGAACCCGTATGGCTTC
TGAACACGCCCCTAGAATCCCCGAAGTTACAGCCCACCTCGTCGAAGCCGGCGGAAA
ACGATTGCGACCTATGCTGACACTTGCTGCTGCCCGACTGTGTGGATACCAGGGCGAA
GATCATGTCAAACTGGCTGCCACTGTTGAATTTATTCACACTGCTACACTTTTGCACGA
TGATGTCGTGGACGAGTCTGGACAAAGACGTGGACGACCTACTGCTAATCTTCTTTGG
GATAACAAGTCCTCTGTTCTTGTGGGCGACTATCTTTTTGCACGATCGTTCCAGCTGAT
GGTCGAAACCGGTTCCCTTCGAGTGCTTGACATCCTCGCTAACGCTGCCGCGACAATT
GCCGAAGGTGAAGTGCTCCAGATGACCGCTGCTTCCGATCTTAGAACTGATGAATCCG
TTTACCTTCAGGTCGTTCGAGGTAAAACTGCCGCTCTTTTTTCTGCTGCTACTGAAGTT
GGTGGTGTTATTGCCGGAGTCCCCGAAGCCCAAGTTCGAGCACTTTTTGAATACGGTG
ATGCGCTGGGAATTGCATTTCAGATTGCTGATGACCTCCTCGACTACCAAGGTGATGC
TAAGGCCACTGGAAAGAATGTTGGAGATGACTTCAGAGAAAGAAAACTCACATTGCC
TGTTATTAAAGCCGTCGCTCAAGCTACTGATGAGGAACGAGCGTTTTGGGTTAGAACT
ATTGAAAAGGGAAAGCAAGCTGAAGGAGATCTTGAACAGGCTCTCGCTCTCATGGAA
AAATACGGAACACTTGCCGCAACCAGAGCCGATGCGCATGCTTGGGCCGAAAAAGCA
CGAACCGCCCTCGAACTGTTGCCGAATCACGAAATCAGAACAATGCTCTCCGACCTCG
CCGATTATGTCGTTGCTAGATTGTCTTAAACGCGT.

[00300] To construct a cassette encoding the decaprenyl diphosphate synthase (dpdpS) from *Loktanella vestfoldensis*, the following sequence was synthesized *de novo*:

(Lv-dpdpS):

GGATCCCGTCTCTTGTCTCTTGATCACGCTGCCACCAAACCTCATGAACAACTTGCCGC
CGCCCTTGCCGACGACCTTACCGCAGTTAACGCTATGATTAGAGACCGAATGGCCAGC
GAACATGCCCCCAGAATTCCACAAGTTACCGCACACCTCGTTGAAGCCGGAGGTAAA
AGACTTCGTCCAATGCTGACCCTTGCCGCCGCCCGTATGTGTGGCTACGACGGACCTT
ACCACATCCACCTTGCAGCCACCGTTGAGTTCATTCACACCGCCACCTTGCTCCATGA
CGATGTTGTTGATGAGTCCTCCCAACGTCGTGGTCGACCTACCGCTAATCTTCTGTGGG
ATAATACCTCTTCTGTTTTGGTTGGAGACTACCTCTTTGCACGATCTTTTCAGTTGATG
GTTGAGACCGGATCGCTTCGAGTTCTTGACATCCTGGCCAATGCTTCTGCTACCATCGC
CGAAGGTGAGGTTCTGCAACTTACCGCCGCCGCTGACCTTGCAACTACCGAGGACATT
TACATCAAAGTTGTTCGAGGAAAGACTGCTGCACTCTTTTCTGCTGCTATGGAAGTTG
GTGGAGAAATCGCCGGTCAGGACCCGGCTATTAAACAGGCTCTCTTTGACTACGGCGA
CGCTCTCGGAATTTCTTTTCAGATTGTTGATGACCTGTTGGATTACGGTGGAACAAAA

GCTACAGGAAAGAACGTTGGTGATGACTTCCGAGAAAGAAAGCTCACCCTCCCTGTT
ATTCGTGCCGTTGCTGCTGCTGATGCTGATGAAAGAGCTTTTTGGGAACGAACAATTC
AAAAAGGAAGACAACAAGATGGAGACCTGGACCATGCAATTGCCCTTCTTCATAGAC
ACGGAACCCTTGAATCCACACGACAAGACGCAATCCTTTGGGCCGCTAAAGCTAAAG
AAGCACTCGGAGTTATCCCGGACCATGCTCTTAAAACCATGCTCGTTGACCTTGCTGA
CTACGTTGTTGCTCGACTCACCTAAACGCGT.

[00301] A NUAMldr-Sp-dpdpS fusion capable of being expressed in *Y. lipolytica* was constructed by ligating the *Xba*I-*Bsm*BI NUAMldr fragment together with the *Bsm*BI-*Mlu*I Sp-dpdpS fragment into pMB4691 cut with *Nhe*I and *Mlu*I, to create pMB4799.

[00302] A NUAMldr-Lv-dpdpS fusion capable of being expressed in *Y. lipolytica* was constructed by ligating the *Xba*I-*Bsm*BI NUAMldr fragment together with the *Bsm*BI-*Mlu*I Lv-dpdpS fragment into pMB4691 cut with *Nhe*I and *Mlu*I, to create pMB4797.

[00303] A Coq1ldr-Sp-dpdpS fusion capable of being expressed in *Y. lipolytica* was constructed by ligating the *Xba*I-*Bsm*BI Coq1ldr fragment together with the *Bsm*BI-*Mlu*I Sp-dpdpS fragment into pMB4691 cut with *Nhe*I and *Mlu*I, to create pMB4798.

[00304] A Coq1ldr-Lv-dpdpS fusion capable of being expressed in *Y. lipolytica* was constructed by ligating the *Xba*I-*Bsm*BI Coq1ldr fragment together with the *Bsm*BI-*Mlu*I Lv-dpdpS fragment into pMB4691 cut with *Nhe*I and *Mlu*I, to create pMB4796.

[00305] To effect the disruption of the native *COQ1* gene and its replacement by the fusions described above, *Y. lipolytica* genomic DNA was amplified with two pairs of primers:

5'- CACACGGTACCGGTATAGGCACAAGTGC [MO4848] with

5'- CACTCGGATCCGTACGTCTGTGGTGCTGTGGT [MO4856], and

5'- CACACGGATCCGCTAGCTCTGAGAAACCTCACCATG [MO4850] with

5'- CACACTCTAGATTTTCTTGGCCATGAACGGT [MO4851],

yielding a fragment of approximately 0.7 kb and 0.85 kb in length, respectively. Fragment MO4848/4856 was cleaved with *Acc*65I and *Bam*HI, fragment MO4850/4851 was cleaved with *Bam*HI and *Xba*I, and pBluescriptSKII$^-$ was cleaved with *Xba*I and *Acc*65I. These three segments were ligated together to yield plasmid pMB4747.

[00306] The 3.6 (or 3.7) kb *Acc*65I-*Xba*I fragments from pMB4796, pMB4797, pMB4798, and pMB4799 containing various *tef*-dpdpS constructs and the *URA3* marker were each ligated to pMB4747 cleaved with *Bsi*WI and *Nhe*I. The resulting plasmids, pMB4800 (Coq1ldr-Lv-dpdpS), pMB4801 (NUAMldr-Lv-dpdpS), pMB4802 (Coq1ldr-Sp-dpdpS), pMB4803 (NUAMldr-Sp-dpdpS), are cleaved with *Acc*65I and *Xba*I and the 5.1 (or 5.3) kb fragment containing various

*coq1-tef1*p-dpdpS-*URA3-coq1* sequences is used to transform *Y. lipolytica* strain MF454 (*MATB ura3 leu2 ade1)* to uracil prototrophy. Transformants were checked by PCR for confirmation of homologous integration based gene replacement which confirmed the presence of the heterologous dpdpS and the absence of the wild type *Y. lypolytica COQ1* allele. The strains were designated MF975 (*MATB ura3 leu2 ade1 coq1ΔNUAMldr-Lv-dpdpS-URA3*), MFL976 (*MATB ura3 leu2 ade1 coq1ΔNUAMldr-Lv-dpdpS-URA3*) as duplicate and MF977 (*MATB ura3 leu2 ade1 coq1ΔNUAMldr-Sp-dpdpS-URA3*). Strains were analyzed for ubiquinone by TLC and HPLC analysis as described in subsequent examples.

Example 2. Increased CoQ10 production resulting from enhanced PHB-polyprenyltransferase activity.

[00307] 4-hydroxybenzoate polyprenyl transferases ("phbPPt") based on the amino acid sequence of those found in *Silicibacter pomeroyi* and in *Bos taurus* are expressed in *Yarrowia lipolytica*, using nucleotide sequences with the appropriate *Yarrowia* codon bias, and in the case of the *S. pomeroyi* sequence, with *Yarrowia* mitochondrial targeting sequences.

[00308] The following sequences are synthesized *de novo*:

[00309] *G: Yarrowia lipolytica* Coq1 signal sequence. + *Silicibacter pomeroyi* phbPPt 5'-

TTCTAGACACAAAAA**TGCTGCGAGTGGGCCGAATCGGCACCAAGACCCTGGCCTC**
TTCTTCTCTGCGATTCGTGGCCGGCGCCCGACCCAAGTCTACCCTGACCGAGGC
CGTGCTGGAGACCACCGGCCTGCTGAAGACCACCCCCCAGAACCCCGAGTGGTC
TGGCGCCGTGAAGCAGGCCTCTCGACTGGTGGAGACCGACACCCCCATCCGAGA
CCCCTTCTCTATCGTGTCTCAGGAGATGCAGGGCCAGGCCCCCACCCCCGACGGCC
AGGTGGCCGACGCCGTGACCGGCAACTGGGTGGACATCCACGCCCCCGCCTGGTCTC
GACCCTACCTGCGACTGTCTCGAGCCGACCGACCCATCGGCACCTGGCTGCTGCTGAT
CCCCTGTTGGTGGGGCCTGGCCCTGGCCATGCTGGACGGCCAGGACGCCCGATGGGG
CGACCTGTGGATCGCCCTGGGCTGTGCCATCGGCGCCTTCCTGATGCGAGGCGCCGGC
TGTACCTGGAACGACATCACCGACCGAGAGTTCGACGGCCGAGTGGAGCGAACCCGA
TCTCGACCCATCCCCTCTGGCCAGGTGTCTGTGCGAATGGCCGTGGTGTGGATGATCG
CCCAGGCCCTGCTGGCCCTGATGATCCTGCTGACCTTCAACCGAATGGCCATCGCCAT
GGGCGTGCTGTCTCTGCTGCCCGTGGCCGTGTACCCCTTCGCCAAGCGATTCACCTGG
TGGCCCCAGGTGTTCCTGGGCCTGGCCTTCAACTGGGGCGCCCTGCTGGCCTGGACCG
CCCACTCTGGCTCTCTGGGCTGGGGCGCCCTGTTCCTGTACCTGGCCGGCATCGCCTG
GACCCTGTTCTACGACACCATCTACGCCCACCAGGACACCGAGGACGACGCCCTGATC
GGCGTGAAGTCTACCGCCCGACTGTTCGGCGCCCAGACCCCCCGATGGATGTCTTACT
TCCTGGTGGCCACCGTGTCTCTGATGGGCATCGCCGTGTTCGAGGCCGCCCTGCCCGA
CGCCTCTATCCTGGCCCTGGTGCTGGCCCTGGCCGGCCCCTGGGCCATGGGCTGGCAC

ATGGCCTGGCAGCTGCGAGGCCTGGACCTGGACGACAACGGCAAGCTGCTGCAGCTG
TTCCGAGTGAACCGAGACACCGGCCTGATCCCCCTGATCTTCTTCGTGATCGCCCTGTT
CGCCTAACGCGT

[00310] *H: Bos taurus* phpPPt 5'-
TTCTAGACACAAAAATGCTGGGCTCTTGTGGCGCCGGCCTGGTGCGAGGCCTGCGAGC
CGAGACCCAGGCCTGGCTGTGGGGCACCCGAGGCCGATCTCTGGCCCTGGTGCACGC
CGCCCGAGGCCTGCACGCCGCCAACTGGCAGCCCTCTCCCGGCCAGGGCCCCCGAGG
CCGACCCCTGTCTCTGTCTGCCGCCGCCGTGGTGAACTCTGCCCCCCGACCCCTGCAG
CCCTACCTGCGACTGATGCGACTGGACAAGCCCATCGGCACCTGGCTGCTGTACCTGC
CCTGTACCTGGTCTATCGGCCTGGCCGCCGACCCCGGCTGTCTGCCCGACTGGTACAT
GCTGTCTCTGTTCGGCACCGGCGCCGTGCTGATGCGAGGCGCCGGCTGTACCATCAAC
GACATGTGGGACCGAGACTACGACAAGAAGGTGACCCGAACCGCCTCTCGACCCATC
GCCGCCGGCGACATCTCTACCTTCCGATCTTTCGTGTTCCTGGGCGGCCAGCTGACCCT
GGCCCTGGGCGTGCTGCTGTGTCTGAACTACTACTCTATCGCCCTGGGCGCCGCCTCTC
TGCTGCTGGTGACCACCTACCCCCTGATGAAGCGAATCACCTACTGGCCCCAGCTGGC
CCTGGGCCTGACCTTCAACTGGGGCGCCCTGCTGGGCTGGTCTGCCGTGAAGGGCTCT
TGTGACCCCTCTGTGTGTCTGCCCCTGTACTTCTCTGGCATCATGTGGACCCTGATCTA
CGACACCATCTACGCCCACCAGGACAAGAAGGACGACGCCCTGATCGGCCTGAAGTC
TACCGCCCTGCTGTTCCGAGAGGACACCAAGAAGTGGCTGTCTGGCTTCTCTGTGGCC
ATGCTGGGCGCCCTGTCTCTGGTGGGCGTGAACTCTGGCCAGACCATGCCCTACTACA
CCGCCCTGGCCGCCGTGGGCGCCCACCTGGCCCACCAGATCTACACCCTGGACATCAA
CCGACCCGAGGACTGTTGGGAGAAGTTCACCTCTAACCGAACCATCGGCCTGATCATC
TTCCTGGGCATCGTGCTGGGCAACCTGTGTAAGGCCAAGGAGACCGACAAGACCCGA
AAGAACATCGAGAACCGAATGGAGAACTAACGCGT

[00311] The above sequences are cleaved with *Mlu*I and *Xba*I, and inserted into *Nhe*I- and *Mlu*I-cleaved pMB4603, placing the genes under the control of the *Y. lipolytica TEF1* promoter, and adjacent to a functional *Y. lipolytica LEU2* gene. These plasmids are designated tef-transS (from sequence G) and tef-transB (from sequence H).

[00312] These plasmids can be used to transform *Y. lipolytica* strain MF454, ML975, MF976, or MF977 to leucine prototrophy by cleaving with enzymes that lie within plasmid backbone sequences to favor nonhomologous integration events. Transformants can be checked by Southern analysis for confirmation of ectopic integration. Production of CoQ10 can be assessed using HPLC or TLC analysis.

Example 3: Extraction of ubiquinone from Yarrowia lipolytica cells

[00313] Shake-flask testing was conducted using 20 ml cultures containing YPD medium (1% yeast extract, 2% peptone, 2% glucose) in 125 ml flasks grown at 30°C. *Y. lipolytica* cells were harvested from 24 hour cultures, and extractions are performed to determine ubiquinone form and quantity. Entire culture was pelleted and washed with 50 ml H_2O. Pelleted cells may be frozen at -80°C and stored. 0.5ml of cubic zirconium beads was added to cell pellets, along with 1 ml ice-cold extraction solvent (a 50/50 v/v mix of hexane and ethyl acetate containing 0.01% butylhydroxytoluene (BHT)). The mixture was then agitated (Mini-BeadBeater-8, BioSpec Products, Inc.) at maximum speed for 5 minutes at 4°C. The mixture was then spun at maximum speed for 2 minutes, and the supernatant collected and deposited in a cold 16 ml glass vial. The remaining cell debris was re-extracted at least three times, without the addition of zirconium beads; all supernatants were pooled in the 16 ml glass vial. A Speed Vac was used to concentrate the supernatant (room temperature in dark), and the samples were stored at -20°C or -80°C until immediately before TLC and HPLC analysis. Prior to TLC analysis, the samples were resuspended in 50µl ice-cold solvent and then transferred to a cold amber vial. In an alternative similar protocol, *Y. lipolytica* cells can be harvested from 72-96 hour 20 ml cultures grown in 125 ml flasks grown at 30°C. 1.8 ml of culture is placed into a pre-weighed tube with a hole poked in the top. Cells are pelleted and washed with 1 ml H_2O. The washing procedure is repeated and then cells are lyophilized overnight. After drying to completion, the tube is weighed in order to calculate dry cell weight. 1 ml from the same shake flask culture is placed into a screw-cap tube for ubiquinone extraction. Cells are pelleted and washed once with 1 ml H_2O and once with 1 M potassium phosphate solution, pH 7.1. Pelleted cells may be frozen at -80°C and stored. Cubic zirconium beads addition and extraction is performed as describe above. Following extraction, the glass vial is spun for 5 minutes at 2000 rpm at 4°C in a Sorvall tabletop centrifuge, and the supernatant is transferred to a new cold 16 ml glass vial. A Speed Vac is used to concentrate the supernatant (room temperature in dark), and the samples are stored at -20°C or -80°C until immediately before HPLC analysis. Prior to HPLC analysis, the samples are resuspended in 1 ml ice-cold solvent and then transferred to a cold amber vial. Throughout the extraction protocols, care is taken to avoid contact with oxygen, light, heat, and acids.

Example 4a: Purification of Ubiquinones from crude extract by Thin Layer Chromatography (TLC)

[00314] Ubiquinone containing samples from the primary extraction in example 3 were spotted to immobilized silica gel plates next to the primary standards (Coenzyme Q9 (Sigma 275970) and Coenzyme Q10 (Sigma 27595)) and resolved in a 80:40:1 hexanes:diethyl ether:acetic acid solvent mixture. Ubiquinone containing bands were identified by UV shadowing and migration with the purified ubiquinone standard and excised from the TLC plate. Samples

were extracted from the silica gel with 50µl acetone followed by mixing, centrifugation, decanting and drying before HPLC analysis.

Example 4b: Quantification of ubiquinone production by HPLC

[00315] Ubiquinone-containing samples are resuspended in ice-cold extraction solvent (a 50/50 v/v mix of hexane and ethyl acetate containing 0.01% butylhydroxytoluene (BHT)). An Alliance 2795 HPLC (Waters) equipped with a Waters XBridge C18 column (3.5 µm, 2.1 x 50 mm) and Thermo Basic 8 guard column (2.1 x 10 mm) is used to resolve ubiquinone at 25°C; authentic ubiquinone samples are used as standards. Ubiquinone molecules were detected at 275 nm (alternatively, they can also be detected at 405 nm), and retention times include CoQ10 (4.272 min) and CoQ9 (4.164 min). The mobile phases and flow rates are shown in Table 45 (Solvent A= Ethyl Acetate; Solvent B= Water; Solvent C= Methanol; Solvent D= Acetonitrile). The injection volume was 10 µL. The detector was a Waters 996 photodiode array detector. A peak corresponding to Coenzyme Q10 was observed in strains MF975, MF976, and MF977.

[00316] The retention times for additional lipophilic molecules include astaxanthin (1.159 min), zeaxanthin (1.335), β-apo-8'-carotenal (2.86 min), ergosterol (3.11 min), lycopene (3.69 min), β-Carotene (4.02 min), and phytoene (4.13 min). Astaxanthin, zeaxanthin, β-apo-8'-carotenal, lycopene and β-Carotene are detected at 475 nm, whereas ergosterol and phytoene are detected at 286 nm.

TABLE 45: Mobile Phases and Flow Rates for Ubiquinone Resolution

Time (min)	Flow (mL/min)	% A	% B	% C	% D	Curve
	0.50	0.0	20.0	0.0	80.0	
3.00	1.00	20.0	0.0	0.0	80.0	6
4.50	1.00	80.0	0.0	20.0	0.0	6
5.50	1.00	0.0	0.0	60.0	40.0	6
6.50	1.00	0.0	0.0	80.0	20.0	6
7.50	1.00	0.0	0.0	100.0	0.0	6
8.50	1.00	0.0	0.0	100.0	0.0	6
9.50	1.00	0.0	20.0	0.0	80.0	6
10.50	0.50	0.0	20.0	0.0	80.0	6

Example 5. Engineering of PHB biosynthetic pathway genes results in increased para-hydroxybenzoic acid production.

[00317] Production of *para*-hydroxybenzoic acid (PHB) is increased by overexpression of a heterologous 3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP) synthase and a heterologous chorismate lyase (UbiC). Both genes are codon-optimized variants of the *Erwinia carotovora* coding sequences. The DAHP synthase is based on the amino acid sequence of that found in *Erwinia* is expressed in *Yarrowia lipolytica*, using nucleotide sequences with the appropriate *Yarrowia* codon bias, and containing a P148L substitution. The P148L substitution can be employed to alleviate tyrosine-mediated allosteric regulation of the *Erwinia* DAHP synthase. The following sequences are synthesized:

[00318] J: DAHP *E. carotovora* (optimized)(AroF with P148L substitution) 5'-

TTCTAGACACAAAAATGCAGAAGGACTCTCTGAACAACATCAACATCTCTGCCGAGC
AGGTGCTGATCACCCCCGACGAGCTGAAGGCCAAGTTCCCCCTGAACGACGTGGAGC
AGCGAGACATCGCCCAGGCCCGAGCCACCATCGCCGACATCATCCACGGCCGAGACG
ACCGACTGCTGATCGTGTGTGGCCCCTGTTCTATCCACGACACCGACGCCGCCCTGGA
GTACGCCCGACGACTGCAGCTGCTGGCCGCCGAGCTGAACGACCGACTGTACATCGT
GATGCGAGTGTACTTCGAGAAGCCCCGAACCACCGTGGGCTGGAAGGGCCTGATCAA
CGACCCCTTCATGGACGGCTCTTTCGACGTGGAGTCTGGCCTGCACATCGCCCGAGGC
CTGCTGCTGCAGCTGGTGAACATGGGCCTGCCCCTGGCCACCGAGGCCCTGGAC**CTG**
AACTCTCCCCAGTACCTGGGCGACCTGTTCTCTTGGTCTGCCATCGGCGCCCGAACCA
CCGAGTCTCAGACCCACCGAGAGATGGCCTCTGGCCTGTCTATGCCCGTGGGCTTCAA
GAACGGCACCGACGGCTCTCTGGGCACCGCCATCAACGCCATGCGAGCCGCCGCCAT
GCCCCACCGATTCGTGGGCATCAACCAGACCGGCCAGGTGTGTCTGCTGCAGACCCAG
GGCAACGGCGACGGCCACGTGATCCTGCGAGGCGGCAAGACCCCCAACTACTCTGCC
CAGGACGTGGCCGAGTGTGAGAAGCAGATGCAGGAGGCCGGCCTGCGACCCGCCCTG
ATGATCGACTGTTCTCACGGCAACTCTAACAAGGACTACCGACGACAGCCCCTGGTGG
TGGAGTCTGCCATCGAGCAGATCAAGGCCGGCAACCGATCTATCATCGGCCTGATGCT
GGAGTCTCACCTGAACGAGGGCTCTCAGTCTTCTGAGCAGCCCCGATCTGACATGCGA
TACGGCGTGTCTGTGACCGACGCCTGTATCTCTTGGGAGTCTACCGAGACCCTGCTGC
GATCTGTGCACCAGGACCTGTCTGCCGCCCGAGTGAAGCACTCTGGCGAGTAACGCGT

[00319] K: Chorismate lyase *E. carotovora* (optimized) (UbiC) 5'-

TTCTAGACACAAAAATGTCTGACGACGCCTCTACCCTGCTGCGAACCATCTCTTGGTT
CACCGAGCCCCCCTCTGTGCTGCCCGAGCACATCGGCGACTGGCTGATGGAGACCTCT
TCTATGACCCAGCGACTGGAGAAGTACTGTGCCCAGCTGCGAGTGACCCTGTGTCGAG
AGGGCTTCATCACCCCCCAGATGCTGGGCGAGGAGCGAGACCAGCTGCCCGCCGACG
AGCGATACTGGCTGCGAGAGGTGGTGCTGTACGGCGACGACCGACCCTGGCTGTTCG

GCCGAACCATCGTGCCCCAGCAGACCCTGGAGGGCTCTGGCGCCGCCCTGACCAAGA
TCGGCAACCAGCCCCTGGGGCGATACCTGTTCGAGCAGAAGTCTCTGACCCGAGACTA
CATCCACACCGGCTGTTGTGAGGGCCTGTGGGCCCGACGATCTCGACTGTGTCTGTCT
GGCCACCCCCTGCTGCTGACCGAGCTGTTCCTGCCCGAGTCTCCCGTGTACTACACCC
CCGGCGACGAGGGCTGGCAGGTGATCTAACGCGT

[00320] The above sequences are cleaved with *Mlu*I and *Xba*I. Sequence J is inserted into *Nhe*I- and *Mlu*I-cleaved pMB4603, and sequence K is inserted into *Nhe*I- and *Mlu*I-cleaved pMB4691, placing the genes under the control of the *Y. lipolytica TEF1* promoter, and adjacent to a functional *Y. lipolytica LEU2* (J) or *URA3* (K) gene. These plasmids are designated tef-aroF P148L (from sequence J) and tef-ubiC (from sequence K). They can be integrated sequentially, by cleavage of tef-aroF P148L with *Ssp*I and of tef-ubiC with *Sal*I, into the genome of *Y. lipolytica* strain ATCC201249 (*MATA ura3 leu2 lys8*), and screened for confirmation of homologous integration as well as for increased PHB and ubiquinone production.

Example 6: Production of CoQ10 in Yarrowia lipolytica strains harboring multiple exogenous ubiquinogenic pathway genes.

[00321] The PHB overproducing strain produced in Example 5 is mated with CoQ10-producing strains described in Example 1 or Example 2, and diploids are selected on minimal medium. Upon meiosis and sporulation, haploid recombinants may be selected that harbor all four heterologous genes: AroF P148L, ubiC, dpdpS, and phbPPt. Genotypes of selected segregants can be confirmed by Southern blotting and polymerase chain reaction (PCR) analysis. Furthermore, increased production of CoQ10 in the selected recombinants is assessed as described in prior examples. In addition, segregants can be chosen that also harbor an *ade1* auxotrophy to facilitate further manipulation.

Example 7. Decreasing carbon flow to the competing sterol pathway results in enhanced ubiquinone production.

[00322] In order to partially inactivate the *ERG9* gene encoding squalene synthase, the neighboring *FOL3* gene is disrupted, resulting in a folinic acid requirement. This strain is then transformed with a mutagenized fragment of DNA partially spanning the two genes, and Fol^+ transformants are screened for decreased squalene synthase activity.

[00323] The following oligonucleotides are synthesized:

5'-CCTTCTAGT**CGTACG**TAGTCAGC [L];

5'-CCACTGA**TCTAGA**ATCTCTTTCTGG [M].

[00324] They are used to amplify a 2.3 kb fragment from *Y. lipolytica* genomic DNA spanning most of the *FOL3* gene, using *Pfu* polymerase. The fragment is cleaved with *Xba*I and

phosphorylated, and ligated into pBluescriptSK⁻ (GenBank accession number X52330) that has been cleaved with *Kpn*I, treated with T4 DNA polymerase (T4pol) in the presence of dNTPs, and subsequently cleaved with *Xba*I. The resultant plasmid, designated BS-fol3, is then cleaved with *Acc*65I and *Eco*RI, treated with T4pol as above, and ligated to the 3.4 kb *Eco*RV-*Spe*I *ADE1* fragment (treated with T4pol) from pMB4529.

[00325] The resulting plasmid, pBSfol3Δade, can be cleaved with *Bsi*WI and *Xba*I to liberate a 5.5 kb fragment that is used to transform the *ade1* CoQ10-overproducing strains described above to adenine prototrophy. Ade^+ transformants are screened for a folinic acid requirement, and for homologous integration by PCR analysis.

[00326] Strains that harbor the resultant *fol3ΔADE1* allele can be transformed with a 3.5 kb DNA fragment generated by mutagenic PCR amplification using the primers:

5'-GGCTCATTGCGCATGCTAACATCG [N];

5'-CGACGATGCTATGAGCTTCTAGACG [P],

and *Y. lipolytica* genomic DNA as template. This fragment contains the N-terminal three-quarters of the *FOL3* ORF and the C-terminal nine-tenths of the *ERG9* ORF. Fol^+ Ade^- transformants are screened for decreased squalene synthase activity by sensitivity to agents such as zaragozic acid, itraconazole, or fluconazole, or by resistance to reactive oxygen species-generating agents such as antimycin.

[00327] In addition, the above fragment could be cloned, and altered in such a way as to remove the 3'-untranslated region of *ERG9*. Replacement of the *fol3ΔADE1* disruption by this fragment results in decreased expression of squalene synthase [Schuldiner et al. (2005), Cell 123:507–519][Muhlrad and Parker (1999), RNA 5:1299–1307], which can be confirmed as described above. This approach may also be used in a Fol^+ Ade^- strain, using the *ADE1* marker to disrupt the *ERG9* 3'-UTR.

[00328] Partially defective *ERG9* alleles can also be identified in *S. cerevisiae* using plasmid shuffling techniques [Boeke et al. (1987), Methods Enzymol. 154:164-175], and using drug sensitivities as a phenotype. Defective genes can be transferred to *Y. lipolytica* using standard molecular genetic techniques.

Example 8. Expression of a truncated form of HMG-CoA reductase to elevate CoQ10 production

[00329] In order to further increase CoQ10 production, carbon flow through the isoprenoid pathway is enhanced by introducing a truncated variant of the *Y. lipolytica* HMG-CoA reductase gene, which also encodes a 77 amino acid leader sequence derived from *S. cerevisiae* Hmg1.

[00330] The following oligonucleotides are synthesized:

5'-TTCTAGACACAAAAATGGCTGCAGACCAATTGGTGA [Q];

5'-CATTAATTCTTCTAAAGGACGTATTTTCTTATC [R];

5'-GTTCTCTGGACGACCTAGAGG [S];

5'-CACACACGCGTACACCTATGACCGTATGCAAAT [T].

Q and R are used to amplify a 0.23 kb fragment encoding Met-Ala followed by residues 530 to 604 of the Hmg1 protein of *S. cerevisiae*, using genomic DNA as template. S and T are used to amplify a 1.4 kb fragment encoding the C-terminal 448 residues of the Hmg1 protein of *Y. lipolytica*, using genomic DNA as template. These fragments are ligated to the appropriate cloning vector, and the resultant plasmids, designated pQR and pST, are verified by sequencing. The QR fragment is liberated with *Xba*I and *Ase*I, and the ST fragment is liberated with *Mae*I and *Mlu*I. These fragments are then ligated to the *ADE1 tef1*p expression vector pMB4629 cut with *Nhe*I and *Mlu*I.

[00331] The resulting plasmid, pTefHMG, can be cleaved with *Sna*BI, *Bbv*CI, or *Bsu*36I to direct integration at the *ade1* locus, or with *Bam*HI to direct integration at the *HMG1* locus, of the CoQ10-producing strains described above, restoring them to adenine prototrophy. Ade^+ transformants are screened for increased CoQ10 production.

[00332] Alternatively, the native *HMG1* gene from *Y. lipolytica* may be modified through truncation, and without *S. cerevisiae* sequences, by amplifying *Y. lipolytica* genomic DNA with primer T above and

[00333] T2 5'-CACACTCTAGACACAAAAATGACCCAGTCTGTGAAGGTGG

[00334] yielding a 1.5 kb fragment that is cleaved with *Xba*I and *Mlu*I and ligated to pMB4629 cut with *Nhe*I and *Mlu*I to create pMB4637. pMB4637 may be cut with *Sna*BI, *Bsu*36I, or *Bbv*CI to direct integration at the *ade1* locus, or with *Bam*HI to direct integration at the *HMG1* locus, of the CoQ10-producing strains described above, restoring them to adenine prototrophy. Ade^+ transformants are screened for increased CoQ10 production.

Example 9: Constructing an oleaginous strain of Saccharomyces cerevisiae

[00335] Genes encoding the two subunits of ATP-citrate lyase from *N. crassa*, the AMP deaminase from *Saccharomyces cerevisiae*, and the cytosolic malic enzyme from *M. circinelloides* are overexpressed in *S. cereviseae* strains in order to increase the total lipid content. Similar approaches to enhance lipid production could be employed in other host organisms such as *Xanthophyllomyces dendrorhous* (*Phaffia rhodozyma*), using the same, homologous, or functionally similar oleaginic polypeptides.

[00336] Qiagen RNAEasy kits (Qiagen, Valencia, CA.) are used to prepare messenger RNA from lyophilized biomass prepared from cultures of *N. crassa*. Subsequently, RT-PCR is performed in two reactions containing the mRNA template and either of the following primer pairs.

acl1: 1fwd: 5' CACACGGATCCTATAatgccttccgcaacgaccg

1rev: 5' CACACACTAGttaaatttggacctcaacacgaccc

acl2: 2fwd: 5' CACACGGATCCAATATAAatgtctgcgaagagcatcctcg

2rev: 5' CACACGCATGCttaagcttggaactccaccgcac

[00337] The resulting fragment from the acl1 reaction is cleaved with *Spe*I and *Bam*HI, and that from the acl2 reaction is cleaved with *Bam*HI and *Sph*I, and both are ligated together into YEp24 that has been digested with *Nhe*I and *Sph*I, creating the plasmid **"p12"**. The bi-directional *GAL1-10* promoter is amplified from *S. cerevisiae* genomic DNA using the primers.

gal10: 5' CACACGGATCCaattttcaaaaattcttacttttttttggatggac

gal1: 5' CACACGGATCCtttttctccttgacgttaaagtatagagg,

and the resulting 0.67 kb fragment is cleaved with *Bam*HI and ligated in either orientation to *Bam*HI-digested **"p12"** to create **"p1gal2"** and **"p2gal1"**, containing *GAL1-acl1/GAL10-acl2* and *GAL10-acl1/GAL1-acl2*, respectively (Genbank accession: *acl1*: CAB91740.2; *acl2*: CAB91741.2).

[00338] In order to amplify the *S. cereviseae* gene encoding AMP deaminase and a promoter suitable for expressing this gene, *S. cerevisiae* genomic DNA is amplified using two primer pairs in separate reactions:

AMD1 ORF:

AMD1FWD: 5' CACACGAGCTCAAAAatggacaatcaggctacacagag

AMD1rev: 5' CACACCCTAGGtcacttttcttcaatggttctcttgaaattg

GAL7p:

gal7prox: 5' CACACGAGCTCggaatattcaactgttttttttatcatgttgatg

gal7dist: 5' CACACGGAtccttcttgaaaatatgcactctatatcttttag,

The resulting fragment from the AMD1 reaction (2.4 kb) is cleaved with *Sac*I and *Avr*II, and that from the GAL7 reaction (0.7 kb) is cleaved with *Bam*HI and *Sph*I, and both are ligated together into YEp13 that has been digested with *Nhe*I and *Bam*HI, creating the plasmid **"pAMPD"**. This plasmid carries the *S. cerevisiae* gene, *AMD1*, encoding AMP deaminase, under the control of the galactose-inducible *GAL7* promoter.

[00339] Messenger RNA is prepared from lyophilized biomass of *M. circinelloides*, as described above, and the mRNA template is used in a RT-PCR reaction with two primers:

MAEfwd: 5' CACACGCTAGCTACAAAatgttgtcactcaaacgcatagcaac

MAErev: 5' CACACGTCGACttaatgatctcggtatacgagaggaac,

and the resulting fragment is cleaved with *Nhe*I and *Sal*I, and ligated to *Xba*I- and *Xho*I-digested pRS413TEF (Mumberg, D. et al. (1995) Gene, 156:119-122), creating the plasmid **"pTEFMAE"**, which contains sequences encoding the cytosolic $NADP^+$-dependant malic enzyme from *M. circinelloides* (E.C. 1.1.1.40; *mce* gene; Genbank accession: AY209191) under the control of the constitutive *TEF1* promoter.

[00340] The plasmids **"p1gal2"**, **"pAMPD"**, and **"pTEFMAE"** are sequentially transformed into a strain of *S. cereviseae* to restore prototrophy for uracil ("p1gal2"), leucine ("pAMPD"), and histidine ("pTEFMAE") (Guthrie and Fink *Methods in Enzymology* 194:1-933, 1991). The resulting transformants are tested for total lipid content following shake flask testing (e.g., 20 ml cultures in 125 ml flasks grown at 30°C for 72-96 hour cultures) in either synthetic complete (SC) medium lacking uracil, leucine and histidine or in a 2-step fermentation process. In the 2-step process, 1.5 ml of cells from an overnight 2 ml roll tube culture containing SC medium lacking uracil, leucine and histidine are centrifuged, washed in distilled water, and resuspended in 20 ml of a nitrogen-limiting medium suitable for lipid accumulation (30 g/L glucose, 1.5 g/L yeast extract, 0.5 g/L NH_4Cl, 7 g/L KH_2PO_4, 5 g/L Na_2HPO_4-$12H_2O$, 1.5 g/L $MgSO_4$-$7H_2O$, 0.08 g/L $FeCl_3$-$6H_2O$, 0.01 g/L $ZnSO_4$-$7H_2O$, 0.1 g/L $CaCl_2$-$2H_2O$, 0.1 mg/L $MnSO_4$-$5H_2O$, 0.1 mg/L $CuSO_4$-$5H_2O$, 0.1 mg/L $Co(NO_3)_2$-$6H_2O$; pH 5.5 (J Am Oil Chem Soc 70:891-894 (1993)).

[00341] Intracellular lipid content of the modified and control *S. cerevisiae* strains is analyzed using the fluorescent probe, Nile Red (J Microbiol Meth (2004) 56:331-338). In brief, cells diluted in buffer are stained with Nile Red, excited at 488 nm, and the fluorescent emission spectra in the wavelength region of 400-700 nm are acquired and compared to the corresponding spectra from cells not stained with Nile Red. To confirm results from the rapid estimation method, the total lipid content is determined by gas chromatographic analysis of the total fatty acids directly transmethylesterified from dried cells, as described (Appl Microbiol Biotechnol. 2002 Nov;60(3):275-80). Yeast strains expressing multiple oleaginic polypeptides produce elevated total lipid (for example, in the range of 17% and 25% dry cell weight basis) following growth in YPD and lipid accumulation medium when compared to non-transformed *S. cerevisiae* strains which may, for example, produce in the range of 6% and 10% total lipid after growth in YPD and lipid accumulation medium.

Example 10: Y. lipolytica oleaginic and isoprenoid biosynthesis genes

[00342] Figure 11 is a list of *Y. lipolytica* genes representing various polypeptides (e.g. oleaginic and isoprenoid biosynthesis peptides) useful in the fungal strains and methods described herein. The Genbank accession number and GI number is given for each polypeptide in addition to oligo pairs which can be used to amplify the coding region for each gene from *Y. lipolytica* genomic DNA or cDNA. Resulting PCR fragments can be cleaved with restriction enzyme pairs (e.g. depending on what site is present within the oligo sequence, XbaI/MluI or NheI/MluI or XbaI/AscI or NheI/AscI) and inserted into expression vectors (e.g. fungal expression vectors including *Y. lipolytica* expression vectors such as MB4629 and MB4691 described herein).

[00343] The DNA and proteins they encode of the *Y. lipolytica* genes represented in Figure 11 are as follows (intron sequence is underlined):

YALI0F30481g
DNA:
atgtcgcaaccccagaacgttggaatcaaagccctcgagatctacgtgccttctcgaattgtcaaccaggctgagctcgagaagcacgacggt
gtcgctgctggcaagtacaccattggtcttggtcagaccaacatggcctttgtcgacgacagagaggacatctattcctttgccctgaccgccgt
ctctcgactgctcaagaacaacaacatcgaccctgcatctattggtcgaatcgaggttggtactgaaacccttctggacaagtccaagtccgtca
agtctgtgctcatgcagctctttggcgagaacagcaacattgagggtgtggacaacgtcaacgcctgctacggaggaaccaacgccctgttca
acgctatcaactgggttgagggtcgatcttgggacggccgaaacgccatcgtcgttgccggtgacattgccctctacgcaaagggcgctgcc
cgacccaccggaggtgccggctgtgttgccatgctcattggccccgacgctcccctggttcttgacaacgtccacggatcttacttcgagcatg
cctacgatttctacaagcctgatctgacctccgagtacccctatgttgatggccactactccctgacctgttacacaaaggccctcgacaaggcc
tacgctgcctacaacgccccgagccgagaaggtcggtctgttcaaggactccgacaagaagggtgctgaccgatttgactactctgccttccac
gtgcccacctgcaagcttgtcaccaagtcttacgctcgacttctctacaacgactacctcaacgacaagagcctgtacgagggccaggtcccc
gaggaggttgctgccgtctcctacgatgcctctctcaccgacaagaccgtcgagaagaccttccttggtattgccaaggctcagtccgccgag
cgaatggctccttctctccagggacccaccaacaccggtaacatgtacaccgcctctgtgtacgcttctctcatctctctgctgacttttgtcccg
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atggtgacatgcagcttatctgcgaggcttacgacctcatgaagcgaggtgctggtttcaccaatgaggagattggagacgttttcgccaagtg
gaacaacggtatcctcgactccttcctcattgagatcacccgagacatcttcaagtacgacgacggctctggaactcctctcgttgagaagatct
ccgacactgctggccagaagggtactggaaagtggaccgctatcaacgctcttgaccttggtatgcccgtcaccctgatcggtgaggccgtct
tcgctcgatgcctttctgccctcaagcaggagcgtgtccgagcttccaaggttcttgatggccccgagcccgtcaagttcactggtgacaagaa
ggagtttgtcgaccagctcgagcaggccctttacgcctccaagatcatctcttacgcccagggtttcatgcttatccgagaggccgccaagacc
tacggctgggagctcaacaacgccggtattgccctcatgtggcgaggtggttgcatcatccgatccgtcttccttgctgacatcaccaaggctta
ccgacaggaccccaacctcgagaacctgctgttcaacgacttcttcaagaacgccatctccaaggccaaccccctcttggcgagctaccgtggc
caaggctgtcacctggggtgttcccactcccgcctttgcctcggctctggctttctacgacggttaccgatctgccaagctccccgctaacctgct
ccaggcccagcgagactacttcggcgcccacacctaccagctcctcgatggtgatggaaagtggatccacaccaactggaccggccgaggt
ggtgaggtttcttcttccacttacgatgcttaa
Protein:
mtdtsnikpvadialiglavmgqnlilnmadhgyevvaynrttskvdhfleneakgksiigahsikelcallkrprriillvkagaavdsfie
qllpyldkgdiiidggnshfpdsnrryeelnekgilfvgsgvsggeegarygpsimpggnkeawphikkifqdisakadgepccdwvg
dagaghfvkmvhngieygdmqliceaydlmkrgagftneeigdvfakwnngildsflieitrdifkyddgsgtplvekisdtagqkgtg
kwtainaldlgmpvtligeavfarclsalkqervraskvldgpepvkftgdkkefvdqleqalyaskiisyaqgfmlireaaktygwelnn
agialmwrggciirsvfladitkayrqdpnlenllfndffknaiskanpswratvakavtwgvptpafasalafydgyrsaklpanllqaqr
dyfgahtyqlldgdgkwihtnwtgrggevssstyda

YALI0D06303g
DNA:

atgctcaaccttagaaccgcccttcgagctgtgcgacccgtcactctggtgagtatctcggagcccgggacggctaccaacacacaagcaag
atgcaacagaaaccggacttttaaatgcggattgcggaaaatttgcatggcggcaacgactcggagaaggagcgggacaattgcaatggca
ggatgccattgacgaactgagggtgatgagagaccgggcctccgatgacgtggtggtgacgacagcccggctggtgttgccgggactgtct
ctgaaaagcaatttctctatctccggtctcaacagactccccttctctagctcaattggcattgtcttcagaaggtgtcttagtggtatccccattgtta
tcttcttttccccaatgtcaatgtcaatgtcaatggctccgacctctttcacattaacacggcgcaaacacagataccacggaaccgactcaaaca
aatccaaagagacgcagcggaataattggcatcaacgaacgatttgggatactctggcgagaatgccgaaatatttcgcttgtcttgttgtttctct
tgagtgagttgtttgtgaagtcgtttggaagaaggttcccaatgtcacaaaccataccaactcgttacagccagcttgtaatcccccacctcttcaa
tacatactaacgcagacccgatcctacgccacttccgtggcctctttcaccggccagaagaactccaacggcaagtacactgtgtctctgattga
gggagacggtatcggaaccgagatctccaaggctgtcaaggacatctaccatgccgccaaggtccccatcgactgggaggttgtcgacgtc
acccccactctggtcaacggcaagaccaccatccccgacagcgccattgagtccatcaaccgaaacaaggttgccctcaagggtcccctcgc
caccccatcggtaagggccacgtttccatgaacctgactctgcgacgaaccttcaacctgttcgccaacgtccgaccttgcaagtccgtcgtg
ggctacaagacccttacgagaacgtcgacaccctgctcatccgagagaacactgagggtgagtactccggtatcgagcacaccgtcgtccc
cggtgtcgttcagtccatcaagctgatcacccgagaggcttccgagcgagtcatccggtacgcttacgagtacgccctgtcccgaggcatgaa
gaaggtccttgttgtccacaaggcctctattatgaaggtctccgatggtcttttccttgaggttgctcgagagctcgccaaggagtacccctccatt
gacctttccgtcgagctgatcgacaacacctgtctgcgaatggtccaggacccgctctctaccgagatgtcgtcatggtcatgcccaaccttta
cggtgacattctgtccgatcttgcctccggtcttatcggtggtcttggtctgacccctccggtaacatgggtgacgaggtctccatcttcgaggc
cgtccacggatccgctcccgacattgctggcaagggtcttgctaaccccactgctctgctgctctcctccgtgatgatgctgcgacacatgggtc
tcaacgacaacgccaccaacatcgagcaggccgtctttggcaccattgcttccggccccgagaaccgaaccaaggatcttaagggtaccgcc
accacttctcactttgctgagcagattatcaagcgactcaagtag
Protein:
mlnlrtalravrpvtltrsyatsvasftgqknsngkytvsliegdgigteiskavkdiyhaakvpidwevvdvtptlvngkttipdsaiesinr
nkvalkgplatpigkghvsmnltlrrtfnlfanvrpcksvvgyktpyenvdtllirentegeysgiehtvvpgvvqsiklitreaserviryay
eyalsrgmkkvlvvhkasimkvsdglflevarelakeypsidlsvelidntclrmvqdpalyrdvvmvmpnlygdilsdlasgligglglt
psgnmgdevsifeavhgsapdiagkglanptalllssvmmlrhmglndnatnieqavfgtiasgpenrtkdlkgtattshfaeqiikrlk

Example 11: Regulatory Sequences

[00344] Sequences which consist of, consist essentially of, or comprise the following regulatory sequences (e.g. promoters and terminator sequences, including functional fragments thereof) may be useful to control expression of endogenous and heterologous genes in recombinant fungi described herein.

Met2 promoter

5'cctctcactttgtgaatcgtgaaacatgaatcttcaagccaagaatgttaggcaggggaagctttctttcagacttttggaattggtcctcttttg
gacattattgacgatattattattttttccccgtccaatgttgacccttgtaagccattccggttctggagcgcatctcgtctgaaggagtcttcgtgtg
gctataactacaagcgttgtatggtggatcctatgaccgtctatatagggcaacttttgctcttgttcttcccccctccttgagggacgtatggcaatg
gctatgacaactatcgtagtgagcctctataacccattgaagtacaagtcctccaccttgctgccaaactcgcgagaaaaaaagtccaccaactc
cgccgggaaatactggagaacacctctaagacgtgggcttctgcacctgtgtggcttgggtctgggttttgcgagctctgagccacaacctaag
gacggtgtgattgggagataagtagtcgttggttttctaatcgcacgtgatatgcaagccacacttataacacaatgaagacaggccgatgaact
gcatgtcattgtacaggtgcggagagcaagaaactctggggcggaggtgaaagatgagacaaaaagcctcaggtgcaaggtagggagttg
atcaacgtcaaacacaaataatctaggttgttaggcagctaaacatgtatataactgggctgccaccgagtgttacttgtcattaacgtcgcattttc
gcctacacaaaatttgggttactcgccactacactgctcaaatctttcagctgtgcaacaagctttcaggtcacacatagactcgcataaggaccc
gggtcatctgttattctccactggtaaaccaatagtcctagctgatttgggtacagaagctcactttcacatcttttcatcttcttctacaaccatc

Met3 promoter

5'atctgtgaggagcccctggcgtcactgtcgactgtgccggcatttctgatggtatttccagccccgcagttctcgagacccccgaacaaatgt
gccacacccttgccaaaatgacgaatacacggcgtcgcggccgggaatcgaactcttggcaccgccacaggagtgaaatttgaaatttgaaa
tttgaaaaataattcacattttgagtttcaataatatatcgatgaccctcccaaaagacccaagtcgagacgcaaaaaaacacccagacgacatg
gatgcggtcacgtgaccgcaaaaaccgccccggaaatccgtttgtgacgtgttcaattccatctctatgtttttctgcggtttctacgatgccgcaa
tggtggccaatgtgcgtttcactgccgtagtggctggaacaagccacaggggtcgtcgggccaatcagacggtccctgacatggttctgcg
ccctaacccgggaactctaacccccgtggtggcgcaatcgctgtcttcatgtgctttatctcacgtgacggctggaatctggcagaagacggag
tatgtacattttgtcgttggtcacgttatccctaaaacgtggtgtttaaactggtcgaatgcttggcccagaacacaagaagaaaaaaacgagaca
acttgatcagtttcaacgccacagcaagcttgtcttcactgtggttggtcttctccacgccacaagcaacacgtacatgtcaattacgtcagggtct
tttaagttctgtggcttttgaaccagttataaagaaccaaccacccttttttcaaagctaatcaagacggggaaatttttttttgatatttttcgaca

Met6 promoter

5'gatactgcagacggtgcattacttacccgtgtcgactgagagtctacttggtacttggccctgtggctaagcagtatttgagcaacaatgcaat
gcagttgctgactcggttccagatccccttgccccgatgtgtggaagcgttgtttttggggcaagggcatgtgggggctgcatcatactgtggct
ggggccgttggaagagccgtcggcagcgagcctgagtcgcttctcggggccttattccccccgcctctaggtcagcggcggccgaagtgtc
gtactcagctcgcctgtacagtatgacgtgaccgaatagcctctggaaggttggagaagtacagtgcaaaaaaaagttgcaaaatttcattttag
cgttcgatccgacgtggcagttggacaatgaatcgatggagacatgatcatgggcagaaatagaaggtctccatgttcaatggcagtaccaatt
gagcaacagacgggtcgacaggcggcgggcacaccatccgccctccacatggcgcaatcgtcagtgcagcgattcgtactcggattgcatc
atgttgcaccgaaagttggggcccgcacgttggagaggcgaggagccagggttagctttggtggggtcctttgttgtcacgtggcatcagcga
atggcgtcctccaatcagggccgtcagcgaagtcggcgtgtgatagtgcgtggggagcgaatagagtttctgggggggggcggcccaaaa
cgtgaaatccgagtacgcatgtagagtgtaaattgggtgtatagtgacattgtttgactctgaccctgagagtaatatataatgtgtacgtgtcccc
ctccgttggtcttctttttttctcctttctcctaaccaacacccaaactaatcaatc

Met25 promoter

5'aagtcgtattaacataactttccttacatttttttaaagcacgtcactatccacgtgacctagccacgcgataccaagtattcatccataatgacac
actcatgacgtccggaggacgtcatcatcgtccagtcacgtgccaaggcacatgactaatcataacaccttatgactagcttctgaatcgctaca
cagttccaattcgcaaataaactcgaaatgacgaaatgccataataaaaatgacgaaactcgagattgagagcagcacatgcactgaagtggt
ggacaaccagcgtatccggagacacgacggatccagcaccatggaagctggccgaaaaagagatccccagcacattgagcaaccaagtc
agctcaattgagtaacatcacacactcagatcgagtctgatggtggtccccttttgttccttcacttgaaaaataattgaaaataacaataacaataa
aaataaaaacaaaataaaaataaaaataaaaataaaaataaaaaaaataaaaaaaccttgccgcatttagcgtcagccacccccgcattgacct
gagtacgttggattgaccccgatcctgcacgtcgagcgtggtcggccaaaaagcgcccgtggctggtgagtcagaaatagcagggttgcaa
gagagagctgcgcaacgagcaataaacggtgtttttttcgcttctgtgctgcttagagtggagagccgaccctcgccatgctcacgtgaccattc
acgtggttgcaaactccaccttagtatagccgtgtccctctcgctacccattatcgcatcgtactccagccacatttttttgttccccgctaaatccg
gaaccttatctgggtcacgtgaaattgcaatctcgacaggaggttatacttatagagtgagacactccacgcaaggtgttgcaagtcaattgaca
ccacctcacctcagactaacatccaca

Pox2 promoter

5'gaatctgccccacattttatctccgcttttgactgtttttctcccccctttcacactctgcttttggctacataaaccccgcaccgtttggaactctg
ttggtccggggaagccgccgttaggtgtgtcagatggagagcgccagacgagcagaaccgagggacagcggatcgggggagggctgtca
cgtgacgaagggcactgttgacgtggtgaatgtcgcccgttctcacgtgacccgtctcctctatatgtgtatccgcctctttgtttggttttttttctgc
ttccccccccccccccccacccccaatcacatgctcagaaagtagacatctgcatcgtcctgcatgccatcccacaagacgaacaagtgatagg
ccgagagccgaggacgaggtggagtgcacaaggggtaggcgaatggtacgattccgccaagtgagactggcgatcgggagaagggttgg
tggtcatgggggatagaatttgtacaagtggaaaaaccactacgagtagcggatttgataccacaagtagcagagatatacagcaatggtggg
agtgcaagtatcggaatgtactgtacctcctgtactcgtactcgtacggcactcgtagaaacggggcaatacgggggagaagcgatcgcccgt
ctgttcaatcgccacaagtccgagtaatgctcgagtatcgaagtcttgtacctccctgtcaatcatggcaccactggtcttgacttgtctattcatac
tggacaagcgccagagttaagcttgtagcgaatttcgccctcggacatcaccccatacgacggacacacatgcccgacaaacagcctctctta
ttgtagctgaaagtatattgaatgtgaacgtgtacaatatcaggtaccagcgggaggttacggccaaggtgataccggaataaccctggcttgg
agatggtcggtccattgtactgaagtgtccgtgtcgtttccgtcactgccccaattggacatgtttgtttttccgatctttcgggcgccctctccttgt
ctccttgtctgtctcctggactgttgctaccccatttctttggcctccattggttcctccccgtctttcacgtcgtctatggttgcatggtttcccttatac
ttttccccacagtcacatgttatggaggggtctagatggaggcctaattttgacgtgcaaggggcgaattggggcgagaaacacgtcgtggac
atggtgcaaggcccgcagggttgattcgacgcttttccgcgaaaaaaacaagtccaaatacccccgtttattctccctcggctctcggtatttcac
atgaaaactataacctagactacacgggcaaccttaaccccagagtatacttatataccaaagggatgggtcctcaaaaatcacacaagcaac
g

Yef3 (YALI0E13277g) promoter

5'cgccattcggttccttccagaccattccagatcaatccacctcttcttatctcaggtgggtgtgctgacatcagaccccgtagcccttctcccag
tggcgaacagcaggcataaaacagggccattgagcagagcaaacaaggtcggtgaaatcgtcgaaaaagtcggaaaacggttgcaagaaa
ttggagcgtcacctgccaccctccaggctctatataaagcattgccccaattgctaacgcttcatatttacacctttggcaccccagtccatccctc
caataaaatgtactacatgggacacaacaagagaggatgcgcgcccaaaccctaacctagcacatgcacgatgattctctttgtctgtgaaaaa
atttttccaccaaaatttccccattgggatgaaaccctaaccgcaaccaaaagtttttaactatcatcttgtacgtcacggtttccgattcttctcttctc
tttcatcatcatcacttgtgacc

Cam1 (YALI0C24420g) promoter

5'aactaccataaagtaccgagaaatataggcaattgtacaaattgtccacctccttcacttacattaccgaaccatggccatatcaccaaaatac
cccgagtgctaaaacacctccctccaaatgttctcttaccttccaccgaaaaccgatcttattatcccaacgcttgttgtggcttgacgcgccgca
cccgctgggcttgccatttcgataccaatccaagaggaaaagctcatgagaaacaatcggaatatcacgagaacggcctggcgaaccaaca
ggatatttttgaatataattacccctcgaatctagtcatatctatgtctactgtagacttgggcggcatcatgatgtacattatttttagcgtctggaacc
ctaaagttcacgtacaatcatgtgacaaacgaggctaaaaaatgtcaatttcgtatattagtgttattacgtggctcacatttccgaatcatctacca
ccccccacctaaaaa

YALI0D16467g promoter

5'ttttttaattttcatatttatttttcatatttatttttcatttatttattcatgtatttatttattacttttttaagtattttaaactcctcactaaaccgt
cgattgcacaatattaaccttcattacacctgcagcgtggttttttgtggtcgttagccgaagtcttccaacgtgggtataagtaggaacaattgggc
cgatttttttgagccgtctaaatctctcgactcaattgatctgctgtcgaaaatccggctctctagctccttttccccgtccgctggagctcctcttcatt

gtgccgtttttccaacatttaactttgccacccaccaccacccccactaccatcacccactcgatctctgttcgtgtcaccacgactttgtcttctcac
acatactctgtttgtgcaccacacattgcgaa

Tef4 (YALI0B12562g) promoter

5'gctacaatagctttattggccctattgagcacgctacaattcggtccagtatgtacaacgtctatgcgcactaacggccatacagtgagttaca
gcacacccaaaagtaaccctgcctgacctgtctgcctgagacaggaagattaactcttgtagtgaccgagctcgataagactcaagccacaca
attttttttatagccttgcttcaagagtcgccaaaatgacattacacaactccacggaccgtcggttccatgtccacacccttggatgggtaagcgct
ccacgcacgtaccacgtgcattgagtttaaccacaaacataggtctgtgtcccagagttaccctgctgcatcagccaagtcttgaaagcaaaatt
tcttgcacaatttttcctcttcttttcttcactgatcgcagtccaaacacaaaca

YALI0D12903g promoter

5'gcgctctgatccacttgtatggctccaagttcagtgtaccaagtagttggtgatgcagggagggatgtctctatccaccaataatgaactcatg
ggcgaaattgtttctgttaaacactccaactgtcgttttaaatctcattctctttgcatttggactccattcgcttccgttgggccaatataatccatcgt
aacgtactttagatggaaatttagttacctgctacttgtctcaacaccccaacaggggctgttcgacagaggtaatagagcgtcaatgggttaata
aaaacacactgtcgattttcactcattgtctttatgatattacctgttttccgctgttatcaatgccgagcatcgtgttatatcttccaccccaactacttg
catttacttaactattacctcaactatttacaccccgaattgttacctcccaataagtaactttatttcaaccaatgggacgagagcatctctgagaac
atcgatctatctctgtcaatattgcccagaatcgttcgaaaaaaaacaccaaaaggtttacagcgccattataaatataaattcgttgtcaattcccc
cgcaatgtctgttgaaatctcattttgagaccttccaacattaccctctctcccgtctggtcacatgacgtgactgcttcttcccaaaacgaacactc
ccaactcttcccccccgtcagtgaaaagtatacatccgacctccaaatcttttcttcactcaac

Tef1 (YALI0C09141g) promoter

5'agagacgggttggcggcgtatttgtgtcccaaaaaacagccccaattgccccaattgaccccaaattgacccagtagcgggcccaaccccc
ggcgagagccccccttcaccccacatatcaaacctcccccggttcccacacttgccgttaagggcgtagggtactgcagtctggaatctacgctt
gttcagactttgtactagtttctttgtctggccatccgggtaacccatgccggacgcaaaatagactactgaaaatttttttgctttgtggttgggactt
tagccaagggtataaaagaccaccgtccccgaattacctttcctcttctttttctctctctccttgtcaactcacacccgaaatcgttaagcatttccttc
tgagtataagaatcattc

Fba1 (YALI0E26004g) promoter

5'gctgcgctgatctggacaccacagaggttccgagcactttaggttgcaccaaatgtcccaccaggtgcaggcagaaaacgctggaacagc
gtgtacagtttgtcttagcaaaaagtgaaggcgctgaggtcgagcagggtggtgtgacttgttatagcctttagagctgcgaaagcgcgtatgg
atttggctcatcaggccagattgagggtctgtggacacatgtcatgttagtgtacttcaatcgccccctggatatagccccgacaataggccgtg
gcctcatttttttgccttccgcacatttccattgctcggtacccacaccttgcttctcctgcacttgccaacccttaatactggtttacattgaccaacatc
ttacaagcgggggggcttgtctagggtatatataaacagtggctctcccaatcggttgccagtctcttttttcctttctttccccacagattcgaaatct
aaactacacatc

Pox2 terminator:

5'gatgaggaatagacaagcgggtatttattgtatgaataaagattatgtattgattgcaaaaaagtgcatttgtagatgtggtttattgtagagagt
acggtatgtactgtacgaacattaggagctacttctacaagtagattttcttaacaagggtgaaatttactaggaagtacatgcatatttcgttagta
gaatcacaaaagaaatgtacaagcacgtactacttgtactccacaatgtggagtgggagcaaaaaaattggacgacaccggaatcgaaccgg
ggacctcgcgcatgctaagcgcatgtgataaccaactacaccagacgcccaagaactttcttggtgattatggaatacgtggtctgctatatctc
aattttgctgtaatgaatcattagaattaaaaaaaaaaccccatttttgtgtgattgtcggccaagagatggaacaggaagaatacgtgaacaagc
gagcacgaatgccatatgctcttctgaacaaccgagtccgaatccgatttgtgggtatcacatgtctcaagtagctgaaatgtatttcgctagaat
aaaataaatgagattaagaattaaaaatattggaatatattttcctagaatagaaactttggatttttttttcggctattacagtctgaactggacaaacg
gctgactatatataaatattattgggtctgttttcttgtttatgtcgaaattatctgggttttactactgtgtcgtcgagtatagagtggcctgactggag
aaaatgcagtagtatggacagtaggtactgccagccagagaagttttttggaattgatacttgagtcatttttccattccccattccccattccaacac
aatcaactgtttctgaacattttccaaaacgcggagatgtatgtcacttggcactgcaagtctcgattcaaaatgcatctctttcagaccaaagtgtc
atcagctttgtttggccccaaattaccgcaaatacttgtcgaaattgaagtgcaatacggcctcgtctgccatgaaacctgcctattctcttcaaatt
ggcgtcaggtttcacgtccagcattcctcgcccagacagagttgctatggttgaatcgtgtactgttaatatatgtatgtattatactcgtactacgat
atactgttcaatagagtctcttataatcgtacgacgattctgggca

Example 12: Cultures conditions, such as limitation for nitrogen, magnesium or phosphate, can promote lipid accumulation in Y. lipolytica.

12a. Strains used to analyze lipid accumulation during growth under various conditions.

[00345] Strains MF760, MF858, and MF921 were grown under an array of culture conditions, and then harvested cells were extracted and analyzed for total lipid content and levels of specific lipophilic metabolites. Figure 12 depicts schematic representations of certain plasmids generated and described in this example. Strain MF760 has genotype MATB ura2::URA2/tef-GGS1 ChrA-1635618::tef-carB ura3-302 ade1::?ADE1/tef-HMG1trunc leu2::?LEU2/tef-carRP (questions marks denote presumed loci of chromosomal integration). Strain MF760 harbors four insertion plasmids, pMB4637, pMB4591, pMB4705, and pMB4660, which encode native or heterologous genes required for synthesis of either isoprenoid metabolites in general, or carotenoid metabolites specifically. In all insertion plasmids, except pMB4789, described in this example, the *Y. lipolytica* TEF1 promoter and XPR2 terminator were the regulatory sequences used to control expression of genes of interest. Also, in some instances multiple URA3-containing plasmids can be utilized in the same strain, since 5-fluoroorotic acid can be used to select for Ura$^-$ segregants following transformation with a URA3 plasmid. pMB4637 is an ADE1 plasmid that encodes a truncated variant of the Y. lipolytica HMG-CoA reductase. pMB4591 is a URA5 plasmid that encodes the Y. lipolytica geranylgeranylpyrophosphate synthase. pMB4705 is a LEU2 plasmid that encodes the phytoene synthase/lycopene cyclase (CarRP) from *Mucor circinelloides*. pMB4660 is a URA3 plasmid that encodes a phytoene dehydrogenase from *M. circinelloides*.

[00346] Strain MF858 has genotype MATB ura2::URA2/tef-GGS1 ChrA-1635618::tef-carB ura3-302::?URA3/tef-plasmid ade1::?ADE1/tef-HMG1trunc leu2::?LEU2/tef-carRP. Strain

MF858 harbors the same four plasmids as MF760, and an addition control plasmid (pMB4691), which is a URA3 plasmid that contains regulatory sequences but no gene of interest.

[00347] Strain MF921 has genotype MATB erg9-3'UTR::URA3 ura2::URA2/tef-GGS1 ChrA-1635618::tef-carB ura3-302 ade1::?ADE1/tef-HMG1trunc leu2::?LEU2/tef-carRP. Strain MF921 harbors the same four plasmids as MF760, and an addition URA3 plasmid, pMB4789, which contains sequences for insertion into the 3' UTR of the native ERG9. Insertion into 3' UTR of ERG9 is presumed to result in a hypomorphic mutation to decrease squalene synthase activity.

12b. Lipid accumulation in media containing various carbon:nitrogen ratios

[00348] Shake flask testing was conducted using carbon to nitrogen (C/N) ratios of 160, 80, 60, 40, 30, 20, and 10 with yeast nitrogen base being the base medium providing vitamins, trace elements and salts. Ammonium sulfate (which contains 21% nitrogen) was used as the nitrogen source and glucose (which contains 40% carbon) was used as the carbon source at a concentration of 30 g/L. The concentrations of ammonium sulfate corresponding to these ratios are: 0.36, 0.71, 0.95, 1.43, 1.91, 2.86, and 4.6 g/L, respectively. Uracil was supplemented at 0.2mM. As controls, strains were also grown in yeast extract-peptone with 50 g/L of glucose (media in which lipids do not accumulate at high levels) and yeast extract-peptone with 5% olive oil (v/v) (media in which lipids accumulate at high levels). Strain MF760 (10- 14 ml of culture) was harvested after 4 days of growth at 30°C, during which time the cultures were shaking at 250 rpm. Following harvesting, cells were washed three times with water, with the exception of the oil-grown cells which were washed three times in 0.5% BSA and one time with water before lipid extractions. Lipids were extracted as described in Folch J, Lees, M, and Stanley, G.H.S. *J. Biol. Chem.* 226: 497-509, 1957. In brief, cell pellets were resuspended in 6 ml of water. A 1 ml aliquot was transferred to a pre-weighed tube with a hole on the lid, spun down and the cell pellet lyophilized overnight to determine the dry cell weight. The remaining 5 ml were placed in a 15 ml Falcon tube and spun down. Cell pellets were frozen at -20°C until extractions were performed. Two to three volumes of a Zymolyase solution (2 mg/ml Zymolyase 100T in 1M Sorbitol, 50 mM EDTA and 0.01% β-mercaptoethanol) was added to each cell pellet and placed at 37°C with constant agiatation for 1 hr. Two volumes of cubic zirconia beads were added to each tube and vortexed for 15-20 min. Samples were viewed under a microscope to ensure cell breakage before continuing with extractions. After cell breakage was complete, 6 ml of extraction solvent was added (a 2:1 mix of chloroform and methanol) and mixed. The mixture was spun down for 5 min at 3000 rpm and the organic layer was transferred to a clean tube. NaCl was added to the remaining aqueous layer to make it a 0.29% NaCl solution. 6 ml of extraction solvent was added and mixed, and the mixture was spun down for 5 min. The organic layers were pooled and filtered through a 0.2 μm filter to get rid of any cell debris. The extract was washed with 0.2 volumes of

0.29 % NaCl solution and another 6 ml of extraction solvent added and mixed. Mixtures were spun and the organic layer was placed in a pre-weighed glass vial, the solvent was evaporated under a flow on nitrogen and the vial was weighed again to determine the weight of the lipid extracted. The dry cell weight is used to determine the percentage of lipid per dry cell weight. The lipid accumulation results are in the Table 66 below:

Table 66. Lipid accumulation under various carbon:nitrogen ratio growth conditions

	C/N Ratio	% lipid
YNB 3%Glucose	160	61
	80	49
	60	34
	40	17
	30	16
	20	14
	10	15
YEP	5% Glucose	22
	5% olive oil	38

Other nitrogen sources tested were proline (12 % nitrogen), sodium glutamate (7% nitrogen), soy acid hydrolysate (12% nitrogen), and yeast extract-peptone (26.8% nitrogen). All nitrogen sources tested at C/N ratios of 80 (with glucose as a carbon source), had significantly larger lipid bodies than at C/N ratios of 10 (also with glucose as a carbon source).

Strains MF858 and MF921 were harvested after 4 days of growth at 30°C (3% glucose was used as the carbon source). Cells were washed three times with water and lipids extracted as described above. Lipid accumulation data for soy hydrolysate, yeast extract-peptone and yeast nitrogen base, used as a control, are listed in Table 67 below.

Table 67. Lipid accumulation under different carbon and nitrogen conditions with various nitrogen sources

		% lipid	
	C/N Ratio	MF858	MF921
Soy hydrolysate	80	36	36
	60	36	35
	10	14	15
	80	37	37

Yeast Extract-	80	37	37
Peptone	10	15	14
Yeast Nitrogen	80	37	38
Base	10	13	11

12c. Determination of lipid levels under high carbon and phosphate or magnesium limiting conditions.

[00349] To test whether other nutrient limitations, under high carbon conditions, will allow for higher lipid accumulation, phosphate or magnesium limiting conditions were tested. For phosphate limiting conditions, yeast nitrogen base medium without phosphate was prepared. Shake flask testing was performed using carbon to phosphate ratios ranging from 5376 down to 42. This range corresponds to 7.8 mg/L up to 1 g/L, respectively, and the latter concentration corresponds to that are commonly used in yeast nitrogen base medium. Glucose, at 30 g/L, was used at the carbon source. Potassium phosphate monobasic (containing 28.7 % phosphate) was used as the phosphate source.

[00350] For magnesium limiting conditions, yeast nitrogen base medium without magnesium was prepared. Shake flask testing was conducted using carbon to magnesium ratios ranging from 31360 down to 245. This range corresponds to 0.375 mg/L up to 0.5 g/L, and the latter magnesium concentration corresponds to that commonly used in yeast nitrogen base. Glucose, at 30 g/L, was used as the carbon source. Magnesium sulfate (containing 9.8% magnesium) was used as the magnesium source.

[00351] Strains MF858 and MF921 were harvested after 4 days of growth at 30°C, during which time the cultures were shaking at 250 rpm. Cells were washed three times with water before lipid extraction. Lipids were extracted as described above. Lipid accumulation data is listed in the Table 68 below:

Table 68. Lipid accumulation in phosphate or magnesium limiting growth conditions

		% Lipid	
	g/L	**MF858**	**MF921**
phosphate	1	14	14
	0.0625	18	20
	0.0313	34	41
	0.0156	62	63
	0.0078	83	76
magnesium	0.5	12	11

	0.0313	NA	16
	0.0156	NA	25
	0.0078	NA	42
	0.0039	48	48

[00352] The following tables are referenced throughout the description. Each reference and information designated by each of the Genbank Accession and GI numbers are hereby incorporated by reference in their entirety.

Table 1. Examples of acetyl-CoA carboxylase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
XP_410263	49097606	hypothetical protein AN6126. 2 [Aspergillus nidulans FGSC A4]
XP_329580	32418204	hypothetical protein [Neurospora crassa]
XP_386756	46124405	hypothetical protein FG06580. 1 [Gibberella zeae PH-1]
XP_367702	39972623	hypothetical protein MG07613. 4 [Magnaporthe grisea 70-15]
XP_501721	50548503	hypothetical protein [Yarrowia lipolytica]
EAK99708	46440402	hypothetical protein CaO19. 7466 [Candida albicans SC5314]
XP_457211	50413128	unnamed protein product [Debaryomyces hansenii]
NP_982612	45184894	AAR071Wp [Eremothecium gossypii]
XP_449236	50293649	unnamed protein product [Candida glabrata]
NP_593271	19114183	acetyl-coa carboxylase [Schizosaccharomyces pombe]
NP_014413	6324343	Acc1p [Saccharomyces cerevisiae]
XP_455355	50310667	unnamed protein product [Kluyveromyces lactis]
T42531	11272737	acetyl-CoA carboxylase (EC 6. 4. 1. 2) - fission yeast (Schizosaccharomyces pombe)
AAA20073	171504	acetyl-CoA carboxylase
EAL20176	50257469	hypothetical protein CNBF2520 [Cryptococcus neoformans var. neoformans B-3501A]
XP_571316	58268320	acetyl-CoA carboxylase, putative [Cryptococcus neoformans var. neoformans JEC21]
XP_402244	49076566	hypothetical protein UM04629. 1 [Ustilago maydis 521]
S60200	2133343	acetyl-CoA carboxylase (EC 6. 4.1.2) - smut fungus (Ustilago maydis)
BAA24410	2804173	acetyl-coenzyme A carboxylase like carboxylase [Saccharomyces cerevisiae]
P32874	1708192	HFA1 protein
S55089	7438088	probable acetyl-CoA carboxylase (EC 6.4.1.2) HFA1 - yeast (Saccharomyces cerevisiae)
NP_990836	45382859	acetyl-Coenzyme A carboxylase alpha [Gallus gallus]
CAE01471	32526576	Acetyl-CoA carboxylase 2 [Homo sapiens]
AAR37018	40019048	acetyl-CoA carboxylase 2 [Homo sapiens]
NP_001....	57164283	acetyl-CoA carboxylase [Ovis aries]
NP_776649	27806341	acetyl-coenzyme A carboxylase alpha [acetyl-coA carboxylase] [Bos taurus]
CAI25271	56205878	acetyl-Coenzyme A carboxylase [Mus musculus]
XP_109883	51828611	PREDICTED: acetyl-Coenzyme A carboxylase [Mus musculus]
NP_942134	38679971	acetyl-Coenzyme A carboxylase alpha isoform 3 [Homo sapiens]
NP_942131	38679960	acetyl-Coenzyme A carboxylase alpha isoform 1 [Homo sapiens]
NP_942135	38679974	acetyl-Coenzyme A carboxylase alpha isoform 4 [Homo sapiens]
NP_942136	38679977	acetyl-Coenzyme A carboxylase alpha isoform 2 [Homo sapiens]
AAP94122	33112885	acetyl-CoA carboxylase 1 [Homo sapiens]
NP_071529	11559962	acetyl-coenzyme A carboxylase alpha [Rattus norvegicus]
2006242A	740964	Ac-CoA carboxylase
AAS13685	42405896	acetyl-CoA carboxylase 1 [Mus musculus]
NP_598665	48976025	acetyl-Coenzyme A carboxylase beta [Mus musculus]
Q13085	2493311	Acetyl-CoA carboxylase 1 (ACC-alpha) [Includes: Biotin carboxylase]
XP_548250	57091783	PREDICTED: similar to acetyl-CoA carboxylase [Canis familiaris]
XP_314071	58385597	ENSANGP00000015662 [Anopheles gambiae str. PEST]
CAG08536	47226520	unnamed protein product [Tetraodon nigroviridis]
NP_724636	24586460	CG11198-PB, isoform B [Drosophila melanogaster]
NP_610342	24586458	CG11198-PA, isoform A [Drosophila melanogaster]

NP_001084	4501855	acetyl-Coenzyme A carboxylase beta [Homo sapiens]
NP_446374	16758804	acetyl-Coenzyme A carboxylase beta [Rattus norvegicus]
EAL63219	60465120	acetyl-CoA carboxylase [Dictyostelium discoideum]
NP_921034	37533464	putative acetyl-CoA carboxylase [Oryza sativa (japonica cultivar-group)]
T07084	7438099	acetyl-CoA carboxylase (EC 6.4.1.2) A - soybean
AAP78896	32264940	acetyl-coenzyme A carboxylase ACC1A [Zea mays]
AAO62903	29123370	acetyl-coenzyme A carboxylase [Setaria italica]
BAA07012	1100253	acetyl-CoA carboxylase [Arabidopsis thaliana]
AAL02056	15558947	acetyl-coenzyme A carboxylase [Setaria italica]
AAG40563	11869927	acetyl-CoA carboxylase 1 [Arabidopsis thaliana]
D86483	25293894	protein F5J5.19 [imported] - Arabidopsis thaliana
T07920	7438090	probable acetyl-CoA carboxylase (EC 6.4.1.2) - rape
A57710	2130099	acetyl-CoA carboxylase (EC 6.4.1.2) - wheat
AAO62902	29123376	acetyl-coenzyme A carboxylase [Setaria italica]
2208491A	1588584	Ac-CoA carboxylase
T09538	7438102	acetyl-CoA carboxylase (EC 6.4.1.2) - alfalfa
CAC19875	12057067	acetyl-CoA carboxylase [Brassica napus]
AAP78897	32264942	acetyl-coenzyme A carboxylase ACC1B [Zea mays]
T02235	7438095	acetyl-CoA carboxylase (EC 6.4.1.2) - maize
AAG40564	11869928	acetyl-CoA carboxylase 2 [Arabidopsis thaliana]
E86483	25293893	probable acetyl-CoA carboxylase, 9984-22276 [imported] - Arabidopsis thaliana
CAC84161	20975574	acetyl-coenzyme A carboxylase [Alopecurus myosuroides]
T07081	7438097	acetyl-CoA carboxylase (EC 6.4.1.2) B - soybean (fragment)
CAC19876	12057069	acetyl-CoA carboxylase [Brassica napus]

Table 2. Examples of pyruvate decarboxylase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
1QPBB	7245977	Chain B, Pyruvate Decarboyxlase From Yeast (Form B) Complexed With Pyruvamide
CAA54522	871533	pyruvate decarboxylase [Saccharomyces cerevisiae]
1PYDB	515237	Chain B, Pyruvate Decarboxylase (Pdc) (E.C. 4.1.1.1)
CAA28380	4109	pyruvate decarboxylase [Saccharomyces cerevisiae]

1PVDB	1127233	Chain B, Pyruvate Decarboxylase (Pdc) (E.C. 4.1.1.1)
CAA33709	4114	unnamed protein product [Saccharomyces cerevisiae]
AAN77243	25992752	pyruvate decarboxylase [Candida glabrata]
NP_013235	6323163	Minor isoform of pyruvate decarboxylase, key enzyme in alcoholic fermentation [Saccharomyces cerevisiae]
Q6FJA3	57012668	Pyruvate decarboxylase
S36363	486942	pyruvate decarboxylase (EC 4.1.1.1) - yeast (Kluyveromyces marxianus)
Q12629	52788279	Pyruvate decarboxylase
AAP75898	37359468	pyruvate decarboxylase [Saccharomyces kluyveri]
S70684	2131152	pyruvate decarboxylase (EC 4.1.1.1) - yeast (Kluyveromyces marxianus var.lactis)
NP_011601	6321524	Minor isoform of pyruvate decarboxylase, key enzyme in alcoholic fermentation [Saccharomyces cerevisiae]
AAQ73618	34500072	pyruvate decarboxylase [Saccharomyces kluyveri]
NP_983270	45185554	ACL134Cp [Eremothecium gossypii]
AAF78895	8745337	putative pyruvate decarboxylase [Saccharomyces kluyveri]
CAB65554	6689662	putative pyruvate decarboxylase [Zygosaccharomyces bisporus]
AAP75899	37359470	pyruvate decarboxylase [Saccharomyces kluyveri]
NP_982469	45184751	AAL073Wp [Eremothecium gossypii]
CAA97091	1945321	PDC6 [Saccharomyces cerevisiae]
S50700	1086157	pyruvate decarboxylase (EC 4.1.1.1) - yeast (Hanseniaspora uvarum)
XP_446491	50288125	unnamed protein product [Candida glabrata]
XP_462338	50427451	unnamed protein product [Debaryomyces hansenii]
AAC03164	17066784	pyruvate decarboxylase 1 [Pichia stipitis]
EAK96569	46437219	hypothetical protein CaO19.10395 [Candida albicans SC5314]
XP_457131	50412425	unnamed protein product [Debaryomyces hansenii]
AAC03165	2734883	pyruvate decarboxylase 2 [Pichia stipitis]
XP_459224	50421349	unnamed protein product [Debaryomyces hansenii]
CAH56494	52673248	pyruvate decarboxylase [Pichia anomala]
XP_502647	50550349	hypothetical protein [Yarrowia lipolytica]
NP_010203	6320123	Probable decarboxylase, [Saccharomyces cerevisiae]
BAA04886	1786148	THI3 regulatory protein [Saccharomyces cerevisiae]
XP_449074	50293325	unnamed protein product [Candida glabrata]
EAL04098	46444826	hypothetical protein CaO19. 12078 [Candida albicans SC5314]
CAD60727	27803024	unnamed protein product [Podospora anserina]
T38759	25777585	probable pyruvate decarboxylase (EC 4.1.1.1) - fission yeast (Schizosaccharomyces pombe)
XP_331173	32421459	hypothetical protein [Neurospora crassa]
NP_594083	19114995	pyruvate decarboxylase [Schizosaccharomyces pombe]
XP_401609	49075036	hypothetical protein UM03994.1 [Ustilago maydis 521]
XP_390010	46136637	hypothetical protein FG09834.1 [Gibberella zeae PH-1]
XP_409025	49095128	DCPY_EMENI Pyruvate decarboxylase [Aspergillus nidulans FGSC A4]
NP_984350	45188127	ADR254Wp [Eremothecium gossypii]
AAD16178	4323053	pyruvate decarboxylase [Aspergillus oryzae]
P87208	2501326	Pyruvate decarboxylase
EAL18331	50255598	hypothetical protein CNBJ2540 [Cryptococcus neoformans var. neoformans B-3501A]
XP_567475	58260130	pyruvate decarboxylase, putative [Cryptococcus neoformans var. neoformans JEC21]
AAM73540	21666011	pyruvate decarboxylase PdcB [Rhizopus oryzae]
AAM73539	21666009	pyruvate decarboxylase PdcA [Rhizopus oryzae]

XP_502508	50550071	hypothetical protein [Yarrowia lipolytica]
CAA93158	1177659	SPAC3H8.01 [Schizosaccharomyces pombe]
XP_412533	49123327	hypothetical protein AN8396.2 [Aspergillus nidulans FGSC A4]
P51844	1706333	Pyruvate decarboxylase
XP_455842	50311631	unnamed protein product [Kluyveromyces lactis]
CAA61155	3688422	pyruvate decarboxylase [Kluyveromyces lactis]
XP_444902	50284947	unnamed protein product [Candida glabrata]
CAA47319	4118	pyruvate decarboxylase [Saccharomyces cerevisiae]

Table 3. Examples of isocitrate dehydrogenase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
O13285	3023996	Isocitrate dehydrogenase [NADP], mitochondrial precursor (IDH) (NADP+-specific ICDH) (IDP) (CtIDP1)
EAK91676	46432179	hypothetical protein CaO19.5211 [Candida albicans SC5314]
O13285	3023996	Isocitrate dehydrogenase [NADP], mitochondrial precursor (IDH) (NADP+-specific ICDH) (IDP) (CtIDP1)
EAK94305	46434909	hypothetical protein CaO19.3733 [Candida albicans SC5314]
XP_451683	50303483	unnamed protein product [Kluyveromyces lactis]
XP_459772	50422415	unnamed protein product [Debaryomyces hansenii]
O13294	27805482	Isocitrate dehydrogenase [NADP] peroxisomal (Oxalosuccinate decarboxylase) (IDH) (PS-NADP-IDH) (CtIDP2)
XP_460289	50423413	unnamed protein product [Debaryomyces hansenii]
XP_390523	46137663	hypothetical protein FG10347. 1 [Gibberella zeae PH-1]

XP_367343	39971905	hypothetical protein MG07268.4 [Magnaporthe grisea 70-15]
XP_323176	32405126	hypothetical protein [Neurospora crassa]
XP_445447	50286037	unnamed protein product [Candida glabrata]
AAK76730	15027826	mitochondrial NADP-dependent isocitrate dehydrogenase [Aspergillus nidulans]
NP_010217	6320137	Idp1p [Saccharomyces cerevisiae]
NP_984921	45190667	AER061Cp [Eremothecium gossypii]
AAK76731	15027827	peroxisomal NADP-dependent isocitrate dehydrogenase [Aspergillus nidulans]
P79089	3023999	Isocitrate dehydrogenase [NADP], mitochondrial precursor (IDH) (NADP+-specific ICDH) (IDP)
NP_013275	6323203	Cytosolic NADP-specific isocitrate dehydrogenase [Saccharomyces cerevisiae]
XP_407136	49091350	IDHP_ASPNG ISOCITRATE DEHYDROGENASE [NADP], MITOCHONDRIAL PRECURSOR (IDP) [Aspergillus nidulans FGSC A4]
NP_982520	45184802	AAL022Wp [Eremothecium gossypii]
XP_446953	50289047	unnamed protein product [Candida glabrata]
XP_445184	50285511	unnamed protein product [Candida glabrata]
XP_455638	50311227	unnamed protein product [Kluyveromyces lactis]
AAA64516	736722	isocitrate dehydrogenase
NP_970434	42525054	isocitrate dehydrogenase (NADP) [Bdellovibrio bacteriovorus HD100]
AAT93173	51013759	YNL009W [Saccharomyces cerevisiae]
XP_569233	58264154	isocitrate dehydrogenase (NADP+), putative [Cryptococcus neoformans var. neoformans JEC21]
XP_569234	58264156	isocitrate dehydrogenase (NADP+), putative [Cryptococcus neoformans var. neoformans JEC21]
XP_403726	49080406	hypothetical protein UM06111.1 [Ustilago maydis 521]
XP_503571	50552322	
XP_458151	50428131	unnamed protein product [Debaryomyces hansenii]
O13302	13124301	Isocitrate dehydrogenase [NAD] subunit 1, mitochondrial precursor (NAD+-specific ICDH)
XP_409927	49096934	IDH1_AJECA Isocitrate dehydrogenase [NAD] subunit 1, mitochondrial precursor[Aspergillus nidulans FGSC A4]
XP_385909	46122711	IDH1_AJECA Isocitrate dehydrogenase [NAD] subunit 1, mitochondrial precursor [Gibberella zeae PH-1]
XP_365293	39967489	hypothetical protein MG01995.4 [Magnaporthe grisea 70-15]
NP_983873	45187650	ADL223Wp [Eremothecium gossypii]
XP_455266	50310493	IDH1_KLULA [Kluyveromyces lactis]
NP_594397	19115309	putative isocitrate dehydrogenase (EC 1.1.1.41) [Schizosaccharomyces pombe]
XP_324955	32408949	hypothetical protein [Neurospora crassa]
CAE81942	38636405	probable isocitrate dehydrogenase [NAD] subunit 1, mitochondrial precursor [Neurospora crassa]
NP_014361	6324291	Idh1p [Saccharomyces cerevisiae]
XP_446479	50288101	unnamed protein product [Candida glabrata]
XP_567378	58259936	isocitrate dehydrogenase (NAD+), putative [Cryptococcus neoformans var. neoformans JEC21]
XP_398944	49069310	hypothetical protein UM01329.1 [Ustilago maydis 521]
XP_502479	50550013	hypothetical protein [Yarrowia lipolytica]
EAK96238	46436883	hypothetical protein CaO19.13213 [Candida albicans SC5314]
EAK96305	46436951	hypothetical protein CaO19.5791 [Candida albicans SC5314]

XP_461797	50426401	unnamed protein product [Debaryomyces hansenii]
XP_328403	32415850	hypothetical protein [Neurospora crassa]
CAF31997	42820684	isocitrate dehydrogenase, putative [Aspergillus fumigatus]
XP_389756	46136129	hypothetical protein FG09580.1 [Gibberella zeae PH-1]
XP_363786	39952139	hypothetical protein MG01712.4 [Magnaporthe grisea 70-15]
AAL73035	18463935	isocitrate dehydrogenase [Coccidioides immitis]
XP_405140	49086142	hypothetical protein AN1003.2 [Aspergillus nidulans FGSC A4]
NP_595203	19111995	probable isocitrate dehydrogenase [nad] subunit 2, mitochondrial precursor [Schizosaccharomyces pombe]
NP_014779	6324709	Idh2p [Saccharomyces cerevisiae]
XP_447564	50290265	unnamed protein product [Candida glabrata]
NP_985684	45198655	AFR137Cp [Eremothecium gossypii]
XP_566837	58258849	isocitrate dehydrogenase, putative [Cryptococcus neoformans var. neoformans JEC21]
XP_454086	50308171	IDH2_KLULA [Kluyveromyces lactis]
XP_398943	49069308	hypothetical protein UM01328.1 [Ustilago maydis 521]

Table 4. Examples of ATP-citrate lyase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
XP_327071	32413182	hypothetical protein [Neurospora crassa]
O93988	30912679	ATP-citrate synthase subunit 1 (ATP-citrate (pro-S-)-lyase 1) (Citrate cleavage enzyme subunit 1)
XP_370222	39977669	hypothetical protein MG06719.4 [Magnaporthe grisea 70-15]
XP_406573	49090008	ACL1_NEUCR Probable ATP-citrate synthase subunit 1 [Aspergillus nidulans FGSC A4]
XP_504787	50554757	hypothetical protein [Yarrowia lipolytica]
Q9P7W3	30912748	Probable ATP-citrate synthase subunit 1 (ATP-citrate (pro-S-)-lyase 1) (Citrate cleavage enzyme subunit 1)
XP_398620	49068662	hypothetical protein UM01005.1 [Ustilago maydis 521]
NP_596202	19112994	probable ATP citrate lyase [Schizosaccharomyces pombe]
XP_567460	58260100	conserved hypothetical protein [Cryptococcus neoformans var. neoformans JEC21]
NP_001008	56118260	acly-prov protein [Xenopus tropicalis]
XP_418154	50760837	PREDICTED: similar to ATP citrate lyase [Gallus gallus]
AAH84253	54038148	LOC495086 protein [Xenopus laevis]
NP_942127	38569423	ATP citrate lyase isoform 2 [Homo sapiens]
NP_001087	38569421	ATP citrate lyase isoform 1 [Homo sapiens]
P53396	20141248	ATP-citrate synthase (ATP-citrate (pro-S-)-lyase) (Citrate cleavage

		enzyme)
AAL34316	17028103	ATP-citrate lyase [Rattus norvegicus]
NP_001002	50540366	zgc:92008 [Danio rerio]
AAH84776	54311201	LOC495316 protein [Xenopus laevis]
S21173	105392	ATP citrate (pro-S)-lyase - human
AAT94429	51092031	RE70805p [Drosophila melanogaster]
AAD34754	28372804	LD21334p [Drosophila melanogaster]
AAH21502	18204829	Acly protein [Mus musculus]
XP_319323	58392375	ENSANGP00000012364 [Anopheles gambiae str. PEST]
NP_725514	24653990	CG8322-PB, isoform B [Drosophila melanogaster]
EAL26601	54637198	GA20986-PA [Drosophila pseudoobscura]
CAE56725	39579419	Hypothetical protein CBG24512 [Caenorhabditis briggsae]
CAE64663	39593194	Hypothetical protein CBG09435 [Caenorhabditis briggsae]
XP_511495	55645405	PREDICTED: similar to ATP citrate lyase isoform 1 [Pan troglodytes]
CAF95829	47210997	unnamed protein product [Tetraodon nigroviridis]
AAO22565	27754223	putative ATP citrate lyase [Arabidopsis thaliana]
AAL33788	17065616	putative ATP citrate lyase [Arabidopsis thaliana]
CAB46077	5304837	ATP citrate lyase [Cyanophora paradoxa]
CAF96044	47204726	unnamed protein product [Tetraodon nigroviridis]
AAK13318	13160653	ATP:citrate lyase [Capsicum annuum]
AAQ75159	34558815	citrate lyase subunit 2 [Alvinella pompejana epibiont 7G3]
AAQ75128	34558783	citrate lyase subunit 2 [Alvinella pompejana epibiont 6C6]
XP_537640	57091075	PREDICTED: similar to ATP citrate lyase isoform 2 [Canis familiaris]
XP_327069	32413178	hypothetical protein ((AJ243817) ATP citrate lyase, subunit 2 [Sordaria macrospora]) [Neurospora crassa]
CAB76164	7160184	ATP citrate lyase, subunit 2 [Sordaria macrospora]
XP_370223	39977671	hypothetical protein MG06720.4 [Magnaporthe grisea 70-15]
XP_386215	46123323	hypothetical protein FG06039.1 [Gibberella zeae PH-1]
CAA10666	7159697	ATP-citrat-lyase [Gibberella pulicaris]
XP_406572	49090004	conserved hypothetical protein [Aspergillus nidulans FGSC A4]
XP_503231	50551515	hypothetical protein [Yarrowia lipolytica]
NP_593246	19114158	putative ATP-citrate (pro-S-) lyase (EC 4.1.3.8) [Schizosaccharomyces pombe]
XP_398620	49068662	hypothetical protein UM01005.1 [Ustilago maydis 521]
XP_567460	58260100	conserved hypothetical protein [Cryptococcus neoformans var. neoformans JEC21]
AAT94429	51092031	RE70805p [Drosophila melanogaster]
NP_725514	24653990	CG8322-PB, isoform B [Drosophila melanogaster]
AAD34754	28372804	LD21334p [Drosophila melanogaster]
EAL26601	54637198	GA20986-PA [Drosophila pseudoobscura]
XP_319323	58392375	ENSANGP00000012364 [Anopheles gambiae str. PEST]
AAH84776	54311201	LOC495316 protein [Xenopus laevis]
BAB00624	9229902	ATP citrate-lyase [Ciona intestinalis]
NP_001008	56118260	acly-prov protein [Xenopus tropicalis]
AAH84253	54038148	LOC495086 protein [Xenopus laevis]
AAH56378	38614162	ATP citrate lyase [Mus musculus]
NP_001087	38569421	ATP citrate lyase isoform 1 [Homo sapiens]
NP_942127	38569423	ATP citrate lyase isoform 2 [Homo sapiens]
P53396	20141248	ATP-citrate synthase (ATP-citrate (pro-S-)-lyase) (Citrate cleavage enzyme)
XP_511495	55645405	PREDICTED: similar to ATP citrate lyase isoform 1 [Pan

		troglodytes]
NP_058683	8392839	ATP citrate lyase [Rattus norvegicus]
NP_001002	50540366	zgc:92008 [Danio rerio]
S21173	105392	ATP citrate (pro-S)-lyase - human
NP_508280	17551266	atp citrate lyase (XC101) [Caenorhabditis elegans]
CAE64663	39593194	Hypothetical protein CBG09435 [Caenorhabditis briggsae]
CAE56725	39579419	Hypothetical protein CBG24512 [Caenorhabditis briggsae]
NP_506267	17557344	ATP citrate lyase (120.6 kD) (5N599) [Caenorhabditis elegans]
XP_537640	57091075	PREDICTED: similar to ATP citrate lyase isoform 2 [Canis familiaris]
CAF96059	47204551	unnamed protein product [Tetraodon nigroviridis]
F96633	25404292	hypothetical protein F8A5.32 [imported] - Arabidopsis thaliana
AAM91141	22136126	similar to ATP-citrate-lyase [Arabidopsis thaliana]
NP_849634	30681854	expressed protein [Arabidopsis thaliana]
AAO23582	27764922	At1g09430/F19J9_9 [Arabidopsis thaliana]
AAM65078	21593129	ATP citrate-lyase, putative [Arabidopsis thaliana]
CAC86996	15919089	ATP citrate lyase b-subunit [Lupinus albus]
AAQ75158	34558814	citrate lyase subunit 1 [Alvinella pompejana epibiont 7G3]
AAQ75127	34558782	citrate lyase subunit 1 [Alvinella pompejana epibiont 6C6]

Table 5. Examples of malic enzyme polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
NP_012896	6322823	Mae1p [Saccharomyces cerevisiae]
XP_448858	50292851	unnamed protein product [Candida glabrata]
XP_454793	50309563	unnamed protein product [Kluyveromyces lactis]
NP_986598	45201028	AGL068Wp [Eremothecium gossypii]
XP_460887	50424595	unnamed protein product [Debaryomyces hansenii]
EAK97738	46438407	hypothetical protein CaO19.3419 [Candida albicans SC5314]
XP_504112	50553402	hypothetical protein [Yarrowia lipolytica]
XP_330094	32419237	hypothetical protein [Neurospora crassa]
XP_380981	46107844	hypothetical protein FG00805.1 [Gibberella zeae PH-1]
XP_411070	49102552	hypothetical protein AN6933.2 [Aspergillus nidulans FGSC A4]
XP_362875	39946676	hypothetical protein MG08562.4 [Magnaporthe grisea 70-15]
NP_587760	19075260	malate oxidoreductase [nad] [Schizosaccharomyces pombe]
NP_978189	42780942	malate oxidoreductase [Bacillus cereus ATCC 10987]
YP_035982	49481098	NAD-dependent malic enzyme [Bacillus thuringiensis serovar konkukian str.97-27]
YP_027934	49184682	malate oxidoreductase [Bacillus anthracis str. Sterne]
YP_018438	47527089	malate oxidoreductase [Bacillus anthracis str.. 'Ames Ancestor']
ZP_002365	47565532	malate oxidoreductase VC1188 [Bacillus cereus G9241]
YP_083209	52143619	NAD-dependent malic enzyme [Bacillus cereus ZK]
XP_571672	58269032	malate dehydrogenase, putative [Cryptococcus neoformans var. neoformans JEC21]
NP_391586	16080758	hypothetical protein BSU37050 [Bacillus subtilis subsp. subtilis str. 168]
YP_092693	52786864	MalS [Bacillus licheniformis ATCC 14580]
NP_831516	30019885	NAD-dependent malic enzyme [Bacillus cereus ATCC 14579]
YP_093460	52787631	YwkA [Bacillus licheniformis ATCC 14580]

YP_081030	52082239	Malic oxidoreductase [Bacillus licheniformis ATCC 14580]
NP_822689	29828055	putative malate dehydrogenase [Streptomyces avermitilis MA-4680]
O34389	33517449	Probable NAD-dependent malic enzyme 3 (NAD-ME 3)
EAL19111	50256386	hypothetical protein CNBH2110 [Cryptococcus neoformans var. neoformans B-3501A]
NP_825047	29830413	putative malate dehydrogenase [Streptomyces avermitilis MA-4680]
ZP_002340	47096498	NADP-dependent malic enzyme [Listeria monocytogenes str. 1/2a F6854]
NP_928837	37525493	malate dehydrogenase (oxaloacetate-decarboxylating) [Photorhabdus luminescens subsp. laumondii TTO1]
NP_230833	15641201	malate oxidoreductase [Vibrio cholerae O1 biovar eltor str. N16961]
NP_934257	37679648	malic enzyme [Vibrio vulnificus YJ016]
NP_761613	27366085	Malic enzyme [Vibrio vulnificus CMCP6]
AC1314	25283688	malolactic enzyme (malate dehydrogenase) homolog lmo1915 - Listeria monocytogenes (strain EGD-e)
YP_055602	50842375	NAD-dependent malic enzyme [Propionibacterium acnes KPA171202]
YP_095310	52841511	malate oxidoreductase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]
ZP_002315	47093832	NADP-dependent malic enzyme [Listeria monocytogenes str. 4b H7858]
AC1686	25283689	malolactic enzyme (malate dehydrogenase) homolog lin2029 [imported] - Listeria innocua (strain Clip11262)
YP_126594	54294179	malate oxidoreductase [Legionella pneumophila str. Lens]
YP_123567	54297198	malate oxidoreductase [Legionella pneumophila str. Paris]
EAJ76260	44510091	unknown [environmental sequence]
YP_114273	53803890	malate oxidoreductase [Methylococcus capsulatus str. Bath]
NP_797637	28898032	malate oxidoreductase [Vibrio parahaemolyticus RIMD 2210633]
YP_040250	49483026	putative malolactic enzyme [Staphylococcus aureus subsp. aureus MRSA252]
ZP_001276	53693400	COG0281: Malic enzyme [Pseudomonas syringae pv. syringae B728a]
YP_044961	50083451	NAD-linked malate dehydrogenase, Rossman fold [Acinetobacter sp. ADP1]
YP_128226	54295811	hypothetical protein lpl2901 [Legionella pneumophila str. Lens]
NP_719387	24375344	malate oxidoreductase [Shewanella oneidensis MR-1]
XP_572853	58271394	nad-dependent malic enzyme, putative [Cryptococcus neoformans var. neoformans JEC21]
NP_252161	15598667	probable malic enzyme [Pseudomonas aeruginosa PAO1]
ZP_001368	46164263	COG0281: Malic enzyme [Pseudomonas aeruginosa UCBPP-PA14]
YP_125345	54298976	hypothetical protein lpp3043 [Legionella pneumophila str. Paris]
NP_793695	28871076	malate dehydrogenase [Pseudomonas syringae pv. tomato str. DC3000]
YP_096964	52843165	malate dehydrogenase (NAD-linked) [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]
EAH92280	44245125	unknown [environmental sequence]
YP_154988	56459707	Malic enzyme [Idiomarina loihiensis L2TR]
EAI68195	44354928	unknown [environmental sequence]
YP_070054	51595863	NAD-dependent malic enzyme [Yersinia pseudotuberculosis IP 32953]

YP_133025	54303032	putative malate oxidoreductase [Photobacterium profundum SS9]
NP_969623	42524243	NAD-dependent malic enzyme [Bdellovibrio bacteriovorus HD100]
NP_856009	31793516	PROBABLE [NAD] DEPENDENT MALATE OXIDOREDUCTASE MEZ (MALIC ENZYME) (NAD-MALIC ENZYME) (MALATE DEHYDROGENASE TATE
DECARBOXY	ATING))	PYRUVIC-MALIC CARBOXYLASE) (NAD-ME) [Mycobacterium bovis AF2122/97]
NP_935035	37680426	malic enzyme [Vibrio vulnificus YJ016]
YP_050922	50121755	NAD-dependent malic enzyme [Erwinia carotovora subsp. atroseptica SCRI1043]
E70705	7431223	probable malate oxidoreductase - Mycobacterium tuberculosis (strain H37RV)
NP_216848	57116971	PROBABLE [NAD] DEPENDENT MALATE OXIDOREDUCTASE MEZ (MALIC ENZYME) (NAD-MALIC ENZYME) (MALATE DEHYDROGENASE TATE
DECARBOXY	ATING))	PYRUVIC-MALIC CARBOXYLASE) (NAD-ME) [Mycobacterium tuberculosis H37Rv]
YP_143786	55980489	NAD-dependent malic enzyme (malate dehydrogenase) [Thermus thermophilus HB8]
YP_130202	54309182	putative malate oxidoreductase [Photobacterium profundum SS9]
NP_415996	16129438	NAD-linked malate dehydrogenase [Escherichia coli K12]
NP_819843	29654151	malate oxidoreductase [Coxiella burnetii RSA 493]
NP_753809	26247769	NAD-dependent malic enzyme [Escherichia coli CFT073]
NP_707611	56479957	NAD-linked malate dehydrogenase (malic enzyme) [Shigella flexneri 2a str. 301]
F85728	25283682	NAD-linked malate dehydrogenase (malic enzyme) - Escherichia coli (strain O157:H7, substrain EDL933)
YP_163690	56552851	malic enzyme [Zymomonas mobilis subsp. mobilis ZM4]
YP_150562	56413487	NAD-linked malic enzyme [Salmonella enterica subsp. enterica serovar Paratypi A str. ATCC 9150]
NP_720610	24378655	malolactic enzyme [Streptococcus mutans UA159]
NP_460525	16764910	NAD-linked malate dehydrogenase [Salmonella typhimurium LT2]
ZP_003193	48865537	COG0281: Malic enzyme [Oenococcus oeni PSU-1]
NP_784797	28377905	malolactic enzyme [Lactobacillus plantarum WCFS1]
T13496	7431227	malolactic enzyme (EC 1.1.1.-) - Leuconostoc oenos
AAV65766	55793550	malolactic enzyme [Oenococcus oeni]
A97096	25283683	malic enzyme [imported] - Clostridium acetobutylicum
YP_193951	58337366	malolactic enzyme [Lactobacillus acidophilus NCFM]
H97096	25283684	malic enzyme [imported] - Clostridium acetobutylicum
ZP_003237	48870993	COG0281: Malic enzyme [Pediococcus pentosaceus ATCC 25745]
ZP_001460	41689468	COG0281: Malic enzyme [Psychrobacter sp. 273-4]
D86737	25283676	malolactic enzyme [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
ZP_002870	48825851	COG0281: Malic enzyme [Enterococcus faecium]
ZP_001439	34762975	Malolactic enzyme [Fusobacterium nucleatum subsp. vincentii ATCC 49256]
1922245A	737262	malolactic enzyme
YP_169914	56708018	NAD-dependent malic enzyme [Francisella tularensis subsp. tularensis Schu 4]
YP_055027	50841800	putative malate oxidoreductase [Propionibacterium acnes KPA171202]
ZP_000625	23023297	COG0281: Malic enzyme [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]

NP_296302	15807565	malate oxidoreductase [Deinococcus radiodurans R1]
NP_285599	15807938	malate oxidoreductase [Deinococcus radiodurans R1]
YP_132069	54302076	hypothetical malate oxidoreductase [Photobacterium profundum SS9]
CAA50716	467569	malolactic enzyme [Lactococcus lactis]
ZP_002906	48833596	COG0281: Malic enzyme [Magnetococcus sp. MC-1]
ZP_003155	48861632	COG0281: Malic enzyme [Microbulbifer degradans 2-40]
NP_773109	27381580	malic enzyme [Bradyrhizobium japonicum USDA 110]
AAQ95658	37622953	malic enzyme [Dictyostelium discoideum]
CAC19505	56204311	malic enzyme 1, NADP(+)-dependent, cytosolic [Homo sapiens]
AAH80660	51873855	Mod1 protein [Mus musculus]
P40927	729986	NADP-dependent malic enzyme (NADP-ME)
AAT02533	46850200	NADP-dependent malic enzyme 1 [Hydrilla verticillata]
BAC37086	26346875	unnamed protein product [Mus musculus]
T02763	7431235	probable malate dehydrogenase (oxaloacetate-decarboxylating) (NADP) (EC 1.1.1.40) - maize
XP_387367	46125627	hypothetical protein FG07191. 1 [Gibberella zeae PH-1]
AAC50613	1465733	cytosolic NADP(+)-dependent malic enzyme
CAA39421	669118	sbcA8 recE fusion [Escherichia coli]
CAA39420	669117	sbcA8 recE fusion [Escherichia coli]
NP_032641	6678912	malic enzyme, supernatant [Mus musculus]
CAA39419	581228	sbcA8 recE fusion [Escherichia coli]
AAB01380	1335389	NADP-dependent malic enzyme
JC4160	1085347	malate dehydrogenase (oxaloacetate-decarboxylating) (NADP) (EC 1.1.1.40) - human
E96828	25283677	probable malate oxidoreductase, 93001-96525 [imported] - Arabidopsis thaliana
BAD87910	57899974	cytosolic NADP malic enzyme [Oryza sativa (japonica cultivar-group)]
EAJ77083	44511304	unknown [environmental sequence]
P13697	266504	NADP-dependent malic enzyme (NADP-ME) (Malic enzyme 1)
NP_036732	7106353	malic enzyme 1 [Rattus norvegicus]
YP_065939	51246055	related to NAD-dependent malic enzyme [Desulfotalea psychrophila LSv54]
CAC18164	16944467	related to malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) [Neurospora crassa]
XP_322953	32404680	hypothetical protein [Neurospora crassa]
AAK91502	18460985	NADP-dependent malic enzyme [Zea mays]
AAQ88396	37147841	non-photosynthetic NADP-malic enzyme [Zea mays]
NP_001003	57525624	zgc:100941 [Danio rerio]
1GQ2P	21465488	Chain P, Malic Enzyme From Pigeon Liver
AAO26053	28195290	malic enzyme [Mucor circinelloides]
AAH84250	54038006	Me2 protein [Xenopus laevis]
XP_362590	39946106	hypothetical protein MG08173.4 [Magnaporthe grisea 70-15]
AAH03287	13096987	Mod1 protein [Mus musculus]
Q29558	2497785	NADP-dependent malic enzyme (NADP-ME) (Malic enzyme 1)
XP_532217	57094622	PREDICTED: similar to malate dehydrogenase decarboxylase (NADP+) [Canis familiaris]
P28227	126734	NADP-dependent malic enzyme (NADP-ME)
NP_496968	17537199	malic enzyme nadp-dependent (2O518) [Caenorhabditis elegans]
NP_914533	34906372	unnamed protein product [Oryza sativa (japonica cultivar-group)]
AAD10504	4096786	NADP-malic enzyme [Zea mays]
AAO67523	50897495	mitochondrial malic enzyme 2 [Xenopus laevis]

P43279	1170871	NADP-dependent malic enzyme, chloroplast precursor (NADP-ME)
AAK83074	15077109	putative cytosolic NADP-malic enzyme [Flaveria pringlei]
AAP33011	30575690	NADP-malic enzyme [Zea mays]
AAN86690	27357017	malic enzyme [Mastigamoeba balamuthi]
P78715	41017288	Malic enzyme, hydrogenosomal precursor (ME)
AAP32204	30526303	NADP-dependent malic enzyme [Sorghum bicolor]
AAV31249	54287505	NADP malic enzyme [Oryza sativa (japonica cultivar-group)]
T06402	7431232	malate dehydrogenase (oxaloacetate-decarboxylating) (NADP) (EC 1.1.1.40) 2, cytosolic - tomato
Q99KE1	55583978	NAD-dependent malic enzyme, mitochondrial precursor (NAD-ME) (Malic enzyme 2)
XP_399922	49071266	hypothetical protein UM02307.1 [Ustilago maydis 521]
P36444	547886	NADP-dependent malic enzyme, chloroplast precursor (NADP-ME)
AAO30034	28059162	malate oxidoreductase (malic enzyme) [Arabidopsis thaliana]
AAK83073	15077107	putative cytosolic NADP-malic enzyme [Flaveria pringlei]
NP_002387	4505145	malic enzyme 2, NAD(+)-dependent, mitochondrial [Homo sapiens]
AAA33487	168528	NADP-dependent malic enzyme (EC 1.1.1.40)
BAA74735	4239891	NADP-malic enzyme [Aloe arborescens]
NP_989634	45383538	malic enzyme 1, NADP(+)-dependent, cytosolic [Gallus gallus]
1GZ3D	31615316	Chain D, The Regulation Of Human Mitochondrial Nad(P)+-Dependent Malic Enzyme By Atp And Fumarate
AAW56450	57791240	chloroplast NADP-dependent malic enzyme precursor [Flaveria bidentis]
AAT02534	46850202	NADP-dependent malic enzyme 2 [Hydrilla verticillata]
S29742	422339	malate dehydrogenase (oxaloacetate-decarboxylating) (NADP) (EC 1.1.1.40) - pig roundworm
1O0SB	34811253	Chain B, Crystal Structure Of Ascaris Suum Malic Enzyme Complexed With Nadh
P27443	126732	NAD-dependent malic enzyme, mitochondrial precursor (NAD-ME)
T06401	7431231	malate dehydrogenase (oxaloacetate-decarboxylating) (NADP) (EC 1.1.1.40) precursor - tomato
AAL16175	16226466	AT5g11670/T22P22_60 [Arabidopsis thaliana]
AAF73006	8118507	NADP-dependent malic protein [Ricinus communis]
AAK97530	15420975	malic enzyme [Meleagris gallopavo]
EAI90348	44385841	unknown [environmental sequence]
P51615	1708924	NADP-DEPENDENT MALIC ENZYME (NADP-ME)
AAA19575	169327	NADP-dependent malic enzyme
S43718	1084300	malate dehydrogenase (oxaloacetate-decarboxylating) (NADP) (EC 1.1.1.40) - common ice plant
P34105	1346485	NADP-DEPENDENT MALIC ENZYME (NADP-ME)
AAS38597	42733630	similar to Mastigamoeba balamuthi Malic enzyme (EC 1.1.1.38) [Dictyostelium discoideum]
BAC54101	27530932	cytosolic NADP-malic enzyme [Lithospermum erythrorhizon]
AAT02535	46850204	NADP-dependent malic enzyme 3 [Hydrilla verticillata]
CAB66003	6706333	NADP-dependent malate dehydrogenase (decarboxylating) [Apium graveolens]
AAH84860	54311418	LOC495390 protein [Xenopus laevis]
CAA39422	669119	sbcA8 recE fusion [Escherichia coli]
NP_916713	34910732	P0022F10.12 [Oryza sativa (japonica cultivar-group)]
CAA56354	510876	NADP dependent malic enzyme [Phaseolus vulgaris]

DEFBC	7427668	malate dehydrogenase (oxaloacetate-decarboxylating) (NADP) (EC 1.1.1.40) - kidney bean
JC5967	7431234	malate dehydrogenase (oxaloacetate-decarboxylating) (NADP) (EC 1.1.1.40) - aloe
NP_197960	15239517	malate oxidoreductase, putative [Arabidopsis thaliana]
NP_651959	21356279	CG5889-PA [Drosophila melanogaster]
CAB64263	6634090	malate dehydrogenase (NADP-dependent oxaloacetate decarboxylating), malic enzyme [Drosophila melanogaster]
BAB20887	54606800	NADP dependent malic enzyme [Oryza sativa (japonica cultivar-group)]
EAL27424	54638022	GA19206-PA [Drosophila pseudoobscura]
NP_006671	5729920	malic enzyme 3, NADP(+)-dependent, mitochondrial [Homo sapiens]
AAB08874	1561774	malate dehydrogenase [Vitis vinifera]
1PJLH	33358128	Chain H, Crystal Structure Of Human M-Nad-Me In Ternary Complex With Nad And Lu3+
1GZ4D	22218682	Chain D, The Regulation Of Human Mitochondrial Nad(P)+-Dependent Malic Enzyme By Atp And Fumarate
1QR6B	5822327	Chain B, Human Mitochondrial Nad(P)-Dependent Malic Enzyme
1PJ3D	39654475	Chain D, Crystal Structure Of Human Mitochondrial Nad(P)+-Dependent Malic Enzyme
P22178	126736	NADP-dependent malic enzyme, chloroplast precursor (NADP-ME)
XP_410305	49097690	hypothetical protein AN6168.2 [Aspergillus nidulans FGSC A4]
AAH22472	18490280	Malic enzyme 3, NADP(+)-dependent, mitochondrial [Homo sapiens]

Table 6. Examples of AMP deaminase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
AAA34420	171053	AMP deaminase (EC 3.5.4.6)
XP_446684	50288509	unnamed protein product [Candida glabrata]
NP_983153	45185436	ABR204Cp [Eremothecium gossypii]
XP_453337	50306727	unnamed protein product [Kluyveromyces lactis]
EAL02322	46443037	adenosine/AMP deaminase [Candida albicans SC5314]
XP_460211	50423261	unnamed protein product [Debaryomyces hansenii]
XP_503822	50552824	hypothetical protein [Yarrowia lipolytica]
XP_413009	49131023	hypothetical protein AN8872.2 [Aspergillus nidulans FGSC A4]
XP_360256	39941438	hypothetical protein MG05630.4 [Magnaporthe grisea 70-15]
XP_381547	46108978	hypothetical protein FG01371.1 [Gibberella zeae PH-1]
XP_330167	32419447	probable AMP deaminase [MIPS] [Neurospora crassa]
CAB97316	16945394	probable AMP deaminase [Neurospora crassa]
T50996	11359582	probable AMP deaminase [imported] - Neurospora crassa
NP_595153	19111945	amp deaminase [Schizosaccharomyces pombe]
EAL22226	50259553	hypothetical protein CNBC3640 [Cryptococcus neoformans var. neoformans B-3501A]
XP_402237	49076548	hypothetical protein UM04622.1 [Ustilago maydis 521]
CAA62797	995562	AMP deaminase [Schizosaccharomyces pombe]
AAF65407	7638159	AMP deaminase [Dictyostelium discoideum]
XP_537039	57088163	PREDICTED: similar to AMP deaminase 2 (AMP deaminase isoform L) [Canis familiaris]
AAH49119	29145073	Adenosine monophosphate deaminase 2 (isoform L) [Mus musculus]
XP_569691	58265070	AMP deaminase, putative [Cryptococcus neoformans var. neoformans JEC21]
AAD56303	5922018	AMP deaminase isoform L [Homo sapiens]
NP_004028	21264318	adenosine monophosphate deaminase 2 (isoform L) isoform 1 [Homo sapiens]
A44313	345738	AMP deaminase (EC 3.5.4.6) isoform L - human
CAI19307	56206061	adenosine monophosphate deaminase 2 (isoform L) [Homo sapiens]
AAA62126	644509	AMP deaminase isoform L splicing variant
CAI19305	56206059	adenosine monophosphate deaminase 2 (isoform L) [Homo sapiens]
XP_310497	58424203	ENSANGP00000017310 [Anopheles gambiae str. PEST]
CAI19306	56206060	adenosine monophosphate deaminase 2 (isoform L) [Homo sapiens]
AAC50308	608499	AMP deaminase
CAG06825	47229629	unnamed protein product [Tetraodon nigroviridis]
NP_727741	45551453	CG32626-PD, isoform D [Drosophila melanogaster]
NP_727739	45551452	CG32626-PA, isoform A [Drosophila melanogaster]
NP_727740	24641890	CG32626-PB, isoform B [Drosophila melanogaster]
AAN09337	22832227	CG32626-PC, isoform C [Drosophila melanogaster]
T01259	7484807	AMP deaminase homolog F16M14.21 - Arabidopsis thaliana
XP_506591	51963676	PREDICTED P0034A04.129 gene product [Oryza sativa (japonica cultivar-group)]
NP_850294	30687456	AMP deaminase, putative / myoadenylate deaminase, putative [Arabidopsis thaliana]
CAG07509	47228777	unnamed protein product [Tetraodon nigroviridis]

NP_494974	32564190	Adenosine/AMP deaminase (85.4 kD) (2F499) [Caenorhabditis elegans]
T15771	7497030	hypothetical protein C34F11.3 - Caenorhabditis elegans
CAE59064	39596837	Hypothetical protein CBG02349 [Caenorhabditis briggsae]
NP_494973	32564194	Adenosine/AMP deaminase family member (2F499) [Caenorhabditis elegans]
BAA06505	1321635	erythrocyte-type AMP deaminase [Homo sapiens]
NP_000471	4502079	adenosine monophosphate deaminase (isoform E) [Homo sapiens]
S68147	2134756	AMP deaminase (EC 3.5.4.6), erythrocte, splice form 1c - human
AAH56380	38614134	Ampd3 protein [Mus musculus]
O08739	2494043	AMP DEAMINASE 3 (AMP DEAMINASE ISOFORM E) (AMP DEAMINASE H-TYPE) (HEART-TYPE AMPD)
NP_113732	13928736	adenosine monophosphate deaminase 3 [Rattus norvegicus]
O09178	2494044	AMP deaminase 3 (AMP deaminase isoform E)
XP_420973	50747746	PREDICTED: similar to AMP deaminase 3 (Erythrocyte AMP deaminase) [Gallus gallus]
NP_956142	41054127	AMP deaminase 3 [Danio rerio]
CAG01709	47222742	unnamed protein product [Tetraodon nigroviridis]
NP_957187	41053780	hypothetical protein MGC77905 [Danio rerio]
XP_392957	48104570	similar to ENSANGP00000017310 [Apis mellifera]
AAH07183	13938134	Ampd3 protein [Mus musculus]
CAG05605	47220579	unnamed protein product [Tetraodon nigroviridis]
NP_620231	20302047	adenosine monophosphate deaminase 1 (isoform M) [Rattus norvegicus]
XP_540247	57098851	PREDICTED: similar to AMP deaminase 1 (AMP deaminase isoform M) [Canis familiaris]
CAF99638	47230445	unnamed protein product [Tetraodon nigroviridis]
XP_513671	55587796	PREDICTED: adenosine monophosphate deaminase 1 (isoform M) [Pan troglodytes]
CAI18828	56203368	adenosine monophosphate deaminase 1 (isoform M) [Homo sapiens]
CAI18829	56203369	OTTHUMP00000059283 [Homo sapiens]
CAI18830	56203370	adenosine monophosphate deaminase 1 (isoform M) [Homo sapiens]
EAA19931	23484684	AMP deaminase homolog [Plasmodium yoelii yoelii]
CAH99706	56500932	AMP deaminase, putative [Plasmodium berghei]
XP_131103	38076931	similar to AMP deaminase 1 (Myoadenylate deaminase) (AMP deaminase isoform M) [Mus musculus]
CAH77387	56523366	AMP deaminase, putative [Plasmodium chabaudi]

Table 7. Examples of acetoacetyl-CoA thiolase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
P10551	135758	Acetyl-CoA acetyltransferase (Acetoacetyl-CoA thiolase)
Q04677	418002	Acetyl-CoA acetyltransferase IB (Peroxisomal acetoacetyl-CoA thiolase) (Thiolase IB)
Q12598	34925109	Acetyl-CoA acetyltransferase IA (Peroxisomal acetoacetyl-CoA thiolase) (Thiolase IA)
T10247	7433657	acetyl-CoA C-acetyltransferase (EC 2.3.1.9), cytosolic - radish
T42741	11257345	probable acetyl-CoA C-acetyltransferase (EC 2.3.1.9) - fission yeast (Schizosaccharomyces pombe)
AAL18924	16417944	acetyl Co-A acetyltransferase [Hevea brasiliensis]
AAM67058	21618008	acetoacyl-CoA-thiolase [Arabidopsis thaliana]
AAO51605	28829030	similar to acetyl-coa acetyltransferase (EC 2.3.1.9) [Schizosaccharomyces pombe]
AAU95618	53854350	cytosolic acetoacetyl-coenzyme A thiolase [Nicotiana tabacum]
AAU95619	53854352	peroxisomal acetoacetyl-coenzyme A thiolase [Nicotiana tabacum]
BAA97003	8777413	acetyl-CoA C-acetyltransferase [Arabidopsis thaliana]
CAE76429	38567134	probable acetoacetyl-CoA thiolase [Neurospora crassa]
EAK90852	46431255	hypothetical protein CaO19.1591 [Candida albicans SC5314]
EAL32264	54643520	GA10651-PA [Drosophila pseudoobscura]
NP_015297	6325229	Acetyl-CoA C-acetyltransferase (acetoacetyl-CoA thiolase) [Saccharomyces cerevisiae]
NP_568694	30695411	acetyl-CoA C-acyltransferase, putative /.3-ketoacyl-CoA thiolase, putative [Arabidopsis thaliana]
NP_572414	24640423	CG10932-PA [Drosophila melanogaster]
NP_596686	19113478	acetyl-coa acetyltransferase (EC 2.3.1.9) [Schizosaccharomyces pombe]
NP_851154	30695409	acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative [Arabidopsis thaliana]
NP_908411	34894172	putative acetoacetyl-coenzyme A thiolase [Oryza sativa (japonica cultivar-group)]
NP_974900	42573608	acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative [Arabidopsis thaliana]
NP_974901	42573610	acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative [Arabidopsis thaliana]
NP_984262	45188039	ADR165Cp [Eremothecium gossypii]
XP_389497	46134945	hypothetical protein FG09321.1 [Gibberella zeae PH-1]
XP_401186	49074048	hypothetical protein UM03571.1 [Ustilago maydis 521]
XP_405546	49087148	hypothetical protein AN1409.2 [Aspergillus nidulans FGSC A4]
XP_449306	50293789	unnamed protein product [Candida glabrata]
XP_449306	50293789	unnamed protein product [Candida glabrata]
XP_450298	50899020	putative acetyl-CoA C-acyltransferase [Oryza sativa (japonica cultivar-group)]
XP_453599	50307241	unnamed protein product [Kluyveromyces lactis]
XP_460741	50424309	unnamed protein product [Debaryomyces hansenii]
XP_500646	50546253	hypothetical protein [Yarrowia lipolytica]

Table 8. Examples of HMG-CoA synthase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
B55729	1083370	hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5), mitochondrial - mouse

P54869	1708235	Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor (HMG-CoA synthase)
S13887	86312	hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - chicken
S27197	284048	hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5), cytosolic, fibroblast isoform - human
AAA37076	387072	3-hydroxy-3-methylglutaryl coenzyme A synthase (HMG CoA)
AAF89580	9621905	3-hydroxy-3-methylglutaryl coenzyme A synthase [Dendroctonus jeffreyi]
AAH00297	33991031	HMGCS1 protein [Homo sapiens]
AAH31363	21618633	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 [Mus musculus]
AAH42929	27552834	Hmgcs1-prov protein [Xenopus laevis]
AAH79694	50925193	MGC80816 protein [Xenopus laevis]
AAH83543	54035469	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 [Rattus norvegicus]
AAO52569	28830079	similar to Homo sapiens (Human). Hypothetical protein FLJ40785 [Dictyostelium discoideum]
AAP35966	30583443	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble) [Homo sapiens]
BAB23657	12836439	unnamed protein product [Mus musculus]
BAC04559	21754758	unnamed protein product [Homo sapiens]
BAC05233	21758044	unnamed protein product [Mus musculus]
CAA52032	1772495	hydroxymethylglutaryl-CoA synthase [Blattella germanica]
CAC18553	11602786	putative 3-hydroxy-3-methylglutaryl coenzyme A synthase [Phycomyces blakesleeanus]
CAG33131	48145817	HMGCS2 [Homo sapiens]
CAH92111	55730782	hypothetical protein [Pongo pygmaeus]
CAI22408	56205097	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial) [Homo sapiens]
EAK97451	46438115	hypothetical protein CaO19.7312 [Candida albicans SC5314]
EAL25034	54635631	GA18098-PA [Drosophila pseudoobscura]
NP_002121	54020720	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble) [Homo sapiens]
NP_013580	6323509	3-hydroxy-3-methylglutaryl-CoA (HMG-CoA) synthase [Saccharomyces cerevisiae]
NP_032282	31560689	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 [Mus musculus]
NP_058964	8393538	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 [Rattus norvegicus]
NP_593859	19114771	hydroxymethylglutaryl-coa synthase (EC 4.1.3.5) [Schizosaccharomyces pombe]
NP_666054	31981842	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 [Mus musculus]
NP_725570	24654139	CG4311-PE, isoform E [Drosophila melanogaster]
NP_775117	27465521	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 [Rattus norvegicus]
NP_957379	41055180	similar to 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 [Danio rerio]
NP_983739	45187516	ADL356Cp [Eremothecium gossypii]
NP_990742	45382279	3-hydroxy-3-methylglutaryl-CoA synthase [Gallus gallus]
NP_999545	47523816	hydroxymethylglutaryl-CoA synthase [Sus scrofa]
XP_315872	58387870	ENSANGP00000017491 [Anopheles gambiae str. PEST]
XP_323241	32405256	probable hydroxymethylglutaryl-CoA synthase [MIPS] [Neurospora

		crassa]
XP_368218	39973655	hypothetical protein MG01026.4 [Magnaporthe grisea 70-15]
XP_389442	46134253	conserved hypothetical protein [Gibberella zeae PH-1]
XP_397202	48141273	similar to CG4311-PA [Apis mellifera]
XP_402977	49078452	hypothetical protein UM05362.1 [Ustilago maydis 521]
XP_409060	49095198	hypothetical protein AN4923.2 [Aspergillus nidulans FGSC A4]
XP_446972	50289085	unnamed protein product [Candida glabrata]
XP_453529	50307101	unnamed protein product [Kluyveromyces lactis]
XP_456470	50405663	unnamed protein product [Debaryomyces hansenii]
XP_506052	50557288	hypothetical protein [Yarrowia lipolytica]
XP_513693	55587844	PREDICTED: 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial) [Pan troglodytes]
XP_536483	57085299	PREDICTED: similar to HMGCS1 protein [Canis familiaris]
XP_569805	58265298	hydroxymethylglutaryl-CoA synthase, putative [Cryptococcus
XP_571930	58269548	conserved hypothetical protein [Cryptococcus neoformans var. neoformans JEC21]

Table 9. Examples of HMG-CoA reductase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
A23586	90238	hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) - golden hamster
O74164	11132850	3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMG-CoA reductase)
P51639	1708252	3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMG-CoA reductase)
P54960	1708251	3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMG-CoA reductase)
Q12649	18276268	3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMG-CoA

		reductase)
Q29512	2495262	3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMG-CoA reductase)
Q9Y7D2	11133211	3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMG-CoA reductase)
S30338	422383	hydroxymethylglutaryl-CoA reductase (NADPH2) (EC 1.1.1.34) - German cockroach
S72194	7450066	hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) - fission yeast (Schizosaccharomyces pombe)
AAA36989	387052	3-hydroxy-3-methylglutaryl coenzyme A [Mesocricetus auratus]
AAA37077	305355	3-hydroxy-3-methylglutaral coenzyme A reductase (EC 1.1.1.34)
AAA49740	214237	3-hydroxy-3-methylglutaryl-coenzyme A reductase
AAD20975	9817458	3-hydroxy-3-methylglutaryl coenzyme A reductase [Ips paraconfusus]
AAH74197	49257596	Unknown (protein for MGC:82101) [Xenopus laevis]
AAL09351	15824453	3-hydroxy-3-methylglutaryl coenzyme A reductase [Ips pini]
AAO85434	29468180	HMG-CoA reductase [Aspergillus nidulans]
AAP72015	32165622	3-hydroxy-3-methylglutaryl-Coenzyme A reductase [Homo sapiens]
AAR02862	45272118	HMG-CoA reductase [Dicentrarchus labrax]
AAT92819	51013051	YLR450W [Saccharomyces cerevisiae]
BAC20567	23574646	HMG-CoA reductase [Penicillium citrinum]
CAA63970	4376229	HMG-CoA-reductase; hydroxymethylglutaryl-CoA reductase (NADPH) [Gibberella fujikuroi]
CAE47850	41581201	3-hydroxy-3-methylglutaryl-coenzyme a reductase, putative [Aspergillus fumigatus]
CAF92135	47213283	unnamed protein product [Tetraodon nigroviridis]
CAH92577	55731745	hypothetical protein [Pongo pygmaeus]
EAK94577	46435190	hypothetical protein CaO19.8633 [Candida albicans SC5314]
EAL20195	50257490	hypothetical protein CNBF0070 [Cryptococcus neoformans var. neoformans B-3501A]
AAF80374	8886086	HMG-CoA reductase [Dendroctonus jeffreyi]
NP_013555	6323483	Hmg2p [Saccharomyces cerevisiae]
NP_013636	6323565	Hmg1p [Saccharomyces cerevisiae]
NP_032281	56119096	3-hydroxy-3-methylglutaryl-Coenzyme A reductase [Mus musculus]
NP_037266	40538852	3-hydroxy-3-methylglutaryl-Coenzyme A reductase [Rattus norvegicus]
NP_588235	19075735	3-hydroxy-3-methylglutaryl-coenzyme a reductase [Schizosaccharomyces pombe]
NP_985010	45190756	AER152Wp [Eremothecium gossypii]
NP_989816	45383193	3-hydroxy-3-methylglutaryl-CoA reductase [Gallus gallus]
NP_999724	47551099	HMGCoA reductase [Strongylocentrotus purpuratus]
XP_324892	32408825	hypothetical protein [Neurospora crassa]
XP_364130	39955070	hypothetical protein MG08975.4 [Magnaporthe grisea 70-15]
XP_389373	46134115	hypothetical protein FG09197.1 [Gibberella zeae PH-1]
XP_400629	49072680	hypothetical protein UM03014.1 [Ustilago maydis 521]
XP_405730	49087632	hypothetical protein AN1593.2 [Aspergillus nidulans FGSC A4]
XP_407954	49092986	hypothetical protein AN3817.2 [Aspergillus nidulans FGSC A4]
XP_449268	50293713	unnamed protein product [Candida glabrata]
XP_451740	50303597	unnamed protein product [Kluyveromyces lactis]
XP_458872	50420671	unnamed protein product [Debaryomyces hansenii]
XP_503558	50552167	hypothetical protein [Yarrowia lipolytica]
XP_536323	57084803	PREDICTED: similar to 3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMG-CoA reductase) [Canis s]

XP_571450	58268588	hydroxymethylglutaryl-CoA reductase (NADPH), putative [Cryptococcus neoformans var.neoformans JEC21]

Table 10. Examples of mevalonate kinase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
XP_386088	46123069	hypothetical protein FG05912.1 [Gibberella zeae PH-1]
XP_408006	49093090	hypothetical protein AN3869.2 [Aspergillus nidulans FGSC A4]
XP_370449	39978123	hypothetical protein MG06946.4 [Magnaporthe grisea 70-15]
EAL04797	46445529	hypothetical protein CaO19.4809 [Candida albicans SC5314]
XP_322935	32404644	hypothetical protein ((AL513444) related to MEVALONATE KINASE [Neurospora crassa])
NP_001007	55925207	zgc:103473 [Danio rerio]
XP_460851	50424525	unnamed protein product [Debaryomyces hansenii]
XP_567851	58260882	cystathionine beta-lyase, putative [Cryptococcus neoformans var. neoformans JEC21]
XP_567850	58260880	cystathionine beta-lyase, putative [Cryptococcus neoformans var. neoformans JEC21]
AAQ02416	33303805	mevalonate kinase [synthetic construct]
CAA53059	450346	unnamed protein product [Hepatitis B virus]

AAH16140	16359371	MVK protein [Homo sapiens]
AAH05606	13542811	Mevalonate kinase [Mus musculus]
XP_403111	49078786	hypothetical protein UM05496.1 [Ustilago maydis 521]
XP_452532	50305147	unnamed protein product [Kluyveromyces lactis]
CAG08527	47226511	unnamed protein product [Tetraodon nigroviridis]
XP_446138	50287417	unnamed protein product [Candida glabrata]
AAO51522	28828936	similar to Rattus norvegicus (Rat). Mevalonate kinase (EC 2.7.1.36) (MK) [Dictyostelium discoideum]
NP_985191	45190937	AER335Wp [Eremothecium gossypii]
XP_500956	50546973	hypothetical protein [Yarrowia lipolytica]
NP_013935	6323864	Erg12p [Saccharomyces cerevisiae]
AAD45421	5578718	mevalonate kinase [Arabidopsis thaliana]
NP_920723	37532842	putative mevalonate kinase [Oryza sativa (japonica cultivar-group)]
NP_851084	30690651	mevalonate kinase (MK) [Arabidopsis thaliana]
AAL18925	16417946	mevalonate kinase [Hevea brasiliensis]
NP_788338	28573850	CG33009-PA, isoform A [Drosophila melanogaster]
AAU20834	51988124	Hypothetical protein Y42G9A.4b [Caenorhabditis elegans]
AAU87813	52839819	Hypothetical protein Y42G9A.4d [Caenorhabditis elegans]
AAU20835	51988125	Hypothetical protein Y42G9A.4c [Caenorhabditis elegans]
YP_183887	57641409	mevalonate kinase [Thermococcus kodakaraensis KOD1]
NP_143478	14591399	mevalonate kinase [Pyrococcus horikoshii OT3]
BAA24409	2804172	mevalonate kinase [Saccharomyces cerevisiae]
NP_126232	14520757	mevalonate kinase [Pyrococcus abyssi GE5]
XP_522574	55639331	PREDICTED: similar to Mevalonate kinase (MK) [Pan troglodytes]
NP_071114	11499870	mevalonate kinase (mvk) [Archaeoglobus fulgidus DSM 4304]
XP_423949	50797461	PREDICTED: similar to mevalonate kinase [Gallus gallus]
NP_633786	21227864	Mevalonate kinase [Methanosarcina mazei Go1]
ZP_002971	48840229	COG1577: Mevalonate kinase [Methanosarcina barkeri str. fusaro]
EAH50787	44170778	unknown [environmental sequence]
NP_615566	20089491	mevalonate kinase [Methanosarcina acetivorans C2A]
1VISA	40890012	Chain A, Crystal Structure Of Mevalonate Kinase
EAK03559	44549994	unknown [environmental sequence]
NP_248080	15669275	mevalonate kinase [Methanocaldococcus jannaschii DSM 2661]
1KKHA	20150886	Chain A, Crystal Structure Of The Methanococcus Jannaschii Mevalonate Kinase
Q50559	2497518	Mevalonate kinase (MK)
CAF88123	47200914	unnamed protein product [Tetraodon nigroviridis]
NP_275189	15678075	mevalonate kinase [Methanothermobacter thermautotrophicus str. Delta H]
EAI88745	44383877	unknown [environmental sequence]
ZP_002040	46141948	COG1577: Mevalonate kinase [Methanococcoides burtonii DSM 6242]
XP_543435	57105916	PREDICTED: similar to Mevalonate kinase (MK) [Canis familiaris]
EAI38920	44313360	unknown [environmental sequence]
NP_148611	14602065	mevalonate kinase [Aeropyrum pernix K1]
EAD08953	43286228	unknown [environmental sequence]
EAD45697	43361720	unknown [environmental sequence]
YP_134862	55377012	mevalonate kinase [Haloarcula marismortui ATCC 43049]
NP_720650	24378695	putative mevalonate kinase [Streptococcus mutans UA159]
NP_614276	20094429	Mevalonate kinase [Methanopyrus kandleri AV19]
E84270	25409931	mevalonate kinase [imported] - Halobacterium sp. NRC-1
NP_691146	23097680	mevalonate kinase [Oceanobacillus iheyensis HTE831]
ZP_003233	48870579	COG1577: Mevalonate kinase [Pediococcus pentosaceus ATCC

		25745]
AAG02440	9937386	mevalonate kinase [Enterococcus faecalis]
EAD12278	43292898	unknown [environmental sequence]
NP_498328	17555862	mevalonate kinase (64.1 kD) (3H214) [Caenorhabditis elegans]
EAB31483	42928976	unknown [environmental sequence]
ZP_003319	50590618	COG1577: Mevalonate kinase [Streptococcus suis 89/1591]
NP_814642	29375488	mevalonate kinase [Enterococcus faecalis V583]
AC1434	25514495	mevalonate kinase homolog lin0010 [imported] - Listeria innocua (strain Clip11262)
ZP_003577	53796847	COG1577: Mevalonate kinase [Chloroflexus aurantiacus]
EAD82048	43454743	unknown [environmental sequence]
CAE73618	39586491	Hypothetical protein CBG21109 [Caenorhabditis briggsae]
YP_012624	46906235	mevalonate kinase [Listeria monocytogenes str. 4b F2365]
NP_988455	45358898	Mevalonate kinase [Methanococcus maripaludis S2]
ZP_002348	47097293	mevalonate kinase [Listeria monocytogenes str. 1/2a F6854]
ZP_002862	48824993	COG1577: Mevalonate kinase [Enterococcus faecium]
ZP_002307	47093020	mevalonate kinase [Listeria monocytogenes str. 4b H7858]
NP_597102	19173299	MEVALONATE KINASE [Encephalitozoon cuniculi]
CAD24422	20429111	phosphomevalonate kinase [Paracoccus zeaxanthinifaciens]
NP_785308	28378416	mevalonate kinase [Lactobacillus plantarum WCFS1]
EAA39098	29247539	GLP_305_18405_19430 [Giardia lamblia ATCC 50803]
NP_819638	29653946	phosphomevalonate kinase, putative [Coxiella burnetii RSA 493]
EAH49746	44168765	unknown [environmental sequence]
EAH49745	44168764	unknown [environmental sequence]
NP_378182	15922513	hypothetical protein ST2185 [Sulfolobus tokodaii str. 7]
ZP_000459	23002259	COG1577: Mevalonate kinase [Lactobacillus gasseri]
H90181	25393827	mevalonate kinase [imported] - Sulfolobus solfataricus
YP_054120	50405028	Mevalonate kinase, putative [Paramecium tetraurelia]
BAB07790	9695270	mevalonate kinase [Streptomyces sp. CL190]
AAG02435	9937379	mevalonate kinase [Staphylococcus epidermidis]
NP_560495	18313828	mevalonate kinase [Pyrobaculum aerophilum str. IM2]
YP_187834	57866187	mevalonate kinase [Staphylococcus epidermidis RP62A]
EAK40782	44602942	unknown [environmental sequence]
CAC51370	15212070	mevalonate kinase [Lactobacillus helveticus]
AAG02424	9937364	mevalonate kinase [Staphylococcus aureus]
YP_185521	57651465	mevalonate kinase [Staphylococcus aureus subsp. aureus COL]
YP_040044	49482820	mevalonate kinase [Staphylococcus aureus subsp. aureus MRSA252]
YP_194037	58337452	mevalonate kinase [Lactobacillus acidophilus NCFM]
D86675	25400965	mevalonate kinase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
NP_763916	27467279	mevalonate kinase [Staphylococcus epidermidis ATCC 12228]
CAF89434	47197810	unnamed protein product [Tetraodon nigroviridis]
EAF38333	43767792	unknown [environmental sequence]
EAK46841	44611394	unknown [environmental sequence]
H89827	25507776	mevalonate kinase [imported] - Staphylococcus aureus (strain N315)
ZP_003149	48861061	COG0153: Galactokinase [Microbulbifer degradans 2-40]
EAK17824	44570143	unknown [environmental sequence]
EAH86276	44235719	unknown [environmental sequence]
YP_118418	54024176	putative mevalonate kinase [Nocardia farcinica IFM 10152]
ZP_003196	48865749	COG1577: Mevalonate kinase [Oenococcus oeni PSU-1]
AAG02430	9937372	mevalonate kinase [Staphylococcus haemolyticus]
NP_269075	15674901	mevalonate kinase [Streptococcus pyogenes M1 GAS]

NP_802520	28896170	putative mevalonate kinase [Streptococcus pyogenes SSI-1]
AAL97579	19748102	mevalonate kinase [Streptococcus pyogenes MGAS8232]
ZP_003666	56808907	COG1577: Mevalonate kinase [Streptococcus pyogenes M49 591]
NP_965060	42519130	mevalonate kinase [Lactobacillus johnsonii NCC 533]
NP_819639	29653947	mevalonate kinase, putative [Coxiella burnetii RSA 493]
EAD97024	43484567	unknown [environmental sequence]
BAD86800	57753870	mevalonate kinase [Streptomyces sp. KO-3988]

Table 11. Examples of phosphomevalonate kinase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
AAA34596	171479	phosphomevalonate kinase
XP_452514	50305111	unnamed protein product [Kluyveromyces lactis]
NP_985210	45190956	AER354Wp [Eremothecium gossypii]
XP_446144	50287429	unnamed protein product [Candida glabrata]
XP_462340	50427455	unnamed protein product [Debaryomyces hansenii]
EAL04096	46444824	hypothetical protein CaO19.12076 [Candida albicans SC5314]
EAL03941	46444668	hypothetical protein CaO19.4606 [Candida albicans SC5314]
XP_503619	50552418	hypothetical protein [Yarrowia lipolytica]
XP_389940	46136497	hypothetical protein FG09764.1 [Gibberella zeae PH-1]
XP_329795	32418634	hypothetical protein [Neurospora crassa]
XP_369652	39976529	hypothetical protein MG05812.4 [Magnaporthe grisea 70-15]
XP_406448	49089559	hypothetical protein AN2311.2 [Aspergillus nidulans FGSC A4]
NP_593421	19114333	putative phosphomevalonate kinase [Schizosaccharomyces pombe]
XP_568385	58261950	expressed protein [Cryptococcus neoformans var. neoformans JEC21]
EAL17628	50254887	hypothetical protein CNBM0120 [Cryptococcus neoformans var. neoformans B-3501A]
AAL18926	16417948	phosphomevalonate kinase [Hevea brasiliensis]
BAD43274	51969164	hypothetical protein [Arabidopsis thaliana]
BAD44652	51971975	hypothetical protein [Arabidopsis thaliana]
XP_398375	49068172	hypothetical protein UM00760. 1 [Ustilago maydis 521]
BAD44486	51971643	hypothetical protein [Arabidopsis thaliana]
F90479	25393214	(Phospho) mevalonate kinase, probable [imported] - Sulfolobus solfataricus
YP_194039	58337454	phosphomevalonate kinase [Lactobacillus acidophilus NCFM]

Table 12. Examples of mevalonate pyrophosphate decarboxylase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
AAT93171	51013755	YNR043W [Saccharomyces cerevisiae]
1FI4A	13786942	Chain A, The X-Ray Crystal Structure Of Mevalonate 5-Diphosphate Decarboxylase At 2.3 Angstrom Resolution.
XP_455548	50311049	unnamed protein product [Kluyveromyces lactis]
XP_445335	50285813	unnamed protein product [Candida glabrata]
XP_456912	50409853	unnamed protein product [Debaryomyces hansenii]
NP_986435	45200865	AGL232Cp [Eremothecium gossypii]
AAF19399	6625790	diphosphomevalonate decarboxylase MVD1 [Candida albicans]
XP_328845	32416734	hypothetical protein [Neurospora crassa]
XP_505041	50555265	hypothetical protein [Yarrowia lipolytica]
NP_594027	19114939	diphosphomevalonate decarboxylase [Schizosaccharomyces pombe]
XP_364905	39963452	hypothetical protein MG09750.4 [Magnaporthe grisea 70-15]
XP_390600	46137817	hypothetical protein FG10424.1 [Gibberella zeae PH-1]
XP_408551	49094180	hypothetical protein AN4414.2 [Aspergillus nidulans FGSC A4]
AAA34506	7544604	ORF [Saccharomyces cerevisiae]
EAL18927	50256200	hypothetical protein CNBI1880 [Cryptococcus neoformans var. neoformans B-3501A]
XP_568247	58261674	diphosphomevalonate decarboxylase, putative [Cryptococcus neoformans var. neoformans JEC21]
XP_402794	49077992	hypothetical protein UM05179.1 [Ustilago maydis 521]
AAH81784	51980639	Mevalonate (diphospho) decarboxylase [Rattus norvegicus]
EAL00166	46440864	hypothetical protein CaO19.6105 [Candida albicans SC5314]
NP_619597	20149736	mevalonate (diphospho) decarboxylase [Mus musculus]
NP_112324	13592005	mevalonate (diphospho) decarboxylase [Rattus norvegicus]
BAC40852	26354448	unnamed protein product [Mus musculus]
XP_546783	57087071	Mevalonate pyrophosphate decarboxylase [Canis familiaris]
Q99JF5	23814095	Diphosphomevalonate decarboxylase (Mevalonate pyrophosphate decarboxylase)

AAH63907	39645379	LOC394871 protein [Xenopus tropicalis]
CAF99534	47230341	unnamed protein product [Tetraodon nigroviridis]
AAP35576	30582699	mevalonate (diphospho) decarboxylase [Homo sapiens]
AAP36301	30584105	Homo sapiens mevalonate (diphospho) decarboxylase [synthetic construct]
AAL18927	16417950	mevalonate disphosphate decarboxylase [Hevea brasiliensis]
AAV32433	54292590	mevalonate disphosphate decarboxylase [Ginkgo biloba]
AAP68208	31711704	At2g38700 [Arabidopsis thaliana]
AAM64988	21593039	mevalonate diphosphate decarboxylase [Arabidopsis thaliana]
NP_566995	18410026	mevalonate diphosphate decarboxylase, putative [Arabidopsis thaliana]
XP_423130	50771155	PREDICTED: similar to mevalonate pyrophosphate decarboxylase [Gallus gallus]
AAM65192	21593243	diphosphomevalonate decarboxylase-like protein [Arabidopsis thaliana]
NP_001007	55925435	zgc:100824 [Danio rerio]
NP_573068	28571205	CG8239-PA [Drosophila melanogaster]
BAD27942	50252009	putative mevalonate disphosphate decarboxylase [Oryza sativa (japonica cultivar-group)]
T47584	11281655	diphosphomevalonate decarboxylase (EC 4.1.1.33) F24B22.210 [similarity] - Arabidopsis thaliana
XP_307373	31196851	ENSANGP00000013738 [Anopheles gambiae str. PEST]
CAE73245	39591192	Hypothetical protein CBG20661 [Caenorhabditis briggsae]
NP_496966	17537201	mevalonate decarboxylase (41.5 kD) (2O512) [Caenorhabditis elegans]
XP_393230	48121058	similar to mevalonate pyrophosphate decarboxylase [Apis mellifera]
G90479	25393662	diphosphomevalonate decarboxylase, probable [imported] - Sulfolobus solfataricus
NP_496967	17537203	mevalonate decarboxylase (2O512) [Caenorhabditis elegans]
NP_691147	23097681	mevalonate diphosphate decarboxylase [Oceanobacillus iheyensis HTE831]
EAL29282	54640164	GA20922-PA [Drosophila pseudoobscura]
AD1434	25515042	mevalonate diphosphate decarboxylase homolog lin0011 [imported] - Listeria innocua (strain Clip11262)
ZP_002308	47093021	diphosphomevalonate decarboxylase [Listeria monocytogenes str. 4b H7858]
YP_012625	46906236	diphosphomevalonate decarboxylase [Listeria monocytogenes str. 4b F2365]
ZP_002348	47097294	diphosphomevalonate decarboxylase [Listeria monocytogenes str. 1/2a F6854]
NP_819637	29653945	diphosphomevalonate decarboxylase [Coxiella burnetii RSA 493]
NP_376888	15921219	hypothetical diphosphomevalonate decarboxylase [Sulfolobus tokodaii str. 7]
ZP_003319	50590617	COG3407: Mevalonate pyrophosphate decarboxylase [Streptococcus suis 89/1591]
NP_585805	19074299	MEVALONATE PYROPHOSPHATE DECARBOXYLASE [Encephalitozoon cuniculi]
YP_187835	57866188	mevalonate diphosphate decarboxylase [Staphylococcus epidermidis RP62A]
CAD24423	20429112	mevalonate diphosphate decarboxylase [Paracoccus zeaxanthinifaciens]
AAG02431	9937373	mevalonate diphosphate decarboxylase [Staphylococcus haemolyticus]

NP_763917	27467280	mevalonate diphosphate decarboxylase [Staphylococcus epidermidis ATCC 12228]
AAG02446	9937394	mevalonate diphosphate decarboxylase [Enterococcus faecium]
ZP_002863	48824994	COG3407: Mevalonate pyrophosphate decarboxylase [Enterococcus faecium]
AAG02441	9937387	mevalonate diphosphate decarboxylase [Enterococcus faecalis]
YP_185522	57651466	mevalonate diphosphate decarboxylase [Staphylococcus aureus subsp. aureus COL]
A89828	25505863	mevalonate diphosphate decarboxylase [imported] - Staphylococcus aureus (strain N315)
NP_814641	29375487	mevalonate diphosphate decarboxylase [Enterococcus faecalis V583]
YP_040045	49482821	mevalonate diphosphate decarboxylase [Staphylococcus aureus subsp. aureus MRSA252]
NP_785307	28378415	diphosphomevalonate decarboxylase [Lactobacillus plantarum WCFS1]
ZP_003196	48865750	COG3407: Mevalonate pyrophosphate decarboxylase [Oenococcus oeni PSU-1]
ZP_003233	48870580	COG3407: Mevalonate pyrophosphate decarboxylase [Pediococcus pentosaceus ATCC 25745]
E86675	25400967	diphosphomevalonate decarboxylase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
EAE31110	43552684	unknown [environmental sequence]
BAB07791	9695271	diphosphomevalonate decarboxylase [Streptomyces sp. CL190]
CAC51371	15212071	mevalonate diphosphate decarboxylase [Lactobacillus helveticus]
ZP_000459	23002258	COG3407: Mevalonate pyrophosphate decarboxylase [Lactobacillus gasseri]
NP_965061	42519131	mevalonate pyrophosphate decarboxylase [Lactobacillus johnsonii NCC 533]
BAD86801	57753871	mevalonate diphosphate decarboxylase [Streptomyces sp. KO-3988]
YP_194038	58337453	mevalonate diphosphate decarboxylase [Lactobacillus acidophilus NCFM]
YP_118419	54024177	putative diphosphomevalonate decarboxylase [Nocardia farcinica IFM 10152]
EAK18820	44571499	unknown [environmental sequence]
EAI85935	44379784	unknown [environmental sequence]
NP_721336	24379381	putative mevalonate diphosphate decarboxylase [Streptococcus mutans UA159]
D95044	25388338	diphosphomevalonate decarboxylase [imported] - Streptococcus pneumoniae (strain TIGR4)
AAG02456	9937408	mevalonate diphosphate decarboxylase [Streptococcus pneumoniae]
C97914	25511486	diphosphomevalonate decarboxylase (EC 4.1.1.33) [imported] - Streptococcus pneumoniae (strain R6)
EAK47683	44612560	unknown [environmental sequence]
EAB86425	43039778	unknown [environmental sequence]
YP_140971	55822530	mevalonate pyrophosphate decarboxylase [Streptococcus thermophilus CNRZ1066]
YP_139081	55820639	mevalonate pyrophosphate decarboxylase [Streptococcus thermophilus LMG 18311]
BAD07376	40882372	mevalonate diphosphate decarboxylase [Actinoplanes sp. A40644]
NP_968512	42523132	Diphosphomevalonate decarboxylase [Bdellovibrio bacteriovorus HD100]
EAI06705	44265427	unknown [environmental sequence]
YP_060018	50914046	Diphosphomevalonate decarboxylase [Streptococcus pyogenes

		MGAS10394]
AAG02451	9937401	mevalonate diphosphate decarboxylase [Streptococcus pyogenes]
NP_269076	15674902	mevalonate pyrophosphate decarboxylase [Streptococcus pyogenes M1 GAS]
ZP_003666	56808906	COG3407: Mevalonate pyrophosphate decarboxylase [Streptococcus pyogenes M49 591]
NP_688323	22537472	diphosphomevalonate decarboxylase [Streptococcus agalactiae 2603V/R]
NP_735832	25011437	hypothetical protein gbs1395 [Streptococcus agalactiae NEM316]
EAC40267	43149093	unknown [environmental sequence]
AAL97580	19748103	mevalonate pyrophosphate decarboxylase [Streptococcus pyogenes MGAS8232]
EAI76915	44367119	unknown [environmental sequence]
EAD35042	43339207	unknown [environmental sequence]
YP_073129	51598941	mevalonate pyrophosphate decarboxylase [Borrelia garinii PBi]
EAI90092	44385501	unknown [environmental sequence]
BAB07818	9711347	mevalonate diphosphate decaroboxylase [Kitasatospora griseola]
EAD72850	43433025	unknown [environmental sequence]
NP_212820	15595031	mevalonate pyrophosphate decarboxylase [Borrelia burgdorferi B31]
YP_124337	54297968	hypothetical protein lpp2023 [Legionella pneumophila str. Paris]
YP_096056	52842257	mevalonate diphosphate decarboxylase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]
EAA39903	29248368	GLP_479_14176_13169 [Giardia lamblia ATCC 50803]
EAH06252	44088237	unknown [environmental sequence]
YP_127354	54294939	hypothetical protein lpl2018 [Legionella pneumophila str. Lens]
EAD45753	43361830	unknown [environmental sequence]
NP_802519	28896169	putative mevalonate pyrophosphate decarboxylase [Streptococcus pyogenes SSI-1]

Table 13. Examples of IPP isomerase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
NP_015208	6325140	Idi1p [Saccharomyces cerevisiae]
XP_448008	50291151	unnamed protein product [Candida glabrata]
NP_983828	45187605	ADL268Cp [Eremothecium gossypii]
XP_455121	50310203	unnamed protein product [Kluyveromyces lactis]
XP_462358	50427491	unnamed protein product [Debaryomyces hansenii]
EAL01685	46442395	potential isopentenyl diphosphate isomerase [Candida albicans SC5314]
XP_504974	50555131	hypothetical protein [Yarrowia lipolytica]
XP_328425	32415894	hypothetical protein [Neurospora crassa]
XP_367200	39971619	hypothetical protein MG07125.4 [Magnaporthe grisea 70-15]
XP_389898	46136413	conserved hypothetical protein [Gibberella zeae PH-1]
XP_404716	49085144	hypothetical protein AN0579.2 [Aspergillus nidulans FGSC A4]
CAD37150	21627818	isopentenyl-diphosphate delta-isomerase [Aspergillus fumigatus]
NP_595164	19111956	isopentenyl-diphosphate delta-isomerase [Schizosaccharomyces pombe]
XP_566641	58258457	isopentenyl-diphosphate delta-isomerase, putative [Cryptococcus neoformans var. neoformans JEC21]
XP_402453	49077100	hypothetical protein UM04838.1 [Ustilago maydis 521]
O35586	6225528	Isopentenyl-diphosphate delta-isomerase 1 (IPP isomerase 1)
AAP36609	30584713	Homo sapiens isopentenyl-diphosphate delta isomerase [synthetic construct]
AAF37873	7188790	isopentenyl pyrophosphate isomerase [Dictyostelium discoideum]
NP_445991	16758306	isopentenyl-diphosphate delta isomerase [Rattus norvegicus]
O42641	6225529	Isopentenyl-diphosphate delta-isomerase (IPP isomerase) (Isopentenyl pyrophosphate isomerase)
BAA33979	3790386	IPP isomerase [Xanthophyllomyces dendrorhous]
Q13907	6225527	Isopentenyl-diphosphate delta-isomerase 1 (IPP isomerase 1)
AAH22418	48257241	IDI1 protein [Homo sapiens]
AAH19227	48257312	IDI1 protein [Homo sapiens]
AAH57827	35505325	IDI1 protein [Homo sapiens]
NP_004499	40018633	isopentenyl-diphosphate delta isomerase [Homo sapiens]
AAH89786	58477715	Unknown (protein for MGC:108635) [Rattus norvegicus]
CAH91844	55730243	hypothetical protein [Pongo pygmaeus]
XP_418561	50732281	PREDICTED: similar to isopentenyl-diphosphate delta isomerase; IPP isomerase [Gallus gallus]
AAH06999	48257093	IDI1 protein [Homo sapiens]
CAF98782	47225155	unnamed protein product [Tetraodon nigroviridis]
NP_808875	29366820	isopentenyl-diphosphate delta isomerase [Mus musculus]
XP_507622	55633353	PREDICTED: similar to isopentenyl-diphosphate delta isomerase; IPP isomerase [Pan troglodytes]
AAH82648	52139082	LOC494671 protein [Xenopus laevis]

NP_001011	58332496	hypothetical LOC496783 [Xenopus tropicalis]
AAF29976	6856556	isopentenyl pyrophosphate:dimethyllallyl pyrophosphate isomerase [Lactuca sativa]
AAG10423	9971806	isopentenyl pyrophosphate:dimethyllallyl pyrophosphate isomerase [Tagetes erecta]
O48964	6225525	Isopentenyl-diphosphate delta-isomerase I (IPP isomerase I) (Isopentenyl pyrophosphate isomerase I)
AAF29973	6856550	isopentenyl pyrophosphate:dimethyllallyl pyrophosphate isomerase [Adonis palaestina]
AAF29977	6856558	isopentenyl pyrophosphate:dimethyllallyl pyrophosphate isomerase [Tagetes erecta]
AAQ84167	35186998	isopentenyl pyrophosphate isomerase [Pueraria montana var. lobata]
AAF29974	6856552	isopentenyl pyrophosphate:dimethyllallyl pyrophosphate isomerase [Adonis palaestina]
Q39472	6225526	Isopentenyl-diphosphate delta-isomerase I (IPP isomerase I) (Isopentenyl pyrophosphate isomerase I)
S49588	1085973	isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) 1 - Clarkia breweri (fragment)
AAL91980	19568939	isopentenyl pyrophosphate isomerase IDI1 [Melaleuca alternifolia]
BAB40973	13603406	isopentenyl diphosphate isomerase 1 [Nicotiana tabacum]
AAF29975	6856554	isopentenyl pyrophosphate:dimethyllallyl pyrophosphate isomerase [Lactuca sativa]
T52027	25493162	isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) 1 [validated] - Haematococcus pluvialis
AAL91979	19568937	isopentenyl pyrophosphate isomerase IDI2 [Melaleuca alternifolia]
T46812	11362218	isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) [imported] - Haematococcus pluvialis
T51248	11362217	isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) 2 [validated] - Haematococcus pluvialis
BAB40974	13603408	isopentenyl diphosphate isomerase 2 [Nicotiana tabacum]
O48965	6225532	Isopentenyl-diphosphate delta-isomerase II (IPP isomerase II) (Isopentenyl pyrophosphate isomerase II)
XP_225509	34877710	similar to isopentenyl diphosphate delta-isomerase type 2 [Rattus norvegicus]
XP_506401	51963472	PREDICTED OJ1612_A04.101 gene product [Oryza sativa (japonica cultivar-group)]
AAF29978	6856560	isopentenyl pyrophosphate:dimethyllallyl pyrophosphate isomerase [Oryza sativa]
AAH76541	50369278	Unknown (protein for IMAGE:7037641) [Danio rerio]
AAT94033	51038230	putative isopentenyl-diphosphate delta-isomerase [Oryza sativa (japonica cultivar-group)]
XP_225502	34876517	similar to isopentenyl diphosphate delta-isomerase type 2 [Rattus norvegicus]
Q39471	6225533	Isopentenyl-diphosphate delta-isomerase II (IPP isomerase II) (Isopentenyl pyrophosphate isomerase II)
AAB67743	1213450	isopentenyl pyrophosphate isomerase [Clarkia breweri]
NP_197148	22326844	isopentenyl-diphosphate delta-isomerase I [Arabidopsis thaliana]
BAB09611	9759126	isopentenyl pyrophosphate:dimethyllallyl pyrophosphate isomerase [Arabidopsis thaliana]
AAD41766	5305669	isopentenyl pyrophosphate isomerase [Hevea brasiliensis]
AAB67741	1213442	isopentenyl pyrophosphate isomerase [Arabidopsis thaliana]
XP_395125	48101420	similar to CG8646-PA [Apis mellifera]
AAN28784	23505849	At3g02780/F13E7_28 [Arabidopsis thaliana]

AAF36996	7110585	isopentenyl pyrophosphate:dimethylallyl pyrophosphate isomerase [Brassica oleracea var. botrytis]
BAB16690	15289752	putative IPP isomerase [Eucommia ulmoides]
AAQ14869	33340598	isopentenyl pyrophosphate isomerase [Zea mays]
BAC65421	28971819	isopentenyl-diphosphate delta-isomerase [Periploca sepium]
S71369	2129625	isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) 1 - Arabidopsis thaliana
AAF29979	6856562	isopentenyl pyrophosphate:dimethyllallyl pyrophosphate isomerase [Arabidopsis thaliana]
AAF29980	6856564	isopentenyl pyrophosphate:dimethyllallyl pyrophosphate isomerase [Arabidopsis thaliana]
AAP21674	30267831	isopentenyl diphosphate delta-isomerase type 2 [Mus musculus]
Q39664	6225534	Isopentenyl-diphosphate delta-isomerase II (IPP isomerase II) (Isopentenyl pyrophosphate isomerase II)
NP_650962	24648688	CG5919-PA [Drosophila melanogaster]
AAM50284	21429130	RE22306p [Drosophila melanogaster]
XP_321388	58395620	ENSANGP00000011643 [Anopheles gambiae str. PEST]
Q9BXS1	20978506	Isopentenyl-diphosphate delta-isomerase 2 (IPP isomerase 2))
T07979	7484383	isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) ipi1 - Chlamydomonas reinhardtii
XP_225508	34876527	similar to diphosphate dimethylallyl diphosphate isomerase 2 [Rattus norvegicus]
AAT92102	51011386	isopentenyl-diphosphate delta-isomerase [Ixodes pacificus]
XP_225507	34876555	similar to isopentenyl diphosphate delta-isomerase type 2 [Rattus norvegicus]
XP_344623	34876537	similar to isopentenyl diphosphate delta-isomerase type 2 [Rattus norvegicus]
S44843	630677	K06H7.3 protein - Caenorhabditis elegans
XP_225498	27687955	similar to diphosphate dimethylallyl diphosphate isomerase 2 [Rattus norvegicus]
AAT08468	47013849	isopentenyl-diphosphate isomerase [Caenorhabditis elegans]
EAI79636	44370808	unknown [environmental sequence]
CAE75055	39587401	Hypothetical protein CBG22969 [Caenorhabditis briggsae]
EAL04047	46444775	potential isopentenyl diphosphate isomerase fragment [Candida albicans SC5314]
XP_225528	34876543	similar to isopentenyl diphosphate delta-isomerase type 2 [Rattus norvegicus]
XP_544282	57040602	PREDICTED: similar to isopentenyl-diphosphate delta isomerase [Canis familiaris]
XP_225511	27688013	similar to diphosphate dimethylallyl diphosphate isomerase 2 [Rattus norvegicus]
P26173	114853	Isopentenyl-diphosphate delta-isomerase (IPP isomerase) (Bacteriochlorophyll synthase 20 kDa chain)
EAJ04069	44405322	unknown [environmental sequence]
EAH27496	44127513	unknown [environmental sequence]
AAF91499	9653280	isopentenyl pyrophosphate isomerase [Daucus carota]
AAM48661	21328655	isopentyl-diphosphate delta-isomerase [uncultured proteobacterium]
EAK17826	44570145	unknown [environmental sequence]
EAD59515	43391069	unknown [environmental sequence]
YP_128702	54307682	hypothetical isopentenyldiphosphate isomerase [Photobacterium profundum SS9]
EAK66656	44639203	unknown [environmental sequence]
YP_118189	54023947	putative isopentenyldiphosphate isomerase [Nocardia farcinica IFM

		10152]
T50740	11282665	isopentenyl diphosphate isomerase homolog [imported] - Rhodobacter sphaeroides
ZP_002077	46193541	COG1443: Isopentenyldiphosphate isomerase [Rhodobacter sphaeroides 2.4.1]
EAK16470	44568229	unknown [environmental sequence]
YP_165403	56695056	isopentyl-diphosphate delta-isomerase [Silicibacter pomeroyi DSS-3]
EAD08775	43285885	unknown [environmental sequence]
YP_195623	58616494	putative isopentenyl-diphosphate delta-isomerase [Azoarcus sp. EbN1]
EAI38918	44313358	unknown [environmental sequence]
NP_930583	37527239	hypothetical protein plu3365 [Photorhabdus luminescens subsp. laumondii TTO1]
YP_160254	56478665	isopentenyl-diphosphate delta-isomerase [Azoarcus sp. EbN1]
EAH69842	44206571	unknown [environmental sequence]
EAK26254	44582307	unknown [environmental sequence]
AAR24381	38569721	isopentyl-diphosphate delta isomerase [Sus scrofa]
AAM48607	21328600	isopentenyl-diphosphate delta-isomerase, putative [uncultured proteobacterium]
EAD82049	43454744	unknown [environmental sequence]
ZP_001924	45914126	COG1443: Isopentenyldiphosphate isomerase [Mesorhizobium sp. BNC1]
YP_056780	50843553	isopentenyl-diphosphate delta-isomerase [Propionibacterium acnes KPA171202]
YP_050880	50121713	putative isopentenyl-diphosphate delta-isomerase [Erwinia carotovora subsp. atroseptica SCRI1043]
EAF29235	43749645	unknown [environmental sequence]
NP_630823	21225044	putative IPP isomerase [Streptomyces coelicolor A3(2)]
Q82MJ7	34582349	Isopentenyl-diphosphate delta-isomerase (IPP isomerase) (Isopentenyl pyrophosphate isomerase)
ZP_003374	52010110	COG1443: Isopentenyldiphosphate isomerase [Silicibacter sp. TM1040]
AAS75819	45737905	isopentenyl/dimethylallyl diphosphate isomerase [Nicotiana benthamiana]
Q8KP37	30913023	Isopentenyl-diphosphate delta-isomerase (IPP isomerase) (Isopentenyl pyrophosphate isomerase)
XP_507621	55633351	PREDICTED: similar to isopentenyl-diphosphate delta isomerase 2 [Pan troglodytes]
XP_344621	34876521	similar to diphosphate dimethylallyl diphosphate isomerase 2 [Rattus norvegicus]
XP_346322	34880719	similar to diphosphate dimethylallyl diphosphate isomerase 2 [Rattus norvegicus]
YP_152060	56414985	probable isomerase [Salmonella enterica subsp. enterica serovar Paratypi A str. ATCC 9150]
AAT42442	48429280	putative isopentenyl diphosphate isomerase [Edwardsiella ictaluri]
Q9KK75	13878536	Isopentenyl-diphosphate delta-isomerase (IPP isomerase) (Isopentenyl pyrophosphate isomerase)
NP_806649	29143307	probable isomerase [Salmonella enterica subsp. enterica serovar Typhi Ty2]
YP_063124	50955836	isopentenyldiphosphate isomerase [Leifsonia xyli subsp. xyli str. CTCB07]
Q8FND7	46395593	Isopentenyl-diphosphate delta-isomerase (IPP isomerase)

		(Isopentenyl pyrophosphate isomerase)
CAF20647	41326485	ISOPENTENYLDIPHOSPHATE ISOMERASE [Corynebacterium glutamicum ATCC 13032]
Q8NN99	23821718	Isopentenyl-diphosphate delta-isomerase (IPP isomerase) (Isopentenyl pyrophosphate isomerase)
Q7X5H2	46395586	Isopentenyl-diphosphate delta-isomerase (IPP isomerase) (Isopentenyl pyrophosphate isomerase)
NP_336246	15841209	isopentenyl-diphosphate delta-isomerase [Mycobacterium tuberculosis CDC1551]
Q83MJ9	46395588	Isopentenyl-diphosphate delta-isomerase (IPP isomerase) (Isopentenyl pyrophosphate isomerase)
P60923	46395576	Isopentenyl-diphosphate delta-isomerase (IPP isomerase) (Isopentenyl pyrophosphate isomerase)
Q8FE75	31563050	Isopentenyl-diphosphate delta-isomerase (IPP isomerase) (Isopentenyl pyrophosphate isomerase)
1R67A	38493022	Chain A, Y104a Mutant Of E. Coli Ipp Isomerase
Q9KWD1	13878537	Isopentenyl-diphosphate delta-isomerase (IPP isomerase)
Q7VEU0	46395585	Isopentenyl-diphosphate delta-isomerase (IPP isomerase)
B84333	25410326	isopentenyl pyrophosphate isomerase [imported] - Halobacterium sp. NRC-1
NP_417365	16130791	isopentenyl diphosphate isomerase [Escherichia coli K12]
E85944	25355426	probable enzyme Z4227 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
1HZTA	15826050	Chain A, Crystal Structure Of Metal-Free Isopentenyl Diphosphate:dimethylallyl Diphosphate Isomerase
1PVFB	50513321	Chain B, E. Coli Ipp Isomerase In Complex With Diphosphate
EAD63579	43403471	unknown [environmental sequence]
1I9AB	13786886	Chain B, Mevalonate 5-Diphosphate Decarboxylase And Isopentenyl Diphosphate Isomerase
YP_012992	46906603	MutT/nudix family protein [Listeria monocytogenes str. 4b F2365]
ZP_002293	47091503	MutT/nudix family protein [Listeria monocytogenes str. 4b H7858]
EAI37194	44310821	unknown [environmental sequence]
YP_137864	55380014	probable isopentenyl-diphosphate delta-isomerase [Haloarcula marismortui ATCC 43049]
CAD92056	42516867	putative isopentenyl diphosphate isomerase type 1 [Haloferax mediterranei]
1OW2B	42543244	Chain B, Isopentenylpyrophosphate-Dimethylallylpyrophosphate Isomerase: Complex Of C67a Mutant With Eipp

Table 14. Examples of FPP synthase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
Q92250	2497455	Farnesyl pyrophosphate synthetase (FPP synthetase) (FPS) (Farnesyl diphosphate synthetase)
XP_363065	39948036	hypothetical protein MG08649.4 [Magnaporthe grisea 70-15]

XP_386960	46124813	FPPS_GIBFU Farnesyl pyrophosphate synthetase (FPP synthetase) (FPS) [Gibberella zeae PH-1]
Q92235	3122099	Farnesyl pyrophosphate synthetase (FPP synthetase) (FPS) (Farnesyl diphosphate synthetase)
XP_412149	49116518	hypothetical protein AN8012.2 [Aspergillus nidulans FGSC A4]
XP_503599	50552378	hypothetical protein [Yarrowia lipolytica]
NP_593299	19114211	farnesyl pyrophosphate synthetase [Schizosaccharomyces pombe]
CAD42869	21955860	farnesyl pyrophosphate synthase [Mucor circinelloides f. lusitanicus]
XP_448787	50292709	unnamed protein product [Candida glabrata]
NP_012368	6322294	Erg20p [Saccharomyces cerevisiae]
T42081	7433997	farnesyl-pyrophosphate synthetase - fission yeast (Schizosaccharomyces pombe) (fragment)
EAK93751	46434339	likely farnesyl diphosphate synthetase [Candida albicans SC5314]
XP_451300	50302727	FPPS_KLULA [Kluyveromyces lactis]
XP_571137	58267962	isoprenoid biosynthesis-related protein, putative [Cryptococcus neoformans var. neoformans JEC21]
XP_460720	50424267	unnamed protein product [Debaryomyces hansenii]
NP_984739	45190485	AEL122Wp [Eremothecium gossypii]
BAD15361	46367743	farnesyl diphosphate synthase [Lactarius chrysorrheus]
S71433	7433991	farnesyl-pyrophosphate synthetase - ergot fungus (fragment)
CAA65643	1523990	farnesyl pyrophosphate synthetase [Claviceps purpurea]
XP_399061	49069544	hypothetical protein UM01446.1 [Ustilago maydis 521]
S71432	7433990	farnesyl-pyrophosphate synthetase - Sphaceloma manihoticola (fragment)
AAH68912	46249832	MGC83119 protein [Xenopus laevis]
1FPS	1065289	Chain , Avian Farnesyl Diphosphate Synthase (Fps) (E.C.2.5.1.10)
P08836	3915686	Farnesyl pyrophosphate synthetase (FPP synthetase) (FPS) (Farnesyl diphosphate synthetase)
AAH83515	53733369	Unknown (protein for IMAGE:7049076) [Danio rerio]
1UBX	1942050	Chain , Structure Of Farnesyl Pyrophosphate Synthetase
1UBY	1942051	Chain , Structure Of Farnesyl Pyrophosphate Synthetase
AAF37872	7188788	farnesyl diphosphate synthase [Dictyostelium discoideum]
NP_803463	29135293	farnesyl diphosphate synthase [Bos taurus]
AAK63847	14488053	farnesyl diphosphate synthase [Mentha x piperita]
AAV58896	55710092	farnesyl diphosphate synthase [Centella asiatica]
T06272	7433988	farnesyl-pyrophosphate synthetase FPS1 - tomato
JC4846	2117737	farnesyl-pyrophosphate synthetase - Artemisia annua
P05369	120478	Farnesyl pyrophosphate synthetase (FPP synthetase) (FPS) (Farnesyl diphosphate synthetase)
O24241	25452945	Farnesyl pyrophosphate synthetase 1 (FPP synthetase 1)
O24242	25452946	Farnesyl pyrophosphate synthetase 2 (FPP synthetase 2)
AAH59125	37590777	Testis-specific farnesyl pyrophosphate synthetase [Rattus norvegicus]
AAH48497	28913418	Farnesyl diphosphate synthetase [Mus musculus]
AAP74720	32329199	farnesyl diphosphate synthase [Artemisia tridentata subsp. spiciformis]
CAG11850	47225367	unnamed protein product [Tetraodon nigroviridis]
AAM51429	21436457	putative farnesyl-pyrophosphate synthetase FPS2 [Arabidopsis thaliana]
AAP74719	32329197	farnesyl diphosphate synthase [Artemisia tridentata subsp. spiciformis]
AAM08927	20135548	farnesyl pyrophosphate synthase [Malus x domestica]

XP_537252	57089113	PREDICTED: similar to farnesyl diphosphate synthase [Canis familiaris]
AAQ56011	34013692	farnesyl diphosphate synthase [Hevea brasiliensis]
AAQ14872	33340604	truncated geranylgeranyl-diphosphate synthase [Zea mays]
AAQ14871	33340602	geranylgeranyl-diphosphate synthase [Zea mays]
AAD17204	4324960	farnesyl diphosphate synthase [Artemisia annua]
AAH87886	56789674	Farnesyl diphosphate synthetase [Mus musculus]
AAK68152	14573639	farnesyldiphosphate synthase [x Citrofortunella microcarpa]
AAA52423	182399	farnesyl pyrophosphate synthetase (EC 2.5.1.1)
S66470	2129849	farnesyl-pyrophosphate synthetase fps1 - white lupine
CAA29064	4725	unnamed protein product [Saccharomyces cerevisiae]
CAI12715	55957735	farnesyl diphosphate synthase [Homo sapiens]
BAA03523	40788949	KIAA1293 [Homo sapiens]
P14324	1346031	Farnesyl pyrophosphate synthetase (FPP synthetase)
S66471	2129850	farnesyl-pyrophosphate synthetase fps2 - white lupine
AAA35820	182405	farnesyl pyrophosphate synthetase
CAA59170	1491641	dimethylallyltransferase [Capsicum annuum]
BAB16687	15289750	putative FPP synthase 1 [Eucommia ulmoides]
CAA72793	1922251	farnesyl pyrophosphate synthase [Gossypium arboreum]
CAH91070	55728661	hypothetical protein [Pongo pygmaeus]
AAK58594	14279425	farnesyl pyrophosphate synthase [Humulus lupulus]
AAB07264	1146159	farnesyl diphosphate synthase short form [Arabidopsis thaliana]
Q09152	21431776	Farnesyl pyrophosphate synthetase 1, mitochondrial precursor (FPP synthetase 1)
O64905	6016044	Farnesyl pyrophosphate synthetase (FPP synthetase)
BAB60822	14422406	putative FPP synthase 2 [Eucommia ulmoides]
S52009	1076319	farnesyl-pyrophosphate synthetase FPS1 - Arabidopsis thaliana
NP_917118	34911542	putative farnesyl-pyrophosphate synthetase [Oryza sativa (japonica cultivar-group)]
AAD32648	4894899	farnesyl diphosphate synthase [Artemisia annua]
AAA40960	203582	cholesterol-regulated protein CR39
AAR27053	38684029	farnesyl diphosphate synthetase [Ginkgo biloba]
AAU43998	52353430	putative farnesyl pyrophosphate synthase [Oryza sativa (japonica cultivar-group)]
AAL82595	18958450	farnesyl pyrophosphare synthase [Musa acuminata]
NP_917069	34911444	putative farnesyl-pyrophosphate synthetase [Oryza sativa (japonica cultivar-group)]
XP_228802	34879769	similar to testis-specific farnesyl pyrophosphate synthetase [Rattus norvegicus]
BAD81810	56785155	putative farnesyl-pyrophosphate synthetase fps2 [Oryza sativa (japonica cultivar-group)]
AAN62522	24796660	farnesyl pyrophosphate synthetase [Eucommia ulmoides]
NP_595334	19112126	farnesyl pyrophosphate synthetase [Schizosaccharomyces pombe]
T52066	25458583	probable farnesyl pyrophosphate synthase [imported] - rice
AAL49067	17946048	RE52884p [Drosophila melanogaster]
CAA08919	3395483	dimethylallyltransferase; farnesyl pyrophosphate synthase [Drosophila melanogaster]
XP_547662	57089869	PREDICTED: similar to farnesyl diphosphate synthase [Canis familiaris]
EAL26135	54636732	GA11601-PA [Drosophila pseudoobscura]
BAB60821	14422404	putative FPP synthase 1 [Eucommia ulmoides]
AAP74721	32329201	chrysanthemyl diphosphate synthase [Artemisia tridentata subsp. spiciformis]

XP_496902	51466663	PREDICTED: similar to Farnesyl pyrophosphate synthetase (FPP synthetase) [Homo sapiens]
XP_474182	50929309	OSJNBa0071I13.18 [Oryza sativa (japonica cultivar-group)]
CAA87327	1160178	partial sequence [Homo sapiens]
BAD20729	47776234	farnesyl pyrophosphate synthase [Candida glabrata]
BAC53873	30984142	farnesyl pyrophosphate synthase [Phaseolus lunatus]
BAB69490	15991313	farnesyl pyrophosphate syntase [Bombyx mori]
NP_974565	42572937	farnesyl pyrophosphate synthetase 2 (FPS2) / FPP synthetase 2 [Arabidopsis thaliana]
CAA08918	5678609	dimethylallyltransferase; farnesyl pyrophosphate synthase [Agrotis ipsilon]
AAP86267	32527731	Ac2-125 [Rattus norvegicus]
AAO17735	30522953	farnesyl pyrophosphate synthase [Trypanosoma brucei]
AAK71861	14647139	farnesyl pyrophosphate synthase [Trypanosoma cruzi]
AAL73357	18478919	farnesyl diphosphate synthase precursor [Trypanosoma cruzi]
AAO63552	29124957	putative farnesyl pyrophosphate synthase [Plasmodium falciparum]
CAI00471	56498227	farnesyl pyrophosphate synthase, putative [Plasmodium berghei]
NP_701155	23508486	farnesyl pyrophosphate synthase, putative [Plasmodium falciparum 3D7]
XP_474180	50929305	OSJNBa0071I13.16 [Oryza sativa (japonica cultivar-group)]
AAL73358	18478922	farnesyl diphosphate synthase precursor [Trypanosoma cruzi]
EAH48995	44167328	unknown [environmental sequence]
NP_493027	17508563	farnesyl pyrophosphate synthetase (1M510) [Caenorhabditis elegans]
CAE71711	39580204	Hypothetical protein CBG18688 [Caenorhabditis briggsae]
XP_487220	51766977	similar to farnesyl pyrophosphate synthase [Mus musculus]

Table 15. Examples of GGPP synthase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
AAT92871	51013155	YPL069C [Saccharomyces cerevisiae]
XP_447025	50289191	unnamed protein product [Candida glabrata]
NP_984623	45190369	AEL238Cp [Eremothecium gossypii]
XP_390273	46137163	GGPP_GIBFU Geranylgeranyl pyrophosphate synthetase (GGPP synthetase) [Gibberella zeae PH-1]
XP_404791	49085320	hypothetical protein AN0654.2 [Aspergillus nidulans FGSC A4]
XP_368486	39974191	hypothetical protein MG00758.4 [Magnaporthe grisea 70-15]
Q92236	6831550	Geranylgeranyl pyrophosphate synthetase (GGPP synthetase)
AAO85432	29468176	geranylgeranyl diphosphate synthase [Aspergillus nidulans]
XP_572774	58271236	farnesyltranstransferase, putative [Cryptococcus neoformans var. neoformans JEC21]
XP_502923	50550901	hypothetical protein [Yarrowia lipolytica]

AAK11525	13021716	geranylgeranyl pyrophosphate synthase [Penicillium paxilli]
XP_326920	32412880	GERANYLGERANYL PYROPHOSPHATE SYNTHETASE (GGPP SYNTHETASE) [Neurospora crassa]
CAF32032	42820719	geranylgeranyl pyrophosphate synthetase, putative [Aspergillus fumigatus]
BAD29965	50355599	Phoma betae geranylgeranyl diphosphate synthase
XP_384767	46117498	hypothetical protein FG04591.1 [Gibberella zeae PH-1]
BAD29970	50355631	geranylgeranyldiphosphate synthase [Phoma betae]
CAB89115	7649674	geranylgeranyl pyrophosphate synthase [Mucor circinelloides f. lusitanicus]
CAG09545	47229030	unnamed protein product [Tetraodon nigroviridis]
CAI13753	55960163	geranylgeranyl diphosphate synthase 1 [Homo sapiens]
AAH69913	47124116	Geranylgeranyl diphosphate synthase 1 [Mus musculus]
AAH67768	45709211	GGPS1 protein [Homo sapiens]
XP_455003	50309979	unnamed protein product [Kluyveromyces lactis]
P56966	9296978	Geranylgeranyl pyrophosphate synthetase (GGPP synthetase)
NP_001007	56090562	geranylgeranyl diphosphate synthase 1 [Rattus norvegicus]
AAT65717	49409613	geranylgeranyl diphosphate synthase [Aspergillus flavus]
NP_956329	41053321	geranylgeranyl diphosphate synthase 1 [Danio rerio]
BAA90525	6899844	geranylgeranyl diphosphate synthase [Nigrospora sphaerica]
XP_405729	49087630	hypothetical protein AN1592.2 [Aspergillus nidulans FGSC A4]
AAK11531	13021724	geranylgeranyl pyrophosphate synthase [Penicillium paxilli]
XP_412280	49119197	hypothetical protein AN8143.2 [Aspergillus nidulans FGSC A4]
AAC05273	2944400	geranylgeranyl pyrophosphate synthase [Drosophila melanogaster]
NP_523958	24660002	CG8593-PA [Drosophila melanogaster]
XP_402074	49076128	hypothetical protein UM04459.1 [Ustilago maydis 521]
EAL30191	54641441	GA21189-PA [Drosophila pseudoobscura]
XP_536340	57084951	PREDICTED: hypothetical protein XP_536340 [Canis familiaris]
XP_424685	50811194	PREDICTED: similar to geranylgeranyl diphosphate synthase 1, partial [Gallus gallus]
AAH06798	13905030	Ggps1 protein [Mus musculus]
AAP06018	29841005	similar to NM_010282 geranylgeranyl diphosphate synthase 1; GGPP synthase [Schistosoma japonicum]
XP_460338	50423511	unnamed protein product [Debaryomyces hansenii]
AAC05595	2957271	geranylgeranyl pyrophosphate synthase [Drosophila melanogaster]
EAK92197	46432727	hypothetical protein CaO19.6674 [Candida albicans SC5314]
XP_535573	57108760	PREDICTED: similar to geranylgeranyl diphosphate synthase 1 [Canis familiaris]
AAH83212	53734594	Zgc:56514 protein [Danio rerio]
XP_486466	51827552	similar to geranylgeranyl diphosphate synthase 1; GGPP synthase [Mus musculus]
CAH18006	51469024	geranylgeranyl diphosphate synthase [Fusarium proliferatum]
CAA75568	3549881	geranylgeranyl diphosphate synthase [Gibberella fujikuroi]
XP_397455	48143654	similar to CG8593-PA [Apis mellifera]
XP_410947	49101294	hypothetical protein AN6810.2 [Aspergillus nidulans FGSC A4]
XP_381914	46109712	hypothetical protein FG01738.1 [Gibberella zeae PH-1]
XP_364478	39959279	hypothetical protein MG09448.4 [Magnaporthe grisea 70-15]
XP_360889	39942704	hypothetical protein MG03432.4 [Magnaporthe grisea 70-15]
XP_369218	39975655	hypothetical protein MG00026.4 [Magnaporthe grisea 70-15]
XP_406544	49089926	hypothetical protein AN2407.2 [Aspergillus nidulans FGSC A4]
XP_367595	39972409	hypothetical protein MG07506.4 [Magnaporthe grisea 70-15]
XP_363775	39952117	hypothetical protein MG01701.4 [Magnaporthe grisea 70-15]
XP_368486	39974191	hypothetical protein MG00758.4 [Magnaporthe grisea 70-15]

XP_390273	46137163	GGPP_GIBFU Geranylgeranyl pyrophosphate synthetase (GGPP synthetase) [Gibberella zeae PH-1]
Q92236	6831550	Geranylgeranyl pyrophosphate synthetase (GGPP synthetase)
AAK11525	13021716	geranylgeranyl pyrophosphate synthase [Penicillium paxilli]
CAF32032	42820719	geranylgeranyl pyrophosphate synthetase, putative [Aspergillus fumigatus]
XP_404791	49085320	hypothetical protein AN0654.2 [Aspergillus nidulans FGSC A4]
AAO85432	29468176	geranylgeranyl diphosphate synthase [Aspergillus nidulans]
BAD29965	50355599	Phoma betae geranylgeranyl diphosphate synthase
BAD29970	50355631	geranylgeranyldiphosphate synthase [Phoma betae]
BAA90525	6899844	geranylgeranyl diphosphate synthase [Nigrospora sphaerica]
AAT65717	49409613	geranylgeranyl diphosphate synthase [Aspergillus flavus]
XP_384767	46117498	hypothetical protein FG04591.1 [Gibberella zeae PH-1]
CAB89115	7649674	geranylgeranyl pyrophosphate synthase [Mucor circinelloides f. lusitanicus]
XP_572774	58271236	farnesyltranstransferase, putative [Cryptococcus neoformans var. neoformans JEC21]
AAK11531	13021724	geranylgeranyl pyrophosphate synthase [Penicillium paxilli]
XP_502923	50550901	hypothetical protein [Yarrowia lipolytica]
CAI13753	55960163	geranylgeranyl diphosphate synthase 1 [Homo sapiens]
CAG09545	47229030	unnamed protein product [Tetraodon nigroviridis]
XP_412280	49119197	hypothetical protein AN8143.2 [Aspergillus nidulans FGSC A4]
P56966	9296978	Geranylgeranyl pyrophosphate synthetase (GGPP synthetase)
NP_001007	56090562	geranylgeranyl diphosphate synthase 1 [Rattus norvegicus]
AAH69913	47124116	Geranylgeranyl diphosphate synthase 1 [Mus musculus]
AAH67768	45709211	GGPS1 protein [Homo sapiens]
NP_956329	41053321	geranylgeranyl diphosphate synthase 1 [Danio rerio]
EAL30191	54641441	GA21189-PA [Drosophila pseudoobscura]
XP_424685	50811194	PREDICTED: similar to geranylgeranyl diphosphate synthase 1, partial [Gallus gallus]
XP_536340	57084951	PREDICTED: hypothetical protein XP_536340 [Canis familiaris]
NP_523958	24660002	CG8593-PA [Drosophila melanogaster]
AAC05273	2944400	geranylgeranyl pyrophosphate synthase [Drosophila melanogaster]
XP_405729	49087630	hypothetical protein AN1592.2 [Aspergillus nidulans FGSC A4]
AAC05595	2957271	geranylgeranyl pyrophosphate synthase [Drosophila melanogaster]
XP_402074	49076128	hypothetical protein UM04459.1 [Ustilago maydis 521]
AAP06018	29841005	similar to NM_010282 geranylgeranyl diphosphate synthase 1; GGPP synthase [Schistosoma japonicum]
AAH06798	13905030	Ggps1 protein [Mus musculus]
XP_535573	57108760	PREDICTED: similar to geranylgeranyl diphosphate synthase 1 [Canis familiaris]
AAH83212	53734594	Zgc:56514 protein [Danio rerio]
AAP21085	30097620	albino-3 [Neurospora crassa]
NP_984623	45190369	AEL238Cp [Eremothecium gossypii]
XP_447025	50289191	unnamed protein product [Candida glabrata]
AAT92871	51013155	YPL069C [Saccharomyces cerevisiae]
XP_486466	51827552	similar to geranylgeranyl diphosphate synthase 1; GGPP synthase [Mus musculus]
XP_410947	49101294	hypothetical protein AN6810.2 [Aspergillus nidulans FGSC A4]
XP_397455	48143654	similar to CG8593-PA [Apis mellifera]
XP_455003	50309979	unnamed protein product [Kluyveromyces lactis]
EAK92197	46432727	hypothetical protein CaO19.6674 [Candida albicans SC5314]
XP_381914	46109712	hypothetical protein FG01738.1 [Gibberella zeae PH-1]

XP_460338	50423511	unnamed protein product [Debaryomyces hansenii]
CAH18006	51469024	geranylgeranyl diphosphate synthase [Fusarium proliferatum]
XP_360889	39942704	hypothetical protein MG03432.4 [Magnaporthe grisea 70-15]
XP_406544	49089926	hypothetical protein AN2407.2 [Aspergillus nidulans FGSC A4]
XP_364478	39959279	hypothetical protein MG09448.4 [Magnaporthe grisea 70-15]
XP_363775	39952117	hypothetical protein MG01701.4 [Magnaporthe grisea 70-15]
XP_367595	39972409	hypothetical protein MG07506.4 [Magnaporthe grisea 70-15]
XP_369218	39975655	hypothetical protein MG00026.4 [Magnaporthe grisea 70-15]
C39273	483124	phytoene synthase - Erwinia herbicola
BAB79600	18143445	crtE [Pantoea agglomerans pv. milletiae]
BAA14124	216682	crtE [Pantoea ananatis]
AAN85596	27228290	Geranylgeranyl Pyrophosphate Synthase [Pantoea stewartii]
AAA32797	413730	geranylgeranyl pyrophosphate synthase
Q08291	585326	Geranyltranstransferase (Farnesyl-diphosphate synthase) (FPP synthase)
S52584	1073293	crtE protein - Erwinia herbicola
S53722	1076576	farnesyltranstransferase (EC 2.5.1.29) precursor - pepper
AAC44848	1842242	geranylgeranyl synthase
BAA19583	1944371	geranylgeranyl pyrophosphate synthase [Arabidopsis thaliana]
S71230	2129674	geranylgeranyl pyrophosphate synthase (EC 2.5.1.-) 2 precursor - Arabidopsis thaliana
BAA23157	2578822	geranyl geranyl pyrophosphate synthase [Arabidopsis thaliana]
AAC77874	3885426	geranylgeranyl pyrophosphate synthase [Helianthus annuus]
CAB38744	4490594	geranylgeranyl pyrophosphate synthase [Rhodobacter sphaeroides]
BAA78047	4958920	GGPP synthase [Daucus carota]
BAA82613	5631295	geranylgeranyl diphosphate synthase (SelGGPS) [Synechococcus elongatus]
CAB56064	5912297	geranylgeranyl pyrophosphate synthase [Paracoccus marcusii]
BAA86284	6277254	geranylgeranyl pyrophosphate synthase [Croton sublyratus]
T11021	7447356	farnesyltranstransferase (EC 2.5.1.29) - white lupine
AAF78199	8650415	geranylgeranyl synthase [Bradyrhizobium sp. ORS278]
AAG10424	9971808	GGDP synthase [Tagetes erecta]
CAC10561	10637876	gpp synthase large subunit [Mentha x piperita]
T50879	11279298	phytoene synthase [imported] - Rubrivivax gelatinosus
BAB01343	11994221	geranyl geranyl pyrophosphate synthase-like protein [Arabidopsis thaliana]
Q42698	13431546	Geranylgeranyl pyrophosphate synthetase, chloroplast precursor (GGPP synthetase)
Q43133	13431547	Geranylgeranyl pyrophosphate synthetase, chloroplast precursor (GGPP synthetase)
P54976	13878921	Geranylgeranyl pyrophosphate synthetase (GGPP synthetase) (Farnesyltranstransferase)
BAB50600	14023995	geranyltranstransferase; farnesyl-diphosphate synthase [Mesorhizobium loti MAFF303099]
BAB60678	14325238	geranylgeranyl diphosphate synthase [Hevea brasiliensis]
BAB60820	14422402	putative GGPP synthase [Eucommia ulmoides]
NP_189589	15228704	geranylgeranyl pyrophosphate synthase, putative / GGPP synthetase [Arabidopsis thaliana]
NP_188651	15231055	geranylgeranyl pyrophosphate synthase, putative / GGPP synthetase [Arabidopsis thaliana]
NP_188069	15231869	geranylgeranyl pyrophosphate synthase, putative / GGPP synthetase [Arabidopsis thaliana]
NP_188073	15231881	geranylgeranyl pyrophosphate synthase, putative / GGPP synthetase

		[Arabidopsis thaliana]
AAL01997	15553715	farnesyl diphosphate synthase [Xanthobacter sp. Py2]
AAL01998	15553717	geranylgeranyl diphosphate synthase [Xanthobacter sp. Py2]
NP_252732	15599238	geranyltranstransferase [Pseudomonas aeruginosa PAO1]
NP_245470	15602398	IspA [Pasteurella multocida subsp. multocida str. Pm70]
NP_390308	16079484	hypothetical protein BSU24280 [Bacillus subtilis subsp. subtilis str. 168]
NP_440010	16329282	geranylgeranyl pyrophosphate synthase [Synechocystis sp. PCC 6803]
NP_440010	16329282	geranylgeranyl pyrophosphate synthase [Synechocystis sp. PCC 6803]
AAL17614	17352451	geranylgeranyl diphosphate synthase [Abies grandis]
NP_520343	17546941	PROBABLE GERANYLTRANSTRANSFERASE (FARNESYL-DIPHOSPHATE SYNTHASE) PROTEIN [Ralstonia solanacearum GM
AAL76349	18645048	geranyltranstransferase [uncultured proteobacterium]
AAM21638	20386366	geranylgeranyl pyrophosphate synthase [Cistus incanus subsp. creticus]
AAM21639	20386368	geranylgeranyl pyrophosphate synthase [Cistus incanus subsp. creticus]
NP_622916	20807745	Geranylgeranyl pyrophosphate synthase [Thermoanaerobacter tengcongensis MB4]
AAM48650	21328644	geranylgeranyl pyrophosphate synthetase [uncultured proteobacterium]
NP_659794	21492720	probable polyprenyl synthetase. [Rhizobium etli]
AAM64496	21592547	putative geranylgeranyl pyrophosphate synthase GGPS3 [Arabidopsis thaliana]
AAM65107	21593158	geranylgeranyl pyrophosphate synthase [Arabidopsis thaliana]
NP_680811	22297564	geranylgeranyl pyrophosphate synthase [Thermosynechococcus elongatus BP-1]
ZP_000474	23003800	COG0142: Geranylgeranyl pyrophosphate synthase [Lactobacillus gasseri]
ZP_001252	23469933	COG0142: Geranylgeranyl pyrophosphate synthase [Pseudomonas syringae pv. syringae B728a]
NP_698760	23502633	geranyltranstransferase [Brucella suis 1330]
E84566	25313373	probable geranylgeranyl pyrophosphate synthase [imported] - Arabidopsis thaliana
F85434	25313385	geranylgeranyl pyrophosphate synthase [imported] - Arabidopsis thaliana
AC1245	25313389	geranyltranstransferase homolog lmo1363 [imported] - Listeria monocytogenes (strain EGD-e)
E83997	25313393	geranyltranstransferase BH2781 [imported] - Bacillus halodurans (strain C-125)
G84566	25313395	probable geranylgeranyl pyrophosphate synthase [imported] - Arabidopsis thaliana
AH2910	25315863	geranyltranstransferase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
D87505	25398795	geranyltranstransferase [imported] - Caulobacter crescentus
A89932	25505949	hypothetical protein ispA [imported] - Staphylococcus aureus (strain N315)
F97685	25520741	geranyltransferase (AF203881) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
AI3285	25527013	geranyltranstransferase (EC 2.5.1.10) [imported] - Brucella

		melitensis (strain 16M)
BAC42571	26450928	putative geranylgeranyl pyrophosphate synthase GGPS3 [Arabidopsis thaliana]
NP_785195	28378303	geranyltranstransferase [Lactobacillus plantarum WCFS1]
NP_790546	28867927	geranyltranstransferase [Pseudomonas syringae pv. tomato str. DC3000]
AAO63392	28950937	At2g23800 [Arabidopsis thaliana]
AAO93113	29893480	geranylgeranyl pyrophosphate synthetase; CrtE [Rubrivivax gelatinosus]
NP_833891	30022260	Dimethylallyltransferase [Bacillus cereus ATCC 14579]
AAP59037	31621279	CrtE [Thiocapsa roseopersicina]
ZP_001374	32039216	COG0142: Geranylgeranyl pyrophosphate synthase [Pseudomonas aeruginosa UCBPP-PA14]
NP_864766	32471772	geranylgeranyl pyrophosphate synthetase [precursor] [Rhodopirellula baltica SH 1]
NP_875521	33240579	Geranylgeranyl pyrophosphate synthase [Prochlorococcus marinus subsp. marinus str. CCMP1375]
NP_881399	33593755	probable geranyltranstransferase [Bordetella pertussis Tohama I]
NP_884694	33597051	probable geranyltranstransferase [Bordetella parapertussis 12822]
NP_888456	33600896	probable geranyltranstransferase [Bordetella bronchiseptica RB50]
NP_893187	33861626	Polyprenyl synthetase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]
NP_894940	33863380	Polyprenyl synthetase [Prochlorococcus marinus str. MIT 9313]
NP_896835	33865276	geranylgeranyl pyrophosphate synthase [Synechococcus sp. WH 8102]
NP_896835	33865276	geranylgeranyl pyrophosphate synthase [Synechococcus sp. WH 8102]
AAQ65086	34365549	At3g14530 [Arabidopsis thaliana]
NP_945877	39933601	putative geranyltranstransferase (farnesyl-diphosphate synthase) [Rhodopseudomonas palustris CGA009]
NP_946867	39934591	geranylgeranyl pyrophosphate synthase [Rhodopseudomonas palustris CGA009]
NP_952815	39996864	geranyltranstransferase [Geobacter sulfurreducens PCA]
AAR37805	40062934	polyprenyl synthetase [uncultured bacterium 442]
AAR37858	40062988	geranylgeranyl pyrophosphate synthetase [uncultured bacterium 443]
AAR98495	41018904	geranyl geranyl synthase [Bradyrhizobium sp. ORS278]
AAR99082	41059107	geranylgeranyl pyrophosphate synthase [Plectranthus barbatus]
NP_965349	42519419	geranyltranstransferase [Lactobacillus johnsonii NCC 533]
NP_980544	42783297	geranyltranstransferase [Bacillus cereus ATCC 10987]
EAA96348	42858148	unknown [environmental sequence]
EAB36506	42939031	unknown [environmental sequence]
EAB36642	42939300	unknown [environmental sequence]
EAC39208	43146996	unknown [environmental sequence]
EAD26007	43320598	unknown [environmental sequence]
EAE43084	43576643	unknown [environmental sequence]
EAE70061	43630884	unknown [environmental sequence]
EAF70308	43832107	unknown [environmental sequence]
EAG88494	44055952	unknown [environmental sequence]
EAH52060	44173220	unknown [environmental sequence]
EAH78354	44221788	unknown [environmental sequence]
EAH84117	44231960	unknown [environmental sequence]
EAI11762	44272832	unknown [environmental sequence]
EAI49391	44328289	unknown [environmental sequence]

EAI54846	44336042	unknown [environmental sequence]
EAI68356	44355138	unknown [environmental sequence]
EAI68713	44355672	unknown [environmental sequence]
EAI69401	44356609	unknown [environmental sequence]
EAI73873	44362658	unknown [environmental sequence]
EAJ73634	44506168	unknown [environmental sequence]
EAJ77351	44511694	unknown [environmental sequence]
EAK70639	44644254	unknown [environmental sequence]
ZP_001751	45523854	COG0142: Geranylgeranyl pyrophosphate synthase [Crocosphaera watsonii WH 8501]
AAS76253	45752710	At1g49530 [Arabidopsis thaliana]
ZP_001957	45916757	COG0142: Geranylgeranyl pyrophosphate synthase [Mesorhizobium sp. BNC1]
1RTRB	46015556	Chain B, Crystal Structure Of S. Aureus Farnesyl Pyrophosphate Synthase
ZP_001863	46105954	COG0142: Geranylgeranyl pyrophosphate synthase [Rubrobacter xylanophilus DSM 9941]
ZP_002002	46107045	COG0142: Geranylgeranyl pyrophosphate synthase [Rubrobacter xylanophilus DSM 9941]
ZP_001711	46132567	COG0142: Geranylgeranyl pyrophosphate synthase [Ralstonia eutropha JMP134]
ZP_002073	46192680	COG0142: Geranylgeranyl pyrophosphate synthase [Rhodobacter sphaeroides 2.4.1]
ZP_002074	46192861	COG0142: Geranylgeranyl pyrophosphate synthase [Rhodobacter sphaeroides 2.4.1]
AAS82860	46241274	geranyl diphosphate synthase large subunit [Antirrhinum majus]
ZP_002108	46308696	COG0142: Geranylgeranyl pyrophosphate synthase [Ehrlichia canis str.Jake]
YP_010568	46579760	geranylgeranyl diphosphate synthase [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]
BAD18313	47076770	geranyltranstransferase [Geobacillus stearothermophilus]
ZP_002315	47093750	geranyltranstransferase [Listeria monocytogenes str. 4b H7858]
ZP_002335	47095946	geranyltranstransferase [Listeria monocytogenes str. 1/2a F6854]
AAT35222	47531118	fusion of carotene synthesis proteins [synthetic construct]
ZP_002401	47569437	geranyltranstransferase [Bacillus cereus G9241]
ZP_002435	47573473	COG0142: Geranylgeranyl pyrophosphate synthase [Rubrivivax gelatinosus PM1]
ZP_002626	48728941	COG0142: Geranylgeranyl pyrophosphate synthase [Pseudomonas fluorescens Pf0-1]
ZP_002702	48765678	COG0142: Geranylgeranyl pyrophosphate synthase [Rhodospirillum rubrum]
ZP_002705	48766028	COG0142: Geranylgeranyl pyrophosphate synthase [Rhodospirillum rubrum]
ZP_002732	48768894	COG0142: Geranylgeranyl pyrophosphate synthase [Ralstonia metallidurans CH34]
ZP_002914	48834438	COG0142: Geranylgeranyl pyrophosphate synthase [Magnetococcus sp. MC-1]
ZP_003024	48848203	COG0142: Geranylgeranyl pyrophosphate synthase [Novosphingobium aromaticivorans DSM 12444]
ZP_003129	48858958	COG0142: Geranylgeranyl pyrophosphate synthase [Clostridium thermocellum ATCC 27405]
ZP_003177	48863841	COG0142: Geranylgeranyl pyrophosphate synthase [Microbulbifer degradans 2-40]

ZP_003225	48869790	COG0142: Geranylgeranyl pyrophosphate synthase [Pediococcus pentosaceus ATCC 25745]
AAT51323	49086036	PA4043 [synthetic construct]
ZP_003301	49236117	COG0142: Geranylgeranyl pyrophosphate synthase [Moorella thermoacetica ATCC 39073]
YP_034222	49476181	Geranyltranstransferase (farnesyl-diphosphate synthase) [Bartonella henselae str. Houston-1]
YP_040995	49483771	putative geranyltranstransferase [Staphylococcus aureus subsp. aureus MRSA252]
YP_043579	49486358	putative geranyltranstransferase [Staphylococcus aureus subsp. aureus MSSA476]
AAT71982	50253560	At3g32040 [Arabidopsis thaliana]
AAT90315	50952782	putative geranylgeranyl pyrophosphate synthetase [uncultured proteobacterium eBACred25D05]
YP_066435	51246551	probable geranylgeranyl pyrophosphate synthase [Desulfotalea psychrophila LSv54]
YP_075673	51892982	geranylgeranyl pyrophosphate synthase [Symbiobacterium thermophilum IAM 14863]
YP_085511	52141318	geranyltranstransferase [Bacillus cereus ZK]
YP_092166	52786337	YqiD [Bacillus licheniformis ATCC 14580]
ZP_001298	53691368	COG0142: Geranylgeranyl pyrophosphate synthase [Desulfovibrio desulfuricans G20]
YP_105136	53716444	geranyltranstransferase [Burkholderia mallei ATCC 23344]
YP_111769	53722784	geranyltranstransferase [Burkholderia pseudomallei K96243]
ZP_003630	54030933	COG0142: Geranylgeranyl pyrophosphate synthase [Polaromonas sp. JS666]
YP_129021	54308001	putative geranyltranstransferase [Photobacterium profundum SS9]
AAV74395	56122554	geranylgeranyl diphosphate synthase [Adonis palaestina]
AAV74396	56122556	geranylgeranyl diphosphate synthase [Adonis palaestina]
YP_148246	56420928	geranyltranstransferase (farnesyl-diphosphate synthase) [Geobacillus kaustophilus HTA426]
YP_156518	56461237	Geranylgeranyl pyrophosphate synthase [Idiomarina loihiensis L2TR]
YP_162590	56551751	geranyltranstransferase [Zymomonas mobilis subsp. mobilis ZM4]
YP_171470	56750769	geranylgeranyl pyrophosphate synthase [Synechococcus elongatus PCC 6301]
YP_175959	56964228	geranyltranstransferase [Bacillus clausii KSM-K16]
YP_186407	57650478	geranyltranstransferase [Staphylococcus aureus subsp. aureus COL]
YP_190690	58038726	Dimethylallyltransferase [Gluconobacter oxydans 621H]
AAW66658	58201026	geranyl diphosphate synthase [Picrorhiza kurrooa]
YP_194187	58337602	geranylgeranyl diphosphate (GGPP) synthase [Lactobacillus acidophilus NCFM]
YP_197469	58579257	Possible geranyltranstransferase [Ehrlichia ruminantium str. Welgevonden]
YP_201938	58582922	geranyltranstransferase; farnesyl-diphosphate synthase [Xanthomonas oryzae pv. oryzae KACC10331]
YP_196510	58617311	Possible geranyltranstransferase [Ehrlichia ruminantium str. Gardel]

Table 16. Examples of squalene synthase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
AAA34597	171481	squalene synthetase
CAA42583	3686	farnesyl-diphosphate farnesyltransferase [Saccharomyces cerevisiae]
Q9HGZ6	51704336	Farnesyl-diphosphate farnesyltransferase (Squalene synthetase) (SQS) (SS) (FPP:FPP farnesyltransferase)
BAB12207	9955387	squalene synthase [Candida glabrata]
XP_453457	50306959	unnamed protein product [Kluyveromyces lactis]
Q752X9	51701405	Farnesyl-diphosphate farnesyltransferase (Squalene synthetase) (SQS) (SS) (FPP:FPP farnesyltransferase)
O74165	51701378	Farnesyl-diphosphate farnesyltransferase (Squalene synthetase) (SQS) (SS) (FPP:FPP farnesyltransferase)
XP_458579	50420093	unnamed protein product [Debaryomyces hansenii]
EAK95451	46436082	hypothetical protein CaO19.11099 [Candida albicans SC5314]
P78589	2499979	Farnesyl-diphosphate farnesyltransferase (Squalene synthetase) (SQS) (SS) (FPP:FPP farnesyltransferase)
Q9Y753	51701459	Farnesyl-diphosphate farnesyltransferase (Squalene synthetase) (SQS) (SS) (FPP:FPP farnesyltransferase)
XP_407513	49092104	hypothetical protein AN3376.2 [Aspergillus nidulans FGSC A4]
XP_364394	39958237	hypothetical protein MG09239.4 [Magnaporthe grisea 70-15]
Q7S4Z6	51701416	Probable farnesyl-diphosphate farnesyltransferase (Squalene synthetase)
CAD60581	27764301	unnamed protein product [Podospora anserina]
XP_389557	46135731	hypothetical protein FG09381.1 [Gibberella zeae PH-1]
NP_595363	19112155	farnesyl-diphosphate farnesyltransferase [Schizosaccharomyces pombe]
B48057	477750	farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) - fission yeast (Schizosaccharomyces pombe)
NP_034321	34328173	farnesyl diphosphate farnesyl transferase 1 [Mus musculus]
CAH92517	55731622	hypothetical protein [Pongo pygmaeus]
AAF00038	6002565	squalene synthase [Mus musculus]
P53798	1706773	Farnesyl-diphosphate farnesyltransferase (Squalene synthetase) (SQS) (SS) (FPP:FPP farnesyltransferase)
NP_004453	31542632	farnesyl-diphosphate farnesyltransferase 1 [Homo sapiens]
AAP36671	30584837	Homo sapiens farnesyl-diphosphate farnesyltransferase 1 [synthetic construct]
1EZFC	11514497	Chain C, Crystal Structure Of Human Squalene Synthase
AAH09251	14328083	Farnesyl-diphosphate farnesyltransferase 1 [Homo sapiens]
AAH84016	54035372	LOC494973 protein [Xenopus laevis]
I52090	2136196	squalene synthase - human
XP_420043	50745256	PREDICTED: similar to Farnesyl-diphosphate farnesyltransferase 1 [Gallus gallus]

AAH81810	51858605	Farnesyl diphosphate farnesyl transferase 1 [Rattus norvegicus]
CAE48363	50841455	TPA: FDFT1 protein [Bos taurus]
XP_569783	58265254	farnesyl-diphosphate farnesyltransferase, putative [Cryptococcus neoformans var. neoformans JEC21]
XP_569782	58265252	farnesyl-diphosphate farnesyltransferase, putative [Cryptococcus neoformans var. neoformans JEC21]
XP_534557	57105080	PREDICTED: similar to FDFT1 protein [Canis familiaris]
XP_401989	49075920	FDFT_USTMA Farnesyl-diphosphate farnesyltransferase (Squalene synthetase) [Ustilago maydis 521]

Table 17. Examples of phytoene dehydrogenase polypeptides.

ACCESSION	PROTEIN DESCRIPTION
1613414B	crtI gene
1613414F	crtD gene
1904206A	methoxyneurosporene dehydrogenase
2121278A	zeta carotene desaturase
A86203	hypothetical protein [imported] - Arabidopsis thaliana
A96612	hypothetical protein F12K22.18 [imported] - Arabidopsis thaliana
A99470	phytoene dehydrogenase (desaturase) (crtI) [imported] - Sulfolobus solfataricus
AAA24820	phytoene dehydrogenase [Pantoea agglomerans]
AAA34001	phytoene desaturase
AAA50313	photoprotective pigment
AAA64981	phytoene dehydrogenase [Pantoea agglomerans]
AAA91161	zeta-carotene desaturase precursor
AAA99519	phytoene desaturase
AAC44798	hydroxyneurosporene and rhodopin dehydrogenase [Rubrivivax gelatinosus]
AAC44850	phytoene desaturase
AAC48983	phytoene dehydrogenase precursor
AAF78201	phytoene desaturase [Bradyrhizobium sp. ORS278]
AAG10426	phytoene desaturase [Tagetes erecta]
AAG14399	zeta-carotene desaturase precursor [Oryza sativa]
AAG28700	CrtI [Streptomyces griseus]
AAG50743	hypothetical protein [Arabidopsis thaliana]
AAH85048	Unknown (protein for MGC:97898) [Xenopus laevis]
AAK51545	phytoene desaturase [Citrus x paradisi]
AAK51557	zeta-carotene desaturase precursor [Citrus x paradisi]
AAK64299	phytoene desaturase [Corynebacterium glutamicum]
AAL02000	phytoene dehydrogenase [Xanthobacter sp. Py2]
AAL15300	AT4g14210/dl3145c [Arabidopsis thaliana]
AAL38046	phytoene desaturase [Hordeum vulgare]
AAL73986	hypothetical protein MMT-7 [Mus musculus]
AAL80005	phytoene desaturase [Sandersonia aurantiaca]
AAL91366	carotenoid isomerase [Lycopersicon esculentum]
AAM45380	phytoene desaturase [Tagetes erecta]
AAM48646	phytoene dehydrogenase [uncultured proteobacterium]
AAM63349	putative zeta-carotene desaturase precursor [Arabidopsis thaliana]
AAM94364	phytoene desaturase [Agromyces mediolanus]
AAN75037	CrtD [Rhodospirillum rubrum]
AAN85599	Phytoene Desaturase [Pantoea stewartii]
AAO24235	phytoene desaturase [Crocus sativus]
AAO46892	phytoene dehydrogenase [Blakeslea trispora]
AAO46894	phytoene dehydrogenase [Blakeslea trispora]
AAO53257	phytoene desaturase [Xanthophyllomyces dendrorhous]
AAO53258	phytoene desaturase splice variant [Xanthophyllomyces dendrorhous]
AAO64750	At5g49550/K6M13_10 [Arabidopsis thaliana]
AAO93135	phytoene dehydrogenase; CrtI [Rubrivivax gelatinosus]
AAP59036	CrtD [Thiocapsa roseopersicina]
AAP79175	phytoene dehydrogenase [Bigelowiella natans]

AAQ04224	zeta-carotene desaturase ZDS1 [Malus x domestica]
AAQ04225	zeta-carotene desaturase ZDS2 [Malus x domestica]
AAQ65246	phytoene desaturase [Methylobacterium extorquens]
AAQ65246	phytoene desaturase [Methylobacterium extorquens]
AAQ88931	WLPL439 [Homo sapiens]
AAR37797	methoxyneurosporene dehydrogenase [uncultured bacterium 442]
AAR37802	phytoene dehydrogenase [uncultured bacterium 442]
AAR37850	methoxyneurosporene dehydrogenase [uncultured bacterium 443]
AAR37855	phytoene dehydrogenase [uncultured bacterium 443]
AAR86105	phytoene desaturase [Momordica charantia var. abbreviata]
AAR98491	phytoene desaturase [Bradyrhizobium sp. ORS278]
AAR98494	phytoene dehydrogenase [Bradyrhizobium sp. ORS278]
AAR98733	phytoene desaturase [Lilium longiflorum]
AAS17750	phytoene desaturase [Solanum tuberosum]
AAT01639	phytoene desaturase [Petunia x hybrida]
AAT35222	fusion of carotene synthesis proteins [synthetic construct]
AAT74579	PDS [Citrus sinensis]
AAT74580	ZDS [Citrus sinensis]
AAT76050	zeta-carotene desaturase [Citrus clementina]
AAT76434	phytoene desaturase [Hydrilla verticillata]
AAT90316	putative methoxyneurosporene dehydrogenase [uncultured proteobacterium eBACred25D05]
AAU34019	retina and RPE/choroid [Macaca fascicularis]
AAW23161	phytoene dehydrogenase [Rhodococcus erythropolis]
AB2035	phytoene desaturase [imported] - Nostoc sp. (strain PCC 7120)
AB2064	hypothetical protein alr2064 [imported] - Nostoc sp. (strain PCC 7120)
AC2446	hypothetical protein all5123 [imported] - Nostoc sp. (strain PCC 7120)
AF1557	phytoene dehydrogenase homolog lin0999 [imported] - Listeria innocua (strain Clip11262)
AF2029	hypothetical protein alr1788 [imported] - Nostoc sp. (strain PCC 7120)
AG2103	zeta-carotene desaturase [imported] - Nostoc sp. (strain PCC 7120)
AG2509	zeta-carotene desaturase [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha
AH1199	phytoene dehydrogenase homolog lmo1000 [imported] - Listeria monocytogenes (strain EGD-e)
AI2185	hypothetical protein all3040 [imported] - Nostoc sp. (strain PCC 7120)
AI2273	hypothetical protein all3744 [imported] - Nostoc sp. (strain PCC 7120)
B55548	crtN protein - Staphylococcus aureus
B84327	phytoene dehydrogenase [imported] - Halobacterium sp. NRC-1
B90061	squalene synthase [imported] - Staphylococcus aureus (strain N315)
BAA14127	crtI [Pantoea ananatis]
BAA20276	phytoene desaturase [Erythrobacter longus]
BAA76534	Phytoene disaturase [Acidiphilium rubrum]
BAB10768	phytoene dehydrogenase-like [Arabidopsis thaliana]
BAB50520	phytoene dehydrogenase [Mesorhizobium loti MAFF303099]
BAB51896	mlr5446 [Mesorhizobium loti MAFF303099]
BAB68552	zeta-carotene desaturase [Citrus unshiu]
BAB79603	crtI [Pantoea agglomerans pv. milletiae]
BAB82461	phytoene desaturase [Gentiana lutea]
BAB82462	phytoene desaturase [Gentiana lutea]
BAB98016	Phytoene dehydrogenase and related proteins [Corynebacterium glutamicum ATCC 13032]
BAC75676	putative phytoene desaturase [Gordonia sp. TM414]

BAC77668	phytoene desaturase [marine bacterium P99-3]
BAC77671	gamma-carotene desaturase [marine bacterium P99-3]
BAD07279	phytoene desaturase [Citrus sinensis]
BAD07280	zeta-carotene desaturase [Citrus sinensis]
BAD07287	phytoene desaturase [Citrus limon]
BAD07288	zeta-carotene desaturase [Citrus limon]
CAA52098	squalene synthase [Staphylococcus aureus]
CAA60479	Phytoene desaturase [Haematococcus pluvialis]
CAA66626	unnamed protein product [Staphylococcus aureus]
CAB38739	phytoene dehydrogenase [Rhodobacter sphaeroides]
CAB38743	methoxyneurosporene dehydrogenase [Rhodobacter sphaeroides]
CAB40843	phytoene dehydrogenase [Mucor circinelloides f. lusitanicus]
CAB56041	zeta-carotene desaturase [Nostoc sp. PCC 7120]
CAB56062	phytoene desaturase [Paracoccus marcusii]
CAB59726	phytoene desaturase [Lycopersicon esculentum]
CAB65434	zeta carotene desaturase [Synechococcus leopoliensis]
CAB94794	phytoene dehydrogenase [Mycobacterium aurum]
CAC85667	zeta-carotene desaturase [Citrus sinensis]
CAD19989	phytoene dehydrogenase [Gibberella fujikuroi]
CAD27442	putative zeta-carotene desaturase [Helianthus annuus]
CAD55814	putative zeta-carotene desaturase [Helianthus annuus]
CAE00192	phytoene desaturase [Nicotiana benthamiana]
CAE83576	phytoene desaturase [Nicotiana tabacum]
CAF19330	PHYTOENE DEHYDROGENASE (DESATURASE) [Corynebacterium glutamicum ATCC 13032]
CAF21094	PHYTOENE DEHYDROGENASE (DESATURASE) (N-terminal fragment) [Corynebacterium glutamicum ATCC 13032]
CAF21337	phytoene desaturase [Pisum sativum]
CAH91165	hypothetical protein [Pongo pygmaeus]
E90061	hypothetical protein SA2351 [imported] - Staphylococcus aureus (strain N315)
EAA90383	unknown [environmental sequence]
EAA98598	unknown [environmental sequence]
EAB09790	unknown [environmental sequence]
EAB14136	unknown [environmental sequence]
EAB18725	unknown [environmental sequence]
EAB29729	unknown [environmental sequence]
EAB30992	unknown [environmental sequence]
EAB41377	unknown [environmental sequence]
EAB54727	unknown [environmental sequence]
EAB76679	unknown [environmental sequence]
EAB87028	unknown [environmental sequence]
EAB92587	unknown [environmental sequence]
EAB94459	unknown [environmental sequence]
EAB96864	unknown [environmental sequence]
EAC01884	unknown [environmental sequence]
EAC38895	unknown [environmental sequence]
EAC60360	unknown [environmental sequence]
EAD05874	unknown [environmental sequence]
EAD05999	unknown [environmental sequence]
EAD20520	unknown [environmental sequence]
EAE06978	unknown [environmental sequence]
EAE70773	unknown [environmental sequence]
EAF04985	unknown [environmental sequence]

EAF51354	unknown [environmental sequence]
EAF62819	unknown [environmental sequence]
EAF75453	unknown [environmental sequence]
EAG09111	unknown [environmental sequence]
EAG19412	unknown [environmental sequence]
EAG23070	unknown [environmental sequence]
EAG25053	unknown [environmental sequence]
EAG25054	unknown [environmental sequence]
EAG29279	unknown [environmental sequence]
EAG39845	unknown [environmental sequence]
EAG56100	unknown [environmental sequence]
EAG63013	unknown [environmental sequence]
EAG68633	unknown [environmental sequence]
EAG71574	unknown [environmental sequence]
EAG89835	unknown [environmental sequence]
EAH04928	unknown [environmental sequence]
EAH04936	unknown [environmental sequence]
EAH08586	unknown [environmental sequence]
EAH22597	unknown [environmental sequence]
EAH22853	unknown [environmental sequence]
EAH31648	unknown [environmental sequence]
EAH55579	unknown [environmental sequence]
EAH68071	unknown [environmental sequence]
EAH73302	unknown [environmental sequence]
EAH79041	unknown [environmental sequence]
EAH86965	unknown [environmental sequence]
EAH97108	unknown [environmental sequence]
EAH99977	unknown [environmental sequence]
EAI01660	unknown [environmental sequence]
EAI03576	unknown [environmental sequence]
EAI06784	unknown [environmental sequence]
EAI11087	unknown [environmental sequence]
EAI15261	unknown [environmental sequence]
EAI15547	unknown [environmental sequence]
EAI17521	unknown [environmental sequence]
EAI21398	unknown [environmental sequence]
EAI29728	unknown [environmental sequence]
EAI38468	unknown [environmental sequence]
EAI43591	unknown [environmental sequence]
EAI51589	unknown [environmental sequence]
EAI58453	unknown [environmental sequence]
EAI72974	unknown [environmental sequence]
EAI77885	unknown [environmental sequence]
EAI78272	unknown [environmental sequence]
EAI80262	unknown [environmental sequence]
EAI83937	unknown [environmental sequence]
EAI86664	unknown [environmental sequence]
EAJ00517	unknown [environmental sequence]
EAJ05570	unknown [environmental sequence]
EAJ08238	unknown [environmental sequence]
EAJ15524	unknown [environmental sequence]
EAJ18144	unknown [environmental sequence]
EAJ20649	unknown [environmental sequence]

EAJ21683	unknown [environmental sequence]
EAJ24413	unknown [environmental sequence]
EAJ28774	unknown [environmental sequence]
EAJ30522	unknown [environmental sequence]
EAJ35157	unknown [environmental sequence]
EAJ37407	unknown [environmental sequence]
EAJ39929	unknown [environmental sequence]
EAJ54356	unknown [environmental sequence]
EAJ54959	unknown [environmental sequence]
EAJ56207	unknown [environmental sequence]
EAJ58447	unknown [environmental sequence]
EAJ59958	unknown [environmental sequence]
EAJ63347	unknown [environmental sequence]
EAJ66054	unknown [environmental sequence]
EAJ67637	unknown [environmental sequence]
EAJ69812	unknown [environmental sequence]
EAJ74441	unknown [environmental sequence]
EAJ76472	unknown [environmental sequence]
EAJ76473	unknown [environmental sequence]
EAJ80355	unknown [environmental sequence]
EAJ80839	unknown [environmental sequence]
EAJ81408	unknown [environmental sequence]
EAJ86174	unknown [environmental sequence]
EAJ87600	unknown [environmental sequence]
EAJ88203	unknown [environmental sequence]
EAJ88682	unknown [environmental sequence]
EAJ92341	unknown [environmental sequence]
EAJ94774	unknown [environmental sequence]
EAJ97555	unknown [environmental sequence]
EAJ97958	unknown [environmental sequence]
EAK07654	unknown [environmental sequence]
EAK08513	unknown [environmental sequence]
EAK08529	unknown [environmental sequence]
EAK10609	unknown [environmental sequence]
EAK10614	unknown [environmental sequence]
EAK12902	unknown [environmental sequence]
EAK13034	unknown [environmental sequence]
EAK15092	unknown [environmental sequence]
EAK22483	unknown [environmental sequence]
EAK23222	unknown [environmental sequence]
EAK24187	unknown [environmental sequence]
EAK24674	unknown [environmental sequence]
EAK28785	unknown [environmental sequence]
EAK34731	unknown [environmental sequence]
EAK34742	unknown [environmental sequence]
EAK36883	unknown [environmental sequence]
EAK37522	unknown [environmental sequence]
EAK42705	unknown [environmental sequence]
EAK43213	unknown [environmental sequence]
EAK52580	unknown [environmental sequence]
EAK53452	unknown [environmental sequence]
EAK58759	unknown [environmental sequence]
EAK62665	unknown [environmental sequence]

EAK63558	unknown [environmental sequence]
F84187	phytoene dehydrogenase [imported] - Halobacterium sp. NRC-1
F90272	phytoene dehydrogenase related protein [imported] - Sulfolobus solfataricus
G87635	phytoene dehydrogenase-related protein [imported] - Caulobacter crescentus
G90413	phytoene dehydrogenase related protein [imported] - Sulfolobus solfataricus
H83880	hypothetical protein BH1848 [imported] - Bacillus halodurans (strain C-125)
H84320	phytoene dehydrogenase [imported] - Halobacterium sp. NRC-1
JC7723	phytoene desaturase (EC 1.14.99.-) 1 - citrus
NP_060220	all-trans-13,14-dihydroretinol saturase [Homo sapiens]
NP_080435	all-trans-13,14-dihydroretinol saturase [Mus musculus]
NP_193157	phytoene dehydrogenase, chloroplast / phytoene desaturase (PDS) [Arabidopsis thaliana]
NP_214383	protoporphyrinogen oxidase [Aquifex aeolicus VF5]
NP_276913	phytoene dehydrogenase [Methanothermobacter thermautotrophicus str. Delta H]
NP_293819	phytoene dehydrogenase, putative [Deinococcus radiodurans R1]
NP_294534	dehydrogenase, putative [Deinococcus radiodurans R1]
NP_294585	phytoene dehydrogenase [Deinococcus radiodurans R1]
NP_295972	methoxyneurosporene dehydrogenase [Deinococcus radiodurans R1]
NP_338490	oxidoreductase, putative [Mycobacterium tuberculosis CDC1551]
NP_376437	hypothetical protein ST0549 [Sulfolobus tokodaii str. 7]
NP_377056	hypothetical protein ST1130 [Sulfolobus tokodaii str. 7]
NP_388895	protoporphyrinogen IX and coproporphyrinogen III oxidase [Bacillus subtilis subsp. subtilis str. 168]
NP_441167	phytoene desaturase [Synechocystis sp. PCC 6803]
NP_441254	hypothetical protein sll0254 [Synechocystis sp. PCC 6803]
NP_442491	b-carotene ketolase [Synechocystis sp. PCC 6803]
NP_442727	hypothetical protein sll0033 [Synechocystis sp. PCC 6803]
NP_562475	probable diapophytoene dehydrogenase [Clostridium perfringens str. 13]
NP_568712	amine oxidase-related [Arabidopsis thaliana]
NP_601630	hypothetical protein NCgl2346 [Corynebacterium glutamicum ATCC 13032]
NP_601630	hypothetical protein NCgl2346 [Corynebacterium glutamicum ATCC 13032]
NP_616426	phytoene dehydrogenase family protein [Methanosarcina acetivorans C2A]
NP_624522	putative phytoene dehydrogenase (phytoene desaturase) (putative secreted protein) [Streptomyces coelicolor A3(2)]
NP_626360	putative carotenoid dehydrogenase (putative secreted protein) [Streptomyces coelicolor A3(2)]
NP_630834	putative phytoene dehydrogenase [Streptomyces coelicolor A3(2)]
NP_643053	phytoene dehydrogenase [Xanthomonas axonopodis pv. citri str. 306]
NP_647302	hypothetical protein MW2485 [Staphylococcus aureus subsp. aureus MW2]
NP_659552	all-trans-13,14-dihydroretinol saturase [Rattus norvegicus]
NP_661086	lycopene cyclase, putative [Chlorobium tepidum TLS]
NP_661546	carotenoid isomerase, putative [Chlorobium tepidum TLS]
NP_661701	phytoene desaturase [Chlorobium tepidum TLS]
NP_662300	zeta-carotene desaturase [Chlorobium tepidum TLS]
NP_681023	putative phytoene dehydrogenase [Thermosynechococcus elongatus BP-1]
NP_681127	zeta-carotene desaturase [Thermosynechococcus elongatus BP-1]
NP_682351	phytoene dehydrogenase / phytoene desaturase [Thermosynechococcus elongatus BP-1]
NP_693380	phytoene dehydrogenase [Oceanobacillus iheyensis HTE831]
NP_693382	phytoene dehydrogenase [Oceanobacillus iheyensis HTE831]
NP_737250	phytoene desaturase [Corynebacterium efficiens YS-314]
NP_763380	hypothetical protein VV21505 [Vibrio vulnificus CMCP6]

NP_786524	squalene synthase [Lactobacillus plantarum WCFS1]
NP_822198	phytoene desaturase [Streptomyces avermitilis MA-4680]
NP_822828	squalene/phytoene dehydrogenase [Streptomyces avermitilis MA-4680]
NP_827278	putative phytoene dehydrogenase [Streptomyces avermitilis MA-4680]
NP_851528	putative phytoene dehydrogenase [Streptomyces rochei]
NP_857496	PUTATIVE DEHYDROGENASE [Mycobacterium bovis AF2122/97]
NP_868798	probable phytoene dehydrogenase [Rhodopirellula baltica SH 1]
NP_869339	phytoene dehydrogenase [Rhodopirellula baltica SH 1]
NP_870237	phytoene dehydrogenase [Rhodopirellula baltica SH 1]
NP_874530	Zeta-carotene desaturase [Prochlorococcus marinus subsp. marinus str. CCMP1375]
NP_874561	Phytoene dehydrogenase, phytoene desaturase [Prochlorococcus marinus subsp. marinus str. CCMP1375]
NP_874977	Phytoene dehydrogenase / carotenoid isomerase [Prochlorococcus marinus subsp. marinus str. CCMP1375]
NP_892236	zeta-carotene desaturase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]
NP_892265	phytoene desaturase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]
NP_892458	Bacterial-type phytoene dehydrogenase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]
NP_893232	putative carotenoid isomerase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]
NP_894882	putative carotenoid isomerase [Prochlorococcus marinus str. MIT 9313]
NP_895385	NAD binding site [Prochlorococcus marinus str. MIT 9313]
NP_895793	zeta-carotene desaturase [Prochlorococcus marinus str. MIT 9313]
NP_895829	phytoene desaturase [Prochlorococcus marinus str. MIT 9313]
NP_896854	hypothetical protein SYNW0761 [Synechococcus sp. WH 8102]
NP_896994	Carotenoid isomerase [Synechococcus sp. WH 8102]
NP_898304	zeta-carotene desaturase [Synechococcus sp. WH 8102]
NP_898346	phytoene desaturase [Synechococcus sp. WH 8102]
NP_902647	hypothetical protein CV2977 [Chromobacterium violaceum ATCC 12472]
NP_923340	beta-carotene ketolase [Gloeobacter violaceus PCC 7421]
NP_923639	hypothetical protein gll0693 [Gloeobacter violaceus PCC 7421]
NP_923813	phytoene dehydrogenase [Gloeobacter violaceus PCC 7421]
NP_925079	hypothetical protein gvip293 [Gloeobacter violaceus PCC 7421]
NP_931515	phytoene dehydrogenase (phytoene desaturase) [Photorhabdus luminescens subsp. laumondii TTO1]
NP_936379	hypothetical protein VVA0323 [Vibrio vulnificus YJ016]
NP_940208	phytoene dehydrogenase related enzyme [Corynebacterium diphtheriae NCTC 13129]
NP_945754	NAD binding site:Amine oxidase [Rhodopseudomonas palustris CGA009]
NP_946860	phytoene dehydrogenase CrtI [Rhodopseudomonas palustris CGA009]
NP_946866	methoxyneurosporene dehydrogenase [Rhodopseudomonas palustris CGA009]
NP_948851	phytoene dehydrogenase-related protein [Rhodopseudomonas palustris CGA009]
NP_962004	hypothetical protein MAP3070 [Mycobacterium avium subsp. paratuberculosis str. k10]
NP_968600	Phytoene dehydrogenase [Bdellovibrio bacteriovorus HD100]
NP_974222	zeta-carotene desaturase (ZDS1) / carotene 7,8-desaturase [Arabidopsis thaliana]
NP_974545	phytoene dehydrogenase, chloroplast / phytoene desaturase (PDS) [Arabidopsis thaliana]
O49901	Zeta-carotene desaturase, chloroplast precursor (Carotene 7,8-desaturase)
P17059	Methoxyneurosporene dehydrogenase

P54971	Phytoene dehydrogenase (Phytoene desaturase)
P54978	Phytoene dehydrogenase (Phytoene desaturase)
P54979	Phytoene dehydrogenase (Phytoene desaturase)
P54981	Phytoene dehydrogenase (Phytoene desaturase)
P54982	Phytoene dehydrogenase (Phytoene desaturase)
P74306	Zeta-carotene desaturase (Carotene 7,8-desaturase)
Q01671	Methoxyneurosporene dehydrogenase
Q02861	Phytoene dehydrogenase (Phytoene desaturase)
Q38893	Zeta-carotene desaturase, chloroplast precursor (Carotene 7,8-desaturase)
Q40406	Phytoene dehydrogenase, chloroplast precursor (Phytoene desaturase)
Q9FV46	Zeta-carotene desaturase, chloroplast precursor (Carotene 7,8-desaturase)
Q9SE20	Zeta-carotene desaturase, chloroplast precursor (Carotene 7,8-desaturase)
Q9SMJ3	Zeta-carotene desaturase, chloroplast precursor (Carotene 7,8-desaturase)
Q9ZTN9	Phytoene dehydrogenase, chloroplast precursor (Phytoene desaturase)
Q9ZTP4	Zeta-carotene desaturase, chloroplast precursor (Carotene 7,8-desaturase)
S29314	phytoene dehydrogenase (EC 1.3.-.-) - pepper
S32171	hydroxyneurosporene dehydrogenase (EC 1.3.-.-) - Myxococcus xanthus
S49624	methoxyneurosporene dehydrogenase (EC 1.3.-.-) CrtD - Rhodobacter sphaeroides
S52586	phytoene dehydrogenase (EC 1.3.-.-) - Erwinia herbicola
S65060	phytoene desaturase precursor - maize
T10701	probable phytoene dehydrogenase (EC 1.3.-.-) - green alga (Dunaliella bardawil)
T31463	probable diapophytoene dehydrogenase crtN - Heliobacillus mobilis
T46822	phytoene desaturase (EC 1.3.-.-) [validated] - Xanthophyllomyces dendrorhous
T48646	phytoene dehydrogenase (EC 1.-.-.-) [validated] - Cercospora nicotianae
T50745	phytoene dehydrogenase (EC 1.3.-.-) [imported] - Rhodobacter sphaeroides
T50749	methoxyneurosporene dehydrogenase (EC 1.3.-.-) crtD [imported] - Rhodobacter sphaeroides
T50893	methoxyneurosporene dehydrogenase [imported] - Rubrivivax gelatinosus
T50910	phytoene dehydrogenase [imported] - Rubrivivax gelatinosus
T51119	phytoene desaturase crtI [imported] - Brevibacterium linens
T51123	betacarotene desaturase [imported] - Brevibacterium linens
XP_324732	PHYTOENE DEHYDROGENASE (PHYTOENE DESATURASE) (ALBINO-1 PROTEIN) [Neurospora crassa]
XP_383241	hypothetical protein FG03065.1 [Gibberella zeae PH-1]
XP_401825	hypothetical protein UM04210.1 [Ustilago maydis 521]
XP_470568	Putative phytoene dehydrogenase precursor [Oryza sativa]
XP_473486	OSJNBa0084K11.8 [Oryza sativa (japonica cultivar-group)]
XP_477063	putative zeta-carotene desaturase precursor [Oryza sativa (japonica cultivar-group)]
XP_525801	PREDICTED: hypothetical protein XP_525801 [Pan troglodytes]
XP_540198	PREDICTED: hypothetical protein XP_540198 [Canis familiaris]
YP_006049	phytoene dehydrogenase [Thermus thermophilus HB27]
YP_013621	phytoene dehydrogenase, putative [Listeria monocytogenes str. 4b F2365]
YP_024310	phytoene dehydrogenase [Picrophilus torridus DSM 9790]
YP_041986	squalene synthase [Staphylococcus aureus subsp. aureus MRSA252]
YP_041988	putative phytoene dehydrogenase related protein [Staphylococcus aureus subsp. aureus MRSA252]
YP_044561	squalene synthase [Staphylococcus aureus subsp. aureus MSSA476]
YP_044564	putative phytoene dehydrogenase related protein [Staphylococcus aureus subsp. aureus MSSA476]
YP_062471	phytoene dehydrogenase [Leifsonia xyli subsp. xyli str. CTCB07]
YP_117947	putative phytoene desaturase [Nocardia farcinica IFM 10152]

YP_120612	putative phytoene desaturase [Nocardia farcinica IFM 10152]
YP_135077	phytoene dehydrogenase [Haloarcula marismortui ATCC 43049]
YP_136483	phytoene dehydrogenase [Haloarcula marismortui ATCC 43049]
YP_145331	probable phytoene dehydrogenase [Thermus thermophilus HB8]
YP_145348	phytoene dehydrogenase [Thermus thermophilus HB8]
YP_171014	carotene isomerase [Synechococcus elongatus PCC 6301]
YP_172823	phytoene dehydrogenase [Synechococcus elongatus PCC 6301]
YP_173078	carotene isomerase [Synechococcus elongatus PCC 6301]
YP_173207	zeta-carotene desaturase [Synechococcus elongatus PCC 6301]
YP_184572	predicted oxidoreductase [Thermococcus kodakaraensis]
YP_187368	dehydrosqualene desaturase [Staphylococcus aureus subsp. aureus COL]
YP_187371	phytoene dehydrogenase [Staphylococcus aureus subsp. aureus COL]
YP_187371	phytoene dehydrogenase [Staphylococcus aureus subsp. aureus COL]
YP_187371	phytoene dehydrogenase [Staphylococcus aureus subsp. aureus COL]
ZP_000490	COG1233: Phytoene dehydrogenase and related proteins [Magnetospirillum magnetotacticum MS-1]
ZP_000509	COG1233: Phytoene dehydrogenase and related proteins [Magnetospirillum magnetotacticum MS-1]
ZP_000518	COG1233: Phytoene dehydrogenase and related proteins [Magnetospirillum magnetotacticum MS-1]
ZP_000566	COG0562: UDP-galactopyranose mutase [Magnetospirillum magnetotacticum MS-1]
ZP_000627	COG1233: Phytoene dehydrogenase and related proteins [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]
ZP_000627	COG1233: Phytoene dehydrogenase and related proteins [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]
ZP_001073	COG1233: Phytoene dehydrogenase and related proteins [Nostoc punctiforme PCC 73102]
ZP_001081	COG1233: Phytoene dehydrogenase and related proteins [Nostoc punctiforme PCC 73102]
ZP_001091	COG3349: Uncharacterized conserved protein [Nostoc punctiforme PCC 73102]
ZP_001116	COG1233: Phytoene dehydrogenase and related proteins [Nostoc punctiforme PCC 73102]
ZP_001117	COG3349: Uncharacterized conserved protein [Nostoc punctiforme PCC 73102]
ZP_001119	COG3349: Uncharacterized conserved protein [Nostoc punctiforme PCC 73102]
ZP_001124	COG1233: Phytoene dehydrogenase and related proteins [Nostoc punctiforme PCC 73102]
ZP_001510	COG1233: Phytoene dehydrogenase and related proteins [Dechloromonas aromatica RCB]
ZP_001591	COG3349: Uncharacterized conserved protein [Anabaena variabilis ATCC 29413]
ZP_001593	COG1233: Phytoene dehydrogenase and related proteins [Anabaena variabilis ATCC 29413]
ZP_001602	COG3349: Uncharacterized conserved protein [Anabaena variabilis ATCC 29413]
ZP_001614	COG3349: Uncharacterized conserved protein [Anabaena variabilis ATCC 29413]
ZP_001645	COG3349: Uncharacterized conserved protein [Synechococcus elongatus PCC 7942]
ZP_001650	COG3349: Uncharacterized conserved protein [Synechococcus elongatus PCC 7942]
ZP_001722	COG1233: Phytoene dehydrogenase and related proteins [Methylobacillus flagellatus KT]

ZP_001746	COG3349: Uncharacterized conserved protein [Crocosphaera watsonii WH 8501]
ZP_001752	COG3349: Uncharacterized conserved protein [Crocosphaera watsonii WH 8501]
ZP_001770	COG1232: Protoporphyrinogen oxidase [Crocosphaera watsonii WH 8501]
ZP_001777	COG1233: Phytoene dehydrogenase and related proteins [Crocosphaera watsonii WH 8501]
ZP_001787	COG3349: Uncharacterized conserved protein [Crocosphaera watsonii WH 8501]
ZP_001837	COG1233: Phytoene dehydrogenase and related proteins [Exiguobacterium sp. 255-15]
ZP_001867	COG1233: Phytoene dehydrogenase and related proteins [Rubrobacter xylanophilus DSM 9941]
ZP_002073	COG1233: Phytoene dehydrogenase and related proteins [Rhodobacter sphaeroides 2.4.1]
ZP_002077	COG1233: Phytoene dehydrogenase and related proteins [Rhodobacter sphaeroides 2.4.1]
ZP_002339	phytoene dehydrogenase, putative [Listeria monocytogenes str. 1/2a F6854]
ZP_002680	COG1233: Phytoene dehydrogenase and related proteins [Rhodospirillum rubrum]
ZP_002705	COG1233: Phytoene dehydrogenase and related proteins [Rhodospirillum rubrum]
ZP_002771	COG1232: Protoporphyrinogen oxidase [Burkholderia fungorum LB400]
ZP_002892	hypothetical protein Mmc102002317 [Magnetococcus sp. MC-1]
ZP_002916	COG3349: Uncharacterized conserved protein [Thermobifida fusca]
ZP_002963	COG1233: Phytoene dehydrogenase and related proteins [Methanosarcina barkeri str. fusaro]
ZP_003022	COG1233: Phytoene dehydrogenase and related proteins [Novosphingobium aromaticivorans DSM 12444]
ZP_003036	COG1233: Phytoene dehydrogenase and related proteins [Novosphingobium aromaticivorans DSM 12444]
ZP_003107	COG1233: Phytoene dehydrogenase and related proteins [Cytophaga hutchinsonii]
ZP_003202	COG1233: Phytoene dehydrogenase and related proteins [Oenococcus oeni PSU-1]
ZP_003258	COG1233: Phytoene dehydrogenase and related proteins [Trichodesmium erythraeum IMS101]
ZP_003268	COG3349: Uncharacterized conserved protein [Trichodesmium erythraeum IMS101]
ZP_003269	COG3349: Uncharacterized conserved protein [Trichodesmium erythraeum IMS101]
ZP_003276	COG1233: Phytoene dehydrogenase and related proteins [Trichodesmium erythraeum IMS101]
ZP_003283	COG1233: Phytoene dehydrogenase and related proteins [Trichodesmium erythraeum IMS101]
ZP_003557	COG1233: Phytoene dehydrogenase and related proteins [Exiguobacterium sp. 255-15]
ZP_003559	COG3349: Uncharacterized conserved protein [Chloroflexus aurantiacus]
ZP_003565	COG1233: Phytoene dehydrogenase and related proteins [Chloroflexus aurantiacus]
ZP_003577	COG1233: Phytoene dehydrogenase and related proteins [Chloroflexus aurantiacus]
ZP_003593	COG1233: Phytoene dehydrogenase and related proteins [Chloroflexus

	aurantiacus]
ZP_003595	COG1233: Phytoene dehydrogenase and related proteins [Chloroflexus aurantiacus]
ZP_003685	carotenoid isomerase, putative [Campylobacter lari RM2100]

Table 18. Examples of phytoene synthase and lycopene cyclase polypeptides.

Accession Number	GI Number	Description
1613414C	227040	crtB gene
A49558	1076590	phytoene synthase 2 precursor - tomato (fragment)
AAA19428	506623	phytoene synthase [Neurospora crassa]
AAA32836	413732	phytoene synthase
AAA64982	148413	phytoene synthase [Pantoea agglomerans]
AAB87738	29893495	phytoene synthase [Rubrivivax gelatinosus]
AAC44849	1842243	phytoene synthase
AAD38051	13542332	phytoene synthase [Citrus x paradisi]
AAF78202	8650418	phytoene synthase [Bradyrhizobium sp. ORS278]
AAF82616	9081847	phytoene synthase [Tagetes erecta]
AAG10427	9971814	phytoene synthase [Tagetes erecta]
AAG28701	11066678	CrtB [Streptomyces griseus]
AAK07734	18476085	phytoene synthase [Oryza sativa (japonica cultivar-group)]
AAK07735	18476089	phytoene synthase [Oryza sativa (japonica cultivar-group)]
AAK15621	13195243	phytoene synthase [Haematococcus pluvialis]
AAL02001	15553721	phytoene synthase [Xanthobacter sp. Py2]
AAL76346	18645045	phytoene synthase [uncultured proteobacterium]
AAL82578	21326700	phytoene synthase radicle isoform [Oryza sativa (indica cultivar-group)]
AAM45379	21360353	phytoene synthase [Tagetes erecta]
AAM48647	21328641	phytoene synthase [uncultured proteobacterium]
AAM62787	21553694	phytoene synthase [Arabidopsis thaliana]
AAM94363	22296799	phytoene synthase [Agromyces mediolanus]
AAN85600	27228294	Phytoene Synthase [Pantoea stewartii]
AAO24767	27903500	phytoene synthase [Citrus maxima]
AAO39835	28403302	phytoene synthase [Citrus sinensis]
AAO46895	37729028	lycopene cyclase / phytoene synthase [Blakeslea trispora]
AAO47570	33465823	phytoene-beta carotene synthase [Xanthophyllomyces dendrorhous]
AAO73816	33465821	crtYB [Xanthophyllomyces dendrorhous]
AAP22038	30349414	phytoene synthase 2 [Zea mays]
AAP55451	32350232	phytoene synthase 2 [Zea mays]
AAP55453	32350236	phytoene synthase 2 [Zea mays]
AAP55461	32350252	phytoene synthase 2 [Zea mays]

AAP55471	32350272	phytoene synthase 2 [Zea mays]
AAP55484	32350298	phytoene synthase 2 [Zea mays]
AAP55486	32350302	phytoene synthase 2 [Zea mays]
AAP56083	32349564	phytoene synthase [Zea mays]
AAP56124	32349646	phytoene synthase [Zea mays]
AAP56127	32349652	phytoene synthase [Zea mays]
AAP56136	32349670	phytoene synthase [Zea mays]
AAP56148	32349694	phytoene synthase [Zea mays]
AAP56155	32349708	phytoene synthase [Zea mays]
AAP56156	32349710	phytoene synthase [Zea mays]
AAP56157	32349712	phytoene synthase [Zea mays]
AAP56158	32349714	phytoene synthase [Zea mays]
AAP79176	32307542	phytoene synthase [Bigelowiella natans]
AAQ91837	37499616	phytoene synthase 2 [Zea mays]
AAR08445	38037628	chloroplast phytoene synthase 1 [Zea mays]
AAR31885	39842609	chloroplast phytoene synthase [Zea mays]
AAR37803	40062932	phytoene synthase [uncultured bacterium 442]
AAR37856	40062986	phytoene synthase [uncultured bacterium 443]
AAR86104	40456029	phytoene synthase [Momordica charantia var. abbreviata]
AAR87868	40557193	phytoene synthase [Oncidium cv. 'Gower Ramsey']
AAR98492	41018901	phytoene synthase [Bradyrhizobium sp. ORS278]
AAS02284	41394357	phytoene synthase 2 [Zea mays]
AAS17009	42491736	phytoene synthase 2 [Oryza sativa (japonica cultivar-group)]
AAS18307	42521626	phytoene synthase 1; PSY1 [Oryza sativa (indica cultivar-group)]
AAT28184	47498515	phytoene synthase [Dunaliella salina]
AAT35222	47531118	fusion of carotene synthesis proteins [synthetic construct]
AAT38473	47779181	chloroplast phytoene synthase precursor [Chlamydomonas reinhardtii]
AAT46069	48686711	phytoene synthase [Dunaliella salina]
AAT74581	50313418	PSY [Citrus sinensis]
AAT90319	50952786	putative phytoene synthase [uncultured proteobacterium eBACred25D05]
AAV74394	56122551	phytoene synthase [Adonis palaestina]
AAW23162	56698928	phytoene synthase [Rhodococcus erythropolis]
AC2035	25366683	phytoene synthase [imported] - Nostoc sp. (strain PCC 7120)
AC2035	25366683	phytoene synthase [imported] - Nostoc sp. (strain PCC 7120)
BAB18514	11344507	phytoene synthase [Citrus unshiu]
BAB79604	18143449	crtB [Pantoea agglomerans pv. milletiae]
BAD07278	40809739	phytoene synthase [Citrus sinensis]
BAD07286	40809755	phytoene synthase [Citrus limon]
BAD62106	54291340	phytoene synthase [Oryza sativa (japonica cultivar-group)]
BAD62107	54291341	phytoene synthase-like [Oryza sativa (japonica cultivar-group)]
C90061	25506636	squalene desaturase [imported] - Staphylococcus aureus (strain N315)
CAA47625	19347	mutant phytoene synthase [Lycopersicon esculentum]
CAA68575	19341	unnamed protein product [Lycopersicon esculentum]
CAB07958	1934837	unknown [Bacillus subtilis]
CAB38740	4490590	phytoene synthase [Rhodobacter sphaeroides]
CAB51949	5690074	phytoene-beta carotene synthase [Xanthophyllomyces dendrorhous]
CAB56063	5912296	phytoene synthase [Paracoccus marcusii]

CAB86388	7453011	phytoene synthase/lycopene cyclase [Phycomyces blakesleeanus]
CAB93661	8250520	lycopene cyclase/phytoene synthase [Phycomyces blakesleeanus]
CAB94795	8574392	phytoene synthase [Mycobacterium aurum]
CAC19567	11990226	phytoene synthase [Helianthus annuus]
CAC27383	12584564	phytoene synthase [Helianthus annuus]
CAD19988	18307500	carotene cyclase [Gibberella fujikuroi]
CAD29284	57282088	putative phytoene synthase [Oryza sativa]
CAE76609	38567321	geranylgeranyl-diphosphate geranylgeranyltransferase (AL-2) [Neurospora crassa]
E37802	95606	crtB protein - Erwinia uredovora
E84320	25410251	phytoene synthase [imported] - Halobacterium sp. NRC-1
EAA98758	42863045	unknown [environmental sequence]
EAB01965	42869439	unknown [environmental sequence]
EAB04170	42873822	unknown [environmental sequence]
EAB07138	42879858	unknown [environmental sequence]
EAB09791	42885235	unknown [environmental sequence]
EAB19826	42905452	unknown [environmental sequence]
EAB35029	42936011	unknown [environmental sequence]
EAB41375	42948740	unknown [environmental sequence]
EAB78706	43024004	unknown [environmental sequence]
EAB92586	43052355	unknown [environmental sequence]
EAC06949	43081493	unknown [environmental sequence]
EAC18360	43104624	unknown [environmental sequence]
EAC25793	43119723	unknown [environmental sequence]
EAC29883	43128092	unknown [environmental sequence]
EAC32813	43133973	unknown [environmental sequence]
EAC33105	43134560	unknown [environmental sequence]
EAC38486	43145552	unknown [environmental sequence]
EAC52233	43173313	unknown [environmental sequence]
EAC60029	43189028	unknown [environmental sequence]
EAC68026	43204953	unknown [environmental sequence]
EAC96197	43261031	unknown [environmental sequence]
EAD08701	43285745	unknown [environmental sequence]
EAD20866	43310220	unknown [environmental sequence]
EAD32755	43334458	unknown [environmental sequence]
EAD38008	43345761	unknown [environmental sequence]
EAD50152	43370658	unknown [environmental sequence]
EAD50402	43371147	unknown [environmental sequence]
EAD81123	43452903	unknown [environmental sequence]
EAD93882	43478303	unknown [environmental sequence]
EAE12860	43516265	unknown [environmental sequence]
EAE16121	43522884	unknown [environmental sequence]
EAE31084	43552634	unknown [environmental sequence]
EAE35665	43561764	unknown [environmental sequence]
EAE44717	43579862	unknown [environmental sequence]
EAE46627	43583580	unknown [environmental sequence]
EAE47846	43586023	unknown [environmental sequence]
EAE72264	43635190	unknown [environmental sequence]
EAE76009	43642573	unknown [environmental sequence]
EAE86335	43662748	unknown [environmental sequence]
EAE89581	43669163	unknown [environmental sequence]

EAF18881	43728007	unknown [environmental sequence]
EAF64277	43819669	unknown [environmental sequence]
EAF67931	43827263	unknown [environmental sequence]
EAF84745	43861327	unknown [environmental sequence]
EAF94004	43880040	unknown [environmental sequence]
EAG06083	43903395	unknown [environmental sequence]
EAG21950	43933540	unknown [environmental sequence]
EAG43625	43973477	unknown [environmental sequence]
EAG50171	43985555	unknown [environmental sequence]
EAG57517	43999205	unknown [environmental sequence]
EAG62787	44009110	unknown [environmental sequence]
EAG65580	44014171	unknown [environmental sequence]
EAG68110	44018715	unknown [environmental sequence]
EAG72283	44026322	unknown [environmental sequence]
EAG78750	44037938	unknown [environmental sequence]
EAG80445	44041116	unknown [environmental sequence]
EAG93220	44064453	unknown [environmental sequence]
EAH04927	44085694	unknown [environmental sequence]
EAH08972	44093217	unknown [environmental sequence]
EAH10377	44095788	unknown [environmental sequence]
EAH22151	44117864	unknown [environmental sequence]
EAH31461	44134654	unknown [environmental sequence]
EAH50033	44169323	unknown [environmental sequence]
EAH64480	44196848	unknown [environmental sequence]
EAH79040	44223009	unknown [environmental sequence]
EAH99976	44255671	unknown [environmental sequence]
EAI02786	44259828	unknown [environmental sequence]
EAI02787	44259829	unknown [environmental sequence]
EAI03575	44260943	unknown [environmental sequence]
EAI05900	44264266	unknown [environmental sequence]
EAI61004	44344824	unknown [environmental sequence]
EAI70669	44358327	unknown [environmental sequence]
EAI83938	44377067	unknown [environmental sequence]
EAJ05110	44406802	unknown [environmental sequence]
EAJ05569	44407471	unknown [environmental sequence]
EAJ08876	44412338	unknown [environmental sequence]
EAJ35156	44449986	unknown [environmental sequence]
EAJ38900	44455130	unknown [environmental sequence]
EAJ49645	44470504	unknown [environmental sequence]
EAJ54357	44477026	unknown [environmental sequence]
EAJ60475	44485647	unknown [environmental sequence]
EAJ64125	44492007	unknown [environmental sequence]
EAJ67499	44497025	unknown [environmental sequence]
EAJ76471	44510405	unknown [environmental sequence]
EAJ76950	44511114	unknown [environmental sequence]
EAJ78637	44513596	unknown [environmental sequence]
EAJ78787	44513824	unknown [environmental sequence]
EAJ79616	44515082	unknown [environmental sequence]
EAJ80356	44516200	unknown [environmental sequence]
EAJ81914	44518489	unknown [environmental sequence]
EAJ87417	44526623	unknown [environmental sequence]
EAK08514	44557109	unknown [environmental sequence]
EAK08523	44557119	unknown [environmental sequence]

EAK12901	44563097	unknown [environmental sequence]
EAK22180	44576315	unknown [environmental sequence]
EAK24859	44580262	unknown [environmental sequence]
EAK28345	44585276	unknown [environmental sequence]
EAK34732	44594324	unknown [environmental sequence]
EAK34736	44594329	unknown [environmental sequence]
EAK37296	44597942	unknown [environmental sequence]
EAK37521	44598256	unknown [environmental sequence]
EAK56335	44624430	unknown [environmental sequence]
G84363	25410528	hypothetical protein ggt [imported] - Halobacterium sp. NRC-1
NP_274195	15677043	phytoene synthase, putative [Neisseria meningitidis MC58]
NP_284085	15794263	poly-isoprenyl transferase [Neisseria meningitidis Z2491]
NP_294586	15805888	phytoene synthase [Deinococcus radiodurans R1]
NP_388961	16078144	hypothetical protein BSU10810 [Bacillus subtilis subsp. subtilis str. 168]
NP_441168	16330440	phytoene synthase [Synechocystis sp. PCC 6803]
NP_443763	16519643	Y4aC [Rhizobium sp. NGR234]
NP_624523	21218744	putative phytoene synthase [Streptomyces coelicolor A3(2)]
NP_630832	21225053	putative phytoene synthase [Streptomyces coelicolor A3(2)]
NP_662273	21674208	phytoene desaturase [Chlorobium tepidum TLS]
NP_682350	22299103	phytoene synthase [Thermosynechococcus elongatus BP-1]
NP_693381	23099915	phytoene synthase [Oceanobacillus iheyensis HTE831]
NP_786525	28379633	phytoene synthase [Lactobacillus plantarum WCFS1]
NP_822199	29827565	phytoene synthase [Streptomyces avermitilis MA-4680]
NP_822829	29828195	squalene/phytoene synthase [Streptomyces avermitilis MA-4680]
NP_851527	30795077	putative phytoene synthase [Streptomyces rochei]
NP_868799	32475805	probable phytoene synthase [Rhodopirellula baltica SH 1]
NP_874560	33239618	Phytoene synthase, CrtB [Prochlorococcus marinus subsp. marinus str. CCMP1375]
NP_879992	33592348	putative phytoene synthase [Bordetella pertussis Tohama I]
NP_884101	33596458	putative phytoene synthase [Bordetella parapertussis 12822]
NP_889809	33602249	putative phytoene synthase [Bordetella bronchiseptica RB50]
NP_892264	33860703	Squalene and phytoene synthases [Prochlorococcus marinus subsp. pastoris str. CCMP1986]
NP_895828	33864268	Squalene and phytoene synthases [Prochlorococcus marinus str. MIT 9313]
NP_898345	33866786	phytoene synthases [Synechococcus sp. WH 8102]
NP_902648	34498433	probable geranylgeranyl-diphosphate geranylgeranyltransferase [Chromobacterium violaceum ATCC 12472
NP_902649	34498434	probable phytoene synthase-related protein [Chromobacterium violaceum ATCC 12472]
NP_924690	37521313	phytoene synthase [Gloeobacter violaceus PCC 7421]
NP_931516	37528171	phytoene synthase [Photorhabdus luminescens subsp. laumondii TTO1]
NP_946861	39934585	CrtB phytoene synthase [Rhodopseudomonas palustris CGA009]
NP_949079	39936803	putative poly-isoprenyl transferase [Rhodopseudomonas palustris CGA009]
NP_962005	41409169	hypothetical protein MAP3071 [Mycobacterium avium subsp. paratuberculosis str. k10]

NP_968601	42523221	phytoene synthase [Bdellovibrio bacteriovorus HD100]
O07333	3913360	Phytoene synthase
P08196	585746	Phytoene synthase 1, chloroplast precursor (Fruit ripening specific protein pTOM5)
P21683	30923192	Phytoene synthase
P37269	585009	Phytoene synthase
P37271	27735222	Phytoene synthase, chloroplast precursor
P37272	585749	Phytoene synthase, chloroplast precursor
P53797	1709885	Phytoene synthase, chloroplast precursor
P54975	1706137	Phytoene synthase
P54977	1706139	Phytoene synthase
P65860	54041032	Probable phytoene synthase
Q9SSU8	8928282	Phytoene synthase, chloroplast precursor
Q9UUQ6	34922667	CarRP protein [Includes: Lycopene cyclase ; Phytoene synthase]
S22474	7489041	phytoene synthase (EC 2.5.1.-) - tomato
S32170	321671	phytoene synthetase - Myxococcus xanthus
S52587	1073300	prephytoene pyrophosphate synthase - Erwinia herbicola
S56668	2129505	geranylgeranyl-diphosphate geranylgeranyltransferase (EC 2.5.1.32) precursor - muskmelon
S68307	2130144	phytoene synthase - maize
T10702	7484346	phytoene synthase (EC 2.5.1.-) - green alga (Dunaliella bardawil)
T46594	11291807	phytoene synthase (EC 2.5.1.-) [validated] - Mycobacterium marinum
T50746	11356347	phytoene synthase (EC 2.5.1.-) [imported] - Rhodobacter sphaeroides
T50895	11291816	prephytoene pyrophosphate synthase [imported] - Rubrivivax gelatinosus
XP_324765	32408567	PHYTOENE SYNTHASE [Neurospora crassa]
XP_383242	46114448	hypothetical protein FG03066.1 [Gibberella zeae PH-1]
XP_403902	49080862	hypothetical protein UM06287.1 [Ustilago maydis 521]
YP_006040	46255128	phytoene synthase [Thermus thermophilus HB27]
YP_103126	53723680	phytoene synthase, putative [Burkholderia mallei ATCC 23344]
YP_112342	53723357	squalene/phytoene synthase [Burkholderia pseudomallei K96243]
YP_117945	54023703	putative phytoene synthase [Nocardia farcinica IFM 10152]
YP_120611	54026369	putative phytoene synthase [Nocardia farcinica IFM 10152]
YP_136628	55378778	lycopene cyclase [Haloarcula marismortui ATCC 43049]
YP_136629	55378779	phytoene synthase [Haloarcula marismortui ATCC 43049]
YP_145340	55978284	phytoene synthase [Thermus thermophilus HB8]
YP_145343	55978287	phytoene synthase-related protein [Thermus thermophilus HB8]
YP_160917	56479328	probable terpenoid synthase-related protein [Azoarcus sp. EbN1]
YP_160918	56479329	putative terpenoid synthase [Azoarcus sp. EbN1]
YP_162605	56551766	phytoene/squalene synthetase [Zymomonas mobilis subsp. mobilis ZM4]
YP_172822	56752121	phytoene synthase [Synechococcus elongatus PCC 6301]
YP_187369	57652299	dehydrosqualene synthase [Staphylococcus aureus subsp. aureus COL]
YP_192648	58040684	Putative phytoene synthase [Gluconobacter oxydans 621H]

ZP_000044	22956752	COG1562: Phytoene/squalene synthetase [Rhodobacter sphaeroides 2.4.1]
ZP_001091	53688068	COG1562: Phytoene/squalene synthetase [Nostoc punctiforme PCC 73102]
ZP_001591	53763709	COG1562: Phytoene/squalene synthetase [Anabaena variabilis ATCC 29413]
ZP_001657	45514234	COG1562: Phytoene/squalene synthetase [Ralstonia eutropha JMP134]
ZP_001690	46132223	COG1562: Phytoene/squalene synthetase [Ralstonia eutropha JMP134]
ZP_001746	45523280	COG1562: Phytoene/squalene synthetase [Crocosphaera watsonii WH 8501]
ZP_001837	53771530	COG1562: Phytoene/squalene synthetase [Exiguobacterium sp. 255-15]
ZP_001867	45546711	COG1562: Phytoene/squalene synthetase [Rubrobacter xylanophilus DSM 9941]
ZP_002096	46204978	COG1562: Phytoene/squalene synthetase [Magnetospirillum magnetotacticum MS-1]
ZP_002248	46324513	COG1562: Phytoene/squalene synthetase [Burkholderia cepacia R1808]
ZP_002450	47575031	COG1562: Phytoene/squalene synthetase [Rubrivivax gelatinosus PM1]
ZP_002680	48763469	COG1562: Phytoene/squalene synthetase [Rhodospirillum rubrum]
ZP_002710	48766450	COG1562: Phytoene/squalene synthetase [Rhodospirillum rubrum]
ZP_002791	48782680	COG1562: Phytoene/squalene synthetase [Burkholderia fungorum LB400]
ZP_002892	48832182	COG1562: Phytoene/squalene synthetase [Magnetococcus sp. MC-1]
ZP_002916	48834623	COG1562: Phytoene/squalene synthetase [Thermobifida fusca]
ZP_003036	48849426	COG1562: Phytoene/squalene synthetase [Novosphingobium aromaticivorans DSM 12444]
ZP_003269	48893702	COG1562: Phytoene/squalene synthetase [Trichodesmium erythraeum IMS101]
ZP_003351	52007802	COG1562: Phytoene/squalene synthetase [Thiobacillus denitrificans ATCC 25259]
ZP_003487	53730362	COG1562: Phytoene/squalene synthetase [Dechloromonas aromatica RCB]
ZP_003501	53759405	COG1562: Phytoene/squalene synthetase [Methylobacillus flagellatus KT]
ZP_003591	53798896	COG1562: Phytoene/squalene synthetase [Chloroflexus aurantiacus]
ZP_003628	54030691	COG1562: Phytoene/squalene synthetase [Polaromonas sp. JS666]

Table 19. Examples of carotenoid ketolase polypeptides.

Accession Number	GI Number	Description
AAA99932	609575	fatty acid desaturase
AAB48668	1870215	ORF [Emericella nidulans]
AAC25611	2541936	unknown [Pseudomonas syringae]
AAF78203	8650419	beta-carotene ketolase [Bradyrhizobium sp. ORS278]
AAH16427	16741158	2210008A03Rik protein [Mus musculus]
AAN03484	22597194	BKT [Haematococcus pluvialis]
AAN85497	26541510	putative fatty acid desaturase [Streptomyces atroolivaceus]
AAN86030	33439708	beta-carotene C4 oxygenase [Brevundimonas aurantiaca]
AAO64399	28976134	putative beta-carotene ketolase [Nodularia spumigena]

AAQ23139	33621091	CrtW/CrtY fusion protein [synthetic construct]
AAT35222	47531118	fusion of carotene synthesis proteins [synthetic construct]
AAT35555	47558911	beta-carotene ketolase [Haematococcus pluvialis]
AAV41372	55139370	beta-carotene ketolase/oxygenase ['Chlorella' zofingiensis]
AB2307	25530134	hypothetical protein alr4009 [imported] - Nostoc sp. (strain PCC 7120)
AF2204	25533132	beta-carotene ketolase [imported] - Nostoc sp. (strain PCC 7120)
BAB54999	14028447	mlr9395 [Mesorhizobium loti MAFF303099]
BAB58879	14270087	membrane fatty acid desaturase [Toxoplasma gondii]
BAC98366	37360914	alkane hydroxylase [Alcanivorax borkumensis]
CAA60478	2654318	beta-carotene C-4 oxygenase (ketolase) [Haematococcus pluvialis]
CAB56059	5912292	beta-carotene C-4-oxygenase (ketolase) [Paracoccus marcusii]
D87673	25398945	conserved hypothetical protein CC3422 [imported] - Caulobacter crescentus
EAA79304	42823978	unknown [environmental sequence]
EAA80363	42826055	unknown [environmental sequence]
EAA81403	42828115	unknown [environmental sequence]
EAA84711	42834481	unknown [environmental sequence]
EAB82380	43031476	unknown [environmental sequence]
EAB86624	43040184	unknown [environmental sequence]
EAC05755	43079085	unknown [environmental sequence]
EAD12219	43292778	unknown [environmental sequence]
EAD71182	43427899	unknown [environmental sequence]
EAD94927	43480380	unknown [environmental sequence]
EAF11582	43712986	unknown [environmental sequence]
EAF98072	43888329	unknown [environmental sequence]
EAG19345	43928738	unknown [environmental sequence]
EAG38273	43963688	unknown [environmental sequence]
EAG79800	44039853	unknown [environmental sequence]
EAG96474	44070318	unknown [environmental sequence]
EAH00349	44077315	unknown [environmental sequence]
EAH36448	44143633	unknown [environmental sequence]
EAH40683	44151265	unknown [environmental sequence]
EAH53180	44175316	unknown [environmental sequence]
EAH96648	44250729	unknown [environmental sequence]
EAI05260	44263397	unknown [environmental sequence]
EAI17468	44281329	unknown [environmental sequence]
EAI53009	44333409	unknown [environmental sequence]
EAI54054	44334878	unknown [environmental sequence]
EAI67818	44354362	unknown [environmental sequence]
EAI68153	44354875	unknown [environmental sequence]
EAI89684	44384943	unknown [environmental sequence]
EAJ27674	44439188	unknown [environmental sequence]
EAJ45589	44464684	unknown [environmental sequence]
EAJ45589	44464684	unknown [environmental sequence]
EAJ67118	44496466	unknown [environmental sequence]
EAJ74221	44507022	unknown [environmental sequence]
EAJ74653	44507662	unknown [environmental sequence]
EAJ88396	44528064	unknown [environmental sequence]
EAJ88887	44528792	unknown [environmental sequence]
EAK06069	44553531	unknown [environmental sequence]

EAK11467	44561166	unknown [environmental sequence]
EAK16824	44568733	unknown [environmental sequence]
EAK28828	44585942	unknown [environmental sequence]
EAK28828	44585942	unknown [environmental sequence]
EAK31112	44589271	unknown [environmental sequence]
EAK42591	44605441	unknown [environmental sequence]
NP_045063	11465545	fatty-acid desaturase [Cyanidium caldarium]
NP_081575	27754029	sphingolipid delta 4 desaturase/C-4 hydroxylase [Mus musculus]
NP_338204	15843167	fatty acid desaturase, putative/ferredoxin reductase, electron transfer component [Mycobacterium tuberculosis CDC1551]
NP_440788	16330060	b-carotene hydroxylase [Synechocystis sp. PCC 6803]
NP_441220	16330492	hypothetical protein sll1611 [Synechocystis sp. PCC 6803]
NP_682690	22299443	beta-carotene hydroxylase [Thermosynechococcus elongatus BP-1]
NP_770721	27379192	hypothetical protein blr4081 [Bradyrhizobium japonicum USDA 110]
NP_848964	30468077	beta-carotene hydroxylase [Cyanidioschyzon merolae strain 10D]
NP_857223	31794730	POSSIBLE ELECTRON TRANSFER PROTEIN FDXB [Mycobacterium bovis AF2122/97]
NP_881760	33594116	putative fatty acid desaturase [Bordetella pertussis Tohama I]
NP_882469	33594826	putative fatty acid desaturase [Bordetella parapertussis 12822]
NP_886657	33599097	putative fatty acid desaturase [Bordetella bronchiseptica RB50]
NP_895643	33864083	beta carotene hydroxylase [Prochlorococcus marinus str. MIT 9313]
NP_896386	33864827	beta-carotene hydroxylase [Synechococcus sp. WH 8102]
NP_897461	33865902	possible beta-carotene ketolase [Synechococcus sp. WH 8102]
NP_924674	37521297	beta-carotene ketolase [Gloeobacter violaceus PCC 7421]
NP_927525	37524181	hypothetical protein plu0159 [Photorhabdus luminescens subsp. laumondii TTO1]
NP_947075	39934799	Fatty acid desaturase family [Rhodopseudomonas palustris CGA009]
P54972	1706150	Beta-carotene ketolase (Beta-carotene oxygenase)
Q39982	2498257	Beta-carotene ketolase (Beta-carotene oxygenase)
Q44261	2498256	Beta-carotene ketolase (Beta-carotene oxygenase)
T31123	11361063	hypothetical protein 15 - Sphingomonas aromaticivorans plasmid pNL1
XP_330780	32420673	hypothetical protein [Neurospora crassa]
XP_368852	39974923	hypothetical protein MG00392.4 [Magnaporthe grisea 70-15]
XP_380194	46102628	hypothetical protein FG00018.1 [Gibberella zeae PH-1]
XP_383758	46115480	hypothetical protein FG03582.1 [Gibberella zeae PH-1]
XP_405100	49086048	hypothetical protein AN0963.2 [Aspergillus nidulans FGSC A4]
XP_409222	49095522	hypothetical protein AN5085.2 [Aspergillus nidulans FGSC A4]
YP_102417	53725671	alkane-1 monooxygenase [Burkholderia mallei ATCC 23344]
YP_108945	53719959	putative alkane monooxygenase [Burkholderia pseudomallei K96243]
YP_132414	54302421	hypothetical putative delta-9 fatty acid desaturase [Photobacterium profundum SS9]
YP_154670	56459389	Fatty-acid desaturase [Idiomarina loihiensis L2TR]
YP_166682	56696325	fatty acid desaturase family protein [Silicibacter pomeroyi

		DSS-3]
YP_168846	56698471	fatty acid desaturase family protein [Silicibacter pomeroyi DSS-3]
YP_172377	56751676	beta-carotene hydroxylase [Synechococcus elongatus PCC 6301]
ZP_001068	23124870	COG3239: Fatty acid desaturase [Nostoc punctiforme PCC 73102]
ZP_001112	53688676	COG3239: Fatty acid desaturase [Nostoc punctiforme PCC 73102]
ZP_001607	53764743	COG3239: Fatty acid desaturase [Anabaena variabilis ATCC 29413]
ZP_001757	46118877	COG3239: Fatty acid desaturase [Crocosphaera watsonii WH 8501]
ZP_001787	53736018	COG3239: Fatty acid desaturase [Crocosphaera watsonii WH 8501]
ZP_002218	46321435	COG3239: Fatty acid desaturase [Burkholderia cepacia R1808]
ZP_002456	47575608	COG3239: Fatty acid desaturase [Rubrivivax gelatinosus PM1]
ZP_003028	48848557	COG3239: Fatty acid desaturase [Novosphingobium aromaticivorans DSM 12444]
ZP_003107	48856640	COG3239: Fatty acid desaturase [Cytophaga hutchinsonii]
ZP_003264	48893204	COG3239: Fatty acid desaturase [Trichodesmium erythraeum IMS101]
ZP_003458	53688805	hypothetical protein Npun02000865 [Nostoc punctiforme PCC 73102]
ZP_003513	53763576	COG3239: Fatty acid desaturase [Anabaena variabilis ATCC 29413]

Table 20. Examples of carotenoid hydroxylase polypeptides.

Accession Number	GI Number	Description
AAC44852	1842246	b-carotene hydroxylase
AAC49443	1575296	beta-carotene hydroxylase [Arabidopsis thaliana]
AAD54243	5852870	carotenoid hydroxylase [Haematococcus pluvialis]
AAG10430	9971820	beta hydroxylase [Tagetes erecta]
AAG10793	9988836	beta-carotene hydroxylase [Citrus unshiu]
AAG33636	11245486	beta-carotene hydroxylase [Citrus unshiu]
AAL80006	19071768	beta carotene hydroxylase [Sandersonia aurantiaca]
AAM44971	21280903	putative beta-carotene hydroxylase [Arabidopsis thaliana]
AAM51300	21436107	putative beta-carotene hydroxylase [Arabidopsis thaliana]
AAM77007	21734857	beta-carotene hydroxylase [Vitis vinifera]
AAN85601	27228295	Beta-Carotene Hydroxylase [Pantoea stewartii]
AAO53295	28911949	carotenoid hydroxylase [Haematococcus pluvialis]
AAS48097	44887642	beta-carotene hydroxylase [Citrus sinensis]
AAS55552	45184599	putative beta-carotene hydroxylase [Brassica rapa]
AAS88426	46326968	beta-carotene hydroxylase [Glycine max]
AAT48741	49036137	beta-carotene hydroxylase [Citrus sinensis]
AAT84408	50844570	beta carotene hydroxylase [Crocus sativus]
AAV85452	56267980	beta-ring oxygenase AdKeto1 [Adonis palaestina]
AAV85453	56267982	beta-ring oxygenase AdKeto2 [Adonis palaestina]

BAA14129	216687	crtZ [Pantoea ananatis]
BAB79605	18143450	crtZ [Pantoea agglomerans pv. milletiae]
BAC77670	31790567	gamma-carotene hydroxylase [marine bacterium P99-3]
BAD07283	40809749	beta-ring hydroxylase [Citrus sinensis]
BAD07291	40809765	beta-ring hydroxylase [Citrus limon]
CAA70427	2956671	beta-carotene hydrolase [Capsicum annuum]
CAA70888	2956717	beta-carotene hydroxylase 2 [Capsicum annuum]
CAB55625	5870598	beta-carotene hydroxylase [Lycopersicon esculentum]
CAB55626	5870600	beta-carotene hydroxylase [Lycopersicon esculentum]
CAB56060	5912293	carotene hydroxylase [Paracoccus marcusii]
CAC06712	9968545	beta-carotene hydroxylase [Narcissus pseudonarcissus]
CAC95130	33145986	beta-carotene hydroxylase [Crocus sativus]
EAB30128	42926157	unknown [environmental sequence]
EAC49462	43167766	unknown [environmental sequence]
EAC86129	43241003	unknown [environmental sequence]
EAD61089	43395962	unknown [environmental sequence]
EAD76156	43443111	unknown [environmental sequence]
EAD88640	43467793	unknown [environmental sequence]
EAE27903	43546376	unknown [environmental sequence]
EAE28203	43546980	unknown [environmental sequence]
EAE78743	43647896	unknown [environmental sequence]
EAF12173	43714211	unknown [environmental sequence]
EAH29370	44130906	unknown [environmental sequence]
EAH44202	44158360	unknown [environmental sequence]
EAI00766	44256844	unknown [environmental sequence]
EAI29017	44298625	unknown [environmental sequence]
EAJ30844	44443849	unknown [environmental sequence]
EAJ72524	44504516	unknown [environmental sequence]
EAK10611	44559981	unknown [environmental sequence]
EAK53455	44620561	unknown [environmental sequence]
EAK63955	44635271	unknown [environmental sequence]
H90469	25394049	beta carotene hydroxylase (crtZ) [imported] - Sulfolobus solfataricus
NP_745389	26989964	beta-carotene hydroxylase [Pseudomonas putida KT2440]
NP_922503	37536402	putative beta-carotene hydroxylase [Oryza sativa (japonica cultivar-group)]
P54973	1706152	Beta-carotene hydroxylase
Q44262	2498258	Beta-carotene hydroxylase
S52982	1073291	beta-carotene hydroxylase - Erwinia herbicola
XP_473611	50928167	OSJNBa0011J08.7 [Oryza sativa (japonica cultivar-group)]
YP_024309	48478603	beta carotene hydroxylase [Picrophilus torridus DSM 9790]
ZP_003055	48851297	COG3000: Sterol desaturase [Novosphingobium aromaticivorans DSM 12444]
ZP_003107	48856620	COG3000: Sterol desaturase [Cytophaga hutchinsonii]

Table 21. Examples of astaxanthin synthase polypeptides and putative astaxanthin synthase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
AAM56288	21501451	Astaxanthin synthase [Xanthophyllomyces dendrorhous]
XP_571276	58268240	Cytochrome P450, putative [Cryptococcus neoformans var. neoformans JEC21]
EAL20013	50257304	hypothetical protein CNBF3400 [Cryptococcus neoformans var. neoformans B-3501A]
XP_401804	49075484	hypothetical protein UM04189.1 [Ustilago maydis 521]
XP_397817	49067054	hypothetical protein UM00202.1 [Ustilago maydis 521]
XP_399595	49070612	hypothetical protein UM01980.1 [Ustilago maydis 521]
XP_403279	49079218	hypothetical protein UM05664.1 [Ustilago maydis 521]
XP_382294	46110473	hypothetical protein FG02118.1 [Gibberella zeae PH-1]
XP_406021	49088382	hypothetical protein AN1884.2 [Aspergillus nidulans FGSC A4]
XP_381224	46108332	hypothetical protein FG01048.1 [Gibberella zeae PH-1]
XP_391479	46139577	hypothetical protein FG11303.1 [Gibberella zeae PH-1]
XP_569261	58264210	conserved hypothetical protein [Cryptococcus neoformans var. neoformans JEC21]
EAL22841	50260180	hypothetical protein CNBB0620 [Cryptococcus neoformans var. neoformans B-3501A]
XP_359866	39940658	hypothetical protein MG04911.4 [Magnaporthe grisea 70-15]

TABLE 22: Examples of mitochondrial targeting sequences.

Species	**Protein (residues)**	**GI**	**Sequence**
Yarrowia lipoylitica	NUAM (AA 1-34)	6689648	MLSRNLSKFARAGLIRPATTSTHTRLFSVSARR L
Yarrowia lipoylitica	NUHM (AA 1-32)	50549567	MLRLIRPRLAALARPTTRAPQALNARTHIVSV
Saccharomyces cerevisiae	Coq1 (AA 1-53)	536190	MFQRSGAAHHIKLISSRRCRFKSSFAVALNAA SKLVTPKILWNNPISLVSKEM
Yarrowia lipoylitica	Coq1 (AA 1-77)	60389562	MLRVGRIGTKTLASSSLRFVAGARPKSTLTEA VLETTGLLKTTPQNPEWSGAVKQASRLVETD TPIRDPFSIVSQEM

Table 23: Examples of prenyldiphosphate synthase polypeptides.

23A: Bacteria Proteins that require a mitochondrial targeting sequence		
Accession	**GI**	**Description**
ZP_009...	83373595	Trans-hexaprenyltranstransferase [Rhodobacter sphaeroides ATCC 17029]
ZP_009...	83371280	Trans-hexaprenyltranstransferase [Rhodobacter sphaeroides ATCC 17025]
CAD24417	20429105	decaprenyl diphosphate synthase [Paracoccus zeaxanthinifaciens]
ZP_010...	85705714	Geranylgeranyl pyrophosphate synthase/Polyprenyl synthetase [Roseovarius sp. 217]
ZP_010...	84515724	decaprenyl diphosphate synthase [Loktanella vestfoldensis SKA53]
YP_165582	56695234	decaprenyl diphosphate synthase [Silicibacter pomeroyi DSS-3]
ZP_010...	86139019	decaprenyl diphosphate synthase [Roseobacter sp. MED193]
ZP_009...	83941379	decaprenyl diphosphate synthase [Sulfitobacter sp. EE-36]
ZP_009...	83854856	decaprenyl diphosphate synthase [Sulfitobacter sp. NAS-14.1]
ZP_006...	69299873	Farnesyltranstransferase [Silicibacter sp. TM1040]
ZP_010...	84683979	Geranylgeranyl pyrophosphate synthase/Polyprenyl synthetase [Rhodobacterales bacterium HTCC2654]
ZP_009...	84500217	decaprenyl diphosphate synthase [Oceanicola batsensis HTCC2597]
ZP_009...	83952381	decaprenyl diphosphate synthase [Roseovarius nubinhibens ISM]
ZP_006...	69937106	Trans-hexaprenyltranstransferase [Paracoccus denitrificans PD1222]
ZP_005...	68180845	Trans-hexaprenyltranstransferase [Jannaschia sp. CCS1]
ZP_008...	78495595	Polyprenyl synthetase [Rhodopseudomonas palustris BisB18]
AAY82368	67866738	decaprenyl diphosphate synthase [Agrobacterium tumefaciens]
NP_353656	15887975	hypothetical protein AGR_C_1125 [Agrobacterium tumefaciens str. C58]
ZP_008...	77688465	Farnesyltranstransferase [Rhodopseudomonas palustris BisB5]
NP_531334	17934544	octaprenyl-diphosphate synthase [Agrobacterium tumefaciens str. C58]
YP_484709	86748213	Farnesyltranstransferase [Rhodopseudomonas palustris HaA2]
AAP56240	37903500	decaprenyl diphosphate synthase [Agrobacterium tumefaciens]

YP_192388	58040424	Decaprenyl diphosphate synthase [Gluconobacter oxydans 621H]
23B: Subunit 1- Proteins that contain mitochondrial targeting sequence		
Accession	**GI**	**Description**
T43193	11279237	trans-pentaprenyltranstransferase homolog - fission yeast (Schizosaccharomyces pombe)
AAD28559	4732024	trans-prenyltransferase [Homo sapiens]
AAI07275	78070698	Trans-prenyltransferase [Mus musculus]
BAE48216	81157931	subunit 1 of decaprenyl diphosphate synthase [Homo sapiens]
AAH49211	29165656	PDSS1 protein [Homo sapiens]
Q33DR2	85700953	Decaprenyl-diphosphate synthase subunit 1 (Solanesyl-diphosphate synthase subunit 1) (Trans-prenyltransferase)
XP_507706	55633583	PREDICTED: similar to TPRT protein [Pan troglodytes]
XP_586717	76632198	PREDICTED: similar to trans-prenyltransferase [Bos taurus]
XP_849908	73948851	PREDICTED: similar to trans-prenyltransferase [Canis familiaris]
23C: Subunit 2- Proteins that contain mitochondrial targeting sequence		
Accession	**GI**	**Description**
O13851	60389474	Decaprenyl-diphosphate synthase subunit 2 (Decaprenyl pyrophosphate synthetase subunit 2)
BAE48218	81157935	subunit 2 of solanesyl diphosphate synthase [Mus musculus]
BAE48217	81157933	subunit 2 of decaprenyl diphosphate synthase [Homo sapiens]

Table 24: Examples of PHB-polyprenyltransferase polypeptides.

GI	PROTEIN DESCRIPTION
51013645	YNR041C [Saccharomyces cerevisiae]
50285815	unnamed protein product [Candida glabrata]
50311051	unnamed protein product [Kluyveromyces lactis]
45200866	AGL231Wp [Eremothecium gossypii]
50555263	hypothetical protein [Yarrowia lipolytica]
68473193	*para*-hydroxybenzoate: polyprenyl transferase [Candida albicans SC5314]
50410039	hypothetical protein DEHA0A14212g [Debaryomyces hansenii CBS767]
83769349	unnamed protein product [Aspergillus oryzae]
70994900	*para*-hydroxybenzoate-polyprenyltransferase precursor [Aspergillus fumigatus Af293]
19114131	hypothetical protein SPAC56F8.04c [Schizosaccharomyces pombe 972h-]
39973573	hypothetical protein MG01067.4 [Magnaporthe grisea 70-15]
85078920	protein related to *para*-hydroxybenzoate polyprenyltransferase precursor [Neurospora crassa N150]
76660839	PREDICTED: similar to *para*-hydroxybenzoate-polyprenyltransferase, mitochondrial [Bos taurus]
52138578	*para*-hydroxybenzoate-polyprenyltransferase, mitochondrial [Homo sapiens]
18088424	COQ2 protein [Homo sapiens]
47221448	unnamed protein product [Tetraodon nigroviridis]
58385249	ENSANGP00000012220 [Anopheles gambiae str. PEST]
50746583	PREDICTED: similar to hypothetical protein CL640 [Gallus gallus]
54638587	GA21912-PA [Drosophila pseudoobscura]
21355567	CG9613-PA [Drosophila melanogaster]
71005862	hypothetical protein UM01450.1 [Ustilago maydis 521]

Table 25: Examples of O-methyltransferase polypeptides.

GI	PROTEIN DESCRIPTION
37362692	O-methyltransferase, Coq3p [Saccharomyces cerevisiae]
50290295	hypothetical protein CAGL0I07601g [Candida glabrata CBS138]
50304805	unnamed protein product [Kluyveromyces lactis]
45187988	ADR115Wp [Eremothecium gossypii]
7673983	Hexaprenyldihydroxybenzoate methyltransferase, mitochondrial precursor
68478536	O-methyltransferase Coq3-like protein [Candida albicans SC5314]
50424601	hypothetical protein DEHA0F13189g [Debaryomyces hansenii CBS767]
50546961	hypothetical protein [Yarrowia lipolytica]
85090891	hypothetical protein [Neurospora crassa N150]
46128151	hypothetical protein FG08453.1 [Gibberella zeae PH-1]
19075739	hypothetical protein SPCC162.05 [Schizosaccharomyces pombe 972h-]
39973611	hypothetical protein MG01048.4 [Magnaporthe grisea 70-15]

Table 26: Examples of CoQ4 related family member polypeptides.

Accession	GI	PROTEIN DESCRIPTION
S61567	2131314	hypothetical protein YD8142A.01 - yeast (Saccharomyces cerevisiae) (fragment)
XP_446206	50287553	unnamed protein product [Candida glabrata]
XP_453897	50307807	unnamed protein product [Kluyveromyces lactis]
NP_986564	45200994	AGL103Wp [Eremothecium gossypii]
XP_721235	68469441	hypothetical protein CaO19_10526 [Candida albicans SC5314]
XP_462229	50427233	hypothetical protein DEHA0G16852g [Debaryomyces hansenii CBS767]
XP_505938	50557060	hypothetical protein [Yarrowia lipolytica]
XP_754965	71000563	hypothetical protein Afu3g06410 [Aspergillus fumigatus Af293]
XP_964516	85113402	hypothetical protein [Neurospora crassa N150]
XP_662361	67537174	hypothetical protein AN4757.2 [Aspergillus nidulans FGSC A4]
BAE63342	83773215	unnamed protein product [Aspergillus oryzae]
EAQ71080	86196442	hypothetical protein MGG_ch7g487 [Magnaporthe grisea 70-15]
EAQ89817	88182349	hypothetical protein CHGG_06436 [Chaetomium globosum CBS 148.51]
XP_314100	58385631	ENSANGP00000010400 [Anopheles gambiae str. PEST]
CAJ81453	89268068	coenzyme Q4 homolog (yeast) [Xenopus tropicalis]
NP_057119	7705807	coenzyme Q4 homolog [Homo sapiens]
Q9Y3A0	24211604	Ubiquinone biosynthesis protein COQ4 homolog (Coenzyme Q biosynthesis protein 4 homolog)
EAL29530	54640779	GA16732-PA [Drosophila pseudoobscura]
CAI13487	55958820	coenzyme Q4 homolog (yeast) [Homo sapiens]
XP_851315	73968120	PREDICTED: similar to coenzyme Q4 homolog [Canis familiaris]
CAF99178	47223569	unnamed protein product [Tetraodon nigroviridis]
Q9VVG6	29428064	Ubiquinone biosynthesis protein COQ4 homolog
XP_567895	58260970	ubiquinone metabolism-related protein [Cryptococcus neoformans var. neoformans JEC21]
EAF12010	43713866	unknown [environmental sequence]
EAL18027	50255292	hypothetical protein CNBK0480 [Cryptococcus neoformans var. neoformans B-3501A]
NP_491246	71990052	COenzyme Q (ubiquinone) biosynthesis family member (coq-4) [Caenorhabditis elegans]
XP_395030	66530721	PREDICTED: similar to CG3874-PA [Apis mellifera]
XP_795398	72055534	PREDICTED: similar to Ubiquinone biosynthesis protein COQ4 homolog (Coenzyme Q biosynthesis protein 4 homolog) [Strongylocentrotus purpuratus]
AAZ94908	74039764	putative ubiquinone bioshynthesis protein COQ4 [Moneuplotes crassus]
XP_687876	68361418	PREDICTED: similar to coenzyme Q4 homolog [Danio rerio]
XP_629528	66801205	hypothetical protein DDB0184480 [Dictyostelium discoideum]
XP_474322	50929589	OSJNBa0018M05.9 [Oryza sativa (japonica cultivar-group)]
XP_760642	71020823	hypothetical protein UM04495.1 [Ustilago maydis 521]
C84451	25411031	probable ubiquinone biosynthesis protein [imported] - Arabidopsis thaliana
AAV31201	54287457	putaitve coenzyme Q biosynthesis protein [Oryza sativa (japonica

		cultivargroup)]
XP_829414	74025696	ubiquinone biosynthesis protein [Trypanosoma brucei TREU927]
EAB01941	42869393	unknown [environmental sequence]
XP_815382	71653491	ubiquinone biosynthesis protein-like protein [Trypanosoma cruzi]
XP_811857	71421652	ubiquinone biosynthesis protein-like protein [Trypanosoma cruzi]
CAJ03081	68124611	ubiquinone biosynthesis protein-like protein, putative [Leishmania major]
EAR95772	89297784	hypothetical protein TTHERM_00275760 [Tetrahymena thermophila SB210]
CAE66639	39586228	Hypothetical protein CBG11976 [Caenorhabditis briggsae]
CAE66638	39586227	Hypothetical protein CBG11975 [Caenorhabditis briggsae]
EAF65991	43823163	unknown [environmental sequence]
XP_745261	70952146	hypothetical protein [Plasmodium chabaudi chabaudi]
XP_674591	68065214	hypothetical protein [Plasmodium berghei strain ANKA]
XP_726273	82596465	ubiquinone biosynthesis protein [Plasmodium yoelii yoelii str. 17XNL]
NP_700989	23508320	hypothetical protein PF11_0128 [Plasmodium falciparum 3D7]
XP_627898	66361868	similar to ubiquinone biosynthesis protein [Cryptosporidium parvum]
AAH39570	24660465	Coq4 protein [Mus musculus]
XP_520291	55632385	PREDICTED: similar to Ubiquinone biosynthesis protein COQ4 homolog (Coenzyme Q biosynthesis protein 4 homolog) (CGI-92) [Pan troglodytes]

Table 27: Examples of C-methyltransferase polypeptides.

Accession	GI	Description
XP_453146	50306345	unnamedproteinproduct[Kluyveromyceslactis]
XP_447997	50291129	unnamedproteinproduct[Candidaglabrata]
AAT93213	51013839	YML110C[Saccharomycescerevisiae]
XP_714936	68482357	hypotheticalproteinCaO19.3577[CandidaalbicansSC5314]
XP_458944	50420807	hypotheticalproteinDEHA0D12100g[DebaryomyceshanseniiCBS767]
XP_501966	50548991	hypotheticalprotein[Yarrowialipolytica]
XP_659347	67522573	hypotheticalproteinAN1743.2[AspergillusnidulansFGSCA4]
BAE57068	83766928	unnamedproteinproduct[Aspergillusoryzae]
XP_750774	70991851	ubiquinonebiosynthesismethlytransferaseCoq5[Aspergillusfumigatus Af293]
P87230	57013807	Ubiquinonebiosynthesismethyltransferasecoq5
XP_757235	71005138	hypotheticalproteinUM01088.1[Ustilagomaydis521]
XP_389415	46134199	hypotheticalproteinFG09239.1[GibberellazeaePH-1]
XP_641323	66814288	hypotheticalproteinDDB0206461[Dictyosteliumdiscoideum]
XP_960179	85095977	hypotheticalprotein[NeurosporacrassaN150]
XP_566576	58258327	ubiquinonebiosynthesismethyltransferase[Cryptococcusneoformansvar.neoformansJEC21]
Q8FUZ3	48474468	Ubiquinone/menaquinonebiosynthesismethyltransferaseubiE
YP_419160	83269869	SAMbindingmotif:methyltransferase:UbiE/COQ5:Ubiquinone/menaquinone[BrucellamelitensisbiovarAbortus2308]
CAH90854	55728214	hypotheticalprotein[Pongopygmaeus]
NP_572865	24641702	CG2453-PA[Drosophilamelanogaster]
AAM52653	21483356	GM25741p[Drosophilamelanogaster]
AAI07875	81294347	Unknown(proteinforMGC:104303)[Homosapiens]
BAD96330	62896779	hypotheticalproteinMGC4767variant[Homosapiens]
NP_115690	58036498	hypotheticalproteinLOC84274[Homosapiens]
XP_854268	73995311	PREDICTED:similartoCG2453-PA[Canisfamiliaris]
AAM14112	20258881	putativeubiquinone/menaquinonebiosynthesismethyltransferase[Arabidopsisthaliana]
ZP_000...	23010342	COG2226:Methylaseinvolvedinubiquinone/menaquinonebiosynthesis[MagnetospirillummagnetotacticumMS-1]
ZP_009...	83369205	Ubiquinone/menaquinonebiosynthesismethyltransferase[RhodobacterspharoidesATCC17025]
CAG08176	47221514	unnamedproteinproduct[Tetraodonnigroviridis]
ZP_009...	83372227	Ubiquinone/menaquinonebiosynthesismethyltransferase[RhodobacterspharoidesATCC17029]
AAH04916	38196988	COQ5protein[Homosapiens]
NP_001...	52218926	hypotheticalproteinLOC447802[Daniorerio]
NP_001...	84781656	hypotheticalproteinLOC304542[Rattusnorvegicus]
AAH52345	30802047	HypotheticalproteinLOC52064[Musmusculus]
BAB29289	12852138	unnamedproteinproduct[Musmusculus]
EAL32141	54643397	GA15370-PA[Drosophilapseudoobscura]
XP_307798	58376000	ENSANGP00000018068[Anophelesgambiaestr. PEST]
Q89WD0	48474428	Ubiquinone/menaquinonebiosynthesismethyltransferaseubiE
XP_396701	66501438	PREDICTED:similartoCG2453-PA[Apismellifera]

ZP_009...	83750758	COG2226:Methylaseinvolvedinubiquinone/menaquinonebiosynthesis[BartonellabacilliformisKC583]
YP_428879	83595127	Ubiquinone/menaquinonebiosynthesismethyltransferase[RhodospirillumrubrumATCC11170]
ZP_001...	34581345	ubiquinone/menaquinonebiosynthesismethlytransferaseubiE[Rickettsiasibirica246]
ZP_001...	53732282	COG2226:Methylaseinvolvedinubiquinone/menaquinonebiosynthesis[Rickettsiarickettsii]
E97829	25304993	hypotheticalproteinubiE[imported]-Rickettsiaconorii(strainMalish7)
YP_484242	86747746	ubiquinone/menaquinonebiosynthesismethyltransferases[RhodopseudomonaspalustrisHaA2]
Q6G577	61217251	Ubiquinone/menaquinonebiosynthesismethyltransferaseubiE
NP_001...	57525205	hypotheticalproteinLOC416975[Gallusgallus]
ZP_006...	69930221	Ubiquinone/menaquinonebiosynthesismethyltransferase[NitrobacterhamburgensisX14]
Q98GV1	48474615	Ubiquinone/menaquinonebiosynthesismethyltransferaseubiE
ZP_006...	69278661	Ubiquinone/menaquinonebiosynthesismethyltransferase[Mesorhizobiumsp. BNC1]
YP_467903	86356011	ubiquinone/menaquinonebiosynthesismethyltransferaseprotein[RhizobiumetliCFN42]
ZP_010...	84684526	methyltransferase[RhodobacteralesbacteriumHTCC2654]
Q6NDM2	61217267	Ubiquinone/menaquinonebiosynthesismethyltransferaseubiE
ZP_010...	86139423	ubiquinone/menaquinonebiosynthesismethyltransferaseUbiE[Roseobactersp. MED193]
ZP_008...	78694883	Ubiquinone/menaquinonebiosynthesismethyltransferase[Bradyrhizobiumsp. BTAi1]
ZP_006...	69257590	Ubiquinone/menaquinonebiosynthesismethyltransferase[Magnetococcussp. MC-1]
YP_316661	75674240	ubiquinone/menaquinonebiosynthesismethyltransferase[NitrobacterwinogradskyiNb-255]
ZP_009...	84501267	ubiquinone/menaquinonebiosynthesismethyltransferaseUbiE[OceanicolabatsensisHTCC2597]
ZP_010...	85714158	ubiquinone/menaquinonebiosynthesismethyltransferase[Nitrobactersp.Nb-311A]
P34666	21431890	Ubiquinonebiosynthesismethyltransferasecoq-5
ZP_009...	83941661	ubiquinone/menaquinonebiosynthesismethyltransferaseUbiE[Sulfitobactersp. EE-36]
ZP_000...	23014783	COG2226:Methylaseinvolvedinubiquinone/menaquinonebiosynthesis[MagnetospirillummagnetotacticumMS-1]
ZP_008...	77691323	Ubiquinone/menaquinonebiosynthesismethyltransferase[RhodopseudomonaspalustrisBisB5]
ZP_006...	69300808	Ubiquinone/menaquinonebiosynthesismethyltransferase[Silicibactersp. TM1040]
ZP_003...	52699248	COG2226:Methylaseinvolvedinubiquinone/menaquinonebiosynthesis[Rickettsiaakaristr. Hartford]
ZP_008...	78493819	Ubiquinone/menaquinonebiosynthesismethyltransferase[RhodopseudomonaspalustrisBisB18]

Q6G1I2	61217248	Ubiquinone/menaquinonebiosynthesismethyltransferaseubiE
ZP_010...	84514658	ubiquinone/menaquinonebiosynthesismethyltransferaseUbiE[Loktanellavestfoldensis SKA53]
NP_384470	15964117	ubiquinone/menaquinonebiosynthesismethyltransferase[Sinorhizobiummeliloti1021]
Q92SK7	48474592	Ubiquinone/menaquinonebiosynthesismethyltransferaseubiE
AAH97761	66910809	Unknown(proteinforMGC:115452)[Xenopuslaevis]
ZP_006...	69936420	Ubiquinone/menaquinonebiosynthesismethyltransferase[Paracoccusdenitrificans PD1222]
ZP_008...	77739893	Ubiquinone/menaquinonebiosynthesismethyltransferase[Rhodopseudomonaspalustris BisA53]
CAE66876	39589641	HypotheticalproteinCBG12254[Caenorhabditisbriggsae]
AH2615	25305007	hypotheticalproteinubiE[imported]-Agrobacteriumtumefaciens(strainC58,Dupont)
Q8UIH5	48474890	Ubiquinone/menaquinonebiosynthesismethyltransferaseubiE
EAJ68789	44498928	unknown[environmentalsequence]
ZP_010...	85709425	ubiquinonemethyltransferase[Erythrobactersp. NAP1]
ZP_005...	68180386	Ubiquinone/menaquinonebiosynthesismethyltransferase[Jannaschiasp. CCS1]
ZP_010...	85706183	ubiquinone/menaquinonebiosynthesismethyltransferaseUbiE[Roseovariussp. 217]
Q68W57	56749693	Ubiquinone/menaquinonebiosynthesismethyltransferaseubiE
EAF74963	43841414	unknown[environmentalsequence]
EAG73295	44028151	unknown[environmentalsequence]
Q9ZCP3	21542473	Ubiquinone/menaquinonebiosynthesismethyltransferaseubiE
NP_221041	15604523	ubiquinone/menaquinonebiosynthesismethyltransferase[Rickettsiaprowazekiistr. MadridE]
EAI61571	44345679	unknown[environmentalsequence]
YP_165417	56695070	ubiquinone/menaquinonebiosynthesismethyltransferaseUbiE[Silicibacterpomeroyi DSS-3]
EAI08753	44268414	unknown[environmentalsequence]
YP_246259	67458635	ubiquinone/menaquinonebiosynthesismethyltransferase[Rickettsiafelis URRWXCal2]
ZP_005...	68537811	Ubiquinone/menaquinonebiosynthesismethyltransferase[Sphingopyxisalaskensis RB2256]
EAB75777	43018113	unknown[environmentalsequence]
EAD48352	43367051	unknown[environmentalsequence]
YP_495876	87198619	ubiquinone/menaquinonebiosynthesismethyltransferases[Novosphingobiumaromaticivorans DSM12444]
ZP_009...	83950594	ubiquinone/menaquinonebiosynthesismethyltransferaseUbiE[Roseovariusnubinhibens ISM]
YP_341403	77361828	2-octaprenyl-6-methoxy-1,4-benzoquinonemethylase/S-adenosylmethionine[Pseudoalteromonashaloplanktis
YP_045153	50083643	SAM:2-DMKmethyltransferaseand2-octaprenyl-6-methoxy-1,4-benzoquinonemethylase[Acinetobactersp. ADP1]

EAI09300	44269223	unknown[environmentalsequence]
NP_472972	16804943	UbiE-likemethlytransferase,putative[Plasmodiumfalciparum3D7]
ZP_009...	83944874	ubiquinone/menaquinonebiosynthesismethlytransferaseUbiE[Oceanic aulisalexandriiHTCC2633]
ZP_010...	87120355	ubiquinone/menaquinonebiosynthesismethyltransferaseUbiE[Marino monassp. MED121]
ZP_009...	82742409	Ubiqu
EAH88886	44240640	unknown[environmentalsequence]
XP_814279	71651194	ubiquinonebiosynthesismethyltransferase[TrypanosomacruzistrainCL Brener]
YP_192885	58040921	Ubiquinone/menaquinonebiosynthesismethyltransferase[Gluconobacte roxydans621H]
AAK14902	13177631	temperaturesensitiveprotein[Leishmaniadonovani]
Q9A258	48474624	Ubiquinone/menaquinonebiosynthesismethyltransferaseubiE
XP_815230	71653177	ubiquinonebiosynthesismethyltransferase[TrypanosomacruzistrainCL Brener]
YP_313973	74316233	ubiquinone/menaquinonebiosynthesismethyltransferase[Thiobacillusd enitrificansATCC25259]
CAJ09508	68130197	ubiquinonebiosynthesismethyltransferase,putative[Leishmaniamajor]
YP_264006	71065279	probableubiquinone/menaquinonebiosynthesismethyltransferase[Psyc hrobacterarcticus273-4]
ZP_006...	69941453	Ubiquinone/menaquinonebiosynthesismethyltransferase[Shewanellade nitrificansOS-217]
Q9X3X2	59803065	Ubiquinone/menaquinonebiosynthesismethyltransferaseubiE
EAH78668	44222354	unknown[environmentalsequence]
ZP_005...	68541992	Ubiquinone/menaquinonebiosynthesismethyltransferase[Shewanellaba lticaOS155]
Q8E9R7	48474457	Ubiquinone/menaquinonebiosynthesismethyltransferaseubiE
YP_458999	85374937	ubiquinonemethyltransferase[ErythrobacterlitoralisHTCC2594]
YP_432387	83643952	Methylaseinvolvedinubiquinone/menaquinonebiosynthesis[Hahellach ejuensisKCTC2396]
ZP_005...	68546475	Ubiquinone/menaquinonebiosynthesismethyltransferase[Shewanellaa mazonensisSB2B]
EAK68100	44641208	unknown[environmentalsequence]
AAD21548	4511988u	biquinonemethyltransferase[Zymomonasmobilis]
ZP_008...	77953062	Ubiquinone/menaquinonebiosynthesismethyltransferase[Marinobacter aquaeoleiVT8]
ZP_006...	71364836	Ubiquinone/menaquinonebiosynthesismethyltransferase[Psychrobacte rcryohalolentisK5]
YP_267060	71280787	ubiquinone/menaquinonebiosynthesismethlytransferaseUbiE[Colwelli apsychrerythraea34H]
EAD10368	43289030	unknown[environmentalsequence]
EAH05696	44087209	unknown[environmentalsequence]

BAE77468	85676218	bifunctional2-octaprenyl-6-methoxy-1,4-benzoquinonemethylaseandSAM:2-DMKmethyltransferase[Escherichiacoli]
ZP_009...	83569331	COG2226:Methylaseinvolvedinubiquinone/menaquinonebiosynthesis[Shigelladysenteriae1012]
YP_218855	62182438	ubiquinone/menaquinonebiosynthesismethyltransferase[Salmonellaentericasubsp. enterica]
ZP_007...	76793309	Ubiquinone/menaquinonebiosynthesismethyltransferase[PseudoalteromonasatlanticaT6c]
ZP_007...	75237632	COG2226:Methylaseinvolvedinubiquinone/menaquinonebiosynthesis[EscherichiacoliF11]
ZP_008...	78366176	Ubiquinone/menaquinonebiosynthesismethyltransferase[Shewanellasp. PV-4]
ZP_006...	69949855	Ubiquinone/menaquinonebiosynthesismethyltransferase[ShewanellafrigidimarinaNCIMB400]
ZP_004...	67676228	Ubiquinone/menaquinonebiosynthesismethyltransferase[ChromohalobactersalexigensDSM3043]
ZP_008...	82497401	Ubiquinone/menaquinonebiosynthesismethyltransferase[Shewanellasp. MR-4]
EAJ07041	44409543	unknown[environmentalsequence]
EAH02013	44080298	unknown[environmentalsequence]
EAJ84762	44522732	unknown[environmentalsequence]
ZP_005...	67848069	Ubiquinone/menaquinonebiosynthesismethyltransferase[Polaromonas sp. JS666]
EAJ16045	44422453	unknown[environmentalsequence]
AAA67628	148231o2	51[Escherichiacoli]
ZP_010...	84709882	Ubiquinone/menaquinonebiosynthesismethyltransferase[PolaromonasnaphthalenivoransCJ2]
Q8P558	48474489	Ubiquinone/menaquinonebiosynthesismethyltransferaseubiE
YP_241773	66767011	ubiquinone/menaquinonebiosynthesismethyltransferase[Xanthomonascampestrispv.campestrisstr. 8004]
Q606J9	61217211	Ubiquinone/menaquinonebiosynthesismethyltransferaseubiE
EAJ79965	44515607	unknown[environmentalsequence]
EAJ47458	44467411	unknown[environmentalsequence]
XP_829115	74025098	ubiquinonebiosynthesismethyltransferase[TrypanosomabruceiTREU927]
EAB98740	43064873	unknown[environmentalsequence]
EAC73387	43215714	unknown[environmentalsequence]
ZP_008...	77973692	COG2226:Methylaseinvolvedinubiquinone/menaquinonebiosynthesis[YersiniafrederikseniiATCC33641]
NP_407228	16123915	ubiquinone/menaquinonebiosynthesismethyltransferase[YersiniapestisCO92]
ZP_007...	77633882	COG2226:Methylaseinvolvedinubiquinone/menaquinonebiosynthesis[YersiniapestisAngola]
EAC00995	43069433	unknown[environmentalsequence]
EAB52674	42971393	unknown[environmentalsequence]

ZP_008...	77978480	COG2226:Methylaseinvolvedinubiquinone/menaquinonebiosynthesis[YersiniaintermediaATCC29909]
ZP_003...	58699058	ubiquinone/menaquinonebiosynthesismethlytransferaseUbiE[WolbachiaendosymbiontofDrosophila]
YP_203429	59710653	ubiquinone/menaquinonebiosynthesismethyltransferase[VibriofischeriES114]
YP_452787	84625415	ubiquinone/menaquinonetransferase[Xanthomonasoryzae pv. oryzaeMAFF311018]
YP_202626	58583610	ubiquinone/menaquinonebiosynthesismethyltransferase[Xanthomonasoryzaepv. oryzaeKACC10331]
EAH40497	44150931	unknown[environmentalsequence]
ZP_008...	77961745	COG2226:Methylaseinvolvedinubiquinone/menaquinonebiosynthesis[YersiniamollaretiiATCC43969]
Q8PPP2	48474873	Ubiquinone/menaquinonebiosynthesismethyltransferaseubiE
EAJ37631	44453326	unknown[environmentalsequence]
YP_362429	78046254	ubiquinone/menaquinonebiosynthesismethyltransferase[Xanthomonascampestrispv. vesicatoriastr. 85-10]
EAI94987	44392321	unknown[environmentalsequence]
YP_390672	78484747	ubiquinone/menaquinonebiosynthesismethyltransferase[ThiomicrospiracrunogenaXCL-2]
EAK24181	44579264	unknown[environmentalsequence]
EAJ20767	44429280	unknown[environmentalsequence]
EAI56325	44338235	unknown[environmentalsequence]
EAF16609	43723279	unknown[environmentalsequence]
ZP_001...	32033562	COG2226:Methylaseinvolvedinubiquinone/menaquinonebiosynthesis[Actinobacilluspleuropneumoniaestr. 4074]
Q7MQ33	61217315	Ubiquinone/menaquinonebiosynthesismethyltransferaseubiE
EAG95272	44068140	unknown[environmentalsequence]
ZP_009...	84323851	COG2226:Methylaseinvolvedinubiquinone/menaquinonebiosynthesis[Pseudomonasaeruginosa2192]
Q73HZ4	59799058	Ubiquinone/menaquinonebiosynthesismethyltransferaseubiE
ZP_007...	75829374	COG2226:Methylaseinvolvedinubiquinone/menaquinonebiosynthesis[VibriocholeraeMO10]
ZP_004...	67158081	Ubiquinone/menaquinonebiosynthesismethyltransferase[AzotobactervinelandiiAvOP]
Q5NFE1	61217184	Ubiquinone/menaquinonebiosynthesismethyltransferaseubiE
EAI42505	44318564	unknown[environmentalsequence]
EAI87953	44382719	unknown[environmentalsequence]
EAH78177	44221477	unknown[environmentalsequence]
Q9Z439	48474719	Ubiquinone/menaquinonebiosynthesismethyltransferaseubiE
ZP_007...	75820016	COG2226:Methylaseinvolvedinubiquinone/menaquinonebiosynthesis[VibriocholeraeV51]
EAF83842	43859479	unknown[environmentalsequence]
P59911	37999899	Ubiquinone/menaquinonebiosynthesismethyltransferaseubiE

ZP_009...	84386296	ubiquinone/menaquinonebiosynthesismethyltransferase[Vibriosplendidus12B01]
EAJ66843	44496055	unknown[environmentalsequence]
ZP_003...	48861804	COG2226:Methylaseinvolvedinubiquinone/menaquinonebiosynthesis[Microbulbiferdegradans2-40]
Q5QYG2	61217193	UbiquinoneMenaquinonebiosynthesismethyltransferaseubiE
Q9K075	48474972	UbiquinoneMenaquinonebiosynthesismethyltransferaseubiE
NP_900659	34496444	ubiquinone/menaquinonebiosynthesismethyltransferase[ChromobacteriumviolaceumATCC12472]
YP_207480	59800768	ubiquinone/menaquinonebiosynthesismethyltransferase[NeisseriagonorrhoeaeFA1090]
EAB87563	43042105	unknown[environmentalsequence]
EAF16632	43723327	unknown[environmentalsequence]
EAF34015	43759153	unknown[environmentalsequence]
EAG69427	44021114	unknown[environmentalsequence]
ZP_008...	82736190	Ubiquinone/menaquinonebiosynthesismethyltransferase[PseudomonasputidaF1]
EAI73896	44362692	unknown[environmentalsequence]
ZP_010...	86146605	ubiquinone/menaquinonebiosynthesismethyltransferase[Vibriosp.MED222]
EAJ40962	44457991	unknown[environmentalsequence]
EAC53325	43175475	unknown[environmentalsequence]

Table 28: Examples of Monooxygenase CoQ6 related polypeptides.

Accession	GI	Description
XP_452320	50304729	unnamedproteinproduct[Kluyveromyceslactis]
NP_011771	6321694	Putativeflavin-dependentmonooxygenase;Coq6p[Saccharomycescerevisiae]
XP_446327	50287795	unnamedproteinproduct[Candidaglabrata]
XP_721285	68469544	COQ6monooxygenase[CandidaalbicansSC5314]
XP_459945	50422737	hypotheticalproteinDEHA0E15301g[DebaryomyceshanseniiCBS767]
XP_380551	46105494	hypotheticalproteinFG00375.1[GibberellazeaePH-1]
XP_965667	85119586	hypotheticalprotein[NeurosporacrassaN150]
XP_499891	50543450	hypotheticalprotein[Yarrowialipolytica]
CAA56705	522109	orf2[Saccharomycescerevisiae]
XP_751538	70993382	ubiquinonebiosynthesismonooxgenaseCoq6[AspergillusfumigatusAf293]
EAQ92855	88185387	hypotheticalproteinCHGG_01090[ChaetomiumglobosumCBS148.51]
BAE54773	83764629	unnamedproteinproduct[Aspergillusoryzae]
XP_661190	67526257	hypotheticalproteinAN3586.2[AspergillusnidulansFGSCA4]
NP_595401	19112193	monooxygenase[Schizosaccharomycespombe972h-]
XP_782348	72009737	PREDICTED:similartocoenzymeQ6homolog(yeast)(predicted)[Strongylocentrotuspurpuratus]
NP_001...	55741992	coenzymeQ6homolog[Xenopustropicalis]
AAI12595	86438095	Unknown(proteinforMGC:137363)[Bostaurus]

XP_576073	62651056	PREDICTED:coenzymeQ6homolog(yeast)(predicted)[Rattusnorvegicus]
BAD96685	62897491	CGI-10proteinisoformavariant[Homosapiens]
NP_872282	32967305	coenzymeQ6homologisoforma[Homosapiens]
AAH14483	15680256	CoenzymeQ6homolog,isoforma[Homosapiens]
AAH24135	18848355	Coq6protein[Musmusculus]
BAE20853	74203378	unnamedproteinproduct[Musmusculus]
Q8R1S0	26006706	UbiquinonebiosynthesismonooxgenaseCOQ6
AAH51055	30047245	Coq6protein[Musmusculus]
XP_547900	57090727	PREDICTED:similartoUbiquinonebiosynthesismonooxgenaseCOQ6[Canisfamiliaris]
NP_766170	27369832	coenzymeQ6homolog[Musmusculus]
AAH97912	67678277	Unknown(proteinforMGC:115711)[Xenopuslaevis]
AAD27719	4680659	CGI-10protein[Homosapiens]
CAG10598	47230184	unnamedproteinproduct[Tetraodonnigroviridis]
XP_572612	58270912	ubiquinonebiosynthesismonooxygenase[Cryptococcusneoformansvar.neoformansJEC21]
NP_872286	32967307	coenzymeQ6homologisoformb[Homosapiens]
XP_311042	58381158	ENSANGP00000019848[Anophelesgambiaestr.PEST]
XP_395883	66509969	PREDICTED:similartoUbiquinonebiosynthesismonooxgenaseCOQ6(CGI-10)[Apismellifera]
CAD62332	28193180	unnamedproteinproduct[Homosapiens]
O01884	32172411	Probableubiquinonebiosynthesismonooxgenasecoq-6
EAL34550	54645812	GA20231-PA[Drosophilapseudoobscura]
NP_608934	19920760	CG7277-PA[Drosophilamelanogaster]
CAA56704	522108	orf1[Saccharomycescerevisiae]
CAE72156	39594578	HypotheticalproteinCBG19254[Caenorhabditisbriggsae]
XP_872593	76628365	PREDICTED:similartoUbiquinonebiosynthesismonooxgenaseCOQ6isoform2[Bostaurus]
YP_344564	77166039	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[NitrosoccusoceaniATCC19707]
NP_189062	79416711	monooxygenase/oxidoreductase[Arabidopsisthaliana]
NP_001...	79313357	monooxygenase/oxidoreductase[Arabidopsisthaliana]
XP_684723	68421322	PREDICTED:similartoUbiquinonebiosynthesismonooxgenaseCOQ6,partial[Danio rerio]
BAD43118	51968852	monooxygenase,putatve[Arabidopsisthaliana]
XP_635209	66802674	hypotheticalproteinDDB0183892[Dictyosteliumdiscoideum]
XP_470364	50920007	putativeoxygenase[Oryzasativa(japonicacultivar-group)]
YP_351159	77461652	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinolhydroxylase[PseudomonasfluorescensPfO-1]
ZP_008...	82736761	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[PseudomonasputidaF1]
NP_747298	26991873	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinolhydroxylase[PseudomonasputidaKT2440]
YP_233433	66043592	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinolhydroxylase[Pseudomonassyringaepv.syringaeB728a]
YP_263023	70733250	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinolhydroxylase[PseudomonasfluorescensPf-5]
NP_794952	28872333	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinolhydroxylase[Pseudomonassyringaepv.tomatostr.DC3000]
BAB01361	11994239	unnamedproteinproduct[Arabidopsisthaliana]
ZP_009...	84324075	COG0654:2-polyprenyl-6-methoxyphenolhydroxylase[Pseudomonasaeruginosa2192]

YP_428788	83595036	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[Rhodospirillumrubrum ATCC11170]
ZP_009...	84317910	COG0654:2-polyprenyl-6-methoxyphenolhydroxylaseandrelatedFAD-dependentoxidoreductases[PseudomonasaC3719]
NP_253908	15600414	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinolhydroxylase[PseudomonasaeruginosaPAO1]
ZP_008...	77953072	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[Marinobacteraquaeolei VT8]
XP_780895	72116657	PREDICTED:similartoUbiquinonebiosynthesismonooxgenaseCOQ6[Strongylocentrotuspurpuratus]
YP_272612	71735583	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinolhydroxylase[Pseudomonassyringaepv.phaseolicola1448A]
ZP_004...	67155409	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[Azotobactervinelandii AvOP]
ZP_008...	78702761	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[Alkalilimnicolaehrlichei MLHE-1]
NP_698877	23502750	2-octaprenyl-6-methoxyphenylhydroxylase[Brucellasuis1330]
NP_539083	17986449	2-octaprenyl-6-methoxyphenylhydroxylase[Brucellamelitensis16M]
NP_440170	16329442	2-octaprenyl-6-methoxyphenylhydroxylase[Synechocystissp.PCC6803]
YP_415240	82700666	NADbindingsite:UbiH/COQ6monooxygenase[Brucellamelitensisbiov arAbortus2308]
YP_321745	75907449	2-octaprenyl-6-methoxyphenylhydroxylase[AnabaenavariabilisATCC29413]
ZP_004...	67674617	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[Chromohalobactersalexigens DSM3043]
NP_488314	17231766	2-octaprenyl-6-methoxyphenylhydroxylase[Nostocsp.PCC7120]
ZP_010...	86136929	ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6familyprotein[Roseobactersp.MED193]
ZP_001...	46143421	COG0654:2-polyprenyl-6-methoxyphenolhydroxylase[Actinobacilluspleuropneumoniaeserovar1 str.4074]
ZP_006...	69935442	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[Paracoccusdenitrificans PD1222]
ZP_009...	83372105	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[Rhodobactersphaeroides ATCC17029]
ZP_009...	83952498	ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6familyprotein[Roseovariusnubinhibens ISM]
ZP_010...	86146371	hypotheticalproteinMED222_22361[Vibriosp.MED222]
YP_114193	53804217	monooxygenase,FAD-binding[Methylococcuscapsulatusstr.Bath]
ZP_005...	68212612	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[Methylobacillusflagellatus KT]
NP_798965	28899360	hypotheticalproteinVP2586[VibrioparahaemolyticusRIMD2210633]
NP_900802	34496587	monooxygenase[ChromobacteriumviolaceumATCC12472]
EAK27563	44584154	unknown[environmentalsequence]
ZP_009...	84390090	hypotheticalproteinV12B01_07895[Vibriosplendidus12B01]
YP_351534	77462030	UbiH/COQ6monooxygenasefamily[Rhodobactersphaeroides2.4.1]
ZP_009...	83750872	COG0654:2-polyprenyl-6-methoxyphenolhydroxylase[BartonellabacilliformisKC583]
ZP_006...	69300866	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[Silicibactersp.TM1040]
ZP_005...	68545515	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[Shewanellaamazonensis SB2B]

AAR37526	40062597	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinolhydroxylase,putative[unculturedbacterium311]
ZP_001...	23127034	COG0654:2-polyprenyl-6-methoxyphenolhydroxylase[NostocpunctiformePCC73102]
BAB50951	14024347	2-octaprenyl-6-methoxyphenol4-monoxygenase;UbiH[MesorhizobiumlotiMAFF303099]
ZP_006...	69274742	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[Mesorhizobiumsp.BNC1]
EAJ25028	44435391	unknown[environmentalsequence]
NP_245939	15602867	hypotheticalproteinPM1002[Pasteurellamultocidasubsp.multocidastr.Pm70]
EAK45724	44609867	unknown[environmentalsequence]
NP_533420	17936630	2-octaprenyl-6-methoxyphenylhydroxylase[Agrobacteriumtumefaciensstr.C58]
NP_387293	15966940	2-octaprenyl-6-methoxyphenylhydroxylase[Sinorhizobiummeliloti1021]
EAJ73686	44506250	unknown[environmentalsequence]
P_010...	85703939	ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6familyprotein[Roseovariussp.217]
P_007...	75829334	COG0654:2-polyprenyl-6-methoxyphenolhydroxylaseandrelatedFAD-dependentoxidoreductases[VibriocholeraeMO10]
YP_471448	86359556	probableFAD-dependentmonooxygenaseprotein[RhizobiumetliCFN42]
ZP_006...	69950407	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[ShewanellafrigidimarinaNCIMB400]
NP_716808	24372766	oxidoreductase,FAD-binding[ShewanellaoneidensisMR-1]
ZP_005...	68180785	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[Jannaschiasp.CCS1]
YP_131234	54310214	hypotheticalproteinPBPRA3117[PhotobacteriumprofundumSS9]
YP_131021	54310001	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinolhydroxylase[PhotobacteriumprofundumSS9]
EAJ30362	44443121	unknown[environmentalsequence]
NP_874216	33152863	Putative2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinolhydroxylase[Haemophilusducreyi35000HP]
EAG57760	43999646	unknown[environmentalsequence]
YP_034248	49476207	2-octaprenyl-6-methoxyphenylhydroxylase[Bartonellahenselaestr.Houston-1]
ZP_008...	78702226	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[AlkalilimnicolaehrlicheiMLHE-1]
ZP_007...	77630161	COG0654:2-polyprenyl-6-methoxyphenolhydroxylase[YersiniapseudotuberculosisIP31758]
EAJ51467	44472887	unknown[environmentalsequence]
ZP_007...	77635837	COG0654:2-polyprenyl-6-methoxyphenolhydroxylase[YersiniapestisAngola]
NP_935638	37681029	hypotheticalproteinVV2845[VibriovulnificusYJ016]
NP_760450	27364922	hypotheticalproteinVV11553[VibriovulnificusCMCP6]
EAH93271	44246441	unknown[environmentalsequence]
ZP_008...	78691821	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[Shewanellasp.MR-7]
YP_032771	49474729	2-octaprenyl-6-methoxyphenylhydroxylase[Bartonellaquintanastr.Toulouse]
EAE30141	43550738	unknown[environmentalsequence]
YP_170175	56708279	monooxygenasefamilyprotein[Francisellatularensissubsp.tularensisSC

		HUS4]
AAV29244	54113221	NT02FT1272[syntheticconstruct]
ZP_008...	78368767	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[Shewanellasp.PV-4]
ZP_001...	23466876	COG0654:2-polyprenyl-6-methoxyphenolhydroxylase[Haemophilussomnus129PT]
ZP_008...	78694407	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[Bradyrhizobiumsp.BTAi1]
NP_298124	15837436	hypotheticalproteinXF0834[Xylellafastidiosa9a5c]
ZP_006...	69950714	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[ShewanellafrigidimarinaNCIMB400]
ZP_007...	76794964	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[PseudoalteromonasatlanticaT6c]
ZP_009...	84500683	ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6familyprotein[OceanicolabatsensisHTCC2597]
CAD42832	32328570	putative2-octaprenyl-6-methoxyphenol4-monoxygenase[Bartonellatribocorum]
YP_432082	83643647	2-polyprenyl-6-methoxyphenolhydroxylaseandrelatedFAD-dependentoxidoreductase[HahellachejuensisKCTC2396]
ZP_005...	68548424	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[ShewanellaamazonensisSB2B]
YP_048575	50119408	hypotheticalproteinECA0457[Erwiniacarotovorasubsp.atrosepticaSCRI1043]
ZP_003...	48861543	COG0654:2-polyprenyl-6-methoxyphenolhydroxylase[Microbulbiferdegradans2-40]
ZP_010...	84515144	ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6family[LoktanellavestfoldensisSKA53]
ZP_009...	82741012	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[Shewanellasp.W3-18-1]
ZP_008...	82498448	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[Shewanellasp.MR-4]
ZP_006...	71899117	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[XylellafastidiosaAnn-1]
ZP_008...	77816356	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[ShewanellaputrefaciensCN-32]
ZP_007...	75854007	COG0654:2-polyprenyl-6-methoxyphenolhydroxylaseandrelatedFAD-dependentoxidoreductases[Vibriosp.Ex25]
BAA14326	216628	UbiH(VisB)[Escherichiacoli]
ZP_006...	71899686	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[XylellafastidiosaAnn-1]
NP_780021	28199707	hypotheticalproteinPD1838[XylellafastidiosaTemecula1]
BAE76972	85675719	2-octaprenyl-6-methoxyphenolhydroxylase,FAD/NAD(P)-binding[EscherichiacoliW3110]
NP_683079	22299832	2-octaprenyl-6-methoxyphenylhydroxylase[ThermosynechococcuselongatusBP-1]
YP_205483	59712707	hypotheticalproteinVF2100[VibriofischeriES114]
YP_156477	56461196	FAD-bindingoxidoreductase,UbiH/Coq6family[IdiomarinaloihiensisL2TR]
NP_289475	15803442	2-octaprenyl-6-methoxyphenylhydroxylase[EscherichiacoliO157:H7EDL933]
ZP_010...	85711155	FAD-bindingoxidoreductase,UbiH/Coq6familyprotein[IdiomarinabalticaOS145]

NP_767243	27375714	2-octaprenyl-6-methoxyphenylhydroxylase[BradyrhizobiumjaponicumUSDA110]
NP_311805	15833032	2-octaprenyl-6-methoxyphenylhydroxylase[EscherichiacoliO157:H7]
ZP_009...	83941776	ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6familyprotein[Sulfitobactersp.EE-36]
YP_413125	82703559	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6family[NitrosospiramultiformisATCC25196]
EAF25138	43741236	unknown[environmentalsequence]
XP_510056	55641039	PREDICTED:similartoUbiquinonebiosynthesismonooxgenaseCOQ6(CGI-10)[Pantroglodytes]
NP_928624	37525280	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinolhydroxylase[Photorhabdusluminescenssubsp.laumondiiTTO1]
YP_477026	86608264	ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6family[CyanobacteriabacteriumYellowstoneB-Prime]
AAR38107	40063289	ubiH/COQ6monooxygenasefamilyprotein[unculturedbacterium578]
ZP_006...	71550561	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[NitrosomonaseutrophaC71]
ZP_009...	83855254	ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6familyprotein[Sulfitobactersp.NAS-14.1]
ZP_007...	75234635	COG0654:2-polyprenyl-6-methoxyphenolhydroxylase[EscherichiacoliE110019]
NP_838389	30064218	2-octaprenyl-6-methoxyphenylhydroxylase[Shigellaflexneri2astr.2457T]
YP_409418	82545471	UbiH[ShigellaboydiiSb227]
ZP_007...	75515309	COG0654:2-polyprenyl-6-methoxyphenolhydroxylase[Escherichiacoli53638]
YP_168615	56698242	ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6family[SilicibacterpomeroyiDSS-3]
YP_419375	83309111	2-polyprenyl-6-methoxyphenolhydroxylase[MagnetospirillummagneticumAMB-1]
ZP_006...	69942812	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[ShewanelladenitrificansOS-217]
EAE77605	43645644	unknown[environmentalsequence]
ZP_007...	75258507	COG0654:2-polyprenyl-6-methoxyphenolhydroxylaseandrelatedFAD-dependentoxidoreductases[EscherichiacoliE22]
YP_498059	87200802	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6family[NovosphingobiumaromaticivoransDSM12444]
ZP_006...	69950715	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[ShewanellafrigidimarinaNCIMB400]
YP_094133	52840334	2-polyprenyl-6-methoxyphenolhydroxylase[Legionellapneumophilasubsp.pneumophilastr.Philadelphia1]
YP_244496	66769734	hypotheticalproteinXC_3432[Xanthomonascampestrispv.campestrisstr.8004]
YP_344563	77166038	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[NitrosoccoccusoceaniATCC19707]
EAH95544	44249260	unknown[environmentalsequence]
NP_755364	26249324	2-octaprenyl-6-methoxyphenylhydroxylase[EscherichiacoliCFT073]
BAE76971	85675718	predictedoxidoreductase,FAD/NAD(P)-bindingdomain[EscherichiacoliW3110]
YP_432378	83643943	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinolhydroxylase[HahellachejuensisKCTC2396]

ZP_008...	78366680	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[Shewanellasp.PV-4]
BAA14327	216629	VisC[Escherichiacoli]
NP_819129	29653437	visCprotein[CoxiellaburnetiiRSA493]
ZP_008...	77978893	COG0654:2-polyprenyl-6-methoxyphenolhydroxylase[YersiniaintermediaATCC29909]
NP_418926	16124362	2-octaprenyl-6-methoxyphenolhydroxylase[CaulobactercrescentusCB15]
ZP_007...	75813937	COG0654:2-polyprenyl-6-methoxyphenolhydroxylaseandrelatedFAD-dependentoxidoreductases[VibriocholeraeV52]
ZP_008...	77691290	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[RhodopseudomonaspalustrisBisB5]
ZP_008...	78493608	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[RhodopseudomonaspalustrisBisB18]
YP_268015	71279860	2-octaprenyl-6-methoxyphenolhydroxylase[Colwelliapsychrerythraea34H]
YP_125459	54293044	hypotheticalproteinlpl0081[Legionellapneumophilastr.Lens]
NP_641225	21241643	hypotheticalproteinXAC0873[Xanthomonasaxonopodispv.citristr.306]
ZP_010...	84683893	ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6familyprotein[RhodobacteralesbacteriumHTCC2654]
NP_933711	37679102	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinolhydroxylase[VibriovulnificusYJ016]
NP_311804	15833031	hypotheticalproteinECs3777[EscherichiacoliO157:H7]
ZP_009...	83569122	COG0654:2-polyprenyl-6-methoxyphenolhydroxylase[Shigelladysenteriae1012]
YP_404677	82778328	UbiH[ShigelladysenteriaeSd197]
ZP_010...	85714113	2-octaprenyl-6-methoxyphenylhydroxylase[Nitrobactersp.Nb-311A]
ZP_008...	77979052	COG0654:2-polyprenyl-6-methoxyphenolhydroxylase[YersiniaintermediaATCC29909]
ZP_007...	75239249	COG0654:2-polyprenyl-6-methoxyphenolhydroxylaseandrelatedFAD-dependentoxidoreductases[EscherichiacoliF11]
ZP_008...	77739784	Ubiquinonebiosynthesishydroxylase,UbiH/UbiF/VisC/COQ6[RhodopseudomonaspalustrisBisA53]
YP_311884	74313465	2-octaprenyl-6-methoxyphenylhydroxylase[ShigellasonneiSs046]
ZP_006...	75178799	COG0654:2-polyprenyl-6-methoxyphenolhydroxylaseandrelatedFAD-dependentoxidoreductases[ShigellaboydiiBS512]

Table 29: Examples of Monooxygenase CoQ7 related polypeptides.

Accession	GI	Description
P41735	82658569	CataboliterepressionproteinCAT5(UbiquinonebiosynthesisproteinCOQ7)
XP_448666	50292467	unnamedproteinproduct[Candidaglabrata]
XP_454057	50308113	unnamedproteinproduct[Kluyveromyceslactis]
NP_983242	45185526	ACL162Cp[Eremotheciumgossypii]
XP_715646	68480760	hypotheticalproteinCaO19_9495[CandidaalbicansSC5314]
XP_459962	50422771	hypotheticalproteinDEHA0E15675g[DebaryomyceshanseniiCBS767]
XP_503973	50553126	hypotheticalprotein[Yarrowialipolytica]
NP_595416	19112208	hypotheticalproteinSPBC337.15c[Schizosaccharomycespombe972h-]
EAQ84651	88177183	hypotheticalproteinCHGG_08665[ChaetomiumglobosumCBS148.51]
XP_957596	85085894	hypotheticalprotein[NeurosporacrassaN150]
XP_749324	70988947	hypotheticalproteinAfu2g01890[AspergillusfumigatusAf293]
BAE64957	83774834	unnamedproteinproduct[Aspergillusoryzae]
NP_001...	62859549	coenzymeQ7homolog,ubiquinone[Xenopustropicalis]
AAH91075	60551324	Unknown(proteinforIMAGE:7024122)[Xenopustropicalis]
XP_570414	58266516	ubiquinonemetabolism-relatedprotein[Cryptococcusneoformansvar.neoformansJEC21]
AAH82481	51950191	MGC84727protein[Xenopuslaevis]
NP_036917	25453396	demethyl-Q7[Rattusnorvegicus]
AAC69179	3806019	ubiquinonebiosynthesisproteincoq7[Musmusculus]
Q99807	12643397	UbiquinonebiosynthesisproteinCOQ7homolog(CoenzymeQbiosynthesisprotein7homolog)
NP_057222	25453484	COQ7protein[Homosapiens]
AAH43272	71297300	COQ7protein[Homosapiens]
AAM21346	20385593	placentalproteinKG-20[Homosapiens]
AAC69451	3811295	timingproteinCLK-1;ubiquinonebiosynthesisproteinCOQ7[Homosapiens]
XP_536955	73958985	PREDICTED:similartoUbiquinonebiosynthesisproteinCOQ7homolog[Canisfamiliaris]
ABD36098	87248091	ubiquinonebiosynthesisproteinCOQ7-likeprotein[Bombyxmori]
NP_001...	62460390	COQ7protein[Bostaurus]
CAB66582	12052820	hypotheticalprotein[Homosapiens]
XP_311027	58381140	ENSANGP00000019901[Anophelesgambiaestr.PEST]
CAB64656	6682311	putativeCOQ7isologue[Drosophilamelanogaster]
NP_651967	24640215	CG14437-PA[Drosophilamelanogaster]
XP_392748	66509055	PREDICTED:similartoubiquinonebiosynthesisproteinCOQ7-likeprotein[Apismellifera]
AAW27401	56758522	SJCHGC09044protein[Schistosomajaponicum]
XP_687941	68394515	PREDICTED:similartodemethyl-Q7[Daniorerio]
ZP_000...	46202110	COG2941:UbiquinonebiosynthesisproteinCOQ7[MagnetospirillummagnetotacticumMS-1]
XP_316597	31218166	ENSANGP00000011540[Anophelesgambiaestr.PEST]

YP_420895	83310631	UbiquinonebiosynthesisproteinCOQ7[MagnetospirillummagneticumAMB-1]
EAL32634	54643891	GA12984-PA[Drosophilapseudoobscura]
CAG03316	47220282	unnamedproteinproduct[Tetraodonnigroviridis]
XP_641196	66814034	hypotheticalproteinDDB0205223[Dictyosteliumdiscoideum]
EAJ47066	44466825	unknown[environmentalsequence]
ZP_010...	85709756	ubiquinonebiosynthesisprotein[Erythrobactersp.NAP1]
EAC77522	43223892	unknown[environmentalsequence]
EAJ53843	44476245	unknown[environmentalsequence]
EAG57298	43998802	unknown[environmentalsequence]
EAJ31519	44444847	unknown[environmentalsequence]
EAC25090	43118241	unknown[environmentalsequence]
EAK63205	44634136	unknown[environmentalsequence]
EAF53425	43797609	unknown[environmentalsequence]
EAF86145	43864205	unknown[environmentalsequence]
EAC85045	43238865	unknown[environmentalsequence]
S71353	7446710	Coq7proteinhomolog-rat
NP_421000	16126436	Coq7familyprotein[CaulobactercrescentusCB15]
CAE73680	39586553	HypotheticalproteinCBG21190[Caenorhabditisbriggsae]
EAK44603	44608294	unknown[environmentalsequence]
EAG86836	44052973	unknown[environmentalsequence]
EAE52263	43594793	unknown[environmentalsequence]
NP_498128	17552756	CLocK(biologicaltiming)abnormalityfamilymember(clk-1)[Caenorhabditiselegans]
YP_495336	87198079	UbiquinonebiosynthesisproteinCOQ7[NovosphingobiumaromaticivoransDSM12444]
EAJ91256	44532313	unknown[environmentalsequence]
EAA88936	42843054	unknown[environmentalsequence]
EAK57582	44626217	unknown[environmentalsequence]
YP_459540	85375478	ubiquinonebiosynthesisprotein[ErythrobacterlitoralisHTCC2594]
EAF00804	43691181	unknown[environmentalsequence]
XP_662173	67536798	hypotheticalproteinAN4569.2[AspergillusnidulansFGSCA4]
EAJ95415	44538384	unknown[environmentalsequence]
EAD63880	43404368	unknown[environmentalsequence]
ZP_005...	68539280	UbiquinonebiosyntheisproteinCOQ7[SphingopyxisalaskensisRB2256]
ZP_003...	58698317	Coq7familyprotein[WolbachiaendosymbiontofDrosophilaananassae]
EAE52310	43594894	unknown[environmentalsequence]
YP_163404	56552565	ubiquinonebiosynthesisprotein[Zymomonasmobilissubsp.mobilisZM4]
EAE97466	43684615	unknown[environmentalsequence]
EAI91294	44387145	unknown[environmentalsequence]
EAA82480	42830167	unknown[environmentalsequence]
AAH28276	20380261	Coq7protein[Musmusculus]
ZP_010...	84703893	Coq7familyprotein[ParvularculabermudensisHTCC2503]
YP_302872	73666856	Coq7familyprotein[Ehrlichiacanisstr.Jake]
EAB15593	42896823	unknown[environmentalsequence]
YP_196146	58616947	hypotheticalproteinERGA_CDS_02200[Ehrlichiaruminantiumstr.Gardel]
YP_197100	58578888	similartohumanUbiquinonebiosynthesisproteinCoq7[Ehrlichiaruminantiumstr.Welgevonden]
XP_826564	71905315	ubiquinonebiosynthesisproteinCOQ7[TrypanosomabruceiTREU927]
EAK36297	44596505	unknown[environmentalsequence]
EAJ89456	44529635	unknown[environmentalsequence]

EAD28662	43326122	unknown[environmentalsequence]
EAK59279	44628538	unknown[environmentalsequence]
YP_198414	58584841	UbiquinonebiosynthesisproteinCOQ7[WolbachiaendosymbiontstrainTRSofBrugiamalayi]
YP_153684	56416610	ubiquinonebiosynthesisprotein[Anaplasmamarginalestr.St.Maries]
EAB52099	42970264	unknown[environmentalsequence]
EAC57506	43183868	unknown[environmentalsequence]
EAB92271	43051725	unknown[environmentalsequence]
EAK62249	44632766	unknown[environmentalsequence]
EAI37514	44311290	unknown[environmentalsequence]
EAI92143	44388293	unknown[environmentalsequence]
ZP_009...	83859752	Coq7familyprotein[OceanicaulisalexandriiHTCC2633]
EAF22482	43735524	unknown[environmentalsequence]
EAG67211	44017101	unknown[environmentalsequence]
EAJ06849	44409219	unknown[environmentalsequence]
EAB94738	43056733	unknown[environmentalsequence]
EAK62019	44632424	unknown[environmentalsequence]
EAI47985	44326281	unknown[environmentalsequence]
EAC87443	43243586	unknown[environmentalsequence]
YP_505484	88607535	Coq7familyprotein[AnaplasmaphagocytophilumHZ]
EAE22675	43536004	unknown[environmentalsequence]
EAB20442	42906701	unknown[environmentalsequence]
EAH67880	44203052	unknown[environmentalsequence]
EAK01095	44546495	unknown[environmentalsequence]
EAC11358	43090346	unknown[environmentalsequence]
EAD59294	43390384	unknown[environmentalsequence]
EAK61612	44631860	unknown[environmentalsequence]
EAK39492	44601038	unknown[environmentalsequence]
EAK27662	44584302	unknown[environmentalsequence]
EAD74693	43438687	unknown[environmentalsequence]
XP_804058	71402240	ubiquinonebiosynthesisprotein[Trypanosomacruzi]
EAJ23958	44433827	unknown[environmentalsequence]
EAB76994	43020564	unknown[environmentalsequence]
EAB64054	42994223	unknown[environmentalsequence]
EAJ20396	44428732	unknown[environmentalsequence]
EAI35508	44308400	unknown[environmentalsequence]
EAB63560	42993283	unknown[environmentalsequence]
EAI29963	44300011	unknown[environmentalsequence]
EAC95617	43259878	unknown[environmentalsequence]
EAJ10790	44415211	unknown[environmentalsequence]
XP_822048	71660665	ubiquinonebiosynthesisprotein[Trypanosomacruzi]
EAB48106	42962322	unknown[environmentalsequence]
EAJ28183	44439935	unknown[environmentalsequence]
EAG56172	43996702	unknown[environmentalsequence]
EAE99716	43689092	unknown[environmentalsequence]
EAJ19549	44427483	unknown[environmentalsequence]
EAE48403	43587122	unknown[environmentalsequence]
EAJ32166	44445791	unknown[environmentalsequence]
EAF99075	43890209	unknown[environmentalsequence]
YP_247093	67459469	UbiquinonebiosynthesisproteinCoq7[RickettsiafelisURRWXCal2]
YP_507668	88658272	Coq7familyprotein[Ehrlichiachaffeensisstr.Arkansas]
EAF44135	43779252	unknown[environmentalsequence]
EAB04184	42873849	unknown[environmentalsequence]

EAH87661	44237850	unknown[environmentalsequence]
EAF56081	43803012	unknown[environmentalsequence]
EAC27316	43122883	unknown[environmentalsequence]
XP_847900	73536963	hypotheticalproteinLMJ_0878[LeishmaniamajorstrainFriedlin]
EAC83012	43234815	unknown[environmentalsequence]
EAH03602	44083176	unknown[environmentalsequence]
EAG71098	44024161	unknown[environmentalsequence]
EAC81193	43231211	unknown[environmentalsequence]
EAJ85338	44523557	unknown[environmentalsequence]
EAI58773	44341681	unknown[environmentalsequence]
EAK05851	44553225	unknown[environmentalsequence]
EAK37509	44598239	unknown[environmentalsequence]
EAB09578	42884813	unknown[environmentalsequence]
EAK52843	44619709	unknown[environmentalsequence]
EAG15177	43920690	unknown[environmentalsequence]
EAI22948	44289502	unknown[environmentalsequence]
EAK33632	44592678	unknown[environmentalsequence]
EAE93617	43677072	unknown[environmentalsequence]
EAH91819	44244498	unknown[environmentalsequence]
EAI26579	44295000	unknown[environmentalsequence]
ZP_001...	42453390	COG2941:UbiquinonebiosynthesisproteinCOQ7[Rickettsiarickettsii]
EAH05825	44087451	unknown[environmentalsequence]
EAJ28569	44440496	unknown[environmentalsequence]
EAC35418	43139311	unknown[environmentalsequence]
EAK29884	44587500	unknown[environmentalsequence]
EAI42461	44318495	unknown[environmentalsequence]
EAE05259	43501002	unknown[environmentalsequence]
EAH24199	44121565	unknown[environmentalsequence]
EAK12556	44562590	unknown[environmentalsequence]
AAC53055	1841536	COQ7[Musmusculus]
NP_359876	15892162	ubiquinonebiosynthesisproteincoq7[Rickettsiaconoriistr.Malish7]
EAG14310	43918853	unknown[environmentalsequence]
EAI63504	44348400	unknown[environmentalsequence]
ZP_001...	34580808	ubiquinonebiosynthesisproteincoq7[Rickettsiasibirica246]
EAH68487	44204140	unknown[environmentalsequence]
EAF57169	43805250	unknown[environmentalsequence]
YP_265844	71083125	Coq7familyprotein[CandidatusPelagibacterubiqueHTCC1062]
EAC42254	43153188	unknown[environmentalsequence]
EAD25605	43319796	unknown[environmentalsequence]
EAG87757	44054623	unknown[environmentalsequence]
EAJ74530	44507478	unknown[environmentalsequence]
EAJ19120	44426874	unknown[environmentalsequence]
EAJ36771	44452066	unknown[environmentalsequence]
NP_220579	15604064	UBIQUINONEBIOSYNTHESISPROTEINCOQ7(coq7)[Rickettsiaprowazekiistr.MadridE]
EAF45740	43782424	unknown[environmentalsequence]
EAJ44656	44463331	unknown[environmentalsequence]
EAD43046	43356360	unknown[environmentalsequence]
EAC84824	43238438	unknown[environmentalsequence]
EAC52460	43173755	unknown[environmentalsequence]
EAI58386	44341140	unknown[environmentalsequence]
EAJ38065	44453957	unknown[environmentalsequence]
EAI84950	44378449	unknown[environmentalsequence]

EAJ68670	44498750	unknown[environmentalsequence]
EAB77871	43022290	unknown[environmentalsequence]
EAG11254	43912898	unknown[environmentalsequence]
EAJ67153	44496520	unknown[environmentalsequence]
EAJ22334	44431517	unknown[environmentalsequence]
EAJ30845	44443851	unknown[environmentalsequence]
EAI95064	44392433	unknown[environmentalsequence]
EAK52124	44618702	unknown[environmentalsequence]
EAG01741	43895326	unknown[environmentalsequence]
EAG61133	44006044	unknown[environmentalsequence]
EAF60912	43812788	unknown[environmentalsequence]
EAG32267	43952637	unknown[environmentalsequence]
EAE48264	43586856	unknown[environmentalsequence]
YP_506228	88608210	Coq7familyprotein[Neorickettsiasennetsustr.Miyayama]

Table 30: Examples of Monooxygenase CoQ8 Related polypeptides.

Accession	GI	Description
XP_451554	50303225	unnamedproteinproduct[Kluyveromyceslactis]
NP_011396	6321319	Proteinrequiredforubiquinone(coenzymeQ)biosynthesisandforrespiratorygrowth;Abc1p
XP_446281	50287703	unnamedproteinproduct[Candidaglabrata]
XP_718424	68475077	putativemitochondrialchaperonin[CandidaalbicansSC5314]
XP_718154	68475612	putativemitochondrialchaperonin[CandidaalbicansSC5314]
XP_456738	50407820	hypotheticalproteinDEHA0A09603g[DebaryomyceshanseniiCBS767]
XP_500941	50546943	hypotheticalprotein[Yarrowialipolytica]
BAE61853	83771723	unnamedproteinproduct[Aspergillusoryzae]

XP_664176	67540804	hypotheticalproteinAN6572.2[AspergillusnidulansFGSCA4]
XP_961212	85101761	hypotheticalprotein((AL451018)probableabc1proteinprecursor[NeurosporacrassaN150])
XP_747640	70984246	molecularchaperone[AspergillusfumigatusAf293]
XP_387573	46126039	hypotheticalproteinFG07397.1[GibberellazeaePH-1]
AAL16909	16304010	ABC1protein[Magnaporthegrisea]
NP_596237	19113029	hypotheticalproteinSPBC2D10.18[Schizosaccharomycespombe972h-]
XP_570839	58267366	ubiquinonebiosynthesis-relatedprotein[CryptococcusneoformansvarneoformansJEC21]
XP_791783	72159100	similartoChaperone-activityofbc1complex-like,mitochondrialprecursor[Strongylocentrotuspurpuratus]
XP_758611	71013530	hypotheticalproteinUM02464.1[Ustilagomaydis521]
CAG01797	47219134	unnamedproteinproduct[Tetraodonnigroviridis]
XP_574399	62639199	PREDICTED:aarFdomaincontainingkinase4(predicted)[Rattusnorvegicus]
XP_690929	68392390	PREDICTED:similartoChaperone-activityofbc1complex-like,mitochondrialprecursor[Daniorerio]
XP_691266	68392398	PREDICTED:similartoChaperone-activityofbc1complex-like,mitochondrialprecursor[Daniorerio]
AAH93498	62471517	Adck4protein[Musmusculus]
XP_592153	76641677	PREDICTED:similartoaarFdomaincontainingkinase4isoform1[Bostaurus]
CAG06439	47224869	unnamedproteinproduct[Tetraodonnigroviridis]
XP_624948	66551973	PREDICTED:similartoCG32649-PA[Apismellifera]
XP_415040	50756155	PREDICTED:similartoCabc1protein[Gallusgallus]
NP_079152	27363457	aarFdomaincontainingkinase4[Homosapiens]
AAF48209	22832168	CG32649-PA[Drosophilamelanogaster]
AAH79816	50927238	MGC86474protein[Xenopuslaevis]
EAL31495	54642750	GA17042-PA[Drosophilapseudoobscura]
XP_881803	76671827	similartoChaperone-activityofbc1complex-like,mitochondrialprecursorisoform3[Bostaurus]
XP_881921	76671831	similartoChaperone-activityofbc1complex-like,mitochondrialprecursorisoform5[Bostaurus]
XP_311995	58382519	ENSANGP00000018621[Anophelesgambiaestr. PEST]
NP_075830	70778882	chaperone,ABC1activityofbc1complexlike[Musmusculus]
BAB29459	26380702	unnamedproteinproduct[Musmusculus]
CAI19106	56206212	chaperone,ABC1activityofbc1complexlike(S.pombe)[Homosapiens]
CAI19105	56206211	chaperone,ABC1activityofbc1complexlike(S.pombe)[Homosapiens]
CAI19104	56206210	chaperone,ABC1activityofbc1complexlike(S.pombe)[Homosapiens]
CAI19103	56206209	chaperone,ABC1activityofbc1complexlike(S.pombe)[Homosapiens]
CAI12066	55962365	novelproteinsimilartovertebratechaperone,ABC1activityofbc1complexlike(CABC1)[Daniorerio]
BAC11143	22760302	unnamedproteinproduct[Homosapiens]
NP_001...	61557218	chaperone,ABC1activityofbc1complexlike(S.pombe)(predicted)[Rattusnorvegicus]
CAG13211	47221275	unnamedproteinproduct[Tetraodonnigroviridis]
NP_908650	34894650	putativeABC(ATPbindingcassette)1protein[Oryzasativa(japonicaculti var-group)]
NP_498014	32565180	COenzymeQ(ubiquinone)biosynthesisfamilymember(coq-8)[Caenorhabditiselegans]

Table 31: Examples of chorismate lyase (UbiC/CoQ9) Related polypeptides.

Accession	GI	Description
67010XP	453611	50307265unnamedproteinproduct[Kluyveromyceslactis]
63110NP	13302	6323230MitochondrialinnermembraneproteinCoq9p[Saccharomycesc erevisiae]
XP_444938	50285019	hypotheticalproteinCAGL0A03949g[CandidaglabrataCBS138]
XP_390015	46136647	hypotheticalproteinFG09839.1[GibberellazeaePH-1]
XP_461856	50426519	hypotheticalproteinDEHA0G07733g[DebaryomyceshanseniiCBS767]
CAD60732	27803029	unnamedproteinproduct[Podosporaanserina]
NP_594426	19115338	hypotheticalproteinSPAC19G12.11[Schizosaccharomycespombe972h -]
XP_711301	68489737	hypotheticalproteinCaO19.6602[CandidaalbicansSC5314]
XP_959723	85093576	hypotheticalprotein[NeurosporacrassaN150]
EAQ92196	88184728	hypotheticalproteinCHGG_00431[ChaetomiumglobosumCBS148.51]
XP_505941	50557066	hypotheticalprotein[Yarrowialipolytica]
XP_661342	67526561	hypotheticalproteinAN3738.2[AspergillusnidulansFGSCA4]
BAE54683	83764539	unnamedproteinproduct[Aspergillusoryzae]

XP_751109	70992521	hypotheticalproteinAfu6g12310[AspergillusfumigatusAf293]
EAL25313	54635910	GA15880-PA[Drosophilapseudoobscura]
AAI04703	75775127	LOC498909protein[Rattusnorvegicus]
NP_001...	78214350	hypotheticalproteinLOC498909[Rattusnorvegicus]
AAH54340	56078960	HypotheticalproteinLOC57017[Homosapiens]
AAL68377	18447632	SD02734p[Drosophilamelanogaster]
NP_724594	24586344	CG30493-PB[Drosophilamelanogaster]
BAE34754	74186535	unnamedproteinproduct[Musmusculus]
XP_470923	50921125	unknownprotein[Oryzasativa(japonicacultivar-group)]
XP_510991	55643929	PREDICTED:hypotheticalproteinXP_510991[Pantroglodytes]
AAI11145	84708700	Unknown(proteinforMGC:134146)[Bostaurus]
NP_001...	58332064	hypotheticalproteinLOC496601[Xenopustropicalis]
AAI06648	77748499	Unknown(proteinforIMAGE:6953475)[Xenopuslaevis]
AAH87448	56269534	LOC496049protein[Xenopuslaevis]
XP_624508	66512029	PREDICTED:similartoENSANGP00000025105[Apismellifera]
AAF29004	6841302	HSPC326[Homosapiens]
AAW26355	56756364	SJCHGC05554protein[Schistosomajaponicum]
XP_314349	58385978	ENSANGP00000025105[Anophelesgambiaestr. PEST]
XP_314351	58385982	ENSANGP00000025000[Anophelesgambiaestr. PEST]
AAH01478	33987999	COQ9protein[Homosapiens]

Table 32: Examples of Anthranilate Synthase polypeptides.

32A. Anthranilate synthase Component I		
Accession	GI	Description
XP_454856	50309689	unnamedproteinproduct[Kluyveromyceslactis]
XP_447468	50290073	hypotheticalproteinCAGL0I05016g[CandidaglabrataCBS138]
NP_011014	6320935	Anthranilatesynthase,catalyzesinitialstepoftryptophanbiosynthesis,Trp2p[Saccharomycescerevisiae]
XP_503954	50553088	hypotheticalprotein[Yarrowialipolytica]
XP_456652	50406654	hypotheticalproteinDEHA0A07612g[DebaryomyceshanseniiCBS767]
XP_718214	68475383	putativeanthranilatesynthasecomponentI[CandidaalbicansSC5314]
XP_718312	68475188	putativeanthranilatesynthasecomponentI[CandidaalbicansSC5314]
XP_751136	70992575	anthranilatesynthasecomponentI[AspergillusfumigatusAf293]
BAE57556	83767417	unnamedproteinproduct[Aspergillusoryzae]
XP_661299	67526475	hypotheticalproteinAN3695.2[AspergillusnidulansFGSCA4]
AAA35175	173043	anthranilatesynthaseComponentI
O94582	30913348	Probableanthranilatesynthasecomponent I
XP_756451	71003570	hypotheticalproteinUM00304.1[Ustilagomaydis521]

CAD70536	28881419	hypotheticalprotein[Neurosporacrassa]
XP_957115	85083387	hypotheticalprotein[NeurosporacrassaN150]
XP_386701	46124295	hypotheticalproteinFG06525.1[GibberellazeaePH-1]
EAL20329	50257624	hypotheticalproteinCNBF1400[Cryptococcusneoformansvar.neoformansB-3501A]
XP_571668	58269024	anthranilatesynthase[Cryptococcusneoformansvar.neoformansJEC21]
T43181	11268473	probableanthranilatesynthase(EC4.1.3.27)chainI-fissionyeast(Schizosaccharomycespombe)

32B. Anthranilate synthase Component II

Accession	GI	Description
AAA35176	173045	anthranilatesynthaseComponentII:indole-3-glycerolphosphatesynthase(TRP3)
XP_445985	50287111	unnamedproteinproduct[Candidaglabrata]
XP_452170	50304441	unnamedproteinproduct[Kluyveromyceslactis]
XP_502685	50550425	hypotheticalprotein[Yarrowialipolytica]
NP_985301	45191047	AER446Wp[Eremotheciumgossypii]
P20409	136358	AnthranilatesynthasecomponentII(PRAI)
AAA33633	169014	trifunctionalprotein
AAA34450	171126	glutamineamidotransferase(TRP3)
XP_716312	68479266	putativebifunctionaltryptophanbiosynthesisenzymeTrp3p[CandidaalbicansSC5314]
EAQ88984	88181516	hypotheticalproteinCHGG_05603[ChaetomiumglobosumCBS148.51]
XP_385717	46122327	hypotheticalproteinFG05541.1[GibberellazeaePH-1]
P24773	136296	AnthranilatesynthasecomponentII(PRAI)
P05328	136286	AnthranilatesynthasecomponentII(PRAI)
XP_752679	70995848	anthranilatesynthasemultifunctionalprotein[AspergillusfumigatusAf293]
XP_457477	50415562	hypotheticalproteinDEHA0B12276g[DebaryomyceshanseniiCBS767]
CAA37640	1069996	unnamedproteinproduct[Aspergillusniger]
BAE60735	83770602	unnamedproteinproduct[Aspergillusoryzae]
NP_596823	19113615	hypotheticalproteinSPBC1539.09c[Schizosaccharomycespombe972h-]
P06531	136287	AnthranilatesynthasecomponentII(PRAI)
CAA70348	1666213	trp-1[Schizosaccharomycespombe]
CAC41002	14330265	anthranilatesynthase[Coprinopsisscobicola]
BAD14308	46092404	trifunctionaltryptophanbiosynthesisenzyme[Schizophyllumcommune]
AAO62633	29123601	trifunctionaltryptophanbiosynthesisenzyme[Metarhiziumanisopliae]
CAC40999	14329790	trifunctionaltryptophanbiosynthesisenzyme[Agaricusbisporus]
P09575	136354	AnthranilatesynthasecomponentII(PRAI)
CAE84138	48473841	anthranilatesynthasecomponentII[Hebelomacylindrosporum]
P25170	136297	AnthranilatesynthasecomponentII(PRAI)
CAA26232	2423	unnamedproteinproduct[Emericellanidulans]
Q5KC22	68053034	AnthranilatesynthasecomponentII(PRAI)
EAL19359	50256636	hypotheticalproteinCNBH0530[Cryptococcusneoformansvar.neoformansB-3501A]
P27710	68067603	AnthranilatesynthasecomponentII(PRAI)
XP_758523	71012739	hypotheticalproteinUM02376.1[Ustilagomaydis521]

Q92411	2494752	AnthranilatesynthasecomponentII(PRAI)

Table 33: Examples of Shikimate pathway polypeptides.

Accession	GI	Description
XP_449840	50294858	hypotheticalproteinCAGL0M11484g[CandidaglabrataCBS138]
XP_455965	50311867	unnamedproteinproduct[Kluyveromyceslactis]
NP_986731	45201161	AGR066Wp[Eremotheciumgossypii]
AAW33954	57117457	AROMpentafunctionalenzyme[Pichiapastoris]
XP_459982	50422811	hypotheticalproteinDEHA0E16247g[DebaryomyceshanseniiCBS767]
XP_722916	68466283	hypotheticalproteinCaO19_12175[CandidaalbicansSC5314]
XP_722769	68466574	hypotheticalproteinCaO19_4704[CandidaalbicansSC5314]
XP_505337	50555858	hypotheticalprotein[Yarrowialipolytica]
XP_956000	85077284	hypotheticalprotein[NeurosporacrassaN150]
XP_384463	46116890	hypotheticalproteinFG04287.1[GibberellazeaePH-1]
AAU95677	53854589	arom[Sclerotiniasclerotiorum]
NP_594681	19115593	hypotheticalproteinSPAC1834.02[Schizosaccharomycespombe972h-]
BAE60669	83770536	unnamedproteinproduct[Aspergillusoryzae]
XP_752744	70995978	pentafunctionalpolypeptideAroM[AspergillusfumigatusAf293]
CAD29607	44889967	pentafunctionalarompolypeptide[includes:3-dehydroquinatesynthase],putative[Aspergillusfumigatus]
AAN70992	25005077	arompolypeptide[Thanatephoruscucumeris]
P07547	6226554	PentafunctionalAROMpolypeptide
XP_569127	58263434	aromaticaminoacidfamilybiosynthesis-relatedprotein[Cryptococcusneoformansvar.neoformansJEC21]

EAQ83900	88176432	hypotheticalproteinCHGG_10304[ChaetomiumglobosumCBS 148.51]
Q12659	2492977	PentafunctionalAROMpolypeptide
XP_759754	71019047	hypotheticalproteinUM03607.1[Ustilagomaydis521]

Table 34. Examples of Chorismate mutase.

Accession	GI	Description
1CSMB	1127168	ChainB,Mol_id:1;Molecule:ChorismateMutase;Chain:A,B;Ec:4.1.3.27;Mutation:AlleleMutant,Thr226Ile;
3CSMB	2914555	ChainB,StructureOfYeastChorismateMutaseWithBoundTrpAndAnEndooxabicyclicInhibitor
5CSMA	2914565	ChainA,YeastChorismateMutase,T226sMutant,ComplexWithTrp
XP_451906	50303917	unnamedproteinproduct[Kluyveromyceslactis]
XP_448747	50292629	unnamedproteinproduct[Candidaglabrata]
NP_983770	45187547	ADL326Wp[Eremotheciumgossypii]
XP_713036	68486172	chorismatemutase[CandidaalbicansSC5314]
AAW33953	57117455	chorismatemutase[Pichiapastoris]
XP_461407	50425621	hypotheticalproteinDEHA0F26004g[DebaryomyceshanseniiCBS767]
AAF87954	9502025	chorismatemutase[Pichiaangusta]
XP_504065	50553308	hypotheticalprotein[Yarrowialipolytica]
BAD21145	47846873	chorismatemutase[Roselliniasp. PF1022]
XP_961975	85105491	hypotheticalprotein[NeurosporacrassaN150]
XP_753341	70997175	chorismatemutase[AspergillusfumigatusAf293]
BAE63016	83772888	unnamedproteinproduct[Aspergillusoryzae]
XP_664470	67541392	hypotheticalproteinAN6866.2[AspergillusnidulansFGSCA4]
NP_594216	19115128	hypotheticalproteinSPAC16E8.04c[Schizosaccharomycespombe972h-]
AAD48923	5732018	chorimatemutase[Lycopersiconesculentum]
BAD87142	57899563	putativechorismatemutaseprecursor[Oryzasativa(japonicacultivar-group)]
NP_916250	34909806	putativechorismatemutaseprecursor[Oryzasativa(japonicacultivar-group)]
ABA54871	76782202	putativechorismatemutase[Fagussylvatica]
AAO63370	28950893	At1g69370[Arabidopsisthaliana]
P42738	17380436	Chorismatemutase,chloroplastprecursor(CM-1)

NP_566846	18406100	CM1;chorismatemutase[Arabidopsisthaliana]
XP_760367	71020273	hypotheticalproteinUM04220.1[Ustilagomaydis521]
CAA81286	429153	chorismatemutaseprecursor[Arabidopsisthaliana]
CAB54518	5824343	chorismatemutase[Arabidopsisthaliana]
XP_568424	58262028	chorismatemutase[Cryptococcusneoformansvar. neoformansJEC21]
AAK83369	15077828	chorismatemutase[Filobasidiellaneoformans]
AAD21624	4512122	chorismatemutase3[Arabidopsisthaliana]
ABA99067	77556271	chorismatemutase,putative[Oryzasativa(japonicacultivar-group)]
XP_464326	50905675	putativechorismatemutase,cytosolic[Oryzasativa(japonicacultivar-group)]
AAM91774	22136860	putativechorismatemutaseCM2[Arabidopsisthaliana]
EAD61241	43396431	unknown[environmentalsequence]
XP_389778	46136173	hypotheticalproteinFG09602.1[GibberellazeaePH-1]
XP_482629	50946203	putativechorimatemutase[Oryzasativa(japonicacultivar-group)]

Table 35: Examples of Chorismate Synthase polypeptides.

Accession	GI	Description
1R53A	40889609	ChainA,CrystalStructureOfTheBifunctionalChorismateSynthaseFromSaccharomycesCerevisiae
XP_445906	50286953	unnamedproteinproduct[Candidaglabrata]
XP_454358	50308709	unnamedproteinproduct[Kluyveromyceslactis]
NP_983809	45187586	ADL287Cp[Eremotheciumgossypii]
XP_459489	50421863	hypotheticalproteinDEHA0E04510g[DebaryomyceshanseniiCBS767]
XP_710110	68492225	hypotheticalproteinCaO19.1986[CandidaalbicansSC5314]
XP_710211	68492031	chorismatesynthase[CandidaalbicansSC5314]
XP_502961	50550975	hypotheticalprotein[Yarrowialipolytica]
NP_588359	63054453	chorismatesynthase[Schizosaccharomycespombe972h-]
XP_750443	70991188	chorismatesynthase[AspergillusfumigatusAf293]
XP_963243	85074621	NADPH-dependentchorismatesynthase/flavinreductase[NeurosporacrassaN150]
BAE57314	83767175	unnamedproteinproduct[Aspergillusoryzae]
XP_663335	67539122	hypotheticalproteinAN5731.2[AspergillusnidulansFGSCA4]
2120340A	1583263	chorismatesynthase/flavinreductase
EAQ84101	88176633	hypotheticalproteinCHGG_10505[ChaetomiumglobosumCBS148.51]
XP_381819	46109522	hypotheticalproteinFG01643.1[GibberellazeaePH-1]
XP_572438	58270564	chorismatesynthase[Cryptococcusneoformansvar. neoformansJEC21]
XP_757549	71005766	hypotheticalproteinUM01402.1[Ustilagomaydis521]
YP_066794	51246910	chorismatesynthase[DesulfotaleapsychrophilaLSv54]
Q6AIP3	67460262	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
Q8DLM1	67460401	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
NP_440735	16330007	chorismatesynthase[Synechocystissp. PCC6803]
YP_399231	81299023	chorismatesynthase[SynechococcuselongatusPCC7942]
ZP_005...	67924165	Chorismatesynthase[CrocosphaerawatsoniiWH8501]

Q5N2I0	67460182	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
Q7V364	67460362	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
YP_321108	75906812	chorismatesynthase[AnabaenavariabilisATCC29413]
ZP_001...	23126882	COG0082:Chorismatesynthase[NostocpunctiformePCC73102]
EAJ73729	44506310	unknown[environmentalsequence]
ABA54870	76782200	putativechorismatesynthase[Fagussylvatica]
YP_396724	78778612	chorismatesynthase[Prochlorococcusmarinusstr. MIT9312]
Q42884	2492952	Chorismatesynthase1,chloroplastprecursor(5-enolpyruvylshikimate-3-phosphatephospholyase1)
ZP_006...	71677678	Chorismatesynthase[TrichodesmiumerythraeumIMS101]
YP_292784	72383429	chorismatesynthase[Prochlorococcusmarinusstr. NATL2A]
YP_473819	86605056	chorismatesynthase[CyanobacteriabacteriumYellowstoneA-Prime]
P46894	37154600	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
P27793	114182	Chorismatesynthase,chloroplastprecursor(5-enolpyruvylshikimate-3-phosphatephospholyase)
ZP_010...	87125048	chorismatesynthase[Synechococcussp. RS9917]
ZP_010...	84518705	chorismatesynthase[Prochlorococcusmarinusstr. MIT9211]
YP_477740	86608978	chorismatesynthase[CyanobacteriabacteriumYellowstoneB-Prime]
Q42885	2492953	Chorismatesynthase2,chloroplastprecursor(5-enolpyruvylshikimate-3-phosphatephospholyase2)
Q7U9F0	67460361	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
ZP_010...	87301885	chorismatesynthase[Synechococcussp. WH5701]
ZP_003...	48855812	COG0082:Chorismatesynthase[Cytophagahutchinsonii]
YP_378041	78185607	chorismatesynthase[Synechococcussp. CC9902]
EAI68558	44355446	unknown[environmentalsequence]
Q7V4Y9	67460363	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
YP_380635	78211856	chorismatesynthase[Synechococcussp. CC9605]
CAB40781	4584699	SPCC297.01[Schizosaccharomycespombe]
AAG50662	12321114	chorismatesynthase,putative[Arabidopsisthaliana]
ABA90483	77547031	chorismatesynthase[Glycinemax]
Q8F9N4	67460408	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
EAJ82888	44519924	unknown[environmentalsequence]
ZP_010...	86141575	chorismatesynthase[Flavobacteriumsp. MED217]
YP_213181	60683037	chorismatesynthase[BacteroidesfragilisNCTC9343]
Q64PP7	67460246	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
Q8A602	67460395	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
ZP_009...	83857326	chorismatesynthase[CroceibacteratlanticusHTCC2559]
EAH64755	44197337	unknown[environmentalsequence]
ZP_010...	86132299	chorismatesynthase[Cellulophagasp. MED134]
ZP_010...	86133890	chorismatesynthase[Tenacibaculumsp. MED152]
EAI60943	44344733	unknown[environmentalsequence]
EAK03675	44550154	unknown[environmentalsequence]
Q8PW84	23813697	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
YP_304976	73668961	chorismatesynthase[Methanosarcinabarkeristr. fusaro]

YP_247913	68248801	chorismatesynthase[Haemophilusinfluenzae86-028NP]
EAE15364	43521398	unknown[environmentalsequence]
NP_438365	16272160	chorismatesynthase[HaemophilusinfluenzaeRdKW20]
Q7MV04	67460355	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
Q5X2Y6	67460219	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
Q5ZT62	67460229	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
Q5WUE6	67460215	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
ZP_001...	46128950	COG0082:Chorismatesynthase[HaemophilusinfluenzaeR2846]
ZP_001...	42630499	COG0082:Chorismatesynthase[HaemophilusinfluenzaeR2866]
Q65U87	67460251	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
ZP_001...	46143241	COG0082:Chorismatesynthase[Actinobacilluspleuropneumoniaeserovar1str. 4074]
EAJ34873	44449592	unknown[environmentalsequence]
Q8TT87	23813707	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
ZP_007...	76260956	Chorismatesynthase[ChloroflexusaurantiacusJ-10-fl]
ZP_005...	68210573	Chorismatesynthase[MethanococcoidesburtoniiDSM6242]
ZP_007...	75429471	Chorismatesynthase[Actinobacillussuccinogenes130Z]
EAJ41923	44459321	unknown[environmentalsequence]
NP_245296	15602224	chorismatesynthase[Pasteurellamultocidasubsp. multocidastr. Pm70]
ZP_001...	32029118	COG0082:Chorismatesynthase[Haemophilussomnus2336]
Q6LNN4	67460285	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
Q7VLX2	67460366	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
NP_248169	15669364	chorismatesynthase[MethanocaldococcusjannaschiiDSM2661]
AAA21830	497783	2,3-dihydroxybenzoicacid
P39198	12230992	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
Q5E3U6	67460141	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
Q9ZHE9	22654227	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
A55510	1073744	chorismatesynthase(EC4.2.3.5)-Vibrioanguillarum
BAA16185	85675358	chorismatesynthase[EscherichiacoliW3110]
ZP_009...	83588353	COG0082:Chorismatesynthase[Escherichiacoli101-1]
Q87MM9	32129420	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
NP_754757	26248717	chorismatesynthase[EscherichiacoliCFT073]
ZP_007...	75187111	COG0082:Chorismatesynthase[EscherichiacoliE24377A]
O29587	12229689	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
ZP_009...	83570060	COG0082:Chorismatesynthase[Shigelladysenteriae1012]
Q5PCX2	67460192	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
ZP_007...	75259789	COG0082:Chorismatesynthase[EscherichiacoliE22]
YP_344913	77166388	chorismatesynthase[NitrosococcusoceaniATCC19707]

Q57LX0	67460138	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
NP_708211	56480091	chorismatesynthase[Shigellaflexneri2astr. 301]
YP_408757	82544810	chorismatesynthase[ShigellaboydiiSb227]
EAK23118	44577658	unknown[environmentalsequence]
YP_269847	71279712	chorismatesynthase[Colwelliapsychrerythraea34H]
EAJ40457	44457285	unknown[environmentalsequence]
NP_935227	37680618	chorismatesynthase[VibriovulnificusYJ016]
Q7MIT1	56748606	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
EAI90130	44385558	unknown[environmentalsequence]
ZP_010...	86148780	chorismatesynthase[Vibriosp. MED222]
Q8TXN1	23813708	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
ZP_007...	75830306	COG0082:Chorismatesynthase[VibriocholeraeMO10]
Q8DB42	32129424	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
YP_278007	71892273	chorimatesynthase[CandidatusBlochmanniapennsylvanicusstr. BPEN]
EAJ92903	44534640	unknown[environmentalsequence]
ZP_008...	77979080	COG0082:Chorismatesynthase[YersiniaintermediaATCC29909]
ZP_008...	77975539	COG0082:Chorismatesynthase[YersiniafrederikseniiATCC33641]
AAA27029	153878	chorismatesynthase(EC4.6.1.4)
Q89AX9	31076612	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
NP_993740	45442201	chorismatesynthase[YersiniapestisbiovarMedievalisstr. 91001]
ZP_007...	77635298	COG0082:Chorismatesynthase[YersiniapestisAngola]
ZP_008...	77960624	COG0082:Chorismatesynthase[YersiniamollaretiiATCC43969]
Q668V5	67460253	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
AAC97352	4038312	chorismatesynthase[Buchneraaphidicola]
EAD56104	43382436	unknown[environmentalsequence]
EAJ03832	44404977	unknown[environmentalsequence]
EAK01926	44547711	unknown[environmentalsequence]
ZP_008...	77956337	COG0082:Chorismatesynthase[YersiniabercovieriATCC43970]
NP_804338	29140996	chorismatesynthase[Salmonellaentericasubsp. entericaserovarTyphiTy2]
ZP_007...	75854943	COG0082:Chorismatesynthase[Vibriosp. Ex25]
ZP_007...	75824680	COG0082:Chorismatesynthase[VibriocholeraeRC385]
YP_433655	83645220	chorismatesynthase[HahellachejuensisKCTC2396]
Q6D2M6	67460268	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
EAJ94359	44536803	unknown[environmentalsequence]
YP_461859	85859657	chorismatesynthase[SyntrophusaciditrophicusSB]
NP_284644	15794822	chorismatesynthase[NeisseriameningitidisZ2491]
ZP_010...	87122382	chorismatesynthase[Marinomonassp. MED121]
ZP_008...	77955543	Chorismatesynthase[MarinobacteraquaeoleiVT8]
YP_495292	87198035	Chorismatesynthase[NovosphingobiumaromaticivoransDSM12444]
ZP_007...	76792635	Chorismatesynthase[PseudoalteromonasatlanticaT6c]
Q6MCU1	67460289	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
ZP_006...	74020660	Chorismatesynthase[RhodoferaxferrireducensDSM15236]

Q5F756	67460147	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
EAK59027	44628183	unknown[environmentalsequence]
ZP_005...	68547898	Chorismatesynthase[ShewanellaamazonensisSB2B]
H84940	25292291	chorismatesynthase(EC4.2.3.5)[imported]-Buchnerasp. (strainAPS)
NP_274684	15677528	chorismatesynthase[NeisseriameningitidisMC58]
Q7N299	67460357	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
CAA68707	40970	chorismatesynthase[Escherichiacoli]
AAU83947	52550098	chorismatesynthase[unculturedarchaeonGZfos35A2]
YP_391804	78485879	chorismatesynthase[ThiomicrospiracrunogenaXCL-2]
Q72DN5	67460334	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
ZP_008...	78368433	Chorismatesynthase[Shewanellasp. PV-4]
Q6LXL7	67460288	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
EAK57706	44626388	unknown[environmentalsequence]
ZP_008...	78700295	Chorismatesynthase[AlkalilimnicolaehrlicheiMLHE-1]
EAK27283	44583774	unknown[environmentalsequence]
EAK65066	44636899	unknown[environmentalsequence]
ZP_009...	82743562	Chorismatesynthase[Shewanellasp. W3-18-1]
ZP_004...	67675591	Chorismatesynthase[ChromohalobactersalexigensDSM3043]
EAK59299	44628563	unknown[environmentalsequence]
EAI54083	44334914	unknown[environmentalsequence]
YP_455307	85059605	chorismatesynthase[Sodalisglossinidiusstr. 'morsitans']
EAI60092	44343509	unknown[environmentalsequence]
Q5NGG6	67460183	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
ZP_008. . .	77816154	Chorismatesynthase[ShewanellaputrefaciensCN-32]
EAK50038	44615937	unknown[environmentalsequence]
YP_284084	71906497	Chorismatesynthase[DechloromonasaromaticaRCB]
EAI59376	44342539	unknown[environmentalsequence]
EAI97240	44395486	unknown[environmentalsequence]
ZP_008...	78687720	Chorismatesynthase[Shewanellasp. ANA-3]
ZP_008...	82496538	Chorismatesynthase[Shewanellasp. MR-4]
YP_266036	71083317	chorismatesynthase[CandidatusPelagibacterubiqueHTCC1062]
EAJ61884	44487705	unknown[environmentalsequence]
Q7NYT5	67460359	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
EAI24483	44291825	unknown[environmentalsequence]
EAJ70270	44501151	unknown[environmentalsequence]
EAJ99006	44543462	unknown[environmentalsequence]
EAI44821	44321908	unknown[environmentalsequence]
AAV29123	54112979	NT02FT0667[syntheticconstruct]
EAI27648	44296619	unknown[environmentalsequence]
Q5QW40	67460201	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
ZP_004...	67546996	Chorismatesynthase[BurkholderiavietnamiensisG4]
EAJ59012	44483458	unknown[environmentalsequence]
Q83D67	67460387	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)

Q7VRU6	67460367	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
EAJ87211	44526318	unknown[environmentalsequence]
ZP_005...	68555811	ChorismatesynthaseRalstoniametalliduransCH34]
EAJ56902	44480510	unknown[environmentalsequence]
ZP_009...	84321644	COG0082:ChorismatesynthasePseudomonasaeruginosaC3719]
EAH98922	44254138	unknown[environmentalsequence]
EAJ54935	44477846	unknown[environmentalsequence]
ZP_005...	68213830	ChorismatesynthaseMethylobacillusflagellatusKT]
EAJ45490	44464541	unknown[environmentalsequence]
Q60AY5	67460234	Chorismatesynthase(5-enolpyruvylshikimate-3-phosphatephospholyase)
EAI53063	44333485	unknown[environmentalsequence]
ZP_001...	32041730	COG0082:ChorismatesynthasePseudomonasaeruginosaUCBPP-PA14]
EAI90416	44385937	unknown[environmentalsequence]

Table 36: Examples of DAHP Synthase polypeptides.

Accession	GI	Description
XP_447238	50289613	unnamed protein product [Candida glabrata]
AAS55983	45269207	YDR035W [Saccharomyces cerevisiae]
NP_982845	45185128	ABL102Cp [Eremothecium gossypii]
XP_461930	50426665	hypothetical protein DEHA0G09584 [Debaryomyces hansenii CBS767]
P34725	461538	Phenylalanine-inhibited DAHP synthase
XP_501119	50547299	hypothetical protein [Yarrowia lipolytica]
EAQ92521	88185053	conserved hypothetical protein [Chaetomium globosum CBS 148.51]
XP_380654	46107190	conserved hypothetical protein [Gibberella zeae PH-1]
XP_657958	67516145	hypothetical protein AN0354.2 [Aspergillus nidulans FGSC A4]
AAG36950	11527262	phe-inhibited DAHP synthase [Aspergillus nidulans]
BAE55893	83765750	unnamed protein product [Aspergillus oryzae]
XP_749961	70990224	phospho-2-dehydro-3-deoxyheptonate aldolase [Aspergillus fumigatus Af293]
XP_963757	85111064	hypothetical protein [Neurospora crassa N150]
1OG0H	48425119	Chain H, Crystal Structure Of The Mutant G226s Of The Tyrosine-Regulated DAHP synthase From S. cerevisiae
1OF6H	49258352	Chain H, Crystal Structure Of The Tyrosine-Regulated DAHP synthase From Saccharomyces Cerevisiae
XP_388514	46127921	hypothetical protein FG08338.1 [Gibberella zeae PH-1]
XP_710729	68490922	tyrosine-sensitive DAHP synthase [Candida albicans SC5314]
NP_985501	45198472	AFL047Wp [Eremothecium gossypii]
XP_445243	50285629	unnamed protein product [Candida glabrata]
XP_456529	50405777	hypothetical protein DEHA0A04796g [Debaryomyces hansenii CBS767]
XP_960510	85097818	hypothetical protein [Neurospora crassa N150]
EAQ84788	88177320	conserved hypothetical protein [Chaetomium globosum CBS 148.51]
XP_749101	70987245	phospho-2-dehydro-3-deoxyheptonate aldolase [Aspergillus fumigatus Af293]
XP_455377	50310711	unnamed protein product [Kluyveromyces lactis]
NP_594946	19115858	hypothetical protein SPAP8A3.07c [Schizosaccharomyces pombe 972h-]
AAX07693	59803020	phospho-2-dehydro-3-deoxyheptonate aldolase-like protein [Magnaporthe grisea]
XP_663305	67539062	hypothetical protein AN5701.2 [Aspergillus nidulans FGSC A4]
BAE55202	83765059	unnamed protein product [Aspergillus oryzae]
XP_722423	68467016	hypothetical protein CaO19_9092 [Candida albicans SC5314]
NP_592942	19113854	hypothetical protein SPAC24H6.10c [Schizosaccharomyces pombe 972h-]
XP_758532	71012850	hypothetical protein UM02385.1 [Ustilago maydis 521]
YP_391662	78485737	phospho-2-dehydro-3-deoxyheptonate aldolase [Thiomicrospira crunogena XCL-2]
AAX51844	61676641	3-deoxy-7-phosphoheptulonate synthase [Paxillus involutus]
YP_206352	59713577	3-deoxy-7-phosphoheptulonate synthase [Vibrio fischeri ES114]
YP_049487	50120320	3-deoxy-7-phosphoheptulonate synthase [Erwinia carotovora subsp. atroseptica SCRI1043]

EAJ93797	44535951	unknown [environmental sequence]
XP_568187	58261554	phospho-2-dehydro-3-deoxyheptonate aldolase [Cryptococcus neoformans var.neoformans JEC21]
EAL19008	50256282	hypothetical protein CNBI0210 [Cryptococcus neoformans var. neoformans B-3501A]
XP_759307	71018153	hypothetical protein UM03160.1 [Ustilago maydis 521]
ZP_004...	67542259	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Burkholderia vietnamiensis G4]
XP_570499	58266686	3-deoxy-7-phosphoheptulonate synthase [Cryptococcus neoformans var. neoformans JEC21]
YP_286523	71908936	3-deoxy-7-phosphoheptulonate synthase [Dechloromonas aromatica RCB]
YP_460636	85858434	phospho-2-dehydro-3-deoxyheptonate aldolase [Syntrophus aciditrophicus SB]
YP_309691	74311272	3-deoxy-7-phosphoheptulonate synthase [Shigella sonnei Ss046]
NP_883658	33596015	3-deoxy-7-phosphoheptulonate synthase [Bordetella parapertussis 12822]
NP_888962	33601402	3-deoxy-7-phosphoheptulonate synthase [Bordetella bronchiseptica RB50]
ZP_009...	83584861	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Escherichia coli 101-1]
YP_151203	56414128	3-deoxy-7-phosphoheptulonate synthase [Salmonella enterica ATCC 9150]
ZP_007...	75189768	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Escherichia coli E24377A]
1N8FD	30749576	Chain D, Crystal Structure Of E24q Mutant Of Phenylalanine-Regulated Dahp Synthase From Escherichia Coli
NP_953340	39997389	3-deoxy-7-phosphoheptulonate synthase [Geobacter sulfurreducens PCA]
ZP_004...	67664891	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Burkholderia cenocepacia HI2424]
ZP_006...	74018758	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Burkholderia ambifaria AMMD]
ZP_007...	75237090	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Escherichia coli F11]
NP_640898	21241316	3-deoxy-7-phosphoheptulonate synthase [Xanthomonas axonopodis pv. citri str. 306]
ZP_007...	75831890	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Vibrio cholerae MO10]
YP_370847	78060939	3-deoxy-7-phosphoheptulonate synthase [Burkholderia sp. 383]
YP_215746	62179329	3-deoxy-7-phosphoheptulonate synthase [Salmonella enterica subsp. enterica str. SC-B67]
NP_752760	26246720	3-deoxy-7-phosphoheptulonate synthase [Escherichia coli CFT073]
ZP_007...	75235771	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Escherichia coli E110019]
NP_884719	33597076	3-deoxy-7-phosphoheptulonate synthase [Bordetella parapertussis 12822]
NP_805875	29142533	3-deoxy-7-phosphoheptulonate synthase [Salmonella enterica subsp. enterica serovar Typhi Ty2]
NP_928766	37525422	3-deoxy-7-phosphoheptulonate synthase [Photorhabdus luminescens subsp. laumondii TTO1]
YP_454573	85058871	3-deoxy-D-arabino-heptulosonate-7-phosphate synthase [Sodalis glossinidius str. 'morsitans']

ZP_009...	84360842	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Burkholderia dolosa AUO158]
NP_273357	15676225	3-deoxy-7-phosphoheptulonate synthase [Neisseria meningitidis MC58]
ZP_004...	67547628	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Burkholderia vietnamiensis G4]
NP_459740	16764125	3-deoxy-7-phosphoheptulonate synthase [Salmonella typhimurium LT2]
NP_888480	33600920	3-deoxy-7-phosphoheptulonate synthase [Bordetella bronchiseptica RB50]
ZP_008...	78696746	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Bradyrhizobium sp. BTAi1]
YP_362305	78046130	3-deoxy-7-phosphoheptulonate synthase [Xanthomonas campestris pv.vesicatoria str. 85-10]
AAW77538	58428501	phospho-2-dehydro-3-deoxyheptonate aldolase, phe-sensitive [Xanthomonas oryzae pv. oryzae KACC10331]
YP_453068	84625696	phospho-2-dehydro-3-deoxyheptonate aldolase [Xanthomonas oryzae pv. oryzae MAFF 311018]
NP_836261	30062090	3-deoxy-7-phosphoheptulonate synthase [Shigella flexneri 2a str. 2457T]
ZP_009...	83568956	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Shigella dysenteriae 1012]
ZP_006...	74017092	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Burkholderia ambifaria AMMD]
NP_800695	28901040	3-deoxy-7-phosphoheptulonate synthase [Vibrio parahaemolyticus RIMD 2210633]
YP_368071	78065302	3-deoxy-7-phosphoheptulonate synthase [Burkholderia sp. 383]
NP_284873	15795051	3-deoxy-7-phosphoheptulonate synthase [Neisseria meningitidis Z2491]
ZP_006...	69298960	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Silicibacter sp. TM1040]
ZP_007...	75820777	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Vibrio cholerae V51]
NP_899843	34495628	3-deoxy-7-phosphoheptulonate synthase [Chromobacterium violaceum ATCC 12472]
ZP_009...	84353080	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Burkholderia cenocepacia PC184]
YP_295249	73540729	3-deoxy-7-phosphoheptulonate synthase [Ralstonia eutropha JMP134]
YP_241649	66766887	3-deoxy-7-phosphoheptulonate synthase [Xanthomonas campestris pv.campestris str. 8004]
NP_840905	30248835	3-deoxy-7-phosphoheptulonate synthase [Nitrosomonas europaea ATCC 19718]
YP_441842	83718583	phospho-2-dehydro-3-deoxyheptonate aldolase [Burkholderia thailandensis E264]
NP_762515	27366988	3-deoxy-7-phosphoheptulonate synthase [Vibrio vulnificus CMCP6]
NP_771029	27379500	3-deoxy-7-phosphoheptulonate synthase [Bradyrhizobium japonicum USDA 110]
ZP_009...	84356885	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Burkholderia cenocepacia PC184]
EAK32325	44590917	unknown [environmental sequence]
ZP_009...	84358961	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Burkholderia dolosa AUO158]

NP_937162	37676766	3-deoxy-7-phosphoheptulonate synthase [Vibrio vulnificus YJ016]
YP_269491	71282168	3-deoxy-7-phosphoheptulonate synthase [Colwellia psychrerythraea 34H]
YP_088376	52425239	3-deoxy-7-phosphoheptulonate synthase [Mannheimia succiniciproducens MBEL55E]
YP_334707	76808557	3-deoxy-7-phosphoheptulonate synthase [Burkholderia pseudomallei 1710b]
ZP_009...	83677258	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Burkholderia pseudomallei 406e]
ZP_006...	71900167	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Xylella fastidiosa Ann-1]
ZP_006...	68562271	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Rubrobacter xylanophilus DSM 9941]
ZP_010...	86144399	3-deoxy-7-phosphoheptulonate synthase [Vibrio sp. MED222]
YP_208731	59802019	3-deoxy-7-phosphoheptulonate synthase [Neisseria gonorrhoeae FA 1090]
1KFLH	23200241	Chain H, Phenylalanine-Regulated 3-Deoxy-D- Arabino-Heptulosonate-7-Phosphate Synthase (Dahp Synthase)
ZP_004...	67674181	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Burkholderia pseudomallei 1655]
NP_778276	77747623	3-deoxy-7-phosphoheptulonate synthase [Xylella fastidiosa Temecula1]
AAO27925	28056022	phospho-2-dehydro-3-deoxyheptonate aldolase [Xylella fastidiosa Temecula1]
NP_297319	77747482	3-deoxy-7-phosphoheptulonate synthase [Xylella fastidiosa 9a5c]
AAF82839	9104790	phospho-2-dehydro-3-deoxyheptonate aldolase [Xylella fastidiosa 9a5c]
ZP_010...	84523704	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Burkholderia mallei SAVP1]
ZP_009...	82742183	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Shewanella sp. W3-18-1]
EAK46973	44611560	unknown [environmental sequence]
ZP_008...	77815397	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Shewanella putrefaciens CN-32]
ZP_006...	71549218	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Nitrosomonas eutropha C71]
ZP_008...	77688859	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Rhodopseudomonas palustris BisB5]
ZP_001...	53732821	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Haemophilus influenzae R2846]
AAN31488	23394399	DAHP synthase [Phytophthora infestans]
ZP_010...	87316601	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Burkholderia mallei 2002721280]
ZP_006...	71899720	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Xylella fastidiosa Ann-1]
ZP_005...	68178152	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Desulfuromonas acetoxidans DSM 684]
YP_343507	77164982	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Nitrosococcus oceani ATCC 19707]
ZP_005...	68555668	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Ralstonia metallidurans CH34]
ZP_009...	83746166	Phospho-2-dehydro-3-deoxyheptonate aldolase [Ralstonia

		solanacearum UW551]
ZP_010...	87315604	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Burkholderia mallei 2002721280]
ZP_009...	84387592	3-deoxy-7-phosphoheptulonate synthase [Vibrio splendidus 12B01]
YP_132933	54302940	3-deoxy-7-phosphoheptulonate synthase [Photobacterium profundum SS9]
YP_290406	72162749	phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Thermobifida fusca YX]
ZP_007...	75829548	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Vibrio cholerae MO10]
ZP_007...	75824087	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Vibrio cholerae RC385]
YP_157562	56475973	3-deoxy-7-phosphoheptulonate synthase [Azoarcus sp. EbN1]
ZP_008...	77976568	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Yersinia intermedia ATCC 29909]
NP_945383	39933107	3-deoxy-7-phosphoheptulonate synthase [Rhodopseudomonas palustris CGA009]
ZP_007...	75819386	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Vibrio cholerae V51]
YP_249050	68249938	3-deoxy-7-phosphoheptulonate synthase [Haemophilus influenzae 86-028NP]
NP_439696	16273447	3-deoxy-7-phosphoheptulonate synthase [Haemophilus influenzae Rd KW20]
ZP_002...	48786648	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Burkholderia fungorum LB400]
ZP_001...	42631619	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Haemophilus influenzae R2866]
NP_873888	33152535	3-deoxy-7-phosphoheptulonate synthase [Haemophilus ducreyi 35000HP]
ZP_007...	77636410	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Yersinia pestis Angola]
BAB51519	14024917	2-dehydro-3-deoxyphosphoheptonate aldolase [Mesorhizobium loti MAFF303099]
EAH95568	44249284	unknown [environmental sequence]
NP_245500	15602428	3-deoxy-7-phosphoheptulonate synthase [Pasteurella multocida subsp. multocida str. Pm70]
ZP_007...	75826054	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Vibrio cholerae O395]
NP_518864	17545462	3-deoxy-7-phosphoheptulonate synthase [Ralstonia solanacearum GMI1000]
ZP_008...	78685198	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Shewanella sp. ANA-3]
ZP_005...	68544665	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Shewanella baltica OS155]
EAI90598	44386184	unknown [environmental sequence]
ZP_008...	77973952	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Yersinia frederiksenii ATCC 33641]
NP_796925	28897320	3-deoxy-7-phosphoheptulonate synthase [Vibrio parahaemolyticus RIMD 2210633]
ZP_006...	69952674	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Shewanella frigidimarina NCIMB 400]
ZP_010...	86135796	phospho-2-dehydro-3-deoxyheptonate aldolase [Roseobacter sp. MED193]

ZP_006...	69953103	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Shewanella frigidimarina NCIMB 400]
NP_819990	29654298	3-deoxy-7-phosphoheptulonate synthase [Coxiella burnetii RSA 493]
ZP_002...	48783624	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Burkholderia fungorum LB400]
YP_314272	74316532	3-deoxy-7-phosphoheptulonate synthase [Thiobacillus denitrificans ATCC 25259]
EAK66242	44638614	unknown [environmental sequence]
ZP_008...	77960615	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Yersinia mollaretii ATCC 43969]
NP_716387	24372345	3-deoxy-7-phosphoheptulonate synthase [Shewanella oneidensis MR-1]
ZP_008...	78689982	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Shewanella sp. MR-7]
ZP_008...	82494841	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Shewanella sp. MR-4]
ZP_001...	32035348	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Actinobacillus pleuropneumoniae]
XP_746312	70981566	phospho-2-dehydro-3-deoxyheptonate aldolase [Aspergillus fumigatus Af293]
YP_385325	78223578	3-deoxy-7-phosphoheptulonate synthase [Geobacter metallireducens GS-15]
EAJ18299	44425730	unknown [environmental sequence]
ZP_007...	75430869	3-deoxy-7-phosphoheptulonate synthase [Actinobacillus succinogenes 130Z]
EAK54737	44622389	unknown [environmental sequence]
EAK47950	44612934	unknown [environmental sequence]
YP_439321	83717638	phospho-2-dehydro-3-deoxyheptonate aldolase [Burkholderia thailandensis E264]
ZP_007...	75854868	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Vibrio sp. Ex25]
ZP_008...	77956874	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Yersinia bercovieri ATCC 43970]
ZP_009...	83747243	Phospho-2-dehydro-3-deoxyheptonate aldolase [Ralstonia solanacearum UW551]
ZP_006...	69945782	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Shewanella denitrificans OS-217]
YP_433739	83645304	phospho-2-dehydro-3-deoxyheptonate aldolase [Hahella chejuensis KCTC 2396]
YP_466161	86159376	phospho-2-dehydro-3-deoxyheptonate aldolase [Anaeromyxobacter dehalogenans 2CP-C]
ZP_001...	32030060	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Haemophilus somnus 2336]
YP_469876	86357984	phospho-2-dehydro-3-deoxyheptonate aldolase protein, Phe-sensitive [Rhizobium etli CFN 42]
EAK21196	44574903	unknown [environmental sequence]
EAK21185	44574888	unknown [environmental sequence]
NP_520781	17547379	3-deoxy-7-phosphoheptulonate synthase [Ralstonia solanacearum GMI1000]
EAI94964	44392288	unknown [environmental sequence]
EAJ01592	44401791	unknown [environmental sequence]
YP_046933	50085423	3-deoxy-7-phosphoheptulonate synthase [Acinetobacter sp.

		ADP1]
EAI46330	44323998	unknown [environmental sequence]
NP_873017	33151664	3-deoxy-7-phosphoheptulonate synthase [Haemophilus ducreyi 35000HP]
ZP_007...	75429314	3-deoxy-7-phosphoheptulonate synthase [Actinobacillus succinogenes 130Z]
ZP_009...	84393583	3-deoxy-7-phosphoheptulonate synthase [Vibrio splendidus 12B01]
EAJ15572	44421750	unknown [environmental sequence]
ZP_002...	47573313	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Rubrivivax gelatinosus PM1]
ZP_005...	68557629	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Ralstonia metallidurans CH34]
ZP_004...	67677476	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Chromohalobacter salexigens DSM 3043]
ZP_010...	86148427	3-deoxy-7-phosphoheptulonate synthase [Vibrio sp. MED222]
ZP_006...	69944508	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Shewanella denitrificans OS-217]
NP_716981	24372939	3-deoxy-7-phosphoheptulonate synthase [Shewanella oneidensis MR-1]
ZP_006...	69943657	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Shewanella denitrificans OS-217]
YP_131156	54310136	3-deoxy-7-phosphoheptulonate synthase [Photobacterium profundum SS9]
ZP_006...	74020452	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Rhodoferax ferrireducens DSM 15236]
YP_088296	52425159	3-deoxy-7-phosphoheptulonate synthase [Mannheimia succiniciproducens MBEL55E]
YP_051441	50122274	3-deoxy-7-phosphoheptulonate synthase [Erwinia carotovora subsp. atroseptica SCRI1043]
YP_298478	73538111	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Ralstonia eutropha JMP134]
EAJ50911	44472105	unknown [environmental sequence]
ZP_003...	48863129	COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Microbulbifer degradans 2-40]
ZP_008...	82496144	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1 [Shewanella sp. MR-4]

Table 37: Examples of Transketolase polypeptides.

Accession	GI	Description
1TKCB	809445	Chain B, Transketolase (E.C.2.2.1.1) Complexed With 6'-Methyl-Thiamin Diphosphate And Calcium
1AY0B	3212469	Chain B, Identification Of Catalytically Important Residues In Yeast Transketolase
XP_445471	50286085	unnamed protein product [Candida glabrata]
AAA35168	173022	transkelotase
XP_451936	50303973	TKT1_KLULA [Kluyveromyces lactis]
NP_983730	45187507	ADL366Wp [Eremothecium gossypii]
NP_009675	6319593	Transketolase, similar to Tkl1p; needed for synthesis of aromatic amino acids; Tkl2p
XP_460538	50423907	hypothetical protein DEHA0F04378g [Debaryomyces hansenii CBS767]
O94039	18202255	Transketolase 1 (TK 1)
XP_717574	68476858	hypothetical protein CaO19_12578 [Candida albicans SC5314]
XP_503628	50552436	hypothetical protein [Yarrowia lipolytica]
XP_390174	46136965	conserved hypothetical protein [Gibberella zeae PH-1]
P34736	464895	Transketolase (TK)
CAC18218	11595598	probable TRANSKETOLASE [Neurospora crassa]
XP_961414	85102892	hypothetical protein ((AL451017) probable TRANSKETOLASE [Neurospora crassa N150])
EAQ90716	88183248	conserved hypothetical protein [Chaetomium globosum CBS 148.51]
XP_752720	70995930	transketolase TktA [Aspergillus fumigatus Af293]
BAE60691	83770558	unnamed protein product [Aspergillus oryzae]
XP_570402	58266492	hypothetical protein [Cryptococcus neoformans var.neoformans JEC21]
CAF32073	42820760	transketolase, putative [Aspergillus fumigatus]
XP_658292	67516813	hypothetical protein AN0688.2 [Aspergillus nidulans FGSC A4]
CAD80256	29409959	transketolase [Aspergillus niger]

Q9URM2	41688744	Probable transketolase (TK)
XP_761114	71021767	hypothetical protein UM04967.1 [Ustilago maydis 521]
NP_682660	22299413	transketolase [Thermosynechococcus elongatus BP-1]
YP_399557	81299349	transketolase [Synechococcus elongatus PCC 7942]
ZP_001...	23124098	COG0021: Transketolase [Nostoc punctiforme PCC 73102]
YP_475736	86606973	transketolase [Cyanobacteria bacterium Yellowstone A-Prime]
YP_477359	86608597	transketolase [Cyanobacteria bacterium Yellowstone B-Prime]
EAI59672	44342928	unknown [environmental sequence]
NP_895782	33864222	transketolase [Prochlorococcus marinus str. MIT 9313]
YP_398200	78780088	transketolase [Prochlorococcus marinus str. MIT 9312]
CAJ05341	68126790	transketolase, putative [Leishmania major]
ZP_010...	84519077	transketolase [Prochlorococcus marinus str. MIT 9211]
1R9JB	56965909	Chain B, Transketolase From Leishmania Mexicana
CAD20572	22217844	transketolase [Leishmania mexicana mexicana]
XP_823559	71898191	transketolase [Trypanosoma brucei TREU927]
EAJ68618	44498674	unknown [environmental sequence]
XP_817929	71661828	transketolase [Trypanosoma cruzi strain CL Brener]
YP_376186	78183752	transketolase [Synechococcus sp. CC9902]
ZP_010...	87123206	transketolase [Synechococcus sp. RS9917]
ZP_010...	87301979	transketolase [Synechococcus sp. WH 5701]
YP_324146	75909850	transketolase [Anabaena variabilis ATCC 29413]
YP_292380	72383025	transketolase [Prochlorococcus marinus str. NATL2A]
NP_487384	17230836	transketolase [Nostoc sp. PCC 7120]
YP_380455	78211676	transketolase [Synechococcus sp. CC9605]
NP_876161	33241219	transketolase [Prochlorococcus marinus subsp. marinus str. CCMP1375]
NP_893727	33862166	transketolase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]
NP_896236	33864677	transketolase [Synechococcus sp. WH 8102]
CAA75777	3559814	transketolase 1 [Capsicum annuum]
S58083	2117700	transketolase (EC 2.2.1.1) precursor - potato (fragment)
NP_440630	16329902	transketolase [Synechocystis sp. PCC 6803]
Q43848	2501356	Transketolase, chloroplast precursor (TK)
NP_925243	37521866	transketolase [Gloeobacter violaceus PCC 7421]
AAO29950	28058762	Unknown protein [Arabidopsis thaliana]
AAM91794	22136900	putative transketolase [Arabidopsis thaliana]
ZP_006...	71675415	transketolase [Trichodesmium erythraeum IMS101]
AAM62766	21553673	transketolase-like protein [Arabidopsis thaliana]
Q42677	2501354	Transketolase 7 (TK)
CAB82679	7329685	transketolase-like protein [Arabidopsis thaliana]
1ITZC	28948384	Chain C, Maize Transketolase In Complex With Tpp
AAN65341	25067747	thioredoxin/transketolase fusion protein [synthetic construct]
YP_147185	56419867	transketolase [Geobacillus kaustophilus HTA426]
O20250	68052991	Transketolase, chloroplast precursor (TK)
YP_091619	52785790	Tkt [Bacillus licheniformis ATCC 14580]
AAO33154	28190676	putative transketolase [Oryza sativa (japonica cultivar-group)]
YP_313917	74316177	transketolase [Thiobacillus denitrificans ATCC 25259]
NP_980015	42782768	transketolase [Bacillus cereus ATCC 10987]
Q42675	2501355	Transketolase 10 (TK)
AAW79357	58613541	chloroplast transketolase [Heterocapsa triquetra]
NP_833410	30021779	transketolase [Bacillus cereus ATCC 14579]
ZP_002...	47569206	transketolase [Bacillus cereus G9241]
YP_084972	52141859	transketolase [Bacillus cereus E33L]
CAB58135	6048212	putative transketolase precursor [Cyanophora paradoxa]
YP_029725	49186473	transketolase [Bacillus anthracis str. Sterne]

Q9KAD7	18203172	Transketolase (TK)
YP_037757	49478325	transketolase [Bacillus thuringiensis serovar konkukian str. 97-27]
NP_957656	41057053	putative transketolase [Bacillus methanolicus]
XP_966097	86170850	transketolase [Plasmodium falciparum 3D7]
XP_743287	70947319	transketolase [Plasmodium chabaudi chabaudi]
NP_389672	16078852	transketolase [Bacillus subtilis subsp. subtilis str. 168]
YP_143374	55980077	transketolase [Thermus thermophilus HB8]
YP_174605	56962878	transketolase [Bacillus clausii KSM-K16]
ZP_006...	71549767	transketolase [Nitrosomonas eutropha C71]
YP_005865	46200198	transketolase [Thermus thermophilus HB27]
XP_731078	83317250	transketolase [Plasmodium yoelii yoelii str. 17XNL]
NP_840415	30248345	transketolase [Nitrosomonas europaea ATCC 19718]
NP_621887	20806716	Transketolase [Thermoanaerobacter tengcongensis MB4]
YP_460297	85858095	transketolase [Syntrophus aciditrophicus SB]
ZP_003...	65320951	COG0021: Transketolase [Bacillus anthracis str. A2012]
ZP_001...	46143789	COG0021: Transketolase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]
ZP_010...	84713578	transketolase [Polaromonas naphthalenivorans CJ2]
YP_329002	76787695	transketolase [Streptococcus agalactiae A909]
ZP_001...	23467867	COG0021: Transketolase [Haemophilus somnus 129PT]
ZP_001...	32029978	COG0021: Transketolase [Haemophilus somnus 2336]
YP_441742	83719441	transketolase [Burkholderia thailandensis E264]
NP_734737	25010342	transketolase [Streptococcus agalactiae NEM316]
ZP_009...	84360784	COG0021: Transketolase [Burkholderia dolosa AUO158]
ZP_006...	74019726	transketolase [Burkholderia ambifaria AMMD]
AAB82634	20196914	putative transketolase precursor [Arabidopsis thaliana]
EAK32589	44591183	unknown [environmental sequence]
ZP_003...	66797882	transketolase [Deinococcus geothermalis DSM 11300]
NP_687313	22536462	transketolase [Streptococcus agalactiae 2603V/R]
YP_248708	68249596	transketolase [Haemophilus influenzae 86-028NP]
ZP_002...	48785143	COG0021: Transketolase [Burkholderia fungorum LB400]
ZP_007...	75856523	COG0021: Transketolase [Vibrio sp. Ex25]
YP_115427	53802849	transketolase [Methylococcus capsulatus str. Bath]
YP_115433	53802834	transketolase [Methylococcus capsulatus str. Bath]
Q7MDD4	81755355	Transketolase 2 (TK 2)
YP_109547	53720561	transketolase [Burkholderia pseudomallei K96243]
YP_334838	76811793	transketolase [Burkholderia pseudomallei 1710b]
ZP_004...	67666970	transketolase [Burkholderia cenocepacia HI2424]
ZP_009...	84385129	transketolase [Vibrio splendidus 12B01]
ZP_001...	46133244	COG0021: Transketolase [Haemophilus influenzae R2866]
NP_439183	16272957	transketolase [Haemophilus influenzae Rd KW20]
ZP_009...	83680107	COG0021: Transketolase [Burkholderia pseudomallei 406e]
ZP_009...	84356730	COG0021: Transketolase [Burkholderia cenocepacia PC184]
ZP_001...	42630153	COG0021: Transketolase [Haemophilus influenzae R2846]
Q8D6H8	81447400	Transketolase 2 (TK 2)
YP_367967	78065198	transketolase [Burkholderia sp. 383]
NP_662747	21674682	transketolase [Chlorobium tepidum TLS]
YP_104015	53725663	transketolase [Burkholderia mallei ATCC 23344]
Q87GY4	81725569	Transketolase 2 (TK 2)
NP_899861	34495646	transketolase [Chromobacterium violaceum ATCC 12472]
ZP_010...	86144326	transketolase [Vibrio sp. MED222]
ZP_004...	67737605	COG0021: Transketolase [Burkholderia pseudomallei 668]
Q5DZP0	75352704	Transketolase 2 (TK 2)

ZP_005...	67761770	COG0021: Transketolase [Burkholderia pseudomallei S13]
ZP_009...	82747679	transketolase [Clostridium beijerincki NCIMB 8052]
ZP_007...	75437583	transketolase [Actinobacillus succinogenes 130Z]
NP_786741	28379849	transketolase [Lactobacillus plantarum WCFS1]
ZP_010...	85065618	COG0021: Transketolase [Burkholderia mallei 10229]
YP_181386	57234617	transketolase [Dehalococcoides ethenogenes 195]
YP_344785	77166260	transketolase [Nitrosococcus oceani ATCC 19707]
NP_692593	23099127	transketolase [Oceanobacillus iheyensis HTE831]
ZP_009...	82744860	transketolase [Clostridium beijerincki NCIMB 8052]
ZP_004...	67546170	transketolase [Burkholderia vietnamiensis G4]
ZP_009...	82746570	transketolase [Clostridium beijerincki NCIMB 8052]
NP_756618	26250578	transketolase [Escherichia coli CFT073]
YP_156595	56461314	transketolase [Idiomarina loihiensis L2TR]
YP_087249	52424112	transketolase [Mannheimia succiniciproducens MBEL55E]
NP_760436	27364908	transketolase [Vibrio vulnificus CMCP6]
ZP_009...	82748032	transketolase [Clostridium beijerincki NCIMB 8052]
ZP_007...	75825874	COG0021: Transketolase [Vibrio cholerae O395]
NP_274468	15677313	transketolase [Neisseria meningitidis MC58]
NP_874093	33152740	transketolase [Haemophilus ducreyi 35000HP]
NP_230127	15640500	transketolase [Vibrio cholerae O1 biovar eltor str. N16961]
NP_470679	16800411	tkt [Listeria innocua Clip11262]
ZP_007...	75817228	COG0021: Transketolase [Vibrio cholerae V52]
ZP_007...	75825446	COG0021: Transketolase [Vibrio cholerae O395]
NP_347580	15894231	Transketolase [Clostridium acetobutylicum ATCC 824]
NP_284385	15794563	transketolase [Neisseria meningitidis Z2491]
ZP_007...	75818756	COG0021: Transketolase [Vibrio cholerae V51]
YP_175660	56963929	transketolase [Bacillus clausii KSM-K16]
XP_550612	55775372	putative transketolase 1 [Oryza sativa (japonica cultivar-group)]
ZP_007...	75820098	COG0021: Transketolase [Vibrio cholerae V51]
ZP_007...	75831530	COG0021: Transketolase [Vibrio cholerae MO10]
ZP_010...	85711777	Transketolase [Idiomarina baltica OS145]
NP_879793	33592149	transketolase [Bordetella pertussis Tohama I]
NP_887926	33600366	transketolase [Bordetella bronchiseptica RB50]
YP_208116	59801404	transketolase [Neisseria gonorrhoeae FA 1090]
BAB62078	14787119	transketolase [Polygonum tinctorium]
ZP_009...	83746772	Transketolase [Ralstonia solanacearum UW551]
ZP_009...	84394076	transketolase [Vibrio splendidus 12B01]
ZP_008...	77687242	transketolase [Alkaliphilus metalliredigenes QYMF]
Q87LK8	81726913	Transketolase 1 (TK 1)
ZP_007...	75823597	COG0021: Transketolase [Vibrio cholerae RC385]
NP_233013	15601382	transketolase [Vibrio cholerae O1 biovar eltor str. N16961]
ZP_007...	76258375	transketolase [Chloroflexus aurantiacus J-10-fl]
NP_883480	33595837	transketolase [Bordetella parapertussis 12822]
AAL98225	19748806	putative transketolase [Streptococcus pyogenes MGAS8232]
NP_246179	15603107	transketolase [Pasteurella multocida subsp. multocida str. Pm70]
NP_801666	28895316	transketolase [Streptococcus pyogenes SSI-1]
YP_013921	46907532	transketolase [Listeria monocytogenes str. 4b F2365]
NP_269713	15675539	transketolase [Streptococcus pyogenes M1 GAS]
YP_282738	71911188	transketolase [Streptococcus pyogenes MGAS5005]
NP_464830	16803345	hypothetical protein lmo1305 [Listeria monocytogenes EGD-e]
ZP_010...	86146387	transketolase [Vibrio sp. MED222]
NP_520871	17547469	transketolase [Ralstonia solanacearum GMI1000]
YP_278020	71892286	transketolase [Candidatus Blochmannia pennsylvanicus str. BPEN]

ZP_005...	68055292	transketolase [Exiguobacterium sibiricum 255-15]
NP_246577	15603503	transketolase [Pasteurella multocida subsp. multocida str. Pm70]
ZP_007...	75240114	COG0021: Transketolase [Escherichia coli F11]
NP_708304	56480111	transketolase [Shigella flexneri 2a str. 301]
ZP_009...	83586887	COG0021: Transketolase [Escherichia coli 101-1]
ZP_002...	47096930	transketolase [Listeria monocytogenes str. 1/2a F6854]
ZP_002...	47573633	COG0021: Transketolase [Rubrivivax gelatinosus PM1]
YP_060741	50914769	transketolase [Streptococcus pyogenes MGAS10394]
YP_307719	73748480	transketolase [Dehalococcoides sp. CBDB1]
NP_928282	37524938	transketolase [Photorhabdus luminescens subsp. laumondii TTO1]
ZP_007...	75196470	COG0021: Transketolase [Escherichia coli HS]
NP_935655	37681046	transketolase [Vibrio vulnificus YJ016]
YP_411088	82701522	transketolase [Nitrosospira multiformis ATCC 25196]
ZP_007...	75237651	COG0021: Transketolase [Escherichia coli F11]
ZP_007...	75237792	COG0021: Transketolase [Escherichia coli E110019]
YP_311409	74312990	transketolase [Shigella sonnei Ss046]
NP_311354	15832581	transketolase [Escherichia coli O157:H7]

Table 38. Examples of carotenoid epsilon hydroxylase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
ABB52076	79155148	putative epsilon-ring carotene hydroxylase [Daucus carota subsp. sativus]
BAD94136	62319017	Cytochrom P450 -like protein [Arabidopsis thaliana]
ABD28565	87162770	E-class P450, group I [Medicago truncatula]
AAT28222	47498772	putative 97B2-like cytochrome P450 [Ginkgo biloba]
ABC68396	85001685	cytochrome P450 monooxygenase CYP97A [Glycine max]
ABC59110	84514203	cytochrome P450 monooxygenase CYP97B [Medicago truncatula]
NP_190881	42565881	LUT1 (LUTEIN DEFICIENT 1); oxygen binding [Arabidopsis thaliana]
ABB47954	78708979	cytochrome P450 monooxygenase, putative [Oryza sativa (japonica cultivar-group)]
NP_922604	37536604	putative cytochrome P450 monooxygenase [Oryza sativa (japonica cultivar-group)]

Table 39. Examples of lycopene cyclase polypeptides, beta and epsilon subunits.

ACCESSION	GI	PROTEIN DESCRIPTION
AAK07431	12746307	lycopene epsilon-cyclase [Adonis palaestina]
ABB52073	79154988	putative lycopene epsilon cyclase [Daucus carota subsp. sativus]
Q38932	27735211	Lycopene epsilon cyclase, chloroplast precursor
AAB53336	1399181	lycopene epsilon cyclase
AAG10428	9971816	epsilon cyclase [Tagetes erecta]
AAK07434	12746313	lycopene epsilon-cyclase [Lactuca sativa]
AAM45382	21360359	epsilon cyclase [Tagetes erecta]
O65837	11132841	Lycopene epsilon cyclase, chloroplast precursor
AAL69394	18419661	lycopene epsilon-cyclase [Spinacia oleracea]
BAE79549	87299433	lycopene epsilon-cyclase [Chrysanthemum x morifolium]
XP_463351	50901836	putative lycopene epsilon-cyclase [Oryza sativa (japonica cultivar-group)]
AAS48096	44887640	epsilon lycopene cyclase [Citrus sinensis]
AAX92679	62638188	lycopene epsilon cyclase [Citrus maxima]
AAL92114	19569601	lycopene epsilon-cyclase [Citrus x paradisi]
AAK07433	12746311	lycopene epsilon-cyclase [Solanum tuberosum]
AAL47019	17864021	lycopene epsilon-cyclase [Citrus sinensis]
AAT46065	48686703	chloroplast lycopene epsilon-cyclase precursor [Chlamydomonas reinhardtii]
BAD07293	40809769	lycopene epsilon-cyclase [Citrus limon]
BAD07285	40809753	lycopene epsilon-cyclase [Citrus sinensis]
BAD07277	40809737	lycopene epsilon-cyclase [Citrus unshiu]
EAJ62839	44489138	unknown [environmental sequence]
BAE43547	73993068	putative lycopene beta cyclase [Taxodium distichum var. distichum]
BAE43550	73993074	putative lycopene beta cyclase [Taxodium distichum var. distichum]
BAE43557	73993088	putative lycopene beta cyclase [Taxodium distichum var. imbricarium]
BAE43558	73993090	putative lycopene beta cyclase [Taxodium distichum var. imbricarium]
BAE43553	73993080	putative lycopene beta cyclase [Taxodium distichum var. imbricarium]
BAE43545	73993064	putative lycopene beta cyclase [Taxodium distichum var. distichum]
BAE43556	73993086	putative lycopene beta cyclase [Taxodium distichum var. imbricarium]
BAE43552	73993078	putative lycopene beta cyclase [Taxodium distichum var. distichum]
BAE43560	73993094	putative lycopene beta cyclase [Taxodium distichum var. imbricarium]
BAE43554	73993082	putative lycopene beta cyclase [Taxodium distichum var. imbricarium]
BAE43551	73993076	putative lycopene beta cyclase [Taxodium distichum var. distichum]
BAE43519	73993012	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43535	73993044	putative lycopene beta cyclase [Cryptomeria japonica]

BAE43541	73993056	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43542	73993058	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43517	73993008	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43534	73993042	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43537	73993048	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43533	73993040	putative lycopene beta cyclase [Cryptomeria japonica]
BAD02774	38603277	putative lycopene beta cyclase [Cryptomeria japonica]
BAD02766	38603261	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43540	73993054	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43514	73993002	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43544	73993062	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43538	73993050	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43528	73993030	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43546	73993066	putative lycopene beta cyclase [Taxodium distichum var. distichum]
BAE43526	73993026	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43543	73993060	putative lycopene beta cyclase [Cryptomeria japonica]
BAD02742	38603213	putative lycopene beta cyclase [Cryptomeria japonica]
BAD02770	38603269	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43522	73993018	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43559	73993092	putative lycopene beta cyclase [Taxodium distichum var. imbricarium]
BAE43527	73993028	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43548	73993070	putative lycopene beta cyclase [Taxodium distichum var. distichum]
AAF44700	14550425	lycopene beta-cyclase [Citrus sinensis]
BAE43555	73993084	putative lycopene beta cyclase [Taxodium distichum var. imbricarium]
BAE43549	73993072	putative lycopene beta cyclase [Taxodium distichum var. distichum]
AAU14144	51922063	lycopene beta-cyclase [Citrus sinensis]
AAN86060	27261727	lycopene cyclase [Citrus unshiu]
AAR89632	40756518	lycopene-beta-cyclase [Citrus maxima]
AAM21152	20530862	lycopene beta-cyclase [Citrus sinensis]
AAD38049	13959731	lycopene cyclase [Citrus x paradisi]
AAU05146	51511939	lycopene beta-cyclase [Citrus sinensis]
AAU05145	51511937	lycopene beta-cyclase [Citrus sinensis]
AAK07430	12746305	lycopene beta-cyclase [Adonis palaestina]
ABB72443	82394885	lycopene beta-cyclase [Citrus sinensis]
BAE79544	87299423	lycopene beta-cyclase [Chrysanthemum x morifolium]
BAE78471	85717882	lycopene beta cyclase [Taraxacum officinale]
Q43415	11133019	Lycopene beta cyclase, chloroplast precursor
AAF23013	6665782	lycopene epsilon-cyclase [Daucus carota]
ABB52071	79154899	putative lycopene beta cyclase [Daucus carota subsp. sativus]
AAW88382	59665024	lycopene beta-cyclase [Lycium barbarum]
AAG10429	9971818	beta cyclase [Tagetes erecta]
AAM45381	21360357	beta cyclase [Tagetes erecta]
AAM14335	20259239	putative lycopene beta cyclase [Arabidopsis thaliana]
AAO18661	27728515	lycopene beta-cyclase [Zea mays]
AAA81880	735882	lycopene cyclase
Q43503	11133022	Lycopene beta cyclase, chloroplast precursor
S66350	2129931	lycopene beta-cyclase (EC 5.5.1.-) - tomato
XP_464409	50905841	putative lycopene beta-cyclase [Oryza sativa (japonica

		cultivar-group)]
CAD70565	45237491	lycopene cyclase [Bixa orellana]
Q43578	11133025	Lycopene beta cyclase, chloroplast precursor
AAL92175	19569782	beta-lycopene cyclase [Sandersonia aurantiaca]
AAX54906	61742130	putative chloroplast lycopene beta cyclase precursor [Chlamydomonas reinhardtii]
S66349	2129954	lycopene beta-cyclase (EC 5.5.1.-) - common tobacco
AAG21133	10644119	chromoplast-specific lycopene beta-cyclase [Lycopersicon esculentum]
CAB92977	8247354	neoxanthin synthase [Solanum tuberosum]
CAB93342	8249885	neoxanthin synthase [Lycopersicon esculentum]
Q9SEA0	11131528	Capsanthin/capsorubin synthase, chloroplast precursor
Q42435	12643508	Capsanthin/capsorubin synthase, chloroplast precursor
AAO64977	37730608	lycopene beta cyclase [Haematococcus pluvialis]
Q40424	11133011	Lycopene beta cyclase, chloroplast precursor
ABB52072	79154940	putative capsanthin-capsorubin synthase [Daucus carota subsp. sativus]
AAQ02668	33304511	lycopene cyclase [Setaria italica]
CAA54961	840729	putative chromoplastic oxydo-reductase [Capsicum annuum]
EAJ62838	44489136	unknown [environmental sequence]
YP_401079	81300871	Lycopene cyclase, beta and epsilon [Synechococcus elongatus PCC 7942]
YP_172741	56752040	lycopene cyclase [Synechococcus elongatus PCC 6301]
ZP_011...	88808972	lycopene beta cyclase [Synechococcus sp. WH 7805]
EAK50052	44615956	unknown [environmental sequence]
NP_892751	33861190	putative lycopene epsilon cyclase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]
NP_875182	33240240	Lycopene epsilon cyclase [Prochlorococcus marinus subsp. marinus str. CCMP1375]
YP_382237	78213458	Lycopene cyclase, beta and epsilon [Synechococcus sp. CC9605]
YP_397130	78779018	Lycopene cyclase, beta and epsilon [Prochlorococcus marinus str. MIT 9312]
NP_896821	33865262	lycopene beta cyclase [Synechococcus sp. WH 8102]
YP_397570	78779458	Lycopene cyclase, beta and epsilon [Prochlorococcus marinus str. MIT 9312]
ZP_010...	87302144	lycopene cyclase [Synechococcus sp. WH 5701]
EAK17149	44569190	unknown [environmental sequence]
YP_291882	72382527	lycopene cyclase, beta and epsilon [Prochlorococcus marinus str. NATL2A]
NP_875528	33240586	Lycopene beta cyclase related dehydrogenase [Prochlorococcus marinus subsp. marinus str. CCMP1375]
NP_893181	33861620	putative lycopene beta cyclase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]
NP_895600	33864040	putative lycopene epsilon cyclase [Prochlorococcus marinus str. MIT 9313]
EAI47456	44325573	unknown [environmental sequence]
YP_291268	72381913	lycopene cyclase, beta and epsilon [Prochlorococcus marinus str. NATL2A]
ZP_010...	84517806	Lycopene beta cyclase related dehydrogenase [Prochlorococcus marinus str. MIT 9211]
AAF34191	6970079	lycopene epsilon cyclase [Daucus carota]
ZP_010...	84518202	Lycopene epsilon cyclase [Prochlorococcus marinus str. MIT

		9211]
YP_376736	78184301	Lycopene cyclase, beta and epsilon [Synechococcus sp. CC9902]
ZP_003...	66796756	Lycopene cyclase, beta and epsilon [Deinococcus geothermalis DSM 11300]
NP_894954	33863394	putative lycopene beta cyclase [Prochlorococcus marinus str. MIT 9313]
AAT76051	50365502	lycopene cyclase [Citrus clementina]
EAK22047	44576122	unknown [environmental sequence]
NP_294525	15805827	lycopene cyclase [Deinococcus radiodurans R1]

Table 40. Examples of carotenoid glucosyltransferase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
AAA21261	148395	CrtX [Pantoea agglomerans]
AAN85597	27228291	Zeaxanthin Glucosyl Transferase [Pantoea stewartii]
BAB79601	18143446	crtX [Pantoea agglomerans pv. milletiae]
AAZ73147	72536082	zeaxanthin glucosyl transferase [Enterobacteriaceae bacterium DC413]
AAZ73128	72536060	zeaxanthin glucosyl transferase [Enterobacteriaceae bacterium DC260]
AAZ73140	72536074	zeaxanthin glucosyl transferase [Enterobacteriaceae bacterium

		DC416]
Q01330	231911	Zeaxanthin glucosyl transferase
ZP_006...	71674312	UDP-glycosyltransferase, MGT [Trichodesmium erythraeum IMS101]
NP_439972	16329244	zeaxanthin glucosyl transferase [Synechocystis sp. PCC 6803]
EAH29368	44130903	unknown [environmental sequence]
ZP_005...	67926135	zeaxanthin glucosyl transferase, hypothetical protein [Crocosphaera watsonii WH 8501]
YP_378763	78188425	hypothetical protein Cag_0447 [Chlorobium chlorochromatii CaD3]
ZP_005...	68549418	Glycosyl transferase, group 1 [Pelodictyon phaeoclathratiforme BU-1]
ZP_010...	85713606	glycosyl transferase, group 1 [Nitrobacter sp. Nb-311A]
YP_317171	75674750	glycosyl transferase, group 1 [Nitrobacter winogradskyi Nb-255]
ZP_006...	69929171	Glycosyl transferase, group 1 [Nitrobacter hamburgensis X14]
ZP_009...	84500589	hypothetical protein OB2597_11541 [Oceanicola batsensis HTCC2597]
ZP_009...	83953176	hypothetical protein NAS141_12746 [Sulfitobacter sp. NAS-14.1]
ZP_009...	83942121	hypothetical protein EE36_07793 [Sulfitobacter sp. EE-36]
YP_508020	89052569	glycosyl transferase, group 1 [Jannaschia sp. CCS1]
ZP_010...	85704103	hypothetical protein ROS217_13931 [Roseovarius sp. 217]
ZP_009...	83370850	probable glycosyltransferase [Rhodobacter sphaeroides ATCC 17025]
ZP_006...	69934465	Glycosyl transferase, group 1 [Paracoccus denitrificans PD1222]
ZP_009...	83949880	probable glycosyltransferase [Roseovarius nubinhibens ISM]
YP_376237	78183803	putative glycosyltransferase [Synechococcus sp. CC9902]
YP_376129	78183695	probable glycosyltransferase [Synechococcus sp. CC9902]
YP_374296	78186253	hypothetical protein Plut_0365 [Pelodictyon luteolum DSM 273]
ZP_010...	87301651	Putative glycosyltransferase [Synechococcus sp. WH 5701]
ZP_011...	88809938	Putative glycosyltransferase [Synechococcus sp. WH 7805]
BAE47471	78483937	carotenoid glucosyltransferase [Paracoccus sp. N81106]
ZP_010...	87303273	probable glycosyltransferase [Synechococcus sp. WH 5701]
YP_376127	78183693	probable glycosyltransferase [Synechococcus sp. CC9902]
YP_501334	88196509	hypothetical protein SAOUHSC_02880 [Staphylococcus aureus subsp. aureus NCTC 8325]
YP_187370	57652300	glycosyl transferase, group 2 family protein [Staphylococcus aureus subsp. aureus COL]
CAA66627	1340131u	nnamed protein product [Staphylococcus aureus]
YP_041987	49484763	putative glycosyl transferase [Staphylococcus aureus subsp. aureus MRSA252]
YP_417885	82752144	hypothetical protein SAB2436c [Staphylococcus aureus RF122]
YP_252404	70725490	hypothetical protein SH0489 [Staphylococcus haemolyticus JCSC1435]
NP_693379	23099913	hypothetical protein OB2458 [Oceanobacillus iheyensis HTE831]
ZP_008...	82501285	conserved hypothetical protein [Caldicellulosiruptor saccharolyticus DSM 8903]

ZP_010...	87303565	hypothetical protein WH5701_09900 [Synechococcus sp. WH 5701]

Table 41. Examples of acyl CoA:diacyglycerol acyltransferase (DGAT) polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
XP_957022	85082953	hypothetical protein [Neurospora crassa N150]
XP_386864	46124621	hypothetical protein FG06688.1 [Gibberella zeae PH-1]
XP_755172	71000982	diacylglycerol O-acyltransferase DGAT [Aspergillus fumigatus Af293]
XP_663763	67539978	hypothetical protein AN6159.2 [Aspergillus nidulans FGSC A4]
BAE65302	83775179	unnamed protein product [Aspergillus oryzae]
XP_502557	50550169	hypothetical protein [Yarrowia lipolytica]
AAS78662	56199782	diacylglycerol acyltransferase [Glycine max]
ABB84383	82582915	diacylglycerol acyltransferase [Jatropha curcas]
AAV31083	54145459	1,2-diacyl-sn-glycerol:acyl-CoA acyltransferase [Euonymus alatus]
AAG23696	10803053	diacylglycerol acyltransferase [Perilla frutescens]
AAF64065	7576941	putative diacylglycerol acyltransferase [Brassica napus]
AAS01606	41387497	acyl-CoA:diacylglycerol acyltransferase 1 [Olea europaea]
AAT73629	50299542	acyl CoA:diacylglycerol acyltransferase [Glycine max]

AAM03340	67043496	putative diacylglycerol acyltransferase [Tropaeolum majus]
XP_645633	66824557	hypothetical protein DDB0202877 [Dictyostelium discoideum]
AAF19345	6625653	diacylglycerol acylCoA acyltransferase [Nicotiana tabacum]
AAY40785	63376239	diacylglycerol acyltransferase DGAT2 [Brassica juncea]
AAW47581	57231736	diacylglycerol acyltransferase [Oryza sativa (japonica cultivar-group)]
AAR11479	38146080	diacylglycerol acyltransferase [Ricinus communis]
AAY40784	63376226	diacylglycerol acyltransferase DGAT1 [Brassica juncea]
AAP68322	31711932	At2g19450 [Arabidopsis thaliana]
AAW51456	57545061	diacylglycerol acyltransferase [Lotus corniculatus var. japonicus]
AAD45536	5579408	putative diacylglycerol acyltransferase [Brassica napus]
BAD53762	53791817	putative acyl-CoA:diacylglycerol acyltransferase [Oryza sativa (japonica cultivar-group)]
NP_956024	41054343	hypothetical protein LOC325875 [Danio rerio]
AAL49962	18642598	diacylglycerol acyltransferase 1 [Bos taurus]
XP_930884	89028385	similar to Diacylglycerol O-acyltransferase 1 (Diglyceride acyltransferase) (ACAT-related gene) [Homo sapiens]
NP_777118	27819636	diacylglycerol O-acyltransferase 1 [Bos taurus]
Q9GMF1	18202926	Diacylglycerol O-acyltransferase 1 (Diglyceride acyltransferase)
NP_036211	6912332	diacylglycerol O-acyltransferase 1 [Homo sapiens]
AAH06263	34782946	DGAT1 protein [Homo sapiens]
XP_780515	72006039	similar to Diacylglycerol O-acyltransferase 1 [Strongylocentrotus purpuratus]
AAD40881	5225382	putative diacylglycerol acyltransferase [Brassica napus]
XP_539214	73974769	similar to Diacylglycerol O-acyltransferase 1 (ACAT related gene product 1) isoform 1 [Canis familiaris]
AAZ22403	71063860	diacylglycerol O-acyltransferase 1 [Bubalus bubalis]
NP_999216	47522918	diacylglycerol acyltransferase [Sus scrofa]
NP_001...	50539976	hypothetical protein LOC436731 [Danio rerio]
XP_849176	73974767	similar to Diacylglycerol O-acyltransferase 1 (ACAT related gene product 1) isoform 2 [Canis familiaris]
NP_505828	71997360	H19N07.4 [Caenorhabditis elegans]
AAF82410	9049538	diacylglycerol acyltransferase [Caenorhabditis elegans]
CAE75170	39591950	Hypothetical protein CBG23107 [Caenorhabditis briggsae]
XP_626337	66358318	diacylglycerol acyltransferase 1 [Cryptosporidium parvum Iowa II]
XP_668402	67624239	acyl-CoA:diacylglycerol acyltransferase 1-related enzyme [Cryptosporidium hominis TU502]
AAP94208	33113253	acyl-CoA:diacylglycerol acyltransferase 1-related enzyme [Toxoplasma gondii]
AAP94209	33113255	acyl-CoA:diacylglycerol acyltransferase 1-related enzyme [Toxoplasma gondii]
XP_579557	62652535	PREDICTED: diacylglycerol O-acyltransferase 1 [Rattus norvegicus]
BAC66171	29170489	diacylglycerol acyltransferase [Mus musculus]
Q9ERM3	18202872	Diacylglycerol O-acyltransferase 1 (Diglyceride acyltransferase)
AAL78366	18698659	acyl coenzyme A:diacylglycerol acyltransferase [Drosophila melanogaster]
NP_995724	45552403	CG31991-PD, isoform D [Drosophila melanogaster]

NP_724017	24584734	CG31991-PC, isoform C [Drosophila melanogaster]
XP_858062	73974765	similar to Diacylglycerol O-acyltransferase 1 (ACAT related gene product 1) isoform 3 [Canis familiaris]
XP_728984	82915156	hypothetical protein PY01256 [Plasmodium yoelii yoelii str. 17XNL]
CAG11944	47225461	unnamed protein product [Tetraodon nigroviridis]
BAD27526	50199438	acyl-CoA:diacylglycerol acyltransferase [eukaryotic synthetic construct]
XP_317656	31226099	ENSANGP00000002281 [Anopheles gambiae str. PEST]
AAV59457	55733950	putative diacylglycerol acyltransferase [Oryza sativa . (japonica cultivar-group)]
EAL33593	54644853	GA16599-PA [Drosophila pseudoobscura]
XP_678753	68073677	diacylglycerol O-acyltransferase [Plasmodium berghei strain ANKA]
XP_520014	55631434	PREDICTED: similar to Diacylglycerol O-acyltransferase 1 (Diglyceride acyltransferase) [Pan troglodytes]
CAG10815	47219451	unnamed protein product [Tetraodon nigroviridis]
XP_624754	66522700	PREDICTED: similar to ENSANGP00000002281 [Apis mellifera]
CAC69884	15620769	diacylglycerol acyltransferase I [Rattus norvegicus]
XP_686181	68363630	PREDICTED: similar to Diacylglycerol O-acyltransferase 1 (Diglyceride acyltransferase) [Danio rerio]
XP_734008	70921323	diacylglycerol O-acyltransferase [Plasmodium chabaudi chabaudi]
XP_673128	68062248	hypothetical protein PB300300.00.0 [Plasmodium berghei strain ANKA]
AAS72376	45642963	acyl-CoA:cholesterol acyltransferase beta [Toxoplasma gondii]
AAS72375	45642961	acyl-CoA:cholesterol acyltransferase alpha [Toxoplasma gondii]
NP_586145	19074639	STEROL O-ACYLTRANSFERASE [Encephalitozoon cuniculi GB-M1]
XP_640280	66812202	hypothetical protein DDB0205259 [Dictyostelium discoideum]
AAY40783	63376221	diacylglycerol acyltransferase [Brassica juncea]
XP_765774	71032265	diacylglycerol O-acyltransferase [Theileria parva strain Muguga]
Q876L2	34582301	Sterol O-acyltransferase 2 (Sterol-ester synthase 2)
XP_571260	58268208	sterol O-acyltransferase [Cryptococcus neoformans var. neoformans JEC21]
EAL20032	50257323	hypothetical protein CNBF3580 [Cryptococcus neoformans var. neoformans B-3501A]
XP_954478	84999514	acyl transferase [Theileria annulata strain Ankara]
XP_505086	50555355	hypothetical protein [Yarrowia lipolytica]
NP_588558	19076058	hypothetical protein SPCP1E11.05c [Schizosaccharomyces pombe 972h-]
AAC49441	1389739	acyl-CoA:sterol acyltransferase
NP_014416	6324346	Acyl-CoA:sterol acyltransferase, isozyme of Are1p; Are2p [Saccharomyces cerevisiae]
XP_750354	70991010	sterol o-acyltransferase APE2 [Aspergillus fumigatus Af293]
XP_382192	46110268	hypothetical protein FG02016.1 [Gibberella zeae PH-1]
BAE54934	83764790	unnamed protein product [Aspergillus oryzae]
XP_885914	76617939	similar to Sterol O-acyltransferase 2 (Cholesterol

		acyltransferase 2) (ACAT-2) isoform 2 [Bos taurus]
XP_591251	76617937	similar to Sterol O-acyltransferase 2 (Cholesterol acyltransferase 2) (ACAT-2) isoform 1 [Bos taurus]
BAC00846	21392392	AcylCoA:Cholesterol Acyltransferase 2 [Rattus norvegicus]
NP_649816	28571583	CG8112-PA [Drosophila melanogaster]
NP_666176	22122547	sterol O-acyltransferase 2 [Mus musculus]
O88908	18202245	Sterol O-acyltransferase 2 (Cholesterol acyltransferase 2) (ACAT-2)
XP_761502	71022545	hypothetical protein UM05355.1 [Ustilago maydis 521]
NP_714950	40254723	sterol O-acyltransferase 2 [Rattus norvegicus]
EAQ86094	88178626	hypothetical protein CHGG_07347 [Chaetomium globosum CBS 148.51]
XP_461395	50425599	hypothetical protein DEHA0F25652g [Debaryomyces hansenii CBS767]
XP_661812	67527926	hypothetical protein AN4208.2 [Aspergillus nidulans FGSC A4]
AAH96091	64654094	Sterol O-acyltransferase 2 [Homo sapiens]
O75908	18202149	Sterol O-acyltransferase 2 (Cholesterol acyltransferase 2) (ACAT-2)
AAH96090	64652990	Sterol O-acyltransferase 2 [Homo sapiens]
AAK48829	13898623	acyl coenzyme A: cholesterol acyltransferase-2 [Homo sapiens]
XP_543637	73996435	PREDICTED: similar to sterol O-acyltransferase 2 [Canis familiaris]
O77759	18202176	Sterol O-acyltransferase 2 (Cholesterol acyltransferase 2) (ACAT-2)
AAO32474	28564191	ARE2 [Saccharomyces castellii]
XP_323485	32405744	hypothetical protein [Neurospora crassa]
NP_982606	45184888	AAR065Cp [Eremothecium gossypii]
NP_593708	19114620	hypothetical protein SPAC13G7.06 [Schizosaccharomyces pombe 972h-]
AAO32554	28564940	ARE2 [Saccharomyces kluyveri]
EAL28962	54639560	GA20833-PA [Drosophila pseudoobscura]
XP_449806	50294790	hypothetical protein CAGL0M10571g [Candida glabrata CBS138]
NP_033256	84619697	sterol O-acyltransferase 1 [Mus musculus]
Q61263	18202591	Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (ACAT-1)
BAC34925	26342537	unnamed protein product [Mus musculus]
XP_452607	50305295	unnamed protein product [Kluyveromyces lactis]
NP_001...	77735363	hypothetical protein LOC504287 [Bos taurus]
Q60457	18202585	Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (ACAT-1)
XP_320321	58393811	ENSANGP00000016512 [Anopheles gambiae str. PEST]
XP_320320	58393809	ENSANGP00000016486 [Anopheles gambiae str. PEST]
O70536	18202126	Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (ACAT-1)
XP_714776	68482533	acyl-CoA cholesterol acyltransferase [Candida albicans SC5314]
P84285	56404462	Sterol O-acyltransferase 2 (Sterol-ester synthase) (ASAT)
AAH77916	50416229	Soat1-prov protein [Xenopus laevis]
XP_692855	68364838	PREDICTED: similar to Soat1-prov protein [Danio rerio]
CAI13574	55960156	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol

		acyltransferase) 1 [Homo sapiens]
AAL56227	18028942	cholesterol acyltransferase 1 [Gorilla gorilla]
AAL56228	18028944	cholesterol acyltransferase 1 [Pongo pygmaeus]
AAC37532	4878022	acyl-coenzyme A: cholesterol acyltransferase [Homo sapiens]
2201440A	1585676	acyl-CoA/cholesterol acyltransferase
Q876L3	34582302	Sterol O-acyltransferase 1 (Sterol-ester synthase 1)
BAE01048	67969393	unnamed protein product [Macaca fascicularis]
XP_514030	55588858	PREDICTED: hypothetical protein XP_514030 [Pan troglodytes]
XP_547445	73961286	similar to Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (ACAT-1) [Canis familiaris]
EAQ84619	88177151	hypothetical protein CHGG_08633 [Chaetomium globosum CBS 148.51]
O77761	18202178	Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (ACAT-1)
XP_422267	50751122	PREDICTED: similar to Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (ACAT-1) [Gallus gallus]
XP_693284	68392980	PREDICTED: similar to Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (ACAT-1) [Danio rerio]
AAT92940	51013293	YCR048W [Saccharomyces cerevisiae]
XP_956576	85080625	hypothetical protein [Neurospora crassa N150]
XP_624691	66564061	PREDICTED: similar to ENSANGP00000016486 [Apis mellifera]
CAF96514	47222847	unnamed protein product [Tetraodon nigroviridis]
XP_788209	72085563	PREDICTED: similar to sterol O-acyltransferase 1 [Strongylocentrotus purpuratus]
XP_445307	50285757	unnamed protein product [Candida glabrata]
CAE70002	39596364	Hypothetical protein CBG16409 [Caenorhabditis briggsae]
CAG07990	47225647	unnamed protein product [Tetraodon nigroviridis]
NP_510623	17549960	B0395.2 [Caenorhabditis elegans]
AAX28331	76157393	SJCHGC04421 protein [Schistosoma japonicum]
CAI96158	66347204	Diacylglycerol O-acyltransferase [Bubalus bubalis]
XP_390039	46136695	hypothetical protein FG09863.1 [Gibberella zeae PH-1]
XP_643169	66819019	hypothetical protein DDB0203882 [Dictyostelium discoideum]
AAO53095	28850306	hypothetical protein [Dictyostelium discoideum]
AAB06959	1515472	acyl-CoA:cholesterol acyltransferase [Oryctolagus cuniculus]
NP_945619	39933343	putative alginate o-acetyltransferase AlgI [Rhodopseudomonas palustris CGA009]
ZP_008...	77691302	Membrane bound O-acyl transferase, MBOAT [Rhodopseudomonas palustris BisB5]
XP_465546	50908115	putative wax synthase [Oryza sativa (japonica cultivar-group)]

Table 46. Examples of MenF polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	ZP_007...	75238054	COG1169: Isochorismate synthase [Escherichia coli E110019]
2	ZP_007...	75512743	COG1169: Isochorismate synthase [Escherichia coli 53638]
3	ZP_007...	75259729	COG1169: Isochorismate synthase [Escherichia coli E22]
4	ZP_007...	75230348	COG1169: Isochorismate synthase [Escherichia coli B7A]
5	ZP_006...	75177942	COG1169: Isochorismate synthase [Shigella boydii BS512]
6	NP_754695	26248655	menaquinone-specific isochorismate synthase [Escherichia coli CFT073]
7	YP_689752	110806232	isochorismate hydroxymutase 2 [Shigella flexneri 5 str. 8401]
8	YP_541547	91211561	menaquinone-specific isochorismate synthase [Escherichia coli UTI89]
9	ZP_007...	75187052	COG1169: Isochorismate synthase [Escherichia coli E24377A]
10	NP_311180	38704070	menaquinone-specific isochorismate synthase [Escherichia coli O157:H7 str. Sakai]
11	AAC44303	1399684	isochorismate synthase
12	YP_670204	110642474	menaquinone-specific isochorismate synthase [Escherichia coli 536]
13	G64997	7466604	isochorismate synthase (EC 5.4.99.6) - Escherichia coli (strain 12)
14	NP_708151	56480082	menaquinone-specific isochorismate synthase [Shigella flexneri str. 301]
15	YP_408694	82544747	isochorismate hydroxymutase 2 [Shigella boydii Sb227]
16	YP_311206	74312787	isochorismate hydroxymutase 2 [Shigella sonnei Ss046]
17	BAB36576	13362623	isochorismate hydroxymutase 2 [Escherichia coli O157:H7 str. Sakai]
18	NP_288843	15802816	menaquinone-specific isochorismate synthase [Escherichia coli O157:H7 EDL933]
19	YP_404023	82777674	isochorismate hydroxymutase 2, menaquinone biosynthesis [Shigella dysenteriae Sd197]
20	YP_217297	62180880	menaquinone-specific isochorismate synthase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
21	NP_804410	29141068	menaquinone-specific isochorismate synthase [Salmonella enterica subsp. enterica serovar Typhi Ty2]
22	YP_149867	56412792	menaquinone-specific isochorismate synthase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]
23	YP_049316	50120149	menaquinone-specific isochorismate synthase [Erwinia carotovora subsp. atroseptica SCRI1043]
24	ZP_008...	77976633	COG1169: Isochorismate synthase [Yersinia intermedia ATCC 29909]
25	AAB02729	1381658	isochorismate synthase
26	NP_406060	16122747	menaquinone-specific isochorismate synthase [Yersinia pestis CO92]
27	ZP_007...	77629614	COG1169: Isochorismate synthase [Yersinia pseudotuberculosis 31758]
28	YP_648052	108812285	menaquinone-specific isochorismate synthase [Yersinia pestis Nepal516]
29	YP_071071	51596880	menaquinone-specific isochorismate synthase [Yersinia pseudotuberculosis IP 32953]
30	ZP_008...	77957626	COG1169: Isochorismate synthase [Yersinia bercovieri ATCC 43970]
31	ZP_008...	77975455	COG1169: Isochorismate synthase [Yersinia frederiksenii ATC

			33641]
32	ZP_008...	77961206	COG1169: Isochorismate synthase [Yersinia mollaretii ATCC 43969]
33	NP_930306	37526962	menaquinone-specific isochorismate synthase [Photorhabdus luminescens subsp. laumondii TTO1]
34	ZP_012...	90579267	menaquinone-specific isochorismate synthase [Vibrio angustu S14]
35	YP_130806	54309786	menaquinone-specific isochorismate synthase [Photobacterium profundum SS9]
36	ZP_011...	89073241	menaquinone-specific isochorismate synthase [Photobacterium SKA34]
37	ZP_012...	90410794	menaquinone-specific isochorismate synthase [Photobacterium profundum 3TCK]
38	YP_205055	59712279	menaquinone-specific isochorismate synthase [Vibrio fischeri ES114]
39	YP_088987	52425850	menaquinone-specific isochorismate synthase [Mannheimia succiniciproducens MBEL55E]
40	AAW66012	58198740	menaquinone-specific isochorismate synthase [Listonella anguillarum]
41	ZP_007...	75818951	COG1169: Isochorismate synthase [Vibrio cholerae V51]
42	NP_873159	33151806	menaquinone-specific isochorismate synthase [Haemophilus ducreyi 35000HP]
43	ZP_007...	75823560	COG1169: Isochorismate synthase [Vibrio cholerae RC385]
44	NP_231610	15641978	menaquinone-specific isochorismate synthase [Vibrio cholerae biovar eltor str. N16961]
45	ZP_007...	75830783	COG1169: Isochorismate synthase [Vibrio cholerae MO10]
46	ZP_007...	75815080	COG1169: Isochorismate synthase [Vibrio cholerae V52]
47	ZP_010...	86148511	menaquinone-specific isochorismate synthase [Vibrio sp. MED222]
48	ZP_009...	84387746	menaquinone-specific isochorismate synthase [Vibrio splendid 12B01]
49	NP_933908	37679299	menaquinone-specific isochorismate synthase [Vibrio vulnifici YJ016]
50	YP_718830	113460763	isochorismate synthase [Haemophilus somnus 129PT]
51	ZP_001...	53728666	COG1169: Isochorismate synthase [Haemophilus somnus 233
52	ZP_007...	75434665	isochorismate synthase [Actinobacillus succinogenes 130Z]
53	NP_797307	28897702	menaquinone-specific isochorismate synthase [Vibrio parahaemolyticus RIMD 2210633]
54	ZP_012...	91228605	menaquinone-specific isochorismate synthase [Vibrio alginolyt 12G01]
55	ZP_007...	75854295	COG1169: Isochorismate synthase [Vibrio sp. Ex25]
56	YP_248001	68248889	menaquinone-specific isochorismate synthase [Haemophilus influenzae 86-028NP]
57	NP_438452	16272240	menaquinone-specific isochorismate synthase [Haemophilus influenzae Rd KW20]
58	ZP_001...	53733183	COG1169: Isochorismate synthase [Haemophilus influenzae R2866]
59	Q9CPI5	20138722	Menaquinone-specific isochorismate synthase (Isochorismate mutase)
60	ZP_001...	46143565	COG1169: Isochorismate synthase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]
61	ZP_006...	69951380	Isochorismate synthase [Shewanella frigidimarina NCIMB 400
62	NP_720229	24376185	menaquinone-specific isochorismate synthase, putative

			[Shewanella oneidensis MR-1]
63	ZP_008...	78684523	Isochorismate synthase [Shewanella sp. ANA-3]
64	YP_735988	113972195	isochorismate synthases [Shewanella sp. MR-4]
65	ZP_005...	68545383	Isochorismate synthase [Shewanella amazonensis SB2B]
66	YP_739995	114049445	isochorismate synthases [Shewanella sp. MR-7]
67	ZP_009...	82742433	Isochorismate synthase [Shewanella sp. W3-18-1]
68	ZP_005...	68541057	Isochorismate synthase [Shewanella baltica OS155]
69	ZP_008...	78366054	Isochorismate synthase [Shewanella sp. PV-4]
70	ZP_005...	68551549	Isochorismate synthase [Prosthecochloris aestuarii DSM 271]
71	ZP_012...	90407329	menaquinone-specific isochorismate synthase, putative [Psychromonas sp. CNPT3]
72	NP_662717	21674652	menaquinone-specific isochorismate synthase [Chlorobium tepidum TLS]
73	YP_645620	108805683	isochorismate synthases [Rubrobacter xylanophilus DSM 9941
74	ZP_013...	106882319	isochorismate synthases [Psychromonas ingrahamii 37]
75	ZP_005...	67938335	Isochorismate synthase [Chlorobium phaeobacteroides BS1]
76	YP_379995	78189657	Isochorismate synthase [Chlorobium chlorochromatii CaD3]
77	ZP_006...	71481159	Isochorismate synthase [Prosthecochloris vibrioformis DSM 2(
78	YP_374263	78186220	Isochorismate synthase [Pelodictyon luteolum DSM 273]
79	ZP_005...	67935846	Isochorismate synthase [Chlorobium phaeobacteroides DSM 2(
80	ZP_005...	68548706	Isochorismate synthase [Pelodictyon phaeoclathratiforme BU-1
81	ZP_011...	88948981	Isochorismate synthase [Halorhodospira halophila SL1]
82	YP_148729	56421411	menaquinone-specific isochorismate synthase [Geobacillus kaustophilus HTA426]
83	YP_445474	83814242	putative isochorismate synthase [Salinibacter ruber DSM 1385
84	ZP_013...	110596947	isochorismate synthases [Chlorobium ferrooxidans DSM 1303
85	YP_135525	55377675	menaquinone-specific isochorismate synthase [Haloarcula marismortui ATCC 43049]
86	YP_260591	70730850	salicylate biosynthesis isochorismate synthase [Pseudomonas fluorescens Pf-5]
87	YP_462926	85860724	isochorismate synthase [Syntrophus aciditrophicus SB]
88	ZP_005...	67921375	Isochorismate synthase [Crocosphaera watsonii WH 8501]
89	YP_475840	86607077	isochorismate synthase [Synechococcus sp. JA-3-3Ab]
90	YP_401205	81300997	isochorismate synthase [Synechococcus elongatus PCC 7942]
91	ZP_005...	67918346	Isochorismate synthase [Chlorobium limicola DSM 245]
92	Q9ZPC0	20138529	Isochorismate synthase, chloroplast precursor
93	NP_441449	16330721	menaquinone-specific isochorismate synthase [Synechocystis s PCC 6803]
94	YP_275086	71735977	isochorismate synthase [Pseudomonas syringae pv. phaseolicol 1448A]
95	AAW66457	58200403	isochorismate synthase [Capsicum annuum]
96	YP_440027	83716790	isochorismate synthase family protein, putative [Burkholderia thailandensis E264]
97	NP_974143	42572105	ICS1 (ISOCHORISMATE SYNTHASE1); isochorismate synth [Arabidopsis thaliana]
98	T51711	11358652	probable isochorismate synthase (EC 5.4.99.6) [imported] - Arabidopsis thaliana
99	YP_623232	107025721	isochorismate synthases [Burkholderia cenocepacia AU 1054]
100	NP_792404	28869785	salicylate biosynthesis isochorismate synthase [Pseudomonas syringae pv. tomato str. DC3000]
101	ZP_011...	88810531	salicylate biosynthesis isochorismate synthase [Nitrococcus mobilis Nb-231]
102	YP_478502	86609740	isochorismate synthase [Synechococcus sp. JA-2-3B'a(2-13)]

103	ABE91019	92891975	isochorismate synthases, putative [Medicago truncatula]
104	AAM70573	21700899	At1g74710/F25A4.31 [Arabidopsis thaliana]
105	AAG52358	12324796	isochorismate synthase (icsI); 127003-130218 [Arabidopsis thaliana]
106	YP_327012	76802004	isochorismate synthase [Natronomonas pharaonis DSM 2160]
107	ZP_013...	100122709	hypothetical protein BpseS_03003489 [Burkholderia pseudom S13]
108	YP_110602	53721617	salicylate biosynthesis isochorismate synthase [Burkholderia pseudomallei K96243]
109	ZP_013...	100062175	hypothetical protein BpseP_03002327 [Burkholderia pseudom Pasteur]
110	ZP_013...	99912008	hypothetical protein Bpse1_03001777 [Burkholderia pseudom 1655]
111	ZP_008...	82535543	hypothetical protein Bpse110_02003219 [Burkholderia pseudomallei 1106b]
112	ZP_012...	90295215	hypothetical protein Bpse17_02000208 [Burkholderia pseudomallei 1710a]
113	ZP_004...	67736224	COG1169: Isochorismate synthase [Burkholderia pseudomalle 668]
114	NP_484076	17227528	menaquinone-specific isochorismate synthase [Nostoc sp. PCC 7120]
115	ZP_013...	100231616	hypothetical protein Bpse4_03004458 [Burkholderia pseudom 406e]
116	YP_723556	113477495	isochorismate synthases [Trichodesmium erythraeum IMS101]
117	YP_371425	78061517	salicylate biosynthesis isochorismate synthase [Burkholderia s 383]
118	YP_323141	75908845	menaquinone-specific isochorismate synthase [Anabaena varia ATCC 29413]
119	NP_045108	11465501	isochorismate synthase [Cyanidium caldarium]
120	ZP_007...	76261303	Isochorismate synthase [Chloroflexus aurantiacus J-10-fl]
121	NP_682003	22298756	menaquinone-specific isochorismate synthase [Thermosynechococcus elongatus BP-1]
122	YP_631721	108758468	isochorismate synthase [Myxococcus xanthus DK 1622]
123	NP_173321	15221882	isochorismate synthase [Arabidopsis thaliana]
124	NP_806015	29142673	isochorismate synthase [Salmonella enterica subsp. enterica serovar Typhi Ty2]
125	NP_459587	16763972	isochorismate synthase [Salmonella typhimurium LT2]
126	YP_215613	62179196	isochorismate synthase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
127	ZP_011...	89099709	menaquinone-specific isochorismate synthase [Bacillus sp. NR B-14911]
128	YP_151343	56414268	isochorismate synthase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]
129	NP_280001	15790177	MenF [Halobacterium sp. NRC-1]
130	YP_092776	52786947	menaquinone-specific isochorismate synthase [Bacillus licheniformis ATCC 14580]
131	ZP_013...	106889325	isochorismate synthases [Roseiflexus sp. RS-1]
132	AAG42414	11992028	isochorismate synthase [Brucella melitensis biovar Abortus]
133	NP_541054	17988421	isochorismate synthase [Brucella melitensis 16M]
134	NP_699223	23499783	isochorismate synthase [Brucella suis 1330]
135	AAA50397	557488	Unknown
136	ZP_001...	23124228	COG1169: Isochorismate synthase [Nostoc punctiforme PCC 73102]

137	YP_048595	50119428	isochorismate synthase [Erwinia carotovora subsp. atroseptica SCRI1043]
138	YP_418262	83268971	Isochorismate synthase:Anthranilate synthase component I and chorismate binding protein [Brucella melitensis biovar Abortus 2308]
139	NP_693247	23099781	menaquinone-specific isochorismate synthase [Oceanobacillus iheyensis HTE831]
140	NP_390961	16080135	menaquinone-specific isochorismate synthase [Bacillus subtilis subsp. subtilis str. 168]
141	ZP_007...	75229521	COG1169: Isochorismate synthase [Escherichia coli B7A]
142	ZP_009...	83586971	COG1169: Isochorismate synthase [Escherichia coli 101-1]
143	NP_752611	26246572	isochorismate synthase [Escherichia coli CFT073]
144	YP_406986	82543039	isochorismate hydroxymutase 2, enterochelin biosynthesis [Shigella boydii Sb227]
145	ZP_012...	94414311	hypothetical protein PaerP_01003892 [Pseudomonas aeruginos PA7]
146	ZP_013...	107103747	hypothetical protein PaerPA_01004818 [Pseudomonas aerugin PACS2]
147	YP_668552	110640824	Isochorismate synthase EntC [Escherichia coli 536]
148	ZP_006...	75177504	COG1169: Isochorismate synthase [Shigella boydii BS512]
149	ZP_007...	75194778	COG1169: Isochorismate synthase [Escherichia coli HS]
150	ZP_007...	75514688	COG1169: Isochorismate synthase [Escherichia coli 53638]
151	YP_539626	91209640	isochorismate synthase [Escherichia coli UTI89]
152	AP_001240	89107460	isochorismate synthase 1 [Escherichia coli W3110]
153	YP_309547	74311128	isochorismate hydroxymutase 2 [Shigella sonnei Ss046]
154	ZP_001...	32039448	COG1169: Isochorismate synthase [Pseudomonas aeruginosa UCBPP-PA14]
155	YP_437626	83649191	Isochorismate synthase [Hahella chejuensis KCTC 2396]
156	YP_047342	50085832	isochorismate synthetase [Acinetobacter sp. ADP1]
157	AAN28933	30348890	isochorismate synthase DhbC [Acinetobacter baumannii]
158	BAC87913	35210435	probable acinetobactin biosynthesis protein [Acinetobacter baumannii]
159	AAA18491	145840	iron chelator protein [Escherichia coli]
160	ZP_006...	69288475	Isochorismate synthase [Kineococcus radiotolerans SRS30216
161	NP_898397	33866838	Isochorismate synthase [Synechococcus sp. WH 8102]
162	YP_378121	78185687	Isochorismate synthase [Synechococcus sp. CC9902]
163	ZP_009...	83570420	COG1169: Isochorismate synthase [Shigella dysenteriae 1012]
164	ZP_011...	88809870	Isochorismate synthase [Synechococcus sp. WH 7805]
165	ZP_008...	77974176	COG1169: Isochorismate synthase [Yersinia frederiksenii ATC 33641]
166	NP_874596	33239654	Isochorismate synthase [Prochlorococcus marinus subsp. marin str. CCMP1375]
167	ZP_006...:	74020257	Isochorismate synthase [Burkholderia ambifaria AMMD]
168	AAK95838	22073888	putative isochorismate synthase PhbC [Photorhabdus luminesc
169	AAF19052	6606080	neutral sphingomyelinase [Homo sapiens]
170	ZP_011...	89201879	Isochorismate synthase [Bacillus cereus subsp. cytotoxis NVH 391-98]
171	ZP_005...	68054683	Isochorismate synthase [Exiguobacterium sibiricum 255-15]
172	AAA21935	141868	amonabactin
173	NP_895885	33864325	Isochorismate synthase [Prochlorococcus marinus str. MIT 931
174	CAA70528	4150886	isochorismate synthase [Pseudomonas fluorescens]
175	YP_292736	72383381	isochorismate synthase [Prochlorococcus marinus str. NATL2A
176	NP_276767	15679650	anthranilate synthase component I [Methanothermobacter

			thermautotrophicus str. Delta H]
177	ZP_010...	87300853	Isochorismate synthase [Synechococcus sp. WH 5701]
178	NP_901155	34496940	isochorismate synthase [Chromobacterium violaceum ATCC 12472]
179	NP_849025	30468138	menaquinone-specific isochorismate synthase [Cyanidioschyz merolae strain 10D]
180	ZP_010...	87123565	Isochorismate synthase [Synechococcus sp. RS9917]
181	YP_382726	78213947	isochorismate synthase [Synechococcus sp. CC9605]
182	AAA73028	149745	anthranilate synthase alpha-subunit
183	NP_814231	29375078	menaquinone-specific isochorismate synthase [Enterococcus faecalis V583]
184	NP_266888	15672714	menaquinone-specific isochorismate synthase [Lactococcus la subsp. lactis Il1403]
185	YP_286023	71908436	Isochorismate synthase [Dechloromonas aromatica RCB]
186	1QDLA	5822246	Chain A, The Crystal Structure Of Anthranilate Synthase Fron Sulfolobus Solfataricus
187	NP_342385	15897780	Anthranilate synthase component I (trpE) [Sulfolobus solfatari P2]
188	CAA90311	1004323	anthranilate synthase component 1 [Sulfolobus solfataricus]
189	ZP_011...	88858731	putative isochorismate synthase [Pseudoalteromonas tunicata I
190	YP_657637	110667826	isochorismate synthase [Haloquadratum walsbyi DSM 16790]
191	ZP_010...	84518759	Isochorismate synthase [Prochlorococcus marinus str. MIT 92
192	NP_213409	15606032	anthranilate synthase component I [Aquifex aeolicus VF5]
193	NP_691876	23098410	isochorismate synthase [Oceanobacillus iheyensis HTE831]
194	ZP_000...	53689595	COG1169: Isochorismate synthase [Leuconostoc mesenteroide subsp. mesenteroides ATCC 8293]
195	YP_093408	52787579	isochorismate synthase [Bacillus licheniformis ATCC 14580]
196	NP_764298	27467661	putative menaquinone-specific isochorismate synthase [Staphylococcus epidermidis ATCC 12228]
197	YP_080979	52082188	isochorismate synthase [Bacillus licheniformis ATCC 14580]
198	YP_251072	68536367	putative isochorismate synthase [Corynebacterium jeikeium K
199	YP_188214	57866508	isochorismate synthase family protein [Staphylococcus epidermidis RP62A]
200	ZP_011...	89199776	Isochorismate synthase [Bacillus cereus subsp. cytotoxis NVH 391-98]

Table 47. Examples of MenD polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	ZP_007...	75259728	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Escherichia coli E22]
2	ZP_007...	75238053	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Escherichia coli E110019]
3	ZP_007...	75230349	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Escherichia coli B7A]
4	NP_708150	56480081	2-oxoglutarate decarboxylase [Shigella flexneri 2a str. 301]
5	YP_689751	110806231	2-oxoglutarate decarboxylase [Shigella flexneri 5 str. 8401]
6	YP_408693	82544746	2-oxoglutarate decarboxylase [Shigella boydii Sb227]
7	ZP_007...	75187051	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Escherichia coli E24377A]
8	ZP_006...	75177943	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Shigella boydii BS512]
9	YP_311205	74312786	2-oxoglutarate decarboxylase [Shigella sonnei Ss046]
10	NP_311179	15832406	2-oxoglutarate decarboxylase [Escherichia coli O157:H7 str. Sakai]
11	NP_754694	26248654	2-oxoglutarate decarboxylase [Escherichia coli CFT073]
12	YP_670203	110642473	menaquinone biosynthesis protein menD [Escherichia coli 536]
13	ZP_007...	75243080	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Escherichia coli F11]
14	YP_541546	91211560	Menaquinone biosynthesis protein MenD [Escherichia coli UT
15	NP_288842	15802815	2-oxoglutarate decarboxylase [Escherichia coli O157:H7 EDL9
16	YP_404022	82777673	2-oxoglutarate decarboxylase [Shigella dysenteriae Sd197]

17	NP_461251	16765636	2-oxoglutarate decarboxylase [Salmonella typhimurium LT2]
18	YP_217296	62180879	2-oxoglutarate decarboxylase [Salmonella enterica subsp. enter serovar Choleraesuis str. SC-B67]
19	YP_149868	56412793	2-oxoglutarate decarboxylase [Salmonella enterica subsp. enter serovar Paratyphi A str. ATCC 9150]
20	NP_804411	29141069	2-oxoglutarate decarboxylase [Salmonella enterica subsp. enter serovar Typhi Ty2]
21	ZP_008...	77957627	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Yersinia bercovieri ATCC 43970]
22	ZP_008...	77961207	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Yersinia mollaretii ATCC 43969]
23	ZP_008...	77975454	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Yersinia frederiksenii ATCC 33641]
24	YP_071070	51596879	2-oxoglutarate decarboxylase [Yersinia pseudotuberculosis IP 32953]
25	ZP_007...	77629613	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Yersinia pseudotuberculosis IP 31758]
26	ZP_007...	77636596	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Yersinia pestis Angola]
27	YP_648051	108812284	menaquinone biosynthesis protein [Yersinia pestis Nepal516]
28	YP_049317	50120150	2-oxoglutarate decarboxylase [Erwinia carotovora subsp. atroseptica SCRI1043]
29	NP_930305	37526961	2-oxoglutarate decarboxylase [Photorhabdus luminescens subsp laumondii TTO1]
30	AAA24153	146813	2-succinyl-6-hydroxy-2,4-cyclohexadiene- 1-carboxylate synth (mendD)
31	YP_088986	52425849	2-oxoglutarate decarboxylase [Mannheimia succiniciproducens MBEL55E]
32	AAB59060	146815	menaquinone [Escherichia coli]
33	ZP_008...	77976634	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Yersinia intermedia ATCC 29909]
34	Q9CPI4	20138721	Menaquinone biosynthesis protein menD [Includes: 2-succinyl-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase (SHCHC synthase); 2-oxoglutarate decarboxylase (Alpha-ketoglutarate decarboxylase) (KDC)]
35	ZP_001...	53728665	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Haemophilus somnus 2336]
36	YP_718829	113460762	2-oxoglutarate decarboxylase [Haemophilus somnus 129PT]
37	NP_438451	16272239	2-oxoglutarate decarboxylase [Haemophilus influenzae Rd KW
38	ZP_001...	53733182	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Haemophilus influenzae R2866]
39	ZP_001...	32035279	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Actinobacillus pleuropneumoniae serova str. 4074]
40	YP_248000	68248888	2-oxoglutarate decarboxylase [Haemophilus influenzae 86-028
41	NP_874205	33152852	2-oxoglutarate decarboxylase [Haemophilus ducreyi 35000HP]
42	ZP_001...	53732929	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Haemophilus influenzae R2846]
43	ZP_012...	90410795	2-oxoglutarate decarboxylase [Photobacterium profundum 3TC
44	YP_130805	54309785	2-oxoglutarate decarboxylase [Photobacterium profundum SS9
45	ZP_011...	89073242	2-oxoglutarate decarboxylase [Photobacterium sp. SKA34]
46	ZP_012...	90579266	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synth [Vibrio angustum S14]

47	YP_205054	59712278	2-oxoglutarate decarboxylase [Vibrio fischeri ES114]
48	ZP_007...	75823559	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Vibrio cholerae RC385]
49	ZP_007...	75818950	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Vibrio cholerae V51]
50	ZP_007...	75830782	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Vibrio cholerae MO10]
51	NP_797308	28897703	2-oxoglutarate decarboxylase [Vibrio parahaemolyticus RIMD 2210633]
52	NP_933909	37679300	2-oxoglutarate decarboxylase [Vibrio vulnificus YJ016]
53	ZP_009...	84387747	2-oxoglutarate decarboxylase [Vibrio splendidus 12B01]
54	NP_761961	27366433	2-oxoglutarate decarboxylase [Vibrio vulnificus CMCP6]
55	ZP_006...	69950064	Menaquinone biosynthesis protein [Shewanella frigidimarina NCIMB 400]
56	ZP_010...	86148510	2-oxoglutarate decarboxylase [Vibrio sp. MED222]
57	ZP_005...	68545141	Menaquinone biosynthesis protein [Shewanella amazonensis SB2B]
58	ZP_009...	82741682	Menaquinone biosynthesis protein [Shewanella sp. W3-18-1]
59	ZP_008...	77814932	Menaquinone biosynthesis protein [Shewanella putrefaciens C 32]
60	ZP_008...	78684419	Menaquinone biosynthesis protein [Shewanella sp. ANA-3]
61	ZP_007...	75434666	2-oxoglutarate decarboxylase [Actinobacillus succinogenes 13
62	AAK72376	15822636	2-ketoglutarate decarboxylase MenD [Shewanella putrefaciens
63	YP_735887	113972094	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Shewanella sp. MR-4]
64	YP_739874	114049324	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Shewanella sp. MR-7]
65	ZP_007...	75854296	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Vibrio sp. Ex25]
66	NP_720089	24376046	2-oxoglutarate decarboxylase [Shewanella oneidensis MR-1]
67	ZP_005...	68542841	Menaquinone biosynthesis protein [Shewanella baltica OS155]
68	ZP_012...	91228604	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synth [Vibrio alginolyticus 12G01]
69	ZP_008...	78365984	Menaquinone biosynthesis protein [Shewanella sp. PV-4]
70	ZP_013...	106882316	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Psychromonas ingraha 37]
71	ZP_012...	90407330	2-oxoglutarate decarboxylase [Psychromonas sp. CNPT3]
72	NP_662718	21674653	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synth [Chlorobium tepidum TLS]
73	ZP_011...	88948982	Menaquinone biosynthesis protein [Halorhodospira halophila S
74	YP_645619	108805682	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Rubrobacter xylanophi DSM 9941]
75	YP_379994	78189656	Menaquinone biosynthesis protein [Chlorobium chlorochromat CaD3]
76	ZP_005...	68548707	Menaquinone biosynthesis protein [Pelodictyon phaeoclathratiforme BU-1]
77	YP_445475	83815108	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Salinibacter ruber DSM 13855]
78	YP_374262	78186219	Menaquinone biosynthesis protein [Pelodictyon luteolum DSM 273]

79	ZP_005...	67938336	Menaquinone biosynthesis protein [Chlorobium phaeobacteroi BS1]
80	ZP_008...	77976635	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Yersinia intermedia ATCC 29909]
81	ZP_005...	67935847	Menaquinone biosynthesis protein [Chlorobium phaeobacteroi DSM 266]
82	ZP_013...	110596948	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Chlorobium ferrooxid DSM 13031]
83	ZP_005...	68551550	Menaquinone biosynthesis protein [Prosthecochloris aestuarii DSM 271]
84	BAE99027	110742201	hypothetical protein [Arabidopsis thaliana]
85	AAZ40195	71738181	chloroplast Phyllo [Arabidopsis thaliana]
86	ZP_005...	67918347	Menaquinone biosynthesis protein [Chlorobium limicola DSM 245]
87	ZP_006...	71481158	Menaquinone biosynthesis protein [Prosthecochloris vibriofor DSM 265]
88	NP_177055	15221555	2-oxoglutarate decarboxylase [Arabidopsis thaliana]
89	NP_680921	22297674	2-oxoglutarate decarboxylase [Thermosynechococcus elongat BP-1]
90	YP_462925	85860723	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synth [Syntrophus aciditrophicus SB]
91	NP_484356	17227808	2-oxoglutarate decarboxylase [Nostoc sp. PCC 7120]
92	ZP_005...	67921252	Menaquinone biosynthesis protein [Crocosphaera watsonii WH 8501]
93	YP_325198	75910902	2-oxoglutarate decarboxylase [Anabaena variabilis ATCC 294
94	YP_631722	108759318	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Myxococcus xanthus I 1622]
95	YP_285551	71907964	Menaquinone biosynthesis protein [Dechloromonas aromatica RCB]
96	ZP_011...	89099708	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synth [Bacillus sp. NRRL B-14911]
97	NP_465200	16803715	2-oxoglutarate decarboxylase [Listeria monocytogenes EGD-e
98	YP_478254	86609492	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Synechococcus sp. JA 3B'a(2-13)]
99	NP_390960	16080134	2-oxoglutarate decarboxylase [Bacillus subtilis subsp. subtilis 168]
100	ZP_002...	47096748	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Listeria monocytogene str. 1/2a F6854]
101	ZP_001...	23126172	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Nostoc punctiforme PCC 73102]
102	ZP_013...	106889324	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Roseiflexus sp. RS-1]
103	ZP_007...	76261302	Menaquinone biosynthesis protein [Chloroflexus aurantiacus J fl]
104	YP_014295	46907906	2-oxoglutarate decarboxylase [Listeria monocytogenes str. 4b F2365]
105	ZP_002...	47093554	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Listeria monocytogene str. 4b H7858]

106	AAC37014	1185289	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1- carboxylate synt
107	YP_135526	55377676	2-succinyl-6-hydroxy-2 4-cyclohexadiene-1-carboxylate synth [Haloarcula marismortui ATCC 43049]
108	YP_092775	52786946	2-oxoglutarate decarboxylase [Bacillus licheniformis ATCC 14580]
109	NP_471119	16800851	2-oxoglutarate decarboxylase [Listeria innocua Clip11262]
110	YP_148728	56421410	2-oxoglutarate decarboxylase [Geobacillus kaustophilus HTA
111	YP_473574	86604811	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Synechococcus sp. JA 3Ab]
112	YP_400452	81300244	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Synechococcus elonga PCC 7942]
113	NP_849026	30468139	2-succinyl-6-hydroxy-2, 4-cyclohexadiene-1-carboxylate synt [Cyanidioschyzon merolae strain 10D]
114	YP_723559	113477498	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Trichodesmium erythraeum IMS101]
115	YP_289472	72161815	Menaquinone biosynthesis protein [Thermobifida fusca YX]
116	ZP_013...	109647423	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Desulfitobacterium hafniense DCB-2]
117	NP_045109	11465500	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synth [Cyanidium caldarium]
118	NP_814232	29375079	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Enterococcus faecalis V583]
119	ZP_011...	89201878	Menaquinone biosynthesis protein [Bacillus cereus subsp. cytotoxis NVH 391-98]
120	NP_764299	27467662	2-oxoglutarate decarboxylase [Staphylococcus epidermidis AT 12228]
121	NP_693246	23099780	2-oxoglutarate decarboxylase [Oceanobacillus iheyensis HTE8
122	YP_188215	57866509	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Staphylococcus epidermidis RP62A]
123	YP_301838	73663057	menaquinone biosynthesis bifunctional protein [Staphylococc saprophyticus subsp. saprophyticus ATCC 15305]
124	NP_280000	15790176	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synth [Halobacterium sp. NRC-1]
125	YP_657638	110667827	2-oxoglutarate decarboxylase; 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Haloquadratum walsb DSM 16790]
126	YP_038900	49478795	2-oxoglutarate decarboxylase [Bacillus thuringiensis serovar konkukian str. 97-27]
127	YP_327013	76802005	2-oxoglutarate decarboxylase ; 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Natronomonas pharac DSM 2160]
128	ZP_011...	89204353	Menaquinone biosynthesis protein [Bacillus weihenstephanens KBAB4]
129	ZP_002...	47568034	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Bacillus cereus G9241
130	YP_040433	49483209	putative menaquinone biosynthesis bifunctional protein [Staphylococcus aureus subsp. aureus MRSA252]
131	NP_981308	42784061	2-oxoglutarate decarboxylase [Bacillus cereus ATCC 10987]

132	ZP_007...	75762875	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synth 2-oxoglutarate decarboxylase [Bacillus thuringiensis serovar israelensis ATCC 35646]
133	NP_834554	30022923	2-oxoglutarate decarboxylase [Bacillus cereus ATCC 14579]
134	ZP_011...	88808384	Menaquinone biosynthesis protein; 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate [Synechococcus sp. WH 7805]
135	YP_086185	52140644	2-oxoglutarate decarboxylase [Bacillus cereus E33L]
136	YP_416396	82750655	2-oxoglutarate decarboxylase [Staphylococcus aureus RF122]
137	ZP_003...	65322223	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Bacillus anthracis str. A2012]
138	YP_499536	88194740	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Staphylococcus aureu subsp. aureus NCTC 8325]
139	YP_043104	49485883	putative menaquinone biosynthesis bifunctional protein [Staphylococcus aureus subsp. aureus MSSA476]
140	NP_442296	16331568	2-oxoglutarate decarboxylase [Synechocystis sp. PCC 6803]
141	ZP_012...	90586041	Menaquinone biosynthesis protein [Staphylococcus aureus sub aureus JH9]
142	ZP_005...	68054684	Menaquinone biosynthesis protein [Exiguobacterium sibiricum 255-15]
143	ZP_010...	87124200	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acidsynthase/2-oxoglutarate decarboxylase [Synechococcus sp RS9917]
144	ZP_009...	84494939	2-oxoglutarate decarboxylase [Janibacter sp. HTCC2649]
145	YP_253834	70726920	menaquinone biosynthesis protein [Staphylococcus haemolytic JCSC1435]
146	ZP_000...	23023622	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]
147	ZP_012...	90592096	2-oxoglutarate decarboxylase [Flavobacterium johnsoniae UW
148	YP_381434	78212655	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Synechococcus sp. CC9605]
149	NP_905665	34541186	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Porphyromonas gingiv W83]
150	NP_875446	33240504	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synth [Prochlorococcus marinus subsp. marinus str. CCMP1375]
151	NP_894239	33862679	Menaquinone biosynthesis protein; 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Prochlorococcus mari str. MIT 9313]
152	ZP_010...	87303314	Menaquinone biosynthesis protein [Synechococcus sp. WH 57
153	ZP_009...	83857346	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acidsynthase/2-oxoglutarate decarboxylase [Croceibacter atlan HTCC2559]
154	ZP_006...	69284898	2-oxoglutarate decarboxylase [Kineococcus radiotolerans SRS30216]
155	NP_897090	33865531	Menaquinone biosynthesis protein; 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Synechococcus sp. W 8102]
156	ZP_011...	88713573	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Flavobacteriales bacte HTCC2170]
157	NP_813612	29350109	2-oxoglutarate decarboxylase and 2-succinyl-6-hydroxy-2,4-

			cyclohexadiene-1-carboxylate synthase [Bacteroides thetaiotaomicron VPI-5482]
158	ZP_011...	88802655	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Polaribacter irgensii 2
159	ZP_010...	86132717	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acidsynthase/2-oxoglutarate decarboxylase [Cellulophaga sp. MED134]
160	YP_377342	78184907	Menaquinone biosynthesis protein [Synechococcus sp. CC990
161	ZP_010...	86133842	2-oxoglutarate decarboxylase and2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate [Tenacibaculum sp. MED152]
162	ZP_010...	86143136	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acidsynthase/2-oxoglutarate decarboxylase [Flavobacterium sp MED217]
163	ZP_003...	62463994	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Lactococcus lactis subsp. cremoris SK11
164	ZP_012...	91215739	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Psychroflexus torquis ATCC 700755]
165	YP_678368	110638159	bifunctional menaquinone biosynthesis protein: 2-oxoglutarate decarboxylase; 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Cytophaga hutchinsonii ATCC 33406]
166	ZP_006...	71369870	2-oxoglutarate decarboxylase [Nocardioides sp. JS614]
167	ZP_011...	88805806	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Robiginitalea biformat HTCC2501]
168	YP_210963	60680819	putative menaquinone biosynthesis protein [Bacteroides fragili NCTC 9343]
169	YP_291238	72381883	Menaquinone biosynthesis protein [Prochlorococcus marinus s NATL2A]
170	ZP_011...	89338602	Thiamine pyrophosphate enzyme, N-terminal TPP binding regi [Mycobacterium flavescens PYR-GCK]
171	ZP_010...	84517891	Menaquinone biosynthesis protein [Prochlorococcus marinus s MIT 9211]
172	NP_334990	15839953	2-oxoglutarate decarboxylase [Mycobacterium tuberculosis CDC1551]
173	YP_701962	111018990	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synth 2-oxoglutarate decarboxylase [Rhodococcus sp. RHA1]
174	YP_121349	54027107	2-oxoglutarate decarboxylase [Nocardia farcinica IFM 10152]
175	ZP_012...	92910333	2-oxoglutarate decarboxylase [Mycobacterium sp. JLS]
176	ZP_008...	81255568	COG1165: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Mycobacterium tuberculosis C]
177	YP_637927	108797730	2-oxoglutarate decarboxylase [Mycobacterium sp. MCS]
178	NP_302478	15828215	2-oxoglutarate decarboxylase [Mycobacterium leprae TN]
179	YP_063989	51244105	similar to menaquinone biosynthesis protein (MenD) [Desulfot psychrophila LSv54]
180	YP_397104	78778992	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Prochlorococcus marin str. MIT 9312]
181	YP_251666	68536961	2-oxoglutarate decarboxylase / 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Corynebacterium jeikeium K411]
182	ZP_012...	90201693	2-oxoglutarate decarboxylase [Mycobacterium vanbaalenii PY
183	ABE11059	91070137	menaquinone biosynthesis protein; putative 2-succinyl-6-hydro

			2,4-cyclohexadiene-1-carboxylate synthase [uncultured Prochlorococcus marinus clone HF10-11A3]
184	NP_266887	15672713	2-oxoglutarate decarboxylase [Lactococcus lactis subsp. lactis Il1403]
185	ZP_004...	66966177	Menaquinone biosynthesis protein [Arthrobacter sp. FB24]
186	NP_892725	33861164	Menaquinone biosynthesis protein; probable 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]
187	YP_055614	50842387	menaquinone biosynthesis protein [Propionibacterium acnes KPA171202]
188	AAW66013	58198741	2-succinyl-6-hydroxy-2, 4-cyclohexadiene-1-carboxylate synth [Listonella anguillarum]
189	NP_737088	25027034	2-oxoglutarate decarboxylase [Corynebacterium efficiens YS-3
190	NP_962986	41410150	2-oxoglutarate decarboxylase [Mycobacterium avium subsp. paratuberculosis K-10]
191	NP_938804	38233037	2-oxoglutarate decarboxylase [Corynebacterium diphtheriae N 13129]
192	ABE11189	91070270	menaquinone biosynthesis protein; putative 2-succinyl-6-hydrc 2,4-cyclohexadiene-1-carboxylate synthase [uncultured Prochlorococcus marinus clone HF10-11H7]
193	YP_008067	46446702	putative menaquinone biosynthesis protein, menD [Candidatus Protochlamydia amoebophila UWE25]
194	ABD98165	90811813	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synth [Chlamydomonas reinhardtii]
195	AAA50399	557490	menCF
196	ZP_007...	75434667	2-oxoglutarate decarboxylase [Actinobacillus succinogenes 13
197	YP_061328	50954040	2-oxoglutarate decarboxylase [Leifsonia xyli subsp. xyli str. CTCB07]

Table 48. Examples of MenC polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	FHVA	10120813	Chain A, Crystal Structure Analysis Of O-Succinylbenzoate Synthase From E. Coli Complexed With Mg And Osb
2	R6WA	39654827	Chain A, Crystal Structure Of The K133r Mutant Of O-Succinylbenzoate Synthase (Osbs) From Escherichia Coli. Complex With Shchc
3	ZP_007...	75259725	COG1441: O-succinylbenzoate synthase [Escherichia coli E22
4	P58484	20138544	O-succinylbenzoate synthase (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoi acid synthase)
5	ZP_007...	75238050	COG1441: O-succinylbenzoate synthase [Escherichia coli E110019]
6	ZP_007...	75196304	COG1441: O-succinylbenzoate synthase [Escherichia coli HS]
7	ZP_007...	75230352	COG1441: O-succinylbenzoate synthase [Escherichia coli B7A
8	ZP_006...	75177946	COG1441: O-succinylbenzoate synthase [Shigella boydii BS51
9	AAA71917	146811	4-(2'-carboxyphenyl)-4-oxybutyric acid synthase
10	ZP_007...	75512739	COG1441: O-succinylbenzoate synthase [Escherichia coli 536
11	YP_408690	82544743	o-succinylbenzoyl-CoA synthase [Shigella boydii Sb227]
12	NP_754690	26248650	O-succinylbenzoate synthase [Escherichia coli CFT073]
13	YP_541542	91211556	O-succinylbenzoate-CoA synthase [Escherichia coli UTI89]
14	YP_670200	110642470	O-succinylbenzoate-CoA synthase [Escherichia coli 536]
15	NP_837863	30063692	O-succinylbenzoate synthase [Shigella flexneri 2a str. 2457T]
16	YP_311202	74312783	O-succinylbenzoyl-CoA synthase [Shigella sonnei Ss046]
17	YP_689748	110806228	O-succinylbenzoate synthase [Shigella flexneri 5 str. 8401]
18	NP_804414	29141072	O-succinylbenzoate synthase [Salmonella enterica subsp. enter serovar Typhi Ty2]
19	YP_149871	56412796	O-succinylbenzoate synthase [Salmonella enterica subsp. enter serovar Paratyphi A str. ATCC 9150]
20	YP_217293	62180876	O-succinylbenzoate synthase [Salmonella enterica subsp. enter serovar Choleraesuis str. SC-B67]
21	ZP_008...	77976638	COG1441: O-succinylbenzoate synthase [Yersinia intermedia ATCC 29909]
22	ZP_008...	77961210	COG1441: O-succinylbenzoate synthase [Yersinia mollaretii ATCC 43969]
23	ZP_008...	77975452	COG1441: O-succinylbenzoate synthase [Yersinia frederikseni ATCC 33641]
24	ZP_008...	77957630	COG1441: O-succinylbenzoate synthase [Yersinia bercovieri ATCC 43970]
25	YP_049320	50120153	O-succinylbenzoate synthase [Erwinia carotovora subsp. atroseptica SCRI1043]
26	NP_930302	37526958	O-succinylbenzoate synthase [Photorhabdus luminescens subsp laumondii TTO1]
27	ZP_007...	77629610	COG1441: O-succinylbenzoate synthase [Yersinia pseudotuberculosis IP 31758]
28	YP_648048	108812281	O-succinylbenzoate-CoA synthase [Yersinia pestis Nepal516]
29	YP_071067	51596876	O-succinylbenzoate synthase [Yersinia pseudotuberculosis IP 32953]
30	YP_088983	52425846	O-succinylbenzoate synthase [Mannheimia succiniciproducens MBEL55E]
31	ZP_007...	75429736	O-succinylbenzoate synthase and related enzymes [Actinobacil succinogenes 130Z]
32	YP_130803	54309783	O-succinylbenzoate synthase [Photobacterium profundum SS9

33	ZP_012...	90410797	O-succinylbenzoate synthase [Photobacterium profundum 3TC
34	ZP_011...	89073244	O-succinylbenzoate synthase [Photobacterium sp. SKA34]
35	ZP_012...	90579264	O-succinylbenzoate synthase [Vibrio angustum S14]
36	YP_205050	59712274	O-succinylbenzoate synthase [Vibrio fischeri ES114]
37	Q9CLV7	17368773	O-succinylbenzoate synthase (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzo acid synthase)
38	YP_718774	113460708	O-succinylbenzoate-CoA synthase [Haemophilus somnus 129I
39	ZP_001...	32029563	COG1441: O-succinylbenzoate synthase [Haemophilus somnu 2336]
40	YP_248668	68249556	O-succinylbenzoate synthase [Haemophilus influenzae 86-028
41	ZP_001...	42631291	COG1441: O-succinylbenzoate synthase [Haemophilus influer R2866]
42	NP_873540	33152187	O-succinylbenzoate synthase [Haemophilus ducreyi 35000HP]
43	ZP_001...	46129092	COG1441: O-succinylbenzoate synthase [Haemophilus influer R2846]
44	P44961	17380438	O-succinylbenzoate synthase (OSB synthase) (OSBS) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzo acid synthase)
45	NP_439130	30995414	O-succinylbenzoate synthase [Haemophilus influenzae Rd KW
46	AAC22626	1573992	O-succinylbenzoate-CoA synthase (menC) [Haemophilus influenzae Rd KW20]
47	NP_761958	27366430	O-succinylbenzoate synthase [Vibrio vulnificus CMCP6]
48	NP_933912	37679303	O-succinylbenzoate synthase [Vibrio vulnificus YJ016]
49	ZP_007...	75854299	COG1441: O-succinylbenzoate synthase [Vibrio sp. Ex25]
50	NP_797311	28897706	O-succinylbenzoate synthase [Vibrio parahaemolyticus RIMD 2210633]
51	ZP_007...	75827285	COG1441: O-succinylbenzoate synthase [Vibrio cholerae O39
52	ZP_012...	91228601	O-succinylbenzoate synthase [Vibrio alginolyticus 12G01]
53	ZP_007...	75830779	COG1441: O-succinylbenzoate synthase [Vibrio cholerae MO
54	ZP_007...	75823556	COG1441: O-succinylbenzoate synthase [Vibrio cholerae RC3
55	ZP_007...	75818947	COG1441: O-succinylbenzoate synthase [Vibrio cholerae V51
56	ZP_009...	84387750	O-succinylbenzoate synthase [Vibrio splendidus 12B01]
57	ZP_010...	86148507	O-succinylbenzoate synthase [Vibrio sp. MED222]
58	ZP_001...	46143800	COG1441: O-succinylbenzoate synthase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]
59	ZP_008...	78684421	O-succinylbenzoate-CoA synthase [Shewanella sp. ANA-3]
60	YP_735889	113972096	O-succinylbenzoate-CoA synthase [Shewanella sp. MR-4]
61	YP_739876	114049326	O-succinylbenzoate-CoA synthase [Shewanella sp. MR-7]
62	NP_720091	24376048	O-succinylbenzoate synthase [Shewanella oneidensis MR-1]
63	ZP_005...	68542839	O-succinylbenzoate-CoA synthase [Shewanella baltica OS155]
64	ZP_006...	69950062	O-succinylbenzoate-CoA synthase [Shewanella frigidimarina NCIMB 400]
65	ZP_008...	78365986	O-succinylbenzoate-CoA synthase [Shewanella sp. PV-4]
66	ZP_013...	106883655	putative O-succinylbenzoate-CoA synthase [Psychromonas ingrahamii 37]
67	ZP_008...	77814934	O-succinylbenzoate-CoA synthase [Shewanella putrefaciens C 32]
68	ZP_009...	82741684	O-succinylbenzoate-CoA synthase [Shewanella sp. W3-18-1]
69	ZP_005...	68545140	O-succinylbenzoate-CoA synthase [Shewanella amazonensis SB2B]
70	ZP_011...	88948985	similar to O-succinylbenzoate synthase [Halorhodospira halopl SL1]

71	ZP_012...	90407216	O-succinylbenzoate-CoA synthase [Psychromonas sp. CNPT3
72	YP_445478	83814286	o-succinylbenzoic acid (OSB) synthetase [Salinibacter ruber D 13855]
73	ZP_005...	68551553	Mandelate racemase/muconate lactonizing enzyme [Prosthecochloris aestuarii DSM 271]
74	NP_662725	21674660	O-succinylbenzoate-CoA synthase [Chlorobium tepidum TLS]
75	ZP_005...	68548716	Mandelate racemase/muconate lactonizing enzyme [Pelodictyc phaeoclathratiforme BU-1]
76	YP_374258	78186215	O-succinylbenzoate-CoA synthase [Pelodictyon luteolum DSM 273]
77	YP_645615	108805678	Mandelate racemase/muconate lactonizing enzyme-like protei [Rubrobacter xylanophilus DSM 9941]
78	ZP_005...	67938339	Mandelate racemase/muconate lactonizing enzyme [Chlorobiu phaeobacteroides BS1]
79	ZP_013...	110596953	Mandelate racemase/muconate lactonizing enzyme [Chlorobiu ferrooxidans DSM 13031]
80	YP_380012	78189674	O-succinylbenzoate-CoA synthase [Chlorobium chlorochroma CaD3]
81	YP_284833	71907246	Mandelate racemase/muconate lactonizing enzyme [Dechloromonas aromatica RCB]
82	ZP_005...	67935850	O-succinylbenzoate-CoA synthase [Chlorobium phaeobacteroi DSM 266]
83	ZP_006...	71481154	O-succinylbenzoate-CoA synthase [Prosthecochloris vibriofon DSM 265]
84	YP_008662	46447297	putative o-succinylbenzoate synthase II, menC [Candidatus Protochlamydia amoebophila UWE25]
85	YP_462873	85860671	o-succinylbenzoate synthase [Syntrophus aciditrophicus SB]
86	ZP_005...	67918350	O-succinylbenzoate-CoA synthase [Chlorobium limicola DSM 245]
87	NP_177056	15221557	catalytic/ hydrolase [Arabidopsis thaliana]
88	AAZ40195	71738181	chloroplast Phyllo [Arabidopsis thaliana]
89	BAE99027	110742201	hypothetical protein [Arabidopsis thaliana]
90	YP_327018	76802010	O-succinylbenzoate-CoA synthase (OSB synthase; 4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) [Natronomonas pharaonis DSM 2160]
91	YP_400037	81299829	O-succinylbenzoate-CoA synthase-like [Synechococcus elonga PCC 7942]
92	YP_055613	50842386	O-succinylbenzoate synthase [Propionibacterium acnes KPA171202]
93	ZP_006...	71369872	Mandelate racemase/muconate lactonizing enzyme [Nocardioi sp. JS614]
94	ZP_003...	62425058	COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Brevibacterium linens BL2]
95	NP_938803	38233036	O-succinylbenzoate synthase [Corynebacterium diphtheriae N 13129]
96	ZP_011...	88809872	putative O-succinylbenzoate synthase [Synechococcus sp. WH 7805]
97	NP_532333	17935543	mandelate racemase/muconate lactonizing enzyme family prot [Agrobacterium tumefaciens str. C58]
98	YP_289471	72161814	O-succinylbenzoate synthase [Thermobifida fusca YX]
99	YP_292734	72383379	O-succinylbenzoate-CoA synthase [Prochlorococcus marinus s NATL2A]
100	YP_061322	50954034	O-succinylbenzoate synthase [Leifsonia xyli subsp. xyli str.

			CTCB07]
101	YP_121759	54027517	O-succinylbenzoate synthase [Nocardia farcinica IFM 10152]
102	YP_474694	86605931	O-succinylbenzoate synthetase [Synechococcus sp. JA-3-3Ab]
103	ZP_011...	88855933	O-succinylbenzoate synthase [marine actinobacterium PHSC2
104	YP_135532	55377682	chloromuconate cycloisomerase [Haloarcula marismortui ATC 43049]
105	NP_737087	25027033	O-succinylbenzoate synthase [Corynebacterium efficiens YS-
106	YP_476976	86608214	O-succinylbenzoate synthetase [Synechococcus sp. JA-2-3B'a(13)]
107	ZP_009...	84494961	O-succinylbenzoate-CoA synthase [Janibacter sp. HTCC2649]
108	Q9CBB2	17368727	Probable O-succinylbenzoate synthase (OSB synthase) (OSBS (2'-carboxyphenyl)-4-oxybutyric acid synthase) (O-succinylbenzoic acid synthase)
109	ZP_012...	90201691	Mandelate racemase/muconate lactonizing enzyme [Mycobacterium vanbaalenii PYR-1]
110	ZP_013...	110606236	Mandelate racemase/muconate lactonizing enzyme [Thermofil pendens Hrk 5]
111	ZP_009...	83951694	mandelate racemase/muconate lactonizing enzyme, putative [Roseovarius nubinhibens ISM]
112	ZP_011...	89338607	Mandelate racemase/muconate lactonizing enzyme [Mycobacterium flavescens PYR-GCK]
113	YP_679013	110638804	chloromuconate cycloisomerase [Cytophaga hutchinsonii ATC 33406]
114	ZP_008...	81255566	COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Mycobacterium tuberculosis
115	ZP_012...	92910340	Mandelate racemase/muconate lactonizing enzyme [Mycobacterium sp. JLS]
116	YP_701966	111018994	possible O-succinylbenzoate synthase [Rhodococcus sp. RHA
117	NP_385940	15965587	hypothetical protein SMc00459 [Sinorhizobium meliloti 1021]
118	YP_657641	110667830	O-succinylbenzoate-CoA synthase (OSB synthase; 4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) [Haloquadratum walsbyi DSM 16790]
119	NP_949301	39937025	putative muconate cycloisomerase [Rhodopseudomonas palust CGA009]
120	YP_637920	108797723	Mandelate racemase/muconate lactonizing enzyme-like protein [Mycobacterium sp. MCS]
121	ZP_010...	87123567	putative O-succinylbenzoate synthase [Synechococcus sp. RS9917]
122	ZP_003...	62514958	COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Lactobacillus casei ATCC 33
123	YP_631725	108761657	putative O-succinylbenzoic acid synthase [Myxococcus xanthu DK 1622]
124	ZP_008...	77684669	Mandelate racemase/muconate lactonizing enzyme [Alkaliphil metalliredigenes QYMF]
125	NP_681964	22298717	O-succinylbenzoate synthase [Thermosynechococcus elongatu BP-1]
126	ZP_010...	84518761	O-succinylbenzoate-CoA synthase [Prochlorococcus marinus s MIT 9211]
127	YP_224766	62389364	O-succinylbenzoate synthase [Corynebacterium glutamicum ATCC 13032]
128	YP_326891	76801883	mandelate racemase homolog / muconate lactonizing enzyme homolog [Natronomonas pharaonis DSM 2160]
129	ZP_011...	89203372	Mandelate racemase/muconate lactonizing enzyme [Bacillus

			cereus subsp. cytotoxis NVH 391-98]
130	ZP_010...	87310011	chloromuconate cycloisomerase [Blastopirellula marina DSM 3645]
131	NP_962984	41410148	O-succinylbenzoate synthase [Mycobacterium avium subsp. paratuberculosis K-10]
132	ZP_010...	86133686	chloromuconate cycloisomerase [Tenacibaculum sp. MED152]
133	YP_574532	92114604	mandelate racemase/muconate lactonizing enzyme [Chromohalobacter salexigens DSM 3043]
134	NP_898395	33866836	putative O-succinylbenzoate synthase [Synechococcus sp. WH 8102]
135	YP_063987	51244103	similar to N-acylamino acid racemase (MenC) [Desulfotalea psychrophila LSv54]
136	YP_703750	111020778	probable glucarate dehydratase [Rhodococcus sp. RHA1]
137	XP_383821	46115606	conserved hypothetical protein [Gibberella zeae PH-1]
138	ZP_010...	86131888	chloromuconate cycloisomerase [Cellulophaga sp. MED134]
139	AAC46430	2996615	muconate cycloisomerase [Acinetobacter sp. ADP1]
140	YP_628593	108763693	mandelate racemase/muconate lactonizing enzyme family prot [Myxococcus xanthus DK 1622]
141	YP_580535	93006098	mandelate racemase/muconate lactonizing enzyme [Psychroba cryohalolentis K5]
142	Q43931	51704317	Muconate cycloisomerase 1 (Muconate cycloisomerase I) (Cis, muconate lactonizing enzyme I) (MLE)
143	ZP_008...	77739092	IMP dehydrogenase/GMP reductase:Mandelate racemase/muconate lactonizing enzyme [Rhodopseudomonas palustris BisA53]
144	YP_134998	55377148	chloromuconate cycloisomerase [Haloarcula marismortui ATC 43049]
145	ZP_007...	76258404	Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Chloroflexus aurantia J-10-fl]
146	ZP_009...	83953326	mandelate racemase/muconate lactonizing enzyme family prot [Sulfitobacter sp. NAS-14.1]
147	YP_662355	109899100	Mandelate racemase/muconate lactonizing enzyme-like [Pseudoalteromonas atlantica T6c]
148	YP_168801	56698427	mandelate racemase/muconate lactonizing enzyme family prot [Silicibacter pomeroyi DSS-3]
149	YP_485246	86748750	Mandelate racemase/muconate lactonizing enzyme [Rhodopseudomonas palustris HaA2]
150	ZP_013...	94494991	mandelate racemase [Sphingomonas sp. SKA58]
151	NP_243872	15615568	muconate cycloisomerase [Bacillus halodurans C-125]
152	ZP_010...	86140323	putative muconate cycloisomerase [Flavobacterium sp. MED2
153	NP_279996	15790172	YkfB2 [Halobacterium sp. NRC-1]
154	ZP_009...	83857375	chloromuconate cycloisomerase [Croceibacter atlanticus HTCC2559]
155	YP_611403	99078145	Mandelate racemase/muconate lactonizing enzyme-like [Silicibacter sp. TM1040]
156	YP_098603	53712611	chloromuconate cycloisomerase [Bacteroides fragilis YCH46]
157	YP_568773	91976114	mandelate racemase/muconate lactonizing enzyme [Rhodopseudomonas palustris BisB5]
158	EAO86088	77654347	Mandelate racemase/muconate lactonizing enzyme [Rhodopseudomonas palustris BisB5]
159	YP_531332	90422962	mandelate racemase/muconate lactonizing enzyme [Rhodopseudomonas palustris BisB18]

160	YP_210966	60680822	putative muconate cycloisomerase [Bacteroides fragilis NCTC 9343]
161	ZP_003...	62516188	COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Lactobacillus delbrueckii sul bulgaricus ATCC BAA-365]
162	YP_619492	104774512	hypothetical protein Ldb1742 [Lactobacillus delbrueckii subsp bulgaricus ATCC 11842]
163	YP_657793	110667982	mandelate racemase/muconate lactonizing enzyme family prot [Haloquadratum walsbyi DSM 16790]
164	ZP_012...	91214878	chloromuconate cycloisomerase [Psychroflexus torquis ATCC 700755]
165	NP_789672	28572892	O-succinylbenzoate synthase [Tropheryma whipplei TW08/27
166	NP_787865	28493704	O-succinylbenzoate synthase [Tropheryma whipplei str. Twist
167	AAZ32484	71483050	L-alanine-DL-glutamate epimerase-like [uncultured euryarcha Alv-FOS1]
168	NP_280565	15790741	YkfB1 [Halobacterium sp. NRC-1]
169	NP_813614	29350111	chloromuconate cycloisomerase [Bacteroides thetaiotaomicron VPI-5482]
170	ZP_011...	88806559	chloromuconate cycloisomerase YkfB1 [Robiginitalea biforma HTCC2501]
171	ZP_011...	88805797	chloromuconate cycloisomerase [Robiginitalea biformata HTCC2501]
172	ZP_009...	83944285	mandelate racemase/muconate lactonizing enzyme family prot [Sulfitobacter sp. EE-36]
173	YP_674100	110633892	Mandelate racemase/muconate lactonizing enzyme-like [Mesorhizobium sp. BNC1]
174	YP_469857	86357965	probable muconate cycloisomerase I protein [Rhizobium etli C 42]
175	YP_084167	52142662	mandelate racemase/muconate lactonizing enzyme [Bacillus cereus E33L]
176	YP_036935	49479091	mandelate racemase/muconate lactonizing enzyme [Bacillus thuringiensis serovar konkukian str. 97-27]
177	NP_693887	23100420	muconate cycloisomerase [Oceanobacillus iheyensis HTE831]
178	NP_832599	30020968	Mandelate racemase/muconate lactonizing enzyme family prot [Bacillus cereus ATCC 14579]
179	ZP_012...	90592089	Mandelate racemase/muconate lactonizing enzyme [Flavobacterium johnsoniae UW101]
180	YP_235793	66045952	Mandelate racemase/muconate lactonizing enzyme:Mandelate racemase/muconate lactonizing enzyme [Pseudomonas syringa pv. syringae B728a]
181	ZP_003...	65320143	COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Bacillus anthracis str. A2012
182	AAL93701	19712800	O-succinylbenzoate-CoA synthase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]
183	YP_028918	49185666	mandelate racemase/muconate lactonizing enzyme family prot [Bacillus anthracis str. Sterne]
184	ZP_007...	75761536	L-Ala-D/L-Glu racemase [Bacillus thuringiensis serovar israelensis ATCC 35646]
185	ZP_010...	87303747	putative O-succinylbenzoate synthase [Synechococcus sp. WH 5701]
186	NP_979182	42781935	mandelate racemase/muconate lactonizing enzyme family prot [Bacillus cereus ATCC 10987]
187	YP_576599	92116870	mandelate racemase/muconate lactonizing enzyme [Nitrobacte

			hamburgensis X14]
188	NP_815232	29376078	mandelate racemase/muconate lactonizing enzyme family prot [Enterococcus faecalis V583]
189	NP_905663	34541184	mandelate racemase/muconate lactonizing enzyme family prot [Porphyromonas gingivalis W83]
190	ZP_012...	90201746	Mandelate racemase/muconate lactonizing enzyme [Mycobacterium vanbaalenii PYR-1]
191	YP_274664	71737005	mandelate racemase/muconate lactonizing enzyme family prot [Pseudomonas syringae pv. phaseolicola 1448A]
192	YP_414443	82699869	Mandelate racemase/muconate lactonizing enzyme [Brucella melitensis biovar Abortus 2308]
193	YP_127261	54294846	hypothetical protein lpl1925 [Legionella pneumophila str. Lens
194	YP_095972	52842173	chloromuconate cycloisomerase [Legionella pneumophila subs pneumophila str. Philadelphia 1]
195	XP_658217	67516663	hypothetical protein AN0613.2 [Aspergillus nidulans FGSC A4
196	ZP_009...	84389418	putative muconate cycloisomerase I [Vibrio splendidus 12B01]
197	ZP_010...	86140220	mandelate racemase/muconate lactonizing enzyme family prot [Roseobacter sp. MED193]
198	ZP_010...	86145024	putative muconate cycloisomerase I [Vibrio sp. MED222]
199	NP_753701	26247661	Hypothetical protein ycjG [Escherichia coli CFT073]
200	NP_415841	90111249	L-Ala-D/L-Glu epimerase [Escherichia coli K12]

Table 49. Examples of MenE polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	ZP_009...	83588247	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Escherichia coli 101-1]
2	AAB04893	520813	o-succinylbenzoate-CoA synthase
3	YP_404018	82777669	o-succinylbenzoate-CoA ligase [Shigella dysenteriae Sd197]
4	ZP_007...	75512738	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Escherichia coli 53638]
5	ZP_007...	75259724	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Escherichia coli E22]
6	ZP_007...	75238049	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Escherichia coli E110019]
7	NP_288838	15802811	O-succinylbenzoic acid--CoA ligase [Escherichia coli O157:H EDL933]
8	ZP_007...	75230353	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Escherichia coli B7A]
9	NP_311175	15832402	O-succinylbenzoic acid--CoA ligase [Escherichia coli O157:H str. Sakai]
10	YP_311201	74312782	o-succinylbenzoate-CoA ligase [Shigella sonnei Ss046]
11	ZP_007...	75187047	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Escherichia coli E24377A]
12	YP_689747	110806227	o-succinylbenzoate-CoA ligase [Shigella flexneri 5 str. 8401]
13	NP_837862	30063691	O-succinylbenzoic acid--CoA ligase [Shigella flexneri 2a str. 2457T]
14	NP_708146	24113636	O-succinylbenzoic acid--CoA ligase [Shigella flexneri 2a str. 3
15	YP_670199	110642469	O-succinylbenzoic acid-CoA ligase [Escherichia coli 536]
16	YP_541541	91211555	O-succinylbenzoic acid--CoA ligase [Escherichia coli UTI89]
17	YP_408689	82544742	o-succinylbenzoate-CoA ligase [Shigella boydii Sb227]
18	NP_754689	26248649	O-succinylbenzoic acid--CoA ligase [Escherichia coli CFT073
19	YP_149872	56412797	O-succinylbenzoic acid--CoA ligase [Salmonella enterica subsp enterica serovar Paratyphi A str. ATCC 9150]
20	P37418	17865734	2-succinylbenzoate--CoA ligase (OSB-CoA synthetase) (o-succinylbenzoyl-CoA synthetase)
21	YP_217292	62180875	O-succinylbenzoic acid--CoA ligase [Salmonella enterica subsp enterica serovar Choleraesuis str. SC-B67]
22	NP_804415	29141073	O-succinylbenzoic acid--CoA ligase [Salmonella enterica subsp enterica serovar Typhi Ty2]
23	NP_930301	37526957	O-succinylbenzoic acid--CoA ligase [Photorhabdus luminescen subsp. laumondii TTO1]
24	ZP_008...	77957631	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Yersinia bercovieri ATCC 43970]
25	ZP_008...	77975451	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Yersinia frederiksenii ATCC 33641]
26	ZP_008...	77961211	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Yersinia mollaretii ATCC 43969]
27	YP_071066	51596875	O-succinylbenzoic acid--CoA ligase [Yersinia pseudotuberculo IP 32953]
28	ZP_008...	77976639	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Yersinia intermedia ATCC 29909]
29	ZP_007...	77629609	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Yersinia pseudotuberculosis IP 31758]
30	NP_668982	22125559	O-succinylbenzoic acid--CoA ligase [Yersinia pestis KIM]
31	YP_648047	108812280	O-succinylbenzoic acid--CoA ligase [Yersinia pestis Nepal516

32	YP_049321	50120154	O-succinylbenzoic acid--CoA ligase [Erwinia carotovora subsp atroseptica SCRI1043]
33	ZP_012...	90410798	O-succinylbenzoic acid--CoA ligase [Photobacterium profundi 3TCK]
34	YP_205049	59712273	O-succinylbenzoic acid--CoA ligase [Vibrio fischeri ES114]
35	YP_130802	54309782	O-succinylbenzoic acid--CoA ligase [Photobacterium profundi SS9]
36	AAA21323	405126	unknown
37	ZP_012...	90579263	O-succinylbenzoic acid--CoA ligase [Vibrio angustum S14]
38	ZP_011...	89073245	O-succinylbenzoic acid--CoA ligase [Photobacterium sp. SKA
39	YP_247911	68248799	O-succinylbenzoic acid--CoA ligase [Haemophilus influenzae 028NP]
40	ZP_001...	46128952	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Haemophilus influenzae R2846]
41	ZP_001...	42630497	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Haemophilus influenzae R2866]
42	NP_438363	16272158	O-succinylbenzoic acid--CoA ligase [Haemophilus influenzae KW20]
43	YP_088056	52424919	O-succinylbenzoic acid--CoA ligase [Mannheimia succiniciproducens MBEL55E]
44	YP_719419	113461350	O-succinylbenzoic acid--CoA ligase [Haemophilus somnus 129PT]
45	ZP_001...	46156759	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Haemophilus somnus 2336]
46	NP_245294	15602222	O-succinylbenzoic acid--CoA ligase [Pasteurella multocida sub multocida str. Pm70]
47	ZP_003...	53728977	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Actinobacillus pleuropneumoniae serovar 1 str. 4074
48	ZP_007...	75823555	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Vibrio cholerae RC385]
49	NP_231605	15641973	O-succinylbenzoic acid--CoA ligase [Vibrio cholerae O1 biova eltor str. N16961]
50	ZP_007...	75830778	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Vibrio cholerae MO10]
51	ZP_007...	75827284	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Vibrio cholerae O395]
52	NP_797312	28897707	O-succinylbenzoic acid--CoA ligase [Vibrio parahaemolyticus RIMD 2210633]
53	NP_873708	33152355	O-succinylbenzoic acid--CoA ligase [Haemophilus ducreyi 35000HP]
54	ZP_007...	75818642	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Vibrio cholerae V51]
55	ZP_007...	75429473	acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Actinobacillus succinogenes 130Z]
56	ZP_012...	91228600	O-succinylbenzoic acid--CoA ligase [Vibrio alginolyticus 12G
57	ZP_007...	75854300	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Vibrio sp. Ex25]
58	NP_761957	27366429	O-succinylbenzoic acid--CoA ligase [Vibrio vulnificus CMCP
59	NP_933913	37679304	O-succinylbenzoic acid--CoA ligase [Vibrio vulnificus YJ016]
60	ZP_010...	86148506	O-succinylbenzoic acid--CoA ligase [Vibrio sp. MED222]
61	ZP_011...	88948986	O-succinylbenzoate-CoA ligase [Halorhodospira halophila SL1
62	ZP_009...	84387751	O-succinylbenzoic acid--CoA ligase [Vibrio splendidus 12B01
63	ZP_008...	78684422	O-succinylbenzoate-CoA ligase [Shewanella sp. ANA-3]

64	ZP_005...	68542838	O-succinylbenzoate-CoA ligase [Shewanella baltica OS155]
65	YP_735890	113972097	O-succinylbenzoate-CoA ligase [Shewanella sp. MR-4]
66	YP_739877	114049327	O-succinylbenzoate-CoA ligase [Shewanella sp. MR-7]
67	ZP_009...	82741685	O-succinylbenzoate-CoA ligase [Shewanella sp. W3-18-1]
68	ZP_008...	77814935	O-succinylbenzoate-CoA ligase [Shewanella putrefaciens CN-
69	NP_720092	24376049	O-succinylbenzoic acid--CoA ligase, putative [Shewanella oneidensis MR-1]
70	ZP_008...	78365987	O-succinylbenzoate-CoA ligase [Shewanella sp. PV-4]
71	ZP_005...	68545139	O-succinylbenzoate-CoA ligase [Shewanella amazonensis SB2
72	ZP_006...	69950061	O-succinylbenzoate-CoA ligase [Shewanella frigidimarina NCIMB 400]
73	YP_645614	108805677	O-succinylbenzoate-CoA ligase [Rubrobacter xylanophilus DS 9941]
74	ZP_005...	67935851	O-succinylbenzoate-CoA ligase [Chlorobium phaeobacteroides DSM 266]
75	YP_374257	78186214	O-succinylbenzoate-CoA ligase [Pelodictyon luteolum DSM 2
76	ZP_013...	110596954	O-succinylbenzoate-CoA ligase [Chlorobium ferrooxidans DS 13031]
77	ZP_006...	71481152	O-succinylbenzoate-CoA ligase [Prosthecochloris vibrioformis DSM 265]
78	ZP_005...	68548718	O-succinylbenzoate-CoA ligase [Pelodictyon phaeoclathratifor BU-1]
79	ZP_005...	67918351	O-succinylbenzoate-CoA ligase [Chlorobium limicola DSM 24
80	NP_662726	21674661	O-succinylbenzoic acid-CoA ligase [Chlorobium tepidum TLS
81	ZP_005...	67938340	O-succinylbenzoate-CoA ligase [Chlorobium phaeobacteroides BS1]
82	ZP_013...	106883654	AMP-dependent synthetase and ligase [Psychromonas ingrahar 37]
83	CAB93977	8347017	putative O-succinylbenzoic acid-CoA ligase [Proteus mirabilis
84	ZP_012...	90407217	O-succinylbenzoic acid-CoA ligase [Psychromonas sp. CNPT3
85	YP_379967	78189629	O-succinylbenzoate-CoA ligase [Chlorobium chlorochromatii CaD3]
86	ZP_005...	68551554	O-succinylbenzoate-CoA ligase [Prosthecochloris aestuarii DS 271]
87	YP_445479	83815832	O-succinylbenzoate-CoA ligase [Salinibacter ruber DSM 1385
88	AAO49468	28629104	MenE [Serratia proteamaculans]
89	YP_631726	108763899	O-succinylbenzoate-CoA ligase [Myxococcus xanthus DK 162
90	NP_471116	16800848	O-succinylbenzoic acid--CoA ligase [Listeria innocua Clip112
91	Q92AY8	60416425	2-succinylbenzoate--CoA ligase (OSB-CoA synthetase) (o-succinylbenzoyl-CoA synthetase)
92	YP_516754	89893267	o-succinylbenzoic acid--CoA ligase [Desulfitobacterium hafnie Y51]
93	P23971	20141517	2-succinylbenzoate--CoA ligase (OSB-CoA synthetase) (o-succinylbenzoyl-CoA synthetase)
94	Q71YZ5	60390034	2-succinylbenzoate--CoA ligase (OSB-CoA synthetase) (o-succinylbenzoyl-CoA synthetase)
95	NP_465197	16803712	O-succinylbenzoic acid--CoA ligase [Listeria monocytogenes EGD-e]
96	YP_535073	90961157	O-succinylbenzoic acid--CoA ligase [Lactobacillus salivarius subsp. salivarius UCC118]
97	P58730	60416414	2-succinylbenzoate--CoA ligase (OSB-CoA synthetase) (o-succinylbenzoyl-CoA synthetase)
98	ZP_012...	92088721	O-succinylbenzoate-CoA ligase [Lactobacillus reuteri 100-23]

99	ZP_002...	47096745	O-succinylbenzoate--CoA ligase [Listeria monocytogenes str. F6854]
100	YP_462872	85860670	o-succinylbenzoic acid--CoA ligase [Syntrophus aciditrophicu SB]
101	ZP_011...	89090333	O-succinylbenzoate-CoA ligase [Lactobacillus reuteri JCM 11
102	YP_092772	52786943	O-succinylbenzoic acid--CoA ligase [Bacillus licheniformis A 14580]
103	ZP_013...	109647420	O-succinylbenzoate-CoA ligase [Desulfitobacterium hafniense DCB-2]
104	Q838K1	38502949	2-succinylbenzoate--CoA ligase (OSB-CoA synthetase) (o-succinylbenzoyl-CoA synthetase)
105	YP_658135	110668324	O-succinylbenzoic acid--CoA ligase [Haloquadratum walsbyi DSM 16790]
106	YP_429376	83589367	AMP-dependent synthetase and ligase [Moorella thermoacetic ATCC 39073]
107	YP_148725	56421407	O-succinylbenzoic acid--CoA ligase [Geobacillus kaustophilus HTA426]
108	AAP59034	31621276	long chain fatty acid CoA ligase [Thiocapsa roseopersicina]
109	Q816I1	38502941	2-succinylbenzoate--CoA ligase (OSB-CoA synthetase) (o-succinylbenzoyl-CoA synthetase)
110	ZP_011...	89204350	O-succinylbenzoate-CoA ligase [Bacillus weihenstephanensis KBAB4]
111	Q72YK9	60390047	2-succinylbenzoate--CoA ligase (OSB-CoA synthetase) (o-succinylbenzoyl-CoA synthetase)
112	ZP_002...	47568031	O-succinylbenzoate-CoA ligase [Bacillus cereus G9241]
113	ZP_007...	75762878	O-succinylbenzoic acid--CoA ligase [Bacillus thuringiensis serovar israelensis ATCC 35646]
114	Q6HC29	60390012	2-succinylbenzoate--CoA ligase (OSB-CoA synthetase) (o-succinylbenzoyl-CoA synthetase)
115	ZP_013...	106888974	AMP-dependent synthetase and ligase [Roseiflexus sp. RS-1]
116	ZP_003...	48866140	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Oenococcus oeni PSU-1]
117	YP_004317	46198650	acyl-CoA ligase [Thermus thermophilus HB27]
118	ZP_000...	23025147	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Leuconostoc mesenteroides subsp. mesenteroides A 8293]
119	ZP_011...	89201875	O-succinylbenzoate-CoA ligase [Bacillus cereus subsp. cytoto NVH 391-98]
120	YP_703422	111020450	acyl-CoA synthetase [Rhodococcus sp. RHA1]
121	YP_021759	47530410	O-succinylbenzoic acid--CoA ligase [Bacillus anthracis str. 'An Ancestor']
122	ZP_003...	65322220	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Bacillus anthracis str. A2012]
123	Q632I5	60389924	2-succinylbenzoate--CoA ligase (OSB-CoA synthetase) (o-succinylbenzoyl-CoA synthetase)
124	YP_701480	111018508	AMP-dependent synthetase [Rhodococcus sp. RHA1]
125	NP_961681	41408845	hypothetical protein MAP2747 [Mycobacterium avium subsp. paratuberculosis K-10]
126	ZP_005...	67929307	AMP-dependent synthetase and ligase [Solibacter usitatus Ellin6076]
127	ZP_011...	89099705	O-succinylbenzoic acid--CoA ligase [Bacillus sp. NRRL B-14
128	YP_286022	71908435	AMP-dependent synthetase and ligase [Dechloromonas aromat RCB]

129	YP_327019	76802011	O-succinylbenzoic acid--CoA ligase [Natronomonas pharaonis DSM 2160]
130	ZP_005...	68054687	O-succinylbenzoate-CoA ligase [Exiguobacterium sibiricum 255]
131	ZP_013...	106889322	O-succinylbenzoate-CoA ligase [Roseiflexus sp. RS-1]
132	YP_360441	78043276	long-chain-fatty-acid--CoA ligase [Carboxydothermus hydrogenoformans Z-2901]
133	ZP_006...	69287078	AMP-dependent synthetase and ligase [Kineococcus radiotolei SRS30216]
134	ZP_007...	76796781	AMP-dependent synthetase and ligase [Thermoanaerobacter ethanolicus ATCC 33223]
135	YP_345691	77454823	fatty-acid--CoA ligase [Rhodococcus erythropolis PR4]
136	Q9CHK3	38503173	2-succinylbenzoate--CoA ligase (OSB-CoA synthetase) (o-succinylbenzoyl-CoA synthetase)
137	AAK04826	12723641	O-succinylbenzoic acid-CoA ligase (EC 6.2.1.26) [Lactococcus lactis subsp. lactis Il1403]
138	ZP_013...	106892703	AMP-dependent synthetase and ligase [Roseiflexus sp. RS-1]
139	YP_121358	54027116	O-succinylbenzoic acid--CoA ligase [Nocardia farcinica IFM 10152]
140	NP_967282	42521902	long-chain fatty-acid-CoA ligase [Bdellovibrio bacteriovorus HD100]
141	ZP_012...	90201690	AMP-dependent synthetase and ligase [Mycobacterium vanbaalenii PYR-1]
142	ZP_003...	62463997	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Lactococcus lactis subsp. cremoris SK11]
143	ZP_007...	76260558	AMP-dependent synthetase and ligase [Chloroflexus aurantiac 10-fl]
144	YP_635261	108760531	putative long-chain fatty acid--CoA ligase [Myxococcus xanth DK 1622]
145	YP_076019	51893328	acyl-CoA synthase [Symbiobacterium thermophilum IAM 148
146	YP_703902	111020930	probable O-succinylbenzoate--CoA ligase [Rhodococcus sp. RHA1]
147	ZP_005...	67930904	AMP-dependent synthetase and ligase [Solibacter usitatus Ellin6076]
148	YP_570930	91978271	AMP-dependent synthetase and ligase [Rhodopseudomonas palustris BisB5]
149	ZP_006...	71368939	AMP-dependent synthetase and ligase [Nocardioides sp. JS614
150	ZP_007...	75854275	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Vibrio sp. Ex25]
151	YP_675489	110635281	AMP-dependent synthetase and ligase [Mesorhizobium sp. BN
152	ZP_006...	69276546	AMP-dependent synthetase and ligase [Mesorhizobium sp. BN
153	NP_946096	39933820	putative acid-CoA ligase [Rhodopseudomonas palustris CGA0
154	YP_487676	86751180	AMP-dependent synthetase and ligase [Rhodopseudomonas palustris HaA2]
155	ZP_012...	90201659	AMP-dependent synthetase and ligase [Mycobacterium vanbaalenii PYR-1]
156	YP_119428	54025186	putative acyl-CoA synthetase [Nocardia farcinica IFM 10152]
157	ZP_011...	89201730	AMP-dependent synthetase and ligase [Bacillus cereus subsp. cytotoxis NVH 391-98]
158	ZP_011...	89338610	AMP-dependent synthetase and ligase [Mycobacterium flavesc PYR-GCK]
159	ZP_007...	76260385	AMP-dependent synthetase and ligase [Chloroflexus aurantiac 10-fl]

160	NP_822521	29827887	acid:CoA ligase [Streptomyces avermitilis MA-4680]
161	ZP_011...	88798761	putative acid-CoA ligase [Reinekea sp. MED297]
162	YP_637919	108797722	AMP-dependent synthetase and ligase [Mycobacterium sp. MC
163	NP_623535	20808364	Acyl-CoA synthetase (AMP-forming)/AMP-acid ligase II [Thermoanaerobacter tengcongensis MB4]
164	NP_959714	41406878	acyl-CoA synthase [Mycobacterium avium subsp. paratubercu K-10]
165	ZP_011...	89338645	AMP-dependent synthetase and ligase [Mycobacterium flavesc PYR-GCK]
166	ZP_012...	92910341	AMP-dependent synthetase and ligase [Mycobacterium sp. JLS
167	YP_323145	75908849	O-succinylbenzoic acid--CoA ligase [Anabaena variabilis ATC 29413]
168	NP_302632	15828369	acyl-CoA synthase [Mycobacterium leprae TN]
169	CAC18323	11595497	feruloyl-CoA synthetase [Amycolatopsis sp. HR167]
170	Q5HNB2	81674064	2-succinylbenzoate--CoA ligase (OSB-CoA synthetase) (o-succinylbenzoyl-CoA synthetase)
171	NP_484079	17227531	O-succinylbenzoic acid--CoA ligase [Nostoc sp. PCC 7120]
172	Q8ENZ7	38503019	2-succinylbenzoate--CoA ligase (OSB-CoA synthetase) (o-succinylbenzoyl-CoA synthetase)
173	YP_158159	56476570	putative ADP-producing CoA ligase, similar to feruloyl-CoA synthetase [Azoarcus sp. EbN1]
174	YP_119728	54025486	putative acyl-CoA synthetase [Nocardia farcinica IFM 10152]
175	ZP_007...	76260423	O-succinylbenzoate-CoA ligase [Chloroflexus aurantiacus J-10
176	YP_297767	73537400	acyl-CoA synthase [Ralstonia eutropha JMP134]
177	YP_301060	73662279	O-succinylbenzoic acid-CoA ligase [Staphylococcus saprophyt subsp. saprophyticus ATCC 15305]
178	YP_116921	54022679	acyl-CoA synthase [Nocardia farcinica IFM 10152]
179	YP_713609	111222815	putative acyl-CoA synthetase (long-chain-fatty-acid--CoA liga [Frankia alni ACN14a]
180	YP_293347	72383993	AMP-dependent synthetase and ligase [Ralstonia eutropha JMP134]
181	YP_372175	78062267	acyl-CoA synthase [Burkholderia sp. 383]
182	YP_704436	111021464	probable acyl-CoA synthetase [Rhodococcus sp. RHA1]
183	YP_521606	89899135	AMP-dependent synthetase and ligase [Rhodoferax ferrireduce T118]
184	ZP_009...	83375403	putative acyl-CoA synthetase [Rhodobacter sphaeroides ATCC 17029]
185	ZP_005...	68228842	AMP-dependent synthetase and ligase [Frankia sp. EAN1pec]
186	YP_587262	94314053	AMP-dependent synthetase and ligase [Ralstonia metallidurans CH34]
187	NP_420134	16125570	long-chain-fatty-acid--CoA ligase [Caulobacter crescentus CB1
188	NP_798343	28898738	putative long-chain-fatty-acid-CoA ligase [Vibrio parahaemolyticus RIMD 2210633]
189	YP_702248	111019276	possible long-chain-fatty-acid--CoA ligase [Rhodococcus sp. RHA1]
190	YP_113483	53804874	acyltransferase family protein [Methylococcus capsulatus str. Bath]
191	YP_706623	111023651	probable acyl-CoA synthetases [Rhodococcus sp. RHA1]
192	ZP_011...	89070037	malonyl-CoA synthase [Oceanicola granulosus HTCC2516]
193	YP_496490	87199233	AMP-dependent synthetase and ligase [Novosphingobium aromaticivorans DSM 12444]
194	ZP_011...	89337575	AMP-dependent synthetase and ligase [Mycobacterium flavesc PYR-GCK]

195	YP_120006	54025764	acyl-CoA synthase [Nocardia farcinica IFM 10152]
196	ZP_012...	91228657	putative long-chain-fatty-acid-CoA ligase [Vibrio alginolyticu: 12G01]
197	ZP_009...	83943831	malonyl-CoA synthase [Sulfitobacter sp. EE-36]
198	ZP_009...	83955309	malonyl-CoA synthase [Sulfitobacter sp. NAS-14.1]
199	YP_707396	111024976	possible acid-CoA ligase [Rhodococcus sp. RHA1]
200	ZP_001...	53686856	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Nostoc punctiforme PCC 73102]

Table 50. Examples of MenB polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	YP_408691	82544744	dihydroxynaphtoic acid synthetase [Shigella boydii Sb227]
2	YP_689749	110806229	dihydroxynaphtoic acid synthetase [Shigella flexneri 5 str. 840
3	YP_404020	82777671	dihydroxynaphtoic acid synthetase [Shigella dysenteriae Sd197
4	NP_288840	15802813	naphthoate synthase [Escherichia coli O157:H7 EDL933]
5	YP_149870	56412795	naphthoate synthase [Salmonella enterica subsp. enterica serov Paratyphi A str. ATCC 9150]
6	YP_217294	62180877	naphthoate synthase [Salmonella enterica subsp. enterica serov Choleraesuis str. SC-B67]
7	ZP_008...	77975453	COG0447: Dihydroxynaphthoic acid synthase [Yersinia frederiksenii ATCC 33641]
8	YP_648049	108812282	naphthoate synthase [Yersinia pestis Nepal516]
9	NP_668980	22125557	naphthoate synthase [Yersinia pestis KIM]
10	ZP_008...	77976637	COG0447: Dihydroxynaphthoic acid synthase [Yersinia intermedia ATCC 29909]
11	ZP_008...	77961209	COG0447: Dihydroxynaphthoic acid synthase [Yersinia mollar ATCC 43969]
12	ZP_008...	77957629	COG0447: Dihydroxynaphthoic acid synthase [Yersinia bercov ATCC 43970]
13	YP_049319	50120152	naphthoate synthase [Erwinia carotovora subsp. atroseptica SCRI1043]
14	NP_930303	37526959	naphthoate synthase [Photorhabdus luminescens subsp. laumon TTO1]
15	YP_088984	52425847	naphthoate synthase [Mannheimia succiniciproducens MBEL5
16	ZP_007...	75429737	dihydroxynaphthoic acid synthase [Actinobacillus succinogene 130Z]
17	ZP_001...	46143479	COG0447: Dihydroxynaphthoic acid synthase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]
18	ZP_001...	46129093	COG0447: Dihydroxynaphthoic acid synthase [Haemophilus influenzae R2846]
19	Q9CLV5	18202821	Naphthoate synthase (Dihydroxynaphthoic acid synthetase) (DHNA synthetase)
20	NP_439129	16272905	naphthoate synthase [Haemophilus influenzae Rd KW20]
21	YP_248667	68249555	naphthoate synthase [Haemophilus influenzae 86-028NP]
22	ZP_001...	32029562	COG0447: Dihydroxynaphthoic acid synthase [Haemophilus somnus 2336]
23	NP_874258	33152905	naphthoate synthase [Haemophilus ducreyi 35000HP]
24	NP_933911	37679302	naphthoate synthase [Vibrio vulnificus YJ016]
25	NP_761959	27366431	naphthoate synthase [Vibrio vulnificus CMCP6]
26	ZP_012...	91228602	naphthoate synthase [Vibrio alginolyticus 12G01]
27	ZP_007...	75854298	COG0447: Dihydroxynaphthoic acid synthase [Vibrio sp. Ex25
28	NP_797310	28897705	naphthoate synthase [Vibrio parahaemolyticus RIMD 2210633]
29	ZP_007...	75830780	COG0447: Dihydroxynaphthoic acid synthase [Vibrio cholerae MO10]
30	ZP_007...	75818948	COG0447: Dihydroxynaphthoic acid synthase [Vibrio cholerae V51]
31	ZP_007...	75823557	COG0447: Dihydroxynaphthoic acid synthase [Vibrio cholerae RC385]
32	CAA59693	732732	naphthoate synthase [Haemophilus parahaemolyticus]
33	ZP_010...	86148508	naphthoate synthase [Vibrio sp. MED222]
34	ZP_009...	84387749	naphthoate synthase [Vibrio splendidus 12B01]
35	ZP_013...	106882314	naphthoate synthase [Psychromonas ingrahamii 37]

36	ZP_012...	90407332	naphthoate synthase [Psychromonas sp. CNPT3]
37	ZP_005...	67935849	Naphthoate synthase [Chlorobium phaeobacteroides DSM 266
38	NP_662724	21674659	naphthoate synthase [Chlorobium tepidum TLS]
39	ZP_005...	68548715	Naphthoate synthase [Pelodictyon phaeoclathratiforme BU-1]
40	ZP_006...	71481155	Naphthoate synthase [Prosthecochloris vibrioformis DSM 265
41	ZP_005...	67918349	Naphthoate synthase [Chlorobium limicola DSM 245]
42	YP_380013	78189675	naphthoate synthase [Chlorobium chlorochromatii CaD3]
43	ZP_013...	110596952	naphthoate synthase [Chlorobium ferrooxidans DSM 13031]
44	YP_374259	78186216	naphthoate synthase [Pelodictyon luteolum DSM 273]
45	ZP_005...	67938338	Naphthoate synthase [Chlorobium phaeobacteroides BS1]
46	ZP_005...	68551552	Naphthoate synthase [Prosthecochloris aestuarii DSM 271]
47	ZP_011...	88948984	Naphthoate synthase [Halorhodospira halophila SL1]
48	YP_008063	46446698	probable naphthoate synthase, menB [Candidatus Protochlamy amoebophila UWE25]
49	ZP_005...	68054686	Naphthoate synthase [Exiguobacterium sibiricum 255-15]
50	AAS66445	45478466	1,4 dihydroxy-2-naphthaote synthase [Synechococcus sp. PCC 7002]
51	YP_723569	113477508	naphthoate synthase [Trichodesmium erythraeum IMS101]
52	YP_474010	86605247	naphthoate synthase [Synechococcus sp. JA-3-3Ab]
53	P23966	20141516	Naphthoate synthase (Dihydroxynaphthoic acid synthetase) (DHNA synthetase)
54	YP_148726	56421408	naphthoate synthase [Geobacillus kaustophilus HTA426]
55	AAA50401	557492	dihydroxynapthoic acid (DHNA) synthetase
56	NP_834552	30022921	naphthoate synthase [Bacillus cereus ATCC 14579]
57	ZP_003...	65322221	COG0447: Dihydroxynaphthoic acid synthase [Bacillus anthra str. A2012]
58	ZP_007...	75762877	Naphthoate synthase [Bacillus thuringiensis serovar israelensis ATCC 35646]
59	YP_320687	75906391	naphthoate synthase [Anabaena variabilis ATCC 29413]
60	YP_092773	52786944	naphthoate synthase [Bacillus licheniformis ATCC 14580]
61	NP_981306	42784059	naphthoate synthase [Bacillus cereus ATCC 10987]
62	YP_086183	52140645	naphthoate synthase [Bacillus cereus E33L]
63	ZP_011...	89204351	Naphthoate synthase [Bacillus weihenstephanensis KBAB4]
64	YP_171636	56750935	naphthoate synthase [Synechococcus elongatus PCC 6301]
65	NP_486387	17229839	naphthoate synthase [Nostoc sp. PCC 7120]
66	ZP_002...	47568032	naphthoate synthase [Bacillus cereus G9241]
67	ZP_011...	89201876	Naphthoate synthase [Bacillus cereus subsp. cytotoxis NVH 39 98]
68	YP_476819	86608057	naphthoate synthase [Synechococcus sp. JA-2-3B'a(2-13)]
69	ZP_001...	23126174	COG0447: Dihydroxynaphthoic acid synthase [Nostoc punctiforme PCC 73102]
70	YP_399616	81299408	naphthoate synthase [Synechococcus elongatus PCC 7942]
71	ZP_011...	89099706	naphthoate synthase [Bacillus sp. NRRL B-14911]
72	ZP_005...	67921527	Naphthoate synthase [Crocosphaera watsonii WH 8501]
73	NP_693244	23099778	naphthoate synthase [Oceanobacillus iheyensis HTE831]
74	YP_301836	73663055	dihydroxynaphthoic acid synthase [Staphylococcus saprophyti subsp. saprophyticus ATCC 15305]
75	NP_440855	16330127	naphthoate synthase [Synechocystis sp. PCC 6803]
76	YP_284834	71907247	Naphthoate synthase [Dechloromonas aromatica RCB]
77	NP_683247	22300000	naphthoate synthase [Thermosynechococcus elongatus BP-1]
78	YP_188217	57866511	naphthoate synthase [Staphylococcus epidermidis RP62A]
79	BAF05698	113533315	Os01g0662700 [Oryza sativa (japonica cultivar-group)]
80	YP_253832	70726918	naphthoate synthase [Staphylococcus haemolyticus JCSC1435]

81	Q8CPQ4	81842954	Naphthoate synthase (Dihydroxynaphthoic acid synthetase) (DHNA synthetase)
82	NP_849024	30468137	naphthoate synthase [Cyanidioschyzon merolae strain 10D]
83	YP_645616	108805679	naphthoate synthase [Rubrobacter xylanophilus DSM 9941]
84	ZP_007...	76260425	Naphthoate synthase [Chloroflexus aurantiacus J-10-fl]
85	YP_043106	49485885	naphthoate synthase [Staphylococcus aureus subsp. aureus MSSA476]
86	YP_499538	88194742	enoyl-CoA hydratase/isomerase family protein, putative [Staphylococcus aureus subsp. aureus NCTC 8325]
87	ABC33866	83638332	naphthoate synthase [Rhodococcus sp. T104]
88	ZP_013...	106889323	naphthoate synthase [Roseiflexus sp. RS-1]
89	ZP_012...	90586043	Naphthoate synthase [Staphylococcus aureus subsp. aureus JH
90	YP_416398	82750657	naphthoate synthase [Staphylococcus aureus RF122]
91	NP_176255	30696431	catalytic/ naphthoate synthase [Arabidopsis thaliana]
92	ZP_002...	47093552	naphthoate synthase [Listeria monocytogenes str. 4b H7858]
93	ZP_002...	47096746	naphthoate synthase [Listeria monocytogenes str. 1/2a F6854]
94	BAC42141	26450042	putative enoyl-CoA hydratase/isomerase [Arabidopsis thaliana
95	ZP_010...	84517892	Naphthoate synthase [Prochlorococcus marinus str. MIT 9211]
96	YP_289470	72161813	naphthoate synthase [Thermobifida fusca YX]
97	ZP_010...	87303315	Naphthoate synthase [Synechococcus sp. WH 5701]
98	ZP_013...	109647421	naphthoate synthase [Desulfitobacterium hafniense DCB-2]
99	YP_516753	89893266	dihydroxynapthoic acid synthetase [Desulfitobacterium hafnier Y51]
100	NP_894238	33862678	Naphthoate synthase [Prochlorococcus marinus str. MIT 9313]
101	YP_063988	51244104	naphthoate synthase (MenB) [Desulfotalea psychrophila LSv54
102	ZP_010...	87124201	Naphthoate synthase [Synechococcus sp. RS9917]
103	NP_266885	15672711	naphthoate synthase [Lactococcus lactis subsp. lactis Il1403]
104	ZP_003...	62463996	COG0447: Dihydroxynaphthoic acid synthase [Lactococcus lac subsp. cremoris SK11]
105	YP_291239	72381884	naphthoate synthase [Prochlorococcus marinus str. NATL2A]
106	YP_381435	78212656	naphthoate synthase [Synechococcus sp. CC9605]
107	NP_905664	34541185	naphthoate synthase [Porphyromonas gingivalis W83]
108	YP_210965	60680821	putative naphthoate synthase [Bacteroides fragilis NCTC 9343
109	YP_377341	78184906	Naphthoate synthase [Synechococcus sp. CC9902]
110	ZP_011...	88808385	Naphthoate synthase [Synechococcus sp. WH 7805]
111	NP_813613	29350110	dihydroxynapthoic acid synthetase [Bacteroides thetaiotaomicr VPI-5482]
112	NP_897091	33865532	Naphthoate synthase [Synechococcus sp. WH 8102]
113	YP_595182	94987249	Dihydroxynapthoic acid synthetase [Lawsonia intracellularis PHE/MN1-00]
114	ABE11060	91070138	napthoate synthase [uncultured Prochlorococcus marinus clone HF10-11A3]
115	YP_205052	59712276	naphthoate synthase [Vibrio fischeri ES114]
116	AAB71952	2462733	Putative enoyl-CoA hydratase/isomerase [Arabidopsis thaliana
117	NP_875445	33240503	Dihydroxynaphthoic acid synthase [Prochlorococcus marinus subsp. marinus str. CCMP1375]
118	NP_814229	29375076	naphthoate synthase [Enterococcus faecalis V583]
119	ABE11188	91070269	napthoate synthase [uncultured Prochlorococcus marinus clone HF10-11H7]
120	YP_397105	78778993	naphthoate synthase [Prochlorococcus marinus str. MIT 9312]
121	NP_892726	33861165	Napthoate synthase [Prochlorococcus marinus subsp. pastoris s CCMP1986]
122	ZP_003...	48866139	COG0447: Dihydroxynaphthoic acid synthase [Oenococcus oe

			PSU-1]
123	YP_535072	90961156	Naphthoate synthase [Lactobacillus salivarius subsp. salivarius UCC118]
124	Q9TM10	14423764	Naphthoate synthase (Dihydroxynaphthoic acid synthetase) (DHNA synthetase)
125	ZP_012...	92088720	Naphthoate synthase [Lactobacillus reuteri 100-23]
126	ZP_011...	89090332	Naphthoate synthase [Lactobacillus reuteri JCM 1112]
127	ZP_000...	23024048	COG0447: Dihydroxynaphthoic acid synthase [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]
128	ZP_011...	88802657	naphthoate synthase [Polaribacter irgensii 23-P]
129	ZP_012...	91214786	naphthoate synthase [Psychroflexus torquis ATCC 700755]
130	ZP_011...	88805655	naphthoate synthase [Robiginitalea biformata HTCC2501]
131	ZP_012...	90592093	Naphthoate synthase [Flavobacterium johnsoniae UW101]
132	ZP_011...	88712549	naphthoate synthase [Flavobacteriales bacterium HTCC2170]
133	ZP_012...	89891317	naphthoate synthase [Flavobacteria bacterium BBFL7]
134	ZP_009...	83857229	naphthoate synthase [Croceibacter atlanticus HTCC2559]
135	ZP_010...	86143133	naphthoate synthase [Flavobacterium sp. MED217]
136	ZP_010...	86133839	naphthoate synthase [Tenacibaculum sp. MED152]
137	ZP_010...	86132721	naphthoate synthase [Cellulophaga sp. MED134]
138	YP_678505	110638296	naphthoate synthase (dihydroxynaphtoic acid synthetase) [Cytophaga hutchinsonii ATCC 33406]
139	NP_739390	25029336	putative naphthoate synthase [Corynebacterium efficiens YS-3
140	ABC33875	83638341	naphthoate synthase [Rhodococcus sp. T104]
141	YP_135529	55377678	naphthoate synthase [Haloarcula marismortui ATCC 43049]
142	YP_293289	72383935	Naphthoate synthase [Ralstonia eutropha JMP134]
143	YP_327015	76802007	naphthoate synthase [Natronomonas pharaonis DSM 2160]
144	NP_070020	11498791	dihydroxynaphthoic acid synthase (menB) [Archaeoglobus fulgidus DSM 4304]
145	ZP_006...	71368102	Naphthoate synthase [Nocardioides sp. JS614]
146	NP_970225	42524845	naphthoate synthase [Bdellovibrio bacteriovorus HD100]
147	YP_158103	56476514	2-ketocyclohexanecarboxyl-CoA hydrolase [Azoarcus sp. EbN
148	YP_298117	73537750	Naphthoate synthase [Ralstonia eutropha JMP134]
149	ZP_011...	89360550	Naphthoate synthase [Xanthobacter autotrophicus Py2]
150	YP_702593	111019621	probable naphthoate synthase [Rhodococcus sp. RHA1]
151	YP_061323	50954035	naphthoate synthase [Leifsonia xyli subsp. xyli str. CTCB07]
152	YP_621308	107022981	naphthoate synthase [Burkholderia cenocepacia AU 1054]
153	NP_279999	15790175	naphthoate synthase [Halobacterium sp. NRC-1]
154	ZP_006...	69953506	Naphthoate synthase [Shewanella frigidimarina NCIMB 400]
155	YP_530917	90422547	naphthoate synthase [Rhodopseudomonas palustris BisB18]
156	ZP_014...	113950738	naphthoate synthase [Shewanella baltica OS195]
157	YP_657639	110667828	naphthoate synthase [Haloquadratum walsbyi DSM 16790]
158	YP_568680	91976021	naphthoate synthase [Rhodopseudomonas palustris BisB5]
159	ZP_008...	77742717	Naphthoate synthase [Rhodopseudomonas palustris BisA53]
160	YP_631357	108763330	naphthoate synthase [Myxococcus xanthus DK 1622]
161	ZP_012...	90579759	naphthoate synthase [Vibrio angustum S14]
162	ZP_010...	84713188	Naphthoate synthase [Polaromonas naphthalenivorans CJ2]
163	NP_789065	28572285	naphthoate synthase [Tropheryma whipplei TW08/27]
164	YP_462924	85860722	dihydroxynaphthoic acid synthase [Syntrophus aciditrophicus S
165	ZP_011...	89074926	naphthoate synthase [Photobacterium sp. SKA34]
166	NP_946006	39933730	2-ketocyclohexanecarboxyl-CoA hydrolase [Rhodopseudomon palustris CGA009]
167	YP_446858	83815505	naphthoate synthase [Salinibacter ruber DSM 13855]

168	ZP_008...	78367711	Naphthoate synthase [Shewanella sp. PV-4]
169	NP_938802	38233035	naphthoate synthase [Corynebacterium diphtheriae NCTC 131
170	ZP_011...	89338637	Naphthoate synthase [Mycobacterium flavescens PYR-GCK]
171	ZP_012...	90201669	Naphthoate synthase [Mycobacterium vanbaalenii PYR-1]
172	ZP_009...	82742522	Naphthoate synthase [Shewanella sp. W3-18-1]
173	ZP_012...	90412293	naphthoate synthase [Photobacterium profundum 3TCK]
174	ZP_014...	111615476	2-ketocyclohexanecarboxyl-CoA hydrolase [Verminephrobact eiseniae EF01-2]
175	ZP_011...	88855935	naphthoate synthase [marine actinobacterium PHSC20C1]
176	NP_962978	41410142	naphthoate synthase [Mycobacterium avium subsp. paratuberculosis K-10]
177	ZP_005...	68548540	Naphthoate synthase [Shewanella amazonensis SB2B]
178	YP_740044	114049494	naphthoate synthase [Shewanella sp. MR-7]
179	YP_224763	62389361	naphthoate synthase [Corynebacterium glutamicum ATCC 130
180	YP_736038	113972245	naphthoate synthase [Shewanella sp. MR-4]
181	NP_720255	24376211	naphthoate synthase [Shewanella oneidensis MR-1]
182	YP_637911	108797714	naphthoate synthase [Mycobacterium sp. MCS]
183	ZP_008...	81255561	COG0447: Dihydroxynaphthoic acid synthase [Mycobacterium tuberculosis C]
184	1Q52L	42543406	Chain L, Crystal Structure Of Mycobacterium Tuberculosis Me A Key Enzyme In Vitamin K2 Biosynthesis
185	ZP_011...	88856952	naphthoate synthase [marine actinobacterium PHSC20C1]
186	ZP_003...	62425059	COG0447: Dihydroxynaphthoic acid synthase [Brevibacterium linens BL2]
187	YP_701968	111018996	probable naphthoate synthase [Rhodococcus sp. RHA1]
188	NP_302473	15828210	naphthoate synthase [Mycobacterium leprae TN]
189	ZP_006...	71366728	Naphthoate synthase [Nocardioides sp. JS614]
190	YP_121354	54027112	naphthoate synthase [Nocardia farcinica IFM 10152]
191	ZP_009...	84494963	putative naphthoate synthase [Janibacter sp. HTCC2649]
192	YP_251668	68536963	naphthoate synthase [Corynebacterium jeikeium K411]
193	NP_737085	25027031	naphthoate synthase [Corynebacterium efficiens YS-314]
194	ZP_004...	66966063	Naphthoate synthase [Arthrobacter sp. FB24]
195	YP_708986	111027008	naphthoate synthase [Rhodococcus sp. RHA1]
196	YP_055618	50842391	naphthoate synthase [Propionibacterium acnes KPA171202]
197	YP_556253	91781046	Putative enoyl-CoA hydratase/isomerase [Burkholderia xenovorans LB400]
198	YP_675490	110635282	Enoyl-CoA hydratase/isomerase [Mesorhizobium sp. BNC1]
199	ZP_013...	111611266	dihydroxynapthoic acid synthetase [Verminephrobacter eisenia EF01-2]

Table 51. Example of MenA polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	ZP_006...	75176683	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Shigella boydii BS512]
2	NP_312884	15834111	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Escherichi coli O157:H7 str. Sakai]
3	YP_312849	74314430	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Shigella so Ss046]
4	ZP_009...	83586226	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Escherichia coli 101-1]
5	ZP_007...	75513884	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Escherichia coli 53638]
6	NP_709734	56480484	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Shigella flexneri 2a str. 301]
7	YP_410226	82546279	MenA [Shigella boydii Sb227]
8	YP_671996	110644266	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Escherichia coli 536]
9	YP_543458	91213472	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Escherichia coli UTI89]
10	YP_405243	82778894	MenA [Shigella dysenteriae Sd197]
11	YP_691311	110807791	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Shigella flexneri 5 str. 8401]
12	YP_153009	56415934	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]
13	YP_218966	62182549	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
14	YP_052350	50123183	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Erwinia carotovora subsp. atroseptica SCRI1043]
15	ZP_008...	77977396	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Yersinia intermedia ATCC 29909]
16	ZP_008...	77957390	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Yersinia bercovieri ATCC 43970]
17	YP_068645	51594454	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Yersinia pseudotuberculosis IP 32953]
18	ZP_011...	89105846	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Yersinia pestis biovar Orientalis str. IP275]
19	YP_649676	108813909	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Yersinia pe Nepal516]
20	ZP_008...	77961040	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Yersinia mollaretii ATCC 43969]
21	ZP_008...	77972977	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Yersinia frederiksenii ATCC 33641]
22	ZP_007...	77630825	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Yersinia pseudotuberculosis IP 31758]
23	NP_931924	37528579	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Photorhabd luminescens subsp. laumondii TTO1]
24	ZP_012...	90580885	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Vibrio angustum S14]
25	ZP_011...	89075183	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Photobacter sp. SKA34]
26	YP_128493	54307473	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Photobacterium profundum SS9]
27	ZP_012...	90413626	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Photobacter

			profundum 3TCK]
28	YP_089032	52425895	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Mannheim succiniciproducens MBEL55E]
29	YP_203595	59710819	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Vibrio fisc ES114]
30	NP_873213	33151860	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Haemophi ducreyi 35000HP]
31	NP_246106	15603034	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Pasteurell multocida subsp. multocida str. Pm70]
32	ZP_001...	46156314	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Haemophilus somnus 2336]
33	YP_718428	113460367	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Haemophil somnus 129PT]
34	ZP_007...	75430490	1, 4-dihydroxy-2-naphthoate octaprenyltransferase [Actinobac succinogenes 130Z]
35	ZP_001...	46143691	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]
36	ZP_001...	53733046	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Haemophilus influenzae R2846]
37	ZP_001...	53733299	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Haemophilus influenzae R2866]
38	NP_438667	30995381	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Haemophi influenzae Rd KW20]
39	AAC22167	1573490	1,4-dihydroxy-2-naphthoate octaprenyltransferase (menA) [Haemophilus influenzae Rd KW20]
40	YP_248220	68249108	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Haemophi influenzae 86-028NP]
41	ZP_007...	75830088	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Vibrio cholerae MO10]
42	ZP_007...	75854331	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Vibrio sp. Ex25]
43	ZP_007...	75824015	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Vibrio cholerae RC385]
44	ZP_010...	86147298	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Vibrio sp. MED222]
45	NP_935810	37681201	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Vibrio vulnificus YJ016]
46	ZP_009...	84390848	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Vibrio splendidus 12B01]
47	NP_796627	28897022	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Vibrio parahaemolyticus RIMD 2210633]
48	ZP_012...	91226626	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Vibrio alginolyticus 12G01]
49	ABD78975	89892388	HI0509-like protein [Haemophilus influenzae]
50	ZP_013...	106882320	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Psychromo ingrahamii 37]
51	YP_676956	110636749	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Cytophaga hutchinsonii ATCC 33406]
52	ZP_012...	90592092	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Flavobacte johnsoniae UW101]
53	ZP_010...	86140325	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Flavobacte sp. MED217]
54	ZP_012...	91214657	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Psychrofle

			torquis ATCC 700755]
55	ZP_011...	88713569	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Flavobacteriales bacterium HTCC2170]
56	ZP_012...	90407328	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Psychromo sp. CNPT3]
57	ZP_009...	83857377	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Croceibact atlanticus HTCC2559]
58	ZP_010...	86132755	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Cellulopha sp. MED134]
59	ZP_011...	88805802	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Robiginital biformata HTCC2501]
60	ZP_011...	88803687	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Polaribacte irgensii 23-P]
61	ZP_010...	86133688	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Tenacibacu sp. MED152]
62	YP_445477	83815103	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Salinibacte ruber DSM 13855]
63	ZP_009...	84494968	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Janibacter HTCC2649]
64	ZP_004...	66966061	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Arthrobacte sp. FB24]
65	YP_657640	110667829	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Haloquadra walsbyi DSM 16790]
66	YP_213105	60682961	putative prenyltransferase [Bacteroides fragilis NCTC 9343]
67	ZP_007...	76260424	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Chloroflexu aurantiacus J-10-fl]
68	ZP_013...	106890612	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Roseiflexus RS-1]
69	YP_562676	91793025	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Shewanella denitrificans OS217]
70	ZP_011...	88800363	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Reinekea sp MED297]
71	ZP_013...	110597752	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Chlorobium ferrooxidans DSM 13031]
72	YP_056621	50843394	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Propionibacterium acnes KPA171202]
73	YP_631724	108760974	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Myxococcu xanthus DK 1622]
74	YP_135533	55377683	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Haloarcula marismortui ATCC 43049]
75	YP_375415	78187372	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Pelodictyo luteolum DSM 273]
76	ZP_006...	69284889	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Kineococcu radiotolerans SRS30216]
77	ZP_006...	69950913	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Shewanella frigidimarina NCIMB 400]
78	ZP_005...	67938127	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Chlorobium phaeobacteroides BS1]
79	ZP_005...	68551059	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Pelodictyon phaeoclathratiforme BU-1]
80	YP_251676	68536971	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Corynebacterium jeikeium K411]
81	ZP_008...	78367541	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Shewanella

			PV-4]
82	ZP_005...	68552894	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Prosthecochloris aestuarii DSM 271]
83	YP_379249	78188911	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Chlorobiu chlorochromatii CaD3]
84	YP_701986	111019014	probable 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Rhodococcus sp. RHA1]
85	NP_938799	38233032	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Corynebacterium diphtheriae NCTC 13129]
86	NP_279997	15790173	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Halobacte sp. NRC-1]
87	ZP_006...	71481597	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Prosthecochloris vibrioformis DSM 265]
88	YP_637879	108797682	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Mycobacte sp. MCS]
89	YP_064658	51244774	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Desulfotale psychrophila LSv54]
90	ZP_011...	88945824	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Desulfotomaculum reducens MI-1]
91	ZP_005...	67935682	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Chlorobiu phaeobacteroides DSM 266]
92	NP_737079	25027025	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Corynebacterium efficiens YS-314]
93	ZP_009...	82740894	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Shewanella W3-18-1]
94	ZP_008...	77814697	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Shewanella putrefaciens CN-32]
95	ZP_005...	68547261	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Shewanella amazonensis SB2B]
96	ZP_005...	67918650	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Chlorobiu limicola DSM 245]
97	YP_121363	54027121	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Nocardia farcinica IFM 10152]
98	NP_906235	34541756	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Porphyrom gingivalis W83]
99	ZP_011...	88855937	1,4-dihydroxy-2-naphthoate octaprenyltransferase [marine actinobacterium PHSC20C1]
100	YP_286863	71909276	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Dechlorom aromatica RCB]
101	ZP_008...	78685675	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Shewanella ANA-3]
102	YP_733750	113969957	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Shewanella MR-4]
103	YP_737742	114047192	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Shewanella MR-7]
104	NP_717517	24373474	1,4-dihydroxy-2-naphthoate octaprenyltransferase, putative [Shewanella oneidensis MR-1]
105	ZP_012...	90201608	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Mycobacte vanbaalenii PYR-1]
106	YP_288849	72161192	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Thermobif fusca YX]
107	ZP_011...	89338650	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Mycobacte flavescens PYR-GCK]

108	ZP_014...	113948860	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Shewanella baltica OS195]
109	ZP_007...	76785823	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Mycobacterium tuberculosis F11]
110	P65650	54041528	Probable 1,4-dihydroxy-2-naphthoate octaprenyltransferase (DHNA-octaprenyltransferase)
111	YP_061325	50954037	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Leifsonia x subsp. xyli str. CTCB07]
112	NP_962963	41410127	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Mycobacterium avium subsp. paratuberculosis K-10]
113	NP_302556	15828293	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Mycobacterium leprae TN]
114	YP_224750	62389348	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Corynebacterium glutamicum ATCC 13032]
115	ZP_008...	81255548	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Mycobacterium tuberculosis C]
116	ZP_000...	23015447	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Magnetospirillum magnetotacticum MS-1]
117	ZP_003...	62425061	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Brevibacterium linens BL2]
118	YP_422438	83312174	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Magnetospirillum magneticum AMB-1]
119	ZP_001...	23336626	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Bifidobacterium longum DJO10A]
120	ZP_011...	88949023	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Halorhodos halophila SL1]
121	NP_696805	23466202	probable 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Bifidobacterium longum NCC2705]
122	YP_148730	56421412	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Geobacillu kaustophilus HTA426]
123	BAA94024	7416775	ORF314 [Rubrivivax gelatinosus]
124	NP_967526	42522146	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Bdellovibri bacteriovorus HD100]
125	YP_428469	83594717	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Rhodospiril rubrum ATCC 11170]
126	AAC62694	3599388	menaquinone biosynthesis protein [Cenarchaeum symbiosum]
127	ZP_010...	85666474	hypothetical protein Badol_01001319 [Bifidobacterium adolescentis]
128	AAC62716	3599411	menaquinone biosynthesis protein [Cenarchaeum symbiosum]
129	NP_789028	28572248	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Tropheryma whipplei TW08/27]
130	YP_595132	94987199	hypothetical protein LI0757 [Lawsonia intracellularis PHE/MN 00]
131	YP_462870	85860668	1,4-dihydroxy-2-naphthoate polyprenyltransferase [Syntrophus aciditrophicus SB]
132	YP_008062	46446697	putative 1,4-dihydroxy-2-naphthoate octaprenyltransferase, me [Candidatus Protochlamydia amoebophila UWE25]
133	BAE03294	68445586	hypothetical conserved protein [uncultured crenarchaeote 10-H
134	YP_595134	94987201	hypothetical protein LI0759 [Lawsonia intracellularis PHE/MN 00]
135	YP_092777	52786948	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Bacillus licheniformis ATCC 14580]
136	YP_644726	108804789	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Rubrobacte

			xylanophilus DSM 9941]
137	YP_086187	52140642	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Bacillus ce E33L]
138	NP_981310	42784063	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Bacillus ce ATCC 10987]
139	YP_074900	51892209	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Symbiobacterium thermophilum IAM 14863]
140	ZP_002...	47568036	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Bacillus cer G9241]
141	YP_519104	89895617	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Desulfitobacterium hafniense Y51]
142	ZP_013...	109645932	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Desulfitobacterium hafniense DCB-2]
143	NP_810927	29347424	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Bacteroides thetaiotaomicron VPI-5482]
144	NP_979500	42782253	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Bacillus ce ATCC 10987]
145	ZP_011...	89201880	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Bacillus cer subsp. cytotoxis NVH 391-98]
146	NP_834556	30022925	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Bacillus ce ATCC 14579]
147	ZP_002...	47096750	1,4-dihydroxy-2-naphthoate octaprenyltransferase, putative [Listeria monocytogenes str. 1/2a F6854]
148	ZP_002...	47564318	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Bacillus cer G9241]
149	ZP_009...	82746102	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Clostridium beijerincki NCIMB 8052]
150	ZP_011...	89204355	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Bacillus weihenstephanensis KBAB4]
151	NP_471121	16800853	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Listeria innocua Clip11262]
152	ZP_005...	68054682	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Exiguobacterium sibiricum 255-15]
153	YP_037272	49480090	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Bacillus thuringiensis serovar konkukian str. 97-27]
154	ZP_003...	65320444	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Bacillus anthracis str. A2012]
155	ZP_007...	75763116	1,4-dihydroxy-2-naphthoate polyprenyltransferase [Bacillus thuringiensis serovar israelensis ATCC 35646]
156	YP_301840	73663059	14-dihydroxy-2-naphthodate octaprenyltransferase [Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305]
157	YP_084472	52142358	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Bacillus cer E33L]
158	ZP_006...	71368944	UbiA prenyltransferase [Nocardioides sp. JS614]
159	NP_832890	30021259	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Bacillus cer ATCC 14579]
160	AAH71203	47940171	UbiA prenyltransferase domain containing 1 [Mus musculus]
161	Q9DC60	81906129	UbiA prenyltransferase domain-containing protein 1
162	ZP_011...	89205833	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Bacillus weihenstephanensis KBAB4]
163	NP_624007	20808836	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Thermoanaerobacter tengcongensis MB4]

164	XP_001...	109477705	PREDICTED: similar to transitional epithelia response protein [Rattus norvegicus]
165	XP_317591	58390248	ENSANGP00000010121 [Anopheles gambiae str. PEST]
166	XP_544571	57045207	PREDICTED: similar to transitional epithelia response protein [Canis familiaris]
167	EAL34198	54645459	GA19197-PA [Drosophila pseudoobscura]
168	Q9V3R8	74947346	UbiA prenyltransferase domain-containing protein 1 homolog (Protein heix)
169	NP_391728	16080900	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Bacillus subtilis subsp. subtilis str. 168]
170	XP_001...	108997038	PREDICTED: similar to transitional epithelia response protein [Macaca mulatta]
171	AAX29103	60652817	transitional epithelia response protein [synthetic construct]
172	NP_693248	23099782	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Oceanobacillus iheyensis HTE831]
173	Q9Y5Z9	74753514	UbiA prenyltransferase domain-containing protein 1 (Transitic epithelial response protein 1)
174	XP_514384	55590988	PREDICTED: similar to transitional epithelia response protein [Pan troglodytes]
175	ZP_011...	89099711	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Bacillus sp NRRL B-14911]
176	BAD96528	62897175	transitional epithelia response protein variant [Homo sapiens]
177	XP_637156	66806867	UbiA prenyltransferase family protein [Dictyostelium discoide AX4]
178	Q5ZKS8	82082269	UbiA prenyltransferase domain-containing protein 1
179	XP_585287	76637236	PREDICTED: similar to transitional epithelia response protein [Bos taurus]
180	YP_253836	70726922	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Staphylococcus haemolyticus JCSC1435]
181	Q28HR4	109895230	UbiA prenyltransferase domain-containing protein 1
182	ZP_012...	90586039	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Staphyloco aureus subsp. aureus JH9]
183	YP_040431	49483207	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Staphylococcus aureus subsp. aureus MRSA252]
184	YP_188212	57866499	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Staphylococcus epidermidis RP62A]
185	ZP_005...	67921376	UbiA prenyltransferase [Crocosphaera watsonii WH 8501]
186	YP_423708	83313444	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Magnetospirillum magneticum AMB-1]
187	XP_625148	66562776	PREDICTED: similar to heixuedian CG5876-PA [Apis mellife
188	ZP_000...	23015983	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Magnetospirillum magnetotacticum MS-1]
189	XP_686705	68432583	PREDICTED: similar to transitional epithelia response protein [Danio rerio]
190	AAR24482	38569912	1,4-dihydroxy-2-naphthoate octaprenyltransferase [uncultured crenarchaeote DeepAnt-EC39]
191	ZP_013...	110605369	UbiA prenyltransferase [Thermofilum pendens Hrk 5]
192	ZP_010...	84712924	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Polaromon naphthalenivorans CJ2]
193	YP_462031	85859828	1,4-dihydroxy-2-naphthoate polyprenyltransferase [Syntrophus aciditrophicus SB]
194	XP_973123	91088573	PREDICTED: similar to CG5876-PA [Tribolium castaneum]
195	EAT43537	108879312	1,4-dihydroxy-2-naphthoate octaprenyltransferase [Aedes aegy

196	ZP_013...	94499116	1,4-dihydroxy-2-naphthoate octaprenyltransferase, putative [Oceanobacter sp. RED65]
197	YP_323142	75908846	1,4-dihydroxy-2-naphthoate octaprenyltransferase, [Anabaena variabilis ATCC 29413]
198	ZP_011...	88706563	UbiA prenyltransferase [gamma proteobacterium KT 71]
199	ZP_011...	88939585	1 4-dihydroxy-2-naphthoate octaprenyltransferase-like [Acidiphilium cryptum JF-5]

Table 52. Examples of UbiE polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	YP_671909	110644179	ubiquinone/menaquinone biosynthesis methyltransferase UbiE [Escherichia coli 536]
2	ZP_009...	83569331	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Shigella dysenteriae 1012]
3	AAA67628	148231	o251 [Escherichia coli]
4	YP_218855	62182438	ubiquinone/menaquinone biosynthesis methyltransferase [Salmonella enterica subsp. enterica serovar Choleraesuis str. S B67]
5	YP_650157	108806241	ubiquinone/menaquinone biosynthesis methyltransferase [Yers pestis Antiqua]
6	YP_646116	108810349	ubiquinone/menaquinone biosynthesis methyltransferase [Yers pestis Nepal516]
7	ZP_008...	77978480	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Yersinia intermedia ATCC 29909]
8	ZP_008...	77973692	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Yersinia frederiksenii ATCC 33641]
9	ZP_008...	77961745	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Yersinia mollaretii ATCC 43969]
10	ZP_012...	90581027	ubiquinone/menaquinone biosynthesis methyltransferase [Vibr angustum S14]
11	ZP_011...	89074430	ubiquinone/menaquinone biosynthesis methyltransferase [Photobacterium sp. SKA34]
12	YP_203429	59710653	ubiquinone/menaquinone biosynthesis methyltransferase [Vibr fischeri ES114]
13	Q7MZ81	56749773	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
14	ZP_001...	32033562	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Actinobacillus pleuropneumoniae serovar 1 str. 4074]
15	Q9CKD6	48474949	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
16	ZP_012...	90412766	putative ubiquinone/menaquinone biosynthesis methlytransfera UbiE [Photobacterium profundum 3TCK]
17	YP_453789	85058087	ubiquinone/menaquinone biosynthesis methyltransferase [Soda glossinidius str. 'morsitans']
18	P59911	37999899	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
19	ZP_001...	32029969	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Haemophilus somnus 2336]
20	YP_718753	113460687	ubiquinone/menaquinone biosynthesis methyltransferase [Haemophilus somnus 129PT]
21	ZP_007...	75829374	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Vibrio cholerae MO10]
22	ZP_010...	86146605	ubiquinone/menaquinone biosynthesis methyltransferase [Vibr sp. MED222]
23	ZP_009...	84386296	ubiquinone/menaquinone biosynthesis methyltransferase [Vibr splendidus 12B01]
24	ZP_007...	75820016	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Vibrio cholerae V51]
25	Q6DAQ7	56749696	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
26	Q7MQ33	61217315	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
27	ZP_007...	75856470	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Vibrio sp. Ex25]
28	Q87TH4	48474408	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE

29	ZP_012...	91224931	ubiquinone/menaquinone biosynthesis methyltransferase [Vibr alginolyticus 12G01]
30	YP_341403	77361828	2-octaprenyl-6-methoxy-1,4-benzoquinone methylase / S-adenosylmethionine [Pseudoalteromonas haloplanktis TAC125
31	YP_663762	109900507	ubiquinone/menaquinone biosynthesis methyltransferases [Pseudoalteromonas atlantica T6c]
32	ZP_013...	106882286	ubiquinone/menaquinone biosynthesis methyltransferases [Psychromonas ingrahamii 37]
33	ZP_012...	90407556	UbiE [Psychromonas sp. CNPT3]
34	ZP_005...	68546475	Ubiquinone/menaquinone biosynthesis methyltransferase [Shewanella amazonensis SB2B]
35	Q5QYG2	61217193	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
36	ZP_011...	88861184	bifunctional protein [Pseudoalteromonas tunicata D2]
37	ZP_011...	88794590	ubiquinone/menaquinone biosynthesis methyltransferase [Alteromonas macleodii 'Deep ecotype']
38	YP_128357	54307337	putative ubiquinone/menaquinone biosynthesis methlytransfera UbiE [Photobacterium profundum SS9]
39	YP_736465	114045915	ubiquinone/menaquinone biosynthesis methyltransferases [Shewanella sp. MR-7]
40	ZP_008...	78366176	Ubiquinone/menaquinone biosynthesis methyltransferase [Shewanella sp. PV-4]
41	Q8E9R7	48474457	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
42	ZP_014...	113948769	ubiquinone/menaquinone biosynthesis methyltransferases [Shewanella baltica OS195]
43	YP_267060	71280787	ubiquinone/menaquinone biosynthesis methlytransferase UbiE [Colwellia psychrerythraea 34H]
44	YP_561476	91791825	ubiquinone/menaquinone biosynthesis methyltransferases [Shewanella denitrificans OS217]
45	ZP_010...	87120355	ubiquinone/menaquinone biosynthesis methyltransferase UbiE [Marinomonas sp. MED121]
46	ZP_009...	82742409	Ubiquinone/menaquinone biosynthesis methyltransferase [Shewanella sp. W3-18-1]
47	ZP_010...	85711927	2-polyprenylmethoxybenozoquinol methylase [Idiomarina balti OS145]
48	ZP_006...	69949855	Ubiquinone/menaquinone biosynthesis methyltransferase [Shewanella frigidimarina NCIMB 400]
49	ZP_013...	107104162	hypothetical protein PaerPA_01005235 [Pseudomonas aerugin PACS2]
50	ZP_009...	84323851	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Pseudomonas aeruginosa 2192]
51	ZP_012...	94415433	hypothetical protein PaerP_01002801 [Pseudomonas aeruginos PA7]
52	YP_610489	104783991	ubiquinone biosynthesis methyltransferase [Pseudomonas entomophila L48]
53	Q9Z439	48474719	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
54	YP_346120	77456615	ubiquinone/menaquinone biosynthesis methyltransferase [Pseudomonas fluorescens PfO-1]
55	ZP_008...	82736190	Ubiquinone/menaquinone biosynthesis methyltransferase [Pseudomonas putida F1]
56	YP_572658	92112730	ubiquinone/menaquinone biosynthesis methyltransferases [Chromohalobacter salexigens DSM 3043]
57	Q87UZ2	48474830	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
58	ZP_012...	90417283	ubiquinone/menaquinone biosynthesis methyltransferase UbiE

			[marine gamma proteobacterium HTCC2207]
59	YP_272675	71734036	ubiquinone/menaquinone biosynthesis methlytransferase UbiE [Pseudomonas syringae pv. phaseolicola 1448A]
60	YP_257571	70733931	ubiquinone/menaquinone biosynthesis methyltransferase [Pseudomonas fluorescens Pf-5]
61	ZP_004...	67158081	Ubiquinone/menaquinone biosynthesis methyltransferase [Azotobacter vinelandii AvOP]
62	ZP_011...	89093517	ubiquinone/menaquinone biosynthesis methyltransferase [Oceanospirillum sp. MED92]
63	YP_667382	110670825	menaquinone biosynthesis methyltransferase [Francisella tularensis subsp. tularensis FSC 198]
64	ZP_013...	94500588	ubiquinone/menaquinone biosynthesis methyltransferase [Oceanobacter sp. RED65]
65	YP_513178	89255816	menaquinone biosynthesis methyltransferase [Francisella tularensis subsp. holarctica]
66	YP_045153	50083643	S-adenosylmethionine : 2-DMK methyltransferase and 2-octaprenyl-6-methoxy-1,4-benzoquinone methylase [Acinetob sp. ADP1]
67	ZP_011...	88705221	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE [gamma proteobacterium KT 71]
68	YP_264006	71065279	probable ubiquinone/menaquinone biosynthesis methyltransfer [Psychrobacter arcticus 273-4]
69	ZP_011...	88797351	ubiquinone/menaquinone biosynthesis methyltransferase [Reinekea sp. MED297]
70	YP_579955	93005518	ubiquinone/menaquinone biosynthesis methyltransferases [Psychrobacter cryohalolentis K5]
71	YP_432387	83643952	Methylase involved in ubiquinone/menaquinone biosynthesis [Hahella chejuensis KCTC 2396]
72	YP_528172	90022345	Heat shock protein Hsp70 [Saccharophagus degradans 2-40]
73	ZP_008...	77953062	Ubiquinone/menaquinone biosynthesis methyltransferase [Marinobacter aquaeolei VT8]
74	BAB91365	20502371	ubiquinone biosynthesis methyltransferase homolog protein [Pseudomonas sp. 61-3]
75	ZP_012...	91770275	Ubiquinone/menaquinone biosynthesis methyltransferase [Psychrobacter sp. PRwf-1]
76	YP_344331	77165806	Ubiquinone/menaquinone biosynthesis methyltransferase [Nitrosococcus oceani ATCC 19707]
77	YP_390672	78484747	ubiquinone/menaquinone biosynthesis methyltransferase [Thiomicrospira crunogena XCL-2]
78	Q606J9	61217211	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
79	YP_693966	110835107	methyltransferase, ubiquinone biosynthesis [Alcanivorax borkumensis SK2]
80	YP_278124	71892390	2-octaprenyl-6-methoxy-1,4-benzoquinone methylase [Candid Blochmannia pennsylvanicus str. BPEN]
81	Q5X0X6	61217203	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
82	Q5WSQ8	61217202	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
83	ZP_012...	94492586	hypothetical protein CburD_01000167 [Coxiella burnetii Dugv 7E9-12]
84	Q5ZRH9	61217209	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
85	Q7NZD3	61217326	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
86	NP_900659	34496444	ubiquinone/menaquinone biosynthesis methyltransferase [Chromobacterium violaceum ATCC 12472]
87	YP_544807	91775051	ubiquinone/menaquinone biosynthesis methyltransferases

			[Methylobacillus flagellatus KT]
88	Q7VRJ1	61217333	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
89	YP_287313	71909726	Ubiquinone/menaquinone biosynthesis methyltransferase [Dechloromonas aromatica RCB]
90	Q9JV83	48474665	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
91	YP_207480	59800768	ubiquinone/menaquinone biosynthesis methyltransferase [Neisseria gonorrhoeae FA 1090]
92	Q9K075	48474972	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
93	YP_313973	74316233	ubiquinone/menaquinone biosynthesis methyltransferase [Thiobacillus denitrificans ATCC 25259]
94	YP_158726	56477137	ubiquinone/menaquinone biosynthesis methyltransferase ubiE [Azoarcus sp. EbN1]
95	ZP_006...	71549128	Ubiquinone/menaquinone biosynthesis methyltransferase [Nitrosomonas eutropha C71]
96	Q81ZZ8	48474814	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
97	Q8Y278	48474569	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
98	ZP_009...	83746613	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE [Ralstonia solanacearum UW551]
99	ZP_008...	78701957	Ubiquinone/menaquinone biosynthesis methyltransferase [Alkalilimnicola ehrlichei MLHE-1]
100	ZP_013...	100916089	hypothetical protein Bmal10_03002573 [Burkholderia mallei 10399]
101	YP_582526	94309316	ubiquinone/menaquinone biosynthesis methyltransferases [Ralstonia metallidurans CH34]
102	ZP_009...	84362919	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Burkholderia dolosa AUO158]
103	ZP_013...	110593844	ubiquinone/menaquinone biosynthesis methyltransferases [Acidovorax sp. JS42]
104	YP_412953	82703387	ubiquinone/menaquinone biosynthesis methyltransferase [Nitrosospira multiformis ATCC 25196]
105	YP_370297	78067528	ubiquinone/menaquinone biosynthesis methyltransferase [Burkholderia sp. 383]
106	ZP_004...	67547187	Ubiquinone/menaquinone biosynthesis methyltransferase [Burkholderia vietnamiensis G4]
107	YP_294657	73540137	ubiquinone/menaquinone biosynthesis methyltransferase [Ralstonia eutropha JMP134]
108	ZP_009...	84355659	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Burkholderia cenocepacia PC184]
109	YP_621994	107023667	ubiquinone/menaquinone biosynthesis methyltransferases [Burkholderia cenocepacia AU 1054]
110	Q7WF12	56749776	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
111	YP_557001	91781795	Ubiquinone/menaquinone biosynthesis methyltransferase [Burkholderia xenovorans LB400]
112	ZP_006...	74014209	Ubiquinone/menaquinone biosynthesis methyltransferase [Burkholderia ambifaria AMMD]
113	ZP_013...	94492964	hypothetical protein Rgryl_01001411 [Rickettsiella grylli]
114	Q8P558	48474489	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
115	YP_241773	66767011	ubiquinone/menaquinone biosynthesis methyltransferase [Xanthomonas campestris pv. campestris str. 8004]
116	YP_452787	84625415	ubiquinone/menaquinone transferase [Xanthomonas oryzae pv. oryzae MAFF 311018]
117	YP_202626	58583610	ubiquinone/menaquinone biosynthesis methyltransferase [Xanthomonas oryzae pv. oryzae KACC10331]

118	YP_362429	78046254	ubiquinone/menaquinone biosynthesis methyltransferase [Xanthomonas campestris pv. vesicatoria str. 85-10]
119	ZP_002...	47573577	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Rubrivivax gelatinosus PM1]
120	Q8PPP2	48474873	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
121	Q87DI1	48474404	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
122	ZP_006...	71901200	Ubiquinone/menaquinone biosynthesis methyltransferase [Xyl fastidiosa Ann-1]
123	BAB84082	18307680	probable ubiquinone/menaquinone biosynthesis methyltransfe [Leptothrix cholodnii]
124	ZP_006...	71900274	Ubiquinone/menaquinone biosynthesis methyltransferase [Xyl fastidiosa Ann-1]
125	ZP_010...	84709882	Ubiquinone/menaquinone biosynthesis methyltransferase [Polaromonas naphthalenivorans CJ2]
126	ZP_014...	111616165	ubiquinone/menaquinone biosynthesis methyltransferases [Acidovorax avenae subsp. citrulli AAC00-1]
127	YP_547714	91786762	ubiquinone/menaquinone biosynthesis methyltransferases [Polaromonas sp. JS666]
128	ZP_011...	88813052	ubiquinone/menaquinone biosynthesis methyltransferase [Nitrococcus mobilis Nb-231]
129	Q9PD92	48474677	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
130	YP_522556	89900085	ubiquinone/menaquinone biosynthesis methyltransferases [Rhodoferax ferrireducens T118]
131	ZP_013...	111611725	putative ubiquinone/menaquinone biosynthesis methyltransfer protein [Verminephrobacter eiseniae EF01-2]
132	ZP_006...	69257590	Ubiquinone/menaquinone biosynthesis methyltransferase [Magnetococcus sp. MC-1]
133	ZP_011...	88949054	Ubiquinone/menaquinone biosynthesis methyltransferase [Halorhodospira halophila SL1]
134	Q8D382	48474447	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
135	YP_680618	110677611	ubiquinone/menaquinone biosynthesis methyltransferase UbiE [Roseobacter denitrificans OCh 114]
136	ZP_010...	86139423	ubiquinone/menaquinone biosynthesis methyltransferase UbiE [Roseobacter sp. MED193]
137	ZP_009...	83941661	ubiquinone/menaquinone biosynthesis methyltransferase UbiE [Sulfitobacter sp. EE-36]
138	ZP_010...	84514658	ubiquinone/menaquinone biosynthesis methyltransferase UbiE [Loktanella vestfoldensis SKA53]
139	YP_192885	58040921	Ubiquinone/menaquinone biosynthesis methyltransferase [Gluconobacter oxydans 621H]
140	YP_165417	56695070	ubiquinone/menaquinone biosynthesis methyltransferase UbiE [Silicibacter pomeroyi DSS-3]
141	ZP_009...	83950594	ubiquinone/menaquinone biosynthesis methyltransferase UbiE [Roseovarius nubinhibens ISM]
142	YP_615022	99082868	ubiquinone/menaquinone biosynthesis methyltransferases [Silicibacter sp. TM1040]
143	ZP_009...	84501267	ubiquinone/menaquinone biosynthesis methyltransferase UbiE [Oceanicola batsensis HTCC2597]
144	ZP_010...	84684526	methyltransferase [Rhodobacterales bacterium HTCC2654]
145	YP_512151	89056700	ubiquinone/menaquinone biosynthesis methyltransferases [Jannaschia sp. CCS1]
146	ZP_011...	89069833	ubiquinone/menaquinone biosynthesis methyltransferase UbiE [Oceanicola granulosus HTCC2516]

147	ZP_010...	85706183	ubiquinone/menaquinone biosynthesis methyltransferase UbiE [Roseovarius sp. 217]
148	Q8FUZ3	48474468	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
149	YP_419160	83269869	SAM (and some other nucleotide) binding motif:Generic methyltransferase:UbiE/COQ5 methyltransferase:Ubiquinone/menaquinone bi... [Brucella melitensis biovar Abortus 2308]
150	ZP_000...	23014783	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Magnetospirillum magnetotacticum MS-1]
151	ZP_009...	83372227	Ubiquinone/menaquinone biosynthesis methyltransferase [Rhodobacter sphaeroides ATCC 17029]
152	ZP_009...	83369205	Ubiquinone/menaquinone biosynthesis methyltransferase [Rhodobacter sphaeroides ATCC 17025]
153	Q9Z5E9	48474720	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
154	ZP_011...	88940393	ubiquinone/menaquinone biosynthesis methyltransferases [Acidiphilium cryptum JF-5]
155	Q66L51	82234518	Ubiquinone biosynthesis methyltransferase COQ5, mitochondr precursor
156	XP_641323	66814288	ubiE/COQ5 methyltransferase family protein [Dictyostelium discoideum AX4]
157	ZP_012...	89362653	Ubiquinone/menaquinone biosynthesis methyltransferase [Xanthobacter autotrophicus Py2]
158	ZP_009...	83944874	ubiquinone/menaquinone biosynthesis methlytransferase UbiE [Oceanicaulis alexandrii HTCC2633]
159	ZP_006...	69936420	Ubiquinone/menaquinone biosynthesis methyltransferase [Paracoccus denitrificans PD1222]
160	XP_854268	73995311	PREDICTED: similar to CG2453-PA [Canis familiaris]
161	YP_530272	90421902	ubiquinone/menaquinone biosynthesis methyltransferases [Rhodopseudomonas palustris BisB18]
162	Q4V7R3	82225839	Ubiquinone biosynthesis methyltransferase COQ5, mitochondr precursor
163	AAI20309	112362323	Unknown (protein for MGC:142779) [Bos taurus]
164	EAO83841	77651885	Ubiquinone/menaquinone biosynthesis methyltransferase [Rhodopseudomonas palustris BisB5]
165	YP_567352	91974693	ubiquinone/menaquinone biosynthesis methyltransferases [Rhodopseudomonas palustris BisB5]
166	YP_428879	83595127	Ubiquinone/menaquinone biosynthesis methyltransferase [Rhodospirillum rubrum ATCC 11170]
167	CAG08176	47221514	unnamed protein product [Tetraodon nigroviridis]
168	Q89WD0	48474428	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
169	YP_676621	110636413	ubiquinone/menaquinone biosynthesis methyltransferases [Mesorhizobium sp. BNC1]
170	AAM52653	21483356	GM25741p [Drosophila melanogaster]
171	Q9VYF8	75027708	Ubiquinone biosynthesis methyltransferase COQ5, mitochondr precursor
172	Q5ZLL5	82233903	Ubiquinone biosynthesis methyltransferase COQ5, mitochondr precursor
173	BAD96330	62896779	hypothetical protein MGC4767 variant [Homo sapiens]
174	Q5HYK3	90111987	Ubiquinone biosynthesis methyltransferase COQ5, mitochondr precursor
175	AAH04916	38196988	COQ5 protein [Homo sapiens]
176	ZP_009...	83750758	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Bartonella bacilliformis KC583]

177	YP_484242	86747746	ubiquinone/menaquinone biosynthesis methyltransferases [Rhodopseudomonas palustris HaA2]
178	EAL32141	54643397	GA15370-PA [Drosophila pseudoobscura]
179	ZP_008...	77739893	Ubiquinone/menaquinone biosynthesis methyltransferase [Rhodopseudomonas palustris BisA53]
180	XP_396701	66501438	PREDICTED: similar to CG2453-PA [Apis mellifera]
181	YP_467903	86356011	ubiquinone/menaquinone biosynthesis methyltransferase protei [Rhizobium etli CFN 42]
182	NP_115690	58036498	coenzyme Q5 homolog, methyltransferase [Homo sapiens]
183	Q6NDM2	61217267	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
184	Q92SK7	48474592	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
185	NP_384470	15964117	ubiquinone/menaquinone biosynthesis methyltransferase [Sinorhizobium meliloti 1021]
186	Q5RBK6	75070793	Ubiquinone biosynthesis methyltransferase COQ5, mitochondr precursor
187	Q98GV1	48474615	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
188	CAE66876	39589641	Hypothetical protein CBG12254 [Caenorhabditis briggsae]
189	Q4G064	90111989	Ubiquinone biosynthesis methyltransferase COQ5, mitochondr precursor
190	EAT48827	108884602	ubiquinone/menaquinone biosynthesis methyltransferase [Aede aegypti]
191	ZP_008...	78694883	Ubiquinone/menaquinone biosynthesis methyltransferase [Bradyrhizobium sp. BTAi1]
192	YP_575410	92115681	ubiquinone/menaquinone biosynthesis methyltransferase [Nitrobacter hamburgensis X14]
193	Q6G577	61217251	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
194	BAB29289	12852138	unnamed protein product [Mus musculus]
195	YP_316661	75674240	ubiquinone/menaquinone biosynthesis methyltransferase [Nitrobacter winogradskyi Nb-255]
196	Q9CXI0	90111988	Ubiquinone biosynthesis methyltransferase COQ5, mitochondr precursor
197	ZP_010...	85714158	ubiquinone/menaquinone biosynthesis methyltransferase [Nitrobacter sp. Nb-311A]
198	Q8UIH5	48474890	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE
199	NP_531026	17934236	ubiquinone/menaquinone biosynthesis methyltransferase [Agrobacterium tumefaciens str. C58]
200	YP_537418	91205063	Ubiquinone/menaquinone biosynthesis methlytransferase UbiE [Rickettsia bellii RML369-C]

Table 53. Examples of MenG polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	YP_405244	82778895	menaquinone biosynthesis protein [Shigella dysenteriae Sd197
2	YP_691310	110807790	menaquinone biosynthesis, unknown [Shigella flexneri 5 str. 8
3	YP_153008	56415933	ribonuclease activity regulator protein RraA [Salmonella enter subsp. enterica serovar Paratyphi A str. ATCC 9150]
4	YP_218965	62182548	ribonuclease activity regulator protein RraA [Salmonella enter subsp. enterica serovar Choleraesuis str. SC-B67]
5	Q6CZ89	61215906	Regulator of ribonuclease activity A
6	YP_649677	108813910	S-adenosylmethionine:2-demethylmenaquinone methyltransfe [Yersinia pestis Nepal516]
7	YP_455850	85060148	menaquinone biosynthesis protein [Sodalis glossinidius str. 'morsitans']
8	ZP_008...	77977395	COG0684: Demethylmenaquinone methyltransferase [Yersini intermedia ATCC 29909]
9	ZP_008...	77957391	COG0684: Demethylmenaquinone methyltransferase [Yersini bercovieri ATCC 43970]
10	ZP_008...	77961041	COG0684: Demethylmenaquinone methyltransferase [Yersini mollaretii ATCC 43969]
11	ZP_008...	77972976	COG0684: Demethylmenaquinone methyltransferase [Yersini frederiksenii ATCC 33641]
12	Q7MYB9	61216007	Regulator of ribonuclease activity A
13	ZP_012...	90413627	ribonuclease activity regulator protein RraA [Photobacterium profundum 3TCK]
14	Q8E9R9	37088830	Regulator of ribonuclease activity A protein 2
15	Q6LVI5	61216078	Regulator of ribonuclease activity A 1
16	YP_736467	114045917	regulator of ribonuclease activity A [Shewanella sp. MR-7]
17	ZP_012...	90580886	ribonuclease activity regulator protein RraA [Vibrio angustum S14]
18	YP_561478	91791827	Protein of unknown function 1935 [Shewanella denitrificans OS217]
19	ZP_011...	89075182	ribonuclease activity regulator protein RraA [Photobacterium s SKA34]
20	ZP_006...	69949853	Protein of unknown function 1935 [Shewanella frigidimarina NCIMB 400]
21	ZP_009...	84390849	ribonuclease activity regulator protein RraA [Vibrio splendidu 12B01]
22	ZP_009...	82742407	Protein of unknown function 1935 [Shewanella sp. W3-18-1]
23	ZP_007...	75830087	COG0684: Demethylmenaquinone methyltransferase [Vibrio cholerae MO10]
24	ZP_010...	86147297	ribonuclease activity regulator protein RraA [Vibrio sp. MED2
25	ZP_014...	113948767	Protein of unknown function 1935 [Shewanella baltica OS195]
26	Q87T23	33301271	Regulator of ribonuclease activity A protein 2
27	ZP_008...	78366174	Protein of unknown function 1935 [Shewanella sp. PV-4]
28	Q8DCP6	37088808	Regulator of ribonuclease activity A protein 2
29	ZP_012...	91226625	ribonuclease activity regulator protein RraA [Vibrio alginolyti 12G01]
30	Q7MH54	61216082	Regulator of ribonuclease activity A protein 2
31	ZP_005...	68546473	Protein of unknown function 1935 [Shewanella amazonensis SB2B]
32	ZP_007...	75854332	COG0684: Demethylmenaquinone methyltransferase [Vibrio s Ex25]
33	YP_203594	59710818	ribonuclease activity regulator protein RraA [Vibrio fischeri

			ES114]
34	Q9CLP9	17368770	Regulator of ribonuclease activity A
35	NP_438666	16272452	ribonuclease activity regulator protein RraA [Haemophilus influenzae Rd KW20]
36	YP_248219	68249107	ribonuclease activity regulator protein RraA [Haemophilus influenzae 86-028NP]
37	YP_718427	113460366	regulator of ribonuclease activity A [Haemophilus somnus 129
38	ZP_007...	75430489	demethylmenaquinone methyltransferase [Actinobacillus succinogenes 130Z]
39	ZP_010...	85711520	ribonuclease activity regulator protein RraA [Idiomarina baltic OS145]
40	YP_663623	109900368	regulator of ribonuclease activity A [Pseudoalteromonas atlant T6c]
41	P59885	37088068	Regulator of ribonuclease activity A
42	YP_089031	52425894	ribonuclease activity regulator protein RraA [Mannheimia succiniciproducens MBEL55E]
43	Q65RG4	61215868	Regulator of ribonuclease activity A
44	ZP_001...	32034231	COG0684: Demethylmenaquinone methyltransferase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]
45	ZP_011...	88792846	ribonuclease activity regulator protein RraA [Alteromonas macleodii 'Deep ecotype']
46	Q5QV38	61215798	Regulator of ribonuclease activity A
47	NP_760277	27364749	ribonuclease activity regulator protein RraA [Vibrio vulnificus CMCP6]
48	ZP_012...	90408304	ribonuclease activity regulator protein RraA [Psychromonas sp CNPT3]
49	ZP_013...	106883372	Protein of unknown function 1935 [Psychromonas ingrahamii
50	YP_341224	77361649	regulator of RNase E/rne (Belongs to the rraA) [Pseudoalteromonas haloplanktis TAC125]
51	ZP_011...	88858824	regulator of RNase E/rne protein [Pseudoalteromonas tunicata
52	YP_271023	71279667	hypothetical protein CPS_4374 [Colwellia psychrerythraea 34I
53	ZP_004...	67153424	Protein of unknown function 1935 [Azotobacter vinelandii Av(
54	Q883Q6	37088355	Regulator of ribonuclease activity A
55	ZP_009...	84328093	COG0684: Demethylmenaquinone methyltransferase [Pseudomonas aeruginosa 2192]
56	ZP_009...	82737941	Protein of unknown function 1935 [Pseudomonas putida F1]
57	Q88L51	37088372	Regulator of ribonuclease activity A
58	YP_258990	70729254	ribonuclease activity regulator protein RraA [Pseudomonas fluorescens Pf-5]
59	ZP_013...	107101203	hypothetical protein PaerPA_01002235 [Pseudomonas aerugin PACS2]
60	ZP_012...	94414601	hypothetical protein PaerP_01003676 [Pseudomonas aeruginos PA7]
61	Q9S4U0	17369593	Regulator of ribonuclease activity A
62	YP_235173	66045332	ribonuclease activity regulator protein RraA [Pseudomonas syringae pv. syringae B728a]
63	YP_274282	71737716	protein of unknown function, TIGR01935 [Pseudomonas syrin pv. phaseolicola 1448A]
64	YP_347504	77457999	Protein of unknown function 1935 [Pseudomonas fluorescens I 1]
65	YP_433379	83644944	Demethylmenaquinone methyltransferase [Hahella chejuensis KCTC 2396]
66	ZP_012...	90415933	ribonuclease activity regulator protein RraA [marine gamma

			proteobacterium HTCC2207]
67	ZP_011...	89094366	hypothetical protein MED92_09636 [Oceanospirillum sp. MEI
68	ZP_013...	94502020	ribonuclease activity regulator protein RraA [Oceanobacter sp. RED65]
69	YP_286296	71908709	Protein of unknown function 1935 [Dechloromonas aromatica RCB]
70	ZP_008...	77954841	Protein of unknown function 1935 [Marinobacter aquaeolei V]
71	YP_159562	56477973	ribonuclease activity regulator protein RraA [Azoarcus sp. EbI
72	ZP_008...	78700348	Protein of unknown function 1935 [Alkalilimnicola ehrlichei MLHE-1]
73	Q6FCF4	61215916	Regulator of ribonuclease activity A
74	YP_692965	110834106	s-adenosylmethionine:2-demethylmenaquinonemethyl transfer [Alcanivorax borkumensis SK2]
75	ZP_007...	75829007	COG0684: Demethylmenaquinone methyltransferase [Vibrio cholerae MO10]
76	Q9KPK1	33302630	Regulator of ribonuclease activity A protein 1
77	ZP_011...	88800595	ribonuclease activity regulator protein RraA [Reinekea sp. MED297]
78	YP_364699	78048524	ribonuclease activity regulator protein RraA [Xanthomonas campestris pv. vesicatoria str. 85-10]
79	ZP_011...	89072516	ribonuclease activity regulator protein RraA [Photobacterium s SKA34]
80	YP_242568	66767806	ribonuclease activity regulator protein RraA [Xanthomonas campestris pv. campestris str. 8004]
81	ABH85383	112005081	ribonuclease activity regulator protein [Vibrio fischeri]
82	ZP_001...	32030320	COG0684: Demethylmenaquinone methyltransferase [Haemophilus somnus 2336]
83	Q8PIT8	37089016	Regulator of ribonuclease activity A
84	ZP_012...	90580599	ribonuclease activity regulator protein RraA [Vibrio angustum S14]
85	1VI4A	40889977	Chain A, Crystal Structure Of Regulator Of Ribonuclease Aci A Protein 1
86	YP_574110	92114182	Protein of unknown function 1935 [Chromohalobacter salexig DSM 3043]
87	ZP_011...	88949522	Protein of unknown function 1935 [Halorhodospira halophila S
88	ZP_012...	91771273	Protein of unknown function 1935 [Psychrobacter sp. PRwf-1]
89	AAW74809	58425772	S-adenosylmethionine:2-demethylmenaquinone methyltransfe [Xanthomonas oryzae pv. oryzae KACC10331]
90	YP_450472	84623100	S-adenosylmethionine:2-demethylmenaquinone methyltransfe [Xanthomonas oryzae pv. oryzae MAFF 311018]
91	ZP_005...	68547769	Protein of unknown function 1935 [Shewanella amazonensis SB2B]
92	ZP_010...	87121817	hypothetical protein MED121_00795 [Marinomonas sp. MED
93	BAD44396	51971463	putative S-adenosylmethionine:2- demethylmenaquinone methyltransferase [Arabidopsis thaliana]
94	Q87SD2	33301268	Regulator of ribonuclease activity A protein 1
95	ZP_013...	100918601	hypothetical protein Bmal10_03000386 [Burkholderia mallei 10399]
96	NP_850830	30685861	unknown protein [Arabidopsis thaliana]
97	AAM61756	21537415	S-adenosylmethionine:2-demethylmenaquinone methyltransfe like protein [Arabidopsis thaliana]
98	YP_580926	93006489	Protein of unknown function 1935 [Psychrobacter cryohalolen K5]

99	Q7NXI6	61216011	Regulator of ribonuclease activity A
100	AAR24712	38603934	At5g56260 [Arabidopsis thaliana]
101	YP_144588	55981291	ribonuclease activity regulator protein RraA [Thermus thermophilus HB8]
102	YP_264767	71066040	ribonuclease activity regulator protein RraA [Psychrobacter arcticus 273-4]
103	YP_628661	108758203	putative regulator of ribonuclease activity A [Myxococcus xant DK 1622]
104	Q7MNR7	61216083	Regulator of ribonuclease activity A protein 1
105	NP_933441	37678832	ribonuclease activity regulator protein RraA [Vibrio vulnificus YJ016]
106	ZP_011...	88704122	S-adenosylmethionine:2-demethylmenaquinone methyltransfer [gamma proteobacterium KT 71]
107	ZP_010...	84711560	Protein of unknown function 1935 [Polaromonas naphthalenivorans CJ2]
108	NP_519475	17546073	ribonuclease activity regulator protein RraA [Ralstonia solanacearum GMI1000]
109	Q8XZP1	61252297	Regulator of ribonuclease activity A
110	1J3LF	46014897	Chain F, Structure Of The Rna-Processing Inhibitor Rraa From Thermus Thermophilis
111	ZP_009...	83945186	ribonuclease activity regulator protein RraA [Oceanicaulis alexandrii HTCC2633]
112	Q72J23	61215971	Regulator of ribonuclease activity A
113	ZP_012...	91226804	ribonuclease activity regulator protein RraA [Vibrio alginolytic 12G01]
114	ZP_012...	90413160	ribonuclease activity regulator protein RraA [Photobacterium profundum 3TCK]
115	YP_442516	83721353	regulator of ribonuclease activity A [Burkholderia thailandensi E264]
116	ZP_012...	92908958	Protein of unknown function 1935 [Mycobacterium sp. JLS]
117	ZP_009...	84393241	Demethylmenaquinone methyltransferase [Vibrio splendidus 12B01]
118	BAF10115	113537732	Os02g0762100 [Oryza sativa (japonica cultivar-group)]
119	Q5Z3P5	61215828	Regulator of ribonuclease activity A
120	BAF10114	113537731	Os02g0761900 [Oryza sativa (japonica cultivar-group)]
121	YP_296171	73541651	ribonuclease activity regulator protein RraA [Ralstonia eutroph JMP134]
122	ZP_002...	47573824	COG0684: Demethylmenaquinone methyltransferase [Rubrivi gelatinosus PM1]
123	ZP_008...	81252640	COG0684: Demethylmenaquinone methyltransferase [Mycobacterium tuberculosis C]
124	NP_916709	34910724	S-adenosylmethionine:2-demethylmenaquinone methyltransfer like protein [Oryza sativa (japonica cultivar-group)]
125	ZP_013...	110593137	Protein of unknown function 1935 [Acidovorax sp. JS42]
126	YP_290783	72163126	ribonuclease activity regulator protein RraA [Thermobifida fus YX]
127	ZP_010...	86147386	ribonuclease activity regulator protein RraA [Vibrio sp. MED2
128	Q8FQY0	37088871	Regulator of ribonuclease activity A
129	NP_737597	25027543	ribonuclease activity regulator protein RraA [Corynebacterium efficiens YS-314]
130	ZP_007...	75853842	COG0684: Demethylmenaquinone methyltransferase [Vibrio s Ex25]
131	Q607E7	61215840	Regulator of ribonuclease activity A

132	Q745I2	61215990	Regulator of ribonuclease activity A
133	ZP_008...	78366607	Protein of unknown function 1935 [Shewanella sp. PV-4]
134	YP_642216	108802019	Protein of unknown function 1935 [Mycobacterium sp. MCS]
135	ZP_005...	68541848	Protein of unknown function 1935 [Shewanella baltica OS155
136	YP_523211	89900740	Protein of unknown function 1935 [Rhodoferax ferrireducens T118]
137	ZP_008...	78688287	Protein of unknown function 1935 [Shewanella sp. ANA-3]
138	B86917	25397608	hypothetical protein menG [imported] - Mycobacterium leprae
139	YP_559362	91784156	Protein of unknown function 1935 [Burkholderia xenovorans LB400]
140	ZP_011...	89342451	Protein of unknown function 1935 [Mycobacterium flavescens PYR-GCK]
141	ABE89807	92889308	Dimethylmenaquinone methyltransferase [Medicago truncatul
142	YP_583534	94310324	Protein of unknown function 1935 [Ralstonia metallidurans CI
143	YP_603858	94984494	Protein of unknown function 1935 [Deinococcus geothermalis DSM 11300]
144	ZP_009...	82744293	Protein of unknown function 1935 [Shewanella sp. W3-18-1]
145	ZP_012...	90203781	Protein of unknown function 1935 [Mycobacterium vanbaalen PYR-1]
146	YP_738287	114047737	regulator of ribonuclease activity A [Shewanella sp. MR-7]
147	Q9RW10	17369587	Regulator of ribonuclease activity A
148	ZP_006...	69952580	Protein of unknown function 1935 [Shewanella frigidimarina NCIMB 400]
149	YP_267296	71277832	ribonuclease activity regulator protein RraA [Colwellia psychrerythraea 34H]
150	YP_250682	68535977	S-adenosylmethionine:2-demethylmenaquinone methyltransfe [Corynebacterium jeikeium K411]
151	Q8EE23	37088843	Regulator of ribonuclease activity A protein 1
152	YP_703694	111020722	possible S-adenosylmethionine:2-demethylmenaquinone methyltransferase [Rhodococcus sp. RHA1]
153	ZP_009...	84497544	ribonuclease activity regulator protein RraA [Janibacter sp. HTCC2649]
154	YP_225217	62389815	ribonuclease activity regulator protein RraA [Corynebacterium glutamicum ATCC 13032]
155	Q8NRW6	37088990	Regulator of ribonuclease activity A
156	YP_563031	91793380	Protein of unknown function 1935 [Shewanella denitrificans OS217]
157	ZP_007...	75430509	demethylmenaquinone methyltransferase [Actinobacillus succinogenes 130Z]
158	Q734S7	61215978	Regulator of ribonuclease activity A
159	YP_147666	56420348	ribonuclease activity regulator protein RraA [Geobacillus kaustophilus HTA426]
160	ZP_003...	62423288	COG0684: Demethylmenaquinone methyltransferase [Brevibacterium linens BL2]
161	Q638R8	61215850	Regulator of ribonuclease activity A
162	ZP_002...	47564444	protein of unknown function, TIGR01935 [Bacillus cereus G9
163	ZP_011...	89206547	Protein of unknown function 1935 [Bacillus weihenstephanens KBAB4]
164	YP_037432	49478174	ribonuclease activity regulator protein RraA [Bacillus thuringi serovar konkukian str. 97-27]
165	ZP_007...	75763625	S-adenosylmethionine:2-demethylmenaquinone methyltransfe [Bacillus thuringiensis serovar israelensis ATCC 35646]
166	YP_029379	49186127	ribonuclease activity regulator protein RraA [Bacillus anthraci

			Sterne]
167	ZP_004...	66964056	Protein of unknown function 1935 [Arthrobacter sp. FB24]
168	YP_341690	77362116	putative regulator of ribonuclease E activity (Rra family) [Pseudoalteromonas haloplanktis TAC125]
169	ZP_011...	89094648	hypothetical protein MED92_00445 [Oceanospirillum sp. ME]
170	ZP_009...	82744360	Protein of unknown function 1935 [Shewanella sp. W3-18-1]
171	ZP_004...	67154759	Dimethylmenaquinone methyltransferase [Azotobacter vinelan AvOP]
172	CAG27624	46911569	putative demethylmenaquinone methyltransferase-like [Populu euramericana]
173	ZP_009...	82739104	transferase [Pseudomonas putida F1]
174	YP_348718	77459211	hypothetical protein Pfl_2988 [Pseudomonas fluorescens PfO-
175	YP_532939	90424569	Dimethylmenaquinone methyltransferase [Rhodopseudomonas palustris BisB18]
176	NP_766770	27375241	hypothetical protein bll0130 [Bradyrhizobium japonicum USD 110]
177	ZP_011...	88951779	Orotidine 5'-phosphate decarboxylase:Dimethylmenaquinone methyltransferase:Putative N-acetylmannosamine-6-phosphate epimerase:Protein of unknown function DUF561 [Methanosae thermophila PT]
178	NP_069695	11498467	hypothetical protein AF0861 [Archaeoglobus fulgidus DSM 4
179	NP_884072	33596429	hypothetical protein BPP1802 [Bordetella parapertussis 12822
180	NP_879960	33592316	hypothetical protein BP1186 [Bordetella pertussis Tohama I]
181	NP_889840	33602280	hypothetical protein BB3305 [Bordetella bronchiseptica RB50
182	CAJ73826	91200773	conserved hypothetical protein [Candidatus Kuenenia stuttgartiensis]
183	NP_522505	17549165	hypothetical protein RS05389 [Ralstonia solanacearum GMI10
184	YP_553022	91777814	Putative dimethylmenaquinone methyltransferase [Burkholderi xenovorans LB400]
185	ZP_011...	89095790	hypothetical protein B14911_03634 [Bacillus sp. NRRL B-14
186	ZP_009...	83747877	Demethylmenaquinone methyltransferase family [Ralstonia solanacearum UW551]
187	ZP_012...	91216440	ribonuclease activity regulator protein RraA [Psychroflexus tor ATCC 700755]
188	ZP_007...	75255997	COG0684: Demethylmenaquinone methyltransferase [Escheric coli E22]
189	YP_706882	111023910	methyltransferase [Rhodococcus sp. RHA1]
190	YP_177252	56965519	S-adenosylmethionine:2-demethylmenaquinone methyltransfer [Bacillus clausii KSM-K16]
191	NP_535701	17938913	hypothetical protein Atu5329 [Agrobacterium tumefaciens str. C58]
192	NP_883361	33595718	putative dimethylmenaquinone methyltransferase [Bordetella parapertussis 12822]
193	NP_887802	33600242	putative dimethylmenaquinone methyltransferase [Bordetella bronchiseptica RB50]
194	YP_660173	109896918	Dimethylmenaquinone methyltransferase [Pseudoalteromonas atlantica T6c]
195	YP_532593	90424223	Dimethylmenaquinone methyltransferase [Rhodopseudomonas palustris BisB18]
196	ZP_009...	83368913	demethylmenaquinone methyltransferase [Rhodobacter sphaeroides ATCC 17025]
197	ZP_013...	110604871	Dimethylmenaquinone methyltransferase [Methanoculleus marisnigri JR1]

198	YP_502122	88601944	Orotidine 5'-phosphate decarboxylase [Methanospirillum hung JF-1]

Table 54. Examples of tyrA polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	CAA42950.1	43345	chorismate mutase; prephenate dehydrogenase [Pantoea agglomerans].
2	AAA24868	415010	prephenate dehydrogenase [Pantoea agglomerans]
3	NP_806335	29142993	chorismate mutase [Salmonella enterica subsp. enterica serova Typhi Ty2]
4	ZP_008...	77976462	COG0287: Prephenate dehydrogenase [Yersinia intermedia A 29909]
5	YP_217658	62181241	chorismate mutase T/prephenate dehydrogenase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
6	YP_151709	56414634	chorismate mutase/prephenate dehydrogenase [Salmonella ent subsp. enterica serovar Paratyphi A str. ATCC 9150]
7	ZP_008...	77972190	COG0287: Prephenate dehydrogenase [Yersinia frederiksenii ATCC 33641]
8	YP_541920	91211934	bifunctional chorismate mutase/prephenate dehydratase [Escherichia coli UTI89]
9	ZP_008...	77960429	COG0287: Prephenate dehydrogenase [Yersinia mollaretii AT 43969]
10	YP_690253	110806733	chorismate mutase-T and prephenate dehydrogenase [Shigella flexneri 5 str. 8401]
11	NP_311490	15832717	chorismate mutase-T [Escherichia coli O157:H7 str. Sakai]
12	YP_670491	110642761	chorismate mutase T/prephenate dehydrogenase [Escherichia c 536]
13	ZP_007...	75187347	COG0287: Prephenate dehydrogenase [Escherichia coli E2437
14	NP_838171	30064000	chorismate mutase-T and prephenate dehydrogenase [Shigella flexneri 2a str. 2457T]
15	YP_409003	82545056	chorismate mutase-T and prephenate dehydrogenase [Shigella boydii Sb227]
16	AP_003181	89109401	fused chorismate mutase T and prephenate dehydrogenase [Escherichia coli W3110]
17	ZP_007...	77631814	COG0287: Prephenate dehydrogenase [Yersinia pseudotuberculosis IP 31758]
18	ZP_007...	75513206	COG0287: Prephenate dehydrogenase [Escherichia coli 53638
19	YP_404300	82777951	chorismate mutase-T [Shigella dysenteriae Sd197]
20	YP_646746	108810979	chorismate mutase and prephenate dehydrogenase [Yersinia pe Nepal516]
21	ZP_008...	77956720	COG0287: Prephenate dehydrogenase [Yersinia bercovieri AT 43970]
22	YP_051440	50122273	T-protein [includes: chorismate mutase and prephenate dehydrogenase] [Erwinia carotovora subsp. atroseptica SCRI1
23	YP_454259	85058557	chorismate mutase T/prephenate dehydrogenase [Sodalis glossinidius str. 'morsitans']
24	NP_928574	37525230	T-protein [includes: chorismate mutase (CM); prephenate dehydrogenase (PDH)] [Photorhabdus luminescens subsp. laumondii TTO1]
25	YP_131155	54310135	putative chorismate mutase/prephenate dehydrogenase [Photobacterium profundum SS9]
26	ZP_012...	90414898	putative chorismate mutase/prephenate dehydrogenase [Photobacterium profundum 3TCK]
27	ZP_012...	90580373	putative chorismate mutase/prephenate dehydrogenase [Vibrio angustum S14]
28	ZP_011...	89075043	putative chorismate mutase/prephenate dehydrogenase

			[Photobacterium sp. SKA34]
29	ZP_010...	86148428	chorismate mutase/prephenate dehydrogenase [Vibrio sp. MED222]
30	ZP_007...	75854869	COG0287: Prephenate dehydrogenase [Vibrio sp. Ex25]
31	NP_796926	28897321	chorismate mutase/prephenate dehydrogenase [Vibrio parahaemolyticus RIMD 2210633]
32	ZP_009...	84393584	chorismate mutase/prephenate dehydrogenase [Vibrio splendi 12B01]
33	ZP_007...	75826055	COG0287: Prephenate dehydrogenase [Vibrio cholerae O395]
34	ZP_007...	75824086	COG0287: Prephenate dehydrogenase [Vibrio cholerae RC38
35	YP_203937	59711161	chorismate mutase [Vibrio fischeri ES114]
36	ZP_012...	91227656	chorismate mutase/prephenate dehydrogenase [Vibrio alginol 12G01]
37	ZP_007...	75829549	COG0287: Prephenate dehydrogenase [Vibrio cholerae MO1
38	ZP_007...	75819387	COG0287: Prephenate dehydrogenase [Vibrio cholerae V51]
39	NP_759486	27363958	Prephenate dehydrogenase [Vibrio vulnificus CMCP6]
40	NP_933495	37678886	prephenate dehydrogenase [Vibrio vulnificus YJ016]
41	ZP_013...	106882250	Chorismate mutase, T-protein [Psychromonas ingrahamii 37]
42	ZP_012...	90407526	putative chorismate mutase/prephenate dehydrogenase [Psychromonas sp. CNPT3]
43	YP_277695	71891965	chorismate mutase T [Candidatus Blochmannia pennsylvanicu BPEN]
44	ZP_001...	53728281	COG0287: Prephenate dehydrogenase [Haemophilus somnus 2336]
45	YP_718883	113460816	chorismate mutase [Haemophilus somnus 129PT]
46	YP_088294	52425157	TyrA protein [Mannheimia succiniciproducens MBEL55E]
47	ZP_001...	46133541	COG0287: Prephenate dehydrogenase [Haemophilus influenz R2866]
48	ZP_001...	53732693	COG0287: Prephenate dehydrogenase [Haemophilus influenz R2846]
49	NP_439442	16273204	hypothetical protein HI1290 [Haemophilus influenzae Rd KW
50	YP_249263	68250151	T-protein [Haemophilus influenzae 86-028NP]
51	ZP_005...	68547562	Chorismate mutase, T-protein [Shewanella amazonensis SB2B
52	ZP_009...	82744297	Chorismate mutase, T-protein [Shewanella sp. W3-18-1]
53	NP_245601	15602529	TyrA [Pasteurella multocida subsp. multocida str. Pm70]
54	ZP_007...	75429313	prephenate dehydrogenase [Actinobacillus succinogenes 130Z
55	ZP_008...	78685248	Chorismate mutase, T-protein [Shewanella sp. ANA-3]
56	YP_738956	114048406	chorismate mutase [Shewanella sp. MR-7]
57	ZP_005...	68544265	Chorismate mutase, T-protein [Shewanella baltica OS155]
58	ZP_001...	32034455	COG0287: Prephenate dehydrogenase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]
59	ZP_008...	78368660	Chorismate mutase, T-protein [Shewanella sp. PV-4]
60	NP_716982	24372940	chorismate mutase/prephenate dehydrogenase [Shewanella oneidensis MR-1]
61	YP_563751	91794100	Chorismate mutase, T-protein [Shewanella denitrificans OS21
62	ZP_006...	69952675	Chorismate mutase, T-protein [Shewanella frigidimarina NCI 400]
63	ZP_011...	88796197	bifunctional chorismate mutase T/prephenate dehydrogenase [Alteromonas macleodii 'Deep ecotype']
64	NP_878481	33519649	chorismate mutase/prephenate dehydrogenase [Candidatus Blochmannia floridanus]
65	YP_661164	109897909	chorismate mutase [Pseudoalteromonas atlantica T6c]
66	YP_270611	71281624	chorismate mutase/prephenate dehydrogenase [Colwellia

			psychrerythraea 34H]
67	YP_156103	56460822	Chorismate mutase-T [Idiomarina loihiensis L2TR]
68	ZP_010...	85712465	Chorismate mutase-T [Idiomarina baltica OS145]
69	YP_339470	77359895	chorismate mutase / prephenate dehydrogenase [Pseudoalteromonas haloplanktis TAC125]
70	ZP_011...	88860525	bifunctional protein [Pseudoalteromonas tunicata D2]
71	ZP_008...	77814309	Prephenate dehydrogenase [Shewanella putrefaciens CN-32]
72	XP_561110	57965340	ENSANGP00000026463 [Anopheles gambiae str. PEST]
73	ZP_001...	23128268	COG0287: Prephenate dehydrogenase [Nostoc punctiforme P 73102]
74	NP_484462	17227914	chorismate mutase/prephenate dehydrogenase [Nostoc sp. PC 7120]
75	YP_512856	89255495	prephenate dehydrogenase. [Francisella tularensis subsp. holarctica]
76	ZP_006...	71548230	Prephenate dehydrogenase [Syntrophobacter fumaroxidans M
77	ZP_013...	110604808	Prephenate dehydrogenase [Methanoculleus marisnigri JR1]
78	NP_247596	15668793	prephenate dehydrogenase [Methanocaldococcus jannaschii D 2661]
79	YP_304477	73668462	prephenate dehydrogenase [Methanosarcina barkeri str. fusarc
80	YP_461858	85859656	prephenate dehydrogenase [Syntrophus aciditrophicus SB]
81	NP_988634	45359077	prephenate dehydrogenase [Methanococcus maripaludis S2]
82	NP_614082	20094235	prephenate dehydrogenase [Methanopyrus kandleri AV19]
83	CAJ36601	110621323	prephenate dehydrogenase [uncultured methanogenic archaeo RC-I]
84	NP_633299	21227377	prephenate dehydrogenase [Methanosarcina mazei Go1]
85	NP_619454	20093379	prephenate dehydrogenase [Methanosarcina acetivorans C2A]
86	YP_566626	91773934	Prephenate dehydrogenase [Methanococcoides burtonii DSM 6242]
87	ZP_011...	88952193	Prephenate dehydrogenase:6-phosphogluconate dehydrogenas NAD-binding [Methanosaeta thermophila PT]
88	YP_706040	111023068	bifunctional chorismate mutase/ prephenate dehydrogenase [Rhodococcus sp. RHA1]
89	YP_009688	46578880	prephenate dehydrogenase [Desulfovibrio vulgaris subsp. vulg str. Hildenborough]
90	AAC44867	1575337	PapC
91	NP_378270	15922601	hypothetical protein ST2270 [Sulfolobus tokodaii str. 7]
92	YP_448109	84489877	putative prephenate dehydrogenase [Methanosphaera stadtmai DSM 3091]
93	NP_299617	15838929	prephenate dehydrogenase [Xylella fastidiosa 9a5c]
94	NP_069065	11497843	chorismate mutase/prephenate dehydratase (pheA) [Archaeogl fulgidus DSM 4304]
95	NP_930778	37527434	hypothetical protein plu3562 [Photorhabdus luminescens subs laumondii TTO1]
96	ZP_006...	71900368	Amino acid-binding ACT:Prephenate dehydrogenase [Xylella fastidiosa Ann-1]
97	NP_779566	28199252	prephenate dehydrogenase [Xylella fastidiosa Temecula1]
98	NP_276752	15679635	prephenate dehydrogenase [Methanothermobacter thermautotrophicus str. Delta H]
99	ZP_006...	71898348	Amino acid-binding ACT:Prephenate dehydrogenase [Xylella fastidiosa Ann-1]
100	BAD21141	47846867	4-amino-4-deoxyprephenate dehydrogenase [Streptomyces venezuelae]
101	YP_307541	73748302	prephenate dehydrogenase [Dehalococcoides sp. CBDB1]

102	ZP_011...	88933907	Prephenate dehydrogenase:NADP oxidoreductase, coenzyme F420-dependent:NAD-dependent glycerol-3-phosphate dehydrogenase, N-terminal [Dehalococcoides sp. BAV1]
103	YP_389973	78358524	prephenate dehydrogenase [Desulfovibrio desulfuricans G20]
104	YP_181204	57234714	prephenate dehydrogenase [Dehalococcoides ethenogenes 195
105	NP_341850	15897245	Chorismate mutase/prephenate dehydratase, putative (tyrA) [Sulfolobus solfataricus P2]
106	YP_200673	58581657	prephenate dehydrogenase [Xanthomonas oryzae pv. oryzae KACC10331]
107	YP_633977	108759735	prephenate dehydrogenase/chorismate mutase [Myxococcus xanthus DK 1622]
108	ZP_013...	110609330	Prephenate dehydrogenase:NAD-dependent glycerol-3-phospl dehydrogenase-like [Maricaulis maris MCS10]
109	YP_426060	83592308	Prephenate dehydrogenase [Rhodospirillum rubrum ATCC 11
110	YP_296780	73542260	Chorismate mutase, gamma, beta and epsilon proteobacteria [Ralstonia eutropha JMP134]
111	YP_066011	51246127	similar to P-protein [Desulfotalea psychrophila LSv54]
112	YP_725307	113866818	prephenate dehydratase, Chorismate mutase [Ralstonia eutropl H16]
113	YP_582871	94309661	chorismate mutase [Ralstonia metallidurans CH34]
114	YP_135239	55377389	prephenate dehydrogenase [Haloarcula marismortui ATCC 43
115	YP_157513	56475924	prephenate dehydrogenase [Azoarcus sp. EbN1]
116	YP_617926	103488365	Prephenate dehydrogenase [Sphingopyxis alaskensis RB2256]
117	ZP_003...	62423857	COG1605: Chorismate mutase [Brevibacterium linens BL2]
118	YP_168305	56697934	chorismate mutase family protein [Silicibacter pomeroyi DSS-
119	ZP_006...	69268090	unknown product [Ferroplasma acidarmanus Fer1]
120	YP_471430	86359538	chorismate mutase protein [Rhizobium etli CFN 42]
121	YP_677886	110637679	prephenate dehydrogenase [Cytophaga hutchinsonii ATCC 33
122	ZP_006...	71549758	Prephenate dehydrogenase [Nitrosomonas eutropha C71]
123	ZP_006...	69258402	Chorismate mutase, gamma, beta and epsilon proteobacteria [Magnetococcus sp. MC-1]
124	NP_827386	29832752	chorismate mutase [Streptomyces avermitilis MA-4680]
125	NP_626280	21220501	chorismate mutase [Streptomyces coelicolor A3(2)]
126	YP_412879	82703313	Prephenate dehydrogenase [Nitrosospira multiformis ATCC 25196]
127	NP_534107	17937318	prephenate dehydrogenase [Agrobacterium tumefaciens str. C
128	YP_056453	50843226	chorismate mutase [Propionibacterium acnes KPA171202]
129	YP_192393	58040429	chorismate mutase [Gluconobacter oxydans 621H]
130	NP_357000	15891328	prephenate dehydrogenase [Agrobacterium tumefaciens str. C
131	NP_614892	20095045	Chorismate mutase [Methanopyrus kandleri AV19]
132	YP_628067	108563751	prephenate dehydrogenase [Helicobacter pylori HPAG1]
133	AAL30405	16903098	arogenate dehydrogenase [Arabidopsis thaliana]
134	ZP_011...	89361368	cyclohexadienyl dehydrogenase / prephenate dehydrogenase [Xanthobacter autotrophicus Py2]
135	ZP_011...	89094102	still frameshift 3-phosphoshikimate 1-pcarboxyvinyltransferas prephenate dehydrogenase [Oceanospirillum sp. MED92]
136	YP_046840	50085330	bifunctional protein [Includes: putative prephenate or cyclohexadienyl dehydrogenase; 3-phosphoshikimate 1-carboxyvinyltransferase (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS) (AroA)] [Acinetobacter sp ADP1]
137	NP_224012	15612359	prephenate dehydrogenase [Helicobacter pylori J99]
138	ZP_004...	67546805	Prephenate dehydrogenase [Burkholderia vietnamiensis G4]

139	ZP_014...	111619586	Prephenate dehydrogenase [Acidovorax avenae subsp. citrulli AAC00-1]
140	YP_063084	50955796	chorismate mutase [Leifsonia xyli subsp. xyli str. CTCB07]
141	ZP_009...	83749094	chorismate mutase / prephenate dehydratase [Ralstonia solanacearum UW551]
142	ZP_009...	84357154	COG0077: Prephenate dehydratase [Burkholderia cenocepaci PC184]
143	ZP_012...	94492066	hypothetical protein CburD_01000956 [Coxiella burnetii Dug 7E9-12]
144	YP_368397	78065628	Chorismate mutase/Prephenate dehydratase [Burkholderia sp.
145	ZP_013...	110609017	Prephenate dehydratase [Maricaulis maris MCS10]
146	ZP_009...	84498327	chorismate mutase [Janibacter sp. HTCC2649]
147	ZP_006...	74015881	Chorismate mutase, gamma, beta and epsilon proteobacteria [Burkholderia ambifaria AMMD]
148	ZP_004...	67546806	Chorismate mutase, gamma, beta and epsilon proteobacteria [Burkholderia vietnamiensis G4]
149	ZP_006...	69938509	Chorismate mutase [Paracoccus denitrificans PD1222]
150	ZP_013...	111612462	Prephenate dehydrogenase [Verminephrobacter eiseniae EF01
151	EAU01108	112803764	P-protein [Campylobacter curvus 525.92]
152	NP_819991	29654299	prephenate dehydrogenase family protein [Coxiella burnetii R 493]
153	NP_519025	17545623	PROBABLE BIFUNCTIONAL PROTEIN: CHORISMATE MUTASE AND PREPHENATE DEHYDRATASE [Ralstoni solanacearum GMI1000]
154	ZP_013...	110592958	Prephenate dehydrogenase:NADP oxidoreductase, coenzyme F420-dependent:6-phosphogluconate dehydrogenase, NAD-binding:NAD-dependent glycerol-3-phosphate dehydrogenase [Acidovorax sp. JS42]
155	YP_032817	49474775	chorismate mutase [Bartonella quintana str. Toulouse]
156	YP_504633	88604455	Chorismate mutase [Methanospirillum hungatei JF-1]
157	BAB50405	14023800	cyclohexadienyl dehydrogenase [Mesorhizobium loti MAFF303099]
158	ZP_008...	78700814	Prephenate dehydrogenase [Alkalilimnicola ehrlichei MLHE-
159	ZP_011...	88713205	Prephenate dehydrogenase [Flavobacteriales bacterium HTCC2170]
160	BAB51049	14024446	chorismate mutase [Mesorhizobium loti MAFF303099]
161	YP_620448	107022121	chorismate mutase [Burkholderia cenocepacia AU 1054]
162	ZP_009...	84361153	COG0077: Prephenate dehydratase [Burkholderia dolosa AUC
163	YP_307542	73748303	chorismate mutase/prephenate dehydratase (P-protein) [Dehalococcoides sp. CBDB1]
164	YP_003995	46198328	3-deoxy-7-phosphoheptulonate synthase [Thermus thermophil HB27]
165	ZP_011...	88933906	Prephenate dehydratase:Chorismate mutase:Amino acid-bindi ACT [Dehalococcoides sp. BAV1]
166	YP_143654	55980357	3-deoxy-7-phosphoheptulonate synthase [Thermus thermophil HB8]
167	2D8EA	109157459	Chain A, Structure Of Chorismate Mutase (Form Ii) From The Thermophilus Hb8
168	BAF20453	113596579	Os06g0709000 [Oryza sativa (japonica cultivar-group)]
169	ZP_004...	67665379	Chorismate mutase, gamma, beta and epsilon proteobacteria [Burkholderia cenocepacia HI2424]
170	XP_755378	71001394	prephenate dehydrogenase [Aspergillus fumigatus Af293]
171	NP_213648	15606269	chorismate mutase/prephenate dehydratase [Aquifex aeolicus

172	ZP_006...	71546735	Chorismate mutase, gamma, beta and epsilon proteobacteria [Syntrophobacter fumaroxidans MPOB]
173	ZP_002...	47575153	COG0287: Prephenate dehydrogenase [Rubrivivax gelatinosu PM1]
174	YP_034296	49476255	chorismate mutase [Bartonella henselae str. Houston-1]
175	ZP_013...	100916229	hypothetical protein Bmal10_03002418 [Burkholderia mallei 10399]
176	YP_442172	83719222	chorismate mutase/prephenate dehydratase [Burkholderia thailandensis E264]
177	EAT98964	112801620	P-protein [Campylobacter concisus 13826]
178	NP_533363	17936573	chorismate mutase [Agrobacterium tumefaciens str. C58]
179	ZP_003...	57240749	Prephenate dehydrogenase [Campylobacter lari RM2100]
180	NP_963486	41614988	hypothetical protein NEQ192 [Nanoarchaeum equitans Kin4-I
181	NP_539144	17986510	chorismate mutase [Brucella melitensis 16M]
182	YP_412876	82703310	Chorismate mutase [Nitrosospira multiformis ATCC 25196]
183	YP_415177	82700603	Chorismate mutase [Brucella melitensis biovar Abortus 2308]
184	ZP_010...	85708094	Chorismate mutase [Erythrobacter sp. NAP1]
185	YP_181205	57234713	chorismate mutase/prephenate dehydratase [Dehalococcoides ethenogenes 195]
186	NP_720968	24379013	putative chorismate mutase [Streptococcus mutans UA159]
187	ZP_004...	66964551	Chorismate mutase, bacteria [Arthrobacter sp. FB24]
188	NP_903077	34498862	probable prephenate dehydrogenase [Chromobacterium violac ATCC 12472]
189	ZP_011...	88796198	chorismate mutase/prephenate dehydratase [Alteromonas macleodii 'Deep ecotype']
190	ZP_012...	94266010	Amino acid-binding ACT:Prephenate dehydrogenase [delta proteobacterium MLMS-1]
191	ZP_003...	62527659	COG1605: Chorismate mutase [Streptococcus thermophilus L 9]
192	YP_457621	85373559	chorismate mutase [Erythrobacter litoralis HTCC2594]
193	NP_861039	32267007	chorismate mutase/prephenate dehydratase [Helicobacter hepa ATCC 51449]
194	ABE87267	92884247	Prephenate dehydrogenase; NADP oxidoreductase, coenzyme F420-dependent [Medicago truncatula]
195	YP_615567	103486006	chorismate mutase [Sphingopyxis alaskensis RB2256]
196	YP_545795	91776039	chorismate mutase [Methylobacillus flagellatus KT]
197	ZP_005...	68055955	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 2:Chorismate mutase, G-positive and Deinococcus [Exiguobacterium sibiricum 255-15]
198	ZP_006...	69276036	Chorismate mutase, bacteria [Mesorhizobium sp. BNC1]

Table 55. Examples of pds1(hppd) polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	AAC62457.1	3694811	p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana]
2	1SP9B	55669758	Chain B, 4-Hydroxyphenylpyruvate Dioxygenase
3	NP_172144	30679736	PDS1 (PHYTOENE DESATURATION 1) [Arabidopsis thali
4	AAM96960	22530912	4-hydroxyphenylpyruvate dioxygenase HPD [Arabidopsis thaliana]
5	1TG5A	52695751	Chain A, Crystal Structures Of Plant 4-Hydroxyphenylpyruva Dioxygenases Complexed With Das645
6	AAX59006	62003087	4-hydroxyphenylpyruvate dioxygenase [Medicago truncatula]
7	O23920	3334219	4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acid oxidase)
8	Q9ARF9	17366672	4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acid oxidase)
9	AAN28922	23505684	4-hydroxyphenylpyruvate dioxygenase [Abutilon theophrasti]
10	1SP8D	55669756	Chain D, 4-Hydroxyphenylpyruvate Dioxygenase
11	BAF07924	113535541	Os02g0168100 [Oryza sativa (japonica cultivar-group)]
12	YP_445494	83816571	4-hydroxyphenylpyruvate dioxygenase [Salinibacter ruber DS 13855]
13	ZP_002...	47567476	4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus G924
14	ZP_003...	65317666	COG3185: 4-hydroxyphenylpyruvate dioxygenase and relatec hemolysins [Bacillus anthracis str. A2012]
15	ZP_007...	75760149	4-hydroxyphenylpyruvate dioxygenase [Bacillus thuringiensis serovar israelensis ATCC 35646]
16	NP_830120	30018489	4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus ATC 14579]
17	ZP_011...	89200714	4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus subsp cytotoxis NVH 391-98]
18	ZP_011...	89205757	4-hydroxyphenylpyruvate dioxygenase [Bacillus weihenstephanensis KBAB4]
19	ZP_011...	89098389	4-hydroxyphenylpyruvate dioxygenase [Bacillus sp. NRRL B 14911]
20	ZP_005...	67928870	4-hydroxyphenylpyruvate dioxygenase [Solibacter usitatus Ellin6076]
21	YP_591079	94969031	4-hydroxyphenylpyruvate dioxygenase [Acidobacteria bacteri Ellin345]
22	ZP_010...	86130810	4-hydroxyphenylpyruvate dioxygenase [Cellulophaga sp. MED134]
23	ZP_010...	86143740	4-hydroxyphenylpyruvate dioxygenase [Flavobacterium sp. MED217]
24	YP_054071	50404979	4-hydroxyphenylpyruvate dioxygenase, putative [Paramecium tetraurelia]
25	Q96X22	74630846	4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)
26	ZP_011...	88804748	4-hydroxyphenylpyruvate dioxygenase [Robiginitalea biforma HTCC2501]
27	O42764	3334221	4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)
28	XP_956614	85080847	hypothetical protein [Neurospora crassa OR74A]
29	ZP_007...	76261015	4-hydroxyphenylpyruvate dioxygenase [Chloroflexus aurantia J-10-fl]
30	ZP_012...	89891109	4-hydroxyphenylpyruvate dioxygenase [Flavobacteria bacteri BBFL7]

31	ZP_012...	91215525	4-hydroxyphenylpyruvate dioxygenase [Psychroflexus torqui: ATCC 700755]
32	ZP_011...	88711872	4-hydroxyphenylpyruvate dioxygenase [Flavobacteriales bacterium HTCC2170]
33	ZP_012...	90590734	4-hydroxyphenylpyruvate dioxygenase [Flavobacterium johnsoniae UW101]
34	Q9S2F4	81625146	4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)
35	1T47B	50513703	Chain B, Structure Of Fe2-Hppd Bound To Ntbc
36	ZP_011...	88801956	4-hydroxyphenylpyruvate dioxygenase [Polaribacter irgensii :
37	BAE57420	83767281	unnamed protein product [Aspergillus oryzae]
38	ZP_006...	69270366	4-hydroxyphenylpyruvate dioxygenase [Ferroplasma acidarm Fer1]
39	ZP_010...	86134911	4-hydroxyphenylpyruvate dioxygenase [Tenacibaculum sp. MED152]
40	EAQ86656	88179188	hypothetical protein CHGG_07909 [Chaetomium globosum C 148.51]
41	YP_024147	48478441	4-hydroxyphenylpyruvate dioxygenase [Picrophilus torridus I 9790]
42	AAA50231	555806	4-hydroxyphenylpyruvate acid dioxygenase
43	Q6CDR5	74635204	4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase)
44	XP_386177	46123247	hypothetical protein FG06001.1 [Gibberella zeae PH-1]
45	ZP_009...	83855941	4-hydroxyphenylpyruvate dioxygenase [Croceibacter atlantici HTCC2559]
46	ZP_005...	68232050	4-hydroxyphenylpyruvate dioxygenase [Frankia sp. EAN1pec
47	YP_703131	111020159	4-hydroxyphenylpyruvate dioxygenase [Rhodococcus sp. RH
48	EAS35956	90306325	4-hydroxyphenylpyruvate dioxygenase [Coccidioides immitis
49	Q00415	3334224	4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) (T-cell reactive protein)
50	NP_001...	51230599	hypothetical protein LOC445287 [Danio rerio]
51	XP_853422	73995174	PREDICTED: similar to 4-hydroxyphenylpyruvate dioxygena (4HPPD) (HPD) (HPPDase) [Canis familiaris]
52	AAI05226	75948304	4-hydroxyphenylpyruvate dioxygenase [Bos taurus]
53	XP_798672	72024564	PREDICTED: similar to 4-hydroxyphenylpyruvate dioxygena (4HPPD) (HPD) (HPPDase) [Strongylocentrotus purpuratus]
54	AAH24287	18999511	4-hydroxyphenylpyruvate dioxygenase [Homo sapiens]
55	YP_702005	111019033	4-hydroxyphenylpyruvate dioxygenase [Rhodococcus sp. RH
56	P32755	83303639	4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (4-hydroxyphenylpyruvic acid oxidase) (HPPDase) (F protein) (I Alloantigen)
57	AAC73008	3860238	4-hydroxyphenylpyruvate-dioxygenase [Homo sapiens]
58	EAL30481	54641731	GA11203-PA [Drosophila pseudoobscura]
59	AAA40740	202924	F alloantigen
60	XP_528667	55666795	PREDICTED: 4-hydroxyphenylpyruvate dioxygenase [Pan troglodytes]
61	Q6TGZ5	82187435	4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acid oxidase)
62	JC4215	1362503	T-cell reactive protein - Coccidioides immitis
63	Q5BKL0	82178627	4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acid oxidase)
64	EAS07560	89309572	4-hydroxyphenylpyruvate dioxygenase family protein [Tetrahymena thermophila SB210]

65	XP_001...	109099057	PREDICTED: 4-hydroxyphenylpyruvate dioxygenase isofor [Macaca mulatta]
66	NP_957461	41054723	hypothetical protein LOC394142 [Danio rerio]
67	XP_001...	110755389	PREDICTED: similar to CG11796-PA, isoform A [Apis mel
68	EAT37578	108873353	4-hydroxyphenylpyruvate dioxygenase [Aedes aegypti]
69	P49429	83303597	4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (4-hydroxyphenylpyruvic acid oxidase) (HPPDase) (F protein) (Alloantigen)
70	BAA06267	849053	4-hydroxyphenylpyruvate dioxygenase [Mus musculus]
71	AAS77442	45825069	GH11957p [Drosophila melanogaster]
72	AAH84120	54035226	LOC495029 protein [Xenopus laevis]
73	YP_705013	111022041	4-hydroxyphenylpyruvate dioxygenase [Rhodococcus sp. RH
74	BAE28861	74143620	unnamed protein product [Mus musculus]
75	YP_703002	111020030	4-hydroxyphenylpyruvate dioxygenase [Rhodococcus sp. RH
76	EAT33142	108868917	4-hydroxyphenylpyruvate dioxygenase [Aedes aegypti]
77	CAA42111	1841443	F1 protein [Mus musculus]
78	ZP_006...	71366476	4-hydroxyphenylpyruvate dioxygenase [Nocardioides sp. JS6
79	NP_999389	47523532	4-hydroxyphenylpyruvic acid dioxygenase [Sus scrofa]
80	XP_318007	58390825	ENSANGP00000010800 [Anopheles gambiae str. PEST]
81	XP_642615	66817524	4-hydroxyphenylpyruvate dioxygenase [Dictyostelium discoi AX4]
82	Q4WPV8	74671554	Probable 4-hydroxyphenylpyruvate dioxygenase 2 (4HPPD 2 (HPD 2) (HPPDase 2)
83	XP_001...	111226747	4-hydroxyphenylpyruvate dioxygenase [Dictyostelium discoi AX4]
84	AAI21487	113197875	Unknown (protein for MGC:146689) [Xenopus tropicalis]
85	YP_121297	54027055	putative 4-hydroxyphenylpyruvate dioxygenase [Nocardia farcinica IFM 10152]
86	Q60Y65	74846152	4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) (4-hydroxyphenylpyruvic acid oxidase)
87	NP_499324	17555220	4-HydroxyPhenylpyruvate Dioxygenase (HPD) family memb (hpd-1) [Caenorhabditis elegans]
88	XP_001...	109099059	PREDICTED: 4-hydroxyphenylpyruvate dioxygenase isofor [Macaca mulatta]
89	XP_415144	50756391	PREDICTED: similar to 4-hydroxyphenylpyruvate dioxygen [Gallus gallus]
90	AAH60451	38014668	MGC68535 protein [Xenopus laevis]
91	NP_649225	21356105	CG11796-PB, isoform B [Drosophila melanogaster]
92	CAJ38798	83318921	4-hydroxyphenylpyruvate dioxygenase protein [Platynereis dumerilii]
93	XP_460446	50423723	hypothetical protein DEHA0F02156g [Debaryomyces hanser CBS767]
94	CAF98530	47223760	unnamed protein product [Tetraodon nigroviridis]
95	YP_432268	83643833	4-hydroxyphenylpyruvate dioxygenase [Hahella chejuensis K 2396]
96	YP_481550	86741150	4-hydroxyphenylpyruvate dioxygenase [Frankia sp. CcI3]
97	ABB86496	93209319	HNF-HNF class homeobox protein [Nematostella vectensis]
98	NP_508875	17550752	C31H2.4 [Caenorhabditis elegans]
99	CAE53378	40713178	HmaS protein [Actinoplanes teichomyceticus]
100	CAG15040	45580880	HmaS protein [Actinoplanes teichomyceticus]
101	NP_970275	42524895	4-hydroxyphenylpyruvate dioxygenase [Bdellovibrio bacteriovorus HD100]
102	YP_132852	54302859	putative 4-hydroxyphenylpyruvate dioxygenase [Photobacteri

			profundum SS9]
103	ZP_012...	90414163	putative 4-hydroxyphenylpyruvate dioxygenase [Photobacteri profundum 3TCK]
104	NP_484814	17228266	4-hydroxyphenylpyruvate dioxygenase [Nostoc sp. PCC 712(
105	YP_723660	113477599	4-hydroxyphenylpyruvate dioxygenase [Trichodesmium erythraeum IMS101]
106	YP_343456	77164931	4-hydroxyphenylpyruvate dioxygenase [Nitrosococcus ocean ATCC 19707]
107	XP_659503	67522885	hypothetical protein AN1899.2 [Aspergillus nidulans FGSC A
108	YP_325158	75910862	4-hydroxyphenylpyruvate dioxygenase [Anabaena variabilis ATCC 29413]
109	XP_711490	68489395	4-hydroxyphenylpyruvate dioxygenase [Candida albicans SC5314]
110	CAA11761	2894154	PCZA361.1 [Amycolatopsis orientalis]
111	EAS36112	90306481	hypothetical protein CIMG_01466 [Coccidioides immitis RS]
112	EAT91209	111070089	hypothetical protein SNOG_01560 [Phaeosphaeria nodorum SN15]
113	NP_900639	34496424	4-hydroxyphenylpyruvate dioxygenase [Chromobacterium violaceum ATCC 12472]
114	AAM80551	21911428	HmaS [Streptomyces toyocaensis]
115	AAT09803	47078310	NocF [Nocardia uniformis subsp. tsuyamanensis]
116	CAC48371	15131503	putative hydroxyphenyl pyruvate dioxygenase [Amycolatopsi balhimycina]
117	CAE68701	39598009	Hypothetical protein CBG14622 [Caenorhabditis briggsae]
118	ZP_006...	69951167	4-hydroxyphenylpyruvate dioxygenase [Shewanella frigidima NCIMB 400]
119	YP_236400	66046559	4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringa pv. syringae B728a]
120	AAL59614	18104608	4-hydroxyphenylpyruvate dioxygenase [Listonella anguillaru
121	YP_580816	93006379	4-hydroxyphenylpyruvate dioxygenase [Psychrobacter cryohalolentis K5]
122	ZP_007...	75826731	COG3185: 4-hydroxyphenylpyruvate dioxygenase and relatec hemolysins [Vibrio cholerae O395]
123	ZP_007...	75829730	COG3185: 4-hydroxyphenylpyruvate dioxygenase and relatec hemolysins [Vibrio cholerae MO10]
124	NP_934288	37679679	putitive hemolysin [Vibrio vulnificus YJ016]
125	CAC35138	13508831	human T-cell reactive protein [Uncinocarpus reesii]
126	ZP_011...	89076762	putative 4-hydroxyphenylpyruvate dioxygenase [Photobacteri sp. SKA34]
127	YP_348648	77459142	4-hydroxyphenylpyruvate dioxygenase [Pseudomonas fluores PfO-1]
128	YP_275410	71737014	4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringa pv. phaseolicola 1448A]
129	CAC35133	13508833	human T-cell reactive protein [Uncinocarpus reesii]
130	YP_260492	70730751	4-hydroxyphenylpyruvate dioxygenase [Pseudomonas fluores Pf-5]
131	NP_793333	28870714	4-hydroxyphenylpyruvate dioxygenase [Pseudomonas syringa pv. tomato str. DC3000]
132	AAA26510	152722	melA
133	ZP_008...	77816006	4-hydroxyphenylpyruvate dioxygenase [Shewanella putrefaci CN-32]
134	ZP_001...	23129947	COG3185: 4-hydroxyphenylpyruvate dioxygenase and related hemolysins [Nostoc punctiforme PCC 73102]

135	1CJXD	7766901	Chain D, Crystal Structure Of Pseudomonas Fluorescens Hpı
136	NP_797728	28898123	4-hydroxyphenylpyruvate dioxygenase [Vibrio parahaemolyt RIMD 2210633]
137	YP_466626	86159841	4-hydroxyphenylpyruvate dioxygenase [Anaeromyxobacter dehalogenans 2CP-C]
138	CAC35134	13508695	human T-cell reactive protein [Coccidioides immitis]
139	ZP_009...	82740811	4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. W3-1
140	AAB22111	248959	4-hydroxyphenylpyruvate dioxygenase {EC 1.13.11.27} [Pseudomonas, P.J. 874, Peptide, 357 aa]
141	ZP_012...	90578056	putative 4-hydroxyphenylpyruvate dioxygenase [Vibrio angu S14]
142	CAC35131	13508705	human T-cell reactive protein [Auxarthron zuffianum]
143	CAC35129	13508701	human T-cell reactive protein [Auxarthron zuffianum]
144	YP_155112	56459831	4-hydroxyphenylpyruvate dioxygenase [Idiomarina loihiensis L2TR]
145	ZP_010...	87118546	4-hydroxyphenylpyruvate dioxygenase [Marinomonas sp. MED121]
146	ZP_012...	91223907	4-hydroxyphenylpyruvate dioxygenase [Vibrio alginolyticus 12G01]
147	ZP_005...	68542976	4-hydroxyphenylpyruvate dioxygenase [Shewanella baltica OS155]
148	NP_766979	27375450	4-hydroxyphenylpyruvate dioxygenase [Bradyrhizobium japonicum USDA 110]
149	ZP_012...	91771308	4-hydroxyphenylpyruvate dioxygenase [Psychrobacter sp. PR 1]
150	ZP_009...	83858849	4-hydroxyphenylpyruvate dioxygenase [Oceanicaulis alexand HTCC2633]
151	ABC88387	94449351	4-hydroxyphenylpyruvate dioxygenase [Pseudomonas fluorescens]
152	ZP_008...	82735751	4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida
153	AAO12525	37727200	p-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida]
154	ZP_012...	94418035	hypothetical protein PaerP_01000184 [Pseudomonas aerugino PA7]
155	YP_560699	91785493	4-hydroxyphenylpyruvate dioxygenase (Hpd) [Burkholderia xenovorans LB400]
156	NP_945361	39933085	4-hydroxyphenylpyruvate dioxygenase [Rhodopseudomonas palustris CGA009]
157	ZP_006...	69934333	4-hydroxyphenylpyruvate dioxygenase [Paracoccus denitrifica PD1222]
158	ZP_010...	85712096	4-hydroxyphenylpyruvate dioxygenase [Idiomarina baltica OS145]
159	ZP_008...	78368776	4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. PV-4]
160	AAK81835	15029330	hydroxyphenyl pyruvate dioxygenase [Streptomyces lavendul
161	YP_563168	91793517	4-hydroxyphenylpyruvate dioxygenase [Shewanella denitrific OS217]
162	NP_745571	26990146	4-hydroxyphenylpyruvate dioxygenase [Pseudomonas putida KT2440]
163	ZP_008...	78694655	4-hydroxyphenylpyruvate dioxygenase [Bradyrhizobium sp. BTAi1]
164	YP_738408	114047858	4-hydroxyphenylpyruvate dioxygenase [Shewanella sp. MR-7
165	ZP_013...	107100323	hypothetical protein PaerPA_01001348 [Pseudomonas aerugi PACS2]
166	ZP_001...	32040878	COG3185: 4-hydroxyphenylpyruvate dioxygenase and related

			hemolysins [Pseudomonas aeruginosa UCBPP-PA14]
167	YP_631003	108760279	4-hydroxyphenylpyruvate dioxygenase [Myxococcus xanthus 1622]
168	ZP_009...	84386189	4-hydroxyphenylpyruvate dioxygenase [Vibrio splendidus 12
169	AAP47152	31324014	4-hydroxyphenylpyruvate dioxygenase [uncultured soil bacte
170	YP_469267	86357375	probable 4-hydroxyphenylpyruvate dioxygenase protein [Rhizobium etli CFN 42]
171	ZP_011...	88858042	4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) (HPPDase) [Pseudoalteromonas tunicata D2]
172	ZP_004...	67157862	4-hydroxyphenylpyruvate dioxygenase [Azotobacter vinelanc AvOP]
173	ZP_010...	86144791	4-hydroxyphenylpyruvate dioxygenase [Vibrio sp. MED222]
174	YP_473959	86605196	putative 4-hydroxyphenylpyruvate dioxygenase [Synechococ sp. JA-3-3Ab]
175	ZP_005...	68547720	4-hydroxyphenylpyruvate dioxygenase [Shewanella amazone SB2B]
176	YP_298695	73538328	4-hydroxyphenylpyruvate dioxygenase [Ralstonia eutropha JMP134]
177	NP_926037	37522660	4-hydroxyphenylpyruvate dioxygenase [Gloeobacter violaceu PCC 7421]
178	ZP_014...	113936344	4-hydroxyphenylpyruvate dioxygenase [Caulobacter sp. K31]
179	NP_717569	24373526	4-hydroxyphenylpyruvate dioxygenase [Shewanella oneidens MR-1]
180	AAC45755	2108220	hemolysin [Vibrio vulnificus]
181	NP_421336	16126772	4-hydroxyphenylpyruvate dioxygenase [Caulobacter crescent CB15]
182	AAP47153	31324016	4-hydroxyphenylpyruvate dioxygenase [uncultured soil bacte
183	ZP_010...	85710284	4-hydroxyphenylpyruvate dioxygenase [Erythrobacter sp. NA
184	YP_241552	66766790	4-hydroxyphenylpyruvate dioxygenase [Xanthomonas campe pv. campestris str. 8004]
185	NP_890748	33603188	putative hemolysin [Bordetella bronchiseptica RB50]
186	NP_521224	17547822	PROBABLE 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE OXIDOREDUCTASE PROTEIN [Ralston solanacearum GMI1000]
187	CAJ95874	113529527	4-Hydroxyphenylpyruvate dioxygenase [Ralstonia eutropha H
188	YP_511202	89055751	4-hydroxyphenylpyruvate dioxygenase [Jannaschia sp. CCS1]
189	ZP_002...	47573686	COG3185: 4-hydroxyphenylpyruvate dioxygenase and relatec hemolysins [Rubrivivax gelatinosus PM1]
190	YP_202710	58583694	4-hydroxyphenylpyruvate dioxygenase [Xanthomonas oryzae oryzae KACC10331]
191	YP_452875	84625503	4-hydroxyphenylpyruvate dioxygenase [Xanthomonas oryzae oryzae MAFF 311018]
192	ZP_009...	83746408	4-hydroxyphenylpyruvate dioxygenase [Ralstonia solanacear UW551]
193	ZP_013...	100914100	hypothetical protein Bmal10_03004554 [Burkholderia mallei 10399]
194	YP_443601	83720009	4-hydroxyphenylpyruvate dioxygenase [Burkholderia thailandensis E264]
195	ZP_009...	84363553	COG3185: 4-hydroxyphenylpyruvate dioxygenase and relatec hemolysins [Burkholderia dolosa AUO158]
196	NP_881613	33593969	putative hemolysin [Bordetella pertussis Tohama I]
197	ZP_013...	94495996	4-hydroxyphenylpyruvate dioxygenase [Sphingomonas sp. SKA58]

198	BAE20327	73912494	dioxygenase [Coccidioides posadasii]
199	YP_662559	109899304	4-hydroxyphenylpyruvate dioxygenase [Pseudoalteromonas atlantica T6c]
200	ZP_014...	113872221	4-hydroxyphenylpyruvate dioxygenase [Sinorhizobium medi WSM419]

Table 56. Examples of VTE1 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	NP_567906.1	18418083	VTE1 (VITAMIN E DEFICIENT 1) [Arabidopsis thaliana].
2	T04448	7486416	hypothetical protein F4D11.30 - Arabidopsis thaliana
3	AAP97931	33188419	tocopherol cyclase [Eucalyptus gunnii]
4	AAT09809	47078321	tocopherol cyclase [Solanum tuberosum]
5	ABE41800	91694297	tocopherol cyclase [Triticum aestivum]
6	ABE41799	91694295	tocopherol cyclase [Gossypium hirsutum]
7	BAF08459	113536076	Os02g0276500 [Oryza sativa (japonica cultivar-group)]
8	Q94FY8	24212570	Probable tocopherol cyclase, chloroplast precursor (Sucrose e defective 1)
9	XP_464940	50906903	putative tocopherol cyclase [Oryza sativa (japonica cultivar-group)]
10	YP_721533	113475472	hypothetical protein Tery_1802 [Trichodesmium erythraeum IMS101]
11	ZP_001...	23130125	hypothetical protein Npun02000631 [Nostoc punctiforme PC 73102]
12	YP_323243	75908947	hypothetical protein Ava_2735 [Anabaena variabilis ATCC 2
13	NP_484289	17227741	hypothetical protein all0245 [Nostoc sp. PCC 7120]
14	ZP_005...	67920254	conserved hypothetical protein [Crocosphaera watsonii WH 8
15	NP_926035	37522658	hypothetical protein glr3089 [Gloeobacter violaceus PCC 742

16	NP_441095	16330367	hypothetical protein slr1737 [Synechocystis sp. PCC 6803]
17	YP_476858	86608096	putative tocopherol cyclase [Synechococcus sp. JA-2-3B'a(2-
18	YP_474131	86605368	putative tocopherol cyclase [Synechococcus sp. JA-3-3Ab]
19	YP_474360	86605597	putative tocopherol cyclase [Synechococcus sp. JA-3-3Ab]

Table 57. Examples of HPT1(VTE2) polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	AAL35412.1	17104828	tocopherol polyprenyltransferase [Arabidopsis thaliana].
2	NP_849984.1	30680535	HPT1 (HOMOGENTISATE PHYTYLTRANSFERASE 1); prenyltransferase [Arabidopsis thaliana].
3	ABB70126	81295666	homogentisate phytyltransferase VTE2-1 [Glycine max]
4	AAV74623	56126261	homogentisate geranylgeranyl transferase [Vitis vinifera]
5	AAX56086	61808320	homogentisate phytylprenyltransferase [Glycine max]
6	AAU14795	51949754	homogentisate phytylprenyltransferase [Medicago sativa]
7	ABB70125	81295664	homogentisate phytyltransferase VTE2-1 [Cuphea pulcherrin
8	ABE86613	92882118	UbiA prenyltransferase [Medicago truncatula]
9	ABB70122	81295658	homogentisate phytyltransferase VTE2-1 [Zea mays]
10	ABB70124	81295662	homogentisate phytyltransferase VTE2-1 [Allium porrum]
11	AAP43911	33391138	homogentisic acid geranylgeranyl transferase [Hordeum vulg
12	BAF20116	113596242	Os06g0646900 [Oryza sativa (japonica cultivar-group)]
13	BAD37616	51535642	putative homogentisic acid geranylgeranyl transferase [Oryza sativa (japonica cultivar-group)]
14	ZP_001...	23125851	COG0382: 4-hydroxybenzoate polyprenyltransferase and rela prenyltransferases [Nostoc punctiforme PCC 73102]
15	YP_323974	75909678	hypothetical protein Ava_3472 [Anabaena variabilis ATCC 29413]
16	NP_487488	17230940	hypothetical protein alr3448 [Nostoc sp. PCC 7120]
17	ZP_005...	67923620	UbiA prenyltransferase [Crocosphaera watsonii WH 8501]
18	YP_475205	86606442	prenyltransferase, UbiA family [Synechococcus sp. JA-3-3Ab
19	NP_923229	37519852	hypothetical protein gll0283 [Gloeobacter violaceus PCC 742
20	YP_478442	86609680	prenyltransferase, UbiA family [Synechococcus sp. JA-2-3B'a 13)]
21	YP_723391	113477330	UbiA prenyltransferase [Trichodesmium erythraeum IMS101
22	ABB70127	81295668	homogentisate phytyltransferase VTE2-2 [Arabidopsis thalian
23	NP_187801	30681973	prenyltransferase/ zinc ion binding [Arabidopsis thaliana]
24	ABB70128	81295670	homogentisate phytyltransferase VTE2-2 [Glycine max]
25	ZP_007...	76258671	UbiA prenyltransferase [Chloroflexus aurantiacus J-10-fl]
26	XP_478828	50938601	putative tocopherol polyprenyltransferase [Oryza sativa (japo cultivar-group)]
27	BAB03104	10998133	unnamed protein product [Arabidopsis thaliana]
28	BAD38337	51536164	hypothetical protein [Oryza sativa (japonica cultivar-group)]
29	YP_256171	70607301	hypothetical protein Saci_1565 [Sulfolobus acidocaldarius DS 639]
30	YP_379836	78189498	bacteriochlorophyll a synthase [Chlorobium chlorochromatii CaD3]
31	NP_342106	15897501	4-hydroxybenzoate octaprenyltransferase , putative (ubiA-2) [Sulfolobus solfataricus P2]
32	CAJ35986	110620708	putative 4-hydroxybenzoate octaprenyltransferase [uncultured methanogenic archaeon RC-I]
33	NP_441094.1	16330366	hypothetical protein slr1736 [Synechocystis sp. PCC 6803]

Table 58. Examples of VTE3 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	NP_191900.1	15229430	APG1 (ALBINO OR PALE GREEN MUTANT 1); methyltransferase [Arabidopsis thaliana].
2	BAB62076	15005009	APG1 [Arabidopsis thaliana]
3	ABF85788	108385436	At3g63410 [Arabidopsis thaliana]
4	AAM63077	21553996	putative chloroplast inner envelope protein [Arabidopsis thali
5	CAA64422	1419090	37kDa chloroplast inner envelope membrane polypeptide precursor [Nicotiana tabacum]
6	P23525	124429	37 kDa inner envelope membrane protein, chloroplast precurs (E37)
7	BAF30293	113649781	Os12g0615400 [Oryza sativa (japonica cultivar-group)]
8	XP_476850	50934645	putative 37kDa chloroplast inner envelope membrane polype precursor [Oryza sativa (japonica cultivar-group)]
9	ABA99848	108862965	37 kDa inner envelope membrane protein, chloroplast precurs putative, expressed [Oryza sativa (japonica cultivar-group)]
10	AAQ90413	37265798	MPBQ/MSBQ methyltransferase [Chlamydomonas reinhardt
11	BAF20948	113610570	Os07g0179300 [Oryza sativa (japonica cultivar-group)]
12	AAF19792	6635349	37 kDa chloroplast inner envelope membrane protein [Lactuc sativa]
13	NP_069348	11498123	chloroplast inner envelope membrane protein [Archaeoglobus fulgidus DSM 4304]
14	YP_137564	55379714	ubiquinone/menaquinone biosynthesis methyltransferase [Haloarcula marismortui ATCC 43049]
15	NP_280804	15790980	Hmp [Halobacterium sp. NRC-1]
16	YP_658943	110669132	menaquinone biosynthesis methyltransferase homolog [Haloquadratum walsbyi DSM 16790]
17	YP_331240	76803145	S-adenosylmethionine-dependent methyltransferase 1 [Natronomonas pharaonis DSM 2160]
18	AAF01212	6010668	37 kDa chloroplast inner membrane protein [Petunia x hybrid
19	CAA59422	728630	orf [Oryza sativa]
20	YP_694632	110799969	methyltransferase, UbiE/COQ5 family [Clostridium perfringe ATCC 13124]
21	YP_697501	110802464	methyltransferase, UbiE/COQ5 family [Clostridium perfringe SM101]
22	NP_561091	18309157	hypothetical protein CPE0175 [Clostridium perfringens str. 1

Table 59. Examples of VTE4 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	NP_176677.1	15217804	G-TMT (GAMMA-TOCOPHEROL METHYLTRANSFERA [Arabidopsis thaliana]
2	AAD02882	4106538	gamma-tocopherol methyltransferase [Arabidopsis thaliana]
3	AAM64696	21592747	gamma-tocopherol methyltransferase [Arabidopsis thaliana]
4	ABC73703	85687532	gamma-tocopherol methyltransferase [Arabidopsis thaliana]
5	AAO13806	27448218	gamma-tocopherol methyltransferase [Brassica oleracea]
6	ABF56215	95115896	gamma-tocopherol methyltransferase [Brassica napus]
7	ABI23433	112818155	gamma-tocopherol methyl transferase [Brassica juncea]
8	ABE41798	91694293	gamma-tocopherol methyltransferase [Gossypium hirsutum]
9	AAY52459	66732623	gamma-tocopherol methyltransferase [Lotus corniculatus var. japonicus]
10	AAX63899	62126057	gamma-tocopherol methyltransferase [Glycine max]
11	ABE41794	91694285	gamma-tocopherol methyltransferase [Lycopersicon esculentu
12	ABE41795	91694287	gamma-tocopherol methyltransferase [Solanum tuberosum]
13	AAL36933	17224292	gamma-tocopherol methyltransferase [Perilla frutescens]
14	ABE41797	91694291	gamma-tocopherol methyltransferase [Zea mays]
15	AAX63740	62115031	gamma tocopherol methyltransferase [Medicago truncatula]
16	AAM94332	22208517	putative gamma-tocopherol methyltransferase [Sorghum bicol
17	AAT72494	50261883	AT1G64970 [Arabidopsis lyrata subsp. petraea]
18	CAI59122	61657538	gamma-tocopherol methyltransferase [Chlamydomonas reinhardtii]
19	YP_723394	113477333	Methyltransferase type 11 [Trichodesmium erythraeum IMS1(
20	YP_325298	75911002	Cyclopropane-fatty-acyl-phospholipid synthase [Anabaena variabilis ATCC 29413]
21	YP_478603	86609841	cyclopropane-fatty-acyl-phospholipid synthase family protein [Synechococcus sp. JA-2-3B'a(2-13)]
22	YP_475654	86606891	cyclopropane-fatty-acyl-phospholipid synthase family protein [Synechococcus sp. JA-3-3Ab]
23	ZP_001...	23128517	COG0500: SAM-dependent methyltransferases [Nostoc punctiforme PCC 73102]
24	NP_485843	17229295	gamma-tocopherol methyltransferase [Nostoc sp. PCC 7120]
25	ZP_005...	67925248	similar to Methylase involved in ubiquinone/menaquinone biosynthesis [Crocosphaera watsonii WH 8501]
26	NP_442492	16331764	delta(24)-sterol C-methyltransferase [Synechocystis sp. PCC 6
27	NP_926036	37522659	gamma-tocopherol methyltransferase [Gloeobacter violaceus I 7421]
28	AAQ55554	33943786	MPBQ/MSBQ transferase cyanobacterial type [Chlamydomon reinhardtii]
29	NP_682516	22299269	delta(24)-sterol C-methyltransferase [Thermosynechococcus elongatus BP-1]
30	ZP_005...	67921787	probable delta(24)-sterol C-methyltransferase [Crocosphaera watsonii WH 8501]
31	YP_398093	78779981	SAM (and some other nucleotide) binding motif precursor [Prochlorococcus marinus str. MIT 9312]
32	YP_477217	86608455	cyclopropane-fatty-acyl-phospholipid synthase family protein [Synechococcus sp. JA-2-3B'a(2-13)]
33	ABE11447	91070541	SAM nucleotide binding motif protein [uncultured Prochlorococcus marinus clone HOT0M-5C8]
34	YP_473658	86604895	cyclopropane-fatty-acyl-phospholipid synthase family protein [Synechococcus sp. JA-3-3Ab]
35	YP_721878	113475817	Methyltransferase type 11 [Trichodesmium erythraeum IMS10

36	NP_441807	16331079	sterol-C-methyltransferase [Synechocystis sp. PCC 6803]
37	NP_486161	17229613	hypothetical protein all2121 [Nostoc sp. PCC 7120]
38	YP_321597	75907301	Cyclopropane-fatty-acyl-phospholipid synthase [Anabaena variabilis ATCC 29413]
39	YP_399615	81299407	delta(24)-sterol C-methyltransferase [Synechococcus elongati PCC 7942]
40	ZP_010...	87301870	probable sterol-C-methyltransferase [Synechococcus sp. WH 5701]
41	YP_292264	72382909	UbiE/COQ5 family methyltransferase [Prochlorococcus marii str. NATL2A]
42	ZP_011...	88807947	probable sterol-C-methyltransferase [Synechococcus sp. WH 7805]
43	NP_895612	33864052	SAM (and some other nucleotide) binding motif [Prochloroco marinus str. MIT 9313]
44	YP_380648	78211869	probable sterol-C-methyltransferase [Synechococcus sp. CC9(
45	NP_876052	33241110	ubiE/COQ5 family methyltransferase [Prochlorococcus marin subsp. marinus str. CCMP1375]
46	ZP_010...	84519189	ubiE/COQ5 family protein methyltransferase [Prochlorococci marinus str. MIT 9211]
47	ZP_010...	87125025	probable sterol-C-methyltransferase [Synechococcus sp. RS9
48	ZP_004...	66964960	gamma-tocopherol methyltransferase [Arthrobacter sp. FB24]
49	BAC10678	22535505	putative D-glucose O-methyltransferase [Lechevalieria aerocolonigenes]
50	XP_390917	46138453	hypothetical protein FG10741.1 [Gibberella zeae PH-1]
51	BAC15754	22830829	RebM [Lechevalieria aerocolonigenes]
52	ZP_013...	106889693	Cyclopropane-fatty-acyl-phospholipid synthase:UbiE/COQ5 methyltransferase [Roseiflexus sp. RS-1]
53	XP_961285	85102183	hypothetical protein [Neurospora crassa OR74A]
54	AAC01738	2792343	C-27 O-methyltransferase [Amycolatopsis mediterranei]

Table 60. Examples of GGH polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	NP_177587.1	15221261	geranylgeranyl reductase [Arabidopsis thaliana].
2	CAA74372	2828267	geranylgeranyl reductase [Arabidopsis thaliana]
3	AAN31803	23397035	putative geranylgeranyl reductase [Arabidopsis thaliana]
4	AAX63898	62126055	geranylgeranyl reductase [Medicago truncatula]
5	AAD28640	19749359	geranylgeranyl hydrogenase [Glycine max]
6	AAY52460	66732625	geranylgeranyl hydrogenase [Lotus corniculatus var. japonicu
7	CAA07683	3821254	geranylgeranyl reductase [Nicotiana tabacum]
8	AAP55675	37921345	geranylgeranyl reductase [Prunus persica]
9	AAC19396	3202030	geranylgeranyl hydrogenase [Mesembryanthemum crystallinu
10	ABD73016	89474863	geranylgeranyl reductase [Olea europaea]
11	NP_680941	22297694	geranylgeranyl hydrogenase [Thermosynechococcus elongatu 1]
12	Q55087	2493698	Geranylgeranyl hydrogenase
13	NP_484172	17227624	geranylgeranyl hydrogenase [Nostoc sp. PCC 7120]
14	YP_322015	75907719	Geranylgeranyl reductase [Anabaena variabilis ATCC 29413]
15	AAP79193	32307576	geranyl-geranyl reductase [Bigelowiella natans]
16	ZP_001...	53688760	COG0644: Dehydrogenases (flavoproteins) [Nostoc punctifor PCC 73102]
17	AAW79316	58613459	chloroplast geranylgeranyl reductase/hydrogenase [Heterocap triquetra]
18	YP_721553	113475492	geranylgeranyl reductase [Trichodesmium erythraeum IMS10
19	YP_473565	86604802	geranylgeranyl reductase [Synechococcus sp. JA-3-3Ab]
20	YP_399404	81299196	geranylgeranyl reductase [Synechococcus elongatus PCC 794
21	ABD51929	88770652	chloroplast geranylgeranyl reductase/hydrogenase [Guillardia theta]
22	YP_477981	86609219	geranylgeranyl reductase [Synechococcus sp. JA-2-3B'a(2-13
23	CAH25334	57335865	geranylgeranyl reductase [Guillardia theta]
24	AAW79317	58613461	chloroplast geranylgeranyl reductase/hydrogenase [Isochrysis galbana]
25	NP_897190	33865631	geranylgeranyl hydrogenase [Synechococcus sp. WH 8102]
26	YP_377247	78184812	Geranylgeranyl reductase [Synechococcus sp. CC9902]
27	YP_291359	72382004	geranylgeranyl reductase:Geranylgeranyl reductase, plants an cyanobacteria:Geran
28	ZP_011...	88808504	geranylgeranyl hydrogenase [Synechococcus sp. WH 7805]
29	YP_381550	78212771	geranylgeranyl reductase [Synechococcus sp. CC9605]
30	NP_892878	33861317	Aromatic-ring hydroxylase (flavoprotein monooxygenase) [Prochlorococcus marinus s
31	NP_875224	33240282	Geranylgeranyl hydrogenase ChlP [Prochlorococcus marinus subsp. marinus str. CCMP
32	ZP_010...	87302812	Geranylgeranyl reductase [Synechococcus sp. WH 5701]
33	ABE11215	91070297	aromatic-ring hydroxylase [uncultured Prochlorococcus marin clone HF10-88D1]
34	ZP_010...	84517932	Geranylgeranyl hydrogenase ChlP [Prochlorococcus marinus MIT 9211]
35	YP_397264	78779152	geranylgeranyl reductase [Prochlorococcus marinus str. MIT 9
36	ZP_010...	87124316	geranylgeranyl hydrogenase [Synechococcus sp. RS9917]
37	NP_912887	34903080	unnamed protein product [Oryza sativa (japonica cultivar-grou
38	NP_894410	33862850	Aromatic-ring hydroxylase (flavoprotein monooxygenase) [Prochlorococcus marinus s
39	NP_441659	16330931	43 kD bacteriochlorophyll synthase subunit [Synechocystis sp PCC 6803]

40	NP_927323	37523946	geranylgeranyl hydrogenase [Gloeobacter violaceus PCC 742
41	AAC12646	3023160	geranylgeranyl reductase [Zantedeschia aethiopica]
42	AAN77241	25992742	geranyl-geranyl reductase [Xerophyta humilis]
43	BAD95270	62319720	geranylgeranyl reductase [Arabidopsis thaliana]
44	NP_663129	21675064	geranylgeranyl hydrogenase [Chlorobium tepidum TLS]
45	ZP_005...	68553026	Geranylgeranyl reductase [Prosthecochloris aestuarii DSM 27
46	CAG26756	57283362	putative geranylgeranyl reductase [Silene latifolia]
47	CAG26757	57283364	putative geranylgeranyl reductase [Silene viscosa]
48	YP_378357	78188019	Geranylgeranyl reductase [Chlorobium chlorochromatii CaD3
49	ZP_013...	106888281	geranylgeranyl reductase:Geranylgeranyl reductase, plantal ar prokaryotic [Rosei
50	ZP_005...	67918582	Geranylgeranyl reductase [Chlorobium limicola DSM 245]
51	ZP_007...	76258850	Geranylgeranyl reductase:Geranylgeranyl reductase, plantal a prokaryotic [Chlor
52	ZP_005...	68549969	Geranylgeranyl reductase [Pelodictyon phaeoclathratiforme B
53	ZP_005...	67939529	Geranylgeranyl reductase [Chlorobium phaeobacteroides BS1
54	ZP_013...	110598296	geranylgeranyl reductase:Geranylgeranyl reductase, plantal an prokaryotic [Chlor
55	YP_373951	78185908	Geranylgeranyl reductase [Pelodictyon luteolum DSM 273]
56	ZP_005...	67936116	Geranylgeranyl reductase [Chlorobium phaeobacteroides DSM 266]
57	ZP_006...	71481254	Geranylgeranyl reductase [Prosthecochloris vibrioformis DSM 265]
58	AAM48662	21328656	geranylgeranyl bacteriochlorophyll reductase [uncultured proteobacterium]
59	AAP80828	32401312	geranylgeranyl hydrogenase [Griffithsia japonica]
60	YP_531185	90422815	geranylgeranyl reductase [Rhodopseudomonas palustris BisB1
61	ZP_010...	85703496	Geranylgeranyl hydrogenase [Roseovarius sp. 217]
62	AAR38264	40063464	bacteriochlorophyll reductase [uncultured bacterium 581]
63	AAL76376	18645075	geranylgeranyl bacteriochlorophyll reductase [uncultured proteobacterium]
64	YP_508109	89052658	geranylgeranyl reductase [Jannaschia sp. CCS1]
65	ZP_010...	84514667	Geranylgeranyl hydrogenase [Loktanella vestfoldensis SKA53
66	BAA94066	7416817	geranylgeranyl bacteriochlorophyll reductase [Rubrivivax gelatinosus]
67	NP_946880	39934604	geranylgeranyl reductase [Rhodopseudomonas palustris CGA(
68	ZP_008...	77738701	Geranylgeranyl reductase:Geranylgeranyl reductase, plantal ar prokaryotic [Rhodo
69	YP_680566	110677559	geranylgeranyl hydrogenase [Roseobacter denitrificans OCh 1
70	P26172	114852	Geranylgeranyl hydrogenase
71	ZP_011...	88948384	Geranylgeranyl reductase:Geranylgeranyl reductase, plantal ar prokaryotic [Halor
72	YP_570867	91978208	geranylgeranyl reductase [Rhodopseudomonas palustris BisB5
73	YP_487594	86751098	geranylgeranyl reductase [Rhodopseudomonas palustris HaA2
74	ZP_009...	83373293	Geranylgeranyl reductase:Geranylgeranyl reductase, plantal ar prokaryotic [Rhodo
75	ZP_009...	83370705	Geranylgeranyl reductase:Geranylgeranyl reductase, plantal ar prokaryotic [Rhodo
76	AAX53583	61699159	BchP [Thiocapsa roseopersicina]
77	AAM48623	21328616	geranylgeranyl hydrogenase [uncultured proteobacterium]
78	ZP_011...	88706639	geranylgeranyl hydrogenase [gamma proteobacterium KT 71]
79	ZP_008...	78694729	Geranylgeranyl reductase:Geranylgeranyl reductase, plantal ar prokaryotic [Brady

80	AAT78843	50592003	geranylgeranyl bacteriochlorophyll reductase [Bradyrhizobiur ORS278]
81	ZP_010...	85710607	geranylgeranyl reductase [Erythrobacter sp. NAP1]
82	YP_425720	83591968	Geranylgeranyl reductase [Rhodospirillum rubrum ATCC 111
83	ZP_002...	47573622	COG0644: Dehydrogenases (flavoproteins) [Rubrivivax gelatinosus PM1]
84	YP_305129	73669114	geranylgeranyl reductase [Methanosarcina barkeri str. fusaro]
85	YP_343021	77164496	Geranylgeranyl reductase [Nitrosococcus oceani ATCC 1970
86	ZP_011...	88952109	Geranylgeranyl reductase, plantal and prokaryotic [Methanosa thermophila PT]
87	YP_692969	110834110	hypothetical protein ABO_1249 [Alcanivorax borkumensis SI
88	ZP_012...	91220812	Geranylgeranyl hydrogenase [Psychroflexus torquis ATCC 700755]
89	NP_615651	20089576	geranylgeranyl reductase [Methanosarcina acetivorans C2A]
90	AAU83959	52550110	geranylgeranyl reductase [uncultured archaeon GZfos35A2]
91	AAU84050	52550201	geranylgeranyl reductase [uncultured archaeon GZfos36D8]
92	AAU82394	52548545	geranylgeranyl reductase [uncultured archaeon GZfos17C7]
93	NP_633873	21227951	Geranylgeranyl reductase [Methanosarcina mazei Go1]
94	NP_615652	20089577	geranylgeranyl reductase [Methanosarcina acetivorans C2A]
95	NP_125857	14520382	bacteriochlorophyll synthase 43 kda subunit or geranylgeranyl hydrogenase [Pyroco
96	P96800	85681848	Hypothetical protein Mbar_A1602 (ORF3)
97	NP_577826	18976469	43 kDa subunit bacteriochlorophyll synthase-like protein [Pyrococcus furiosus DSM
98	YP_429669	83589660	Geranylgeranyl reductase [Moorella thermoacetica ATCC 390
99	NP_247511	15668712	bacteriochlorophyll synthase 43 kDa subunit (chlP) [Methanocaldococcus jannaschii
100	YP_305130	73669115	geranylgeranyl reductase [Methanosarcina barkeri str. fusaro]
101	NP_142180	14590116	hypothetical protein PH0181 [Pyrococcus horikoshii OT3]
102	GAA02396	98660359	unnamed protein product [Pelotomaculum thermopropionicum
103	ZP_005...	67918906	geranylgeranyl reductase [Chlorobium limicola DSM 245]
104	YP_183501	57641023	geranylgeranyl hydrogenase [Thermococcus kodakarensis KO
105	YP_502591	88602413	geranylgeranyl reductase [Methanospirillum hungatei JF-1]
106	YP_356793	77918978	geranylgeranyl bacteriochlorophyll reductase-like [Pelobacter carbinolicus DSM 23
107	ZP_012...	91219138	Geranylgeranyl hydrogenase [Psychroflexus torquis ATCC 700755]
108	ZP_010...	84502883	Geranylgeranyl reductase [Oceanicola batsensis HTCC2597]
109	ZP_005...	67930221	similar to Dehydrogenases (flavoproteins) [Solibacter usitatus Ellin6076]
110	ZP_012...	94264329	Monooxygenase, FAD-binding:FAD dependent oxidoreductas [delta proteobacterium ML
111	NP_632742	21226820	oxidoreductase [Methanosarcina mazei Go1]
112	NP_069300	11498075	bacteriochlorophyll synthase, 43 kDa subunit (chlP-1) [Archaeoglobus fulgidus DSM
113	AAY89944	68304933	hypothetical protein [uncultured bacterium BAC13K9BAC]
114	NP_616418	20090343	geranylgeranyl reductase [Methanosarcina acetivorans C2A]
115	ZP_011...	88950678	Geranylgeranyl reductase, plantal and prokaryotic [Methanosa thermophila PT]
116	NP_213068	15605692	hypothetical protein aq_104 [Aquifex aeolicus VF5]
117	YP_591899	94969851	geranylgeranyl reductase [Acidobacteria bacterium Ellin345]
118	ZP_011...	88950766	Geranylgeranyl reductase, plantal and prokaryotic [Methanosa thermophila PT]

119	YP_306875	73670860	geranylgeranyl reductase [Methanosarcina barkeri str. fusaro]
120	CAJ37749	110622471	putative geranylgeranyl reductase (bacterial chlorophyll reduc related) (pyri
121	ZP_013...	110605523	Geranylgeranyl reductase, plantal and prokaryotic [Thermofilu pendens Hrk 5]
122	YP_303737	73667722	bacteriochlorophyll synthase [Methanosarcina barkeri str. fusa
123	NP_625367	21219588	hydrogenase [Streptomyces coelicolor A3(2)]
124	ZP_006...	69269260	conserved hypothetical protein [Ferroplasma acidarmanus Fer
125	NP_822645	29828011	hydrogenase [Streptomyces avermitilis MA-4680]
126	YP_023346	48477640	geranylgeranyl hydrogenase [Picrophilus torridus DSM 9790]
127	AAL93670	19712763	Probable electron transfer flavoprotein-quinone oxidoreductas ydiS [Fusobacteriu
128	NP_634523	21228601	Geranylgeranyl reductase [Methanosarcina mazei Go1]
129	YP_475395	86606632	geranylgeranyl reductase family protein [Synechococcus sp. J 3Ab]
130	YP_565055	91772363	geranylgeranyl reductase [Methanococcoides burtonii DSM 62
131	CAA70994	1890201	hypothetical protein [Methanosarcina barkeri]
132	CAJ37194	110621916	geranylgeranyl reductase [uncultured methanogenic archaeon I]
133	NP_394946	16082457	geranylgeranyl reductase related protein [Thermoplasma acidophilum DSM 1728]
134	ZP_013...	110603814	Geranylgeranyl reductase, plantal and prokaryotic [Methanocu marisnigri JR1]
135	NP_987508	45357951	geranylgeranyl bacterial chlorophyll reductase related [Methanococcus maripaludis
136	NP_618765	20092690	bacteriochlorophyll synthase [Methanosarcina acetivorans C2
137	YP_478529	86609767	geranylgeranyl reductase family protein [Synechococcus sp. J 3B'a(2-13)]
138	YP_429318	83589309	Geranylgeranyl reductase [Moorella thermoacetica ATCC 390
139	ZP_005...	68229518	putative hydrogenase [Frankia sp. EAN1pec]
140	BAB60443	14325540	electron transfer flavoprotein [Thermoplasma volcanium GSS
141	ZP_005...	67936894	Flavoprotein monooxygenase [Chlorobium phaeobacteroides I 266]
142	NP_682194	22298947	putative geranylgeranyl bacteriochlorophyll reductase [Thermosynechococcus elonga
143	NP_485252	17228704	hypothetical protein alr1209 [Nostoc sp. PCC 7120]
144	ZP_001...	34762287	Probable electron transfer flavoprotein-quinone oxidoreductas ydiS [Fusobacteriu
145	AP_002319	89108539	predicted oxidoreductase, FAD/NAD(P)-binding domain [Escherichia coli W3110]
146	YP_689012	110805492	Probable electron transfer flavoprotein-quinone oxidoreductas YdiS [Shigella fle
147	ZP_009...	83586003	COG0644: Dehydrogenases (flavoproteins) [Escherichia coli 1 1]
148	YP_669550	110641820	probable electron transfer flavoprotein-quinone oxidoreductas YdiS [Escherichia
149	YP_388681	78357232	geranylgeranyl reductase [Desulfovibrio desulfuricans G20]
150	ZP_007...	75513800	COG0644: Dehydrogenases (flavoproteins) [Escherichia coli 53638]
151	NP_614928	20095081	Predicted dehydrogenase (flavoprotein) [Methanopyrus kandle AV19]
152	YP_565757	91773065	geranylgeranyl reductase [Methanococcoides burtonii DSM 62
153	YP_565976	91773284	geranylgeranyl reductase [Methanococcoides burtonii DSM 62

154	YP_306417	73670402	hypothetical protein Mbar_A2942 [Methanosarcina barkeri st fusaro]
155	YP_321149	75906853	geranylgeranyl reductase [Anabaena variabilis ATCC 29413]
156	BAB60664	14325761	hypothetical protein [Thermoplasma volcanium GSS1]
157	NP_213081	15605704	hypothetical protein aq_121 [Aquifex aeolicus VF5]
158	YP_565114	91772422	geranylgeranyl reductase [Methanococcoides burtonii DSM 6
159	ZP_007...	75236845	COG0644: Dehydrogenases (flavoproteins) [Escherichia coli E110019]
160	ZP_007...	75190737	COG0644: Dehydrogenases (flavoproteins) [Escherichia coli E24377A]
161	YP_540899	91210913	probable electron transfer flavoprotein-quinone oxidoreductas ydiS [Escherichia
162	ZP_007...	75256657	COG0644: Dehydrogenases (flavoproteins) [Escherichia coli
163	NP_753990	26247950	Probable electron transfer flavoprotein-quinone oxidoreductas ydiS [Escherichia
164	NP_837205	30063034	flavoprotein [Shigella flexneri 2a str. 2457T]
165	NP_628721	21222942	electron transfer oxidoreductase [Streptomyces coelicolor A3(
166	YP_056614	50843387	putative electron transfer oxidoreductase [Propionibacterium a KPA171202]
167	YP_520029	89896542	hypothetical protein DSY3796 [Desulfitobacterium hafniense
168	YP_448327	84490095	predicted dehydrogenase [Methanosphaera stadtmanae DSM
169	NP_393806	16081459	fixC protein related [Thermoplasma acidophilum DSM 1728]
170	NP_310433	15831660	flavoprotein [Escherichia coli O157:H7 str. Sakai]
171	AAU43680	52352391	conserved hypothetical protein [uncultured archaeon GZfos26
172	AAU83107	52549258	conserved hypothetical protein [uncultured archaeon GZfos26
173	YP_448089	84489857	predicted dehydrogenase [Methanosphaera stadtmanae DSM
174	YP_483487	86743087	geranylgeranyl reductase [Frankia sp. CcI3]
175	ZP_006...	75177404	COG0644: Dehydrogenases (flavoproteins) [Shigella boydii BS512]
176	ZP_000...	23004754	hypothetical protein Magn03000692 [Magnetospirillum magnetotacticum MS-1]
177	NP_276830	15679712	bacteriochlorophyll synthase 43 kDa subunit [Methanothermobacter thermautotrophic
178	ZP_010...	85706741	Geranylgeranyl reductase [Roseovarius sp. 217]
179	NP_275420	15678305	bacteriochlorophyll synthase 43 kDa subunit [Methanothermobacter thermautotrophic
180	NP_578183	18976826	bacteriochlorophyll synthase, 43 kDa subunit [Pyrococcus fur DSM 3638]
181	ZP_012...	91218720	oxidoreductase [Psychroflexus torquis ATCC 700755]
182	ZP_013...	110602569	Geranylgeranyl reductase, plantal and prokaryotic [Methanoc marisnigri JR1]
183	NP_393992	16082528	Predicted geranylgeranyl reductase [Thermoplasma acidophil DSM 1728]
184	YP_331010	76802915	predicted electron-transferring-flavoprotein dehydrogenase 2 [Natronomonas pharao
185	ZP_013...	110603704	Geranylgeranyl reductase, plantal and prokaryotic [Methanoc marisnigri JR1]
186	NP_826012	29831378	electron transfer oxidoreductase [Streptomyces avermitilis M 4680]
187	NP_617789	20091714	hypothetical protein MA2893 [Methanosarcina acetivorans C
188	YP_519301	89895814	hypothetical protein DSY3068 [Desulfitobacterium hafniense
189	GAA02534	98660169	unnamed protein product [Pelotomaculum thermopropionicun
190	YP_399527	81299319	geranylgeranyl reductase [Synechococcus elongatus PCC 794

191	ZP_006...	69284899	Flavoprotein monooxygenase:Monooxygenase, FAD-binding [Kineococcus radiotolerans
192	YP_407882	82543935	YdiS [Shigella boydii Sb227]
193	BAB60165	14325261	cofactor biosynthesis protein [Thermoplasma volcanium GSS1
194	NP_924658	37521281	hypothetical protein gll1712 [Gloeobacter violaceus PCC 742
195	YP_720754	113474693	geranylgeranyl reductase [Trichodesmium erythraeum IMS10
196	YP_403394	82777045	YdiS [Shigella dysenteriae Sd197]
197	YP_479427	86739027	hypothetical protein Francci3_0311 [Frankia sp. CcI3]
198	CAC11656	10639684	geranylgeranyl reductase related protein [Thermoplasma acidophilum]
199	ZP_010...	84683402	Geranylgeranyl reductase [Rhodobacterales bacterium HTCC2

Table 61. Examples of pentaprenyl (5) Ec 2.5.1.33 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	YP_023977.1	48478271	farnesyl pyrophosphate synthetase/geranyltransferase/farnesyltransferase/hexaprenyl diphosphatesynthase [Picrophilus torridus DSM 9790].
2	XP_718635.1	68474524	trans-hexaprenyltranstransferase [Candida albicans SC5314].

Table 62. Examples of hexaprenyl (6) polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_445361	50285865	unnamed protein product [Candida glabrata]
2	XP_454724	50309433	unnamed protein product [Kluyveromyces lactis]
3	BAE95384	108743210	hexaprenyl pyrophosphate synthetase [Saccharomyces bayanus
4	NP_984864	45190610	AER004Wp [Eremothecium gossypii]
5	2118405G	1582566	hexaprenyl pyrophosphate synthetase
6	XP_457083	50411851	hypothetical protein DEHA0B02695g [Debaryomyces hansenii CBS767]
7	XP_718635	68474524	trans-hexaprenyltranstransferase [Candida albicans SC5314]
8	Q6CBH3	60389562	Probable hexaprenyl pyrophosphate synthetase, mitochondrial precursor (HPS)
9	BAE63325	83773198	unnamed protein product [Aspergillus oryzae]
10	XP_391109	46138837	hypothetical protein FG10933.1 [Gibberella zeae PH-1]
11	XP_360800	39942526	hypothetical protein MG03343.4 [Magnaporthe grisea 70-15]
12	EAT89776	111068656	hypothetical protein SNOG_03045 [Phaeosphaeria nodorum SI
13	XP_660371	67524619	hypothetical protein AN2767.2 [Aspergillus nidulans FGSC A4
14	XP_959949	85094730	hypothetical protein [Neurospora crassa OR74A]
15	EAQ83196	88175728	conserved hypothetical protein [Chaetomium globosum CBS 148.51]
16	EAS35130	90305499	hypothetical protein CIMG_00484 [Coccidioides immitis RS]
17	XP_757637	71005942	hypothetical protein UM01490.1 [Ustilago maydis 521]
18	XP_572668	58271024	trans-hexaprenyltranstransferase [Cryptococcus neoformans var neoformans JEC21]
19	XP_641356	66814354	trans-prenyltransferase [Dictyostelium discoideum AX4]
20	ZP_011...	88808408	Trans-hexaprenyltranstransferase [Synechococcus sp. WH 7805
21	YP_401379	81301171	Trans-hexaprenyltranstransferase [Synechococcus elongatus PC 7942]
22	XP_973319	91077592	PREDICTED: similar to CG31005-PA [Tribolium castaneum]
23	YP_381447	78212668	Trans-hexaprenyltranstransferase [Synechococcus sp. CC9605]
24	AAI18814	110645682	Unknown (protein for MGC:146437) [Xenopus tropicalis]
25	NP_001...	62955289	hypothetical protein LOC550349 [Danio rerio]
26	CAG05473	47221152	unnamed protein product [Tetraodon nigroviridis]
27	YP_720124	113474063	Trans-hexaprenyltranstransferase [Trichodesmium erythraeum IMS101]
28	XP_781598	72013681	PREDICTED: similar to trans-prenyltransferase [Strongylocent purpuratus]
29	NP_733425	24651612	CG31005-PA [Drosophila melanogaster]
30	EAL27072	54637670	GA15930-PA [Drosophila pseudoobscura]
31	YP_321987	75907691	Polyprenyl synthetase [Anabaena variabilis ATCC 29413]
32	NP_062374	90577181	prenyl diphosphate synthase, subunit 1 [Mus musculus]
33	AAI07275	78070698	Pdss1 protein [Mus musculus]
34	CAE66926	39589691	Hypothetical protein CBG12314 [Caenorhabditis briggsae]
35	XP_586717	76632198	PREDICTED: similar to trans-prenyltransferase [Bos taurus]
36	AAL68276	18447424	RE18374p [Drosophila melanogaster]
37	YP_377328	78184893	Trans-hexaprenyltranstransferase [Synechococcus sp. CC9902]
38	NP_491588	17505681	COenzyme Q (ubiquinone) biosynthesis family member (coq-1) [Caenorhabditis elegans]
39	XP_001...	109088459	PREDICTED: similar to prenyl diphosphate synthase, subunit 1 isoform 1 [Macaca mulatta]
40	XP_507706	55633583	PREDICTED: similar to TPRT protein [Pan troglodytes]
41	AAD28559	4732024	trans-prenyltransferase [Homo sapiens]
42	XP_418592	50732345	PREDICTED: similar to trans-prenyltransferase; polyprenyl

			pyrophosphate synthetase; 2610203G20Rik; 2700031G06Rik [Gallus gallus]
43	AAH49211	29165656	PDSS1 protein [Homo sapiens]
44	NP_043186	11467329	prenyl transferase [Cyanophora paradoxa]
45	XP_849908	73948851	PREDICTED: similar to trans-prenyltransferase [Canis familiar
46	EAT46550	108882325	trans-prenyltransferase [Aedes aegypti]
47	BAF18352	113579989	Os05g0582300 [Oryza sativa (japonica cultivar-group)]
48	ABF58968	98960969	At1g78510 [Arabidopsis thaliana]
49	AAD30584	4836881	Very similar to prenyltransferases [Arabidopsis thaliana]
50	BAD97134	62898389	trans-prenyltransferase variant [Homo sapiens]
51	BAF01575	110739325	polyprenyl diphosphate synthase [Arabidopsis thaliana]
52	XP_565746	57973716	ENSANGP00000027282 [Anopheles gambiae str. PEST]
53	YP_291250	72381895	trans-hexaprenyltranstransferase [Prochlorococcus marinus str. NATL2A]
54	NP_001...	79324330	dimethylallyltranstransferase [Arabidopsis thaliana]
55	NP_850234	30686146	dimethylallyltranstransferase [Arabidopsis thaliana]
56	AAM13005	20260214	putative trans-prenyltransferase [Arabidopsis thaliana]
57	AAD50025	5734760	Very similar to prenyl transferase [Arabidopsis thaliana]
58	ZP_005...	67921668	Trans-hexaprenyltranstransferase [Crocosphaera watsonii WH 8
59	YP_397115	78779003	Trans-hexaprenyltranstransferase [Prochlorococcus marinus str. MIT 9312]
60	ABE11181	91070262	polyprenyl synthetase [uncultured Prochlorococcus marinus clo HF10-11H7]
61	YP_063627	51209963	prenyl transferase [Gracilaria tenuistipitata var. liui]
62	ABE11067	91070145	polyprenyl synthetase [uncultured Prochlorococcus marinus clo HF10-11A3]
63	NP_053878	11465734	prenyl transferase [Porphyra purpurea]
64	Q9TLS1	14195057	Prenyl transferase
65	ABA97399	108862467	Prenyl transferase, putative, expressed [Oryza sativa (japonica cultivar-group)]
66	YP_536950	90994460	prenyl transferase [Porphyra yezoensis]
67	XP_320978	58395068	ENSANGP00000007795 [Anopheles gambiae str. PEST]
68	AAC26705	3128225	putative trans-prenyltransferase [Arabidopsis thaliana]
69	XP_678396	68072963	polyprenyl synthetase [Plasmodium berghei strain ANKA]
70	ZP_005...	68545618	Trans-hexaprenyltranstransferase [Shewanella amazonensis SB2
71	NP_849058	30468171	prenyl transferase [Cyanidioschyzon merolae strain 10D]
72	ZP_008...	78368580	Trans-hexaprenyltranstransferase [Shewanella sp. PV-4]
73	XP_724427	82540178	polyprenyl synthetase [Plasmodium yoelii yoelii str. 17XNL]
74	XP_396188	66532619	PREDICTED: similar to CG31005-PA, partial [Apis mellifera]
75	ZP_011...	89099139	HepT [Bacillus sp. NRRL B-14911]
76	ZP_006...	69949200	Trans-hexaprenyltranstransferase [Shewanella frigidimarina NC 400]
77	ZP_009...	82743940	Trans-hexaprenyltranstransferase [Shewanella sp. W3-18-1]
78	ZP_008...	77813675	Polyprenyl synthetase [Shewanella putrefaciens CN-32]
79	YP_091982	52786153	HepT [Bacillus licheniformis ATCC 14580]
80	YP_733031	113969238	Trans-hexaprenyltranstransferase [Shewanella sp. MR-4]
81	ZP_005...	68541757	Trans-hexaprenyltranstransferase [Shewanella baltica OS155]
82	NP_759657	27364129	Geranylgeranyl pyrophosphate synthase [Vibrio vulnificus CMC
83	YP_430109	83590100	Trans-hexaprenyltranstransferase [Moorella thermoacetica ATC 39073]
84	ZP_013...	95929474	Trans-hexaprenyltranstransferase [Desulfuromonas acetoxidans DSM 684]
85	YP_563929	91794278	Trans-hexaprenyltranstransferase [Shewanella denitrificans OS2

86	NP_472955	16804926	polyprenyl synthetase, putative [Plasmodium falciparum 3D7]
87	YP_248580	68249468	octaprenyl-diphosphate synthase [Haemophilus influenzae 86-028NP]
88	P_501989.1	50549037	hypothetical protein [Yarrowia lipolytica].
89	AA84939.1	536190	COQ1 [Saccharomyces cerevisiae]

Table 63. Examples of heptaprenyl (7) polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	P55784	7676154	Heptaprenyl diphosphate synthase component I (HEPPP syntha subunit 1)
2	P55785	2829443	Heptaprenyl diphosphate synthase component II (HEPPP synth subunit 2)
3	P31114	399776	Heptaprenyl diphosphate synthase component II (HEPPP synth subunit 2) (Spore germination protein C3)
4	P31112	399774	Heptaprenyl diphosphate synthase component I (HEPPP syntha subunit 1) (Spore germination protein C1)
5	CAJ59711.1	111148045	Heptaprenyl diphosphate synthase component II (HEPPP synth subunit 2) [Frankia alni ACN14a]
6	YP_711307.1	111220513	Heptaprenyl diphosphate synthase component II (HEPPP synth subunit 2) [Frankia alni ACN14a]
7	YP_040881.1	49483657	putative heptaprenyl diphosphate synthase component II [Staphylococcus aureus subsp. aureus MRSA252]
8	CAG40477.1	49241786	putative heptaprenyl diphosphate synthase component II [Staphylococcus aureus subsp. aureus MRSA252]
9	ZP_01371157.1	109647253	Heptaprenyl diphosphate synthase component I [Desulfitobacte hafniense DCB-2]
10	EAT52053.1	109642499	Heptaprenyl diphosphate synthase component I [Desulfitobacte hafniense DCB-2]
11	ZP_01361788.1	106894672	Heptaprenyl diphosphate synthase component I [Clostridium sp. OhILAs]
12	ZP_01354679.1	106887372	Heptaprenyl diphosphate synthase component I [Clostridium phytofermentans ISDg]
13	EAT30561.1	106773993	Heptaprenyl diphosphate synthase component I [Clostridium sp. OhILAs]
14	EAT21890.1	106765118	Heptaprenyl diphosphate synthase component I [Clostridium phytofermentans ISDg]
15	BAA08725.1	1731683	component II of heptaprenyl diphosphate synthase [Geobacillus stearothermophilus]
16	BAA08724.1	1731681	component I of heptaprenyl diphosphate synthase [Geobacillus stearothermophilus]
17	YP_535919.1	90962003	Farnesyl pyrophosphate synthetase / Geranyltranstransferase / Farnesyltransferase / Heptaprenyl diphosphate synthase compon II [Lactobacillus salivarius subsp. salivarius UCC118]
18	ABD99836.1	90821197	Farnesyl pyrophosphate synthetase / Geranyltranstransferase / Farnesyltransferase / Heptaprenyl diphosphate synthase compon II [Lactobacillus salivarius subsp. salivarius UCC118]
19	BAD64424.1	56909897	heptaprenyl diphosphate synthase component II [Bacillus clausi KSM-K16]
20	BAD64420.1	56909893	heptaprenyl diphosphate synthase component I [Bacillus clausii KSM-K16]
21	YP_014554.1	46908165	heptaprenyl diphosphate synthase component I, putative [Listeri monocytogenes str. 4b F2365]
22	YP_014552.1	46908163	heptaprenyl diphosphate synthase, component II [Listeria monocytogenes str. 4b F2365]
23	NP_977962.1	42780715	heptaprenyl diphosphate synthase component II [Bacillus cereus ATCC 10987]
24	NP_977960.1	42780713	heptaprenyl diphosphate synthase component I, putative [Bacill cereus ATCC 10987]
25	YP_283297.1	71905710	Heptaprenyl diphosphate synthase component I [Dechloromona aromatica RCB]

26	YP_181134.1	57234813	heptaprenyl diphosphate synthase component II [Dehalococcoi ethenogenes 195]
27	YP_056599.1	50843372	heptaprenyl diphosphate synthase component II [Propionibacte acnes KPA171202]
28	YP_035728.1	49481021	heptaprenyl diphosphate synthase component I [Bacillus thuringiensis serovar konkukian str. 97-27]
29	YP_035730.1	49481018	heptaprenyl diphosphate synthase component II [Bacillus thuringiensis serovar konkukian str. 97-27]
30	YP_027693.1	49184441	heptaprenyl diphosphate synthase component II [Bacillus anthr str. Sterne]
31	YP_027691.1	49184439	heptaprenyl diphosphate synthase component I, putative [Bacill anthracis str. Sterne]
32	YP_018158.1	47526809	heptaprenyl diphosphate synthase component ii [Bacillus anthr str. 'Ames Ancestor']
33	YP_018156.1	47526807	heptaprenyl diphosphate synthase component i, putative [Bacill anthracis str. 'Ames Ancestor']
34	NP_787182.1	28493021	probable heptaprenyl diphosphate synthase component II [Tropheryma whipplei str. Twist]
35	NP_781674.1	28210730	heptaprenyl diphosphate synthase component I [Clostridium tet E88]
36	YP_360049.1	78042835	heptaprenyl diphosphate synthase component II [Carboxydothe hydrogenoformans Z-2901]
37	ZP_01183526.1	89204951	Heptaprenyl diphosphate synthase subunit 1 [Bacillus weihenstephanensis KBAB4]
38	ZP_01179718.1	89200970	Heptaprenyl diphosphate synthase subunit 1 [Bacillus cereus su cytotoxis NVH 391-98]
39	EAR77242.1	89157248	Heptaprenyl diphosphate synthase subunit 1 [Bacillus weihenstephanensis KBAB4]
40	EAR71431.1	89150929	Heptaprenyl diphosphate synthase subunit 1 [Bacillus cereus su cytotoxis NVH 391-98]
41	ZP_01172016.1	89099137	heptaprenyl diphosphate synthase component I (spore germinati protein C1) [Bacillus sp. NRRL B-14911]
42	EAR65389.1	89086267	heptaprenyl diphosphate synthase component I (spore germinati protein C1) [Bacillus sp. NRRL B-14911]
43	EAO24691.1	71492385	Heptaprenyl diphosphate synthase component I [Syntrophomon wolfei subsp. wolfei str. Goettingen]
44	YP_079576.1	52080785	heptaprenyl diphosphate synthase component I [Bacillus licheniformis ATCC 14580]
45	YP_079574.1	52080783	heptaprenyl diphosphate synthase component II [Bacillus licheniformis ATCC 14580]
46	AAO44151.1	28476061	probable heptaprenyl diphosphate synthase component II [Tropheryma whipplei str. Twist]
47	NP_267498.1	15673324	heptaprenyl diphosphate synthase component II [Lactococcus la subsp. lactis Il1403]
48	AAO35611.1	28203168	heptaprenyl diphosphate synthase component I [Clostridium tet E88]
49	AAP25472.1	30255463	heptaprenyl diphosphate synthase component II [Bacillus anthra str. Ames]
50	AAP25470.1	30255461	heptaprenyl diphosphate synthase component I, putative [Bacill anthracis str. Ames]
51	AAP08492.1	29895204	Heptaprenyl diphosphate synthase component I [Bacillus cereus ATCC 14579]
52	AAO82927.1	29345171	heptaprenyl diphosphate synthase, component II, putative [Enterococcus faecalis V583]

53	AAO81790.1	29344030	heptaprenyl diphosphate synthase, component II, putative [Enterococcus faecalis V583]
54	AAS40570.1	42736635	heptaprenyl diphosphate synthase component II [Bacillus cereus ATCC 10987]
55	AAS40568.1	42736633	heptaprenyl diphosphate synthase component I, putative [Bacillus cereus ATCC 10987]
56	CAB14192.1	2634694	heptaprenyl diphosphate synthase component I [Bacillus subtilis subsp. subtilis str. 168]
57	CAB14190.1	2634692	heptaprenyl diphosphate synthase component II [Bacillus subtilis subsp. subtilis str. 168]
58	AAT04731.1	46881435	putative heptaprenyl diphosphate synthase component I [Listeria monocytogenes str. 4b F2365]
59	AAT04729.1	46881433	heptaprenyl diphosphate synthase, component II [Listeria monocytogenes str. 4b F2365]
60	YP_307471.1	73748232	heptaprenyl diphosphate synthase component II [Dehalococcoid sp. CBDB1]
61	YP_082992.1	52143836	heptaprenyl diphosphate synthase component I [Bacillus cereus E33L]
62	YP_082994.1	52143833	heptaprenyl diphosphate synthase component II [Bacillus cereus E33L]
63	YP_043530.1	49486309	putative heptaprenyl diphosphate synthase component II [Staphylococcus aureus subsp. aureus MSSA476]
64	NP_831291.1	30019660	Heptaprenyl diphosphate synthase component I [Bacillus cereus ATCC 14579]
65	NP_816857.1	29377703	heptaprenyl diphosphate synthase, component II, putative [Enterococcus faecalis V583]
66	NP_815720.1	29376566	heptaprenyl diphosphate synthase, component II, putative [Enterococcus faecalis V583]
67	NP_692711.1	23099245	heptaprenyl diphosphate synthase component I [Oceanobacillus iheyensis HTE831]
68	NP_692709.1	23099243	heptaprenyl diphosphate synthase component II [Oceanobacillus iheyensis HTE831]
69	NP_390157.1	16079333	heptaprenyl diphosphate synthase component I [Bacillus subtilis subsp. subtilis str. 168]
70	NP_390155.1	16079331	heptaprenyl diphosphate synthase component II [Bacillus subtilis subsp. subtilis str. 168]
71	NP_242519.1	15614216	heptaprenyl diphosphate synthase component II (spore germinat protein C3) [Bacillus halodurans C-125]
72	NP_242514.1	15614211	heptaprenyl diphosphate synthase component I (spore germinati protein C1) [Bacillus halodurans C-125]
73	YP_175385.1	56963654	heptaprenyl diphosphate synthase component II [Bacillus clausi KSM-K16]
74	YP_175381.1	56963650	heptaprenyl diphosphate synthase component I [Bacillus clausii KSM-K16]
75	NP_843986.1	30261609	heptaprenyl diphosphate synthase component II [Bacillus anthra str. Ames]
76	NP_843984.1	30261607	heptaprenyl diphosphate synthase component I, putative [Bacillus anthracis str. Ames]
77	NP_602368.1	19704873	Heptaprenyl diphosphate synthase component II [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]
78	ABB13849.1	77994950	heptaprenyl diphosphate synthase component II [Carboxydother hydrogenoformans Z-2901]
79	CAI82555.1	73659948	heptaprenyl diphosphate synthase component II [Dehalococcoid sp. CBDB1]

80	ZP_00798791.1	77683341	Heptaprenyl diphosphate synthase component I [Alkaliphilus metalliredigenes QYMF]
81	EAO83284.1	77640946	Heptaprenyl diphosphate synthase component I [Alkaliphilus metalliredigenes QYMF]
82	ZP_00779866.1	76797568	Heptaprenyl diphosphate synthase component I [Thermoanaerobacter ethanolicus ATCC 33223]
83	ZP_00778578.1	76796211	Heptaprenyl diphosphate synthase component I [Thermoanaerobacter ethanolicus ATCC 33223]
84	EAO64886.1	76588481	Heptaprenyl diphosphate synthase component I [Thermoanaerobacter ethanolicus ATCC 33223]
85	EAO63543.1	76587069	Heptaprenyl diphosphate synthase component I [Thermoanaerobacter ethanolicus ATCC 33223]
86	AAU18855.1	51977305	heptaprenyl diphosphate synthase component I [Bacillus cereus E33L]
87	AAU18852.1	51977302	heptaprenyl diphosphate synthase component II [Bacillus cereu E33L]
88	ZP_00743670.1	75764068	Heptaprenyl diphosphate synthase component I [Bacillus thuringiensis serovar israelensis ATCC 35646]
89	ZP_00742587.1	75762757	Heptaprenyl diphosphate synthase component I [Bacillus thuringiensis serovar israelensis ATCC 35646]
90	ZP_00742585.1	75762755	Farnesyl pyrophosphate synthetase / Geranyltranstransferase / Farnesyltransferase / Heptaprenyl diphosphate synthase compoi II [Bacillus thuringiensis serovar israelensis ATCC 35646]
91	EAO53146.1	74489760	Heptaprenyl diphosphate synthase component I [Bacillus thuringiensis serovar israelensis ATCC 35646]
92	EAO53144.1	74489758	Farnesyl pyrophosphate synthetase / Geranyltranstransferase / Farnesyltransferase / Heptaprenyl diphosphate synthase compoi II [Bacillus thuringiensis serovar israelensis ATCC 35646]
93	EAO52061.1	74488447	Heptaprenyl diphosphate synthase component I [Bacillus thuringiensis serovar israelensis ATCC 35646]
94	AAZ44827.1	71845331	Heptaprenyl diphosphate synthase component I [Dechloromona aromatica RCB]
95	ZP_00662850.1	71541033	Heptaprenyl diphosphate synthase component I [Syntrophomon wolfei str. Goettingen]
96	ZP_00604833.1	69248975	Heptaprenyl diphosphate synthase component I [Enterococcus faecium DO]
97	EAN08830.1	68194316	Heptaprenyl diphosphate synthase component I [Enterococcus faecium DO]
98	AAL93667.1	19712760	Heptaprenyl diphosphate synthase component II [Fusobacteriun nucleatum subsp. nucleatum ATCC 25586]
99	ZP_00504372.1	67874759	heptaprenyl diphosphate synthase component I [Clostridium thermocellum ATCC 27405]
100	EAM46611.1	67851042	heptaprenyl diphosphate synthase component I [Clostridium thermocellum ATCC 27405]
101	CAG43188.1	49244752	putative heptaprenyl diphosphate synthase component II [Staphylococcus aureus subsp. aureus MSSA476]
102	AAW40318.1	57225261	heptaprenyl diphosphate synthase component II [Dehalococcoi ethenogenes 195]
103	BAC13746.1	22777474	heptaprenyl diphosphate synthase component I (spore germinat protein C1) [Oceanobacillus iheyensis HTE831]
104	BAC13744.1	22777472	heptaprenyl diphosphate synthase component II (spore germina protein C3) [Oceanobacillus iheyensis HTE831]
105	BAB05372.1	10174270	heptaprenyl diphosphate synthase component II (spore germina protein C3) [Bacillus halodurans C-125]

106	BAB05367.1	10174265	heptaprenyl diphosphate synthase component I (spore germinat protein C1) [Bacillus halodurans C-125]
107	AAU23938.1	52003996	heptaprenyl diphosphate synthase component I [Bacillus licheniformis ATCC 14580]
108	AAU23936.1	52003994	heptaprenyl diphosphate synthase component II [Bacillus licheniformis ATCC 14580]
109	AAT63223.1	49332577	heptaprenyl diphosphate synthase component I [Bacillus thuringiensis serovar konkukian str. 97-27]
110	AAT63220.1	49332574	heptaprenyl diphosphate synthase component II [Bacillus thuringiensis serovar konkukian str. 97-27]
111	AAT83641.1	50840974	heptaprenyl diphosphate synthase component II [Propionibacte acnes KPA171202]
112	AAT30633.1	47501957	heptaprenyl diphosphate synthase component II [Bacillus anthr str. 'Ames Ancestor']
113	AAT30631.1	47501955	heptaprenyl diphosphate synthase component I, putative [Bacill anthracis str. 'Ames Ancestor']
114	AAT53744.1	49178368	heptaprenyl diphosphate synthase component II [Bacillus anthr str. Sterne]
115	AAT53742.1	49178366	heptaprenyl diphosphate synthase component I, putative [Bacill anthracis str. Sterne]
116	AAK05440.1	12724324	heptaprenyl diphosphate synthase component II (EC 2.5.1.30) [Lactococcus lactis subsp. lactis Il1403]
117	ZP_00237012.1	47565974	heptaprenyl diphosphate synthase component I [Bacillus cereus G9241]
118	EAL15221.1	47556891	heptaprenyl diphosphate synthase component I [Bacillus cereus G9241]
119	ZP_00235229.1	47097728	heptaprenyl diphosphate synthase component I, putative [Lister monocytogenes str. 1/2a F6854]
120	ZP_00235227.1	47097726	heptaprenyl diphosphate synthase, component II [Listeria monocytogenes str. 1/2a F6854]
121	ZP_00232135.1	47094455	heptaprenyl diphosphate synthase component I, putative [Listeri monocytogenes str. 4b H7858]
122	ZP_00232133.1	47094453	heptaprenyl diphosphate synthase, component II [Listeria monocytogenes str. 4b H7858]
123	EAL08023.1	47017170	heptaprenyl diphosphate synthase component I, putative [Listeri monocytogenes str. 4b H7858]
124	EAL08021.1	47017168	heptaprenyl diphosphate synthase, component II [Listeria monocytogenes str. 4b H7858]
125	EAL04931.1	47013899	heptaprenyl diphosphate synthase component I, putative [Listeri monocytogenes str. 1/2a F6854]
126	EAL04929.1	47013897	heptaprenyl diphosphate synthase, component II [Listeria monocytogenes str. 1/2a F6854]
127	BAA82615.1	5631299	farnesyl, geranylgeranyl, geranylfarnesyl, hexaprenyl, heptapre diphosphate synthase (SelF-HepPS) [Synechococcus elongatus]
128	ZP_00143289.1	34762284	Farnesyl pyrophosphate synthetase; Geranyltranstransferase; Farnesyltransferase; Heptaprenyl diphosphate synthase compon [Fusobacterium nucleatum subsp. vincentii ATCC 49256]
129	EAA25132.1	27888070	Farnesyl pyrophosphate synthetase; Geranyltranstransferase; Farnesyltransferase; Heptaprenyl diphosphate synthase compon [Fusobacterium nucleatum subsp. vincentii ATCC 49256]
130	NP_217900.1	15610519	POSSIBLE POLYPRENYL SYNTHETASE IDSB (POLYPRENYL TRANSFERASE) (POLYPRENYL DIPHOSPHATE SYNTHASE) [Mycobacterium tuberculosis H37Rv]

131	CAA15768.1	2661662	POSSIBLE POLYPRENYL SYNTHETASE IDSB (POLYPRENYL TRANSFERASE) (POLYPRENYL DIPHOSPHATE SYNTHASE) [Mycobacterium tuberculosis H37Rv]
132	NP_857056.1	31794563	POSSIBLE POLYPRENYL SYNTHETASE IDSB (POLYPRENYL TRANSFERASE) (POLYPRENYL DIPHOSPHATE SYNTHASE) [Mycobacterium bovis AF2122
133	CAD95588.1	31620159	POSSIBLE POLYPRENYL SYNTHETASE IDSB (POLYPRENYL TRANSFERASE) (POLYPRENYL DIPHOSPHATE SYNTHASE) [Mycobacterium bovis AF2122
134	CAC31793.1	13093913	polyprenyl diphosphate synthase component [Mycobacterium leprae]
135	NP_628745.1	21222966	polyprenyl diphosphate synthase [Streptomyces coelicolor A3(2
136	NP_938810.1	38233043	Putative polyprenyl diphosphate synthase component [Corynebacterium diphtheriae NCTC 13129]
137	CAE48933.1	38199302	Putative polyprenyl diphosphate synthase component [Corynebacterium diphtheriae]
138	CAC08284.1	10129728	putative polyprenyl diphosphate synthase [Streptomyces coelicc A3(2)]
139	NP_215504.1	15608129	PROBABLE POLYPRENYL-DIPHOSPHATE SYNTHASE GRCC2 (POLYPRENYL PYROPHOSPHATE SYNTHETASE [Mycobacterium tuberculosis H37Rv]
140	CAB08149.1	2052123	PROBABLE POLYPRENYL-DIPHOSPHATE SYNTHASE GRCC2 (POLYPRENYL PYROPHOSPHATE SYNTHETASE [Mycobacterium tuberculosis H37Rv]
141	NP_854673.1	31792180	PROBABLE POLYPRENYL-DIPHOSPHATE SYNTHASE GRCC2 (POLYPRENYL PYROPHOSPHATE SYNTHETASE [Mycobacterium bovis AF2122/97]
142	CAD93877.1	31617768	PROBABLE POLYPRENYL-DIPHOSPHATE SYNTHASE GRCC2 (POLYPRENYL PYROPHOSPHATE SYNTHETASE [Mycobacterium bovis AF2122/97]
143	NP_215076.1	15607702	PROBABLE POLYPRENYL-DIPHOSPHATE SYNTHASE GRCC1 (POLYPRENYL PYROPHOSPHATE SYNTHETASE [Mycobacterium tuberculosis H37Rv]
144	CAB08957.1	2114024	PROBABLE POLYPRENYL-DIPHOSPHATE SYNTHASE GRCC1 (POLYPRENYL PYROPHOSPHATE SYNTHETASE [Mycobacterium tuberculosis H37Rv]
145	NP_854237.1	31791744	PROBABLE POLYPRENYL-DIPHOSPHATE SYNTHASE GRCC1 (POLYPRENYL PYROPHOSPHATE SYNTHETASE [Mycobacterium bovis AF2122/97]
146	CAD93439.1	31617330	PROBABLE POLYPRENYL-DIPHOSPHATE SYNTHASE GRCC1 (POLYPRENYL PYROPHOSPHATE SYNTHETASE [Mycobacterium bovis AF2122/97]
147	ZP_01369225.1	109645305	Polyprenyl synthetase [Desulfitobacterium hafniense DCB-2]
148	EAT52807.1	109643254	Polyprenyl synthetase [Desulfitobacterium hafniense DCB-2]
149	YP_637947.1	108797750	Trans-hexaprenyltranstransferase [Mycobacterium sp. MCS]
150	ABG06891.1	108768169	Trans-hexaprenyltranstransferase [Mycobacterium sp. MCS]
151	CAD00719.1	16412129	lmo2641 [Listeria monocytogenes]
152	NP_736217.1	25011822	hypothetical protein gbs1783 [Streptococcus agalactiae NEM31
153	YP_091984.1	52786155	HepS [Bacillus licheniformis ATCC 14580]
154	YP_091982.1	52786153	HepT [Bacillus licheniformis ATCC 14580]
155	NP_472119.1	16801851	hypothetical protein lin2790 [Listeria innocua Clip11262]
156	NP_471380.1	16801112	hypothetical protein lin2046 [Listeria innocua Clip11262]

157	NP_471378.1	16801110	hypothetical protein lin2044 [Listeria innocua Clip11262]
158	NP_466164.1	16804679	hypothetical protein lmo2641 [Listeria monocytogenes EGD-e]
159	NP_465456.1	16803971	hypothetical protein lmo1932 [Listeria monocytogenes EGD-e]
160	NP_465454.1	16803969	hypothetical protein lmo1930 [Listeria monocytogenes EGD-e]
161	CAD47442.1	24413363	Unknown [Streptococcus agalactiae NEM316]
162	CAC98016.1	16415326	lin2790 [Listeria innocua]
163	CAC97276.1	16414547	lin2046 [Listeria innocua]
164	CAC97274.1	16414545	lin2044 [Listeria innocua]
165	CAD00010.1	16411385	lmo1932 [Listeria monocytogenes]
166	CAD00008.1	16411383	lmo1930 [Listeria monocytogenes]
167	AAU41291.1	52348657	HepS [Bacillus licheniformis DSM 13]
168	AAU41289.1	52348655	HepT [Bacillus licheniformis DSM 13]
169	AAC45506.1	2281328	GerCC [Lactococcus lactis subsp. cremoris]
170	AAC45505.1	2281327	GerCA [Lactococcus lactis subsp. cremoris]

Table 64. Examples of octaprenyl (8) polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	YP_404850	82778501	octaprenyl diphosphate synthase [Shigella dysenteriae Sd197]
2	YP_671157	110643427	octaprenyl-diphosphate synthase [Escherichia coli 536]
3	NP_312093	15833320	octaprenyl diphosphate synthase [Escherichia coli O157:H7 str. Sakai]
4	NP_755811	26249771	Octaprenyl-diphosphate synthase [Escherichia coli CFT073]
5	YP_152309	56415234	octaprenyl-diphosphate synthase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]
6	YP_218230	62181813	octaprenyl diphosphate synthase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
7	YP_048804	50119637	octaprenyl-diphosphate synthase [Erwinia carotovora subsp. atroseptica SCRI1043]
8	NP_931707	37528362	octaprenyl-diphosphate synthase (octaprenyl pyrophosphate synthetase) (OPP synthetase) [Photorhabdus luminescens subsp laumondii TTO1]
9	YP_649184	108813417	octaprenyl-diphosphate synthase [Yersinia pestis Nepal516]
10	YP_454042	85058340	octaprenyl-diphosphate synthase [Sodalis glossinidius str. 'morsitans']
11	ZP_009...	84394037	octaprenyl-diphosphate synthase [Vibrio splendidus 12B01]
12	ZP_012...	90411954	putative octaprenyl-diphosphate synthase [Photobacterium profundum 3TCK]
13	YP_128627	54307607	putative octaprenyl-diphosphate synthase [Photobacterium profundum SS9]
14	ZP_010...	86147820	octaprenyl-diphosphate synthase [Vibrio sp. MED222]
15	ZP_011...	89075549	putative octaprenyl-diphosphate synthase [Photobacterium sp.

			SKA34]
16	NP_796706	28897101	octaprenyl-diphosphate synthase [Vibrio parahaemolyticus RIM 2210633]
17	ZP_012...	90580809	putative octaprenyl-diphosphate synthase [Vibrio angustum S14
18	NP_230088	15640461	octaprenyl-diphosphate synthase [Vibrio cholerae O1 biovar elt str. N16961]
19	NP_719195	24375152	octaprenyl-diphosphate synthase [Shewanella oneidensis MR-1]
20	YP_248580	68249468	octaprenyl-diphosphate synthase [Haemophilus influenzae 86-028NP]
21	YP_718452	113460390	octaprenyl-diphosphate synthase [Haemophilus somnus 129PT]
22	ZP_011...	88859033	Octaprenyl-diphosphate synthase (Octaprenyl pyrophosphate synthetase)(OPP synthetase) [Pseudoalteromonas tunicata D2]
23	NP_873232	33151879	octaprenyl pyrophosphate synthetase [Haemophilus ducreyi 35000HP]
24	YP_271161	71278535	octaprenyl-diphosphate synthase [Colwellia psychrerythraea 34]
25	YP_341147	77361572	Octaprenyl-diphosphate synthase (Octaprenyl pyrophosphate synthetase)(OPP synthetase) [Pseudoalteromonas haloplanktis TAC125]
26	YP_277610	71891880	octaprenyl-diphosphate synthase [Candidatus Blochmannia pennsylvanicus str. BPEN]
27	ZP_012...	90408282	octaprenyl-diphosphate synthase [Psychromonas sp. CNPT3]
28	ZP_011...	88948625	octaprenyl diphosphate synthase [Halorhodospira halophila SL1
29	NP_520944	17547542	PROBABLE OCTAPRENYL-DIPHOSPHATE SYNTHASE (OCTAPRENYL PYROPHOSPHATE SYNTHASE) PROTEIN [Ralstonia solanacearum GMI1000]
30	NP_882670	33595027	octaprenyl-diphosphate synthase [Bordetella parapertussis 1282
31	NP_879571	33591927	octaprenyl-diphosphate synthase [Bordetella pertussis Tohama I
32	NP_886865	33599305	octaprenyl-diphosphate synthase [Bordetella bronchiseptica RB
33	NP_900517	34496302	octaprenyl-diphosphate synthase [Chromobacterium violaceum ATCC 12472]
34	NP_878401	33519569	octaprenyl-diphosphate synthase [Candidatus Blochmannia floridanus]
35	ZP_010...	87122767	octaprenyl-diphosphate synthase [Marinomonas sp. MED121]
36	NP_284854	15795032	octaprenyl-diphosphate synthase [Neisseria meningitidis Z2491]
37	ZP_008...	77954118	octylprenyl diphosphate synthase [Marinobacter aquaeolei VT8]
38	YP_262398	70732635	octylprenyl diphosphate synthase [Pseudomonas fluorescens Pf-
39	AAD47627	5712726	octylprenyl diphosphate synthase-like protein [Pseudomonas sp. BG33R]
40	YP_115384	53802938	octaprenyl-diphosphate synthase [Methylococcus capsulatus str. Bath]
41	YP_273004	71735497	octylprenyl diphosphate synthase [Pseudomonas syringae pv. phaseolicola 1448A]
42	NP_790643	28868024	octylprenyl diphosphate synthase [Pseudomonas syringae pv. to str. DC3000]
43	NP_742848	26987423	octylprenyl diphosphate synthase [Pseudomonas putida KT2440
44	ZP_009...	82739290	octylprenyl diphosphate synthase [Pseudomonas putida F1]
45	YP_334895	76809882	octaprenyl-diphosphate synthase [Burkholderia pseudomallei 17
46	YP_109601	53720615	octaprenyl-diphosphate synthase [Burkholderia pseudomallei K96243]
47	YP_364781	78048606	Octaprenyl-diphosphate synthase [Xanthomonas campestris pv. vesicatoria str. 85-10]
48	ZP_011...	88704338	Octaprenyl-diphosphate synthase [gamma proteobacterium KT
49	YP_104070	53726074	octaprenyl-diphosphate synthase [Burkholderia mallei ATCC

			23344]
50	YP_450351	84622979	octaprenyl-diphosphate synthase [Xanthomonas oryzae pv. oryz MAFF 311018]
51	AAW74692	58425655	octaprenyl-diphosphate synthase [Xanthomonas oryzae pv. oryz KACC10331]
52	YP_242466	66767704	octaprenyl-diphosphate synthase [Xanthomonas campestris pv. campestris str. 8004]
53	YP_441686	83721521	octaprenyl-diphosphate synthase [Burkholderia thailandensis E
54	NP_643215	21243633	octaprenyl-diphosphate synthase [Xanthomonas axonopodis pv. str. 306]
55	YP_513741	89256379	Octaprenyl-diphosphate synthase [Francisella tularensis subsp. holarctica]
56	YP_667159	110670602	Octaprenyl-diphosphate synthase [Francisella tularensis subsp. tularensis FSC 198]
57	NP_298680	15837992	octaprenyl-diphosphate synthase [Xylella fastidiosa 9a5c]
58	YP_096661	52842862	octaprenyl diphosphate synthase IspB [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]
59	NP_384952	15964599	PUTATIVE OCTAPRENYL-DIPHOSPHATE SYNTHASE PROTEIN [Sinorhizobium meliloti 1021]
60	YP_047477	50085967	octaprenyl-diphosphate synthase (Octaprenyl pyrophosphate synthetase) (OPP synthetase) [Acinetobacter sp. ADP1]
61	NP_531334	17934544	octaprenyl-diphosphate synthase [Agrobacterium tumefaciens s C58]
62	YP_468413	86356521	octaprenyl-diphosphate synthase protein [Rhizobium etli CFN 4
63	NP_952370	39996419	octaprenyl-diphosphate synthase [Geobacter sulfurreducens PC
64	ZP_011...	88937004	octaprenyl-diphosphate synthase [Geobacter uraniumreducens F
65	BAB53531	14026935	octaprenyl-diphosphate synthase [Mesorhizobium loti MAFF303099]
66	NP_769171	27377642	octaprenyl-diphosphate synthase [Bradyrhizobium japonicum USDA 110]
67	NP_946391	39934115	octaprenyl-diphosphate synthase [Rhodopseudomonas palustris CGA009]
68	YP_357394	77919579	octaprenyl-diphosphate synthase [Pelobacter carbinolicus DSM 2380]
69	YP_033257	49475216	Octaprenyl-diphosphate synthase [Bartonella henselae str. Hous 1]
70	YP_264856	71066129	probable octaprenyl-diphosphate synthase [Psychrobacter arctic 273-4]
71	NP_245283	15602211	IspB [Pasteurella multocida subsp. multocida str. Pm70]
72	YP_208712	59802000	IspB [Neisseria gonorrhoeae FA 1090]

Table 65. Examples of solanesyl(nonaprenyl) (9) polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	ABD92707.1	90200410	solanesyl diphosphate synthase [Hevea brasiliensis]
2	BAE48219.1	81157937	subunit 1 of solanesyl diphosphate synthase [Mus musculus]
3	BAE48218.1	81157935	subunit 2 of solanesyl diphosphate synthase [Mus musculus]
4	BAC82428.1	34327936	solanesyl diphosphate synthase [Arabidopsis thaliana]
5	BAD88534.1	57999785	solanesyl diphosphate synthase 2 [Arabidopsis thaliana]
6	BAD88533.1	57999783	solanesyl diphosphate synthase 1 [Arabidopsis thaliana]
7	BAB86941.1	19911233	solanesyl diphosphate synthase [Arabidopsis thaliana]
8	BAA22867.1	2547044	solanesyl diphosphate synthase [Rhodobacter capsulatus]
9	YP_730756.1	113952964	solanesyl diphosphate synthase [Synechococcus sp. CC9311]
10	ABI45273.1	113880315	solanesyl diphosphate synthase [Synechococcus sp. CC9311]
11	NP_439899.1	16329171	solanesyl diphosphate synthase [Synechocystis sp. PCC 6803]
12	BAD79931.1	56686709	solanesyl diphosphate synthase [Synechococcus elongatus PCC 6301]
13	YP_172451.1	56751750	solanesyl diphosphate synthase [Synechococcus elongatus PCC 6301]
14	NP_897104.1	33865545	polyprenyl synthetase; solanesyl diphosphate synthase (sds) [Synechococcus sp. WH 8102]
15	NP_894225.1	33862665	polyprenyl synthetase; solanesyl diphosphate synthase (sds) [Prochlorococcus marinus str. MIT 9313]
16	NP_892736.1	33861175	polyprenyl synthetase; solanesyl diphosphate synthase (sds) [Prochlorococcus marinus subsp. pastoris str. CCMP1986]
17	NP_682547.1	22299300	solanesyl diphosphate synthase [Thermosynechococcus elongati BP-1]
18	BAA16579.2	14595182	solanesyl diphosphate synthase [Synechocystis sp. PCC 6803]
19	XP_754994.1	71000625	solanesyl pyrophosphate synthase [Aspergillus fumigatus Af293
20	YP_476708.1	86607946	solanesyl diphosphate synthase [Synechococcus sp. JA-2-3B'a(2 13)]
21	YP_475675.1	86606912	solanesyl diphosphate synthase [Synechococcus sp. JA-3-3Ab]
22	ABD01445.1	86556488	solanesyl diphosphate synthase [Synechococcus sp. JA-2-3B'a(2 13)]
23	ABD00412.1	86555454	solanesyl diphosphate synthase [Synechococcus sp. JA-3-3Ab]
24	ZP_01086140.1	87303352	polyprenyl synthetase; solanesyl diphosphate synthase (sds) [Synechococcus sp. WH 5701]
25	EAQ73962.1	87282000	polyprenyl synthetase; solanesyl diphosphate synthase (sds) [Synechococcus sp. WH 5701]
26	EAQ69044.1	86167786	polyprenyl synthetase; solanesyl diphosphate synthase (sds) [Synechococcus sp. RS9917]
27	ZP_01080063.1	87124214	polyprenyl synthetase; solanesyl diphosphate synthase (sds) [Synechococcus sp. RS9917]
28	NP_484140.1	17227592	solanesyl diphosphate synthase [Nostoc sp. PCC 7120]
29	ZP_01005253.1	84517904	polyprenyl synthetase; solanesyl diphosphate synthase (sds) [Prochlorococcus marinus str. MIT 9211]
30	EAQ08991.1	84512653	polyprenyl synthetase; solanesyl diphosphate synthase (sds) [Prochlorococcus marinus str. MIT 9211]
31	NP_923699.1	37520322	solanesyl diphosphate synthase [Gloeobacter violaceus PCC 742
32	EAL92956.1	66852631	solanesyl pyrophosphate synthase [Aspergillus fumigatus Af293
33	CAE19077.1	33639907	polyprenyl synthetase; solanesyl diphosphate synthase (sds) [Prochlorococcus marinus subsp. pastoris str. CCMP1986]
34	CAE20567.1	33634581	polyprenyl synthetase; solanesyl diphosphate synthase (sds) [Prochlorococcus marinus str. MIT 9313]
35	CAE07526.1	33632714	polyprenyl synthetase; solanesyl diphosphate synthase (sds)

			[Synechococcus sp. WH 8102]
36	BAC88694.1	35211315	solanesyl diphosphate synthase [Gloeobacter violaceus PCC 74
37	BAC09309.1	22295483	solanesyl diphosphate synthase [Thermosynechococcus elongat BP-1]
38	BAB77620.1	17135074	solanesyl diphosphate synthase [Nostoc sp. PCC 7120]
39	CAD42868.1	21955862	solanesyl pyrophosphate synthase [Mucor circinelloides f. lusitanicus]
40	NP_062374.2	90577181	prenyl diphosphate synthase, subunit 1 [Mus musculus]
41	NP_177972.2	30699332	dimethylallyltranstransferase [Arabidopsis thaliana].
42	NP_055132.2	50659086	prenyl diphosphate synthase, subunit 1 [Homo sapiens]
43	NP_065114.2	29893562	prenyl diphosphate synthase, subunit 2 [Homo sapiens]
44	ABE11067.1	91070145	polyprenyl synthetase [uncultured Prochlorococcus marinus clo HF10-11A3]
45	NP_082048.1	90568030	prenyl diphosphate synthase, subunit 2 [Mus musculus]
46	CAD75219.1	32445217	polyprenyl synthase [Rhodopirellula baltica SH 1]
47	BAF29571.1	113649059	Os12g0271700 [Oryza sativa (japonica cultivar-group)].
48	BAF18352.1	113579989	Os05g0582300 [Oryza sativa (japonica cultivar-group)].
49	ABE11181.1	91070262	polyprenyl synthetase [uncultured Prochlorococcus marinus clo HF10-11H7]
50	NP_867672.1	32474678	polyprenyl synthase [Rhodopirellula baltica SH 1]

Table 69. Examples of malate dehydrogenase polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_503933.1	50553046	hypothetical protein [Yarrowia lipolytica].
2	EAT83219	111062099	predicted protein [Phaeosphaeria nodorum SN15]
3	XP_747556	70984070	malate dehydrogenase, NAD-dependent [Aspergillus fumigatus Af293]
4	BAE61776	83771646	unnamed protein product [Aspergillus oryzae]
5	EAQ89010	88181542	malate dehydrogenase, mitochondrial precursor [Chaetomiu globosum CBS 148.51]
6	EAS37226	90307595	hypothetical protein CIMG_02580 [Coccidioides immitis R
7	XP_572013	58269714	L-malate dehydrogenase [Cryptococcus neoformans var. neoformans JEC21]
8	XP_748936	70986899	malate dehydrogenase, NAD-dependent [Aspergillus fumigatus Af293]
9	BAE55502	83765359	unnamed protein product [Aspergillus oryzae]
10	EAQ88553	88181085	malate dehydrogenase, mitochondrial precursor [Chaetomiu globosum CBS 148.51]
11	ABH10641	111606553	malate dehydrogenase [Coccidioides posadasii]
12	XP_321163	58395331	ENSANGP00000020184 [Anopheles gambiae str. PEST]
13	XP_717047	68477790	putative peroxisomal malate dehydrogenase [Candida albica SC5314]
14	AAY63978	67043759	mitochondrial malate dehydrogenase [Lysiphlebus testaceip
15	AAX19496	60393102	mitochondrial malate dehydrogenase 2b [Xenopus laevis]
16	EAT40089	108875864	malate dehydrogenase [Aedes aegypti]
17	AAI06696	76780392	Mdh2a protein [Xenopus laevis]
18	XP_572038	58269764	malate dehydrogenase [Cryptococcus neoformans var. neoformans JEC21]
19	XP_392478	66513092	PREDICTED: similar to mitochondrial malate dehydrogena precursor isoform 1 [Apis mellifera]
20	XP_973533	91085015	PREDICTED: similar to mitochondrial malate dehydrogena precursor [Tribolium castaneum]
21	CAG12894	47224065	unnamed protein product [Tetraodon nigroviridis]
22	NP_001...	58332672	mitochondrial malate dehydrogenase 2 [Xenopus tropicalis]
23	XP_819104	71664243	malate dehydrogenase [Trypanosoma cruzi strain CL Brene
24	CAJ07715	68129178	malate dehydrogenase [Leishmania major]
25	EAL29124	54639722	GA20754-PA [Drosophila pseudoobscura]
26	XP_708782	68367713	PREDICTED: similar to malate dehydrogenase, mitochondi isoform 6 [Danio rerio]
27	XP_708779	68367700	PREDICTED: similar to malate dehydrogenase, mitochondi isoform 3 [Danio rerio]
28	AAW79319	58613465	malate dehydrogenase [Isochrysis galbana]
29	CAI29601	56403598	hypothetical protein [Pongo pygmaeus]
30	XP_460754	50424335	hypothetical protein DEHA0F09911g [Debaryomyces hansenii CBS767]
31	XP_001...	109066259	PREDICTED: similar to mitochondrial malate dehydrogena precursor [Macaca mulatta]
32	AAK69767	14583133	malate dehydrogenase [Sphyraena idiastes]
33	XP_708778	68367696	PREDICTED: similar to malate dehydrogenase, mitochond isoform 2 [Danio rerio]
34	NP_001...	79327392	PMDH2 [Arabidopsis thaliana]
35	ABE84799	92877831	Malate dehydrogenase, NAD-dependent, eukaryotes and gamma proteobacteria [Medicago truncatula]

36	AAU29200	52139820	glyoxisomal malate dehydrogenase [Lycopersicon esculentum]
37	AAW27425	56758570	SJCHGC06124 protein [Schistosoma japonicum]
38	XP_708781	68367709	PREDICTED: similar to malate dehydrogenase, mitochond isoform 5 [Danio rerio]
39	1SMKH	60593494	Chain H, Mature And Translocatable Forms Of Glyoxysom Malate Dehydrogenase Have Different Activities And Stabilities But Similar Crystal Structures
40	XP_822509	71746908	mitochondrial malate dehydrogenase [Trypanosoma brucei TREU927]
41	1SEVB	60593476	Chain B, Mature And Translocatable Forms Of Glyoxysom Malate Dehydrogenase Have Different Activities And Stabilities But Similar Crystal Structures
42	XP_708780	68367705	PREDICTED: similar to malate dehydrogenase, mitochond isoform 4 [Danio rerio]
43	ABD77290	89574129	mitochondrial malate dehydrogenase 2, NAD [Homo sapier
44	ABD77284	89574117	mitochondrial malate dehydrogenase 2, NAD [Rattus norvegicus]
45	ABD77283	89574115	mitochondrial malate dehydrogenase 2, NAD [Mus musculi
46	ABD77287	89574123	mitochondrial malate dehydrogenase 2, NAD [Oryctolagus cuniculus]
47	ABD77280	89574109	mitochondrial malate dehydrogenase 2, NAD [Loxodonta africana]
48	ABD77288	89574125	mitochondrial malate dehydrogenase 2, NAD [Lepus europaeus]
49	XP_792004	72025672	PREDICTED: similar to mitochondrial malate dehydrogena precursor [Strongylocentrotus purpuratus]
50	ABD77293	89574135	mitochondrial malate dehydrogenase 2, NAD [Canis familiaris]
51	ABD77294	89574137	mitochondrial malate dehydrogenase 2, NAD [Felis catus]
52	ABD77278	89574105	mitochondrial malate dehydrogenase 2, NAD [Didelphis virginiana]
53	XP_809210	71414199	mitochondrial malate dehydrogenase [Trypanosoma cruzi strain CL Brener]
54	ABD77301	89574151	mitochondrial malate dehydrogenase 2, NAD [Sus scrofa]
55	ABD77286	89574121	mitochondrial malate dehydrogenase 2, NAD [Mesocricetus auratus]
56	ABD77298	89574145	mitochondrial malate dehydrogenase 2, NAD [Bos taurus]
57	AAT35230	47531133	mitochondrial malate dehydrogenase [Clonorchis sinensis]
58	ABD77281	89574111	mitochondrial malate dehydrogenase 2, NAD [Dasypus novemcinctus]
59	ABD77296	89574141	mitochondrial malate dehydrogenase 2, NAD [Ceratotheriu simum]
60	ABA99939	108863014	Malate dehydrogenase, glyoxysomal precursor, putative, expressed [Oryza sativa (japonica cultivar-group)]
61	AAU29198	52139816	mitochondrial malate dehydrogenase [Lycopersicon esculentum]
62	ABD77279	89574107	mitochondrial malate dehydrogenase 2, NAD [Sminthopsis douglasi]
63	CAJ07717	68129180	malate dehydrogenase, putative [Leishmania major]
64	XP_519160	55628772	PREDICTED: similar to mitochondrial malate dehydrogena precursor [Pan troglodytes]
65	ABD72702	89473780	putative mitochondrial malate dehydrogenase [Acyrthosiph

			pisum]
66	ABD77299	89574147	mitochondrial malate dehydrogenase 2, NAD [Balaenopter physalus]
67	BAF23792	113623847	Os08g0434300 [Oryza sativa (japonica cultivar-group)]
68	CAI11361	57337458	putative malate dehydrogenase [Orpinomyces sp. OUS1]
69	ABD77289	89574127	mitochondrial malate dehydrogenase 2, NAD [Tadarida brasiliensis]
70	BAF06605	113534222	Os01g0829800 [Oryza sativa (japonica cultivar-group)]
71	ABD77292	89574133	mitochondrial malate dehydrogenase 2, NAD [Tupaia glis]
72	ABD77285	89574119	mitochondrial malate dehydrogenase 2, NAD [Cavia porcellus]
73	BAF18303	113579940	Os05g0574400 [Oryza sativa (japonica cultivar-group)]
74	ZP_010...	85712491	malate dehydrogenase [Idiomarina baltica OS145]
75	XP_539718	57097207	PREDICTED: similar to malate dehydrogenase 2, NAD (mitochondrial) [Canis familiaris]
76	ABD77277	89574103	mitochondrial malate dehydrogenase 2, NAD [Monodelphi domestica]
77	Q5R030	62286970	Malate dehydrogenase
78	YP_660122	109896867	malate dehydrogenase, NAD-dependent [Pseudoalteromon atlantica T6c]
79	Q87SU7	48428249	Malate dehydrogenase
80	ABD77291	89574131	mitochondrial malate dehydrogenase 2, NAD [Aotus trivirgatus]
81	ZP_007...	75854582	COG0039: Malate/lactate dehydrogenases [Vibrio sp. Ex25
82	ZP_011...	88795318	malate dehydrogenase [Alteromonas macleodii 'Deep ecotype']
83	ZP_012...	91228842	malate dehydrogenase [Vibrio alginolyticus 12G01]
84	ZP_011...	89075547	malate dehydrogenase [Photobacterium sp. SKA34]
85	ZP_012...	90580811	malate dehydrogenase [Vibrio angustum S14]
86	YP_671200	110643470	malate dehydrogenase [Escherichia coli 536]
87	ABD77295	89574139	mitochondrial malate dehydrogenase 2, NAD [Equus caball
88	Q5E875	66774139	Malate dehydrogenase
89	ZP_007...	75209673	COG0039: Malate/lactate dehydrogenases [Escherichia coli B171]
90	ZP_009...	84394039	malate dehydrogenase [Vibrio splendidus 12B01]
91	ZP_007...	75228638	COG0039: Malate/lactate dehydrogenases [Escherichia coli B7A]
92	ZP_010...	86147822	malate dehydrogenase [Vibrio sp. MED222]
93	BAD30064	50508045	malate dehydrogenase [Moritella sp. 36B1]
94	Q4QL89	73621201	Malate dehydrogenase
95	YP_404893	82778544	malate dehydrogenase [Shigella dysenteriae Sd197]
96	BAD30059	50508035	malate dehydrogenase [Moritella sp. 47A1]
97	BAD30066	50508049	malate dehydrogenase [Moritella sp. 36G1]
98	ZP_008...	77958772	COG0039: Malate/lactate dehydrogenases [Yersinia bercovieri ATCC 43970]
99	BAD30071	50508059	malate dehydrogenase [Moritella sp. 38F1]
100	ZP_008...	77973999	COG0039: Malate/lactate dehydrogenases [Yersinia frederiksenii ATCC 33641]
101	ZP_008...	77977600	COG0039: Malate/lactate dehydrogenases [Yersinia intermedia ATCC 29909]
102	P48364	1346511	Malate dehydrogenase
103	BAD30062	50508041	malate dehydrogenase [Moritella sp. 16H2]
104	BAD30069	50508055	malate dehydrogenase [Moritella sp. 56A1]

105	ZP_008...	77961850	COG0039: Malate/lactate dehydrogenases [Yersinia mollar ATCC 43969]
106	ZP_012...	90411956	putative malate dehydrogenase [Photobacterium profundun 3TCK]
107	Q6AW21	57012891	Malate dehydrogenase
108	Q57JA9	68052390	Malate dehydrogenase
109	ZP_012...	90407531	malate dehydrogenase [Psychromonas sp. CNPT3]
110	BAD36746	51172588	malate dehydrogenase [Moritella yayanosii]
111	Q6AW23	57012892	Malate dehydrogenase
112	ABG22106	108863015	Malate dehydrogenase, glyoxysomal precursor, putative, expressed [Oryza sativa (japonica cultivar-group)]
113	ZP_005...	68546610	Malate dehydrogenase, NAD-dependent, eukaryotes and gamma proteobacteria [Shewanella amazonensis SB2B]
114	BAD30060	50508037	malate dehydrogenase [Moritella sp. 47B1]
115	EAL31008	54642259	GA10540-PA [Drosophila pseudoobscura]
116	YP_736674	114046124	malate dehydrogenase, NAD-dependent [Shewanella sp. M 7]
117	CAJ07716	68129179	malate dehydrogenase, putative [Leishmania major]
118	ZP_009...	82743617	Malate dehydrogenase, NAD-dependent, eukaryotes and gamma proteobacteria [Shewanella sp. W3-18-1]
119	Q47VL0	83288301	Malate dehydrogenase
120	ZP_011...	88859032	malate dehydrogenase [Pseudoalteromonas tunicata D2]
121	YP_561838	91792187	malate dehydrogenase, NAD-dependent [Shewanella denitrificans OS217]
122	ZP_005...	68544347	Malate dehydrogenase, NAD-dependent, eukaryotes and gamma proteobacteria [Shewanella baltica OS155]
123	ZP_007...	75429373	malate dehydrogenase [Actinobacillus succinogenes 130Z]
124	AAW29940	56788316	malate dehydrogenase [Pasteurella trehalosi]
125	BAD30063	50508043	malate dehydrogenase [Shewanella sp. T4609]
126	EAL31009	54642260	GA10541-PA [Drosophila pseudoobscura]
127	ZP_006...	69950735	Malate dehydrogenase, NAD-dependent, eukaryotes and gamma proteobacteria [Shewanella frigidimarina NCIMB 400]
128	YP_341148	77361573	malate dehydrogenase [Pseudoalteromonas haloplanktis TAC125]
129	ZP_013...	106882260	malate dehydrogenase, NAD-dependent [Psychromonas ingrahamii 37]
130	BAD30068	50508053	malate dehydrogenase [Shewanella sp. 33H2]
131	ZP_008...	78368581	Malate dehydrogenase, NAD-dependent, eukaryotes and gamma proteobacteria [Shewanella sp. PV-4]
132	XP_851105	74004024	PREDICTED: similar to malate dehydrogenase, mitochond [Canis familiaris]
133	ABD77300	89574149	mitochondrial malate dehydrogenase 2, NAD [Hippopotam amphibius]
134	XP_816948	71656813	glycosomal malate dehydrogenase [Trypanosoma cruzi stra CL Brener]
135	CAJ19596	82655060	malate dehydrogenase [Klebsiella pneumoniae]
136	AAW29939	56788314	malate dehydrogenase [Mannheimia glucosida]
137	CAJ19583	82655034	malate dehydrogenase [Klebsiella pneumoniae]
138	CAJ19589	82655046	malate dehydrogenase [Klebsiella pneumoniae]
139	CAJ19580	82655028	malate dehydrogenase [Klebsiella pneumoniae]
140	CAJ19591	82655050	malate dehydrogenase [Klebsiella pneumoniae]
141	CAJ19595	82655058	malate dehydrogenase [Klebsiella pneumoniae]

142	CAJ19593	82655054	malate dehydrogenase [Klebsiella pneumoniae]
143	AAW29937	56788310	malate dehydrogenase [Mannheimia haemolytica]
144	XP_812467	71423452	glycosomal malate dehydrogenase [Trypanosoma cruzi stra CL Brener]
145	AAW29938	56788312	malate dehydrogenase [Mannheimia haemolytica]
146	AAW29936	56788308	malate dehydrogenase [Mannheimia haemolytica]
147	XP_849858	73993436	PREDICTED: similar to malate dehydrogenase, mitochond [Canis familiaris]
148	AAW28048	56718658	malate dehydrogenase [Vibrio cholerae]
149	AAU88998	52856248	malate dehydrogenase [Shigella flexneri]
150	AAW28041	56718644	malate dehydrogenase [Vibrio cholerae]
151	AAW28047	56718656	malate dehydrogenase [Vibrio mimicus]
152	AAW28045	56718652	malate dehydrogenase [Vibrio mimicus]
153	ABD77282	89574113	mitochondrial malate dehydrogenase 2, NAD [Tamandua tetradactyla]
154	AAU89018	52856288	malate dehydrogenase [Shigella boydii]
155	AAU89003	52856258	malate dehydrogenase [Escherichia coli]
156	AAU88960	52856172	malate dehydrogenase [Escherichia coli]
157	AAU88962	52856176	malate dehydrogenase [Shigella flexneri]
158	AAU88996	52856244	malate dehydrogenase [Escherichia coli]
159	AAU88972	52856196	malate dehydrogenase [Shigella boydii]
160	AAU88969	52856190	malate dehydrogenase [Shigella boydii]
161	ZP_007...	75822170	COG0039: Malate/lactate dehydrogenases [Vibrio cholerae RC385]
162	AAU89062	52856376	malate dehydrogenase [Shigella boydii]
163	AAU88982	52856216	malate dehydrogenase [Shigella dysenteriae]
164	AAU88995	52856242	malate dehydrogenase [Escherichia coli]
165	AAU88993	52856238	malate dehydrogenase [Escherichia coli]
166	AAU89044	52856340	malate dehydrogenase [Shigella flexneri]
167	AAU89015	52856282	malate dehydrogenase [Shigella boydii]
168	AAU88971	52856194	malate dehydrogenase [Shigella sonnei]
169	AAW28034	56718629	malate dehydrogenase [Vibrio cholerae]
170	AAU89011	52856274	malate dehydrogenase [Shigella flexneri]
171	AAU88958	52856168	malate dehydrogenase [Escherichia coli]
172	AAU88976	52856204	malate dehydrogenase [Shigella dysenteriae]
173	AAU88991	52856234	malate dehydrogenase [Escherichia coli]
174	XP_850818	73988067	PREDICTED: similar to mitochondrial malate dehydrogena precursor [Canis familiaris]
175	AAU86550	52697626	malate dehydrogenase [Shigella boydii]
176	AAU88979	52856210	malate dehydrogenase [Shigella dysenteriae]
177	AAU89005	52856262	malate dehydrogenase [Escherichia coli]
178	AAU89019	52856290	malate dehydrogenase [Shigella dysenteriae]
179	AAU88983	52856218	malate dehydrogenase [Shigella dysenteriae]
180	AAU86549	52697624	malate dehydrogenase [Escherichia albertii]
181	AAX85842	62532910	Mdh [Escherichia coli]
182	AAU89007	52856266	malate dehydrogenase [Shigella flexneri]
183	AAU88980	52856212	malate dehydrogenase [Shigella flexneri]
184	AAU89000	52856252	malate dehydrogenase [Shigella flexneri]
185	AAU88968	52856188	malate dehydrogenase [Shigella boydii]
186	AAU88988	52856228	malate dehydrogenase [Escherichia coli]
187	AAX85856	62532938	Mdh [Escherichia coli]
188	AAU86566	52697658	malate dehydrogenase [Shigella boydii]

189	AAU86571	52697668	malate dehydrogenase [Escherichia albertii]
190	ABF20150	94468239	Mdh [Escherichia coli]
191	AAU89051	52856354	malate dehydrogenase [Shigella boydii]
192	AAU89059	52856370	malate dehydrogenase [Shigella boydii]
193	AAU89057	52856366	malate dehydrogenase [Shigella boydii]
194	AAU89036	52856324	malate dehydrogenase [Shigella flexneri]
195	AAU86559	52697644	malate dehydrogenase [Shigella boydii]
196	ABF20151	94468241	Mdh [Escherichia coli]
197	ABF20142	94468223	Mdh [Escherichia coli]
198	AAU88990	52856232	malate dehydrogenase [Escherichia coli]
199	AAU86567	52697660	malate dehydrogenase [Shigella boydii]
200	AAU89032	52856316	malate dehydrogenase [Shigella dysenteriae]
201	AAU89012	52856276	malate dehydrogenase [Shigella flexneri]

Table 70. Examples of glucose-6-phosphate dehydrogenase polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_504275	50553728	hypothetical protein [Yarrowia lipolytica]
2	XP_365081	39965237	hypothetical protein MG09926.4 [Magnaporthe grisea 70-1
3	XP_381455	46108794	G6PD_ASPNG Glucose-6-phosphate 1-dehydrogenase (G6PD) [Gibberella zeae PH-1]
4	XP_660585	67525047	glucose-6-phosphate 1-dehydrogenase [Aspergillus nidulan FGSC A4]
5	P48826	1346070	Glucose-6-phosphate 1-dehydrogenase (G6PD)
6	CAA54840	1523782	glucose-6-phosphate 1-dehydrogenase [Aspergillus niger]
7	EAU38380	114196680	glucose-6-phosphate 1-dehydrogenase [Aspergillus terreus NIH2624]
8	EAT83608	111062488	predicted protein [Phaeosphaeria nodorum SN15]
9	EAS28915	90299284	glucose-6-phosphate 1-dehydrogenase [Coccidioides immit RS]
10	XP_754767	71000100	glucose-6-phosphate 1-dehydrogenase [Aspergillus fumiga Af293]
11	XP_958320	85090234	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (G6P [Neurospora crassa OR74A]
12	EAQ93370	88185902	glucose-6-phosphate 1-dehydrogenase [Chaetomium globosum CBS 148.51]
13	CAA58825	642160	unnamed protein product [Emericella nidulans]
14	XP_458129	50419213	hypothetical protein DEHA0C11286g [Debaryomyces hansenii CBS767]
15	AAB25541	299248	glucose-6-phosphate dehydrogenase [Pichia jadinii=yeast, Peptide, 495 aa]
16	XP_723251	68465104	putative glucose-6-phosphate dehydrogenase [Candida albicans SC5314]
17	XP_723440	68464725	putative glucose-6-phosphate dehydrogenase [Candida albicans SC5314]
18	XP_453944	50307901	G6PD_KLULA [Kluyveromyces lactis]
19	NP_982741	45185024	ABL206Cp [Eremothecium gossypii]
20	XP_448038	50291211	unnamed protein product [Candida glabrata]
21	XP_572045	58269778	glucose-6-phosphate 1-dehydrogenase [Cryptococcus neoformans var. neoformans JEC21]
22	NP_014158	6324088	Glucose-6-phosphate dehydrogenase (G6PD), catalyzes the first step of the pentose phosphate pathway; involved in adapting to oxidatve stress; homolog of the human G6PD which is deficient in patients with hemolytic anemia; Zwf1 [Saccharomyces cerevisiae]
23	AAT93017	51013447	YNL241C [Saccharomyces cerevisiae]
24	AAA34619	171545	glucose-6-phosphate dehydrogenase (ZWF1) (EC 1.1.1.49)
25	XP_761077	71021693	hypothetical protein UM04930.1 [Ustilago maydis 521]
26	NP_593344	63054535	glucose-6-phosphate 1-dehydrogenase [Schizosaccharomyc pombe 972h-]

27	XP_644814	66822919	glucose 6-phosphate-1-dehydrogenase [Dictyostelium discoideum AX4]
28	ABD72519	89357348	glucose 6-phosphate dehydrogenase [Trypanosoma cruzi]
29	BAE99888	110735823	glucose-6-phosphate dehydrogenase [Arabidopsis thaliana]
30	CAB52675	5732197	glucose-6-phosphate 1-dehydrogenase [Arabidopsis thalian
31	CAB08746	2104434	SPAC3A12.18 [Schizosaccharomyces pombe]
32	ABD72517	89357344	glucose 6-phosphate dehydrogenase [Trypanosoma cruzi]
33	ABD72518	89357346	glucose 6-phosphate dehydrogenase [Trypanosoma cruzi]
34	BAB96757	21262179	glucose-6-phosphate dehydrogenase 1 [Chlorella vulgaris]
35	XP_822502	71746894	glucose-6-phosphate 1-dehydrogenase [Trypanosoma bruce TREU927]
36	CAJ07708	68129171	glucose-6-phosphate dehydrogenase [Leishmania major]
37	CAC07816	10045209	glucose-6-phosphate 1-dehydrogenase [Trypanosoma bruce
38	BAF15046	113564703	Os04g0485300 [Oryza sativa (japonica cultivar-group)]
39	AAO37825	28261397	glucose-6-phosphate dehydrogenase [Leishmania mexicana
40	AAM64228	27434608	glucose-6-phosphate dehydrogenase [Leishmania mexicana amazonensis]
41	XP_001...	110750934	PREDICTED: similar to Zwischenferment CG12529-PA, isoform A [Apis mellifera]
42	XP_974096	91082561	PREDICTED: similar to CG12529-PA, isoform A [Tribolii castaneum]
43	ABE83959	92876243	Glucose-6-phosphate dehydrogenase [Medicago truncatula]
44	BAE38077	74138546	unnamed protein product [Mus musculus]
45	NP_001...	79313844	G6PD5; glucose-6-phosphate 1-dehydrogenase [Arabidopsi thaliana]
46	CAB52674	5732195	glucose-6-phosphate 1-dehydrogenase [Arabidopsis thalian
47	AAD11426	4206114	cytoplasmic glucose-6-phosphate 1-dehydrogenase [Mesembryanthemum crystallinum]
48	Q42919	3023815	Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform (G6PD)
49	AAL79959	19071787	glucose-6-phosphate dehydrogenase [Oryza sativa (japonica cultivar-group)]
50	CAE62054	39593761	Hypothetical protein CBG06072 [Caenorhabditis briggsae]
51	EAL31619	54642875	GA11679-PA [Drosophila pseudoobscura]
52	Q00612	54037161	Glucose-6-phosphate 1-dehydrogenase X (G6PD)
53	AAH75663	49523350	Glucose-6-phosphate dehydrogenase X-linked [Mus musculus]
54	AAB69319	2352923	cytosolic glucose-6-phosphate dehydrogenase 2 [Petroselin crispum]
55	AAM64230	27434612	glucose-6-phosphate dehydrogenase [Leishmania guyanens
56	ABB29564	78183137	putative Zwischenferment [Drosophila yakuba]

57	AAL57688	18086470	AT3g27300/K17E12_12 [Arabidopsis thaliana]
58	NP_728287	24643352	Zwischenferment CG12529-PB, isoform B [Drosophila melanogaster]
59	EAT38627	108874402	glucose-6-phosphate 1-dehydrogenase [Aedes aegypti]
60	AAR26303	89214190	glucose-6-phosphate dehydrogenase [Populus suaveolens]
61	AAA99073	1304700	glucose-6-phosphate 1-dehydrogenase [Drosophila melanogaster]
62	AAK93503	15292469	SD03244p [Drosophila melanogaster]
63	AAB02809	1304686	glucose-6-phosphate 1-dehydrogenase [Drosophila melanogaster]
64	NP_523411	24643350	Zwischenferment CG12529-PA, isoform A [Drosophila melanogaster]
65	AAA99107	1305086	glucose-6-phosphate 1-dehydrogenase [Drosophila melanogaster]
66	ABB29562	78183133	putative Zwischenferment [Drosophila simulans]
67	NP_502129	17538218	B0035.5 [Caenorhabditis elegans]
68	AAZ23850	71089991	glucose-6-phosphate dehydrogenase [Boophilus microplus]
69	P37830	585165	Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isofor (G6PD)
70	AAB02812	1304692	glucose-6-phosphate 1-dehydrogenase [Drosophila melanogaster]
71	ABB55386	81075965	glucose-6-phosphate 1-dehydrogenase cytoplasmic isoform like [Solanum tuberosum]
72	CAJ83683	89273424	glucose-6-phosphate dehydrogenase [Xenopus tropicalis]
73	NP_001...	62859893	glucose-6-phosphate dehydrogenase 2 [Xenopus tropicalis]
74	ABB29563	78183135	putative Zwischenferment [Drosophila teissieri]
75	AAX45785	61394184	glucose-6-phosphate dehydrogenase isoform B [Ips typographus]
76	AAX45784	61394183	glucose-6-phosphate dehydrogenase isoform A [Ips typographus]
77	AAH81820	51980296	Glucose-6-phosphate dehydrogenase X-linked [Rattus norvegicus]
78	XP_311452	58381765	ENSANGP00000018551 [Anopheles gambiae str. PEST]
79	XP_538209	74009187	PREDICTED: similar to Glucose-6-phosphate 1-dehydrogenase (G6PD) [Canis familiaris]
80	AAH59324	111185531	Unknown (protein for MGC:69058) [Xenopus laevis]
81	ABB29560	78183129	putative Zwischenferment [Drosophila erecta]
82	Q27638	3023810	Glucose-6-phosphate 1-dehydrogenase (G6PD)
83	Q29492	2494652	Glucose-6-phosphate 1-dehydrogenase (G6PD)
84	BAF09259	113536876	Os02g0600400 [Oryza sativa (japonica cultivar-group)]
85	O55044	62510568	Glucose-6-phosphate 1-dehydrogenase (G6PD)
86	CAA04993	3021510	glucose-6-phosphate dehydrogenase [Nicotiana tabacum]

87	ABB29561	78183131	putative Zwischenferment [Drosophila orena]
88	BAA97662	8918502	glucose-6-phosphate dehydrogenase [Triticum aestivum]
89	BAD17920	46849421	glucose-6-phosphate 1-dehydrogenase [Acipenser baerii]
90	XP_699168	68440567	PREDICTED: similar to glucose-6-phosphate dehydrogena [Danio rerio]
91	AAB96363	2734869	glucose-6-phosphate dehydrogenase [Takifugu rubripes]
92	NP_000393	109389365	glucose-6-phosphate dehydrogenase isoform a [Homo sapi
93	NP_001...	108773793	glucose-6-phosphate dehydrogenase isoform b [Homo sapiens]
94	AAA52500	182871	glucose-6-phosphate dehydrogenase variant A- (EC 1.1.1.4
95	P11413	120731	Glucose-6-phosphate 1-dehydrogenase (G6PD)
96	AAA92653	1203978	G6PD [Homo sapiens]
97	AAX43335	61369430	glucose-6-phosphate dehydrogenase [synthetic construct]
98	P41571	1169799	Glucose-6-phosphate 1-dehydrogenase (G6PD) (Zwischenferment)
99	2BHLB	66361518	Chain B, X-Ray Structure Of Human Glucose-6-Phosphate Dehydrogenase (Deletion Variant) Complexed With Gluco 6-Phosphate
100	ABC74527	85700174	glucose-6-phosphate dehydrogenase [Populus trichocarpa]
101	ABC74528	85700176	glucose-6-phosphate dehydrogenase [Populus trichocarpa]
102	AAA51463	157470	glucose-6-phosphate dehydrogenase
103	XP_001...	109132852	PREDICTED: glucose-6-phosphate dehydrogenase isoform [Macaca mulatta]
104	1QKIH	7546530	Chain H, X-Ray Structure Of Human Glucose 6-Phosphate Dehydrogenase (Variant Canton R459l) Complexed With Structural Nadp+
105	XP_001...	109132850	PREDICTED: glucose-6-phosphate dehydrogenase isoform [Macaca mulatta]
106	BAA97663	8918504	glucose-6-phosphate dehydrogenase [Triticum aestivum]
107	CAA04992	3021508	glucose-6-phosphate dehydrogenase [Nicotiana tabacum]
108	AAB69318	2352921	cytosolic glucose-6-phosphate dehydrogenase 1 [Petroselin crispum]
109	XP_307095	58375370	ENSANGP00000012074 [Anopheles gambiae str. PEST]
110	AAA41179	204197	glucose-6-phosphate dehydrogenase
111	AAA63175	182890	glucose-6-phosphate dehydrogenase [Homo sapiens]
112	BAA97664	8918506	glucose-6-phosphate dehydrogenase [Triticum aestivum]
113	AAW24823	56753227	SJCHGC02527 protein [Schistosoma japonicum]
114	CAA58590	5459313	glucose-6-phosphate 1-dehydrogenase [Takifugu rubripes]
115	CAG07451	47228719	unnamed protein product [Tetraodon nigroviridis]
116	CAJ28912	113207852	glucose-6-phosphate 1-dehydrogenase [Crassostrea gigas]

117	ABC25881	83628088	glucose-6-phosphate 1-dehydrogenase [Homo sapiens]
118	ABC25981	83628208	glucose-6-phosphate 1-dehydrogenase [Homo sapiens]
119	ABC25826	83628022	glucose-6-phosphate 1-dehydrogenase [Homo sapiens]
120	BAD17912	46849405	glucose-6-phosphate 1-dehydrogenase [Amia calva]
121	BAD17877	46849335	glucose-6-phosphate 1-dehydrogenase [Protopterus annecte
122	BAD17947	46849475	glucose-6-phosphate 1-dehydrogenase [Callorhinchus callorynchus]
123	AAI20828	111306848	Glucose-6-phosphate dehydrogenase 2 [Mus musculus]
124	BAD17927	46849435	glucose-6-phosphate 1-dehydrogenase [Polypterus ornatipinnis]
125	BAD17898	46849377	glucose-6-phosphate 1-dehydrogenase [Oryzias latipes]
126	BAD17891	46849363	glucose-6-phosphate 1-dehydrogenase [Ambystoma mexicanum]
127	BAD17951	46849483	glucose-6-phosphate 1-dehydrogenase [Lethenteron reissne
128	AAF19030	7629275	glucose-6-phosphate-1-dehydrogenase; G6PD [Pimephales promelas]
129	BAD17941	46849463	glucose-6-phosphate 1-dehydrogenase [Potamotrygon motc
130	BAD17954	46849489	glucose-6-phosphate 1-dehydrogenase [Branchiostoma belcheri]
131	BAD17905	46849391	glucose-6-phosphate 1-dehydrogenase [Lepisosteus osseus]
132	BAD17884	46849349	glucose-6-phosphate 1-dehydrogenase [Lepidosiren parado:
133	BAD17934	46849449	glucose-6-phosphate 1-dehydrogenase [Cephaloscyllium umbratile]
134	ABC74529	85700178	glucose-6-phosphate dehydrogenase [Populus trichocarpa]
135	CAB52685	5734379	plastidic glucose-6-phosphate dehydrogenase [Dunaliella bioculata]
136	Q43793	3023817	Glucose-6-phosphate 1-dehydrogenase, chloroplast precurs (G6PD)
137	AAF87216	9392607	plastidic glucose 6-phosphate dehydrogenase [Nicotiana tabacum]
138	BAC23041	24745908	glucose 6-phosphate dehydrogenase [Solanum tuberosum]
139	CAB52708	5734502	glucose-6-phosphate 1-dehydrogenase [Solanum tuberosum
140	BAF21344	113610966	Os07g0406300 [Oryza sativa (japonica cultivar-group)]
141	AAQ02671	33304517	putative plastidic glucose-6-phosphate dehydrogenase [Ory: sativa (japonica cultivar-group)]
142	AAW82643	58803037	hepatic glucose-6-phosphate dehydrogenase [Rhabdosargus sarba]
143	BAF12270	113548827	Os03g0412800 [Oryza sativa (japonica cultivar-group)]
144	AAN72144	25083966	glucose-6-phosphate dehydrogenase [Arabidopsis thaliana]
145	AAB69317	2352919	plastidic glucose-6-phosphate dehydrogenase [Petroselinum crispum]
146	O24357	3334193	Glucose-6-phosphate 1-dehydrogenase, chloroplast precurs (G6PD)

147	AAO23597	27764952	At1g24280/F3I6_22 [Arabidopsis thaliana]
148	Q8L743	25452975	Glucose-6-phosphate 1-dehydrogenase 3, chloroplast precursor (G6PD3) (G6PDH3)
149	CAA59011	1166405	glucose-6-phosphate 1-dehydrogenase [Arabidopsis thalian
150	CAA59012	1174336	glucose-6-phosphate 1-dehydrogenase [Arabidopsis thalian
151	CAC05439	9955555	glucose-6-phosphate 1-dehydrogenase [Arabidopsis thalian
152	Q9FY99	25452980	Glucose-6-phosphate 1-dehydrogenase 2, chloroplast precursor (G6PD2) (G6PDH2)
153	AAL57678	18086448	AT5g13110/T19L5_70 [Arabidopsis thaliana]
154	Q43839	3023818	Glucose-6-phosphate 1-dehydrogenase, chloroplast precurs (G6PD)
155	CAA04696	3021305	plastidic glucose-6-phosphate dehydrogenase [Arabidopsis thaliana]
156	CAB52681	5734372	glucose-6-phosphate 1-dehydrogenase [Cyanidium caldariu
157	CAA04994	3021532	glucose-6-phosphate dehydrogenase [Nicotiana tabacum]
158	Q7YS37	62510624	Glucose-6-phosphate 1-dehydrogenase (G6PD)
159	CAG04059	47229307	unnamed protein product [Tetraodon nigroviridis]
160	CAD28862	29149997	glucose 6 phosphate dehydrogenase [Acraea encedana]
161	CAD28863	29149999	glucose 6 phosphate dehydrogenase [Acraea encedana]
162	AAM64231	27434614	glucose-6-phosphate dehydrogenase [Leishmania braziliens
163	AAG28728	11066848	glucose-6-phosphate-dehydrogenase [Drosophila mauritian
164	AAG28730	11066852	glucose-6-phosphate-dehydrogenase [Drosophila sechellia]
165	ABF96583	108708788	Glucose-6-phosphate 1-dehydrogenase, chloroplast precurs putative, expressed [Oryza sativa (japonica cultivar-group)]
166	CAA03941	2276348	Glucose-6-phosphate dehydrogenase [Spinacia oleracea]
167	XP_583628	76658972	PREDICTED: similar to Glucose-6-phosphate 1-dehydrogenase (G6PD) [Bos taurus]
168	AAA52499	182869	glucose-6-phosphate dehydrogenase
169	AAM64229	27434610	glucose-6-phosphate dehydrogenase [Leishmania mexicana
170	NP_587749	19075249	hypothetical protein SPCC794.01c [Schizosaccharomyces pombe 972h-]
171	AAR12945	38156652	glucose-6-phosphate dehydrogenase [Drosophila mojavensi
172	AAR12953	38156668	glucose-6-phosphate dehydrogenase [Drosophila mojavensi
173	AAR12946	38156654	glucose-6-phosphate dehydrogenase [Drosophila mojavensi
174	AAR12943	38156648	glucose-6-phosphate dehydrogenase [Drosophila mojavensi
175	AAR12952	38156666	glucose-6-phosphate dehydrogenase [Drosophila mojavensi
176	BAF11858	113548415	Os03g0318500 [Oryza sativa (japonica cultivar-group)]
177	XP_559252	57942974	ENSANGP00000028421 [Anopheles gambiae str. PEST]

178	NP_593614	19114526	hypothetical protein SPAC3C7.13c [Schizosaccharomyces pombe 972h-]
179	BAD94743	62321397	glucose-6-phosphate dehydrogenase [Arabidopsis thaliana]
180	CAJ20381	95007160	glucose-6-phosphate-1-dehydrogenase [Toxoplasma gondii
181	YP_605437	94986073	glucose-6-phosphate 1-dehydrogenase [Deinococcus geothermalis DSM 11300]
182	CAE51228	37651949	glucose 6 phosphate dehydrogenase [Adalia bipunctata]
183	YP_007820	46446455	putative glucose-6-phosphate [Candidatus Protochlamydia amoebophila UWE25]
184	NP_295319	15806604	glucose-6-phosphate 1-dehydrogenase [Deinococcus radiodurans R1]
185	CAE51222	37651937	glucose 6 phosphate dehydrogenase [Adalia bipunctata]
186	CAE51229	37651951	glucose 6 phosphate dehydrogenase [Adalia decempunctata
187	ZP_007...	76260057	Glucose-6-phosphate dehydrogenase [Chloroflexus aurantiacus J-10-fl]
188	ZP_002...	47096622	glucose-6-phosphate 1-dehydrogenase [Listeria monocytogenes str. 1/2a F6854]
189	ZP_004...	66965919	Glucose-6-phosphate dehydrogenase [Arthrobacter sp. FB2
190	ZP_002...	47093301	glucose-6-phosphate 1-dehydrogenase [Listeria monocytogenes str. 4b H7858]
191	NP_471419	16801151	hypothetical protein lin2085 [Listeria innocua Clip11262]
192	NP_693860	23100393	glucose-6-phosphate 1-dehydrogenase [Oceanobacillus iheyensis HTE831]
193	NP_829405	29840299	glucose-6-phosphate 1-dehydrogenase [Chlamydophila cav GPIC]
194	CAJ71041	91203388	strongly similar to glucose-6-phosphate dehydrogenase [Candidatus Kuenenia stuttgartiensis]
195	YP_629214	108761123	glucose-6-phosphate 1-dehydrogenase [Myxococcus xanthu DK 1622]
196	ZP_009...	84387050	glucose-6-phosphate 1-dehydrogenase [Vibrio splendidus 12B01]
197	ZP_011...	88856188	glucose-6-phosphate 1-dehydrogenase [marine actinobacterium PHSC20C1]
198	NP_827489	29832855	glucose-6-phosphate 1-dehydrogenase [Streptomyces avermitilis MA-4680]
199	CAH10104	88319768	putative glucose-6-phosphate-1-dehydrogenase [Streptomyc sp. SCC 2136]
200	YP_148187	56420869	glucose-6-phosphate 1-dehydrogenase [Geobacillus kaustophilus HTA426]
201	ZP_006...	71368421	Glucose-6-phosphate dehydrogenase [Nocardioides sp. JS61

Table 71. Example of 6-phosphogluconate dehydrogenase polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_500938	50546937	hypothetical protein [Yarrowia lipolytica].
2	XP_458726	50420381	hypothetical protein DEHA0D06820g [Debaryomyces hansenii CBS767]
3	XP_451408	50302941	unnamed protein product [Kluyveromyces lactis]
4	O13287	3334110	6-phosphogluconate dehydrogenase, decarboxylating
5	XP_722227	68467588	hypothetical protein CaO19_5024 [Candida albicans SC531
6	NP_012053	6321977	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delt lactone and adaptation to oxidative stress; Gnd1p [Saccharomyces cerevisiae]
7	AAO32396	28564035	GND1 [Saccharomyces bayanus]
8	XP_750696	70991695	6-phosphogluconate dehydrogenase, decarboxylating [Aspergillus fumigatus Af293]
9	CAD80254	29409963	6-phosphogluconate dehydrogenase [Aspergillus niger]
10	XP_661558	67526993	hypothetical protein AN3954.2 [Aspergillus nidulans FGSC A4]
11	AAO32456	28564155	GND1 [Saccharomyces servazzii]
12	AAO32497	28564385	GND1 [Saccharomyces castellii]
13	BAE57349	83767210	unnamed protein product [Aspergillus oryzae]
14	AAT92830	51013073	YGR256W [Saccharomyces cerevisiae]
15	XP_449923	50295024	hypothetical protein CAGL0M13343g [Candida glabrata CBS138]
16	NP_985676	45198647	AFR129Wp [Eremothecium gossypii]
17	EAS35799	90306168	6-phosphogluconate dehydrogenase, decarboxylating [Coccidioides immitis RS]
18	XP_758724	71014537	hypothetical protein UM02577.1 [Ustilago maydis 521]
19	O60037	12229635	6-phosphogluconate dehydrogenase, decarboxylating
20	XP_964959	85115938	hypothetical protein [Neurospora crassa OR74A]
21	XP_381287	46108458	hypothetical protein FG01111.1 [Gibberella zeae PH-1]
22	EAT76717	111055597	predicted protein [Phaeosphaeria nodorum SN15]
23	XP_369069	39975357	hypothetical protein MG00175.4 [Magnaporthe grisea 70-1
24	XP_567793	58260766	phosphogluconate dehydrogenase (decarboxylating) [Cryptococcus neoformans var. neoformans JEC21]
25	NP_595095	19111887	6-phosphogluconate dehydrogenase [Schizosaccharomyces pombe 972h-]
26	EAQ92608	88185140	hypothetical protein CHGG_00843 [Chaetomium globosum CBS 148.51]
27	T42523	11251352	probable phosphogluconate dehydrogenase (decarboxylatin (EC 1.1.1.44) - fission yeast (Schizosaccharomyces pombe) (fragment)
28	XP_781394	72005545	PREDICTED: similar to 6-phosphogluconate dehydrogenas decarboxylating [Strongylocentrotus purpuratus]
29	BAD98151	63003720	6-phosphogluconate dehydrogenase [Ascidia sydneiensis samea]
30	XP_625090	66547531	PREDICTED: similar to 6-phosphogluconate dehydrogenas decarboxylating, partial [Apis mellifera]
31	CAG32303	53134115	hypothetical protein [Gallus gallus]
32	2PGD	999886	Chain , 6-Phosphogluconate Dehydrogenase (6-Pgdh) (E.C.1.1.1.44)

33	NP_001...	57164179	6-phosphogluconate dehydrogenase (decarboxylating) [Ovi aries]
34	XP_911640	82896232	PREDICTED: similar to 6-phosphogluconate dehydrogena decarboxylating isoform 6 [Mus musculus]
35	BAE31577	74225286	unnamed protein product [Mus musculus]
36	AAX43359	61369608	phosphogluconate dehydrogenase [synthetic construct]
37	CAI95751	66347393	phosphogluconate dehydrogenase [Homo sapiens]
38	XP_993478	94374014	PREDICTED: similar to 6-phosphogluconate dehydrogena decarboxylating isoform 4 [Mus musculus]
39	AAH11329	15030150	Phosphogluconate dehydrogenase [Mus musculus]
40	AAI02179	73586529	LOC514939 protein [Bos taurus]
41	AAA75302	984325	phosphogluconate dehydrogenase [Homo sapiens]
42	AAH59958	37747616	MGC68486 protein [Xenopus laevis]
43	ZP_005...	67931108	6-phosphogluconate dehydrogenase, decarboxylating [Solibacter usitatus Ellin6076]
44	EAT42557	108878332	6-phosphogluconate dehydrogenase [Aedes aegypti]
45	XP_535411	73950940	PREDICTED: similar to 6-phosphogluconate dehydrogena decarboxylating isoform 1 [Canis familiaris]
46	XP_313091	58384192	ENSANGP00000012857 [Anopheles gambiae str. PEST]
47	CAG07546	47228814	unnamed protein product [Tetraodon nigroviridis]
48	YP_007316	46445951	6-phosphogluconate dehydrogenase [Candidatus Protochlamydia amoebophila UWE25]
49	NP_998717	47087205	phosphogluconate hydrogenase isoform 2 [Danio rerio]
50	XP_972051	91094851	PREDICTED: similar to phosphogluconate hydrogenase isoform 2 [Tribolium castaneum]
51	CAE70848	39594980	Hypothetical protein CBG17632 [Caenorhabditis briggsae]
52	XP_001...	94372948	PREDICTED: similar to 6-phosphogluconate dehydrogena decarboxylating isoform 9 [Mus musculus]
53	NP_998618	47087439	phosphogluconate hydrogenase isoform 1 [Danio rerio]
54	AAH95571	63102189	Pgd protein [Danio rerio]
55	XP_993446	94374016	PREDICTED: similar to 6-phosphogluconate dehydrogena decarboxylating isoform 3 [Mus musculus]
56	EAL31500	54642755	GA17642-PA [Drosophila pseudoobscura]
57	Q17761	74962414	6-phosphogluconate dehydrogenase, decarboxylating
58	P41573	1168233	6-phosphogluconate dehydrogenase, decarboxylating
59	AAL90185	19528141	AT26455p [Drosophila melanogaster]
60	NP_476860	24639279	Phosphogluconate dehydrogenase CG3724-PA [Drosophila melanogaster]
61	NP_001...	114053253	6-phosphogluconate dehydrogenase [Bombyx mori]
62	P41570	1168228	6-phosphogluconate dehydrogenase, decarboxylating
63	CAJ43391	95140247	6-phosphogluconate dehydrogenase [Bactrocera oleae]
64	CAJ43390	95140245	6-phosphogluconate dehydrogenase [Ceratitis capitata]
65	AAP92648	33086672	Cc2-27 [Rattus norvegicus]
66	YP_661682	109898427	6-phosphogluconate dehydrogenase, decarboxylating [Pseudoalteromonas atlantica T6c]
67	XP_592859	76637462	PREDICTED: similar to 6-phosphogluconate dehydrogena decarboxylating [Bos taurus]
68	YP_526109	90020282	6-phosphogluconate dehydrogenase, decarboxylating [Saccharophagus degradans 2-40]
69	ZP_001...	53733078	COG0362: 6-phosphogluconate dehydrogenase [Haemophi influenzae R2846]
70	NP_761502	27365974	6-phosphogluconate dehydrogenase [Vibrio vulnificus CMCP6]

71	YP_391484	78485559	6-phosphogluconate dehydrogenase, decarboxylating [Thiomicrospira crunogena XCL-2]
72	YP_248262	68249150	6-phosphogluconate dehydrogenase [Haemophilus influenz 86-028NP]
73	NP_934400	37679791	6-phosphogluconate dehydrogenase [Vibrio vulnificus YJ0
74	ZP_007...	75857693	COG0362: 6-phosphogluconate dehydrogenase [Vibrio sp. Ex25]
75	NP_798087	28898482	6-phosphogluconate dehydrogenase [Vibrio parahaemolytic RIMD 2210633]
76	YP_206428	59713653	6-phosphogluconate dehydrogenase [Vibrio fischeri ES114]
77	ZP_001...	53733322	COG0362: 6-phosphogluconate dehydrogenase [Haemophil influenzae R2866]
78	ZP_012...	91224436	6-phosphogluconate dehydrogenase [Vibrio alginolyticus 12G01]
79	AAB20377	239383	6-phosphogluconate dehydrogenase [sheep, Peptide, 466 aa
80	ZP_010...	86145883	6-phosphogluconate dehydrogenase [Vibrio sp. MED222]
81	ZP_007...	75432781	Phosphogluconate dehydrogenase (decarboxylating) [Actinobacillus succinogenes 130Z]
82	ZP_001...	46143450	COG0362: 6-phosphogluconate dehydrogenase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]
83	ZP_012...	90578957	6-phosphogluconate dehydrogenase [Vibrio angustum S14]
84	YP_087205	52424068	6-phosphogluconate dehydrogenase [Mannheimia succiniciproducens MBEL55E]
85	ZP_011...	89073009	6-phosphogluconate dehydrogenase [Photobacterium sp. SKA34]
86	NP_273081	15675963	6-phosphogluconate dehydrogenase [Neisseria meningitidis MC58]
87	ZP_007...	75825242	COG0362: 6-phosphogluconate dehydrogenase [Vibrio cholerae O395]
88	ZP_007...	75822319	COG0362: 6-phosphogluconate dehydrogenase [Vibrio cholerae RC385]
89	ZP_007...	75831146	COG0362: 6-phosphogluconate dehydrogenase [Vibrio cholerae MO10]
90	YP_719859	113461790	6-phosphogluconate dehydrogenase [Haemophilus somnus 129PT]
91	ZP_012...	90411828	6-phosphogluconate dehydrogenase [Photobacterium profundum 3TCK]
92	YP_129657	54308637	6-phosphogluconate dehydrogenase [Photobacterium profundum SS9]
93	ZP_001...	53728695	COG0362: 6-phosphogluconate dehydrogenase [Haemophil somnus 2336]
94	BAD36766	51241757	6-phosphogluconate dehydrogenase [Cyanidioschyzon merolae]
95	P70718	2492494	6-phosphogluconate dehydrogenase, decarboxylating
96	XP_642122	66816225	6-phosphogluconate dehydrogenase (decarboxylating) [Dictyostelium discoideum AX4]
97	Q7VMX4	71152205	6-phosphogluconate dehydrogenase, decarboxylating
98	NP_283102	15793280	6-phosphogluconate dehydrogenase [Neisseria meningitidis Z2491]
99	NP_246493	15603419	6-phosphogluconate dehydrogenase [Pasteurella multocida subsp. multocida str. Pm70]
100	AAO19943	27573087	6-phosphogluconate dehydrogenase, decarboxylating [Neisseria gonorrhoeae]

101	AAO19944	27573089	6-phosphogluconate dehydrogenase, decarboxylating [Neisseria gonorrhoeae]
102	YP_208939	59802227	6-phosphogluconate dehydrogenase [Neisseria gonorrhoeae FA 1090]
103	AAO19934	27573069	6-phosphogluconate dehydrogenase, decarboxylating [Neisseria gonorrhoeae]
104	AAO19942	27573085	6-phosphogluconate dehydrogenase, decarboxylating [Neisseria gonorrhoeae]
105	ZP_013...	106881674	6-phosphogluconate dehydrogenase, decarboxylating [Psychromonas ingrahamii 37]
106	XP_515670	55599346	PREDICTED: similar to 6-phosphogluconate dehydrogenas decarboxylating [Pan troglodytes]
107	ZP_010...	87309497	6-phosphogluconate dehydrogenase [Blastopirellula marina DSM 3645]
108	NP_865160	32472166	6-phosphogluconate dehydrogenase [Rhodopirellula baltica SH 1]
109	AAW29923	56788282	6-phosphogluconate dehydrogenase [Mannheimia haemolytica]
110	AAW29924	56788284	6-phosphogluconate dehydrogenase [Mannheimia glucosida
111	AAW29925	56788286	6-phosphogluconate dehydrogenase [Pasteurella trehalosi]
112	NP_218771	15639322	6-phosphogluconate dehydrogenase [Treponema pallidum subsp. pallidum str. Nichols]
113	YP_148197	56420879	6-phosphogluconate dehydrogenase [Geobacillus kaustophi HTA426]
114	YP_356348	77918533	probable phosphogluconate dehydrogenase (decarboxylatin [Pelobacter carbinolicus DSM 2380]
115	NP_390267	50812264	6-phosphogluconate dehydrogenase [Bacillus subtilis subsp subtilis str. 168]
116	YP_092134	52786305	6-phosphogluconate dehydrogenase [Bacillus licheniformis ATCC 14580]
117	ZP_011...	89099010	6-phosphogluconate dehydrogenase [Bacillus sp. NRRL B-14911]
118	NP_691106	23097640	6-phosphogluconate dehydrogenase [Oceanobacillus iheyen HTE831]
119	YP_219832	62185047	6-phosphogluconate dehydrogenase [Chlamydophila abortu S26/3]
120	ZP_002...	47565365	6-phosphogluconate dehydrogenase, decarboxylating [Bacil cereus G9241]
121	YP_026451	49183199	6-phosphogluconate dehydrogenase [Bacillus anthracis str. Sterne]
122	YP_034514	49476731	6-phosphogluconate dehydrogenase [Bacillus thuringiensis serovar konkukian str. 97-27]
123	YP_081773	52145056	6-phosphogluconate dehydrogenase [Bacillus cereus E33L]
124	YP_515493	89898383	6-phosphogluconate dehydrogenase [Chlamydophila felis Fe/C-56]
125	NP_814782	29375628	6-phosphogluconate dehydrogenase [Enterococcus faecalis V583]
126	ZP_003...	65317607	COG0362: 6-phosphogluconate dehydrogenase [Bacillus anthracis str. A2012]
127	YP_175422	56963691	6-phosphogluconate dehydrogenase [Bacillus clausii KSM-K16]
128	ZP_006...	69247351	6-phosphogluconate dehydrogenase, decarboxylating [Enterococcus faecium DO]

129	NP_810135	29346632	6-phosphogluconate dehydrogenase [Bacteroides thetaiotaomicron VPI-5482]
130	NP_829300	29840194	6-phosphogluconate dehydrogenase [Chlamydophila caviae GPIC]
131	AAL76325	18644678	6-phosphogluconate dehydrogenase [Porphyra yezoensis]
132	YP_546705	91776949	6-phosphogluconate dehydrogenase, decarboxylating [Methylobacillus flagellatus KT]
133	ZP_004...	67546118	6-phosphogluconate dehydrogenase, decarboxylating [Burkholderia vietnamiensis G4]
134	Q9CHU6	18202802	6-phosphogluconate dehydrogenase, decarboxylating
135	ZP_006...	74014955	6-phosphogluconate dehydrogenase, decarboxylating [Burkholderia ambifaria AMMD]
136	YP_372936	78063028	6-phosphogluconate dehydrogenase [Burkholderia sp. 383]
137	YP_624314	107026803	6-phosphogluconate dehydrogenase, decarboxylating [Burkholderia cenocepacia AU 1054]
138	NP_928851	37525507	6-phosphogluconate dehydrogenase [Photorhabdus luminescens subsp. laumondii TTO1]
139	ZP_002...	47095960	6-phosphogluconate dehydrogenase, decarboxylating [Liste monocytogenes str. 1/2a F6854]
140	YP_438830	83717630	6-phosphogluconate dehydrogenase, decarboxylating [Burkholderia thailandensis E264]
141	P96789	8134294	6-phosphogluconate dehydrogenase, decarboxylating
142	NP_924063	37520686	6-phosphogluconate dehydrogenase [Gloeobacter violaceus PCC 7421]
143	AAA24207	146938	6-phosphogluconate dehydrogenase
144	ZP_009...	84360352	COG0362: 6-phosphogluconate dehydrogenase [Burkholde dolosa AUO158]
145	YP_335987	76817886	6-phosphogluconate dehydrogenase [Burkholderia pseudomallei 1710b]
146	AAA24495	147501	6-phosphogluconate dehydrogenase
147	NP_310857	15832084	6-phosphogluconate dehydrogenase [Escherichia coli O157:H7 str. Sakai]
148	ZP_009...	83571257	COG0362: 6-phosphogluconate dehydrogenase [Shigella dysenteriae 1012]
149	ZP_007...	75229110	COG0362: 6-phosphogluconate dehydrogenase [Escherichi coli B7A]
150	ZP_013...	100915196	hypothetical protein Bmal10_03003493 [Burkholderia mall 10399]
151	AAG35219	11464518	6-phosphogluconate dehydrogenase [Escherichia coli]
152	ZP_013...	100236192	hypothetical protein Bpse4_03000697 [Burkholderia pseudomallei 406e]
153	YP_669972	110642242	6-phosphogluconate dehydrogenase, decarboxylating [Escherichia coli 536]
154	ZP_013...	100062231	hypothetical protein BpseP_03002198 [Burkholderia pseudomallei Pasteur]
155	YP_114383	53803994	6-phosphogluconate dehydrogenase [Methylococcus capsulatus str. Bath]
156	AAA24208	146940	6-phosphogluconate dehydrogenase
157	YP_310991	74312572	gluconate-6-phosphate dehydrogenase, decarboxylating [Shigella sonnei Ss046]
158	ZP_003...	48870455	COG0362: 6-phosphogluconate dehydrogenase [Pediococci pentosaceus ATCC 25745]
159	ZP_007...	75514070	COG0362: 6-phosphogluconate dehydrogenase [Escherichi

			coli 53638]
160	YP_049550	50120383	6-phosphogluconate dehydrogenase [Erwinia carotovora subsp. atroseptica SCRI1043]
161	AP_002630	89108850	gluconate-6-phosphate dehydrogenase, decarboxylating [Escherichia coli W3110]
162	ZP_007...	75259178	COG0362: 6-phosphogluconate dehydrogenase [Escherichi coli E22]
163	YP_541301	91211315	6-phosphogluconate dehydrogenase, decarboxylating [Escherichia coli UTI89]
164	YP_013993	46907604	6-phosphogluconate dehydrogenase [Listeria monocytogen str. 4b F2365]
165	YP_403788	82777439	gluconate-6-phosphate dehydrogenase [Shigella dysenteriae Sd197]
166	ZP_009...	83588030	COG0362: 6-phosphogluconate dehydrogenase [Escherichi coli 101-1]
167	AAD50492	5739470	6-phosphogluconate dehydrogenase Gnd [Escherichia coli]
168	ZP_006...	75177157	COG0362: 6-phosphogluconate dehydrogenase [Shigella boydii BS512]
169	AAA24209	146942	6-phosphogluconate dehydrogenase
170	AAG35221	11464522	6-phosphogluconate dehydrogenase [Escherichia coli]
171	ZP_007...	75186836	COG0362: 6-phosphogluconate dehydrogenase [Escherichi coli E24377A]
172	YP_689521	110806001	gluconate-6-phosphate dehydrogenase [Shigella flexneri 5 s 8401]
173	ZP_008...	77959279	COG0362: 6-phosphogluconate dehydrogenase [Yersinia bercovieri ATCC 43970]
174	AAG35224	11464528	6-phosphogluconate dehydrogenase [Escherichia coli]
175	ZP_007...	77636293	COG0362: 6-phosphogluconate dehydrogenase [Yersinia pestis Angola]
176	ZP_008...	77962467	COG0362: 6-phosphogluconate dehydrogenase [Yersinia mollaretii ATCC 43969]
177	ZP_008...	77978861	COG0362: 6-phosphogluconate dehydrogenase [Yersinia intermedia ATCC 29909]
178	AAG35218	11464516	6-phosphogluconate dehydrogenase [Escherichia coli]
179	BAA77736	4867927	6-phosphogluconate dehydrogenase [Escherichia coli]
180	AAA24490	147491	6-phosphogluconate dehydrogenase
181	YP_648367	108812600	6-phosphogluconate dehydrogenase, decarboxylating [Yersinia pestis Nepal516]
182	NP_669932	22126509	6-phosphogluconate dehydrogenase [Yersinia pestis KIM]
183	AAA23918	146232	6-phosphogluconate dehydrogenase (EC 1.1.1.44)
184	CAJ71042	91203389	strongly similar to 6-phosphogluconate dehydrogenase (decarboxylating) [Candidatus Kuenenia stuttgartiensis]
185	AAA24206	146936	6-phosphogluconate dehydrogenase
186	AAA24494	147499	6-phosphogluconate dehydrogenase
187	AAA24492	147495	6-phosphogluconate dehydrogenase
188	YP_099135	53713143	6-phosphogluconate dehydrogenase [Bacteroides fragilis YCH46]
189	AAA23925	146246	6-phosphogluconate dehydrogenase
190	YP_211552	60681408	6-phosphogluconate dehydrogenase [Bacteroides fragilis NCTC 9343]
191	AAV74381	56122509	Gnd [Escherichia coli]
192	NP_992794	45441255	6-phosphogluconate dehydrogenase [Yersinia pestis biovar Microtus str. 91001]

193	YP_650749	108806833	6-phosphogluconate dehydrogenase, decarboxylating [Yersinia pestis Antiqua]
194	NP_876643	33241702	6-phosphogluconate dehydrogenase [Chlamydophila pneumoniae TW-183]
195	NP_357929	15902379	6-phosphogluconate dehydrogenase [Streptococcus pneumoniae R6]
196	ZP_014...	111658214	hypothetical protein SpneT_02000606 [Streptococcus pneumoniae TIGR4]
197	NP_782446	28211502	6-phosphogluconate dehydrogenase [Clostridium tetani E8
198	AAG35223	11464526	6-phosphogluconate dehydrogenase [Escherichia coli]
199	AAA24493	147497	6-phosphogluconate dehydrogenase
200	ZP_007...	75214880	COG0362: 6-phosphogluconate dehydrogenase [Escherichi coli E110019]

Table 72. Examples of Fructose 1,6 bisphosphatase polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_500111	50545147	hypothetical protein [Yarrowia lipolytica].
2	AAP85294	32492043	fructose-1,6-bisphosphatase [Yarrowia lipolytica]
3	XP_460410	50423651	hypothetical protein DEHA0F01309g [Debaryomyces hansenii CBS767]
4	CAC69139	15528447	putative fructose-1,6-bisphosphatase [Pichia anomala]
5	XP_447425	50289987	hypothetical protein CAGL0I04048g [Candida glabrata CBS138]
6	NP_986140	45199111	AFR593Cp [Eremothecium gossypii]
7	XP_454003	50308005	F16P_KLULA [Kluyveromyces lactis]
8	EAT78213	111057093	predicted protein [Phaeosphaeria nodorum SN15]
9	XP_710934	68490480	fructose-1,6-bisphosphatase [Candida albicans SC5314]
10	AAT92835	51013083	YLR377C [Saccharomyces cerevisiae]
11	XP_364050	39954137	hypothetical protein MG08895.4 [Magnaporthe grisea 70-1
12	NP_001...	68006542	fructose-1,6-bisphosphatase [Schizosaccharomyces pombe 972h-]
13	NP_595083	19111875	hypothetical protein SPBC1198.14c [Schizosaccharomyces pombe 972h-]
14	XP_751698	70993702	fructose-1,6-bisphosphatase [Aspergillus fumigatus Af293]
15	XP_447010	50289161	unnamed protein product [Candida glabrata]
16	BAE58185	83768046	unnamed protein product [Aspergillus oryzae]
17	EAQ84924	88177456	conserved hypothetical protein [Chaetomium globosum CB 148.51]
18	AAF34693	6980006	fructose 1,6-bisphosphatase [Candida albicans]
19	BAB12208	9955389	fructose-1,6-bisphosphatase [Aspergillus oryzae]
20	XP_663208	67538868	hypothetical protein AN5604.2 [Aspergillus nidulans FGSC A4]
21	XP_389456	46134281	conserved hypothetical protein [Gibberella zeae PH-1]
22	XP_960423	85097320	hypothetical protein [Neurospora crassa OR74A]
23	EAS36192	90306561	fructose-1,6-bisphosphatase [Coccidioides immitis RS]
24	XP_566475	58258125	fructose-bisphosphatase [Cryptococcus neoformans var. neoformans JEC21]
25	XP_758850	71015920	hypothetical protein UM02703.1 [Ustilago maydis 521]
26	P14766	119748	Fructose-1,6-bisphosphatase, cytosolic (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
27	AAZ86538	73811203	fructose 1,6-bisphosphatase [Brassica rapa subsp. pekinensi
28	Q9MA79	75312318	Fructose-1,6-bisphosphatase, cytosolic (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
29	Q9SDL8	75313310	Fructose-1,6-bisphosphatase, cytosolic (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
30	BAD81916	56785198	fructose-1,6-bisphosphatase [Oryza sativa (japonica cultivar group)]
31	P46267	1169585	Fructose-1,6-bisphosphatase, cytosolic (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
32	P46276	1169586	Fructose-1,6-bisphosphatase, cytosolic (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase) (CY-F1)
33	Q8RW99	75303233	Fructose-1,6-bisphosphatase, cytosolic (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
34	Q43139	76363515	Fructose-1,6-bisphosphatase, cytosolic (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
35	CAB46084	5305145	fructose-1,6-bisphosphatase [Pisum sativum]

36	BAF06820	113534437	Os01g0866400 [Oryza sativa (japonica cultivar-group)]
37	Q42649	76789650	Fructose-1,6-bisphosphatase, cytosolic (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
38	Q9XF47	75315047	Fructose-1,6-bisphosphatase, cytosolic (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
39	CAA61409	895909	fructose-1, 6-bisphosphatase [Saccharum hybrid cultivar H 7052]
40	1906373A	444324	cytosolic fructose bisphosphatase
41	EAR87347	89289359	fructose-1,6-bisphosphatase family protein [Tetrahymena thermophila SB210]
42	NP_915641	34908588	fructose-1,6-bisphosphatase [Oryza sativa (japonica cultiva group)]
43	XP_475314	50931573	putative fructose-1,6-bisphosphatase [Oryza sativa (japonic cultivar-group)]
44	NP_491004	17508131	K07A3.1 [Caenorhabditis elegans]
45	XP_782411	72013871	PREDICTED: similar to fructose-1,6-bisphosphatase 1, lik [Strongylocentrotus purpuratus]
46	CAE60538	39595500	Hypothetical protein CBG04165 [Caenorhabditis briggsae]
47	NP_610001	19921562	fructose-1,6-bisphosphatase CG31692-PA, isoform A [Drosophila melanogaster]
48	NP_724223	45550998	fructose-1,6-bisphosphatase CG31692-PB, isoform B [Drosophila melanogaster]
49	XP_319937	58393257	ENSANGP00000016841 [Anopheles gambiae str. PEST]
50	AAN31471	23394363	fructose-1 6-biphosphatase [Phytophthora infestans]
51	XP_425040	50762393	PREDICTED: similar to fructose 1,6-bisphosphatase [Gallu gallus]
52	EAT47721	108883496	fructose-1,6-bisphosphatase [Aedes aegypti]
53	EAT47722	108883497	fructose-1,6-bisphosphatase [Aedes aegypti]
54	AAH53784	32450356	Fbp-prov protein [Xenopus laevis]
55	YP_001659	45657573	fructose-1,6-bisphosphatase [Leptospira interrogans serova Copenhageni str. Fiocruz L1-130]
56	NP_989145	45361017	Fructose-1,6-bisphosphatase [Xenopus tropicalis]
57	1YZ0B	62738852	Chain B, R-State Amp Complex Reveals Initial Steps Of Tl Quaternary Transition Of Fructose-1,6-Bisphosphatase
58	1Q9DB	39654661	Chain B, Fructose-1,6-Bisphosphatase Complexed With A New Allosteric Site Inhibitor (I-State)
59	NP_999144	47522784	fructose 1,6-bisphosphatase [Sus scrofa]
60	EAL32807	54644065	GA16400-PA [Drosophila pseudoobscura]
61	XP_848306	73946392	PREDICTED: similar to fructose-1,6-bisphosphatase 1 isoform 3 [Canis familiaris]
62	1FJ9B	11514534	Chain B, Fructose-1,6-Bisphosphatase (Mutant Y57w) ProductsZNAMP Complex (T-State)
63	1LEVF	24987566	Chain F, Porcine Kidney Fructose-1,6-Bisphosphatase Complexed With An Amp-Site Inhibitor
64	1BK4A	6729708	Chain A, Crystal Structure Of Rabbit Liver Fructose-1,6-Bisphosphatase At 2.3 Angstrom Resolution
65	Q3SZB7	110808224	Fructose-1,6-bisphosphatase 1 (D-fructose-1,6-bisphosphat 1-phosphohydrolase 1) (FBPase 1)
66	AAA41131	310111	fructose-biphosphatase
67	P46275	2506391	Fructose-1,6-bisphosphatase, chloroplast precursor (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
68	2F3HB	99032142	Chain B, Mechanism Of Displacement Of A Catalytically Essential Loop From The Active Site Of Fructose-1,6-

			Bisphosphatase
69	NP_036690	51036635	fructose-1,6- biphosphatase 1 [Rattus norvegicus]
70	AAC25597	3288991	fructose-1,6-bisphosphatase [Sus scrofa]
71	XP_967802	91077758	PREDICTED: similar to CG31692-PA, isoform A [Triboli castaneum]
72	AAK59929	14318171	fructose-1,6-bisphosphatase [Pisum sativum]
73	1DCUD	6730314	Chain D, Redox Signaling In The Chloroplast: Structure O Oxidized Pea Fructose-1,6-Bisphosphate Phosphatase
74	1DBZD	6730306	Chain D, C153s Mutant Of Pea Fructose-1,6-Bisphosphata
75	CAB39759	4539148	fructose-1,6-bisphosphatase [Pisum sativum]
76	P09199	20141075	Fructose-1,6-bisphosphatase 1 (D-fructose-1,6-bisphosphat 1-phosphohydrolase 1) (FBPase 1)
77	CAA48719	20717	fructose-bisphosphatase [Pisum sativum]
78	1FPIB	1633402	Chain B, Fructose-1,6-Bisphosphatase (D-Fructose-1,6-Bisphosphate 1-Phosphohydrolase) Complexed With Amp, 2,5-Anhydro-D-Glucitol-1,6-Bisphosphate And Potassium Ions (100 Mm)
79	AAB30523	546354	fructose-1,6-biphosphatase, FBPase {EC 3.1.3.11} [Pisum sativum=peas, Lincoln, Peptide Chloroplast, 357 aa]
80	1KZ8F	24987484	Chain F, Crystal Structure Of Porcine Fructose-1,6-Bisphosphatase Complexed With A Novel Allosteric-Site Inhibitor
81	AAW25416	56754457	SJCHGC06706 protein [Schistosoma japonicum]
82	1FRPB	809402	Chain B, Fructose-1,6-Bisphosphatase (D-Fructose-1,6-Bisphosphate 1-Phosphohydrolase) (E.C.3.1.3.11) Comple With Fructose-2,6-Bisphosphate, Adenosine Monophospha (Amp), And Zinc
83	XP_425039	50762391	PREDICTED: similar to fructose-1,6-bisphosphatase [Gall gallus]
84	NP_998297	47085885	fructose-1,6-bisphosphatase 1 [Danio rerio]
85	1RDZB	1942591	Chain B, T-State Structure Of The Arg 243 To Ala Mutant Pig Kidney Fructose 1,6-Bisphosphatase Expressed In E. C
86	1FSAB	2554913	Chain B, The T-State Structure Of Lys 42 To Ala Mutant C The Pig Kidney Fructose 1,6-Bisphosphatase Expressed In Coli
87	BAE28940	74146344	unnamed protein product [Mus musculus]
88	CAG05216	47228396	unnamed protein product [Tetraodon nigroviridis]
89	NP_956236	41053949	fructose-1,6-bisphosphatase 1, like [Danio rerio]
90	Q07204	585118	Fructose-1,6-bisphosphatase, chloroplast precursor (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
91	BAF11578	113548135	Os03g0267300 [Oryza sativa (japonica cultivar-group)]
92	2FIXL	90109451	Chain L, Structure Of Human Liver Fbpase Complexed Wi Potent Benzoxazole Allosteric Inhibitiors
93	2FHYL	90109424	Chain L, Structure Of Human Liver Fpbase Complexed Wi A Novel Benzoxazole As Allosteric Inhibitor
94	XP_001...	109112377	PREDICTED: fructose-1,6-bisphosphatase 1 isoform 2 [Macaca mulatta]
95	1FTAD	1311149	Chain D, Fructose-1,6-Bisphosphatase(D-Fructose-1,6-Bisphosphate, 1-Phosphohydrolase) (E.C.3.1.3.11) Comple With The Allosteric Inhibitor Amp
96	CAH72692	55662224	fructose-1,6-bisphosphatase 1 [Homo sapiens]
97	CAG08190	47221528	unnamed protein product [Tetraodon nigroviridis]
98	XP_533504	73946534	PREDICTED: similar to Fructose-1,6-bisphosphatase isozy

			2 (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBP [Canis familiaris]
99	AAC25774	3293553	fructose-1,6-bisphosphatase [Homo sapiens]
100	AAA35817	182311	fructose-1,6-bisphosphatase
101	AAD12243	4218951	fructose-1,6-bisphosphatase precursor [Brassica napus]
102	NP_001...	114051459	hypothetical protein LOC514066 [Bos taurus]
103	P09195	119745	Fructose-1,6-bisphosphatase, chloroplast precursor (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
104	NP_001...	57524507	hypothetical protein LOC445505 [Danio rerio]
105	NP_001...	114051287	fructose-1,6-bisphosphatase [Bombyx mori]
106	NP_001...	73853862	hypothetical protein LOC613108 [Xenopus tropicalis]
107	AAD25541	4585576	fructose-1,6-bisphosphatase precursor [Solanum tuberosum
108	Q9N0J6	75067927	Fructose-1,6-bisphosphatase isozyme 2 (D-fructose-1,6-bisphosphate 1-phosphohydrolase 2) (FBPase 2)
109	AAN31884	23397203	putative fructose-bisphosphatase precursor [Arabidopsis thaliana]
110	AAH81229	51703601	Unknown (protein for MGC:85456) [Xenopus laevis]
111	P22418	3915687	Fructose-1,6-bisphosphatase, chloroplast precursor (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
112	CAA41154	11242	fructose-bisphosphatase [Arabidopsis thaliana]
113	XP_001...	109112375	PREDICTED: fructose-1,6-bisphosphatase 1 isoform 1 [Macaca mulatta]
114	P70695	76363514	Fructose-1,6-bisphosphatase isozyme 2 (D-fructose-1,6-bisphosphate 1-phosphohydrolase 2) (FBPase 2) (RAE-30)
115	CAG08189	47221527	unnamed protein product [Tetraodon nigroviridis]
116	AAI13633	109731177	Fructose-1,6-bisphosphatase 2 [Homo sapiens]
117	1SPID	999624	Chain D, Fructose-1,6-Bisphosphatase (D-Fructose-1,6-Bisphosphate 1-Phosphohydrolase) (E.C.3.1.3.11)
118	AAF72973	8118281	fructose-1,6-bisphosphatase [Zaocys dhumnades]
119	AAH12720	15215255	Fbp2 protein [Mus musculus]
120	O00757	76789651	Fructose-1,6-bisphosphatase isozyme 2 (D-fructose-1,6-bisphosphate 1-phosphohydrolase 2) (FBPase 2)
121	XP_827196	71745132	fructose-1,6-bisphosphate cytosolic [Trypanosoma brucei TREU927]
122	Q9Z1N1	76364186	Fructose-1,6-bisphosphatase isozyme 2 (D-fructose-1,6-bisphosphate 1-phosphohydrolase 2) (FBPase 2)
123	BAE40306	74212301	unnamed protein product [Mus musculus]
124	CAC70747	15718373	fructose-1,6-bisphosphatase [Trypanosoma brucei]
125	NP_032020	6679761	fructose bisphosphatase 2 [Mus musculus]
126	AAP79192	32307574	fructose-1,6 bisphosphatase [Bigelowiella natans]
127	ZP_010...	86130901	fructose-1,6-bisphosphatase [Cellulophaga sp. MED134]
128	YP_422024	83311760	Fructose-1,6-bisphosphatase [Magnetospirillum magneticur AMB-1]
129	YP_679484	110639275	fructose-1,6-bisphosphatase [Cytophaga hutchinsonii ATC(33406]
130	ZP_000...	23014308	COG0158: Fructose-1,6-bisphosphatase [Magnetospirillum magnetotacticum MS-1]
131	XP_888627	76363832	Leishmania major strain Friedlin cytosolic fructose-1,6-bisphosphatase [Leishmania major strain Friedlin]
132	ZP_009...	83855881	fructose-1,6-bisphosphatase [Croceibacter atlanticus HTCC2559]
133	YP_437516	83649081	Fructose-1,6-bisphosphatase [Hahella chejuensis KCTC 23
134	ZP_011...	88711300	fructose-1,6-bisphosphatase [Flavobacteriales bacterium

			HTCC2170]
135	CAC82800	16519317	fructose 1,6-bisphosphatase [Galdieria sulphuraria]
136	ZP_012...	91215105	fructose-1,6-bisphosphatase [Psychroflexus torquis ATCC 700755]
137	ZP_012...	90591576	Inositol phosphatase/fructose-1,6-bisphosphatase [Flavobacterium johnsoniae UW101]
138	XP_793452	72046390	PREDICTED: similar to fructose-1,6-bisphosphatase 1, lik [Strongylocentrotus purpuratus]
139	CAJ72223	91202584	strongly similar to fructose-1,6-bisphosphatase [Candidatus Kuenenia stuttgartiensis]
140	ZP_011...	88804197	fructose-1,6-bisphosphatase [Robiginitalea biformata HTCC2501]
141	YP_445598	83815956	fructose-1,6-bisphosphatase [Salinibacter ruber DSM 1385
142	ZP_007...	75815977	COG0158: Fructose-1,6-bisphosphatase [Vibrio cholerae V
143	ZP_011...	88802508	fructose-1,6-bisphosphatase [Polaribacter irgensii 23-P]
144	ZP_007...	75827798	COG0158: Fructose-1,6-bisphosphatase [Vibrio cholerae O395]
145	ZP_011...	88797163	Fructose-1,6-bisphosphatase [Reinekea sp. MED297]
146	ZP_005...	68553442	Inositol phosphatase/fructose-1,6-bisphosphatase [Prosthecochloris aestuarii DSM 271]
147	ZP_007...	75830525	COG0158: Fructose-1,6-bisphosphatase [Vibrio cholerae MO10]
148	Q42796	2494415	Fructose-1,6-bisphosphatase, chloroplast precursor (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
149	ZP_007...	75822783	COG0158: Fructose-1,6-bisphosphatase [Vibrio cholerae RC385]
150	NP_933227	37678618	fructose-1,6-bisphosphatase [Vibrio vulnificus YJ016]
151	XP_812636	71423971	fructose-1,6-bisphosphatase, cytosolic [Trypanosoma cruzi strain CL Brener]
152	ZP_006...	71480926	Inositol phosphatase/fructose-1,6-bisphosphatase [Prosthecochloris vibrioformis DSM 265]
153	ZP_007...	75854570	COG0158: Fructose-1,6-bisphosphatase [Vibrio sp. Ex25]
154	NP_931714	37528369	fructose-1,6-bisphosphatase [Photorhabdus luminescens subsp. laumondii TTO1]
155	XP_805839	71406635	fructose-1,6-bisphosphatase, cytosolic [Trypanosoma cruzi strain CL Brener]
156	YP_374392	78186349	fructose-1,6-bisphosphatase [Pelodictyon luteolum DSM 27
157	NP_902097	34497882	fructose-1,6-bisphosphatase [Chromobacterium violaceum ATCC 12472]
158	XP_646323	66825937	D-fructose-1,6-bisphosphate 1-phosphohydrolase [Dictyostelium discoideum AX4]
159	ZP_010...	86147594	fructose-1,6-bisphosphatase [Vibrio sp. MED222]
160	NP_796691	28897086	fructose-1,6-bisphosphatase [Vibrio parahaemolyticus RIM 2210633]
161	YP_052014	50122847	fructose-1,6-bisphosphatase [Erwinia carotovora subsp. atroseptica SCRI1043]
162	ZP_007...	77634762	COG0158: Fructose-1,6-bisphosphatase [Yersinia pestis Angola]
163	ZP_012...	90406722	fructose-1,6-bisphosphatase [Psychromonas sp. CNPT3]
164	ZP_006...	71549000	Inositol phosphatase/fructose-1,6-bisphosphatase [Nitrosomonas eutropha C71]
165	ZP_013...	106882698	Inositol phosphatase/fructose-1,6-bisphosphatase [Psychromonas ingrahamii 37]

166	ZP_008...	77973994	COG0158: Fructose-1,6-bisphosphatase [Yersinia frederiksenii ATCC 33641]
167	ZP_012...	90411963	fructose-1,6-bisphosphatase [Photobacterium profundum 3TCK]
168	ZP_005...	67938188	Inositol phosphatase/fructose-1,6-bisphosphatase [Chlorobi phaeobacteroides BS1]
169	NP_991956	45440417	fructose-1,6-bisphosphatase [Yersinia pestis biovar Microtu str. 91001]
170	NP_840606	30248536	fructose-1,6-bisphosphatase [Nitrosomonas europaea ATC(19718]
171	YP_649191	108813424	fructose-1,6-bisphosphatase [Yersinia pestis Nepal516]
172	ZP_010...	86134593	fructose-1,6-bisphosphatase [Tenacibaculum sp. MED152]
173	ZP_012...	94268582	Inositol phosphatase/fructose-1,6-bisphosphatase [delta proteobacterium MLMS-1]
174	ZP_012...	94264279	Inositol phosphatase/fructose-1,6-bisphosphatase [delta proteobacterium MLMS-1]
175	ZP_005...	67919158	Inositol phosphatase/fructose-1,6-bisphosphatase [Chlorobi limicola DSM 245]
176	NP_661262	21673197	fructose-1,6-bisphosphatase [Chlorobium tepidum TLS]
177	YP_128618	54307598	fructose-1,6-bisphosphatase [Photobacterium profundum S5
178	YP_378918	78188580	fructose-1,6-bisphosphatase [Chlorobium chlorochromatii CaD3]
179	ZP_005...	68551142	Inositol phosphatase/fructose-1,6-bisphosphatase [Pelodicty phaeoclathratiforme BU-1]
180	YP_445968	83814754	fructose-1,6-bisphosphatase [Salinibacter ruber DSM 13855
181	ZP_012...	90580816	fructose-1,6-bisphosphatase [Vibrio angustum S14]
182	ZP_011...	89075542	fructose-1,6-bisphosphatase [Photobacterium sp. SKA34]
183	YP_342093	77163568	fructose-1,6-bisphosphatase [Nitrosococcus oceani ATCC 19707]
184	ZP_009...	84387793	fructose-1,6-bisphosphatase [Vibrio splendidus 12B01]
185	ZP_010...	86141292	fructose-1,6-bisphosphatase [Flavobacterium sp. MED217]
186	ZP_005...	67937321	Inositol phosphatase/fructose-1,6-bisphosphatase [Chlorobi phaeobacteroides DSM 266]
187	ZP_012...	91228829	fructose-1,6-bisphosphatase [Vibrio alginolyticus 12G01]
188	ZP_008...	77961846	COG0158: Fructose-1,6-bisphosphatase [Yersinia mollareti ATCC 43969]
189	ZP_008...	77977605	COG0158: Fructose-1,6-bisphosphatase [Yersinia intermedi ATCC 29909]
190	YP_203647	59710871	fructose-1,6-bisphosphatase [Vibrio fischeri ES114]
191	ZP_013...	110596824	Inositol phosphatase/fructose-1,6-bisphosphatase [Chlorobi ferrooxidans DSM 13031]
192	YP_454036	85058334	fructose-1,6-bisphosphatase [Sodalis glossinidius str. 'morsitans']
193	ZP_001...	32035025	COG0158: Fructose-1,6-bisphosphatase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]
194	YP_011058	46580250	fructose-1,6-bisphosphatase [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]
195	YP_219276	62182859	fructose-1,6-bisphosphatase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
196	YP_560077	91784871	Inositolphosphatase/fructose-1,6-bisphosphatase [Burkholderia xenovorans LB400]
197	YP_316335	74318595	fructose-1,6-bisphosphatase [Thiobacillus denitrificans AT(25259]

198	YP_388561	78357112	fructose-1,6-bisphosphatase [Desulfovibrio desulfuricans G20]
199	NP_313236	15834463	fructose-1,6-bisphosphatase [Escherichia coli O157:H7 str. Sakai]
200	YP_313128	74314709	fructose-bisphosphatase [Shigella sonnei Ss046]
201	ZP_011...	88801533	fructose-1,6-bisphosphatase [Polaribacter irgensii 23-P]

Table 73. Examples of soluble transydrogenase polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	AAD40691	5163507	soluble pyridine nucleotide transhydrogenase [Azotobacter vinelandii
2	ZP_013...	107102541	hypothetical protein PaerPA_01003605 [Pseudomonas aeruginosa PACS2]
3	ZP_012...	94416745	hypothetical protein PaerP_01001583 [Pseudomonas aeruginc PA7]
4	O05139	11135075	Soluble pyridine nucleotide transhydrogenase (STH) (NAD(P)(+) transhydrogenase [B-specific])
5	YP_259077	70729340	soluble pyridine nucleotide transhydrogenase [Pseudomonas fluorescens Pf-5]
6	YP_349590	77460083	soluble pyridine nucleotide transhydrogenase [Pseudomonas fluorescens PfO-1]
7	YP_274087	71735155	soluble pyridine nucleotide transhydrogenase [Pseudomonas syringae pv. phaseolicola 1448A]
8	YP_234983	66045142	soluble pyridine nucleotide transhydrogenase [Pseudomonas syringae pv. syringae B728a]
9	YP_609219	104782721	soluble pyridine nucleotide transhydrogenase (NAD(P)(+) transhydrogenase [B-specific]) [Pseudomonas entomophila L4
10	Q884I6	38258471	Soluble pyridine nucleotide transhydrogenase (STH) (NAD(P)(+) transhydrogenase [B-specific])
11	ZP_009...	82739140	soluble pyridine nucleotide transhydrogenase [Pseudomonas putida F1]
12	YP_573629	92113701	pyridine nucleotide-disulphide oxidoreductase dimerisation region [Chromohalobacter salexigens DSM 3043]
13	ZP_008...	77951906	NAD(P) transhydrogenase [Marinobacter aquaeolei VT8]
14	YP_433907	83645472	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzyme [Hahella chejuensis KCTC 2396]
15	ZP_011...	89094310	soluble pyridine nucleotide transhydrogenase [Oceanospirillur sp. MED92]
16	ZP_013...	94499566	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzyme [Oceanobacter sp. RED65]
17	ZP_011...	88800089	soluble pyridine nucleotide transhydrogenase [Reinekea sp. MED297]
18	ZP_010...	87121312	soluble pyridine nucleotide transhydrogenase [Marinomonas s MED121]
19	ZP_012...	90417525	soluble pyridine nucleotide transhydrogenase [marine gamma proteobacterium HTCC2207]
20	Q7MQ83	47606104	Soluble pyridine nucleotide transhydrogenase (STH) (NAD(P)(+) transhydrogenase [B-specific])
21	YP_527277	90021450	regulatory protein, ArsR [Saccharophagus degradans 2-40]

22	ZP_009...	83586194	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and relate enzymes [Escherichia coli 101-1]
23	YP_219002	62182585	soluble pyridine nucleotide transhydrogenase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
24	YP_543498	91213512	soluble pyridine nucleotide transhydrogenase [Escherichia co UTI89]
25	Q87KN5	33301640	Soluble pyridine nucleotide transhydrogenase (STH) (NAD(P)(+) transhydrogenase [B-specific])
26	YP_153038	56415963	soluble pyridine nucleotide transhydrogenase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]
27	YP_672034	110644304	soluble pyridine nucleotide transhydrogenase [Escherichia co 536]
28	ZP_013...	106883834	FAD-dependent pyridine nucleotide-disulphide oxidoreductase:Pyridine nucleotide-disulphide oxidoreductas dimerisation region:FAD dependent oxidoreductase [Psychromonas ingrahamii 37]
29	ZP_006...	75176647	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and relate enzymes [Shigella boydii BS512]
30	Q8FB93	38258590	Soluble pyridine nucleotide transhydrogenase (STH) (NAD(P)(+) transhydrogenase [B-specific])
31	ZP_007...	75197835	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and relate enzymes [Escherichia coli HS]
32	ZP_007...	75513852	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and relate enzymes [Escherichia coli 53638]
33	Q8X727	21362954	Soluble pyridine nucleotide transhydrogenase (STH) (NAD(P)(+) transhydrogenase [B-specific])
34	YP_267100	71278420	soluble pyridine nucleotide transhydrogenase [Colwellia psychrerythraea 34H]
35	Q83MI1	39932373	Soluble pyridine nucleotide transhydrogenase (STH) (NAD(P)(+) transhydrogenase [B-specific])
36	ZP_007...	75238410	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and relate enzymes [Escherichia coli E110019]
37	ZP_007...	75854141	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and relate enzymes [Vibrio sp. Ex25]
38	YP_052329	50123162	soluble pyridine nucleotide transhydrogenase [Erwinia carotovora subsp. atroseptica SCRI1043]
39	ZP_008...	77973002	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and relate enzymes [Yersinia frederiksenii ATCC 33641]
40	ZP_008...	77957412	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and relate enzymes [Yersinia bercovieri ATCC 43970]
41	ZP_008...	78702791	NAD(P) transhydrogenase (B-specific) [Alkalilimnicola ehrlichei MLHE-1]

42	YP_645986	108810219	soluble pyridine nucleotide transhydrogenase [Yersinia pestis Nepal516]
43	ZP_007...	75828016	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and relate enzymes [Vibrio cholerae O395]
44	Q7MBG9	47606102	Soluble pyridine nucleotide transhydrogenase (STH) (NAD(P)(+) transhydrogenase [B-specific])
45	ZP_008...	77976809	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and relate enzymes [Yersinia intermedia ATCC 29909]
46	ZP_008...	77961066	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and relate enzymes [Yersinia mollaretii ATCC 43969]
47	ZP_010...	86148649	soluble pyridine nucleotide transhydrogenase [Vibrio sp. MED222]
48	YP_205822	59713046	soluble pyridine nucleotide transhydrogenase [Vibrio fischeri ES114]
49	ZP_009...	84394322	pyridine nucleotide-disulfide oxidoreductase, class I [Vibrio splendidus 12B01]
50	ZP_011...	89074500	soluble pyridine nucleotide transhydrogenase [Photobacterium sp. SKA34]
51	YP_154714	56459433	soluble pyridine nucleotide transhydrogenase [Idiomarina loihiensis L2TR]
52	YP_046885	50085375	soluble pyridine nucleotide transhydrogenase [Acinetobacter s ADP1]
53	ZP_012...	90581098	soluble pyridine nucleotide transhydrogenase [Vibrio angustu S14]
54	YP_693290	110834431	NAD(P) transhydrogenase [Alcanivorax borkumensis SK2]
55	ZP_011...	88795508	soluble pyridine nucleotide transhydrogenase [Alteromonas macleodii 'Deep ecotype']
56	ZP_012...	90407259	soluble pyridine nucleotide transhydrogenase [Psychromonas CNPT3]
57	E65203	7431869	probable dehydrogenase (EC 1.8.1.-) udhA - Escherichia coli (strain K-12)
58	YP_410260	82546313	putative oxidoreductase [Shigella boydii Sb227]
59	YP_312883	74314464	putative oxidoreductase [Shigella sonnei Ss046]
60	YP_131541	54310521	soluble pyridine nucleotide transhydrogenase [Photobacterium profundum SS9]
61	AAC43068	396309	ORF_f444 [Escherichia coli]
62	H86087	25284914	probable oxidoreductase udhA [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
63	ZP_012...	90414698	soluble pyridine nucleotide transhydrogenase [Photobacterium profundum 3TCK]

64	NP_709766	56480495	soluble pyridine nucleotide transhydrogenase [Shigella flexn 2a str. 301]
65	YP_405233	82778884	putative oxidoreductase [Shigella dysenteriae Sd197]
66	YP_691341	110807821	putative oxidoreductase [Shigella flexneri 5 str. 8401]
67	NP_667661	22124238	soluble pyridine nucleotide transhydrogenase [Yersinia pesti KIM]
68	YP_341375	77361800	soluble pyridine nucleotide transhydrogenase [Pseudoalteromonas haloplanktis TAC125]
69	YP_455837	85060135	soluble pyridine nucleotide transhydrogenase [Sodalis glossinidius str. 'morsitans']
70	ZP_012...	91771448	FAD-dependent pyridine nucleotide-disulphide oxidoreductase:Pyridine nucleotide-disulphide oxidoreductas dimerisation region:FAD dependent oxidoreductase [Psychrobacter sp. PRwf-1]
71	ZP_011...	88861405	soluble pyridine nucleotide transhydrogenase [Pseudoalteromonas tunicata D2]
72	YP_264617	71065890	soluble pyridine nucleotide transhydrogenase [Psychrobacter arcticus 273-4]
73	YP_580301	93005864	pyridine nucleotide-disulphide oxidoreductase dimerisation region [Psychrobacter cryohalolentis K5]
74	ZP_010...	85710769	soluble pyridine nucleotide transhydrogenase [Idiomarina bal OS145]
75	ZP_012...	91227486	soluble pyridine nucleotide transhydrogenase [Vibrio alginolyticus 12G01]
76	ZP_007...	75814072	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and relate enzymes [Vibrio cholerae V52]
77	YP_666832	110670275	soluble pyridine nucleotide transhydrogenase [Francisella tularensis subsp. tularensis FSC 198]
78	YP_169700	56707804	soluble pyridine nucleotide transhydrogenase [Francisella tularensis subsp. tularensis SCHU S4]
79	YP_513671	89256309	soluble pyridine nucleotide transhydrogenase [Francisella tularensis subsp. holarctica]
80	CAA46822	43237	udhA [Escherichia coli]
81	ZP_005...	67929855	FAD-dependent pyridine nucleotide-disulphide oxidoreductase:Pyridine nucleotide-disulphide oxidoreductas dimerisation region [Solibacter usitatus Ellin6076]
82	YP_592298	94970250	pyridine nucleotide-disulphide oxidoreductase [Acidobacteria bacterium Ellin345]
83	NP_961763	41408927	soluble pyridine nucleotide transhydrogenase [Mycobacterium avium subsp. paratuberculosis K-10]
84	P66006	54042093	Probable soluble pyridine nucleotide transhydrogenase (STH) (NAD(P)(+) transhydrogenase [B-specific])
85	ZP_007...	76783189	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and relate

			enzymes [Mycobacterium tuberculosis F11]
86	YP_716291	111225497	soluble pyridine nucleotide transhydrogenase [Frankia alni ACN14a]
87	ZP_005...	68235154	FAD-dependent pyridine nucleotide-disulphide oxidoreductase:Pyridine nucleotide-disulphide oxidoreductas dimerisation domain [Frankia sp. EAN1pec]
88	ZP_012...	90205475	FAD-dependent pyridine nucleotide-disulphide oxidoreductase:Pyridine nucleotide-disulphide oxidoreductas dimerisation region [Mycobacterium vanbaalenii PYR-1]
89	YP_482962	86742562	pyridine nucleotide-disulphide oxidoreductase dimerisation region [Frankia sp. CcI3]
90	NP_532346	17935556	soluble pyridine nucleotide transhydrogenase [Agrobacterium tumefaciens str. C58]
91	AAY87873	68165826	pyridine nucleotide-disulfide oxidoreductase class I [Vibrio cholerae]
92	AAY87863	68165806	pyridine nucleotide-disulfide oxidoreductase class I [Vibrio cholerae]
93	AAY87865	68165810	pyridine nucleotide-disulfide oxidoreductase class I [Vibrio cholerae]
94	YP_469365	86357473	probable pyridine nucleotide transhydrogenase protein [Rhizobium etli CFN 42]
95	ZP_010...	85706062	soluble pyridine nucleotide transhydrogenase [Roseovarius sp 217]
96	ZP_014...	113873124	putative soluble pyridine nucleotide transhydrogenase [Sinorhizobium medicae WSM419]
97	NP_385835	15965482	soluble pyridine nucleotide transhydrogenase [Sinorhizobium meliloti 1021]
98	YP_169016	56698639	soluble pyridine nucleotide transhydrogenase [Silicibacter pomeroyi DSS-3]
99	ZP_009...	83951172	soluble pyridine nucleotide transhydrogenase [Roseovarius nubinhibens ISM]
100	YP_611681	99078423	pyridine nucleotide-disulphide oxidoreductase dimerisation region [Silicibacter sp. TM1040]
101	ZP_010...	86140117	soluble pyridine nucleotide transhydrogenase [Roseobacter sp MED193]
102	BAB53939	14027670	soluble pyridine nucleotide transhydrogenase [Mesorhizobium loti MAFF303099]
103	YP_630631	108762684	NAD(P) transhydrogenase (B-specific) [Myxococcus xanthus DK 1622]
104	YP_467034	86160249	FAD-dependent pyridine nucleotide-disulphide oxidoreductas [Anaeromyxobacter dehalogenans 2CP-C]
105	YP_007724	46446359	soluble pyridine nucleotide transhydrogenase [Candidatus Protochlamydia amoebophila UWE25]
106	YP_433307	83644872	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and relate enzyme [Hahella chejuensis KCTC 2396]

107	YP_527988	90022161	soluble pyridine nucleotide transhydrogenase [Saccharophagı degradans 2-40]
108	ZP_005...	67931474	FAD-dependent pyridine nucleotide-disulphide oxidoreductase:Pyridine nucleotide-disulphide oxidoreductas dimerisation region [Solibacter usitatus Ellin6076]
109	YP_575887	92116158	Dihydrolipoamide dehydrogenase [Nitrobacter hamburgensis X14]
110	NP_539063	17986429	dihydrolipoamide dehydrogenase [Brucella melitensis 16M]
111	NP_698895	23502768	dihydrolipoamide dehydrogenase [Brucella suis 1330]
112	YP_415258	82700684	Pyridine nucleotide-disulphide oxidoreductase, class-II:NAD binding site:Adrenodoxin reductase:Mercuric reductase:Pyric nu... [Brucella melitensis biovar Abortus 2308]
113	ZP_011...	88945707	Dihydrolipoamide dehydrogenase [Desulfotomaculum reduc MI-1]
114	YP_675936	110635728	dihydrolipoamide dehydrogenase [Mesorhizobium sp. BNC1]
115	YP_483896	86747400	Dihydrolipoamide dehydrogenase [Rhodopseudomonas palus HaA2]
116	ZP_006...	71836831	Dihydrolipoamide dehydrogenase [Pelobacter propionicus DS 2379]
117	BAB50985	14024381	ferric leghemoglobin reductase-2 precursor, dihydrolipoamid dehydrogenase [Mesorhizobium loti MAFF303099]
118	ZP_011...	88946629	Dihydrolipoamide dehydrogenase [Desulfotomaculum reduce MI-1]
119	YP_032854	49474812	dihydrolipoamide dehydrogenase [Bartonella quintana str. Toulouse]
120	YP_317044	75674623	dihydrolipoamide dehydrogenase [Nitrobacter winogradskyi 255]
121	ZP_012...	90421039	2-oxoglutarate dehydrogenase, E3 component, lipoamide dehydrogenase [Aurantimonas sp. SI85-9A1]
122	NP_533297	17936507	dihydrolipoamide dehydrogenase [Agrobacterium tumefacien str. C58]
123	AAR21288	38489206	2-oxoglutarate dehydrogenase E3 component [Bartonella henselae]
124	YP_034342	49476301	dihydrolipoamide dehydrogenase [Bartonella henselae str. Houston-1]
125	ZP_008...	78694497	Dihydrolipoamide dehydrogenase [Bradyrhizobium sp. BTAi
126	ZP_010...	85713709	dihydrolipoamide dehydrogenase [Nitrobacter sp. Nb-311A]
127	YP_471355	86359463	dihydrolipoamide dehydrogenase protein [Rhizobium etli CFI 42]
128	ZP_008...	77739670	Dihydrolipoamide dehydrogenase [Rhodopseudomonas palus BisA53]

129	NP_387154	15966801	dihydrolipoamide dehydrogenase [Sinorhizobium meliloti 10
130	YP_567689	91975030	Dihydrolipoamide dehydrogenase [Rhodopseudomonas palus BisB5]
131	ZP_009...	83750811	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and relate enzymes [Bartonella bacilliformis KC583]
132	NP_767089	27375560	dihydrolipoamide dehydrogenase [Bradyrhizobium japonicun USDA 110]
133	ZP_014...	113873546	dihydrolipoamide dehydrogenase [Sinorhizobium medicae WSM419]
134	ZP_011...	88801370	Pyruvate/2-oxoglutarate dehydrogenase complex [Polaribacte irgensii 23-P]
135	AAN03817	22652790	dihydrolipoamide dehydrogenase [Methylobacterium extorquens]
136	NP_945538	39933262	dihydrolipoamide dehydrogenase [Rhodopseudomonas palust CGA009]
137	ZP_010...	86142639	Dihydrolipoyl dehydrogenase [Flavobacterium sp. MED217]
138	YP_005669	46200002	dihydrolipoamide dehydrogenase [Thermus thermophilus HB
139	ZP_012...	90589077	Dihydrolipoamide dehydrogenase [Flavobacterium johnsonia UW101]
140	YP_143553	55980256	2-oxoglutarate dehydrogenase E3 component (dihydrolipoami dehydrogenase) [Thermus thermophilus HB8]
141	YP_679939	110639729	dihydrolipoyl dehydrogenanse [Cytophaga hutchinsonii ATC 33406]
142	YP_530077	90421707	Dihydrolipoamide dehydrogenase [Rhodopseudomonas palus BisB18]
143	YP_681916	110678909	dihydrolipoamide dehydrogenase [Roseobacter denitrificans OCh 114]
144	ZP_010...	86135035	dihydrolipoamide dehydrogenase [Tenacibaculum sp. MED15
145	ZP_011...	89068141	2-oxoglutarate dehydrogenase, E3 component, dihydrolipoam dehydrogenase [Oceanicola granulosus HTCC2516]
146	ZP_007...	75761004	Dihydrolipoamide dehydrogenase [Bacillus thuringiensis sero israelensis ATCC 35646]
147	ZP_010...	84684243	2-oxoglutarate dehydrogenase, E3 component, dihydrolipoamidedehydrogenase [Rhodobacterales bacterium HTCC2654]
148	ZP_009...	84500199	2-oxoglutarate dehydrogenase, E3 component, dihydrolipoamidedehydrogenase [Oceanicola batsensis HTCC2597]
149	ZP_006...	71900956	Dihydrolipoamide dehydrogenase [Xylella fastidiosa Ann-1]
150	XP_829730	74026328	dihydrolipoyl dehydrogenase [Trypanosoma brucei TREU927

151	ZP_010...	86132778	dihydrolipoamide dehydrogenase [Cellulophaga sp. MED134
152	P71317	11135239	Soluble pyridine nucleotide transhydrogenase (STH) (NAD(P)(+) transhydrogenase [B-specific])
153	ZP_012...	89891405	dihydrolipoyl dehydrogenase (pyruvate 2-oxoglutarate dehydrogenase) [Flavobacteria bacterium BBFL7]
154	ZP_009...	83950445	2-oxoglutarate dehydrogenase, E3 component, dihydrolipoamidedehydrogenase [Roseovarius nubinhibens I
155	AAA21748	472330	dihydrolipoamide dehydrogenase
156	Q04933	416906	Dihydrolipoyl dehydrogenase (Dihydrolipoamide dehydrogenase)
157	ZP_011...	88805521	Pyruvate/2-oxoglutarate dehydrogenase complex [Robiginital biformata HTCC2501]
158	YP_351398	77461891	dihydrolipoamide dehydrogenase [Pseudomonas fluorescens PfO-1]
159	ZP_006...	71900678	Dihydrolipoamide dehydrogenase [Xylella fastidiosa Ann-1]
160	ZP_011...	88936095	Dihydrolipoamide dehydrogenase [Geobacter uraniumreducei Rf4]
161	YP_430607	83590598	Dihydrolipoamide dehydrogenase [Moorella thermoacetica ATCC 39073]
162	YP_165603	56695257	2-oxoglutarate dehydrogenase, E3 component, dihydrolipoam dehydrogenase [Silicibacter pomeroyi DSS-3]
163	ZP_011...	89359154	Dihydrolipoamide dehydrogenase [Xanthobacter autotrophicu Py2]
164	YP_007150	46445785	dihydrolipoamide dehydrogenase [Candidatus Protochlamydi amoebophila UWE25]
165	YP_632394	108758911	alpha keto acid dehydrogenase complex, E3 component, lipoamide dehydrogenase [Myxococcus xanthus DK 1622]
166	ZP_010...	85704799	2-oxoglutarate dehydrogenase, E3 component, dihydrolipoamidedehydrogenase [Roseovarius sp. 217]
167	NP_778978	28198664	dihydrolipoamide dehydrogenase [Xylella fastidiosa Temecul
168	ZP_011...	88949385	Dihydrolipoamide dehydrogenase [Halorhodospira halophila SL1]
169	XP_749345	70988990	dihydrolipoamide dehydrogenase [Aspergillus fumigatus Af2
170	YP_359567	78044229	alpha keto acid dehydrogenase complex, E3 component, lipoamide dehydrogenase [Carboxydothermus hydrogenoformans Z-2901]
171	XP_959535	85092766	hypothetical protein [Neurospora crassa OR74A]
172	ZP_009...	83856665	Dihydrolipoyl dehydrogenase [Croceibacter atlanticus HTCC2559]
173	ZP_006...	69259929	Dihydrolipoamide dehydrogenase [Magnetococcus sp. MC-1]

174	NP_298837	15838149	dihydrolipoamide dehydrogenase [Xylella fastidiosa 9a5c]
175	YP_508779	89053328	Dihydrolipoamide dehydrogenase [Jannaschia sp. CCS1]
176	CAA72131	1854569	dihydrolipoamide dehydrogenase [Trypanosoma cruzi]
177	ZP_011...	88713490	Dihydrolipoyl dehydrogenase [Flavobacteriales bacterium HTCC2170]
178	P90597	6166121	Dihydrolipoyl dehydrogenase (Dihydrolipoamide dehydrogenase)
179	ZP_009...	83944432	2-oxoglutarate dehydrogenase, E3 component, dihydrolipoamidedehydrogenase [Sulfitobacter sp. EE-36]
180	ZP_009...	83953473	2-oxoglutarate dehydrogenase, E3 component, dihydrolipoamidedehydrogenase [Sulfitobacter sp. NAS-14.1]
181	ZP_010...	86141935	dihydrolipoamide dehydrogenase, E3 component of 2-oxoglutarate andpyruvate dehydrogenase complexes [Flavobacterium sp. MED217]
182	XP_818792	71663602	dihydrolipoyl dehydrogenase [Trypanosoma cruzi strain CL Brener]
183	XP_812294	71422952	dihydrolipoyl dehydrogenase [Trypanosoma cruzi strain CL Brener]
184	CAA72132	1854571	dihydrolipoamide dehydrogenase [Trypanosoma cruzi]
185	NP_623271	20808100	Dihydrolipoamide dehydrogenase/glutathione oxidoreductase and related enzyme [Thermoanaerobacter tengcongensis MB4
186	YP_265659	71082940	Dihydrolipoyl dehydrogenase [Candidatus Pelagibacter ubiqu HTCC1062]
187	ZP_012...	91762636	Dihydrolipoyl dehydrogenase [Candidatus Pelagibacter ubiqu HTCC1002]
188	CAA11554	4210334	2-oxoglutarate dehydrogenase, E3 subunit [Arabidopsis thalia
189	NP_566570	30684428	LPD2 (LIPOAMIDE DEHYDROGENASE 2); FAD binding dihydrolipoyl dehydrogenase/ disulfide oxidoreductase/ oxidoreductase [Arabidopsis thaliana]
190	ZP_010...	84515869	2-oxoglutarate dehydrogenase, E3 component, dihydrolipoamidedehydrogenase [Loktanella vestfoldensis SKA53]
191	YP_355777	77917962	2-oxoglutarate dehydrogenase complex, E3 component, lipoamide dehydrogenase [Pelobacter carbinolicus DSM 2380
192	AAS47708	44804791	dihydrolipoamide dehydrogenase [Leishmania major]
193	AAC26053	3309269	ferric leghemoglobin reductase-2 precursor [Glycine max]
194	XP_712334	68487571	putative mitochondrial matrix dihydrolipoamide dehydrogena Lpd1p [Candida albicans SC5314]
195	ZP_008...	78702525	Dihydrolipoamide dehydrogenase [Alkalilimnicola ehrlichei MLHE-1]

196	YP_002403	45658317	dihydrolipoamide dehydrogenase [Leptospira interrogans serc Copenhageni str. Fiocruz L1-130]
197	ZP_008...	82736566	Dihydrolipoamide dehydrogenase [Pseudomonas putida F1]
198	CAD60736	27803033	unnamed protein product [Podospora anserina]
199	NP_747467	26992042	dihydrolipoamide dehydrogenase [Pseudomonas putida KT24
200	ZP_013...	106891371	Dihydrolipoamide dehydrogenase [Roseiflexus sp. RS-1]
201	EAQ92192	88184724	conserved hypothetical protein [Chaetomium globosum CBS 148.51]

Table 74. Examples of transhydrogenase subunit alpha polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	NP_416120	16129561	NAD(P) transhydrogenase subunit alpha [Escherichia coli K1
2	ZP_007...	75512964	COG3288: NAD/NADP transhydrogenase alpha subunit [Escherichia coli 53638]
3	ZP_009...	83587938	COG3288: NAD/NADP transhydrogenase alpha subunit [Escherichia coli 101-1]
4	YP_669455	110641725	NAD(P) transhydrogenase subunit alpha [Escherichia coli 53
5	YP_540800	91210814	NAD(P) transhydrogenase subunit alpha [Escherichia coli UTI89]
6	ZP_007...	75236686	COG3288: NAD/NADP transhydrogenase alpha subunit [Escherichia coli F11]
7	NP_753890	26247850	NAD(P) transhydrogenase subunit alpha [Escherichia coli CFT073]
8	YP_310491	74312072	pyridine nucleotide transhydrogenase, alpha subunit [Shigella sonnei Ss046]
9	ZP_007...	75234916	COG3288: NAD/NADP transhydrogenase alpha subunit [Escherichia coli E110019]
10	YP_403177	82776828	pyridine nucleotide transhydrogenase, alpha subunit [Shigella dysenteriae Sd197]
11	ZP_007...	75190643	COG3288: NAD/NADP transhydrogenase alpha subunit [Escherichia coli E24377A]
12	ZP_009...	83570993	COG3288: NAD/NADP transhydrogenase alpha subunit [Shigella dysenteriae 1012]
13	ZP_007...	75257022	COG3288: NAD/NADP transhydrogenase alpha subunit [Escherichia coli E22]
14	YP_407977	82544030	pyridine nucleotide transhydrogenase, alpha subunit [Shigella boydii Sb227]
15	ZP_006...	75178502	COG3288: NAD/NADP transhydrogenase alpha subunit [Shigella boydii BS512]
16	YP_689096	110805576	pyridine nucleotide transhydrogenase, alpha subunit [Shigella flexneri 5 str. 8401]
17	NP_310336	15831563	NAD(P) transhydrogenase subunit alpha [Escherichia coli O157:H7 str. Sakai]
18	YP_216484	62180067	NAD(P) transhydrogenase subunit alpha [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
19	NP_460439	16764824	NAD(P) transhydrogenase subunit alpha [Salmonella typhimurium LT2]
20	NP_805194	29141852	NAD(P) transhydrogenase subunit alpha [Salmonella enterica subsp. enterica serovar Typhi Ty2]
21	ABF71058	102621428	NADP transhydrogenase alpha subunit [Enterobacter cloacae
22	ZP_008...	77963333	COG3288: NAD/NADP transhydrogenase alpha subunit [Yersinia mollaretii ATCC 43969]
23	ZP_008...	77958020	COG3288: NAD/NADP transhydrogenase alpha subunit [Yersinia bercovieri ATCC 43970]
24	ZP_008...	77975377	COG3288: NAD/NADP transhydrogenase alpha subunit [Yersinia frederiksenii ATCC 33641]
25	YP_647693	108811926	NAD(P) transhydrogenase alpha subunit [Yersinia pestis Nepal516]
26	YP_070740	51596549	NAD(P) transhydrogenase subunit alpha [Yersinia pseudotuberculosis IP 32953]
27	ZP_007...	77629299	COG3288: NAD/NADP transhydrogenase alpha subunit

			[Yersinia pseudotuberculosis IP 31758]
28	YP_050297	50121130	NAD(P) transhydrogenase subunit alpha [Erwinia carotovora subsp. atroseptica SCRI1043]
29	ZP_008...	77979498	COG3288: NAD/NADP transhydrogenase alpha subunit [Yersinia intermedia ATCC 29909]
30	NP_929427	37526083	NAD(P) transhydrogenase subunit alpha [Photorhabdus luminescens subsp. laumondii TTO1]
31	YP_455168	85059466	pyridine nucleotide transhydrogenase alpha subunit [Sodalis glossinidius str. 'morsitans']
32	YP_206544	59713769	NAD(P) transhydrogenase subunit alpha [Vibrio fischeri ES1
33	ZP_007...	75831475	COG3288: NAD/NADP transhydrogenase alpha subunit [Vit cholerae MO10]
34	ZP_010...	86147993	NAD(P) transhydrogenase subunit alpha [Vibrio sp. MED22
35	ZP_009...	84393928	NAD(P) transhydrogenase subunit alpha [Vibrio splendidus 12B01]
36	ZP_007...	75857576	COG3288: NAD/NADP transhydrogenase alpha subunit [Vit sp. Ex25]
37	ZP_012...	91226112	NAD(P) transhydrogenase subunit alpha [Vibrio alginolyticu 12G01]
38	NP_936868	37676472	NAD(P) transhydrogenase subunit alpha [Vibrio vulnificus YJ016]
39	NP_800432	28900777	NAD(P) transhydrogenase subunit alpha [Vibrio parahaemolyticus RIMD 2210633]
40	NP_762287	27366760	NAD(P) transhydrogenase subunit alpha [Vibrio vulnificus CMCP6]
41	ZP_012...	90577759	NAD(P) transhydrogenase subunit alpha [Vibrio angustum S1
42	ZP_011...	89073747	NAD(P) transhydrogenase subunit alpha [Photobacterium sp. SKA34]
43	NP_245690	15602618	NAD(P) transhydrogenase subunit alpha [Pasteurella multoci subsp. multocida str. Pm70]
44	YP_088416	52425279	NAD(P) transhydrogenase subunit alpha [Mannheimia succiniciproducens MBEL55E]
45	YP_718440	113460378	NAD(P)(+) transhydrogenase, alpha subunit (pyridine nucleotide transhydrogenase) [Haemophilus somnus 129PT]
46	ZP_001...	32030098	COG3288: NAD/NADP transhydrogenase alpha subunit [Haemophilus somnus 2336]
47	ZP_005...	68545628	NAD(P) transhydrogenase, alpha subunit [Shewanella amazonensis SB2B]
48	ZP_012...	90412639	NAD(P) transhydrogenase subunit alpha [Photobacterium profundum 3TCK]
49	ZP_007...	75429914	NAD/NADP transhydrogenase alpha subunit [Actinobacillus succinogenes 130Z]
50	YP_249235	68250123	NAD(P) transhydrogenase subunit alpha [Haemophilus influenzae 86-028NP]
51	YP_132574	54302581	NAD(P) transhydrogenase subunit alpha [Photobacterium profundum SS9]
52	NP_439513	16273272	NAD(P) transhydrogenase subunit alpha [Haemophilus influenzae Rd KW20]
53	ZP_009...	82741968	NAD(P) transhydrogenase, alpha subunit [Shewanella sp. W3 18-1]
54	ZP_014...	113949477	NAD(P) transhydrogenase, alpha subunit [Shewanella baltica OS195]
55	YP_561942	91792291	NAD(P) transhydrogenase, alpha subunit [Shewanella

			denitrificans OS217]
56	NP_719279	24375236	NAD(P) transhydrogenase subunit alpha [Shewanella oneiden MR-1]
57	NP_874046	33152693	NAD(P) transhydrogenase subunit alpha [Haemophilus ducre 35000HP]
58	YP_735209	113971416	NAD(P) transhydrogenase, alpha subunit [Shewanella sp. MR 4]
59	ZP_008...	78686308	NAD(P) transhydrogenase, alpha subunit [Shewanella sp. AN 3]
60	YP_736947	114046397	NAD(P) transhydrogenase, alpha subunit [Shewanella sp. MR 7]
61	ZP_006...	69950756	NAD(P) transhydrogenase, alpha subunit [Shewanella frigidimarina NCIMB 400]
62	ZP_007...	75818840	COG3288: NAD/NADP transhydrogenase alpha subunit [Vibi cholerae V51]
63	ZP_013...	106883669	NAD(P) transhydrogenase, alpha subunit [Psychromonas ingrahamii 37]
64	NP_283944	15794122	NAD(P) transhydrogenase subunit alpha [Neisseria meningitic Z2491]
65	YP_434236	83645801	NAD(P) transhydrogenase, alpha subunit [Hahella chejuensis KCTC 2396]
66	NP_274017	15676872	NAD(P) transhydrogenase subunit alpha [Neisseria meningitic MC58]
67	YP_208522	59801810	NAD(P) transhydrogenase subunit alpha [Neisseria gonorrhoe FA 1090]
68	ZP_012...	90408904	PntA [Psychromonas sp. CNPT3]
69	YP_268514	71281713	NAD(P) transhydrogenase subunit alpha [Colwellia psychrerythraea 34H]
70	ZP_001...	32035329	COG3288: NAD/NADP transhydrogenase alpha subunit [Actinobacillus pleuropneumoniae serovar 1 str. 4074]
71	ZP_012...	90202099	NAD(P) transhydrogenase, alpha subunit [Mycobacterium vanbaalenii PYR-1]
72	YP_342322	77163797	NAD(P) transhydrogenase subunit alpha [Nitrosococcus ocear ATCC 19707]
73	ZP_009...	84495285	NAD(P) transhydrogenase subunit alpha [Janibacter sp. HTCC2649]
74	AAY87755	68165590	NAD(P) transhydrogenase alpha subunit [Vibrio cholerae]
75	ZP_011...	89340414	NAD(P) transhydrogenase, alpha subunit [Mycobacterium flavescens PYR-GCK]
76	AAY87751	68165582	NAD(P) transhydrogenase alpha subunit [Vibrio cholerae]
77	AAY87754	68165588	NAD(P) transhydrogenase alpha subunit [Vibrio cholerae]
78	AAY87762	68165604	NAD(P) transhydrogenase alpha subunit [Vibrio cholerae]
79	YP_422187	83311923	NAD/NADP transhydrogenase alpha subunit [Magnetospirillu magneticum AMB-1]
80	YP_637279	108797082	NAD(P) transhydrogenase, alpha subunit [Mycobacterium sp. MCS]
81	YP_115165	53803088	NAD(P) transhydrogenase subunit alpha [Methylococcus capsulatus str. Bath]
82	NP_821578	29826944	NAD(P) transhydrogenase subunit alpha [Streptomyces avermitilis MA-4680]
83	ZP_006...	69261416	NAD(P) transhydrogenase, alpha subunit [Magnetococcus sp. MC-1]
84	NP_440856	16330128	NAD(P) transhydrogenase subunit alpha [Synechocystis sp.

			PCC 6803]
85	ZP_002...	46202292	COG3288: NAD/NADP transhydrogenase alpha subunit [Magnetospirillum magnetotacticum MS-1]
86	YP_298860	73538493	NAD(P) transhydrogenase subunit alpha [Ralstonia eutropha JMP134]
87	ZP_004...	66966825	NAD(P) transhydrogenase, alpha subunit [Arthrobacter sp. FB24]
88	ZP_006...	71366730	NAD(P) transhydrogenase, alpha subunit [Nocardioides sp. JS614]
89	YP_524985	89902514	NAD(P) transhydrogenase, alpha subunit [Rhodoferax ferrireducens T118]
90	YP_055339	50842112	NAD(P) transhydrogenase subunit alpha [Propionibacterium acnes KPA171202]
91	NP_631664	21225885	NAD(P) transhydrogenase subunit alpha [Streptomyces coelicolor A3(2)]
92	ZP_006...	74018096	NAD(P) transhydrogenase, alpha subunit [Burkholderia ambifaria AMMD]
93	CAJ96500	113530153	NAD(P) transhydrogenase subunit alpha [Ralstonia eutropha H16]
94	YP_366916	78060341	NAD(P) transhydrogenase subunit alpha [Burkholderia sp. 38
95	YP_574538	92114610	NAD(P) transhydrogenase, alpha subunit [Chromohalobacter salexigens DSM 3043]
96	ZP_004...	67542770	NAD(P) transhydrogenase, alpha subunit [Burkholderia vietnamiensis G4]
97	YP_702683	111019711	NAD(P) transhydrogenase alpha subunit [Rhodococcus sp. RHA1]
98	ZP_007...	75821435	COG3288: NAD/NADP transhydrogenase alpha subunit [Vib cholerae RC385]
99	ZP_011...	88798022	NAD(P) transhydrogenase subunit alpha [Reinekea sp. MED297]
100	ZP_009...	83371049	NAD(P) transhydrogenase, alpha subunit [Rhodobacter sphaeroides ATCC 17025]
101	ZP_006...	69933435	NAD(P) transhydrogenase, alpha subunit [Paracoccus denitrificans PD1222]
102	YP_353313	77463809	NAD(P) transhydrogenase subunit alpha [Rhodobacter sphaeroides 2.4.1]
103	ZP_009...	83373326	NAD(P) transhydrogenase, alpha subunit [Rhodobacter sphaeroides ATCC 17029]
104	ZP_010...	85704984	NAD(P) transhydrogenase subunit alpha [Roseovarius sp. 217
105	YP_612703	99080549	NAD(P) transhydrogenase, alpha subunit [Silicibacter sp. TM1040]
106	YP_683504	110680497	NAD(P) transhydrogenase, alpha subunit [Roseobacter denitrificans OCh 114]
107	AAQ87369	36958944	NAD(P) transhydrogenase subunit alpha [Rhizobium sp. NGR234]
108	ZP_010...	86137634	NAD(P) transhydrogenase subunit alpha [Roseobacter sp. MED193]
109	XP_799127	72030333	PREDICTED: similar to nicotinamide nucleotide transhydrogenase [Strongylocentrotus purpuratus]
110	ZP_010...	84503572	NAD(P) transhydrogenase subunit alpha [Oceanicola batsensi HTCC2597]
111	ZP_010...	84516763	NAD(P) transhydrogenase subunit alpha [Loktanella vestfoldensis SKA53]

112	NP_533164	17936374	NAD(P) transhydrogenase subunit alpha [Agrobacterium tumefaciens str. C58]
113	XP_562937	57968100	ENSANGP00000025507 [Anopheles gambiae str. PEST]
114	YP_511224	89055773	NAD(P) transhydrogenase, alpha subunit [Jannaschia sp. CCS
115	ZP_009...	83942708	NAD(P) transhydrogenase subunit alpha [Sulfitobacter sp. EE 36]
116	YP_168028	56697658	NAD(P) transhydrogenase subunit alpha [Silicibacter pomero DSS-3]
117	EAT35199	108870974	nadp transhydrogenase [Aedes aegypti]
118	ZP_009...	83953947	NAD(P) transhydrogenase subunit alpha [Sulfitobacter sp. NA 14.1]
119	ZP_009...	83949483	NAD(P) transhydrogenase subunit alpha [Roseovarius nubinhibens ISM]
120	XP_367628	39972475	hypothetical protein MG07539.4 [Magnaporthe grisea 70-15]
121	NP_999921	47550793	nicotinamide nucleotide transhydrogenase [Danio rerio]
122	XP_961047	85100871	hypothetical protein (mitochondrial nicotinamide nucleotide transhydrogenase-related protein [imported] - Neurospora cras OR74A)
123	AAH81117	51703526	MGC83563 protein [Xenopus laevis]
124	CAF99322	47223713	unnamed protein product [Tetraodon nigroviridis]
125	CAB88572	16416047	related to mitochondrial nicotinamide nucleotide transhydrogenase [Neurospora crassa]
126	AAI10544	83405154	Nicotinamide nucleotide transhydrogenase [Homo sapiens]
127	AAI10545	83405537	Nicotinamide nucleotide transhydrogenase [Homo sapiens]
128	NP_509028	17550456	Nicotinamide Nucleotide Transhydrogenase family member (nnt-1) [Caenorhabditis elegans]
129	2211247B	1589396	nicotinamide nucleotide transhydrogenase
130	ZP_010...	84686399	NAD(P) transhydrogenase subunit alpha [Rhodobacterales bacterium HTCC2654]
131	NP_776368	27806831	nicotinamide nucleotide transhydrogenase [Bos taurus]
132	AAA21440	163397	nicotinamide nucleotide transhydrogenase
133	P11024	128400	NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase)
134	XP_536481	73953769	PREDICTED: similar to NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenas (Nicotinamide nucleotide transhydrogenase) isoform 1 [Canis familiaris]
135	XP_970382	91083631	PREDICTED: similar to nicotinamide nucleotide transhydrogenase [Tribolium castaneum]
136	NP_001...	61557127	nicotinamide nucleotide transhydrogenase [Rattus norvegicus]
137	NP_892022	33695086	nicotinamide nucleotide transhydrogenase [Homo sapiens]
138	XP_867928	73953777	PREDICTED: similar to NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenas (Nicotinamide nucleotide transhydrogenase) isoform 5 [Canis familiaris]
139	NP_036475	33695084	nicotinamide nucleotide transhydrogenase [Homo sapiens]
140	XP_424784	50761621	PREDICTED: similar to nicotinamide nucleotide transhydrogenase [Gallus gallus]
141	XP_646840	66826971	NAD(P)+ transhydrogenase (AB-specific) [Dictyostelium discoideum AX4]
142	BAC40113	26352966	unnamed protein product [Mus musculus]
143	EAS31570	90301939	conserved hypothetical protein [Coccidioides immitis RS]

144	XP_867922	73953775	PREDICTED: similar to NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenas (Nicotinamide nucleotide transhydrogenase) isoform 4 [Canis familiaris]
145	CAF99856	47230663	unnamed protein product [Tetraodon nigroviridis]
146	Q61941	51338804	NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase)
147	2211247A	1589395	nicotinamide nucleotide transhydrogenase
148	NP_032736	31543330	nicotinamide nucleotide transhydrogenase [Mus musculus]
149	BAE35294	74198248	unnamed protein product [Mus musculus]
150	XP_748064	70985116	nicotinamide nucleotide transhydrogenase [Aspergillus fumigatus Af293]
151	XP_389182	46130902	hypothetical protein FG09006.1 [Gibberella zeae PH-1]
152	CAE68875	39598183	Hypothetical protein CBG14838 [Caenorhabditis briggsae]
153	AAK18179	13310152	nicotinamide nucleotide transhydrogenase [Acetabularia acetabulum]
154	AAG02246	11597233	NAD(P)H transhydrogenase [Acetabularia acetabulum]
155	AAC41577	6478876	pyridine nucleotidetranshydrogenase [Entamoeba histolytica]
156	XP_627136	66359916	pyridine nucleotide/ NAD(P) transhydrogenase alpha plus bet subunits, duplicated gene, [Cryptosporidium parvum Iowa II]
157	XP_666495	67602649	transhydrogenase 7B2 [Cryptosporidium hominis TU502]
158	BAE40577	74219995	unnamed protein product [Mus musculus]
159	CAH90079	55726630	hypothetical protein [Pongo pygmaeus]
160	AAA80188	571367	nicotinamide nucleotide transhydrogenase
161	EAQ86424	88178956	conserved hypothetical protein [Chaetomium globosum CBS 148.51]
162	AAA29077	305062	transhydrogenase
163	AAA29081	158904	transhydrogenase
164	YP_724141	113478080	NAD(P)(+) transhydrogenase (AB-specific) [Trichodesmium erythraeum IMS101]
165	NP_487450	17230902	nicotinamide nucleotide transhydrogenase, subunit alpha [Nostoc sp. PCC 7120]
166	YP_323932	75909636	Alanine dehydrogenase/PNT-like [Anabaena variabilis ATCC 29413]
167	ZP_005...	67924536	NAD(P)(+) transhydrogenase (AB-specific) [Crocosphaera watsonii WH 8501]
168	ZP_013...	110607624	Alanine dehydrogenase/PNT-like [Maricaulis maris MCS10]
169	ZP_012...	91222948	NAD(P) transhydrogenase subunit alpha [Psychroflexus torqu ATCC 700755]
170	ZP_009...	82737423	NAD/NADP transhydrogenase, NAD(H)-binding DI subunit [Pseudomonas putida F1]
171	YP_000046	45655960	proton-translocating transhydrogenase, subunit alpha part 1 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]
172	YP_257267	70733627	NAD(P) transhydrogenase, alpha subunit part 1 [Pseudomona fluorescens Pf-5]
173	ZP_001...	23130320	COG3288: NAD/NADP transhydrogenase alpha subunit [Nostoc punctiforme PCC 73102]
174	ZP_013...	110593183	NAD(P)(+) transhydrogenase (AB-specific) [Acidovorax sp. JS42]
175	ZP_009...	83859916	nicotinamide nucleotide transhydrogenase, subunit [Oceanicaulis alexandrii HTCC2633]

176	YP_526430	90020603	Glycogen/starch/alpha-glucan phosphorylase [Saccharophagu degradans 2-40]
177	ZP_012...	89362826	nicotinamide nucleotide transhydrogenase, subunit alpha1 [Xanthobacter autotrophicus Py2]
178	YP_277175	71737873	NAD(P) transhydrogenase, subunit alpha part 1 [Pseudomona syringae pv. phaseolicola 1448A]
179	YP_238081	66048240	Alanine dehydrogenase/PNT, C-terminal:Alanine dehydrogenase/PNT, N-terminal [Pseudomonas syringae pv. syringae B728a]
180	YP_675347	110635139	alanine dehydrogenase/PNT-like [Mesorhizobium sp. BNC1]
181	YP_345847	77456342	NAD(P)(+) transhydrogenase (AB-specific) [Pseudomonas fluorescens PfO-1]
182	AAQ87237	36958769	NAD(P) transhydrogenase subunit alpha [Rhizobium sp. NGR234]
183	ZP_013...	94499798	pyridine nucleotide transhydrogenase alpha subunit [Oceanobacter sp. RED65]
184	NP_881481	33593837	NAD(P) transhydrogenase, subunit alpha part 1 [Bordetella pertussis Tohama I]
185	P0C186	91207608	NAD(P) transhydrogenase subunit alpha part 1 (Pyridine nucleotide transhydrogenase subunit alpha 1) (Nicotinamide nucleotide transhydrogenase subunit alpha 1) (Proton-translocating transhydrogenase component 1) (dI)
186	1PTJB	37927621	Chain B, Crystal Structure Analysis Of The Di And Diii Complex Of Transhydrogenase With A Thio-Nicotinamide Nucleotide Analogue
187	YP_485056	86748560	NAD(P)(+) transhydrogenase (AB-specific) [Rhodopseudomonas palustris HaA2]
188	YP_620103	107021776	alanine dehydrogenase/PNT-like [Burkholderia cenocepacia A 1054]
189	ZP_008...	77952426	pyridine nucleotide transhydrogenase alpha subunit [Marinobacter aquaeolei VT8]
190	NP_840933	30248863	Alanine dehydrogenase and pyridine nucleotide transhydrogenase [Nitrosomonas europaea ATCC 19718]
191	2FRDB	90109601	Chain B, Structure Of Transhydrogenase (Di.S138a.Nadh)2(Diii.Nadph)1 Asymmetric Complex
192	NP_888491	33600931	NAD(P) transhydrogenase, subunit alpha part 1 [Bordetella bronchiseptica RB50]
193	XP_726447	82596885	NAD(P) transhydrogenase subunit beta [Plasmodium yoelii yoelii str. 17XNL]
194	YP_551329	91790377	NAD(P)(+) transhydrogenase (AB-specific) [Polaromonas sp. JS666]
195	ZP_006...	71548985	NAD(P)(+) transhydrogenase (AB-specific) [Nitrosomonas eutropha C71]
196	YP_568553	91975894	NAD(P)(+) transhydrogenase (AB-specific) [Rhodopseudomonas palustris BisB5]
197	2FSVB	90109621	Chain B, Structure Of Transhydrogenase (Di.D135n.Nad+) 2(Diii.E155w.Nadp+)1 Asymmetric Complex
198	1NM5B	42543078	Chain B, R. Rubrum Transhydrogenase (Di.Q132n)2(Diii)1 Asymmetric Complex
199	1L7DB	27065343	Chain B, Crystal Structure Of R. Rubrum Transhydrogenase Domain I Without Bound Nad(H)
200	ZP_012...	90418769	NAD(P) transhydrogenase, subunit alpha part 1 [Aurantimona sp. SI85-9A1]
201	2FR8B	90109598	Chain B, Structure Of Transhydrogenase

			(Di.R127a.Nad+)2(Diii.Nadp+)1 Asymmetric Complex

Table 75. Examples of transhydrogenase subunit beta polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	NP_416119	16129560	pyridine nucleotide transhydrogenase [Escherichia coli K12].
2	YP_669454	110641724	NAD(P) transhydrogenase subunit beta [Escherichia coli 536]
3	ZP_007...	75234915	COG1282: NAD/NADP transhydrogenase beta subunit [Escherichia coli E110019]
4	ZP_007...	75230949	COG1282: NAD/NADP transhydrogenase beta subunit [Escherichia coli B7A]
5	YP_407978	82544031	pyridine nucleotide transhydrogenase, beta subunit [Shigella boydii Sb227]
6	YP_150630	56413555	pyridine nucleotide transhydrogenase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]
7	YP_216485	62180068	pyridine nucleotide transhydrogenase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
8	ABF71059	102621429	NADP transhydrogenase beta subunit [Enterobacter cloacae]
9	NP_929428	37526084	pyridine nucleotide transhydrogenase [Photorhabdus luminescens subsp. laumondii TTO1]
10	YP_050298	50121131	pyridine nucleotide transhydrogenase [Erwinia carotovora subsp. atroseptica SCRI1043]
11	ZP_008...	77979497	COG1282: NAD/NADP transhydrogenase beta subunit [Yersinia intermedia ATCC 29909]
12	ZP_008...	77975378	COG1282: NAD/NADP transhydrogenase beta subunit [Yersinia frederiksenii ATCC 33641]
13	ZP_008...	77958019	COG1282: NAD/NADP transhydrogenase beta subunit [Yersinia bercovieri ATCC 43970]
14	ZP_008...	77963332	COG1282: NAD/NADP transhydrogenase beta subunit [Yersinia mollaretii ATCC 43969]
15	YP_647692	108811925	NAD(P) transhydrogenase subunit beta [Yersinia pestis Nepal516]
16	YP_455167	85059465	pyridine nucleotide transhydrogenase beta subunit [Sodalis glossinidius str. 'morsitans']
17	NP_719280	24375237	pyridine nucleotide transhydrogenase [Shewanella oneidensis MR-1]
18	YP_736946	114046396	NAD(P) transhydrogenase, beta subunit [Shewanella sp. MR-
19	ZP_009...	82741967	NAD(P) transhydrogenase, beta subunit [Shewanella sp. W3-1]
20	NP_245689	15602617	pyridine nucleotide transhydrogenase [Pasteurella multocida subsp. multocida str. Pm70]
21	ZP_005...	68541685	NAD(P) transhydrogenase, beta subunit [Shewanella baltica OS155]
22	ZP_012...	90412640	putative NAD(P) transhydrogenase, beta subunit [Photobacterium profundum 3TCK]
23	ZP_001...	53732668	COG1282: NAD/NADP transhydrogenase beta subunit [Haemophilus influenzae R2846]
24	YP_249234	68250122	pyridine nucleotide transhydrogenase [Haemophilus influenza 86-028NP]
25	NP_439514	16273273	pyridine nucleotide transhydrogenase [Haemophilus influenza Rd KW20]
26	ZP_005...	68545629	NAD(P) transhydrogenase, beta subunit [Shewanella

			amazonensis SB2B]
27	YP_132575	54302582	pyridine nucleotide transhydrogenase [Photobacterium profundum SS9]
28	ZP_011...	89073748	pyridine nucleotide transhydrogenase [Photobacterium sp. SKA34]
29	NP_800431	28900776	pyridine nucleotide transhydrogenase [Vibrio parahaemolytic RIMD 2210633]
30	ZP_012...	90577760	pyridine nucleotide transhydrogenase [Vibrio angustum S14]
31	ZP_007...	75857577	COG1282: NAD/NADP transhydrogenase beta subunit [Vibr sp. Ex25]
32	NP_936867	37676471	pyridine nucleotide transhydrogenase [Vibrio vulnificus YJ01
33	ZP_007...	75818461	COG1282: NAD/NADP transhydrogenase beta subunit [Vibr cholerae V51]
34	ZP_007...	75831476	COG1282: NAD/NADP transhydrogenase beta subunit [Vibr cholerae MO10]
35	ZP_012...	91226113	pyridine nucleotide transhydrogenase [Vibrio alginolyticus 12G01]
36	YP_206543	59713768	pyridine nucleotide transhydrogenase [Vibrio fischeri ES114]
37	YP_088415	52425278	pyridine nucleotide transhydrogenase [Mannheimia succiniciproducens MBEL55E]
38	ZP_001...	32035330	COG1282: NAD/NADP transhydrogenase beta subunit [Actinobacillus pleuropneumoniae serovar 1 str. 4074]
39	ZP_006...	69950757	NAD(P) transhydrogenase, beta subunit [Shewanella frigidimarina NCIMB 400]
40	ZP_010...	86147992	pyridine nucleotide transhydrogenase [Vibrio sp. MED222]
41	ZP_009...	84393927	NAD(P) transhydrogenase, beta subunit [Vibrio splendidus 12B01]
42	ZP_007...	75429915	NAD/NADP transhydrogenase beta subunit [Actinobacillus succinogenes 130Z]
43	NP_274015	15676870	pyridine nucleotide transhydrogenase [Neisseria meningitidis MC58]
44	NP_283942	15794120	pyridine nucleotide transhydrogenase [Neisseria meningitidis Z2491]
45	YP_208524	59801812	pyridine nucleotide transhydrogenase [Neisseria gonorrhoeae FA 1090]
46	YP_718441	113460379	NAD(P)(+) transhydrogenase, beta subunit (pyridine nucleoti transhydrogenase) [Haemophilus somnus 129PT]
47	NP_874045	33152692	pyridine nucleotide transhydrogenase [Haemophilus ducreyi 35000HP]
48	YP_561941	91792290	NAD(P) transhydrogenase, beta subunit [Shewanella denitrificans OS217]
49	YP_434235	83645800	NAD/NADP transhydrogenase beta subunit [Hahella chejuens KCTC 2396]
50	YP_268515	71280969	pyridine nucleotide transhydrogenase [Colwellia psychrerythraea 34H]
51	ZP_013...	106883670	NAD(P) transhydrogenase, beta subunit [Psychromonas ingrahamii 37]
52	ZP_009...	84495284	pyridine nucleotide transhydrogenase [Janibacter sp. HTCC2649]

53	YP_637278	108797081	NAD(P) transhydrogenase, beta subunit [Mycobacterium sp. MCS]
54	ZP_012...	90408905	NAD(P) transhydrogenase subunit beta [Psychromonas sp. CNPT3]
55	ZP_011...	89340413	NAD(P) transhydrogenase, beta subunit [Mycobacterium flavescens PYR-GCK]
56	ZP_012...	90202100	NAD(P) transhydrogenase, beta subunit [Mycobacterium vanbaalenii PYR-1]
57	NP_631663	21225884	NAD(P) transhydrogenase beta subunit [Streptomyces coelicolor A3(2)]
58	NP_821577	29826943	pyridine nucleotide transhydrogenase, beta subunit [Streptomyces avermitilis MA-4680]
59	YP_702682	111019710	NAD(P) transhydrogenase beta subunit [Rhodococcus sp. RHA1]
60	YP_422186	83311922	NAD/NADP transhydrogenase beta subunit [Magnetospirillu magneticum AMB-1]
61	ZP_006...	71366731	NAD(P) transhydrogenase, beta subunit [Nocardioides sp. JS614]
62	YP_115164	53803089	NAD(P) transhydrogenase, beta subunit [Methylococcus capsulatus str. Bath]
63	YP_524984	89902513	NAD(P) transhydrogenase, beta subunit [Rhodoferax ferrireducens T118]
64	NP_440860	16330132	pyridine nucleotide transhydrogenase beta subunit [Synechocystis sp. PCC 6803]
65	ZP_004...	66966824	NAD(P) transhydrogenase, beta subunit [Arthrobacter sp. FB
66	ZP_011...	88798021	pyridine nucleotide transhydrogenase [Reinekea sp. MED297
67	YP_342321	77163796	NAD(P) transhydrogenase, beta subunit [Nitrosococcus ocear ATCC 19707]
68	ZP_006...	69261415	NAD(P) transhydrogenase, beta subunit [Magnetococcus sp. MC-1]
69	ZP_004...	67542769	NAD(P) transhydrogenase, beta subunit [Burkholderia vietnamiensis G4]
70	YP_366915	78060340	NAD(P) transhydrogenase, beta subunit [Burkholderia sp. 38
71	ZP_006...	74018097	NAD(P) transhydrogenase, beta subunit [Burkholderia ambifa AMMD]
72	YP_298859	73538492	NAD(P) transhydrogenase, beta subunit [Ralstonia eutropha JMP134]
73	YP_055340	50842113	NAD(P) transhydrogenase subunit beta [Propionibacterium acnes KPA171202]
74	ZP_009...	83949482	NAD(P)+ transhydrogenase, beta subunit [Roseovarius nubinhibens ISM]
75	CAJ96499	113530152	NAD(P) transhydrogenase subunit beta [Ralstonia eutropha H16]
76	ZP_006...	69933434	NAD(P) transhydrogenase, beta subunit [Paracoccus denitrificans PD1222]
77	YP_168027	56697657	NAD(P)+ transhydrogenase, beta subunit [Silicibacter pomer DSS-3]
78	NP_533165	17936375	NAD(P)+ transhydrogenase beta chain [Agrobacterium tumefaciens str. C58]
79	AAQ87370	36958945	NAD(P) transhydrogenase subunit beta [Rhizobium sp. NGR234]

80	ZP_009...	83942707	NAD(P)+ transhydrogenase, beta subunit [Sulfitobacter sp. E 36]
81	ZP_009...	83953946	NAD(P)+ transhydrogenase, beta subunit [Sulfitobacter sp. NAS-14.1]
82	ZP_007...	75813705	COG1282: NAD/NADP transhydrogenase beta subunit [Vibr cholerae V52]
83	ZP_010...	84503573	NAD(P)+ transhydrogenase, beta subunit [Oceanicola batsen: HTCC2597]
84	ZP_010...	84686400	NAD(P)+ transhydrogenase, beta subunit [Rhodobacterales bacterium HTCC2654]
85	YP_612702	99080548	NAD(P) transhydrogenase, beta subunit [Silicibacter sp. TM1040]
86	ZP_010...	84516762	NAD(P)+ transhydrogenase, beta subunit [Loktanella vestfoldensis SKA53]
87	ZP_010...	86137633	NAD(P)+ transhydrogenase, beta subunit [Roseobacter sp. MED193]
88	YP_511223	89055772	NAD(P) transhydrogenase, beta subunit [Jannaschia sp. CCS
89	ZP_010...	85704983	NAD(P)+ transhydrogenase, beta subunit [Roseovarius sp. 21
90	ZP_007...	75822802	COG1282: NAD/NADP transhydrogenase beta subunit [Vibr cholerae RC385]
91	YP_683503	110680496	NAD(P) transhydrogenase, beta subunit [Roseobacter denitrificans OCh 114]
92	NP_949516	39937240	nicotinamide nucleotide transhydrogenase, subunit beta [Rhodopseudomonas palustris CGA009]
93	YP_418478	83269187	NAD(P) transhydrogenase, beta subunit [Brucella melitensis biovar Abortus 2308]
94	YP_485058	86748562	NAD(P) transhydrogenase, beta subunit [Rhodopseudomonas palustris HaA2]
95	ZP_009...	83859918	nicotinamide nucleotide transhydrogenase, subunit beta [Oceanicaulis alexandrii HTCC2633]
96	ZP_008...	77740973	NAD(P) transhydrogenase, beta subunit [Rhodopseudomonas palustris BisA53]
97	ZP_012...	89362731	NAD(P) transhydrogenase, beta subunit [Xanthobacter autotrophicus Py2]
98	ZP_008...	77814001	NAD(P) transhydrogenase, beta subunit [Shewanella putrefaciens CN-32]
99	ZP_010...	84704197	PntB, NAD(P) transhydrogenase, beta subunit [Parvularcula bermudensis HTCC2503]
100	YP_533811	90425441	NAD(P) transhydrogenase, beta subunit [Rhodopseudomonas palustris BisB18]
101	P0C188	91207612	NAD(P) transhydrogenase subunit beta (Pyridine nucleotide transhydrogenase subunit beta) (Nicotinamide nucleotide transhydrogenase subunit beta) (Proton-translocating transhydrogenase NADP(H)-binding component) (dIII)
102	YP_568555	91975896	NAD(P) transhydrogenase, beta subunit [Rhodopseudomonas palustris BisB5]
103	ZP_012...	90418771	NAD(P) transhydrogenase, subunit beta [Aurantimonas sp. SI85-9A1]
104	YP_526432	90020605	NAD(P) transhydrogenase, beta subunit [Saccharophagus degradans 2-40]
105	ZP_008...	78699497	NAD(P)+ transhydrogenase beta chain [Bradyrhizobium sp. BTAi1]

106	XP_424784	50761621	PREDICTED: similar to nicotinamide nucleotide transhydrogenase [Gallus gallus]
107	XP_799127	72030333	PREDICTED: similar to nicotinamide nucleotide transhydrogenase [Strongylocentrotus purpuratus]
108	ZP_010...	85716091	NAD/NADP transhydrogenase beta subunit [Nitrobacter sp. N 311A]
109	YP_605919	104779421	pyridine nucleotide transhydrogenase, beta subunit [Pseudomonas entomophila L48]
110	YP_457359	85373297	PntB, NAD(P) transhydrogenase, beta subunit [Erythrobacter litoralis HTCC2594]
111	XP_970382	91083631	PREDICTED: similar to nicotinamide nucleotide transhydrogenase [Tribolium castaneum]
112	BAB51677	14025075	nicotinamide nucleotide transhydrogenase, subunit beta [Mesorhizobium loti MAFF303099]
113	ZP_012...	94413536	hypothetical protein PaerP_01004711 [Pseudomonas aeruginc PA7]
114	ZP_011...	88938736	NAD/NADP transhydrogenase beta subunit-like [Acidiphiliu cryptum JF-5]
115	NP_795188	28872569	NAD(P) transhydrogenase, beta subunit [Pseudomonas syring pv. tomato str. DC3000]
116	YP_257265	70733625	NAD(P) transhydrogenase, beta subunit [Pseudomonas fluorescens Pf-5]
117	NP_773764	27382235	NAD(P)+ transhydrogenase beta chain [Bradyrhizobium japonicum USDA 110]
118	YP_576517	92116788	NAD(P) transhydrogenase, beta subunit [Nitrobacter hamburgensis X14]
119	ZP_013...	107099186	hypothetical protein PaerPA_01000196 [Pseudomonas aeruginosa PACS2]
120	YP_557045	91781839	Putative NAD(P) transhydrogenase, beta subunit [Burkholder xenovorans LB400]
121	ZP_009...	82737421	pyridine nucleotide transhydrogenase, beta subunit [Pseudomonas putida F1]
122	YP_345845	77456340	NAD(P) transhydrogenase, beta subunit [Pseudomonas fluorescens PfO-1]
123	NP_999921	47550793	nicotinamide nucleotide transhydrogenase [Danio rerio]
124	YP_411848	82702282	NAD(P) transhydrogenase, beta subunit [Nitrosospira multiformis ATCC 25196]
125	CAF99856	47230663	unnamed protein product [Tetraodon nigroviridis]
126	YP_675345	110635137	NAD(P) transhydrogenase, beta subunit [Mesorhizobium sp. BNC1]
127	EAT35199	108870974	nadp transhydrogenase [Aedes aegypti]
128	YP_277177	71736851	NAD(P) transhydrogenase, beta subunit [Pseudomonas syring pv. phaseolicola 1448A]
129	YP_263852	71065125	NAD(P) transhydrogenase, beta subunit [Psychrobacter arctic 273-4]
130	NP_840935	30248865	NAD(P) transhydrogenase beta subunit [Nitrosomonas europa ATCC 19718]
131	XP_867922	73953775	PREDICTED: similar to NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenas (Nicotinamide nucleotide transhydrogenase) isoform 4 [Canis familiaris]

132	XP_867916	73953773	PREDICTED: similar to NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenas (Nicotinamide nucleotide transhydrogenase) isoform 3 [Canis familiaris]
133	XP_536481	73953769	PREDICTED: similar to NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenas (Nicotinamide nucleotide transhydrogenase) isoform 1 [Canis familiaris]
134	XP_867928	73953777	PREDICTED: similar to NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenas (Nicotinamide nucleotide transhydrogenase) isoform 5 [Canis familiaris]
135	NP_001...	61557127	nicotinamide nucleotide transhydrogenase [Rattus norvegicus
136	YP_238083	66048242	NAD(P) transhydrogenase, beta subunit [Pseudomonas syring pv. syringae B728a]
137	BAE40577	74219995	unnamed protein product [Mus musculus]
138	BAC39226	26351179	unnamed protein product [Mus musculus]
139	ZP_013...	94494989	NAD(P) transhydrogenase, beta subunit [Sphingomonas sp. SKA58]
140	NP_032736	31543330	nicotinamide nucleotide transhydrogenase [Mus musculus]
141	BAC40113	26352966	unnamed protein product [Mus musculus]
142	ZP_004...	67155631	NAD(P) transhydrogenase, beta subunit [Azotobacter vinelan AvOP]
143	YP_579812	93005375	NAD(P) transhydrogenase, beta subunit [Psychrobacter cryohalolentis K5]
144	YP_297031	73542511	NAD(P) transhydrogenase, beta subunit [Ralstonia eutropha JMP134]
145	YP_585107	94311897	NAD(P) transhydrogenase, beta subunit [Ralstonia metallidurans CH34]
146	YP_497119	87199862	NAD(P) transhydrogenase, beta subunit [Novosphingobium aromaticivorans DSM 12444]
147	AAQ87239	36958771	NAD(P) transhydrogenase subunit beta [Rhizobium sp. NGR234]
148	NP_888489	33600929	NAD(P) transhydrogenase subunit beta [Bordetella bronchiseptica RB50]
149	Q61941	51338804	NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase)
150	NP_776368	27806831	nicotinamide nucleotide transhydrogenase [Bos taurus]
151	NP_884728	33597085	NAD(P) transhydrogenase subunit beta [Bordetella parapertus 12822]
152	AAA21440	163397	nicotinamide nucleotide transhydrogenase
153	YP_441808	83721084	NAD(P) transhydrogenase, beta subunit [Burkholderia thailandensis E264]
154	AAI10544	83405154	Nicotinamide nucleotide transhydrogenase [Homo sapiens]
155	NP_899769	34495554	NAD(P) transhydrogenase, beta subunit [Chromobacterium

			violaceum ATCC 12472]
156	NP_422097	16127533	NAD(P) transhydrogenase, beta subunit [Caulobacter crescen CB15]
157	XP_312859	58383882	ENSANGP00000016622 [Anopheles gambiae str. PEST]
158	ZP_009...	84360819	COG1282: NAD/NADP transhydrogenase beta subunit [Burkholderia dolosa AUO158]
159	ZP_014...	113935785	NAD(P) transhydrogenase, beta subunit [Caulobacter sp. K31
160	ZP_006...	71548983	NAD(P) transhydrogenase, beta subunit [Nitrosomonas eutro C71]
161	AAH81117	51703526	MGC83563 protein [Xenopus laevis]
162	CAH90079	55726630	hypothetical protein [Pongo pygmaeus]
163	BAE35294	74198248	unnamed protein product [Mus musculus]
164	ZP_014...	113872300	probable NAD(P) transhydrogenase subunit beta transmembr protein [Sinorhizobium medicae WSM419]
165	AAI10545	83405537	Nicotinamide nucleotide transhydrogenase [Homo sapiens]
166	NP_036475	33695084	nicotinamide nucleotide transhydrogenase [Homo sapiens]
167	YP_727574	113869085	NAD(P) transhydrogenase subunit beta [Ralstonia eutropha H16]
168	2211247B	1589396	nicotinamide nucleotide transhydrogenase
169	2211247A	1589395	nicotinamide nucleotide transhydrogenase
170	AAN62246	24461677	putative pyridine nucleotide transhydrogenase, beta subunit [Pseudomonas aeruginosa]
171	P11024	128400	NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase)
172	NP_892022	33695086	nicotinamide nucleotide transhydrogenase [Homo sapiens]
173	NP_386966	15966613	PROBABLE NAD(P) TRANSHYDROGENASE SUBUNIT BETA TRANSMEMBRANE PROTEIN [Sinorhizobium meliloti 1021]
174	YP_299910	73539543	NAD(P) transhydrogenase, beta subunit [Ralstonia eutropha JMP134]
175	ZP_012...	91769178	NAD(P) transhydrogenase, beta subunit [Psychrobacter sp. PRwf-1]
176	YP_293241	72383887	NAD(P) transhydrogenase, beta subunit [Ralstonia eutropha JMP134]
177	YP_299480	73539113	NAD(P) transhydrogenase, beta subunit [Ralstonia eutropha JMP134]
178	YP_293567	72384213	NAD(P) transhydrogenase, beta subunit [Ralstonia eutropha JMP134]
179	YP_725774	113867285	NAD(P) transhydrogenase subunit beta [Ralstonia eutropha H16]
180	YP_620105	107021778	NAD(P) transhydrogenase, beta subunit [Burkholderia cenocepacia AU 1054]

181	YP_725367	113866878	NAD(P) transhydrogenase subunit beta [Ralstonia eutropha H16]
182	NP_520854	17547452	PROBABLE TRANSMEMBRANE NADP TRANSHYDROGENASE (BETA SUBUNIT) OXIDOREDUCTASE PROTEIN [Ralstonia solanacearum GMI1000]
183	ZP_009...	83746755	PntB [Ralstonia solanacearum UW551]
184	ZP_013...	100235717	hypothetical protein Bpse4_03000891 [Burkholderia pseudomallei 406e]
185	YP_334763	76809085	NAD(P) transhydrogenase subunit beta [Burkholderia pseudomallei 1710b]
186	ZP_013...	100917505	hypothetical protein Bmal10_03001254 [Burkholderia mallei 10399]
187	ZP_004...	67667725	NAD(P) transhydrogenase, beta subunit [Burkholderia cenocepacia HI2424]
188	ZP_012...	91762289	NAD(p) transhydrogenase subunit beta [Candidatus Pelagibac ubique HTCC1002]
189	YP_471093	86359201	NAD(P)(+) transhydrogenase (AB-specific), beta subunit protein [Rhizobium etli CFN 42]
190	ZP_010...	85707884	PntB, NAD(P) transhydrogenase, beta subunit [Erythrobacter NAP1]
191	YP_293266	72383912	NAD(P) transhydrogenase, beta subunit [Ralstonia eutropha JMP134]
192	ZP_009...	84356795	COG1282: NAD/NADP transhydrogenase beta subunit [Burkholderia cenocepacia PC184]
193	YP_266000	71083281	NAD(p) transhydrogenase subunit beta [Candidatus Pelagibac ubique HTCC1062]
194	CAE68875	39598183	Hypothetical protein CBG14838 [Caenorhabditis briggsae]
195	YP_368033	78065264	NAD(P) transhydrogenase, beta subunit [Burkholderia sp. 38
196	YP_616428	103486867	NAD(P) transhydrogenase, beta subunit [Sphingopyxis alaskensis RB2256]
197	YP_246075	67458451	NAD(p) transhydrogenase subunit beta [Rickettsia felis URRWXCal2]
198	YP_537194	91204839	NAD(p) transhydrogenase subunit beta [Rickettsia bellii RML369-C]
199	XP_646840	66826971	NAD(P)+ transhydrogenase (AB-specific) [Dictyostelium discoideum AX4]
200	ZP_009...	83747817	NAD(P) transhydrogenase subunit beta [Ralstonia solanacear UW551]
201	YP_047599	50086089	pyridine nucleotide transhydrogenase, beta subunit [Acinetobacter sp. ADP1]

Table 76. Examples of pox2 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_505264.1	50555712	YlPOX2 [Yarrowia lipolytica].
2	O74936	59799074	Acyl-coenzyme A oxidase 3 (Acyl-CoA oxidase 3)
3	XP_504475	50554133	YlPOX4 [Yarrowia lipolytica]
4	XP_502199	50549457	YlPOX5 [Yarrowia lipolytica]
5	O74934	59799072	Acyl-coenzyme A oxidase 1 (Acyl-CoA oxidase 1)
6	XP_504703	50554589	YlPOX1 [Yarrowia lipolytica]
7	XP_503632	50552444	hypothetical protein [Yarrowia lipolytica]
8	XP_760471	71020481	hypothetical protein UM04324.1 [Ustilago maydis 521]
9	XP_571768	58269224	Acyl-coenzyme A oxidase I [Cryptococcus neoformans var. neoformans JEC21]
10	XP_717995	68475844	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
11	P08790	17373073	Acyl-coenzyme A oxidase 5 (Acyl-CoA oxidase 5) (PXP-5)
12	Q6BRD5	59799027	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
13	OXCKX5	66061	acyl-CoA oxidase (EC 1.3.3.6) POX5, peroxisomal - yeast (Candida tropicalis)
14	BAA83482	5763520	acyl-CoA oxidase [Candida tropicalis]
15	XP_457726	50417804	hypothetical protein DEHA0C01155g [Debaryomyces hansen CBS767]
16	BAA83483	5763522	acyl-CoA oxidase [Candida tropicalis]
17	OXCKPM	66060	acyl-CoA oxidase (EC 1.3.3.6) PXP4, peroxisomal - yeast (Candida maltosa)
18	AAA34362	170912	acyl-coenzyme A oxidase II precursor
19	Q9Y7B1	60391213	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
20	XP_721610	68468582	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
21	AAA34361	170910	PXP-2 protein
22	1306283A	225549	oxidase,fatty acyl
23	P06598	17373023	Acyl-coenzyme A oxidase 4 (Acyl-CoA oxidase 4) (PXP-4) (Peroxisomal fatty acyl-CoA oxidase)
24	XP_721613	68468588	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
25	XP_459232	50421365	hypothetical protein DEHA0D18667g [Debaryomyces hansen CBS767]
26	Q00468	2498206	Acyl-coenzyme A oxidase 2 (Acyl-CoA oxidase 2) (AOX 2)
27	Q6CKK7	59799028	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
28	NP_011310	6321233	Fatty-acyl coenzyme A oxidase, involved in the fatty acid beta oxidation pathway; localized to the peroxisomal matrix; Pox1p [Saccharomyces cerevisiae]
29	AAA34891	172217	acyl-coenzyme A oxidase
30	Q6FY63	59799032	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
31	Q756A9	60391210	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
32	O65202	62286589	Acyl-coenzyme A oxidase 1, peroxisomal (AOX 1) (Long-cha acyl-CoA oxidase) (AtCX1)
33	1W07B	58177067	Chain B, Arabidopsis Thaliana Acyl-Coa Oxidase 1
34	NP_567513	18414744	ACX1 (ACYL-COA OXIDASE 1) [Arabidopsis thaliana]
35	H71434	7488059	probable apetala2 domain TINY - Arabidopsis thaliana
36	XP_001...	109118312	PREDICTED: similar to acyl-Coenzyme A oxidase isoform b [Macaca mulatta]
37	Q5RC19	62286600	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA

			oxidase) (AOX)
38	Q15067	17380467	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) (Straight-chain acyl-CoA oxidase) (SCOX)
39	NP_009223	30089974	acyl-Coenzyme A oxidase isoform b [Homo sapiens]
40	AAB30019	7689914	peroxisomal acyl-coenzyme A oxidase [Homo sapiens]
41	CAH90691	55727877	hypothetical protein [Pongo pygmaeus]
42	AAL01888	15553480	acyl-CoA oxidase [Glycine max]
43	AAA19113	458119	acyl-CoA oxidase
44	AAA18595	495475	peroxisomal fatty acyl-coA oxidase
45	XP_540441	73965013	PREDICTED: similar to acyl-Coenzyme A oxidase isoform a [Canis familiaris]
46	NP_001...	54400372	hypothetical protein LOC449662 [Danio rerio]
47	NP_001...	78369480	acyl-Coenzyme A oxidase 1, palmitoyl [Bos taurus]
48	NP_004026	30089972	acyl-Coenzyme A oxidase isoform a [Homo sapiens]
49	AAH08767	14250616	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
50	CAD97622	31873262	hypothetical protein [Homo sapiens]
51	I38095	2117541	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal - human
52	NP_001...	55741614	acyl-Coenzyme A oxidase 1, palmitoyl [Gallus gallus]
53	CAA68660	2673	acyl-coenzyme A oxidase [Candida tropicalis]
54	Q8HYL8	34098564	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
55	B54942	1082171	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal splice form II - human
56	AAH10425	14714578	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
57	CAJ83302	89271321	acyl-Coenzyme A oxidase 2, branched chain [Xenopus tropicalis]
58	AAO15577	27462768	acyl-CoA oxidase type 2 [Phascolarctos cinereus]
59	XP_414406	50754485	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Gallus gallus]
60	AAH97101	67678187	Zgc:92584 protein [Danio rerio]
61	AAH85743	55249685	Acyl-Coenzyme A oxidase 1, palmitoyl [Rattus norvegicus]
62	2DDHA	93279231	Chain A, Crystal Structure Of Acyl-Coa Oxidase Complexed With 3-Oh- Dodecanoate
63	Q9ZQP2	62286640	Putative acyl-coenzyme A oxidase 1.2, peroxisomal
64	AAH63727	39795632	MGC68531 protein [Xenopus laevis]
65	NP_001...	62751552	MGC108278 protein [Xenopus tropicalis]
66	AAH68891	46250227	MGC83074 protein [Xenopus laevis]
67	AAW78689	58531948	peroxisomal acyl-CoA oxidase 1A [Lycopersicon esculentum]
68	2FONC	109157678	Chain C, X-Ray Crystal Structure Of Leacx1, An Acyl-Coa Oxidase From Lycopersicon Esculentum (Tomato)
69	ABE83706	92875906	acyl-CoA oxidase [Medicago truncatula]
70	XP_511690	55645995	PREDICTED: similar to hypothetical protein [Pan troglodytes
71	AAW78691	58531952	peroxisomal acyl-CoA oxidase 1A [Lycopersicon cheesmania
72	AAL01887	15553478	acyl-CoA oxidase [Glycine max]
73	Q9Z1N0	17367267	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
74	BAA86870	6429156	peroxisomal acyl-CoA oxidase [Mus musculus]
75	Q9R0H0	51338830	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
76	BAF18456	113594582	Os06g0103500 [Oryza sativa (japonica cultivar-group)]
77	AAI08648	83318302	Unknown (protein for MGC:131363) [Xenopus laevis]

78	AAB62926	2253380	peroxisomal acyl-CoA oxidase [Mus musculus]
79	NP_056544	66793429	acyl-Coenzyme A oxidase 1, palmitoyl [Mus musculus]
80	XP_320717	58394415	ENSANGP00000020118 [Anopheles gambiae str. PEST]
81	AAH21339	18204156	Acox2 protein [Mus musculus]
82	BAE25794	74188249	unnamed protein product [Mus musculus]
83	Q9QXD1	17367045	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,12 alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (3 alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
84	XP_320718	58394417	ENSANGP00000020032 [Anopheles gambiae str. PEST]
85	EAT39640	108875415	acyl-CoA oxidase [Aedes aegypti]
86	NP_665713	21955130	acyl-Coenzyme A oxidase 2, branched chain [Rattus norvegic
87	XP_625136	66556360	PREDICTED: similar to CG5009-PA, partial [Apis mellifera]
88	CAE63479	39592402	Hypothetical protein CBG07946 [Caenorhabditis briggsae]
89	XP_879996	76648809	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 6 [Bos taurus]
90	BAC26167	26324826	unnamed protein product [Mus musculus]
91	XP_592892	76648807	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 1 [Bos taurus]
92	AAH47700	28839704	Acyl-Coenzyme A oxidase 2, branched chain [Homo sapiens]
93	XP_541826	73985284	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Canis familiaris]
94	XP_782824	72015136	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
95	EAR95568	89297580	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
96	CAE63477	39592400	Hypothetical protein CBG07944 [Caenorhabditis briggsae]
97	NP_510603	17568313	F59F4.1 [Caenorhabditis elegans]
98	EAT48205	108883980	acyl-CoA oxidase [Aedes aegypti]
99	XP_785210	72015040	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
100	O02767	17366131	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,12 alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (3 alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
101	AAW78690	58531950	peroxisomal acyl-CoA oxidase 1B [Lycopersicon esculentum]
102	CAE63480	39592403	Hypothetical protein CBG07947 [Caenorhabditis briggsae]
103	EAS31618	90301987	hypothetical protein CIMG_07097 [Coccidioides immitis RS]
104	CAE63476	39592399	Hypothetical protein CBG07943 [Caenorhabditis briggsae]
105	XP_973660	91082769	PREDICTED: similar to CG5009-PA [Tribolium castaneum]
106	CAE69737	39596101	Hypothetical protein CBG16008 [Caenorhabditis briggsae]
107	NP_611264	24654595	CG5009-PA [Drosophila melanogaster]
108	AAF73843	8163758	acyl-CoA oxidase ACX3 [Arabidopsis thaliana]

109	Q9LLH9	62286634	Acyl-coenzyme A oxidase 3, peroxisomal precursor (AOX 3) (Medium-chain acyl-CoA oxidase) (AtCX3)
110	EAL26359	54636956	GA18591-PA [Drosophila pseudoobscura]
111	AAH54727	68262425	Acox1 protein [Mus musculus]
112	XP_783450	72111190	PREDICTED: similar to acyl-Coenzyme A oxidase 1, palmit [Strongylocentrotus purpuratus]
113	XP_758355	71010163	hypothetical protein UM02208.1 [Ustilago maydis 521]
114	AAL28144	16767852	GH01266p [Drosophila melanogaster]
115	NP_001...	71983346	F08A8.1a [Caenorhabditis elegans]
116	EAS04704	89306716	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
117	NP_493263	17506533	F08A8.3 [Caenorhabditis elegans]
118	BAC35782	74197284	unnamed protein product [Mus musculus]
119	XP_635946	66804335	hypothetical protein DDBDRAFT_0188674 [Dictyostelium discoideum AX4]
120	NP_493264	17506535	F08A8.4 [Caenorhabditis elegans]
121	CAJ58493	85539740	Hypothetical protein F08A8.1c [Caenorhabditis elegans]
122	NP_001...	71983355	F08A8.1b [Caenorhabditis elegans]
123	EAS02716	89304728	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
124	XP_879827	76648805	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 5 [Bos taurus]
125	CAH91864	55730283	hypothetical protein [Pongo pygmaeus]
126	NP_499119	17552648	C48B4.1 [Caenorhabditis elegans]
127	ZP_012...	90587482	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Flavobacterium johnsoni UW101]
128	BAE55537	83765394	unnamed protein product [Aspergillus oryzae]
129	XP_637610	66807775	hypothetical protein DDBDRAFT_0187085 [Dictyostelium discoideum AX4]
130	BAF19505	113595631	Os06g0354500 [Oryza sativa (japonica cultivar-group)]
131	EAT87650	111066530	hypothetical protein SNOG_05259 [Phaeosphaeria nodorum SN15]
132	CAE65171	39590798	Hypothetical protein CBG10043 [Caenorhabditis briggsae]
133	XP_636605	66805767	hypothetical protein DDBDRAFT_0188084 [Dictyostelium discoideum AX4]
134	XP_664356	67541164	hypothetical protein AN6752.2 [Aspergillus nidulans FGSC A
135	EAR99631	89301643	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
136	NP_493262	17506531	F08A8.2 [Caenorhabditis elegans]
137	XP_382463	46110811	hypothetical protein FG02287.1 [Gibberella zeae PH-1]
138	AAL39944	17862934	SD03592p [Drosophila melanogaster]
139	NP_523802	17647123	acyl-Coenzyme A oxidase at 57D proximal CG9707-PA [Drosophila melanogaster]
140	XP_587157	76620513	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Bos taurus]
141	EAR98581	89300593	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
142	Q9LMI7	62286635	Putative acyl-coenzyme A oxidase 3.2, peroxisomal precursor
143	O65201	62286588	Acyl-coenzyme A oxidase 2, peroxisomal precursor (AOX 2) (Long-chain acyl-CoA oxidase) (AtCX2)

144	AAC13497	3044212	acyl-CoA oxidase [Arabidopsis thaliana]
145	CAH91120	55728762	hypothetical protein [Pongo pygmaeus]
146	EAR89261	89291273	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
147	XP_646395	66826081	hypothetical protein DDBDRAFT_0216722 [Dictyostelium discoideum AX4]
148	O64894	62286587	Acyl-coenzyme A oxidase, peroxisomal precursor (AOX) (Long-chain acyl-CoA oxidase)
149	NP_998312	47085909	pristanoyl acyl-Coenzyme A oxidase 3 [Danio rerio]
150	O15254	17366151	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
151	AAL48010	17944231	LD22081p [Drosophila melanogaster]
152	ZP_012...	89890388	acyl-CoA oxidase [Flavobacteria bacterium BBFL7]
153	XP_758113	71007469	hypothetical protein UM01966.1 [Ustilago maydis 521]
154	EAL26647	54637244	GA21980-PA [Drosophila pseudoobscura]
155	NP_109646	34328334	acyl-Coenzyme A oxidase 3, pristanoyl [Mus musculus]
156	YP_290295	72162638	hypothetical protein Tfu_2239 [Thermobifida fusca YX]
157	AAH44725	28703869	Acox3 protein [Mus musculus]
158	NP_445791	16758056	acyl-Coenzyme A oxidase 3, pristanoyl [Rattus norvegicus]
159	YP_445820	83816544	acyl-coenzyme A oxidase I, putative [Salinibacter ruber DSM 13855]
160	AAB67883	1575556	acyl-CoA oxidase homolog [Phalaenopsis sp. 'True Lady']
161	AAR00586	37699750	acyl-CoA oxidase [Phalaenopsis cv. 'True Lady']
162	XP_969513	91093755	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase [Tribolium castaneum]
163	XP_786025	72005645	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase [Strongylocentrotus purpuratus]
164	YP_634556	108758121	putative acyl-CoA dehydrogenase [Myxococcus xanthus DK 1622]
165	EAT87454	111066334	hypothetical protein SNOG_05063 [Phaeosphaeria nodorum SN15]
166	Q9EPL9	17366740	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
167	XP_545908	73951751	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Canis familiaris]
168	EAL26648	54637245	GA21981-PA [Drosophila pseudoobscura]
169	BAC26136	26324764	unnamed protein product [Mus musculus]
170	CAA04688	2370232	putative acyl-CoA oxidase [Hordeum vulgare subsp. vulgare]
171	BAE42553	74143079	unnamed protein product [Mus musculus]
172	YP_702012	111019040	acyl-CoA oxidase [Rhodococcus sp. RHA1]
173	XP_786081	72005647	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase [Strongylocentrotus purpuratus]
174	NP_001...	79332306	ACX2 (ACYL-COA OXIDASE 2); acyl-CoA oxidase [Arabidopsis thaliana]
175	NP_572371	24640268	CG4586-PA [Drosophila melanogaster]
176	NP_961035	41408199	hypothetical protein MAP2101 [Mycobacterium avium subsp paratuberculosis K-10]
177	EAL32329	54643586	GA18278-PA [Drosophila pseudoobscura]
178	ZP_012...	90205075	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium vanbaale PYR-1]
179	ABA94670	108864573	Acyl-coenzyme A oxidase 2, peroxisomal precursor, putative, expressed [Oryza sativa (japonica cultivar-group)]

180	BAE60166	83770031	unnamed protein product [Aspergillus oryzae]
181	ZP_011...	89339305	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium flavesce PYR-GCK]
182	NP_609027	45550141	CG9527-PA [Drosophila melanogaster]
183	EAT48670	108884445	acyl-CoA oxidase [Aedes aegypti]
184	ZP_012...	92908524	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium sp. JLS]
185	AAH17053	16877606	ACOX3 protein [Homo sapiens]
186	ZP_004...	66967405	Acyl-CoA oxidase:Acyl-CoA dehydrogenase, C-terminal [Arthrobacter sp. FB24]
187	NP_508036	17560134	F25C8.1 [Caenorhabditis elegans]
188	ZP_011...	88854811	acyl-CoA oxidase [marine actinobacterium PHSC20C1]
189	AAL48950	17945806	RE34879p [Drosophila melanogaster]
190	YP_640598	108800401	acyl-CoA dehydrogenase-like protein [Mycobacterium sp. MCS]
191	NP_724181	24585195	CG17544-PC, isoform C [Drosophila melanogaster]
192	AAL14003	16186117	SD05719p [Drosophila melanogaster]
193	XP_642669	66817952	hypothetical protein DDBDRAFT_0169270 [Dictyostelium discoideum AX4]
194	CAA96917	1945301	POX1 [Saccharomyces cerevisiae]
195	NP_500943	17540842	F58F9.7 [Caenorhabditis elegans]
196	XP_664369	67541190	hypothetical protein AN6765.2 [Aspergillus nidulans FGSC A

Table 77. Example of pox1a polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_504703	50554589	YlPOX1 [Yarrowia lipolytica].
2	O74934	59799072	Acyl-coenzyme A oxidase 1 (Acyl-CoA oxidase 1)
3	O74936	59799074	Acyl-coenzyme A oxidase 3 (Acyl-CoA oxidase 3)
4	XP_502199	50549457	YlPOX5 [Yarrowia lipolytica]
5	O74935	59799073	Acyl-coenzyme A oxidase 2 (Acyl-CoA oxidase 2)
6	XP_503632	50552444	hypothetical protein [Yarrowia lipolytica]
7	XP_504475	50554133	YlPOX4 [Yarrowia lipolytica]
8	XP_760471	71020481	hypothetical protein UM04324.1 [Ustilago maydis 521]
9	XP_571768	58269224	Acyl-coenzyme A oxidase I [Cryptococcus neoformans var. neoformans JEC21]
10	XP_717995	68475844	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
11	P08790	17373073	Acyl-coenzyme A oxidase 5 (Acyl-CoA oxidase 5) (PXP-5)
12	OXCKX5	66061	acyl-CoA oxidase (EC 1.3.3.6) POX5, peroxisomal - yeast (Candida tropicalis)
13	Q9Y7B1	60391213	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
14	Q6BRD5	59799027	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
15	XP_457726	50417804	hypothetical protein DEHA0C01155g [Debaryomyces hansen CBS767]
16	AAA34362	170912	acyl-coenzyme A oxidase II precursor
17	XP_459232	50421365	hypothetical protein DEHA0D18667g [Debaryomyces hanser CBS767]
18	BAA83482	5763520	acyl-CoA oxidase [Candida tropicalis]
19	BAA83483	5763522	acyl-CoA oxidase [Candida tropicalis]
20	OXCKPM	66060	acyl-CoA oxidase (EC 1.3.3.6) PXP4, peroxisomal - yeast (Candida maltosa)
21	AAA34361	170910	PXP-2 protein
22	XP_721610	68468582	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
23	1306283A	225549	oxidase,fatty acyl
24	P06598	17373023	Acyl-coenzyme A oxidase 4 (Acyl-CoA oxidase 4) (PXP-4) (Peroxisomal fatty acyl-CoA oxidase)
25	XP_721613	68468588	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
26	Q00468	2498206	Acyl-coenzyme A oxidase 2 (Acyl-CoA oxidase 2) (AOX 2)
27	Q6CKK7	59799028	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
28	Q6FY63	59799032	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
29	Q756A9	60391210	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
30	NP_011310	6321233	Fatty-acyl coenzyme A oxidase, involved in the fatty acid beta oxidation pathway; localized to the peroxisomal matrix; Pox1p [Saccharomyces cerevisiae]
31	AAA34891	172217	acyl-coenzyme A oxidase
32	O65202	62286589	Acyl-coenzyme A oxidase 1, peroxisomal (AOX 1) (Long-cha acyl-CoA oxidase) (AtCX1)
33	1W07B	58177067	Chain B, Arabidopsis Thaliana Acyl-Coa Oxidase 1
34	H71434	7488059	probable apetala2 domain TINY - Arabidopsis thaliana
35	NP_567513	18414744	ACX1 (ACYL-COA OXIDASE 1) [Arabidopsis thaliana]
36	Q9ZQP2	62286640	Putative acyl-coenzyme A oxidase 1.2, peroxisomal
37	AAL01888	15553480	acyl-CoA oxidase [Glycine max]

38	CAA68660	2673	acyl-coenzyme A oxidase [Candida tropicalis]
39	AAL01887	15553478	acyl-CoA oxidase [Glycine max]
40	BAF18456	113594582	Os06g0103500 [Oryza sativa (japonica cultivar-group)]
41	NP_001...	55741614	acyl-Coenzyme A oxidase 1, palmitoyl [Gallus gallus]
42	AAH68891	46250227	MGC83074 protein [Xenopus laevis]
43	2FONC	109157678	Chain C, X-Ray Crystal Structure Of Leacx1, An Acyl-Coa Oxidase From Lycopersicon Esculentum (Tomato)
44	NP_001...	54400372	hypothetical protein LOC449662 [Danio rerio]
45	AAW78689	58531948	peroxisomal acyl-CoA oxidase 1A [Lycopersicon esculentum
46	XP_001...	109118312	PREDICTED: similar to acyl-Coenzyme A oxidase isoform b [Macaca mulatta]
47	AAW78691	58531952	peroxisomal acyl-CoA oxidase 1A [Lycopersicon cheesmania
48	Q5RC19	62286600	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
49	ABE83706	92875906	acyl-CoA oxidase [Medicago truncatula]
50	NP_009223	30089974	acyl-Coenzyme A oxidase isoform b [Homo sapiens]
51	Q15067	17380467	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) (Straight-chain acyl-CoA oxidase) (SCOX)
52	AAA18595	495475	peroxisomal fatty acyl-coA oxidase
53	AAA19113	458119	acyl-CoA oxidase
54	NP_001...	78369480	acyl-Coenzyme A oxidase 1, palmitoyl [Bos taurus]
55	AAH63727	39795632	MGC68531 protein [Xenopus laevis]
56	AAB30019	7689914	peroxisomal acyl-coenzyme A oxidase [Homo sapiens]
57	NP_001...	62751552	MGC108278 protein [Xenopus tropicalis]
58	BAA86870	6429156	peroxisomal acyl-CoA oxidase [Mus musculus]
59	Q9R0H0	51338830	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
60	AAH85743	55249685	Acyl-Coenzyme A oxidase 1, palmitoyl [Rattus norvegicus]
61	AAB62926	2253380	peroxisomal acyl-CoA oxidase [Mus musculus]
62	CAH90691	55727877	hypothetical protein [Pongo pygmaeus]
63	CAJ83302	89271321	acyl-Coenzyme A oxidase 2, branched chain [Xenopus tropicalis]
64	AAH97101	67678187	Zgc:92584 protein [Danio rerio]
65	NP_004026	30089972	acyl-Coenzyme A oxidase isoform a [Homo sapiens]
66	AAH08767	14250616	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
67	CAD97622	31873262	hypothetical protein [Homo sapiens]
68	B54942	1082171	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal splice form II - human
69	2DDHA	93279231	Chain A, Crystal Structure Of Acyl-Coa Oxidase Complexed With 3-Oh- Dodecanoate
70	XP_540441	73965013	PREDICTED: similar to acyl-Coenzyme A oxidase isoform a [Canis familiaris]
71	I38095	2117541	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal - human
72	AAH10425	14714578	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
73	NP_056544	66793429	acyl-Coenzyme A oxidase 1, palmitoyl [Mus musculus]
74	AAI08648	83318302	Unknown (protein for MGC:131363) [Xenopus laevis]
75	Q9Z1N0	17367267	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
76	XP_414406	50754485	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Gallus gallus]

77	Q8HYL8	34098564	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
78	XP_511690	55645995	PREDICTED: similar to hypothetical protein [Pan troglodyte
79	AAO15577	27462768	acyl-CoA oxidase type 2 [Phascolarctos cinereus]
80	XP_625136	66556360	PREDICTED: similar to CG5009-PA, partial [Apis mellifera
81	XP_320717	58394415	ENSANGP00000020118 [Anopheles gambiae str. PEST]
82	EAT39640	108875415	acyl-CoA oxidase [Aedes aegypti]
83	BAC26167	26324826	unnamed protein product [Mus musculus]
84	EAS31618	90301987	hypothetical protein CIMG_07097 [Coccidioides immitis RS
85	XP_382463	46110811	hypothetical protein FG02287.1 [Gibberella zeae PH-1]
86	XP_320718	58394417	ENSANGP00000020032 [Anopheles gambiae str. PEST]
87	CAE63479	39592402	Hypothetical protein CBG07946 [Caenorhabditis briggsae]
88	AAW78690	58531950	peroxisomal acyl-CoA oxidase 1B [Lycopersicon esculentum
89	CAE69737	39596101	Hypothetical protein CBG16008 [Caenorhabditis briggsae]
90	AAH21339	18204156	Acox2 protein [Mus musculus]
91	BAE25794	74188249	unnamed protein product [Mus musculus]
92	EAR95568	89297580	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
93	BAE55537	83765394	unnamed protein product [Aspergillus oryzae]
94	Q9QXD1	17367045	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,1 alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
95	NP_510603	17568313	F59F4.1 [Caenorhabditis elegans]
96	XP_785210	72015040	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
97	XP_973660	91082769	PREDICTED: similar to CG5009-PA [Tribolium castaneum]
98	XP_782824	72015136	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
99	AAH47700	28839704	Acyl-Coenzyme A oxidase 2, branched chain [Homo sapiens]
100	CAE63480	39592403	Hypothetical protein CBG07947 [Caenorhabditis briggsae]
101	O02767	17366131	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,12 alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
102	NP_665713	21955130	acyl-Coenzyme A oxidase 2, branched chain [Rattus norvegic
103	XP_664356	67541164	hypothetical protein AN6752.2 [Aspergillus nidulans FGSC A
104	EAT48205	108883980	acyl-CoA oxidase [Aedes aegypti]
105	CAE63477	39592400	Hypothetical protein CBG07944 [Caenorhabditis briggsae]
106	XP_758355	71010163	hypothetical protein UM02208.1 [Ustilago maydis 521]
107	CAE65171	39590798	Hypothetical protein CBG10043 [Caenorhabditis briggsae]
108	XP_637610	66807775	hypothetical protein DDBDRAFT_0187085 [Dictyostelium discoideum AX4]
109	NP_499119	17552648	C48B4.1 [Caenorhabditis elegans]
110	XP_635946	66804335	hypothetical protein DDBDRAFT_0188674 [Dictyostelium discoideum AX4]

111	XP_592892	76648807	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 1 [Bos taurus]
112	XP_879996	76648809	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 6 [Bos taurus]
113	XP_783450	72111190	PREDICTED: similar to acyl-Coenzyme A oxidase 1, palmit [Strongylocentrotus purpuratus]
114	XP_541826	73985284	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Canis familiaris]
115	EAR89261	89291273	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
116	AAH54727	68262425	Acox1 protein [Mus musculus]
117	BAC35782	74197284	unnamed protein product [Mus musculus]
118	NP_493263	17506533	F08A8.3 [Caenorhabditis elegans]
119	AAF14635	6503198	acyl-CoA oxidase [Petroselinum crispum]
120	CAE63476	39592399	Hypothetical protein CBG07943 [Caenorhabditis briggsae]
121	AAL39944	17862934	SD03592p [Drosophila melanogaster]
122	NP_523802	17647123	acyl-Coenzyme A oxidase at 57D proximal CG9707-PA [Drosophila melanogaster]
123	ZP_012...	90587482	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Flavobacterium johnsoni UW101]
124	AAR00586	37699750	acyl-CoA oxidase [Phalaenopsis cv. 'True Lady']
125	XP_758113	71007469	hypothetical protein UM01966.1 [Ustilago maydis 521]
126	AAB67883	1575556	acyl-CoA oxidase homolog [Phalaenopsis sp. 'True Lady']
127	NP_001...	71983346	F08A8.1a [Caenorhabditis elegans]
128	NP_001...	71983355	F08A8.1b [Caenorhabditis elegans]
129	CAJ58493	85539740	Hypothetical protein F08A8.1c [Caenorhabditis elegans]
130	AAC13497	3044212	acyl-CoA oxidase [Arabidopsis thaliana]
131	O65201	62286588	Acyl-coenzyme A oxidase 2, peroxisomal precursor (AOX 2) (Long-chain acyl-CoA oxidase) (AtCX2)
132	EAS04704	89306716	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
133	EAL26359	54636956	GA18591-PA [Drosophila pseudoobscura]
134	XP_636605	66805767	hypothetical protein DDBDRAFT_0188084 [Dictyostelium discoideum AX4]
135	O64894	62286587	Acyl-coenzyme A oxidase, peroxisomal precursor (AOX) (Long-chain acyl-CoA oxidase)
136	NP_611264	24654595	CG5009-PA [Drosophila melanogaster]
137	NP_493264	17506535	F08A8.4 [Caenorhabditis elegans]
138	AAH44725	28703869	Acox3 protein [Mus musculus]
139	NP_109646	34328334	acyl-Coenzyme A oxidase 3, pristanoyl [Mus musculus]
140	XP_786025	72005645	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidas [Strongylocentrotus purpuratus]
141	XP_646395	66826081	hypothetical protein DDBDRAFT_0216722 [Dictyostelium discoideum AX4]
142	EAT87650	111066530	hypothetical protein SNOG_05259 [Phaeosphaeria nodorum SN15]

143	NP_998312	47085909	pristanoyl acyl-Coenzyme A oxidase 3 [Danio rerio]
144	YP_634556	108758121	putative acyl-CoA dehydrogenase [Myxococcus xanthus DK 1622]
145	AAL28144	16767852	GH01266p [Drosophila melanogaster]
146	YP_445820	83816544	acyl-coenzyme A oxidase I, putative [Salinibacter ruber DSM 13855]
147	EAL26647	54637244	GA21980-PA [Drosophila pseudoobscura]
148	XP_786081	72005647	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidas [Strongylocentrotus purpuratus]
149	EAR99631	89301643	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
150	NP_493262	17506531	F08A8.2 [Caenorhabditis elegans]
151	CAH91864	55730283	hypothetical protein [Pongo pygmaeus]
152	Q9LLH9	62286634	Acyl-coenzyme A oxidase 3, peroxisomal precursor (AOX 3 (Medium-chain acyl-CoA oxidase) (AtCX3)
153	AAF73843	8163758	acyl-CoA oxidase ACX3 [Arabidopsis thaliana]
154	XP_969513	91093755	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidas [Tribolium castaneum]
155	O15254	17366151	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
156	Q9EPL9	17366740	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
157	NP_445791	16758056	acyl-Coenzyme A oxidase 3, pristanoyl [Rattus norvegicus]
158	ABA94670	108864573	Acyl-coenzyme A oxidase 2, peroxisomal precursor, putative expressed [Oryza sativa (japonica cultivar-group)]
159	EAT87454	111066334	hypothetical protein SNOG_05063 [Phaeosphaeria nodorum SN15]
160	EAL26648	54637245	GA21981-PA [Drosophila pseudoobscura]
161	EAR98581	89300593	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
162	BAE42553	74143079	unnamed protein product [Mus musculus]
163	BAC26136	26324764	unnamed protein product [Mus musculus]
164	XP_879827	76648805	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 5 [Bos taurus]
165	XP_587157	76620513	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Bos taurus]
166	YP_290295	72162638	hypothetical protein Tfu_2239 [Thermobifida fusca YX]
167	CAH91120	55728762	hypothetical protein [Pongo pygmaeus]
168	EAS02716	89304728	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
169	AAL48010	17944231	LD22081p [Drosophila melanogaster]
170	XP_545908	73951751	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Canis familiaris]
171	ZP_011...	88854811	acyl-CoA oxidase [marine actinobacterium PHSC20C1]
172	NP_001...	79332306	ACX2 (ACYL-COA OXIDASE 2); acyl-CoA oxidase [Arabidopsis thaliana]
173	BAF19505	113595631	Os06g0354500 [Oryza sativa (japonica cultivar-group)]
174	EAL32329	54643586	GA18278-PA [Drosophila pseudoobscura]
175	CAA04688	2370232	putative acyl-CoA oxidase [Hordeum vulgare subsp. vulgare
176	ZP_012...	89890388	acyl-CoA oxidase [Flavobacteria bacterium BBFL7]
177	Q9LMI7	62286635	Putative acyl-coenzyme A oxidase 3.2, peroxisomal precurso

178	XP_395486	66564429	PREDICTED: similar to CG9527-PA [Apis mellifera]
179	YP_702012	111019040	acyl-CoA oxidase [Rhodococcus sp. RHA1]
180	ZP_012...	90205075	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium vanbaal PYR-1]
181	AAL48950	17945806	RE34879p [Drosophila melanogaster]
182	NP_609027	45550141	CG9527-PA [Drosophila melanogaster]
183	ZP_006...	71369913	Acyl-CoA oxidase:Acyl-CoA dehydrogenase, C-terminal:Ac CoA dehydrogenase, central region:Acyl-CoA dehydrogenas N-terminal [Nocardioides sp. JS614]
184	ZP_012...	92908524	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium sp. JLS]
185	EAT48670	108884445	acyl-CoA oxidase [Aedes aegypti]
186	XP_317446	58390030	ENSANGP00000011863 [Anopheles gambiae str. PEST]
187	EAS36523	90306892	hypothetical protein CIMG_01877 [Coccidioides immitis RS
188	NP_572371	24640268	CG4586-PA [Drosophila melanogaster]
189	XP_642669	66817952	hypothetical protein DDBDRAFT_0169270 [Dictyostelium discoideum AX4]
190	CAA96917	1945301	POX1 [Saccharomyces cerevisiae]
191	ZP_011...	89339305	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium flavesce PYR-GCK]
192	ZP_003...	62426247	COG1960: Acyl-CoA dehydrogenases [Brevibacterium linen BL2]
193	YP_640598	108800401	acyl-CoA dehydrogenase-like protein [Mycobacterium sp. MCS]
194	NP_724181	24585195	CG17544-PC, isoform C [Drosophila melanogaster]
195	AAL14003	16186117	SD05719p [Drosophila melanogaster]
196	AAH17053	16877606	ACOX3 protein [Homo sapiens]
197	EAL32912	54644170	GA21857-PA [Drosophila pseudoobscura]

Table 78. Examples of pox4 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_504475.1	50554133	YlPOX4 [Yarrowia lipolytica]
2	O74935	59799073	Acyl-coenzyme A oxidase 2 (Acyl-CoA oxidase 2)
3	O74936	59799074	Acyl-coenzyme A oxidase 3 (Acyl-CoA oxidase 3)
4	XP_502199	50549457	YlPOX5 [Yarrowia lipolytica]
5	O74934	59799072	Acyl-coenzyme A oxidase 1 (Acyl-CoA oxidase 1)
6	XP_504703	50554589	YlPOX1 [Yarrowia lipolytica]
7	XP_503632	50552444	hypothetical protein [Yarrowia lipolytica]
8	XP_760471	71020481	hypothetical protein UM04324.1 [Ustilago maydis 521]
9	XP_571768	58269224	Acyl-coenzyme A oxidase I [Cryptococcus neoformans var. neoformans JEC21]
10	XP_717995	68475844	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
11	BAA83482	5763520	acyl-CoA oxidase [Candida tropicalis]
12	BAA83483	5763522	acyl-CoA oxidase [Candida tropicalis]
13	OXCKPM	66060	acyl-CoA oxidase (EC 1.3.3.6) PXP4, peroxisomal - yeast (Candida maltosa)
14	XP_721610	68468582	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
15	AAA34362	170912	acyl-coenzyme A oxidase II precursor
16	P08790	17373073	Acyl-coenzyme A oxidase 5 (Acyl-CoA oxidase 5) (PXP-5)
17	OXCKX5	66061	acyl-CoA oxidase (EC 1.3.3.6) POX5, peroxisomal - yeast (Candida tropicalis)
18	Q6BRD5	59799027	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
19	XP_457726	50417804	hypothetical protein DEHA0C01155g [Debaryomyces hansei CBS767]
20	P06598	17373023	Acyl-coenzyme A oxidase 4 (Acyl-CoA oxidase 4) (PXP-4) (Peroxisomal fatty acyl-CoA oxidase)
21	1306283A	225549	oxidase,fatty acyl
22	AAA34361	170910	PXP-2 protein
23	XP_459232	50421365	hypothetical protein DEHA0D18667g [Debaryomyces hansei CBS767]
24	Q9Y7B1	60391213	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
25	XP_721613	68468588	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
26	Q00468	2498206	Acyl-coenzyme A oxidase 2 (Acyl-CoA oxidase 2) (AOX 2)
27	Q6FY63	59799032	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
28	NP_011310	6321233	Fatty-acyl coenzyme A oxidase, involved in the fatty acid bet oxidation pathway; localized to the peroxisomal matrix; Pox1 [Saccharomyces cerevisiae]
29	AAA34891	172217	acyl-coenzyme A oxidase
30	Q6CKK7	59799028	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
31	Q756A9	60391210	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
32	O65202	62286589	Acyl-coenzyme A oxidase 1, peroxisomal (AOX 1) (Long-ch acyl-CoA oxidase) (AtCX1)
33	CAA68660	2673	acyl-coenzyme A oxidase [Candida tropicalis]
34	1W07B	58177067	Chain B, Arabidopsis Thaliana Acyl-Coa Oxidase 1
35	AAL01888	15553480	acyl-CoA oxidase [Glycine max]
36	H71434	7488059	probable apetala2 domain TINY - Arabidopsis thaliana
37	NP_567513	18414744	ACX1 (ACYL-COA OXIDASE 1) [Arabidopsis thaliana]
38	AAH63727	39795632	MGC68531 protein [Xenopus laevis]

39	AAL01887	15553478	acyl-CoA oxidase [Glycine max]
40	AAI08648	83318302	Unknown (protein for MGC:131363) [Xenopus laevis]
41	BAF18456	113594582	Os06g0103500 [Oryza sativa (japonica cultivar-group)]
42	Q9ZQP2	62286640	Putative acyl-coenzyme A oxidase 1.2, peroxisomal
43	NP_001...	78369480	acyl-Coenzyme A oxidase 1, palmitoyl [Bos taurus]
44	ABE83706	92875906	acyl-CoA oxidase [Medicago truncatula]
45	NP_001...	62751552	MGC108278 protein [Xenopus tropicalis]
46	NP_001...	55741614	acyl-Coenzyme A oxidase 1, palmitoyl [Gallus gallus]
47	AAW78689	58531948	peroxisomal acyl-CoA oxidase 1A [Lycopersicon esculentum
48	2FONC	109157678	Chain C, X-Ray Crystal Structure Of Leacx1, An Acyl-Coa Oxidase From Lycopersicon Esculentum (Tomato)
49	NP_001...	54400372	hypothetical protein LOC449662 [Danio rerio]
50	AAW78691	58531952	peroxisomal acyl-CoA oxidase 1A [Lycopersicon cheesmania
51	Q5RC19	62286600	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
52	XP_001...	109118312	PREDICTED: similar to acyl-Coenzyme A oxidase isoform b [Macaca mulatta]
53	Q15067	17380467	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) (Straight-chain acyl-CoA oxidase) (SCOX)
54	NP_009223	30089974	acyl-Coenzyme A oxidase isoform b [Homo sapiens]
55	AAO15577	27462768	acyl-CoA oxidase type 2 [Phascolarctos cinereus]
56	AAB30019	7689914	peroxisomal acyl-coenzyme A oxidase [Homo sapiens]
57	AAH97101	67678187	Zgc:92584 protein [Danio rerio]
58	XP_414406	50754485	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Gallus gallus]
59	AAA19113	458119	acyl-CoA oxidase
60	AAA18595	495475	peroxisomal fatty acyl-coA oxidase
61	Q9Z1N0	17367267	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
62	Q8HYL8	34098564	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
63	AAH85743	55249685	Acyl-Coenzyme A oxidase 1, palmitoyl [Rattus norvegicus]
64	AAH10425	14714578	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
65	CAH90691	55727877	hypothetical protein [Pongo pygmaeus]
66	CAD97622	31873262	hypothetical protein [Homo sapiens]
67	AAH08767	14250616	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
68	NP_004026	30089972	acyl-Coenzyme A oxidase isoform a [Homo sapiens]
69	I38095	2117541	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal - human
70	BAA86870	6429156	peroxisomal acyl-CoA oxidase [Mus musculus]
71	CAJ83302	89271321	acyl-Coenzyme A oxidase 2, branched chain [Xenopus tropicalis]
72	Q9R0H0	51338830	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
73	AAB62926	2253380	peroxisomal acyl-CoA oxidase [Mus musculus]
74	B54942	1082171	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal splice form II - human
75	XP_320717	58394415	ENSANGP00000020118 [Anopheles gambiae str. PEST]
76	BAE25794	74188249	unnamed protein product [Mus musculus]
77	AAH21339	18204156	Acox2 protein [Mus musculus]
78	2DDHA	93279231	Chain A, Crystal Structure Of Acyl-Coa Oxidase Complexed With 3-Oh- Dodecanoate

79	Q9QXD1	17367045	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,1 alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
80	AAH68891	46250227	MGC83074 protein [Xenopus laevis]
81	XP_540441	73965013	PREDICTED: similar to acyl-Coenzyme A oxidase isoform a [Canis familiaris]
82	XP_320718	58394417	ENSANGP00000020032 [Anopheles gambiae str. PEST]
83	XP_511690	55645995	PREDICTED: similar to hypothetical protein [Pan troglodyte
84	NP_056544	66793429	acyl-Coenzyme A oxidase 1, palmitoyl [Mus musculus]
85	EAT39640	108875415	acyl-CoA oxidase [Aedes aegypti]
86	XP_783450	72111190	PREDICTED: similar to acyl-Coenzyme A oxidase 1, palmit [Strongylocentrotus purpuratus]
87	NP_665713	21955130	acyl-Coenzyme A oxidase 2, branched chain [Rattus norvegic
88	XP_973660	91082769	PREDICTED: similar to CG5009-PA [Tribolium castaneum]
89	CAE63476	39592399	Hypothetical protein CBG07943 [Caenorhabditis briggsae]
90	XP_625136	66556360	PREDICTED: similar to CG5009-PA, partial [Apis mellifera]
91	XP_592892	76648807	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 1 [Bos taurus]
92	XP_879996	76648809	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 6 [Bos taurus]
93	AAW78690	58531950	peroxisomal acyl-CoA oxidase 1B [Lycopersicon esculentum
94	AAH47700	28839704	Acyl-Coenzyme A oxidase 2, branched chain [Homo sapiens]
95	CAE69737	39596101	Hypothetical protein CBG16008 [Caenorhabditis briggsae]
96	NP_499119	17552648	C48B4.1 [Caenorhabditis elegans]
97	CAE65171	39590798	Hypothetical protein CBG10043 [Caenorhabditis briggsae]
98	XP_541826	73985284	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Canis familiaris]
99	NP_510603	17568313	F59F4.1 [Caenorhabditis elegans]
100	NP_001...	71983346	F08A8.1a [Caenorhabditis elegans]
101	EAR95568	89297580	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
102	NP_001...	71983355	F08A8.1b [Caenorhabditis elegans]
103	CAJ58493	85539740	Hypothetical protein F08A8.1c [Caenorhabditis elegans]
104	EAL26359	54636956	GA18591-PA [Drosophila pseudoobscura]
105	BAC26167	26324826	unnamed protein product [Mus musculus]
106	CAE63479	39592402	Hypothetical protein CBG07946 [Caenorhabditis briggsae]
107	O02767	17366131	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,1 alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
108	NP_611264	24654595	CG5009-PA [Drosophila melanogaster]
109	CAE63480	39592403	Hypothetical protein CBG07947 [Caenorhabditis briggsae]
110	XP_758355	71010163	hypothetical protein UM02208.1 [Ustilago maydis 521]
111	EAT48205	108883980	acyl-CoA oxidase [Aedes aegypti]

112	XP_782824	72015136	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
113	AAL28144	16767852	GH01266p [Drosophila melanogaster]
114	XP_785210	72015040	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
115	EAS31618	90301987	hypothetical protein CIMG_07097 [Coccidioides immitis RS
116	XP_879827	76648805	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 5 [Bos taurus]
117	CAH91864	55730283	hypothetical protein [Pongo pygmaeus]
118	NP_493263	17506533	F08A8.3 [Caenorhabditis elegans]
119	Q9LLH9	62286634	Acyl-coenzyme A oxidase 3, peroxisomal precursor (AOX 3) (Medium-chain acyl-CoA oxidase) (AtCX3)
120	AAF73843	8163758	acyl-CoA oxidase ACX3 [Arabidopsis thaliana]
121	AAL39944	17862934	SD03592p [Drosophila melanogaster]
122	NP_523802	17647123	acyl-Coenzyme A oxidase at 57D proximal CG9707-PA [Drosophila melanogaster]
123	AAH54727	68262425	Acox1 protein [Mus musculus]
124	BAC35782	74197284	unnamed protein product [Mus musculus]
125	BAE55537	83765394	unnamed protein product [Aspergillus oryzae]
126	CAE63477	39592400	Hypothetical protein CBG07944 [Caenorhabditis briggsae]
127	XP_636605	66805767	hypothetical protein DDBDRAFT_0188084 [Dictyostelium discoideum AX4]
128	NP_493264	17506535	F08A8.4 [Caenorhabditis elegans]
129	NP_493262	17506531	F08A8.2 [Caenorhabditis elegans]
130	EAL26648	54637245	GA21981-PA [Drosophila pseudoobscura]
131	AAF14635	6503198	acyl-CoA oxidase [Petroselinum crispum]
132	XP_664356	67541164	hypothetical protein AN6752.2 [Aspergillus nidulans FGSC A
133	EAL26647	54637244	GA21980-PA [Drosophila pseudoobscura]
134	AAL48010	17944231	LD22081p [Drosophila melanogaster]
135	ZP_012...	90587482	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Flavobacterium johnsoni UW101]
136	CAA04688	2370232	putative acyl-CoA oxidase [Hordeum vulgare subsp. vulgare]
137	Q9LMI7	62286635	Putative acyl-coenzyme A oxidase 3.2, peroxisomal precurso
138	EAR89261	89291273	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
139	YP_290295	72162638	hypothetical protein Tfu_2239 [Thermobifida fusca YX]
140	XP_758113	71007469	hypothetical protein UM01966.1 [Ustilago maydis 521]
141	BAF19505	113595631	Os06g0354500 [Oryza sativa (japonica cultivar-group)]
142	XP_317446	58390030	ENSANGP00000011863 [Anopheles gambiae str. PEST]
143	XP_635946	66804335	hypothetical protein DDBDRAFT_0188674 [Dictyostelium discoideum AX4]
144	XP_382463	46110811	hypothetical protein FG02287.1 [Gibberella zeae PH-1]
145	YP_445820	83816544	acyl-coenzyme A oxidase I, putative [Salinibacter ruber DSM 13855]
146	EAR99631	89301643	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
147	EAT87650	111066530	hypothetical protein SNOG_05259 [Phaeosphaeria nodorum SN15]

148	O15254	17366151	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
149	NP_508036	17560134	F25C8.1 [Caenorhabditis elegans]
150	NP_998312	47085909	pristanoyl acyl-Coenzyme A oxidase 3 [Danio rerio]
151	EAL32329	54643586	GA18278-PA [Drosophila pseudoobscura]
152	EAS02716	89304728	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
153	EAT48670	108884445	acyl-CoA oxidase [Aedes aegypti]
154	CAH91120	55728762	hypothetical protein [Pongo pygmaeus]
155	EAS04704	89306716	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
156	ZP_012...	89890388	acyl-CoA oxidase [Flavobacteria bacterium BBFL7]
157	O64894	62286587	Acyl-coenzyme A oxidase, peroxisomal precursor (AOX) (Long-chain acyl-CoA oxidase)
158	XP_969513	91093755	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase [Tribolium castaneum]
159	AAC13497	3044212	acyl-CoA oxidase [Arabidopsis thaliana]
160	O65201	62286588	Acyl-coenzyme A oxidase 2, peroxisomal precursor (AOX 2) (Long-chain acyl-CoA oxidase) (AtCX2)
161	XP_646395	66826081	hypothetical protein DDBDRAFT_0216722 [Dictyostelium discoideum AX4]
162	YP_634556	108758121	putative acyl-CoA dehydrogenase [Myxococcus xanthus DK 1622]
163	XP_587157	76620513	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Bos taurus]
164	EAR98581	89300593	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
165	XP_637610	66807775	hypothetical protein DDBDRAFT_0187085 [Dictyostelium discoideum AX4]
166	NP_572371	24640268	CG4586-PA [Drosophila melanogaster]
167	EAT87454	111066334	hypothetical protein SNOG_05063 [Phaeosphaeria nodorum SN15]
168	AAB67883	1575556	acyl-CoA oxidase homolog [Phalaenopsis sp. 'True Lady']
169	NP_961035	41408199	hypothetical protein MAP2101 [Mycobacterium avium subsp. paratuberculosis K-10]
170	ABA94670	108864573	Acyl-coenzyme A oxidase 2, peroxisomal precursor, putative, expressed [Oryza sativa (japonica cultivar-group)]
171	AAR00586	37699750	acyl-CoA oxidase [Phalaenopsis cv. 'True Lady']
172	XP_545908	73951751	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Canis familiaris]
173	YP_702012	111019040	acyl-CoA oxidase [Rhodococcus sp. RHA1]
174	ZP_012...	90205075	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium vanbaale PYR-1]
175	EAS36523	90306892	hypothetical protein CIMG_01877 [Coccidioides immitis RS]
176	NP_001...	79332306	ACX2 (ACYL-COA OXIDASE 2); acyl-CoA oxidase [Arabidopsis thaliana]
177	CAA68661	2674	44 kD translation product [Candida tropicalis]
178	ZP_012...	92908524	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium sp. JLS]
179	XP_786025	72005645	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase [Strongylocentrotus purpuratus]
180	CAA96917	1945301	POX1 [Saccharomyces cerevisiae]

181	BAE60166	83770031	unnamed protein product [Aspergillus oryzae]
182	ZP_011...	89339305	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium flavesce PYR-GCK]
183	YP_640598	108800401	acyl-CoA dehydrogenase-like protein [Mycobacterium sp. MCS]
184	ZP_006...	71369913	Acyl-CoA oxidase:Acyl-CoA dehydrogenase, C-terminal:Ac CoA dehydrogenase, central region:Acyl-CoA dehydrogenas N-terminal [Nocardioides sp. JS614]
185	AAL14003	16186117	SD05719p [Drosophila melanogaster]
186	NP_724181	24585195	CG17544-PC, isoform C [Drosophila melanogaster]
187	AAH44725	28703869	Acox3 protein [Mus musculus]
188	NP_109646	34328334	acyl-Coenzyme A oxidase 3, pristanoyl [Mus musculus]
189	EAL33335	54644594	GA14550-PA [Drosophila pseudoobscura]
190	ZP_004...	66967405	Acyl-CoA oxidase:Acyl-CoA dehydrogenase, C-terminal [Arthrobacter sp. FB24]
191	NP_445791	16758056	acyl-Coenzyme A oxidase 3, pristanoyl [Rattus norvegicus]
192	XP_786081	72005647	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidas [Strongylocentrotus purpuratus]
193	Q9EPL9	17366740	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
194	NP_609027	45550141	CG9527-PA [Drosophila melanogaster]
195	ZP_006...	69287897	Acyl-CoA dehydrogenase, C-terminal:Acyl-CoA dehydrogenase, central region [Kineococcus radiotolerans SRS30216]
196	BAE47462	78483008	acyl-CoA oxidase [Arthrobacter ureafaciens]

Table 79. Examples of pox1 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_503632	50552444	hypothetical protein [Yarrowia lipolytica].
2	O74935	59799073	Acyl-coenzyme A oxidase 2 (Acyl-CoA oxidase 2)
3	O74936	59799074	Acyl-coenzyme A oxidase 3 (Acyl-CoA oxidase 3)
4	XP_502199	50549457	YlPOX5 [Yarrowia lipolytica]
5	O74934	59799072	Acyl-coenzyme A oxidase 1 (Acyl-CoA oxidase 1)
6	XP_504703	50554589	YlPOX1 [Yarrowia lipolytica]
7	XP_504475	50554133	YlPOX4 [Yarrowia lipolytica]
8	XP_760471	71020481	hypothetical protein UM04324.1 [Ustilago maydis 521]
9	XP_571768	58269224	Acyl-coenzyme A oxidase I [Cryptococcus neoformans var. neoformans JEC21]
10	AAA34362	170912	acyl-coenzyme A oxidase II precursor
11	BAA83482	5763520	acyl-CoA oxidase [Candida tropicalis]
12	XP_717995	68475844	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
13	BAA83483	5763522	acyl-CoA oxidase [Candida tropicalis]
14	XP_721610	68468582	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
15	OXCKPM	66060	acyl-CoA oxidase (EC 1.3.3.6) PXP4, peroxisomal - yeast (Candida maltosa)
16	P08790	17373073	Acyl-coenzyme A oxidase 5 (Acyl-CoA oxidase 5) (PXP-5)
17	OXCKX5	66061	acyl-CoA oxidase (EC 1.3.3.6) POX5, peroxisomal - yeast (Candida tropicalis)
18	XP_721613	68468588	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
19	AAA34361	170910	PXP-2 protein
20	Q6BRD5	59799027	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
21	1306283A	225549	oxidase,fatty acyl
22	P06598	17373023	Acyl-coenzyme A oxidase 4 (Acyl-CoA oxidase 4) (PXP-4) (Peroxisomal fatty acyl-CoA oxidase)
23	XP_459232	50421365	hypothetical protein DEHA0D18667g [Debaryomyces hanser CBS767]
24	Q00468	2498206	Acyl-coenzyme A oxidase 2 (Acyl-CoA oxidase 2) (AOX 2)
25	XP_457726	50417804	hypothetical protein DEHA0C01155g [Debaryomyces hansen CBS767]
26	Q9Y7B1	60391213	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
27	Q6CKK7	59799028	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
28	NP_011310	6321233	Fatty-acyl coenzyme A oxidase, involved in the fatty acid bet oxidation pathway; localized to the peroxisomal matrix; Pox1 [Saccharomyces cerevisiae]
29	AAA34891	172217	acyl-coenzyme A oxidase
30	Q6FY63	59799032	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)

31	Q756A9	60391210	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
32	CAA68660	2673	acyl-coenzyme A oxidase [Candida tropicalis]
33	1W07B	58177067	Chain B, Arabidopsis Thaliana Acyl-Coa Oxidase 1
34	O65202	62286589	Acyl-coenzyme A oxidase 1, peroxisomal (AOX 1) (Long-ch acyl-CoA oxidase) (AtCX1)
35	NP_001...	55741614	acyl-Coenzyme A oxidase 1, palmitoyl [Gallus gallus]
36	AAH85743	55249685	Acyl-Coenzyme A oxidase 1, palmitoyl [Rattus norvegicus]
37	XP_414406	50754485	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Gallus gallus]
38	H71434	7488059	probable apetala2 domain TINY - Arabidopsis thaliana
39	2DDHA	93279231	Chain A, Crystal Structure Of Acyl-Coa Oxidase Complexed With 3-Oh- Dodecanoate
40	NP_567513	18414744	ACX1 (ACYL-COA OXIDASE 1) [Arabidopsis thaliana]
41	NP_001...	62751552	MGC108278 protein [Xenopus tropicalis]
42	AAI08648	83318302	Unknown (protein for MGC:131363) [Xenopus laevis]
43	AAH97101	67678187	Zgc:92584 protein [Danio rerio]
44	AAH63727	39795632	MGC68531 protein [Xenopus laevis]
45	NP_001...	54400372	hypothetical protein LOC449662 [Danio rerio]
46	AAL01888	15553480	acyl-CoA oxidase [Glycine max]
47	ABE83706	92875906	acyl-CoA oxidase [Medicago truncatula]
48	AAL01887	15553478	acyl-CoA oxidase [Glycine max]
49	BAE25794	74188249	unnamed protein product [Mus musculus]
50	NP_056544	66793429	acyl-Coenzyme A oxidase 1, palmitoyl [Mus musculus]
51	XP_001...	109118312	PREDICTED: similar to acyl-Coenzyme A oxidase isoform b [Macaca mulatta]
52	BAA86870	6429156	peroxisomal acyl-CoA oxidase [Mus musculus]
53	Q9R0H0	51338830	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
54	AAB62926	2253380	peroxisomal acyl-CoA oxidase [Mus musculus]
55	AAA18595	495475	peroxisomal fatty acyl-coA oxidase
56	Q5RC19	62286600	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
57	2FONC	109157678	Chain C, X-Ray Crystal Structure Of Leacx1, An Acyl-Coa Oxidase From Lycopersicon Esculentum (Tomato)
58	AAW78689	58531948	peroxisomal acyl-CoA oxidase 1A [Lycopersicon esculentum
59	AAW78691	58531952	peroxisomal acyl-CoA oxidase 1A [Lycopersicon cheesmania
60	CAH90691	55727877	hypothetical protein [Pongo pygmaeus]
61	NP_009223	30089974	acyl-Coenzyme A oxidase isoform b [Homo sapiens]
62	Q15067	17380467	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) (Straight-chain acyl-CoA oxidase) (SCOX)

63	AAH21339	18204156	Acox2 protein [Mus musculus]
64	NP_004026	30089972	acyl-Coenzyme A oxidase isoform a [Homo sapiens]
65	NP_001...	78369480	acyl-Coenzyme A oxidase 1, palmitoyl [Bos taurus]
66	Q9ZQP2	62286640	Putative acyl-coenzyme A oxidase 1.2, peroxisomal
67	AAH08767	14250616	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
68	AAH68891	46250227	MGC83074 protein [Xenopus laevis]
69	Q8HYL8	34098564	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
70	XP_540441	73965013	PREDICTED: similar to acyl-Coenzyme A oxidase isoform a [Canis familiaris]
71	AAB30019	7689914	peroxisomal acyl-coenzyme A oxidase [Homo sapiens]
72	CAD97622	31873262	hypothetical protein [Homo sapiens]
73	I38095	2117541	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal - human
74	BAF18456	113594582	Os06g0103500 [Oryza sativa (japonica cultivar-group)]
75	AAH10425	14714578	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
76	AAA19113	458119	acyl-CoA oxidase
77	B54942	1082171	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal splice form II - human
78	Q9QXD1	17367045	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,12 alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
79	Q9Z1N0	17367267	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
80	CAJ83302	89271321	acyl-Coenzyme A oxidase 2, branched chain [Xenopus tropicalis]
81	XP_511690	55645995	PREDICTED: similar to hypothetical protein [Pan troglodytes
82	XP_592892	76648807	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 1 [Bos taurus]
83	XP_879996	76648809	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 6 [Bos taurus]
84	AAO15577	27462768	acyl-CoA oxidase type 2 [Phascolarctos cinereus]
85	NP_665713	21955130	acyl-Coenzyme A oxidase 2, branched chain [Rattus norvegic
86	XP_320718	58394417	ENSANGP00000020032 [Anopheles gambiae str. PEST]
87	NP_510603	17568313	F59F4.1 [Caenorhabditis elegans]
88	XP_541826	73985284	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Canis familiaris]
89	CAE69737	39596101	Hypothetical protein CBG16008 [Caenorhabditis briggsae]

90	CAE63479	39592402	Hypothetical protein CBG07946 [Caenorhabditis briggsae]
91	XP_782824	72015136	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
92	AAH47700	28839704	Acyl-Coenzyme A oxidase 2, branched chain [Homo sapiens
93	XP_785210	72015040	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
94	EAT39640	108875415	acyl-CoA oxidase [Aedes aegypti]
95	EAS31618	90301987	hypothetical protein CIMG_07097 [Coccidioides immitis RS
96	O02767	17366131	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,1 alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
97	NP_998312	47085909	pristanoyl acyl-Coenzyme A oxidase 3 [Danio rerio]
98	XP_783450	72111190	PREDICTED: similar to acyl-Coenzyme A oxidase 1, palmit [Strongylocentrotus purpuratus]
99	EAR95568	89297580	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
100	XP_320717	58394415	ENSANGP00000020118 [Anopheles gambiae str. PEST]
101	NP_493263	17506533	F08A8.3 [Caenorhabditis elegans]
102	AAF73843	8163758	acyl-CoA oxidase ACX3 [Arabidopsis thaliana]
103	BAC26167	26324826	unnamed protein product [Mus musculus]
104	Q9LLH9	62286634	Acyl-coenzyme A oxidase 3, peroxisomal precursor (AOX 3) (Medium-chain acyl-CoA oxidase) (AtCX3)
105	NP_493264	17506535	F08A8.4 [Caenorhabditis elegans]
106	XP_758355	71010163	hypothetical protein UM02208.1 [Ustilago maydis 521]
107	XP_664356	67541164	hypothetical protein AN6752.2 [Aspergillus nidulans FGSC A
108	EAT48205	108883980	acyl-CoA oxidase [Aedes aegypti]
109	XP_879827	76648805	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 5 [Bos taurus]
110	NP_499119	17552648	C48B4.1 [Caenorhabditis elegans]
111	O15254	17366151	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
112	BAE55537	83765394	unnamed protein product [Aspergillus oryzae]
113	XP_625136	66556360	PREDICTED: similar to CG5009-PA, partial [Apis mellifera]
114	CAE63476	39592399	Hypothetical protein CBG07943 [Caenorhabditis briggsae]
115	NP_523802	17647123	acyl-Coenzyme A oxidase at 57D proximal CG9707-PA [Drosophila melanogaster]
116	AAH54727	68262425	Acox1 protein [Mus musculus]
117	BAC35782	74197284	unnamed protein product [Mus musculus]

118	AAW78690	58531950	peroxisomal acyl-CoA oxidase 1B [Lycopersicon esculentum
119	AAL39944	17862934	SD03592p [Drosophila melanogaster]
120	XP_786081	72005647	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidas [Strongylocentrotus purpuratus]
121	ZP_012...	90587482	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Flavobacterium johnsoni UW101]
122	CAE63477	39592400	Hypothetical protein CBG07944 [Caenorhabditis briggsae]
123	EAR89261	89291273	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
124	CAE65171	39590798	Hypothetical protein CBG10043 [Caenorhabditis briggsae]
125	CAH91120	55728762	hypothetical protein [Pongo pygmaeus]
126	XP_587157	76620513	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Bos taurus]
127	XP_382463	46110811	hypothetical protein FG02287.1 [Gibberella zeae PH-1]
128	XP_973660	91082769	PREDICTED: similar to CG5009-PA [Tribolium castaneum]
129	CAH91864	55730283	hypothetical protein [Pongo pygmaeus]
130	NP_493262	17506531	F08A8.2 [Caenorhabditis elegans]
131	NP_001...	71983346	F08A8.1a [Caenorhabditis elegans]
132	NP_109646	34328334	acyl-Coenzyme A oxidase 3, pristanoyl [Mus musculus]
133	AAH44725	28703869	Acox3 protein [Mus musculus]
134	XP_969513	91093755	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase [Tribolium castaneum]
135	CAE63480	39592403	Hypothetical protein CBG07947 [Caenorhabditis briggsae]
136	CAJ58493	85539740	Hypothetical protein F08A8.1c [Caenorhabditis elegans]
137	NP_001...	71983355	F08A8.1b [Caenorhabditis elegans]
138	XP_635946	66804335	hypothetical protein DDBDRAFT_0188674 [Dictyostelium discoideum AX4]
139	BAF19505	113595631	Os06g0354500 [Oryza sativa (japonica cultivar-group)]
140	XP_786025	72005645	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase [Strongylocentrotus purpuratus]
141	NP_611264	24654595	CG5009-PA [Drosophila melanogaster]
142	NP_445791	16758056	acyl-Coenzyme A oxidase 3, pristanoyl [Rattus norvegicus]
143	Q9EPL9	17366740	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
144	Q9LMI7	62286635	Putative acyl-coenzyme A oxidase 3.2, peroxisomal precursor
145	BAE42553	74143079	unnamed protein product [Mus musculus]
146	AAL28144	16767852	GH01266p [Drosophila melanogaster]
147	EAT87650	111066530	hypothetical protein SNOG_05259 [Phaeosphaeria nodorum SN15]
148	BAC26136	26324764	unnamed protein product [Mus musculus]
149	XP_545908	73951751	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Canis familiaris]

150	EAR99631	89301643	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
151	AAC13497	3044212	acyl-CoA oxidase [Arabidopsis thaliana]
152	O65201	62286588	Acyl-coenzyme A oxidase 2, peroxisomal precursor (AOX 2) (Long-chain acyl-CoA oxidase) (AtCX2)
153	AAF14635	6503198	acyl-CoA oxidase [Petroselinum crispum]
154	EAS02716	89304728	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
155	AAR00586	37699750	acyl-CoA oxidase [Phalaenopsis cv. 'True Lady']
156	EAS04704	89306716	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
157	YP_634556	108758121	putative acyl-CoA dehydrogenase [Myxococcus xanthus DK 1622]
158	O64894	62286587	Acyl-coenzyme A oxidase, peroxisomal precursor (AOX) (Long-chain acyl-CoA oxidase)
159	AAB67883	1575556	acyl-CoA oxidase homolog [Phalaenopsis sp. 'True Lady']
160	ZP_012...	89890388	acyl-CoA oxidase [Flavobacteria bacterium BBFL7]
161	EAL26359	54636956	GA18591-PA [Drosophila pseudoobscura]
162	EAL26647	54637244	GA21980-PA [Drosophila pseudoobscura]
163	EAR98581	89300593	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
164	AAH17053	16877606	ACOX3 protein [Homo sapiens]
165	XP_636605	66805767	hypothetical protein DDBDRAFT_0188084 [Dictyostelium discoideum AX4]
166	YP_445820	83816544	acyl-coenzyme A oxidase I, putative [Salinibacter ruber DSM 13855]
167	EAT87454	111066334	hypothetical protein SNOG_05063 [Phaeosphaeria nodorum SN15]
168	NP_001...	79332306	ACX2 (ACYL-COA OXIDASE 2); acyl-CoA oxidase [Arabidopsis thaliana]
169	YP_290295	72162638	hypothetical protein Tfu_2239 [Thermobifida fusca YX]
170	XP_646395	66826081	hypothetical protein DDBDRAFT_0216722 [Dictyostelium discoideum AX4]
171	XP_317513	58390136	ENSANGP00000010039 [Anopheles gambiae str. PEST]
172	ZP_012...	90205075	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium vanbaale PYR-1]
173	EAS36523	90306892	hypothetical protein CIMG_01877 [Coccidioides immitis RS]
174	XP_758113	71007469	hypothetical protein UM01966.1 [Ustilago maydis 521]
175	XP_395486	66564429	PREDICTED: similar to CG9527-PA [Apis mellifera]
176	ABA94670	108864573	Acyl-coenzyme A oxidase 2, peroxisomal precursor, putative, expressed [Oryza sativa (japonica cultivar-group)]
177	XP_637610	66807775	hypothetical protein DDBDRAFT_0187085 [Dictyostelium discoideum AX4]
178	ZP_003...	62426247	COG1960: Acyl-CoA dehydrogenases [Brevibacterium linens BL2]
179	YP_702012	111019040	acyl-CoA oxidase [Rhodococcus sp. RHA1]

180	NP_500943	17540842	F58F9.7 [Caenorhabditis elegans]
181	EAT39346	108875121	acyl-CoA oxidase [Aedes aegypti]
182	CAA96917	1945301	POX1 [Saccharomyces cerevisiae]
183	NP_609027	45550141	CG9527-PA [Drosophila melanogaster]
184	CAA04688	2370232	putative acyl-CoA oxidase [Hordeum vulgare subsp. vulgare]
185	AAL48010	17944231	LD22081p [Drosophila melanogaster]
186	EAL32329	54643586	GA18278-PA [Drosophila pseudoobscura]
187	CAE61577	39584202	Hypothetical protein CBG05491 [Caenorhabditis briggsae]
188	AAL48950	17945806	RE34879p [Drosophila melanogaster]
189	NP_724181	24585195	CG17544-PC, isoform C [Drosophila melanogaster]
190	AAL14003	16186117	SD05719p [Drosophila melanogaster]
191	XP_317446	58390030	ENSANGP00000011863 [Anopheles gambiae str. PEST]
192	ZP_011...	89339305	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium flavescei PYR-GCK]
193	ZP_004...	66967405	Acyl-CoA oxidase:Acyl-CoA dehydrogenase, C-terminal [Arthrobacter sp. FB24]
194	ZP_011...	88803915	acyl-coenzyme A oxidase I, putative [Robiginitalea biformata HTCC2501]
195	EAL32912	54644170	GA21857-PA [Drosophila pseudoobscura]
196	EAL26648	54637245	GA21981-PA [Drosophila pseudoobscura]
197	ZP_012...	92908524	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium sp. JLS]

Table 80. Examples of pox3 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_503244	50551539	YlPOX3 [Yarrowia lipolytica]
2	XP_502199	50549457	YlPOX5 [Yarrowia lipolytica]
3	O74935	59799073	Acyl-coenzyme A oxidase 2 (Acyl-CoA oxidase 2)
4	O74934	59799072	Acyl-coenzyme A oxidase 1 (Acyl-CoA oxidase 1)
5	XP_504703	50554589	YlPOX1 [Yarrowia lipolytica]
6	XP_504475	50554133	YlPOX4 [Yarrowia lipolytica]
7	XP_503632	50552444	hypothetical protein [Yarrowia lipolytica]
8	XP_571768	58269224	Acyl-coenzyme A oxidase I [Cryptococcus neoformans var. neoformans JEC21]
9	XP_760471	71020481	hypothetical protein UM04324.1 [Ustilago maydis 521]
10	XP_717995	68475844	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
11	Q6BRD5	59799027	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
12	BAA83482	5763520	acyl-CoA oxidase [Candida tropicalis]
13	OXCKPM	66060	acyl-CoA oxidase (EC 1.3.3.6) PXP4, peroxisomal - yeast (Candida maltosa)
14	BAA83483	5763522	acyl-CoA oxidase [Candida tropicalis]
15	AAA34362	170912	acyl-coenzyme A oxidase II precursor
16	P08790	17373073	Acyl-coenzyme A oxidase 5 (Acyl-CoA oxidase 5) (PXP-5)
17	OXCKX5	66061	acyl-CoA oxidase (EC 1.3.3.6) POX5, peroxisomal - yeast (Candida tropicalis)
18	XP_721610	68468582	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
19	Q9Y7B1	60391213	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
20	XP_457726	50417804	hypothetical protein DEHA0C01155g [Debaryomyces hansen CBS767]
21	P06598	17373023	Acyl-coenzyme A oxidase 4 (Acyl-CoA oxidase 4) (PXP-4) (Peroxisomal fatty acyl-CoA oxidase)
22	AAA34361	170910	PXP-2 protein
23	1306283A	225549	oxidase,fatty acyl
24	XP_721613	68468588	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
25	XP_459232	50421365	hypothetical protein DEHA0D18667g [Debaryomyces hansen CBS767]
26	Q00468	2498206	Acyl-coenzyme A oxidase 2 (Acyl-CoA oxidase 2) (AOX 2)
27	Q6FY63	59799032	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
28	Q6CKK7	59799028	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
29	Q756A9	60391210	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
30	NP_011310	6321233	Fatty-acyl coenzyme A oxidase, involved in the fatty acid beta oxidation pathway; localized to the peroxisomal matrix; Pox1p [Saccharomyces cerevisiae]
31	AAA34891	172217	acyl-coenzyme A oxidase
32	CAA68660	2673	acyl-coenzyme A oxidase [Candida tropicalis]
33	BAF18456	113594582	Os06g0103500 [Oryza sativa (japonica cultivar-group)]
34	O65202	62286589	Acyl-coenzyme A oxidase 1, peroxisomal (AOX 1) (Long-cha acyl-CoA oxidase) (AtCX1)
35	H71434	7488059	probable apetala2 domain TINY - Arabidopsis thaliana
36	1W07B	58177067	Chain B, Arabidopsis Thaliana Acyl-Coa Oxidase 1
37	NP_567513	18414744	ACX1 (ACYL-COA OXIDASE 1) [Arabidopsis thaliana]
38	AAH68891	46250227	MGC83074 protein [Xenopus laevis]
39	AAL01888	15553480	acyl-CoA oxidase [Glycine max]

40	ABE83706	92875906	acyl-CoA oxidase [Medicago truncatula]
41	Q9ZQP2	62286640	Putative acyl-coenzyme A oxidase 1.2, peroxisomal
42	CAJ83302	89271321	acyl-Coenzyme A oxidase 2, branched chain [Xenopus tropicalis]
43	BAE25794	74188249	unnamed protein product [Mus musculus]
44	AAL01887	15553478	acyl-CoA oxidase [Glycine max]
45	AAW78689	58531948	peroxisomal acyl-CoA oxidase 1A [Lycopersicon esculentum
46	2FONC	109157678	Chain C, X-Ray Crystal Structure Of Leacx1, An Acyl-Coa Oxidase From Lycopersicon Esculentum (Tomato)
47	AAW78691	58531952	peroxisomal acyl-CoA oxidase 1A [Lycopersicon cheesmani
48	AAH21339	18204156	Acox2 protein [Mus musculus]
49	XP_320717	58394415	ENSANGP00000020118 [Anopheles gambiae str. PEST]
50	Q9QXD1	17367045	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,1 alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
51	XP_414406	50754485	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Gallus gallus]
52	NP_001...	54400372	hypothetical protein LOC449662 [Danio rerio]
53	AAH63727	39795632	MGC68531 protein [Xenopus laevis]
54	EAT39640	108875415	acyl-CoA oxidase [Aedes aegypti]
55	AAH97101	67678187	Zgc:92584 protein [Danio rerio]
56	NP_001...	55741614	acyl-Coenzyme A oxidase 1, palmitoyl [Gallus gallus]
57	NP_001...	62751552	MGC108278 protein [Xenopus tropicalis]
58	NP_665713	21955130	acyl-Coenzyme A oxidase 2, branched chain [Rattus norvegic
59	XP_320718	58394417	ENSANGP00000020032 [Anopheles gambiae str. PEST]
60	AAI08648	83318302	Unknown (protein for MGC:131363) [Xenopus laevis]
61	CAE63479	39592402	Hypothetical protein CBG07946 [Caenorhabditis briggsae]
62	Q8HYL8	34098564	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
63	EAS31618	90301987	hypothetical protein CIMG_07097 [Coccidioides immitis RS]
64	CAH90691	55727877	hypothetical protein [Pongo pygmaeus]
65	Q5RC19	62286600	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
66	XP_001...	109118312	PREDICTED: similar to acyl-Coenzyme A oxidase isoform b [Macaca mulatta]
67	XP_540441	73965013	PREDICTED: similar to acyl-Coenzyme A oxidase isoform a [Canis familiaris]
68	I38095	2117541	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal - human
69	AAH08767	14250616	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
70	NP_004026	30089972	acyl-Coenzyme A oxidase isoform a [Homo sapiens]
71	CAD97622	31873262	hypothetical protein [Homo sapiens]
72	NP_510603	17568313	F59F4.1 [Caenorhabditis elegans]
73	Q15067	17380467	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) (Straight-chain acyl-CoA oxidase) (SCOX)
74	NP_009223	30089974	acyl-Coenzyme A oxidase isoform b [Homo sapiens]
75	NP_001...	78369480	acyl-Coenzyme A oxidase 1, palmitoyl [Bos taurus]
76	B54942	1082171	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal splice form II - human
77	AAA18595	495475	peroxisomal fatty acyl-coA oxidase

78	AAA19113	458119	acyl-CoA oxidase
79	AAB30019	7689914	peroxisomal acyl-coenzyme A oxidase [Homo sapiens]
80	XP_758355	71010163	hypothetical protein UM02208.1 [Ustilago maydis 521]
81	AAH10425	14714578	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
82	CAE65171	39590798	Hypothetical protein CBG10043 [Caenorhabditis briggsae]
83	O02767	17366131	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,1 alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
84	AAH47700	28839704	Acyl-Coenzyme A oxidase 2, branched chain [Homo sapiens
85	AAO15577	27462768	acyl-CoA oxidase type 2 [Phascolarctos cinereus]
86	CAE69737	39596101	Hypothetical protein CBG16008 [Caenorhabditis briggsae]
87	2DDHA	93279231	Chain A, Crystal Structure Of Acyl-Coa Oxidase Complexed With 3-Oh- Dodecanoate
88	NP_499119	17552648	C48B4.1 [Caenorhabditis elegans]
89	XP_625136	66556360	PREDICTED: similar to CG5009-PA, partial [Apis mellifera
90	XP_879996	76648809	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 6 [Bos taurus]
91	XP_592892	76648807	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 1 [Bos taurus]
92	XP_782824	72015136	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
93	Q9LLH9	62286634	Acyl-coenzyme A oxidase 3, peroxisomal precursor (AOX 3) (Medium-chain acyl-CoA oxidase) (AtCX3)
94	AAF73843	8163758	acyl-CoA oxidase ACX3 [Arabidopsis thaliana]
95	AAH85743	55249685	Acyl-Coenzyme A oxidase 1, palmitoyl [Rattus norvegicus]
96	XP_785210	72015040	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
97	XP_511690	55645995	PREDICTED: similar to hypothetical protein [Pan troglodyte
98	NP_493263	17506533	F08A8.3 [Caenorhabditis elegans]
99	XP_973660	91082769	PREDICTED: similar to CG5009-PA [Tribolium castaneum]
100	CAE63477	39592400	Hypothetical protein CBG07944 [Caenorhabditis briggsae]
101	NP_056544	66793429	acyl-Coenzyme A oxidase 1, palmitoyl [Mus musculus]
102	Q9Z1N0	17367267	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
103	EAT48205	108883980	acyl-CoA oxidase [Aedes aegypti]
104	BAA86870	6429156	peroxisomal acyl-CoA oxidase [Mus musculus]
105	Q9R0H0	51338830	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
106	EAR95568	89297580	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
107	AAB62926	2253380	peroxisomal acyl-CoA oxidase [Mus musculus]
108	AAW78690	58531950	peroxisomal acyl-CoA oxidase 1B [Lycopersicon esculentum
109	XP_635946	66804335	hypothetical protein DDBDRAFT_0188674 [Dictyostelium discoideum AX4]
110	NP_493264	17506535	F08A8.4 [Caenorhabditis elegans]

111	CAE63480	39592403	Hypothetical protein CBG07947 [Caenorhabditis briggsae]
112	NP_001...	71983346	F08A8.1a [Caenorhabditis elegans]
113	CAE63476	39592399	Hypothetical protein CBG07943 [Caenorhabditis briggsae]
114	BAC26167	26324826	unnamed protein product [Mus musculus]
115	XP_541826	73985284	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Canis familiaris]
116	BAE55537	83765394	unnamed protein product [Aspergillus oryzae]
117	NP_001...	71983355	F08A8.1b [Caenorhabditis elegans]
118	CAJ58493	85539740	Hypothetical protein F08A8.1c [Caenorhabditis elegans]
119	EAS04704	89306716	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
120	NP_493262	17506531	F08A8.2 [Caenorhabditis elegans]
121	EAT87650	111066530	hypothetical protein SNOG_05259 [Phaeosphaeria nodorum SN15]
122	O64894	62286587	Acyl-coenzyme A oxidase, peroxisomal precursor (AOX) (Long-chain acyl-CoA oxidase)
123	XP_664356	67541164	hypothetical protein AN6752.2 [Aspergillus nidulans FGSC A
124	XP_783450	72111190	PREDICTED: similar to acyl-Coenzyme A oxidase 1, palmit [Strongylocentrotus purpuratus]
125	BAF19505	113595631	Os06g0354500 [Oryza sativa (japonica cultivar-group)]
126	XP_382463	46110811	hypothetical protein FG02287.1 [Gibberella zeae PH-1]
127	XP_879827	76648805	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 5 [Bos taurus]
128	Q9LMI7	62286635	Putative acyl-coenzyme A oxidase 3.2, peroxisomal precursor
129	AAR00586	37699750	acyl-CoA oxidase [Phalaenopsis cv. 'True Lady']
130	CAH91864	55730283	hypothetical protein [Pongo pygmaeus]
131	NP_998312	47085909	pristanoyl acyl-Coenzyme A oxidase 3 [Danio rerio]
132	AAL39944	17862934	SD03592p [Drosophila melanogaster]
133	NP_523802	17647123	acyl-Coenzyme A oxidase at 57D proximal CG9707-PA [Drosophila melanogaster]
134	EAR99631	89301643	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
135	AAB67883	1575556	acyl-CoA oxidase homolog [Phalaenopsis sp. 'True Lady']
136	AAL48010	17944231	LD22081p [Drosophila melanogaster]
137	EAR98581	89300593	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
138	YP_445820	83816544	acyl-coenzyme A oxidase 1, putative [Salinibacter ruber DSM 13855]
139	EAL26648	54637245	GA21981-PA [Drosophila pseudoobscura]
140	O65201	62286588	Acyl-coenzyme A oxidase 2, peroxisomal precursor (AOX 2) (Long-chain acyl-CoA oxidase) (AtCX2)
141	AAC13497	3044212	acyl-CoA oxidase [Arabidopsis thaliana]
142	AAF14635	6503198	acyl-CoA oxidase [Petroselinum crispum]
143	XP_636605	66805767	hypothetical protein DDBDRAFT_0188084 [Dictyostelium discoideum AX4]
144	O15254	17366151	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
145	XP_758113	71007469	hypothetical protein UM01966.1 [Ustilago maydis 521]
146	NP_611264	24654595	CG5009-PA [Drosophila melanogaster]

147	XP_969513	91093755	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidas [Tribolium castaneum]
148	NP_109646	34328334	acyl-Coenzyme A oxidase 3, pristanoyl [Mus musculus]
149	XP_637610	66807775	hypothetical protein DDBDRAFT_0187085 [Dictyostelium discoideum AX4]
150	BAC35782	74197284	unnamed protein product [Mus musculus]
151	EAL26647	54637244	GA21980-PA [Drosophila pseudoobscura]
152	AAH44725	28703869	Acox3 protein [Mus musculus]
153	AAH54727	68262425	Acox1 protein [Mus musculus]
154	XP_587157	76620513	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Bos taurus]
155	ZP_012...	90587482	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Flavobacterium johnsoni UW101]
156	CAA04688	2370232	putative acyl-CoA oxidase [Hordeum vulgare subsp. vulgare]
157	EAL26359	54636956	GA18591-PA [Drosophila pseudoobscura]
158	AAL28144	16767852	GH01266p [Drosophila melanogaster]
159	CAH91120	55728762	hypothetical protein [Pongo pygmaeus]
160	NP_445791	16758056	acyl-Coenzyme A oxidase 3, pristanoyl [Rattus norvegicus]
161	Q9EPL9	17366740	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
162	XP_786081	72005647	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase [Strongylocentrotus purpuratus]
163	EAR89261	89291273	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
164	ZP_012...	89890388	acyl-CoA oxidase [Flavobacteria bacterium BBFL7]
165	XP_646395	66826081	hypothetical protein DDBDRAFT_0216722 [Dictyostelium discoideum AX4]
166	NP_001...	79332306	ACX2 (ACYL-COA OXIDASE 2); acyl-CoA oxidase [Arabidopsis thaliana]
167	BAC26136	26324764	unnamed protein product [Mus musculus]
168	BAE42553	74143079	unnamed protein product [Mus musculus]
169	EAS02716	89304728	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
170	ABA94670	108864573	Acyl-coenzyme A oxidase 2, peroxisomal precursor, putative, expressed [Oryza sativa (japonica cultivar-group)]
171	YP_290295	72162638	hypothetical protein Tfu_2239 [Thermobifida fusca YX]
172	EAL32329	54643586	GA18278-PA [Drosophila pseudoobscura]
173	EAT87454	111066334	hypothetical protein SNOG_05063 [Phaeosphaeria nodorum SN15]
174	YP_634556	108758121	putative acyl-CoA dehydrogenase [Myxococcus xanthus DK 1622]
175	NP_508036	17560134	F25C8.1 [Caenorhabditis elegans]
176	NP_572371	24640268	CG4586-PA [Drosophila melanogaster]
177	ZP_012...	90205075	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium vanbaale PYR-1]
178	XP_545908	73951751	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Canis familiaris]
179	YP_702012	111019040	acyl-CoA oxidase [Rhodococcus sp. RHA1]
180	ZP_011...	89339305	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium flavesce PYR-GCK]

181	XP_786025	72005645	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidas [Strongylocentrotus purpuratus]
182	BAE60166	83770031	unnamed protein product [Aspergillus oryzae]
183	ZP_012...	92908524	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium sp. JLS]
184	NP_961035	41408199	hypothetical protein MAP2101 [Mycobacterium avium subsp paratuberculosis K-10]
185	YP_640598	108800401	acyl-CoA dehydrogenase-like protein [Mycobacterium sp. MCS]
186	XP_317446	58390030	ENSANGP00000011863 [Anopheles gambiae str. PEST]
187	EAT48670	108884445	acyl-CoA oxidase [Aedes aegypti]
188	BAE47462	78483008	acyl-CoA oxidase [Arthrobacter ureafaciens]
189	ZP_003...	62426247	COG1960: Acyl-CoA dehydrogenases [Brevibacterium linen BL2]
190	AAH17053	16877606	ACOX3 protein [Homo sapiens]
191	ZP_011...	88854811	acyl-CoA oxidase [marine actinobacterium PHSC20C1]
192	ZP_006...	71369913	Acyl-CoA oxidase:Acyl-CoA dehydrogenase, C-terminal:Ac CoA dehydrogenase, central region:Acyl-CoA dehydrogenas N-terminal [Nocardioides sp. JS614]
193	ZP_009...	84496319	hypothetical protein JNB_02330 [Janibacter sp. HTCC2649]
194	ZP_004...	66967405	Acyl-CoA oxidase:Acyl-CoA dehydrogenase, C-terminal [Arthrobacter sp. FB24]
195	ZP_011...	88803915	acyl-coenzyme A oxidase I, putative [Robiginitalea biformata HTCC2501]
196	CAA68661	2674	44 kD translation product [Candida tropicalis]

Table 81. Examples of pox5 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_502199	50549457	YlPOX5 [Yarrowia lipolytica].
2	O74936	59799074	Acyl-coenzyme A oxidase 3 (Acyl-CoA oxidase 3)
3	O74934	59799072	Acyl-coenzyme A oxidase 1 (Acyl-CoA oxidase 1)
4	XP_504703	50554589	YlPOX1 [Yarrowia lipolytica]
5	O74935	59799073	Acyl-coenzyme A oxidase 2 (Acyl-CoA oxidase 2)
6	XP_504475	50554133	YlPOX4 [Yarrowia lipolytica]
7	XP_503632	50552444	hypothetical protein [Yarrowia lipolytica]
8	XP_760471	71020481	hypothetical protein UM04324.1 [Ustilago maydis 521]
9	XP_571768	58269224	Acyl-coenzyme A oxidase I [Cryptococcus neoformans var. neoformans JEC21]
10	BAA83482	5763520	acyl-CoA oxidase [Candida tropicalis]
11	BAA83483	5763522	acyl-CoA oxidase [Candida tropicalis]
12	OXCKPM	66060	acyl-CoA oxidase (EC 1.3.3.6) PXP4, peroxisomal - yeast (Candida maltosa)
13	P08790	17373073	Acyl-coenzyme A oxidase 5 (Acyl-CoA oxidase 5) (PXP-5)
14	AAA34362	170912	acyl-coenzyme A oxidase II precursor
15	OXCKX5	66061	acyl-CoA oxidase (EC 1.3.3.6) POX5, peroxisomal - yeast (Candida tropicalis)
16	XP_717995	68475844	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
17	Q9Y7B1	60391213	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
18	XP_721610	68468582	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
19	AAA34361	170910	PXP-2 protein
20	XP_721613	68468588	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
21	P06598	17373023	Acyl-coenzyme A oxidase 4 (Acyl-CoA oxidase 4) (PXP-4) (Peroxisomal fatty acyl-CoA oxidase)
22	Q6BRD5	59799027	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
23	1306283A	225549	oxidase,fatty acyl
24	XP_457726	50417804	hypothetical protein DEHA0C01155g [Debaryomyces hanser CBS767]
25	XP_459232	50421365	hypothetical protein DEHA0D18667g [Debaryomyces hanser CBS767]
26	Q00468	2498206	Acyl-coenzyme A oxidase 2 (Acyl-CoA oxidase 2) (AOX 2)
27	Q756A9	60391210	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
28	Q6FY63	59799032	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
29	NP_011310	6321233	Fatty-acyl coenzyme A oxidase, involved in the fatty acid bet oxidation pathway; localized to the peroxisomal matrix; Pox1 [Saccharomyces cerevisiae]
30	AAA34891	172217	acyl-coenzyme A oxidase
31	Q6CKK7	59799028	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
32	1W07B	58177067	Chain B, Arabidopsis Thaliana Acyl-Coa Oxidase 1
33	O65202	62286589	Acyl-coenzyme A oxidase 1, peroxisomal (AOX 1) (Long-ch acyl-CoA oxidase) (AtCX1)
34	CAA68660	2673	acyl-coenzyme A oxidase [Candida tropicalis]
35	NP_567513	18414744	ACX1 (ACYL-COA OXIDASE 1) [Arabidopsis thaliana]
36	H71434	7488059	probable apetala2 domain TINY - Arabidopsis thaliana
37	AAL01888	15553480	acyl-CoA oxidase [Glycine max]
38	AAL01887	15553478	acyl-CoA oxidase [Glycine max]

39	ABE83706	92875906	acyl-CoA oxidase [Medicago truncatula]
40	BAF18456	113594582	Os06g0103500 [Oryza sativa (japonica cultivar-group)]
41	2FONC	109157678	Chain C, X-Ray Crystal Structure Of Leacx1, An Acyl-Coa Oxidase From Lycopersicon Esculentum (Tomato)
42	AAW78689	58531948	peroxisomal acyl-CoA oxidase 1A [Lycopersicon esculentum
43	AAW78691	58531952	peroxisomal acyl-CoA oxidase 1A [Lycopersicon cheesmania
44	Q9ZQP2	62286640	Putative acyl-coenzyme A oxidase 1.2, peroxisomal
45	NP_001...	54400372	hypothetical protein LOC449662 [Danio rerio]
46	XP_592892	76648807	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 1 [Bos taurus]
47	XP_879996	76648809	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 6 [Bos taurus]
48	AAH68891	46250227	MGC83074 protein [Xenopus laevis]
49	AAH97101	67678187	Zgc:92584 protein [Danio rerio]
50	XP_414406	50754485	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Gallus gallus]
51	NP_001...	55741614	acyl-Coenzyme A oxidase 1, palmitoyl [Gallus gallus]
52	XP_320717	58394415	ENSANGP00000020118 [Anopheles gambiae str. PEST]
53	NP_510603	17568313	F59F4.1 [Caenorhabditis elegans]
54	BAE25794	74188249	unnamed protein product [Mus musculus]
55	CAE69737	39596101	Hypothetical protein CBG16008 [Caenorhabditis briggsae]
56	AAH21339	18204156	Acox2 protein [Mus musculus]
57	CAJ83302	89271321	acyl-Coenzyme A oxidase 2, branched chain [Xenopus tropicalis]
58	XP_320718	58394417	ENSANGP00000020032 [Anopheles gambiae str. PEST]
59	Q9QXD1	17367045	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,12 alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
60	AAH63727	39795632	MGC68531 protein [Xenopus laevis]
61	Q5RC19	62286600	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
62	AAW78690	58531950	peroxisomal acyl-CoA oxidase 1B [Lycopersicon esculentum
63	XP_782824	72015136	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
64	AAH47700	28839704	Acyl-Coenzyme A oxidase 2, branched chain [Homo sapiens]
65	EAT39640	108875415	acyl-CoA oxidase [Aedes aegypti]
66	NP_001...	62751552	MGC108278 protein [Xenopus tropicalis]
67	CAH90691	55727877	hypothetical protein [Pongo pygmaeus]
68	XP_001...	109118312	PREDICTED: similar to acyl-Coenzyme A oxidase isoform b [Macaca mulatta]
69	Q15067	17380467	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) (Straight-chain acyl-CoA oxidase) (SCOX)
70	NP_009223	30089974	acyl-Coenzyme A oxidase isoform b [Homo sapiens]
71	AAA19113	458119	acyl-CoA oxidase

72	AAB30019	7689914	peroxisomal acyl-coenzyme A oxidase [Homo sapiens]
73	XP_785210	72015040	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
74	O02767	17366131	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,1 alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
75	NP_004026	30089972	acyl-Coenzyme A oxidase isoform a [Homo sapiens]
76	AAA18595	495475	peroxisomal fatty acyl-coA oxidase
77	I38095	2117541	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal - human
78	AAH08767	14250616	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
79	B54942	1082171	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal splice form II - human
80	NP_001...	78369480	acyl-Coenzyme A oxidase 1, palmitoyl [Bos taurus]
81	NP_499119	17552648	C48B4.1 [Caenorhabditis elegans]
82	NP_665713	21955130	acyl-Coenzyme A oxidase 2, branched chain [Rattus norvegic
83	CAD97622	31873262	hypothetical protein [Homo sapiens]
84	BAA86870	6429156	peroxisomal acyl-CoA oxidase [Mus musculus]
85	NP_056544	66793429	acyl-Coenzyme A oxidase 1, palmitoyl [Mus musculus]
86	AAH85743	55249685	Acyl-Coenzyme A oxidase 1, palmitoyl [Rattus norvegicus]
87	2DDHA	93279231	Chain A, Crystal Structure Of Acyl-Coa Oxidase Complexed With 3-Oh- Dodecanoate
88	Q9R0H0	51338830	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
89	XP_758355	71010163	hypothetical protein UM02208.1 [Ustilago maydis 521]
90	AAH10425	14714578	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
91	AAB62926	2253380	peroxisomal acyl-CoA oxidase [Mus musculus]
92	CAE65171	39590798	Hypothetical protein CBG10043 [Caenorhabditis briggsae]
93	XP_625136	66556360	PREDICTED: similar to CG5009-PA, partial [Apis mellifera
94	XP_540441	73965013	PREDICTED: similar to acyl-Coenzyme A oxidase isoform a [Canis familiaris]
95	Q8HYL8	34098564	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
96	CAE63476	39592399	Hypothetical protein CBG07943 [Caenorhabditis briggsae]
97	AAI08648	83318302	Unknown (protein for MGC:131363) [Xenopus laevis]
98	XP_879827	76648805	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 5 [Bos taurus]
99	AAF73843	8163758	acyl-CoA oxidase ACX3 [Arabidopsis thaliana]
100	Q9LLH9	62286634	Acyl-coenzyme A oxidase 3, peroxisomal precursor (AOX 3) (Medium-chain acyl-CoA oxidase) (AtCX3)
101	XP_973660	91082769	PREDICTED: similar to CG5009-PA [Tribolium castaneum]
102	EAS31618	90301987	hypothetical protein CIMG_07097 [Coccidioides immitis RS
103	EAR95568	89297580	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
104	Q9Z1N0	17367267	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
105	AAO15577	27462768	acyl-CoA oxidase type 2 [Phascolarctos cinereus]

106	XP_541826	73985284	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Canis familiaris]
107	CAE63479	39592402	Hypothetical protein CBG07946 [Caenorhabditis briggsae]
108	XP_511690	55645995	PREDICTED: similar to hypothetical protein [Pan troglodyte
109	BAC26167	26324826	unnamed protein product [Mus musculus]
110	CAE63477	39592400	Hypothetical protein CBG07944 [Caenorhabditis briggsae]
111	NP_493264	17506535	F08A8.4 [Caenorhabditis elegans]
112	Q9LMI7	62286635	Putative acyl-coenzyme A oxidase 3.2, peroxisomal precurso
113	CAJ58493	85539740	Hypothetical protein F08A8.1c [Caenorhabditis elegans]
114	NP_001...	71983355	F08A8.1b [Caenorhabditis elegans]
115	NP_001...	71983346	F08A8.1a [Caenorhabditis elegans]
116	BAF19505	113595631	Os06g0354500 [Oryza sativa (japonica cultivar-group)]
117	NP_493263	17506533	F08A8.3 [Caenorhabditis elegans]
118	O64894	62286587	Acyl-coenzyme A oxidase, peroxisomal precursor (AOX) (Long-chain acyl-CoA oxidase)
119	NP_493262	17506531	F08A8.2 [Caenorhabditis elegans]
120	CAE63480	39592403	Hypothetical protein CBG07947 [Caenorhabditis briggsae]
121	AAF14635	6503198	acyl-CoA oxidase [Petroselinum crispum]
122	BAE55537	83765394	unnamed protein product [Aspergillus oryzae]
123	NP_998312	47085909	pristanoyl acyl-Coenzyme A oxidase 3 [Danio rerio]
124	O65201	62286588	Acyl-coenzyme A oxidase 2, peroxisomal precursor (AOX 2) (Long-chain acyl-CoA oxidase) (AtCX2)
125	AAC13497	3044212	acyl-CoA oxidase [Arabidopsis thaliana]
126	EAT87650	111066530	hypothetical protein SNOG_05259 [Phaeosphaeria nodorum SN15]
127	XP_587157	76620513	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Bos taurus]
128	EAT48205	108883980	acyl-CoA oxidase [Aedes aegypti]
129	EAT87454	111066334	hypothetical protein SNOG_05063 [Phaeosphaeria nodorum SN15]
130	XP_664356	67541164	hypothetical protein AN6752.2 [Aspergillus nidulans FGSC A
131	AAB67883	1575556	acyl-CoA oxidase homolog [Phalaenopsis sp. 'True Lady']
132	AAR00586	37699750	acyl-CoA oxidase [Phalaenopsis cv. 'True Lady']
133	CAH91864	55730283	hypothetical protein [Pongo pygmaeus]
134	XP_636605	66805767	hypothetical protein DDBDRAFT_0188084 [Dictyostelium discoideum AX4]
135	NP_611264	24654595	CG5009-PA [Drosophila melanogaster]
136	EAS04704	89306716	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
137	XP_635946	66804335	hypothetical protein DDBDRAFT_0188674 [Dictyostelium discoideum AX4]
138	O15254	17366151	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
139	AAL39944	17862934	SD03592p [Drosophila melanogaster]
140	NP_523802	17647123	acyl-Coenzyme A oxidase at 57D proximal CG9707-PA [Drosophila melanogaster]
141	AAL28144	16767852	GH01266p [Drosophila melanogaster]
142	XP_382463	46110811	hypothetical protein FG02287.1 [Gibberella zeae PH-1]
143	EAL26359	54636956	GA18591-PA [Drosophila pseudoobscura]
144	CAA04688	2370232	putative acyl-CoA oxidase [Hordeum vulgare subsp. vulgare]

145	XP_783450	72111190	PREDICTED: similar to acyl-Coenzyme A oxidase 1, palmit [Strongylocentrotus purpuratus]
146	AAL48010	17944231	LD22081p [Drosophila melanogaster]
147	CAH91120	55728762	hypothetical protein [Pongo pygmaeus]
148	XP_646395	66826081	hypothetical protein DDBDRAFT_0216722 [Dictyostelium discoideum AX4]
149	XP_758113	71007469	hypothetical protein UM01966.1 [Ustilago maydis 521]
150	EAR99631	89301643	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
151	EAR89261	89291273	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
152	XP_637610	66807775	hypothetical protein DDBDRAFT_0187085 [Dictyostelium discoideum AX4]
153	ABA94670	108864573	Acyl-coenzyme A oxidase 2, peroxisomal precursor, putative expressed [Oryza sativa (japonica cultivar-group)]
154	EAL26647	54637244	GA21980-PA [Drosophila pseudoobscura]
155	ZP_012...	90587482	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Flavobacterium johnsoni UW101]
156	BAC35782	74197284	unnamed protein product [Mus musculus]
157	EAS02716	89304728	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
158	YP_634556	108758121	putative acyl-CoA dehydrogenase [Myxococcus xanthus DK 1622]
159	AAH54727	68262425	Acox1 protein [Mus musculus]
160	YP_445820	83816544	acyl-coenzyme A oxidase I, putative [Salinibacter ruber DSM 13855]
161	AAH44725	28703869	Acox3 protein [Mus musculus]
162	NP_109646	34328334	acyl-Coenzyme A oxidase 3, pristanoyl [Mus musculus]
163	XP_545908	73951751	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Canis familiaris]
164	NP_001...	79332306	ACX2 (ACYL-COA OXIDASE 2); acyl-CoA oxidase [Arabidopsis thaliana]
165	EAR98581	89300593	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
166	XP_969513	91093755	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase [Tribolium castaneum]
167	ZP_012...	89890388	acyl-CoA oxidase [Flavobacteria bacterium BBFL7]
168	YP_290295	72162638	hypothetical protein Tfu_2239 [Thermobifida fusca YX]
169	BAC26136	26324764	unnamed protein product [Mus musculus]
170	BAE42553	74143079	unnamed protein product [Mus musculus]
171	EAL26648	54637245	GA21981-PA [Drosophila pseudoobscura]
172	NP_445791	16758056	acyl-Coenzyme A oxidase 3, pristanoyl [Rattus norvegicus]
173	Q9EPL9	17366740	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
174	XP_786025	72005645	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase [Strongylocentrotus purpuratus]
175	XP_786081	72005647	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase [Strongylocentrotus purpuratus]
176	EAL32329	54643586	GA18278-PA [Drosophila pseudoobscura]
177	NP_724181	24585195	CG17544-PC, isoform C [Drosophila melanogaster]
178	AAL14003	16186117	SD05719p [Drosophila melanogaster]
179	CAA68661	2674	44 kD translation product [Candida tropicalis]

180	NP_572371	24640268	CG4586-PA [Drosophila melanogaster]
181	ZP_011...	88854811	acyl-CoA oxidase [marine actinobacterium PHSC20C1]
182	EAL33335	54644594	GA14550-PA [Drosophila pseudoobscura]
183	EAS36523	90306892	hypothetical protein CIMG_01877 [Coccidioides immitis RS]
184	EAT48670	108884445	acyl-CoA oxidase [Aedes aegypti]
185	YP_702012	111019040	acyl-CoA oxidase [Rhodococcus sp. RHA1]
186	ZP_003...	62426247	COG1960: Acyl-CoA dehydrogenases [Brevibacterium linens BL2]
187	XP_317446	58390030	ENSANGP00000011863 [Anopheles gambiae str. PEST]
188	XP_317513	58390136	ENSANGP00000010039 [Anopheles gambiae str. PEST]
189	AAH17053	16877606	ACOX3 protein [Homo sapiens]
190	ZP_012...	90205075	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium vanbaalei PYR-1]
191	ZP_011...	88803915	acyl-coenzyme A oxidase I, putative [Robiginitalea biformata HTCC2501]
192	XP_642669	66817952	hypothetical protein DDBDRAFT_0169270 [Dictyostelium discoideum AX4]
193	NP_508036	17560134	F25C8.1 [Caenorhabditis elegans]
194	ZP_006...	71369913	Acyl-CoA oxidase:Acyl-CoA dehydrogenase, C-terminal:Acyl-CoA dehydrogenase, central region:Acyl-CoA dehydrogenase N-terminal [Nocardioides sp. JS614]
195	BAE65934	83775815	unnamed protein product [Aspergillus oryzae]
196	ZP_012...	92908524	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium sp. JLS]

Table 82. Examples of triglyceride lipase (tgl4) polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_505230	50555644	hypothetical protein [Yarrowia lipolytica].
2	XP_459553	50421985	hypothetical protein DEHA0E06127g [Debaryomyces hansen CBS767]
3	XP_387731	46126355	hypothetical protein FG07555.1 [Gibberella zeae PH-1]
4	XP_717704	68476486	putative patatin-like phospholipase [Candida albicans SC531
5	XP_958750	85091127	hypothetical protein [Neurospora crassa OR74A]
6	NP_013015	6322942	Triacylglycerol lipase involved in triacylglycerol mobilizatior and degradation; found in lipid particles; potential Cdc28p substrate; Tgl4p [Saccharomyces cerevisiae]
7	XP_659317	67522513	hypothetical protein AN1713.2 [Aspergillus nidulans FGSC A
8	NP_984327	45188104	ADR231Cp [Eremothecium gossypii]
9	CAD60564	27764284	unnamed protein product [Podospora anserina]
10	EAT92134	111071014	hypothetical protein SNOG_00639 [Phaeosphaeria nodorum SN15]
11	BAE59228	83769091	unnamed protein product [Aspergillus oryzae]
12	XP_446465	50288073	unnamed protein product [Candida glabrata]
13	XP_751982	70994310	patatin-like serine hydrolase [Aspergillus fumigatus Af293]
14	XP_451336	50302799	unnamed protein product [Kluyveromyces lactis]
15	EAS30095	90300464	hypothetical protein CIMG_08841 [Coccidioides immitis RS]
16	EAQ83092	88175624	hypothetical protein CHGG_10910 [Chaetomium globosum CBS 148.51]
17	NP_014724	6324655	Triacylglycerol lipase involved in TAG mobilization; localize to lipid particles; potential Cdc28p substrate; Tgl5p [Saccharomyces cerevisiae]
18	XP_448470	50292075	unnamed protein product [Candida glabrata]
19	ABG79933	110628937	triacylglycerol lipase [Magnaporthe grisea]
20	NP_593197	19114109	hypothetical protein SPAC1A6.05c [Schizosaccharomyces pombe 972h-]
21	EAR86065	89288077	Patatin-like phospholipase family protein [Tetrahymena thermophila SB210]
22	XP_463448	50902030	P0512C01.22 [Oryza sativa (japonica cultivar-group)]
23	BAF06239	113533856	Os01g0762000 [Oryza sativa (japonica cultivar-group)]
24	YP_433865	83645430	predicted esterase of the alpha-beta hydrolase superfamily [Hahella chejuensis KCTC 2396]
25	ZP_008...	77951643	conserved hypothetical protein [Marinobacter aquaeolei VT8]
26	AAM97135	22531263	putative protein [Arabidopsis thaliana]
27	BAF13581	113550138	Os03g0810900 [Oryza sativa (japonica cultivar-group)]
28	ABE78088	92867978	phospholipase, patatin family, putative [Medicago truncatula]
29	YP_693301	110834442	hypothetical protein ABO_1581 [Alcanivorax borkumensis SK2]
30	NP_974449	42572707	unknown protein [Arabidopsis thaliana]
31	BAE56507	83766364	unnamed protein product [Aspergillus oryzae]
32	EAR83738	89285729	Patatin-like phospholipase family protein [Tetrahymena thermophila SB210]
33	ABE94194	92898449	Patatin [Medicago truncatula]
34	XP_752278	70995024	patatin-like serine hydrolase [Aspergillus fumigatus Af293]
35	YP_046026	50084516	hypothetical protein ACIAD1335 [Acinetobacter sp. ADP1]
36	ZP_011...	88794068	predicted esterase of the alpha-beta hydrolase superfamily protein [Alteromonas macleodii 'Deep ecotype']
37	XP_380696	46107274	hypothetical protein FG00520.1 [Gibberella zeae PH-1]

38	ZP_011...	88703608	Patatin-like phospholipase [gamma proteobacterium KT 71]
39	EAT85718	111064598	hypothetical protein SNOG_07067 [Phaeosphaeria nodorum SN15]
40	ZP_011...	88707125	Patatin-like phospholipase [gamma proteobacterium KT 71]
41	XP_757164	71004996	hypothetical protein UM01017.1 [Ustilago maydis 521]
42	YP_615253	103485692	Patatin [Sphingopyxis alaskensis RB2256]
43	XP_964502	85113293	hypothetical protein [Neurospora crassa OR74A]
44	NP_594022	63054585	hypothetical protein SPAC31G5.20c [Schizosaccharomyces pombe 972h-]
45	XP_502898	50550851	hypothetical protein [Yarrowia lipolytica]
46	XP_722550	68466709	putative patatin-like phospholipase [Candida albicans SC5314
47	EAS31687	90302056	hypothetical protein CIMG_07166 [Coccidioides immitis RS]
48	BAE57969	83767830	unnamed protein product [Aspergillus oryzae]
49	XP_722412	68466994	putative patatin-like phospholipase [Candida albicans SC5314
50	EAQ93362	88185894	hypothetical protein CHGG_01597 [Chaetomium globosum CBS 148.51]
51	ZP_010...	85708568	hypothetical protein NAP1_04995 [Erythrobacter sp. NAP1]
52	XP_457141	50412575	hypothetical protein DEHA0B04048g [Debaryomyces hansen CBS767]
53	XP_658012	67516253	hypothetical protein AN0408.2 [Aspergillus nidulans FGSC A
54	EAS33873	90304242	hypothetical protein CIMG_04897 [Coccidioides immitis RS]
55	XP_805126	71404931	hypothetical protein [Trypanosoma cruzi strain CL Brener]
56	CAB88226	7630152	conserved hypothetical protein L5213T.05 [Leishmania majo
57	CAJ06433	68127889	hypothetical protein, conserved [Leishmania major]
58	XP_750246	70990794	patatin-like serine hydrolase [Aspergillus fumigatus Af293]
59	ABG79934	110628939	triacylglycerol lipase [Magnaporthe grisea]
60	XP_386821	46124535	hypothetical protein FG06645.1 [Gibberella zeae PH-1]
61	EAT92413	111071293	hypothetical protein SNOG_00918 [Phaeosphaeria nodorum SN15]
62	NP_588315	19075815	hypothetical protein SPCC1450.16c [Schizosaccharomyces pombe 972h-]
63	EAQ90965	88183497	hypothetical protein CHGG_02900 [Chaetomium globosum CBS 148.51]
64	XP_957267	85084210	hypothetical protein [Neurospora crassa OR74A]
65	XP_451445	50303015	unnamed protein product [Kluyveromyces lactis]
66	CAB11704	2388971	SPAC31G5.20c [Schizosaccharomyces pombe]
67	XP_626587	66358818	hypothetical protein cgd2_4050 [Cryptosporidium parvum Iov II]
68	XP_665308	67588018	hypothetical protein Chro.20432 [Cryptosporidium hominis TU502]
69	XP_449952	50295082	hypothetical protein CAGL0M13981g [Candida glabrata CBS138]
70	XP_722764	68466564	putative lipid particle triacylglycerol lipase fragment [Candid albicans SC5314]
71	NP_986330	45200760	AGL337Cp [Eremothecium gossypii]
72	CAE84405	39722369	Tgl3 protein [Kluyveromyces delphensis]
73	XP_807283	71409928	hypothetical protein [Trypanosoma cruzi strain CL Brener]
74	XP_807016	71409330	hypothetical protein [Trypanosoma cruzi strain CL Brener]
75	XP_502944	50550941	hypothetical protein [Yarrowia lipolytica]
76	NP_014044	6323973	Triacylglycerol lipase of the lipid particle, responsible for all t TAG lipase activity of the lipid particle; contains the consensu sequence motif GXSXG, which is found in lipolytic enzymes; Tgl3p [Saccharomyces cerevisiae]

Table 83. Examples of triglyceride lipase (tgl3) polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_502944	50550941	hypothetical protein [Yarrowia lipolytica].
2	XP_752278	70995024	patatin-like serine hydrolase [Aspergillus fumigatus Af293]
3	BAE56507	83766364	unnamed protein product [Aspergillus oryzae]
4	EAT85718	111064598	hypothetical protein SNOG_07067 [Phaeosphaeria nodorum SN15]
5	XP_380696	46107274	hypothetical protein FG00520.1 [Gibberella zeae PH-1]
6	XP_964502	85113293	hypothetical protein [Neurospora crassa OR74A]
7	EAQ93362	88185894	hypothetical protein CHGG_01597 [Chaetomium globosum CBS 148.51]
8	XP_722764	68466564	putative lipid particle triacylglycerol lipase fragment [Candic albicans SC5314]
9	NP_986330	45200760	AGL337Cp [Eremothecium gossypii]
10	CAE84405	39722369	Tgl3 protein [Kluyveromyces delphensis]
11	XP_449952	50295082	hypothetical protein CAGL0M13981g [Candida glabrata CBS138]
12	XP_451445	50303015	unnamed protein product [Kluyveromyces lactis]
13	NP_014044	6323973	Triacylglycerol lipase of the lipid particle, responsible for all TAG lipase activity of the lipid particle; contains the consens sequence motif GXSXG, which is found in lipolytic enzymes Tgl3p [Saccharomyces cerevisiae]
14	EAS31687	90302056	hypothetical protein CIMG_07166 [Coccidioides immitis RS
15	EAT92134	111071014	hypothetical protein SNOG_00639 [Phaeosphaeria nodorum SN15]
16	XP_387731	46126355	hypothetical protein FG07555.1 [Gibberella zeae PH-1]
17	NP_588315	19075815	hypothetical protein SPCC1450.16c [Schizosaccharomyces pombe 972h-]
18	XP_751982	70994310	patatin-like serine hydrolase [Aspergillus fumigatus Af293]
19	XP_958750	85091127	hypothetical protein [Neurospora crassa OR74A]
20	EAQ83092	88175624	hypothetical protein CHGG_10910 [Chaetomium globosum CBS 148.51]
21	BAE59228	83769091	unnamed protein product [Aspergillus oryzae]
22	YP_693301	110834442	hypothetical protein ABO_1581 [Alcanivorax borkumensis SK2]
23	XP_659317	67522513	hypothetical protein AN1713.2 [Aspergillus nidulans FGSC
24	ZP_011...	88703608	Patatin-like phospholipase [gamma proteobacterium KT 71]
25	BAF06239	113533856	Os01g0762000 [Oryza sativa (japonica cultivar-group)]
26	XP_463448	50902030	P0512C01.22 [Oryza sativa (japonica cultivar-group)]
27	EAS30095	90300464	hypothetical protein CIMG_08841 [Coccidioides immitis RS
28	YP_433865	83645430	predicted esterase of the alpha-beta hydrolase superfamily [Hahella chejuensis KCTC 2396]
29	XP_459553	50421985	hypothetical protein DEHA0E06127g [Debaryomyces hanser CBS767]
30	CAD60564	27764284	unnamed protein product [Podospora anserina]
31	ZP_008...	77951643	conserved hypothetical protein [Marinobacter aquaeolei VT8
32	XP_505230	50555644	hypothetical protein [Yarrowia lipolytica]
33	XP_446465	50288073	unnamed protein product [Candida glabrata]
34	AAM97135	22531263	putative protein [Arabidopsis thaliana]
35	BAF13581	113550138	Os03g0810900 [Oryza sativa (japonica cultivar-group)]
36	ABG79933	110628937	triacylglycerol lipase [Magnaporthe grisea]
37	XP_717704	68476486	putative patatin-like phospholipase [Candida albicans SC531

38	NP_013015	6322942	Triacylglycerol lipase involved in triacylglycerol mobilizatio and degradation; found in lipid particles; potential Cdc28p substrate; Tgl4p [Saccharomyces cerevisiae]
39	NP_594022	63054585	hypothetical protein SPAC31G5.20c [Schizosaccharomyces pombe 972h-]
40	EAR83738	89285729	Patatin-like phospholipase family protein [Tetrahymena thermophila SB210]
41	NP_984327	45188104	ADR231Cp [Eremothecium gossypii]
42	EAR86065	89288077	Patatin-like phospholipase family protein [Tetrahymena thermophila SB210]
43	NP_014724	6324655	Triacylglycerol lipase involved in TAG mobilization; localiz to lipid particles; potential Cdc28p substrate; Tgl5p [Saccharomyces cerevisiae]
44	YP_046026	50084516	hypothetical protein ACIAD1335 [Acinetobacter sp. ADP1]
45	XP_451336	50302799	unnamed protein product [Kluyveromyces lactis]
46	ZP_011...	88794068	predicted esterase of the alpha-beta hydrolase superfamily protein [Alteromonas macleodii 'Deep ecotype']
47	XP_722550	68466709	putative patatin-like phospholipase [Candida albicans SC531
48	XP_722412	68466994	putative patatin-like phospholipase [Candida albicans SC531
49	EAS33873	90304242	hypothetical protein CIMG_04897 [Coccidioides immitis RS
50	ABG79934	110628939	triacylglycerol lipase [Magnaporthe grisea]
51	ZP_011...	88707125	Patatin-like phospholipase [gamma proteobacterium KT 71]
52	NP_593197	19114109	hypothetical protein SPAC1A6.05c [Schizosaccharomyces pombe 972h-]
53	YP_615253	103485692	Patatin [Sphingopyxis alaskensis RB2256]
54	ZP_010...	85708568	hypothetical protein NAP1_04995 [Erythrobacter sp. NAP1]
55	XP_658012	67516253	hypothetical protein AN0408.2 [Aspergillus nidulans FGSC
56	XP_448470	50292075	unnamed protein product [Candida glabrata]
57	XP_807283	71409928	hypothetical protein [Trypanosoma cruzi strain CL Brener]
58	XP_386821	46124535	hypothetical protein FG06645.1 [Gibberella zeae PH-1]

Table 84. Examples of acyl-coA-cholesterol transferase polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_505086.1	50555355	hypothetical protein [Yarrowia lipolytica].
2	XP_449806	50294790	hypothetical protein CAGL0M10571g [Candida glabrata CBS138]
3	AAO32554	28564940	ARE2 [Saccharomyces kluyveri]
4	XP_461395	50425599	hypothetical protein DEHA0F25652g [Debaryomyces hansen CBS767]
5	P84285	56404462	Sterol O-acyltransferase 2 (Sterol-ester synthase) (ASAT)
6	XP_714776	68482533	acyl-CoA cholesterol acyltransferase [Candida albicans SC5314]
7	AAO32474	28564191	ARE2 [Saccharomyces castellii]
8	NP_982606	45184888	AAR065Cp [Eremothecium gossypii]
9	NP_014416	6324346	Acyl-CoA:sterol acyltransferase, isozyme of Are1p; endoplasmic reticulum enzyme that contributes the major ster esterification activity in the presence of oxygen; Are2p [Saccharomyces cerevisiae]
10	AAC49441	1389739	acyl-CoA:sterol acyltransferase
11	XP_452607	50305295	unnamed protein product [Kluyveromyces lactis]
12	Q876L2	34582301	Sterol O-acyltransferase 2 (Sterol-ester synthase 2)
13	Q876L3	34582302	Sterol O-acyltransferase 1 (Sterol-ester synthase 1)
14	AAT92940	51013293	YCR048W [Saccharomyces cerevisiae]
15	XP_445307	50285757	unnamed protein product [Candida glabrata]
16	NP_593707	19114619	hypothetical protein SPAC13G7.05 [Schizosaccharomyces pombe 972h-]
17	XP_370268	39977761	hypothetical protein MG06765.4 [Magnaporthe grisea 70-15]
18	EAQ84619	88177151	hypothetical protein CHGG_08633 [Chaetomium globosum CBS 148.51]
19	XP_961300	85102248	related to acyl-CoA sterol acyltransferase [MIPS] [Neurospor crassa OR74A]
20	XP_750354	70991010	sterol o-acyltransferase APE2 [Aspergillus fumigatus Af293]
21	EAT80792	111059672	hypothetical protein SNOG_11748 [Phaeosphaeria nodorum SN15]
22	XP_661812	67527926	hypothetical protein AN4208.2 [Aspergillus nidulans FGSC A
23	BAE54934	83764790	unnamed protein product [Aspergillus oryzae]
24	EAT89521	111068401	predicted protein [Phaeosphaeria nodorum SN15]
25	EAQ86094	88178626	hypothetical protein CHGG_07347 [Chaetomium globosum CBS 148.51]
26	NP_588558	19076058	hypothetical protein SPCP1E11.05c [Schizosaccharomyces pombe 972h-]
27	XP_956576	85080625	hypothetical protein [Neurospora crassa OR74A]
28	EAS32815	90303184	hypothetical protein CIMG_03839 [Coccidioides immitis RS]
29	XP_382192	46110268	hypothetical protein FG02016.1 [Gibberella zeae PH-1]
30	XP_761502	71022545	hypothetical protein UM05355.1 [Ustilago maydis 521]
31	EAL20032	50257323	hypothetical protein CNBF3580 [Cryptococcus neoformans v neoformans B-3501A]
32	XP_571260	58268208	sterol O-acyltransferase [Cryptococcus neoformans var. neoformans JEC21]
33	EAR83561	89285549	MBOAT family protein [Tetrahymena thermophila SB210]
34	EAS03424	89305436	MBOAT family protein [Tetrahymena thermophila SB210]
35	AAS72375	45642961	acyl-CoA:cholesterol acyltransferase alpha [Toxoplasma gonc
36	AAS72376	45642963	acyl-CoA:cholesterol acyltransferase beta [Toxoplasma gondi

37	XP_640280	111226542	hypothetical protein DDBDRAFT_0205259 [Dictyostelium discoideum AX4]
38	XP_645633	66824557	hypothetical protein DDBDRAFT_0202877 [Dictyostelium discoideum AX4]
39	EAS35506	90305875	hypothetical protein CIMG_00860 [Coccidioides immitis RS
40	XP_386864	46124621	hypothetical protein FG06688.1 [Gibberella zeae PH-1]
41	NP_649816	28571583	CG8112-PA [Drosophila melanogaster]
42	CAE75170	39591950	Hypothetical protein CBG23107 [Caenorhabditis briggsae]
43	NP_033256	84619697	sterol O-acyltransferase 1 [Mus musculus]
44	BAC34925	26342537	unnamed protein product [Mus musculus]
45	XP_359451	39939828	hypothetical protein MG05326.4 [Magnaporthe grisea 70-15]
46	Q61263	18202591	Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (Ac coenzyme A:cholesterol acyltransferase 1) (ACAT-1)
47	XP_975142	91083363	PREDICTED: similar to CG31991-PA, isoform A [Tribolium castaneum]
48	EAL28962	54639560	GA20833-PA [Drosophila pseudoobscura]
49	XP_957022	85082953	hypothetical protein [Neurospora crassa OR74A]
50	XP_547445	73961286	PREDICTED: similar to Sterol O-acyltransferase 1 (Choleste acyltransferase 1) (Acyl coenzyme A:cholesterol acyltransfer 1) (ACAT-1) [Canis familiaris]
51	EAQ89124	88181656	hypothetical protein CHGG_05743 [Chaetomium globosum CBS 148.51]
52	EAT78735	111057615	hypothetical protein SNOG_13711 [Phaeosphaeria nodorum SN15]
53	Q60457	18202585	Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (Ac coenzyme A:cholesterol acyltransferase 1) (ACAT-1)
54	XP_624754	110762262	PREDICTED: similar to midway CG31991-PA, isoform A [Apis mellifera]
55	O70536	18202126	Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (Ac coenzyme A:cholesterol acyltransferase 1) (ACAT-1)
56	XP_728984	82915156	hypothetical protein PY01256 [Plasmodium yoelii yoelii str. 17XNL]
57	NP_505828	71997360	H19N07.4 [Caenorhabditis elegans]
58	NP_001...	77735363	hypothetical protein LOC504287 [Bos taurus]
59	2201440A	1585676	acyl-CoA/cholesterol acyltransferase
60	XP_663763	67539978	hypothetical protein AN6159.2 [Aspergillus nidulans FGSC A
61	CAI13574	55960156	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1 [Homo sapiens]
62	XP_514030	55588858	PREDICTED: hypothetical protein XP_514030 [Pan troglodytes]
63	AAL56227	18028942	cholesterol acyltransferase 1 [Gorilla gorilla]
64	AAL56228	18028944	cholesterol acyltransferase 1 [Pongo pygmaeus]
65	AAC37532	4878022	acyl-coenzyme A: cholesterol acyltransferase [Homo sapiens]
66	EAT47694	108883469	sterol o-acyltransferase [Aedes aegypti]
67	XP_390039	46136695	hypothetical protein FG09863.1 [Gibberella zeae PH-1]
68	BAE01048	67969393	unnamed protein product [Macaca fascicularis]
69	O77761	18202178	Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (Ac coenzyme A:cholesterol acyltransferase 1) (ACAT-1)
70	AAH06263	34782946	DGAT1 protein [Homo sapiens]
71	XP_317656	31226099	ENSANGP00000002281 [Anopheles gambiae str. PEST]
72	XP_320320	58393809	ENSANGP00000016486 [Anopheles gambiae str. PEST]
73	XP_320321	58393811	ENSANGP00000016512 [Anopheles gambiae str. PEST]
74	BAE65302	83775179	unnamed protein product [Aspergillus oryzae]

75	NP_724017	24584734	midway CG31991-PC, isoform C [Drosophila melanogaster]
76	NP_995724	45552403	midway CG31991-PD, isoform D [Drosophila melanogaster]
77	EAL33593	54644853	GA16599-PA [Drosophila pseudoobscura]
78	NP_586145	19074639	STEROL O-ACYLTRANSFERASE [Encephalitozoon cunici GB-M1]
79	XP_502557	50550169	hypothetical protein [Yarrowia lipolytica]
80	XP_885914	76617939	PREDICTED: similar to Sterol O-acyltransferase 2 (Cholester acyltransferase 2) (Acyl coenzyme A:cholesterol acyltransfera 2) (ACAT-2) isoform 2 [Bos taurus]
81	XP_591251	76617937	PREDICTED: similar to Sterol O-acyltransferase 2 (Cholester acyltransferase 2) (Acyl coenzyme A:cholesterol acyltransfera 2) (ACAT-2) isoform 1 [Bos taurus]
82	XP_624691	66564061	PREDICTED: similar to CG8112-PA [Apis mellifera]
83	O75908	18202149	Sterol O-acyltransferase 2 (Cholesterol acyltransferase 2) (Ac coenzyme A:cholesterol acyltransferase 2) (ACAT-2)
84	XP_001...	109096888	PREDICTED: sterol O-acyltransferase 2 [Macaca mulatta]
85	AAK48829	13898623	acyl coenzyme A: cholesterol acyltransferase-2 [Homo sapien
86	AAH77916	50416229	Soat1-prov protein [Xenopus laevis]
87	AAH96091	64654094	Sterol O-acyltransferase 2 [Homo sapiens]
88	EAT38531	108874306	sterol o-acyltransferase [Aedes aegypti]
89	AAH96090	64652990	Sterol O-acyltransferase 2 [Homo sapiens]
90	NP_001...	50539976	hypothetical protein LOC436731 [Danio rerio]
91	NP_714950	40254723	sterol O-acyltransferase 2 [Rattus norvegicus]
92	XP_422267	50751122	PREDICTED: similar to Sterol O-acyltransferase 1 (Cholester acyltransferase 1) (Acyl coenzyme A:cholesterol acyltransfera 1) (ACAT-1) [Gallus gallus]
93	O88908	18202245	Sterol O-acyltransferase 2 (Cholesterol acyltransferase 2) (Ac coenzyme A:cholesterol acyltransferase 2) (ACAT-2)
94	O77759	18202176	Sterol O-acyltransferase 2 (Cholesterol acyltransferase 2) (Ac coenzyme A:cholesterol acyltransferase 2) (ACAT-2)
95	NP_666176	22122547	sterol O-acyltransferase 2 [Mus musculus]
96	BAC00846	21392392	AcylCoA:Cholesterol Acyltransferase 2 [Rattus norvegicus]
97	XP_692855	68364838	PREDICTED: similar to Soat1-prov protein [Danio rerio]
98	XP_543637	73996435	PREDICTED: similar to sterol O-acyltransferase 2 [Canis familiaris]
99	CAG11944	47225461	unnamed protein product [Tetraodon nigroviridis]
100	CAF96514	47222847	unnamed protein product [Tetraodon nigroviridis]
101	CAG10815	47219451	unnamed protein product [Tetraodon nigroviridis]
102	EAR94647	89296659	MBOAT family protein [Tetrahymena thermophila SB210]
103	AAP68322	31711932	At2g19450 [Arabidopsis thaliana]
104	EAR94441	89296453	MBOAT family protein [Tetrahymena thermophila SB210]
105	CAG07990	47225647	unnamed protein product [Tetraodon nigroviridis]
106	XP_788209	72085563	PREDICTED: similar to sterol O-acyltransferase 1 [Strongylocentrotus purpuratus]
107	AAO32475	28564193	ARE2 [Saccharomyces castellii]
108	XP_673128	68062248	hypothetical protein PB300300.00.0 [Plasmodium berghei stra ANKA]

Table 85. Examples of phospholipid-diacylglycerol acyltransferase polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_504038	50553256	hypothetical protein [Yarrowia lipolytica].
2	XP_458897	50420721	hypothetical protein DEHA0D10868g [Debaryomyces hanser CBS767]
3	XP_718878	68473963	hypothetical protein CaO19_13439 [Candida albicans SC531
4	XP_447501	50290139	hypothetical protein CAGL0I05786g [Candida glabrata CBS138]
5	XP_455369	50310695	unnamed protein product [Kluyveromyces lactis]
6	NP_014405	6324335	Acyltransferase that catalyzes diacylglycerol esterification; or of several acyltransferases that contribute to triglyceride synthesis; putative homolog of human lecithin cholesterol acyltransferase; Lro1p [Saccharomyces cerevisiae]
7	NP_985371	45198342	AFL179Cp [Eremothecium gossypii]
8	BAE57684	83767545	unnamed protein product [Aspergillus oryzae]
9	EAS32928	90303297	hypothetical protein CIMG_03952 [Coccidioides immitis RS]
10	EAT89812	111068692	hypothetical protein SNOG_03081 [Phaeosphaeria nodorum SN15]
11	XP_662596	67537644	hypothetical protein AN4992.2 [Aspergillus nidulans FGSC A
12	XP_361017	39942960	hypothetical protein MG03560.4 [Magnaporthe grisea 70-15]
13	CAD60714	27803011	unnamed protein product [Podospora anserina]
14	XP_718980	68473754	hypothetical protein CaO19_6018 [Candida albicans SC5314]
15	XP_386551	46123995	hypothetical protein FG06375.1 [Gibberella zeae PH-1]
16	XP_959598	85092964	hypothetical protein [Neurospora crassa OR74A]
17	XP_754624	70999814	phospholipid:diacylglycerol acyltransferase [Aspergillus fumigatus Af293]
18	O94680	21362753	Phospholipid:diacylglycerol acyltransferase (PDAT) (Pombe LRO1 homolog 1)
19	EAQ92213	88184745	hypothetical protein CHGG_00448 [Chaetomium globosum CBS 148.51]
20	XP_756469	71003606	hypothetical protein UM00322.1 [Ustilago maydis 521]
21	EAL18953	50256226	hypothetical protein CNBI2140 [Cryptococcus neoformans va neoformans B-3501A]
22	XP_568014	58261208	phospholipid:diacylglycerol acyltransferase [Cryptococcus neoformans var. neoformans JEC21]
23	AAP47635	37785695	lecithine cholesterol acyltransferase-like protein [Medicago truncatula]
24	AAS79590	45935132	putative phosphatidylcholine-sterol acyltransferase [Ipomoea trifida]
25	BAF25212	113631531	Os09g0444200 [Oryza sativa (japonica cultivar-group)]
26	AAK96619	15450695	AT5g13640/MSH12_10 [Arabidopsis thaliana]
27	XP_829379	74025626	phospholipid:diacylglycerol acyltransferase-like protein [Trypanosoma brucei TREU927]
28	XP_816552	71655997	phospholipid:diacylglycerol acyltransferase [Trypanosoma cr strain CL Brener]
29	AAO17787	37724553	lecithine cholesterol acyltransferase-like protein [Arabidopsis thaliana]
30	XP_821756	71660075	phospholipid:diacylglycerol acyltransferase [Trypanosoma cr strain CL Brener]
31	CAD38153	27552462	putative phosphatidylcholine-sterol acetyltransferase [Physcomitrella patens]
32	NP_190069	15230521	phosphatidylcholine-sterol O-acyltransferase [Arabidopsis

			thaliana]
33	CAD38155	27552466	putative acetyltransferase [Physcomitrella patens]
34	CAJ02843	68124573	phospholipid:diacylglycerol acyltransferase, putative [Leishmania major]

Table 86. Examples of squalene epoxidase polypeptides

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_503994	50553168	hypothetical protein [Yarrowia lipolytica].
2	EAS30670	90301039	hypothetical protein CIMG_06149 [Coccidioides immitis RS]
3	XP_753858	70998268	squalene monooxygenase Erg1 [Aspergillus fumigatus Af293]
4	XP_711894	68488538	squalene epoxidase [Candida albicans SC5314]
5	ABD48706	88697124	squalene epoxidase [Emericella nidulans]
6	XP_681020	67901528	hypothetical protein AN7751.2 [Aspergillus nidulans FGSC A4
7	AAQ18215	33415411	squalene epoxidase [Trichophyton rubrum]
8	BAE62359	83772229	unnamed protein product [Aspergillus oryzae]
9	AAQ18216	61807216	squalene epoxidase [Trichophyton rubrum]
10	AAZ08563	70797544	squalene epoxidase [Trichophyton rubrum]
11	CAJ18281	90185988	squalene epoxidase [Hypocrea lixii]
12	XP_462160	50427105	hypothetical protein DEHA0G15202g [Debaryomyces hansenii CBS767]
13	NP_011691	6321614	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3 oxidosqualene; plays an essential role in the ergosterol-biosynth pathway and is the specific target of the antifungal drug terbinaf Erg1p [Saccharomyces cerevisiae]
14	AAA34592	171471	squalene epoxidase
15	O13306	51704232	Squalene monooxygenase (Squalene epoxidase) (SE)
16	XP_455763	50311477	unnamed protein product [Kluyveromyces lactis]
17	XP_386391	46123675	hypothetical protein FG06215.1 [Gibberella zeae PH-1]
18	EAQ88139	88180671	hypothetical protein CHGG_04758 [Chaetomium globosum CB 148.51]
19	XP_961806	85104779	hypothetical protein [Neurospora crassa OR74A]
20	XP_758545	71012984	hypothetical protein UM02398.1 [Ustilago maydis 521]
21	XP_369325	39975869	hypothetical protein MG06139.4 [Magnaporthe grisea 70-15]
22	XP_570092	58265872	squalene monooxygenase [Cryptococcus neoformans var. neoformans JEC21]
23	Q9C1W3	51701448	Probable squalene monooxygenase (Squalene epoxidase) (SE)
24	EAT79729	111058609	hypothetical protein SNOG_12929 [Phaeosphaeria nodorum SN
25	CAG38355	108743007	squalene epoxidase [Aspergillus niger]
26	BAE73094	84579321	hypothetical protein [Macaca fascicularis]
27	EAU31524	114189824	hypothetical protein ATEG_08351 [Aspergillus terreus NIH262
28	NP_003120	62865635	squalene monooxygenase [Homo sapiens]
29	CAI46076	57997512	hypothetical protein [Homo sapiens]
30	BAE37374	74200967	unnamed protein product [Mus musculus]
31	XP_850640	73974448	PREDICTED: similar to squalene monooxygenase isoform 1 [C familiaris]
32	Q75F69	51701415	Squalene monooxygenase (Squalene epoxidase) (SE)
33	AAS60234	45388098	squalene epoxidase 1 [Aspergillus fumigatus]
34	Q14534	12644414	Squalene monooxygenase (Squalene epoxidase) (SE)
35	XP_001...	109087424	PREDICTED: similar to squalene monooxygenase [Macaca mu
36	AAH97330	66911977	Sqle protein [Rattus norvegicus]
37	EAU30782	114189082	hypothetical protein ATEG_08650 [Aspergillus terreus NIH262

38	CAF98057	47218525	unnamed protein product [Tetraodon nigroviridis]
39	XP_861944	73974450	PREDICTED: similar to squalene monooxygenase isoform 2 [C familiaris]
40	ABF94794	108706999	Squalene monooxygenase, putative, expressed [Oryza sativa (japonica cultivar-group)]
41	BAF11377	113547934	Os03g0231800 [Oryza sativa (japonica cultivar-group)]
42	XP_470614	50920507	Putative Squalene monooxygenase [Oryza sativa (japonica culti group)]
43	ABF94791	108706996	Squalene monooxygenase, putative, expressed [Oryza sativa (japonica cultivar-group)]
44	AAM61384	21537043	squalene epoxidase-like protein [Arabidopsis thaliana]
45	BAE98940	110742002	hypothetical protein [Arabidopsis thaliana]
46	ABE84801	92877833	Helix-turn-helix, AraC type; NAD-binding site; Fumarate lyase [Medicago truncatula]
47	BAE36598	74183459	unnamed protein product [Mus musculus]
48	XP_693698	68403773	PREDICTED: similar to squalene monooxygenase [Danio rerio
49	CAB80441	7270759	squalene epoxidase-like protein [Arabidopsis thaliana]
50	O48651	6685403	Squalene monooxygenase (Squalene epoxidase) (SE)
51	AAY22200	62945915	squalene monooxygenase [Datura innoxia]
52	BAD15330	46359651	squalene epoxidase [Panax ginseng]
53	CAD23248	27475610	squalene monooxygenase 2 [Medicago truncatula]
54	ABC94943	86371770	squalene epoxidase [Medicago sativa]
55	CAD23249	27475612	squalene monooxygenase 1 [Medicago truncatula]
56	AAN15558	23198062	squalene monooxygenase, putative [Arabidopsis thaliana]
57	NP_179868	15227757	oxidoreductase [Arabidopsis thaliana]
58	AAG50645	12321049	squalene monooxygenase, putative [Arabidopsis thaliana]
59	XP_629022	66800193	hypothetical protein DDBDRAFT_0192021 [Dictyostelium discoideum AX4]
60	CAK11466	94733753	novel protein similar to vertebrate squalene epoxidase (SQLE) [Danio rerio]
61	AAQ13595	33337947	putative squalene epoxidase [Lycopersicon esculentum]
62	ABF94792	108706997	Squalene monooxygenase, putative, expressed [Oryza sativa (japonica cultivar-group)]
63	XP_604908	76660360	PREDICTED: similar to squalene monooxygenase [Bos taurus]
64	BAA11209	1483186	squalene epoxidase [Homo sapiens]
65	NP_197803	15237902	SQP1 [Arabidopsis thaliana]
66	NP_001...	79328611	SQP1 [Arabidopsis thaliana]
67	CAA06772	3123331	squalene epoxidase homologue [Arabidopsis thaliana]
68	O65726	6685410	Squalene monooxygenase 1,2 (Squalene epoxidase 1,2) (SE 1,2
69	O65727	6685411	Squalene monooxygenase 1,1 (Squalene epoxidase 1,1) (SE 1,1
70	NP_197804	15237903	oxidoreductase [Arabidopsis thaliana]
71	CAJ03182	68125205	squalene monooxygenase-like protein [Leishmania major]
72	NP_197802	15237900	SQP2; oxidoreductase [Arabidopsis thaliana]
73	XP_828409	71754989	squalene monooxygenase [Trypanosoma brucei TREU927]
74	XP_808343	71412304	squalene monooxygenase [Trypanosoma cruzi strain CL Brener
75	XP_789059	72038634	PREDICTED: similar to squalene monooxygenase [Strongylocentrotus purpuratus]
76	XP_796297	72133073	PREDICTED: similar to squalene monooxygenase [Strongylocentrotus purpuratus]
77	AAB69189	2352528	squalene epoxidase [Candida glabrata]

78	XP_813434	71649420	squalene monooxygenase [Trypanosoma cruzi strain CL Brener
79	XP_796261	72133071	PREDICTED: similar to squalene monooxygenase [Strongylocentrotus purpuratus]
80	XP_793783	72114550	PREDICTED: similar to squalene monooxygenase, partial [Strongylocentrotus purpuratus]
81	XP_789028	72038632	PREDICTED: similar to squalene monooxygenase [Strongylocentrotus purpuratus]
82	AAT97087	51105054	squalene epoxidase-like protein [Lymnaea stagnalis]
83	XP_804343	71402993	squalene monooxygenase [Trypanosoma cruzi strain CL Brener
84	YP_115265	53803024	monooxygenase family protein [Methylococcus capsulatus str. I
85	AAM91177	22136198	unknown protein [Arabidopsis thaliana]
86	XP_799134	72026766	PREDICTED: similar to Squalene monooxygenase (Squalene epoxidase) (SE), partial [Strongylocentrotus purpuratus]

Table 87. Examples of ERG1 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	AAA34592	171471	squalene epoxidase
2	O13306	51704232	Squalene monooxygenase (Squalene epoxidase) (SE)
3	XP_455763	50311477	unnamed protein product [Kluyveromyces lactis]
4	Q75F69	51701415	Squalene monooxygenase (Squalene epoxidase) (SE)
5	XP_462160	50427105	hypothetical protein DEHA0G15202g [Debaryomyces hansenii CBS767
6	XP_711894	68488538	squalene epoxidase [Candida albicans SC5314]
7	XP_503994	50553168	hypothetical protein [Yarrowia lipolytica]
8	AAB69189	2352528	squalene epoxidase [Candida glabrata]
9	AAQ18215	33415411	squalene epoxidase [Trichophyton rubrum]
10	AAQ18216	61807216	squalene epoxidase [Trichophyton rubrum]
11	AAZ08563	70797544	squalene epoxidase [Trichophyton rubrum]
12	EAS30670	90301039	hypothetical protein CIMG_06149 [Coccidioides immitis RS]
13	Q9C1W3	51701448	Probable squalene monooxygenase (Squalene epoxidase) (SE)
14	XP_758545	71012984	hypothetical protein UM02398.1 [Ustilago maydis 521]
15	XP_681020	67901528	hypothetical protein AN7751.2 [Aspergillus nidulans FGSC A4]
16	ABD48706	88697124	squalene epoxidase [Emericella nidulans]
17	BAE62359	83772229	unnamed protein product [Aspergillus oryzae]
18	XP_753858	70998268	squalene monooxygenase Erg1 [Aspergillus fumigatus Af293]
19	XP_961806	85104779	hypothetical protein [Neurospora crassa OR74A]
20	XP_386391	46123675	hypothetical protein FG06215.1 [Gibberella zeae PH-1]
21	CAJ18281	90185988	squalene epoxidase [Hypocrea lixii]
22	BAE73094	84579321	hypothetical protein [Macaca fascicularis]
23	BAE37374	74200967	unnamed protein product [Mus musculus]
24	XP_570092	58265872	squalene monooxygenase [Cryptococcus neoformans var. neoformans JEC21]
25	NP_003120	62865635	squalene monooxygenase [Homo sapiens]
26	EAT79729	111058609	hypothetical protein SNOG_12929 [Phaeosphaeria nodorum SN15]
27	AAH97330	66911977	Sqle protein [Rattus norvegicus]
28	CAI46076	57997512	hypothetical protein [Homo sapiens]
29	CAF98057	47218525	unnamed protein product [Tetraodon nigroviridis]
30	XP_850640	73974448	PREDICTED: similar to squalene monooxygenase isoform 1 [Canis familiaris]
31	XP_369325	39975869	hypothetical protein MG06139.4 [Magnaporthe grisea 70-15]
32	Q14534	12644414	Squalene monooxygenase (Squalene epoxidase) (SE)
33	XP_001...	109087424	PREDICTED: similar to squalene monooxygenase [Macaca mulatta]
34	EAQ88139	88180671	hypothetical protein CHGG_04758 [Chaetomium globosum CBS 148.51
35	XP_693698	68403773	PREDICTED: similar to squalene monooxygenase [Danio rerio]
36	CAG38355	108743007	squalene epoxidase [Aspergillus niger]
37	XP_861944	73974450	PREDICTED: similar to squalene monooxygenase isoform 2 [Canis familiaris]
38	XP_519950	55631226	PREDICTED: similar to squalene epoxidase [Pan troglodytes]
39	AAS60234	45388098	squalene epoxidase 1 [Aspergillus fumigatus]
40	XP_629022	66800193	hypothetical protein DDBDRAFT_0192021 [Dictyostelium discoideum AX4]
41	CAK11466	94733753	novel protein similar to vertebrate squalene epoxidase (SQLE) [Danio rerio]
42	BAE98940	110742002	hypothetical protein [Arabidopsis thaliana]
43	AAM61384	21537043	squalene epoxidase-like protein [Arabidopsis thaliana]
44	ABC94943	86371770	squalene epoxidase [Medicago sativa]
45	CAB80441	7270759	squalene epoxidase-like protein [Arabidopsis thaliana]
46	CAD23248	27475610	squalene monooxygenase 2 [Medicago truncatula]

47	BAE36598	74183459	unnamed protein product [Mus musculus]
48	AAQ13595	33337947	putative squalene epoxidase [Lycopersicon esculentum]
49	AAY22200	62945915	squalene monooxygenase [Datura innoxia]
50	ABF94791	108706996	Squalene monooxygenase, putative, expressed [Oryza sativa (japonica cultivar-group)]
51	AAN15558	23198062	squalene monooxygenase, putative [Arabidopsis thaliana]
52	ABF94794	108706999	Squalene monooxygenase, putative, expressed [Oryza sativa (japonica cultivar-group)]
53	XP_470614	50920507	Putative Squalene monooxygenase [Oryza sativa (japonica cultivar-grou
54	BAF11377	113547934	Os03g0231800 [Oryza sativa (japonica cultivar-group)]
55	CAD23249	27475612	squalene monooxygenase 1 [Medicago truncatula]
56	AAG50645	12321049	squalene monooxygenase, putative [Arabidopsis thaliana]
57	NP_179868	15227757	oxidoreductase [Arabidopsis thaliana]
58	ABE84801	92877833	Helix-turn-helix, AraC type; NAD-binding site; Fumarate lyase [Medic truncatula]
59	ABF94792	108706997	Squalene monooxygenase, putative, expressed [Oryza sativa (japonica cultivar-group)]
60	BAA11209	1483186	squalene epoxidase [Homo sapiens]
61	XP_604908	76660360	PREDICTED: similar to squalene monooxygenase [Bos taurus]
62	XP_828409	71754989	squalene monooxygenase [Trypanosoma brucei TREU927]
63	XP_808343	71412304	squalene monooxygenase [Trypanosoma cruzi strain CL Brener]
64	CAJ03182	68125205	squalene monooxygenase-like protein [Leishmania major]
65	O65726	6685410	Squalene monooxygenase 1,2 (Squalene epoxidase 1,2) (SE 1,2)
66	NP_197804	15237903	oxidoreductase [Arabidopsis thaliana]
67	O65727	6685411	Squalene monooxygenase 1,1 (Squalene epoxidase 1,1) (SE 1,1)
68	CAA06772	3123331	squalene epoxidase homologue [Arabidopsis thaliana]
69	NP_001...	79328611	SQP1 [Arabidopsis thaliana]
70	NP_197803	15237902	SQP1 [Arabidopsis thaliana]
71	NP_197802	15237900	SQP2; oxidoreductase [Arabidopsis thaliana]

Table 88. Examples of ERG7 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	AAT93062	51013537	YHR072W [Saccharomyces cerevisiae]
2	AAA16975	465105	lanosterol synthase
3	XP_448182	50291499	unnamed protein product [Candida glabrata]
4	XP_451982	50304065	unnamed protein product [Kluyveromyces lactis]
5	NP_987017	45201447	AGR351Wp [Eremothecium gossypii]
6	XP_457937	50418833	hypothetical protein DEHA0C06501g [Debaryomyces hansenii CBS767
7	XP_722471	68467112	2,3-oxidosqualene-lanosterol cyclase [Candida albicans SC5314]
8	XP_722612	68466833	2,3-oxidosqualene-lanosterol cyclase [Candida albicans SC5314]
9	1903190A	383419	oxidosqualene cyclase
10	XP_504990	50555163	hypothetical protein [Yarrowia lipolytica]
11	AAB08472	1549343	inactive oxidosqualene-lansoterol cyclase [Saccharomyces cerevisiae]
12	Q96WJ0	30913110	Lanosterol synthase (Oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene--lanosterol cyclase) (OSC)
13	XP_747936	70984860	oxidosqualene:lanosterol cyclase [Aspergillus fumigatus Af293]
14	BAE61626	83771494	unnamed protein product [Aspergillus oryzae]
15	NP_593702	63054562	lanosterol synthase activity [Schizosaccharomyces pombe 972h-]
16	XP_758387	71010409	hypothetical protein UM02240.1 [Ustilago maydis 521]
17	XP_681529	67902546	hypothetical protein AN8260.2 [Aspergillus nidulans FGSC A4]
18	EAS37438	90307807	hypothetical protein CIMG_02792 [Coccidioides immitis RS]
19	XP_961026	85100788	lanosterol synthase related protein [MIPS] [Neurospora crassa OR74A]
20	XP_751627	70993560	oxidosqualene:lanosterol cyclase [Aspergillus fumigatus Af293]
21	EAQ86439	88178971	hypothetical protein CHGG_07692 [Chaetomium globosum CBS 148.51
22	XP_386126	46123145	hypothetical protein FG05950.1 [Gibberella zeae PH-1]
23	BAE63415	83773288	unnamed protein product [Aspergillus oryzae]
24	EAS31167	90301536	hypothetical protein CIMG_06646 [Coccidioides immitis RS]
25	EAT81661	11106054	hypothetical protein SNOG_11162 [Phaeosphaeria nodorum SN15]
26	XP_570450	58266588	lanosterol synthase [Cryptococcus neoformans var. neoformans JEC21]
27	AAL56020	18028346	oxidosqualene:lanosterol cyclase [Cephalosporium caerulens]
28	BAC37102	26346907	unnamed protein product [Mus musculus]
29	Q8BLN5	62286881	Lanosterol synthase (Oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene--lanosterol cyclase) (OSC)
30	XP_001...	109065021	PREDICTED: lanosterol synthase isoform 2 [Macaca mulatta]
31	1W6KA	56966682	Chain A, Structure Of Human Osc In Complex With Lanosterol
32	BAC31739	26336108	unnamed protein product [Mus musculus]
33	XP_646246	66825783	hypothetical protein DDB_0191311 [Dictyostelium discoideum AX4]
34	AAF80384	8886139	cycloartenol synthase [Dictyostelium discoideum]
35	CAB42828	4808278	lanosterol synthase [Homo sapiens]
36	1W6JA	56966681	Chain A, Structure Of Human Osc In Complex With Ro 48-8071
37	BAA08208	639865	2,3-oxidosqualene:lanosterol cyclase [Rattus norvegicus]
38	NP_112311	13591981	lanosterol synthase [Rattus norvegicus]
39	NP_001...	114053041	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) [Bos taurus]
40	P48450	62296496	Lanosterol synthase (Oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene--lanosterol cyclase) (OSC)
41	NP_001...	57529773	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) [Gallus gallus
42	XP_751356	70993016	oxidosqualene cyclase [Aspergillus fumigatus Af293]
43	CAG08284	47222029	unnamed protein product [Tetraodon nigroviridis]
44	BAB83085	18147590	cycloartenol synthase [Betula platyphylla]
45	BAA76902	4589852	cycloartenol synthase [Glycyrrhiza glabra]
46	BAE61719	83771588	unnamed protein product [Aspergillus oryzae]
47	BAA33460	3688598	Cycloartenol Synthase [Panax ginseng]
48	XP_001...	109065023	PREDICTED: lanosterol synthase isoform 1 [Macaca mulatta]

49	BAD34644	50896401	cycloartenol synthase [Cucurbita pepo]
50	BAA85266	6045133	cycloartenol synthase [Luffa aegyptiaca]
51	BAB83253	18147771	cycloartenol synthase [Costus speciosus]
52	ABB76767	82468805	cycloartenol synthase [Ricinus communis]
53	BAA23533	2627181	cycloartenol synthase [Pisum sativum]
54	BAD34645	50896403	cucurbitadienol synthase [Cucurbita pepo]
55	BAE53431	83016479	cycloartenol synthase [Lotus japonicus]
56	AAS83469	46242746	cycloartenol synthase [Bupleurum kaoi]
57	A49398	541855	cycloartenol synthase (EC 5.4.99.8) - Arabidopsis thaliana
58	AAN64509	24796994	At2g07050/T4E14.16 [Arabidopsis thaliana]
59	BAD34646	50896405	putative oxidosqualene cyclase [Cucurbita pepo]
60	AAC04931	452446	cycloartenol synthase; (S)-2,3-epoxysqualene mutase [Arabidopsis thaliana]
61	BAE95408	108743265	lanosterol synthase [Arabidopsis thaliana]
62	AAG44096	12004573	cycloartenol synthase [Abies magnifica]
63	AAS01524	41387168	cycloartenol synthase [Centella asiatica]
64	BAB83086	18147592	cycloartenol synthase [Betula platyphylla]
65	AAF03375	6090879	putative cycloartenol synthase [Oryza sativa]
66	BAF07762	113535379	Os02g0139700 [Oryza sativa (japonica cultivar-group)]
67	BAE95410	108743269	lanosterol synthase [Lotus japonicus]
68	AAK82995	15076959	lanosterol synthase [Trypanosoma cruzi]
69	XP_820967	71668047	lanosterol synthase [Trypanosoma cruzi strain CL Brener]
70	BAA85267	6045135	oxidosqualene cyclase [Luffa aegyptiaca]
71	NP_190099	42565553	catalytic/ lyase [Arabidopsis thaliana]
72	AAT38889	47834383	cycloartenol synthase [Avena longiglumis]
73	BAA86933	6456469	oxidosqualene cyclase [Taraxacum officinale]
74	AAT38891	47834387	cycloartenol synthase [Avena strigosa]
75	CAC84559	15866702	cycloartenol synthase [Avena strigosa]
76	AAT38890	47834385	cycloartenol synthase [Avena prostrata]
77	AAT38888	47834381	cycloartenol synthase [Avena longiglumis]
78	AAT38887	47834379	cycloartenol synthase [Avena clauda]
79	AAT38892	47834389	cycloartenol synthase [Avena ventricosa]
80	XP_819758	71665580	lanosterol synthase [Trypanosoma cruzi strain CL Brener]
81	BAA86930	6456434	lupeol synthase [Olea europaea]
82	CAA61078	984145	lanosterol synthase [Homo sapiens]
83	BAA33462	3688602	Oxidosqualene Cyclase [Panax ginseng]
84	AAG26328	11023151	lanosterol synthase [Trypanosoma brucei brucei]
85	XP_825673	71752517	lanosterol synthase [Trypanosoma brucei TREU927]
86	BAA86932	6456467	lupeol synthase [Taraxacum officinale]
87	CAD23247	27475608	beta-amyrin synthase [Medicago truncatula]
88	BAA97558	8918271	beta-amyrin synthase [Pisum sativum]
89	BAA86931	6456465	cycloartenol synthase [Olea europaea]
90	BAD08587	41687978	lupeol synthase [Glycyrrhiza glabra]
91	BAA84603	5922599	oxidosqualene cyclase [Allium macrostemon]
92	AAO33578	28194504	beta-amyrin synthase [Medicago truncatula]
93	BAB83087	18147594	lupeol synthase [Betula platyphylla]
94	BAB83254	18147773	multifunctional triterpene synthase [Costus speciosus]
95	BAA89815	6730969	beta-amyrin synthase [Glycyrrhiza glabra]
96	BAE53429	83016474	beta-amyrin synthase [Lotus japonicus]
97	AAO33579	28194506	putative beta-amyrin synthase [Lotus japonicus]
98	BAA33461	3688600	beta-Amyrin Synthase [Panax ginseng]
99	CAB72151	6911851	oxidosqualene cyclase-like protein [Arabidopsis thaliana]

100	CAJ02110	68124127	lanosterol synthase, putative [Leishmania major]
101	BAA33722	3721856	beta-Amyrin Synthase [Panax ginseng]
102	AAX14716	60203059	beta-amyrin synthase [Aster sedifolius]
103	BAE53430	83016477	lupeol synthase [Lotus japonicus]
104	ABE91090	92892072	Prenyltransferase/squalene oxidase [Medicago truncatula]
105	XP_681518	67902524	hypothetical protein AN8249.2 [Aspergillus nidulans FGSC A4]
106	AAC17080	3152599	Strong similarity to lupeol synthase gb|U49919 and cycloartenol synthas gb|U02555 from A. thaliana (the third gene with similar homology). [Arabidopsis thaliana]
107	BAF28067	113644926	Os11g0286800 [Oryza sativa (japonica cultivar-group)]
108	NP_683508	22330736	beta-amyrin synthase [Arabidopsis thaliana]
109	AAS83468	46242744	beta-armyrin synthase [Bupleurum kaoi]
110	AAO33580	28194508	multifunctional beta-amyrin synthase [Lotus japonicus]
111	BAE43642	73991374	beta-amyrin synthase [Euphorbia tirucalli]
112	BAB83088	18147596	beta-amyrin synthase [Betula platyphylla]
113	ABB76766	82468803	lupeol synthase [Ricinus communis]
114	ABG22399	108864084	Cycloartenol synthase, putative, expressed [Oryza sativa (japonica cultiv group)]
115	BAF28063	113644922	Os11g0285000 [Oryza sativa (japonica cultivar-group)]
116	ABG22398	108864083	Cycloartenol synthase, putative, expressed [Oryza sativa (japonica cultiv group)]
117	NP_849903	30699380	LUP1 (LUPEOL SYNTHASE 1); lupeol synthase [Arabidopsis thaliana
118	AAB94341	2738027	2,3-oxidosqualene-triterpenoid cyclase [Arabidopsis thaliana]
119	AAN77001	25991999	2,3-oxidosqualene-triterpene cyclase [Arabidopsis thaliana]
120	AAT38893	47834391	beta-amyrin synthase [Avena clauda]
121	AAD05032	1762150	lupeol synthase [Arabidopsis thaliana]
122	NP_178017	30699377	ATLUP2; lupeol synthase [Arabidopsis thaliana]
123	ABE88599	92887080	squalene/oxidosqualene cyclases [Medicago truncatula]
124	ABG22449	108864253	Cycloartenol synthase, putative, expressed [Oryza sativa (japonica cultiv group)]
125	BAB68529	15787841	isomultiflorenol synthase [Luffa aegyptiaca]
126	AAT38898	47834401	beta-amyrin synthase [Avena ventricosa]
127	AAT38894	47834393	beta-amyrin synthase [Avena longiglumis]
128	AAT38897	47834399	beta-amyrin synthase [Avena strigosa]
129	NP_178016	22330734	catalytic/ lyase [Arabidopsis thaliana]
130	AAT38895	47834395	beta-amyrin synthase [Avena longiglumis]
131	AAT38896	47834397	beta-amyrin synthase [Avena prostrata]
132	BAA97559	8918273	mixed-amyrin synthase [Pisum sativum]
133	AAC98864	4090722	pentacyclic triterpene synthase [Arabidopsis thaliana]
134	BAF28466	113645325	Os11g0562100 [Oryza sativa (japonica cultivar-group)]
135	AAG41762	11934652	pentacyclic triterpene synthase [synthetic construct]
136	XP_480759	50942463	putative Cycloartenol Synthase [Oryza sativa (japonica cultivar-group)]
137	BAE43643	73991380	putative oxidosqulene cyclase [Euphorbia tirucalli]
138	AAC17070	3152589	Strong similarity to lupeol synthase gb|U49919 from A. thaliana (second gene in a series of three with similar homologies). [Arabidopsis thaliana
139	BAD15332	46359655	beta-amyrin synthase [Panax ginseng]
140	AAM23264	23428800	beta-amyrin synthase [Glycine max]
141	ABC33922	83638481	beta-amyrin synthase [Gypsophila paniculata]
142	AAS01523	41387158	putative beta-amyrin synthase [Centella asiatica]
143	BAE99758	110743847	cycloartenol synthase [Arabidopsis thaliana]
144	BAB11065	10177752	cycloartenol synthase [Arabidopsis thaliana]
145	NP_177971	15218390	catalytic [Arabidopsis thaliana]
146	CAD39196	32526539	cycloartenol synthase [Stigmatella aurantiaca]

147	ABG22450	108864254	Cycloartenol synthase, putative, expressed [Oryza sativa (japonica culti group)]
148	CAA93571	1204221	erg7 [Schizosaccharomyces pombe]
149	NP_567462	18414430	ATPEN1; catalytic/ lyase [Arabidopsis thaliana]
150	NP_199612	42568386	catalytic [Arabidopsis thaliana]
151	NP_193272	15233798	catalytic/ lyase [Arabidopsis thaliana]
152	ABE88610	92887091	squalene/oxidosqualene cyclases [Medicago truncatula]
153	AAW30034	56790234	At5g42600 [Arabidopsis thaliana]
154	BAF01935	110740066	putative lupeol synthase [Arabidopsis thaliana]
155	NP_198464	15239312	ATPEN3; catalytic [Arabidopsis thaliana]
156	BAB83089	18147598	putative oxidosqualene cyclase [Betula platyphylla]
157	YP_115266	53803023	squalene cyclase family protein [Methylococcus capsulatus str. Bath]
158	CAB78579	7268284	lupeol synthase like protein [Arabidopsis thaliana]
159	CAB78576	7268281	lupeol synthase like protein [Arabidopsis thaliana]

Table 89. Examples of ERG6 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	CAA89944	854482	Erg6p [Saccharomyces cerevisiae]
2	P25087	462024	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
3	CAA52308	396515	S-adenosyl-methionine:delta-24-sterol-C- methyltransferase [Saccharomyces cerevisiae]
4	AAB31378	619251	putative S-adenosylmethionine-dependent methyltransferase [Saccharomyces cerevisiae]
5	Q6FRZ7	62900214	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
6	AAX73200	62178560	C24 sterol methyltransferase [Candida glabrata]
7	P_446997	50289135	unnamed protein product [Candida glabrata]
8	CAG59930	49526306	unnamed protein product [Candida glabrata CBS138]
9	AAX73199	62178558	C24 sterol methyltransferase [Candida glabrata]
10	Q6CYB3	62900210	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
11	P_451076	50302283	unnamed protein product [Kluyveromyces lactis]
12	CAH02664	49640207	unnamed protein product [Kluyveromyces lactis NRRL Y-1140]
13	Q759S7	62900245	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
14	P_984292	45188069	ADR196Wp [Eremothecium gossypii]
15	AAS52116	44982886	ADR196Wp [Ashbya gossypii ATCC 10895]
16	CAA37826	4122	unnamed protein product [Saccharomyces cerevisiae]
17	Q875K1	62900279	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
18	AAO21936	27803704	S-adenosylmethionine:D24-methyltransferase [Clavispora lusitaniae]
19	Q6BRB7	62900203	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
20	P_459253	50421405	hypothetical protein DEHA0D19151g [Debaryomyces hansenii CBS767]
21	CAG87427	49654920	unnamed protein product [Debaryomyces hansenii CBS767]
22	P_721588	68468538	SAM:delta 24-methyltransferase [Candida albicans SC5314]
23	P_721708	68468297	SAM:delta 24-methyltransferase [Candida albicans SC5314]
24	EAL02920	46443640	hypothetical protein CaO19.1631 [Candida albicans SC5314]
25	EAL02792	46443511	hypothetical protein CaO19.9199 [Candida albicans SC5314]
26	O74198	6015114	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
27	AAC26626	3323500	sterol transmethylase [Candida albicans]
28	Q6C2D9	62900205	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
29	P_505173	50555530	hypothetical protein [Yarrowia lipolytica]
30	CAG77980	49651043	unnamed protein product [Yarrowia lipolytica CLIB122]
31	P_595787	19112579	hypothetical protein SPBC16E9.05 [Schizosaccharomyces pomb 972h-]
32	O14321	6166151	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
33	CAB16897	2467267	SPBC16E9.05 [Schizosaccharomyces pombe]
34	EAT84719	111063599	hypothetical protein SNOG_08443 [Phaeosphaeria nodorum SN1
35	EAS29698	90300067	hypothetical protein CIMG_08444 [Coccidioides immitis RS]
36	EAQ70709	86196071	hypothetical protein MGG_ch7g116 [Magnaporthe grisea 70-15]
37	P_366350	39969919	hypothetical protein MG10568.4 [Magnaporthe grisea 70-15]

38	P_746550	70982043	sterol 24-c-methyltransferase [Aspergillus fumigatus Af293]
39	EAL84512	66844173	sterol 24-c-methyltransferase, putative [Aspergillus fumigatus Af293]
40	BAE64809	83774686	unnamed protein product [Aspergillus oryzae]
41	P_965392	85118140	probable DELTA(24)-STEROL C-METHYLTRANSFERASE [MIPS] [Neurospora crassa OR74A]
42	Q9P3R1	62900336	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
43	EAA36156	28927200	probable DELTA(24)-STEROL C-METHYLTRANSFERASE [MIPS] [Neurospora crassa]
44	CAB97289	9367272	probable DELTA(24)-STEROL C-METHYLTRANSFERASE (ERG6) [Neurospora crassa]
45	P_664750	67541965	hypothetical protein AN7146.2 [Aspergillus nidulans FGSC A4]
46	EAA61398	40742208	hypothetical protein AN7146.2 [Aspergillus nidulans FGSC A4]
47	P_382959	46111803	hypothetical protein FG02783.1 [Gibberella zeae PH-1]
48	EAA70778	42547935	hypothetical protein FG02783.1 [Gibberella zeae PH-1]
49	Q96WX4	62900323	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
50	AAK54439	14192727	S-adenosyl methionine:sterol methyl transferase [Pneumocystis carinii]
51	EAQ89522	88182054	conserved hypothetical protein [Chaetomium globosum CBS 148.51]
52	BAA13793	41688402	unnamed protein product [Schizosaccharomyces pombe]
53	P_385916	46122725	hypothetical protein FG05740.1 [Gibberella zeae PH-1]
54	EAA75815	42552972	hypothetical protein FG05740.1 [Gibberella zeae PH-1]
55	P_361872	39944670	hypothetical protein MG04346.4 [Magnaporthe grisea 70-15]
56	Q5EN22	62900141	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
57	AAX07631	59802827	sterol 24-C-methyltransferase-like protein [Magnaporthe grisea]
58	BAE61033	83770900	unnamed protein product [Aspergillus oryzae]
59	P_759329	71018197	hypothetical protein UM03182.1 [Ustilago maydis 521]
60	EAK84412	46099179	hypothetical protein UM03182.1 [Ustilago maydis 521]
61	AAK00294	12642580	sterol methyl transferase [Pneumocystis carinii f. sp. carinii]
62	P_360548	39942022	hypothetical protein MG10860.4 [Magnaporthe grisea 70-15]
63	P_568887	58262954	sterol 24-C-methyltransferase [Cryptococcus neoformans var. neoformans JEC21]
64	AAW41580	57223537	sterol 24-C-methyltransferase, putative [Cryptococcus neoformar var. neoformans JEC21]
65	EAL22628	50259962	hypothetical protein CNBB2600 [Cryptococcus neoformans var. neoformans B-3501A]
66	AAC34951	3560474	S-adenosyl-methionine-sterol-C- methyltransferase [Nicotiana tabacum]
67	AAC04265	2909846	(S)-adenosyl-L-methionine:delta 24-sterol methyltransferase [Ze mays]
68	AAB49338	1872473	delta-24-sterol methyltransferase [Triticum aestivum]
69	Q9LM02	62901053	Cycloartenol-C-24-methyltransferase (24-sterol C-methyltransfe 1) (Sterol C-methyltransferase 1) (Protein STEROL METHYLTRANSFERASE 1) (Protein CEPHALOPOD)
70	AAN15377	23197700	24-sterol C-methyltransferase [Arabidopsis thaliana]
71	AAM53274	21539443	24-sterol C-methyltransferase [Arabidopsis thaliana]
72	P_196875	15240691	SMT1 (STEROL METHYLTRANSFERASE 1) [Arabidopsis thaliana]
73	AAG28462	11066105	sterol methyltransferase SMT1 [Arabidopsis thaliana]

74	BAB08698	9758037	24-sterol C-methyltransferase [Arabidopsis thaliana]
75	AAF78847	8745241	SAM:cycloartenol-C24-methyltransferase [Arabidopsis thaliana]
76	AAM53553	21434843	cephalopod [Arabidopsis thaliana]
77	AAB70886	1899060	endosperm C-24 sterol methyltransferase [Zea mays]
78	AAB37769	1706965	delta-24-sterol methyltransferase [Triticum aestivum]
79	BAF21068	113610690	Os07g0206700 [Oryza sativa (japonica cultivar-group)]
80	Q6ZIX2	68566037	Cycloartenol-C-24-methyltransferase 1 (24-sterol C-methyltransferase 1) (Sterol C-methyltransferase 1)
81	P_477078	50935101	cycloartenol-C24-methyltransferase [Oryza sativa (japonica cultivar-group)]
82	BAC83238	34393309	cycloartenol-C24-methyltransferase [Oryza sativa (japonica cultivar-group)]
83	AAB04057	1399380	S-adenosyl-L-methionine:delta24-sterol-C-methyltransferase
84	AAB62812	2246458	S-adenosyl-methionine-sterol-C- methyltransferase [Ricinus communis]
85	AAC35787	3603295	S-adenosyl-methionine cycloartenol-C24-methyltransferase [Nicotiana tabacum]
86	AAC34988	3560531	cycloartenol-C24-methyltransferase [Oryza sativa subsp. japonic
87	AAZ83345	73761691	24-sterol C-methyltransferase [Gossypium hirsutum]
88	EAS30660	90301029	hypothetical protein CIMG_06139 [Coccidioides immitis RS]
89	P_470035	50919277	putative endosperm C-24 sterol methyltransferase [Oryza sativa (japonica cultivar-group)]
90	AAP21419	30103006	putative endosperm C-24 sterol methyltransferase [Oryza sativa (japonica cultivar-group)]
91	AAR92099	40806291	S-adenosyl-L-methionine-C-24-delta-sterol-methyltransferase B [Leishmania donovani]
92	AAR92098	40806289	S-adenosyl-L-methionine-C-24-delta-sterol-methyltransferase A [Leishmania donovani]
93	CAJ09197	68129891	sterol 24-c-methyltransferase, putative [Leishmania major]
94	CAJ09196	68129890	sterol 24-c-methyltransferase, putative [Leishmania major]
95	P_802864	71399753	sterol 24-c-methyltransferase [Trypanosoma cruzi strain CL Brer
96	EAN81418	70865128	sterol 24-c-methyltransferase, putative [Trypanosoma cruzi]
97	P_802716	71399140	sterol 24-c-methyltransferase [Trypanosoma cruzi strain CL Brer
98	EAN81270	70864663	sterol 24-c-methyltransferase, putative [Trypanosoma cruzi]
99	P_822930	71747750	sterol 24-c-methyltransferase [Trypanosoma brucei TREU927]
100	AAZ40214	71738257	sterol methyltransferase [Trypanosoma brucei brucei]
101	CAJ16958	70908212	s-adenosyl-L-methionine-c-24-delta-sterol-methy lt ransferase a, putative [Trypanosoma brucei]
102	EAN78102	70832598	sterol 24-c-methyltransferase, putative [Trypanosoma brucei]
103	P_636481	66805519	hypothetical protein DDBDRAFT_0188166 [Dictyostelium discoideum AX4]
104	EAL62977	60464861	hypothetical protein DDBDRAFT_0188166 [Dictyostelium discoideum AX4]
105	ABF99454	108711659	Cyclopropane-fatty-acyl-phospholipid synthase family protein, expressed [Oryza sativa (japonica cultivar-group)]
106	P_802811	71399535	sterol 24-c-methyltransferase [Trypanosoma cruzi strain CL Brer
107	EAN81365	70864963	sterol 24-c-methyltransferase, putative [Trypanosoma cruzi]
108	ABB90541	82780739	c24-sterol methyltransferase [Paracoccidioides brasiliensis]
109	AAB62807	2246452	S-adenosyl-methionine-sterol-C-methyltransferase homolog [Nicotiana tabacum]
110	Q39227	62900893	24-methylenesterol C-methyltransferase 2 (24-sterol C-methyltransferase 2) (Sterol-C-methyltransferase 2)
111	AAM45009	21281107	putative sterol-C-methyltransferase [Arabidopsis thaliana]

112	P_173458	15217917	SMT2 (STEROL METHYLTRANSFERASE 2) [Arabidopsis thaliana]
113	AAK76716	15028255	putative sterol-C-methyltransferase [Arabidopsis thaliana]
114	AAG48780	12083242	putative sterol-C-methyltransferase [Arabidopsis thaliana]
115	AAF88156	9558593	Identical to 24-sterol C-methyltransferase from Arabidopsis thali gi|2129517 and is a member of the ubiE/COQ5 methyltransferas family PF|01209. ESTs gb|T42228, gb|T46520, gb|T41746, gb|N38458, gb|AI993515, gb|AA389843, gb|AI099890, gb|AI099653 come f
116	2207220A	1587694	sterol C-methyltransferase
117	CAA61966	1061040	sterol-C-methyltransferase [Arabidopsis thaliana]
118	AAN72104	25083682	24-sterol C-methyltransferase [Arabidopsis thaliana]
119	AAM91592	22136020	24-sterol C-methyltransferase [Arabidopsis thaliana]
120	Q94JS4	67472706	24-methylenesterol C-methyltransferase 3 (24-sterol C-methyltransferase 3) (Sterol-C-methyltransferase 3)
121	AAM47339	21360447	At1g76090/T23E18_40 [Arabidopsis thaliana]
122	P_177736	15222955	SMT3; S-adenosylmethionine-dependent methyltransferase [Arabidopsis thaliana]
123	AAK52981	14030613	At1g76090/T23E18_40 [Arabidopsis thaliana]
124	AAN31890	23397216	putative sterol-C-methyltransferase [Arabidopsis thaliana]
125	AAB62809	2246456	S-adenosyl-methionine-sterol-C-methyltransferase [Arabidopsis thaliana]
126	AAB62808	2246454	S-adenosyl-methionine-sterol-C- methyltransferase [Nicotiana tabacum]
127	AAM63753	21555010	sterol-C-methyltransferase [Arabidopsis thaliana]
128	BAF10805	113547362	Os03g0136200 [Oryza sativa (japonica cultivar-group)]
129	ABF93854	108706059	24-methylenesterol C-methyltransferase 2, putative, expressed [Oryza sativa (japonica cultivar-group)]
130	O82427	68566013	24-methylenesterol C-methyltransferase 2 (24-sterol C-methyltransferase 2) (Sterol-C-methyltransferase 2)

Table 90. Examples of ERG5 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	P54781	1706693	Cytochrome P450 61 (C-22 sterol desaturase)
2	AAB06217	1235991	cytochrome P450
3	CAA89116	798924	unknown [Saccharomyces cerevisiae]
4	AAU09769	51830482	YMR015C [Saccharomyces cerevisiae]
5	AAX73198	62178556	C22 sterol desaturase [Candida glabrata]
6	AAX73197	62178554	C22 sterol desaturase [Candida glabrata]
7	P_449681	50294540	hypothetical protein CAGL0M07656g [Candida glabrata CBS1
8	CAG62657	49528995	unnamed protein product [Candida glabrata CBS138]
9	P_453562	50307167	unnamed protein product [Kluyveromyces lactis]
10	CAH00658	49642696	unnamed protein product [Kluyveromyces lactis NRRL Y-1140
11	P_982999	45185282	ABR053Cp [Eremothecium gossypii]
12	AAS50823	44980940	ABR053Cp [Ashbya gossypii ATCC 10895]
13	P_458727	50420383	hypothetical protein DEHA0D06842g [Debaryomyces hansenii CBS767]
14	CAG86871	49654394	unnamed protein product [Debaryomyces hansenii CBS767]
15	P_888893	77022898	hypothetical protein CaJ7.0323 [Candida albicans SC5314]
16	BAE44790	76573706	hypothetical protein [Candida albicans]
17	P_716933	68478128	cytochrome P450 [Candida albicans SC5314]
18	P_717000	68477993	hypothetical protein CaO19.5178 [Candida albicans SC5314]
19	EAK98020	46438693	hypothetical protein CaO19.5178 [Candida albicans SC5314]
20	EAK97950	46438622	hypothetical protein CaO19.12645 [Candida albicans SC5314]
21	CAA21953	3850153	cytochrome P450 [Candida albicans]
22	P_500188	50545301	hypothetical protein [Yarrowia lipolytica]
23	CAG84120	49646053	unnamed protein product [Yarrowia lipolytica CLIB122]
24	BAC01142	21624361	sterol C-22 desaturase [Symbiotaphrina buchneri]
25	BAC01140	21624354	sterol C-22 desaturase [Symbiotaphrina buchneri]
26	BAC01141	21624359	sterol C-22 desaturase [Symbiotaphrina kochii]
27	BAC01139	21624352	sterol C22 desaturase [Symbiotaphrina kochii]
28	EAQ88206	88180738	conserved hypothetical protein [Chaetomium globosum CBS 148.51]
29	P_961915	85105220	hypothetical protein [Neurospora crassa OR74A]
30	EAA32679	28923500	hypothetical protein [Neurospora crassa]
31	EAS33985	90304354	hypothetical protein CIMG_05009 [Coccidioides immitis RS]
32	P_750145	70990592	cytochrome P450 sterol C-22 desaturase [Aspergillus fumigatus Af293]
33	EAL88107	66847777	cytochrome P450 sterol C-22 desaturase, putative [Aspergillus fumigatus Af293]
34	EAT87119	111065999	hypothetical protein SNOG_06055 [Phaeosphaeria nodorum SN
35	BAE58068	83767929	unnamed protein product [Aspergillus oryzae]
36	P_382135	46110154	hypothetical protein FG01959.1 [Gibberella zeae PH-1]
37	EAA68855	42546012	hypothetical protein FG01959.1 [Gibberella zeae PH-1]
38	P_661646	67527317	hypothetical protein AN4042.2 [Aspergillus nidulans FGSC A4]
39	EAA59513	40740323	hypothetical protein AN4042.2 [Aspergillus nidulans FGSC A4]
40	P_383862	46115688	hypothetical protein FG03686.1 [Gibberella zeae PH-1]
41	EAA71499	42548656	hypothetical protein FG03686.1 [Gibberella zeae PH-1]
42	P_369417	39976053	hypothetical protein MG06047.4 [Magnaporthe grisea 70-15]
43	BAE57461	83767322	unnamed protein product [Aspergillus oryzae]
44	P_593788	19114700	hypothetical protein SPAC19A8.04 [Schizosaccharomyces pomb 972h-]
45	CAB11640	7007345	SPAC19A8.04 [Schizosaccharomyces pombe]

46	P_756497	71003662	hypothetical protein UM00350.1 [Ustilago maydis 521]
47	EAK81168	46095935	hypothetical protein UM00350.1 [Ustilago maydis 521]
48	P_571445	58268578	C-22 sterol desaturase [Cryptococcus neoformans var. neoforma JEC21]
49	AAW44138	57227680	C-22 sterol desaturase, putative [Cryptococcus neoformans var. neoformans JEC21]
50	EAL20298	50257593	hypothetical protein CNBF1100 [Cryptococcus neoformans var. neoformans B-3501A]
51	EAQ86140	88178672	hypothetical protein CHGG_07393 [Chaetomium globosum CB 148.51]
52	AAO48601	28864257	ERG5 [Clavispora lusitaniae]
53	P_647018	66827327	cytochrome P450 family protein [Dictyostelium discoideum AX
54	EAL73097	60475161	cytochrome P450 family protein [Dictyostelium discoideum AX
55	BAF04287	113531904	Os01g0211200 [Oryza sativa (japonica cultivar-group)]
56	P_913287	34903880	unnamed protein product [Oryza sativa (japonica cultivar-group
57	BAA96196	8096624	putative sterol C-22 desaturase [Oryza sativa (japonica cultivar-group)]
58	BAA96154	8096581	putative sterol C-22 desaturase [Oryza sativa (japonica cultivar-group)]
59	ABC59097	84514177	cytochrome P450 monooxygenase CYP710A15 [Medicago truncatula]
60	P_180452	15226976	CYP710A4; heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana]
61	AAC79590	3927833	putative cytochrome P450 [Arabidopsis thaliana]
62	P_913285	34903876	unnamed protein product [Oryza sativa (japonica cultivar-group
63	BAA96194	8096622	sterol C-22 desaturase -like [Oryza sativa (japonica cultivar-grou
64	BAA96152	8096579	sterol C-22 desaturase -like [Oryza sativa (japonica cultivar-grou
65	P_913291	34903888	unnamed protein product [Oryza sativa (japonica cultivar-group
66	BAA96200	8096628	sterol C-22 desaturase -like [Oryza sativa (japonica cultivar-grou
67	BAA96158	8096585	sterol C-22 desaturase -like [Oryza sativa (japonica cultivar-grou
68	BAF04286	113531903	Os01g0210900 [Oryza sativa (japonica cultivar-group)]
69	P_913284	34903874	unnamed protein product [Oryza sativa (japonica cultivar-group
70	BAA96193	8096621	sterol C-22 desaturase -like [Oryza sativa (japonica cultivar-grou
71	BAA96151	8096578	sterol C-22 desaturase -like [Oryza sativa (japonica cultivar-grou
72	BAE71351	84468537	CYP710 [Arabidopsis thaliana]
73	AAQ65177	34365731	At2g34500 [Arabidopsis thaliana]
74	AAN72080	25083451	putative cytochrome P450 [Arabidopsis thaliana]
75	AAM14944	20197156	putative cytochrome P450 [Arabidopsis thaliana]
76	P_180997	15226758	CYP710A1; heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana]
77	AAC26690	3128210	putative cytochrome P450 [Arabidopsis thaliana]
78	P_180451	15226974	CYP710A3; heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana]
79	AAC79589	3927832	putative cytochrome P450 [Arabidopsis thaliana]
80	BAE80316	89111285	CYP710 protein [Arabidopsis thaliana]
81	AAM26664	20856398	At2g34490/T31E10.17 [Arabidopsis thaliana]
82	AAM14945	20197157	putative cytochrome P450 [Arabidopsis thaliana]
83	AAL75888	18650637	At2g34490/T31E10.17 [Arabidopsis thaliana]
84	P_180996	15226756	CYP710A2; heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana]
85	AAC26691	3128211	putative cytochrome P450 [Arabidopsis thaliana]
86	AAM62799	21553706	putative cytochrome P450 [Arabidopsis thaliana]
87	BAE93156	91204699	sterol 22-desaturase [Lycopersicon esculentum]

Table 91. Examples of ERG3 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	AAT93015	51013443	YLR056W [Saccharomyces cerevisiae]
2	NP_013157	6323085	C-5 sterol desaturase, catalyzes the introduction of a C-5(6)
3	BAA20292	2143190	C-5 sterol desaturase [Saccharomyces cerevisiae]
4	CAA64303	1181277	C-5 sterol desaturase [Saccharomyces cerevisiae]
5	P32353	416963	C-5 sterol desaturase (Sterol-C5-desaturase) (Ergosterol delta
6	AAB39844	233331	C-5 sterol desaturase [Saccharomyces cerevisiae]
7	AAA34595	171477	C-5 sterol desaturase
8	AAA34594	171475	C-5 sterol desaturase
9	XP_446050	50287241	unnamed protein product [Candida glabrata]
10	CAG58974	49525357	unnamed protein product [Candida glabrata CBS138]
11	P50860	1706691	C-5 sterol desaturase (Sterol-C5-desaturase) (Ergosterol delta
12	AAB02330	755695	ERG3
13	Q754B9	51701406	C-5 sterol desaturase (Sterol-C5-desaturase) (Ergosterol delta
14	NP_985698	45198669	AFR151Cp [Eremothecium gossypii]
15	AAS53522	44984679	AFR151Cp [Ashbya gossypii ATCC 10895]
16	XP_455482	50310919	unnamed protein product [Kluyveromyces lactis]
17	CAG98190	49644618	unnamed protein product [Kluyveromyces lactis NRRL Y-1140
18	Q8NJ57	51701432	C-5 sterol desaturase (Sterol-C5-desaturase) (Ergosterol delta
19	CAD13131	22022945	ergosterol delta 5,6 desaturase [Candida dubliniensis]
20	XP_713577	68485022	hypothetical protein CaO19.767 [Candida albicans SC5314]
21	XP_713612	68484947	hypothetical protein CaO19.8387 [Candida albicans SC5314]
22	EAK94507	46435118	hypothetical protein CaO19.8387 [Candida albicans SC5314]
23	EAK94472	46435082	hypothetical protein CaO19.767 [Candida albicans SC5314]
24	O93875	51701379	C-5 sterol desaturase (Sterol-C5-desaturase) (Ergosterol delta
25	AAC99343	4091929	C5,6 desaturase [Candida albicans]
26	XP_460747	50424321	hypothetical protein DEHA0F09757g [Debaryomyces hansenii CBS76
27	CAG89088	49656416	unnamed protein product [Debaryomyces hansenii CBS767]
28	XP_503090	50551233	hypothetical protein [Yarrowia lipolytica]
29	CAG81282	49648958	unnamed protein product [Yarrowia lipolytica CLIB122]
30	XP_664110	67540672	hypothetical protein AN6506.2 [Aspergillus nidulans FGSC A4
31	EAA57846	40738656	hypothetical protein AN6506.2 [Aspergillus nidulans FGSC A4
32	BAE61784	83771654	unnamed protein product [Aspergillus oryzae]
33	XP_747563	70984086	sterol delta 5,6-desaturase ERG3 [Aspergillus fumigatus Af293
34	EAL85525	66845190	sterol delta 5,6-desaturase ERG3 [Aspergillus fumigatus Af293
35	AAU82098	52548218	C-5 sterol desaturase B-like [Aspergillus fumigatus]
36	BAE56076	83765933	unnamed protein product [Aspergillus oryzae]
37	XP_962923	85109451	hypothetical protein [Neurospora crassa OR74A]
38	Q7SBB6	51701418	Probable C-5 sterol desaturase (Sterol-C5-desaturase) (Ergoste
39	EAA33687	28924567	hypothetical protein [Neurospora crassa]
40	EAS37256	90307625	C-5 sterol desaturase [Coccidioides immitis RS]
41	Q8J207	51701428	C-5 sterol desaturase (Sterol-C5-desaturase) (Ergosterol delta
42	AAN27998	23476431	sterol delta 5,6-desaturase ERG3 [Leptosphaeria maculans]
43	XP_363987	39953467	hypothetical protein MG08832.4 [Magnaporthe grisea 70-15]
44	EAT83541	111062421	hypothetical protein SNOG_09349 [Phaeosphaeria nodorum SN
45	O94457	51701380	Probable C-5 sterol desaturase 1 (Sterol-C5-desaturase 1) (Erg
46	NP_593135	19114047	hypothetical protein SPAC1687.16c [Schizosaccharomyces pon
47	CAA22610	4106670	SPAC1687.16c [Schizosaccharomyces pombe]
48	XP_382678	46111241	hypothetical protein FG02502.1 [Gibberella zeae PH-1]
49	EAA67236	42544393	hypothetical protein FG02502.1 [Gibberella zeae PH-1]

50	BAE65607	83775487	unnamed protein product [Aspergillus oryzae]
51	O13666	6015113	Probable C-5 sterol desaturase 2 (Sterol-C5-desaturase 2) (Erg
52	CAA16898	2853109	SPBC27B12.03c [Schizosaccharomyces pombe]
53	BAA21457	2257565	C-5 STEROL DESATURASE [Schizosaccharomyces pombe]

Table 92. Examples of ERG2 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	AAS56448	45270134	YMR202W [Saccharomyces cerevisiae]
2	CAA88643	736299	Erg2p [Saccharomyces cerevisiae]
3	P32352	416962	C-8 sterol isomerase (Delta-8--delta-7 sterol isomerase)
4	AAA34593	171473	C-8 sterol isomerase
5	P_985369	45198340	AFL181Cp [Eremothecium gossypii]
6	AAS53193	44984227	AFL181Cp [Ashbya gossypii ATCC 10895]
7	P_449233	50293643	unnamed protein product [Candida glabrata]
8	CAG62207	49528546	unnamed protein product [Candida glabrata CBS138]
9	P_455367	50310691	unnamed protein product [Kluyveromyces lactis]
10	CAG98075	49644503	unnamed protein product [Kluyveromyces lactis NRRL Y-1140]
11	P_458891	50420709	hypothetical protein DEHA0D10714g [Debaryomyces hansenii CBS767]
12	CAG87043	49654558	unnamed protein product [Debaryomyces hansenii CBS767]
13	P_718886	68473979	sterol C8-C7 isomerase [Candida albicans SC5314]
14	P_718988	68473770	sterol C8-C7 isomerase [Candida albicans SC5314]
15	EAL00087	46440785	hypothetical protein CaO19.6026 [Candida albicans SC5314]
16	EAK99982	46440679	hypothetical protein CaO19.13447 [Candida albicans SC5314]
17	P_504668	50554519	hypothetical protein [Yarrowia lipolytica]
18	CAG80272	49650537	unnamed protein product [Yarrowia lipolytica CLIB122]
19	P_501006	50547073	hypothetical protein [Yarrowia lipolytica]
20	CAG83259	49646872	unnamed protein product [Yarrowia lipolytica CLIB122]
21	Q92254	67476925	C-8 sterol isomerase (Delta-8--delta-7 sterol isomerase)
22	CAC28749	12718205	C-8 sterol isomerase erg-1 [Neurospora crassa]
23	AAB09470	1575320	C-8 sterol isomerase
24	P_658055	67516339	hypothetical protein AN0451.2 [Aspergillus nidulans FGSC A4]
25	EAA66550	40747394	hypothetical protein AN0451.2 [Aspergillus nidulans FGSC A4]
26	P_593324	19114236	hypothetical protein SPAC20G8.07c [Schizosaccharomyces pom 972h-]
27	P87113	3219796	Probable C-8 sterol isomerase (Delta-8--delta-7 sterol isomerase
28	CAB08601	2094862	SPAC20G8.07c [Schizosaccharomyces pombe]
29	P_363040	39947737	hypothetical protein MG08624.4 [Magnaporthe grisea 70-15]
30	P33281	462023	C-8 sterol isomerase (Delta-8--delta-7 sterol isomerase)
31	CAA80454	311322	C-8 sterol isomerase [Magnaporthe grisea]
32	EAQ85888	88178420	hypothetical protein CHGG_07141 [Chaetomium globosum CBS 148.51]
33	P_961312	85102300	C-8 STEROL ISOMERASE (DELTA-8--DELTA-7 STEROL ISOMERASE) [Neurospora crassa OR74A]
34	EAA32076	28922855	C-8 STEROL ISOMERASE (DELTA-8--DELTA-7 STEROL ISOMERASE) [Neurospora crassa]
35	P_844057	72387265	C-8 sterol isomerase, putative [Trypanosoma brucei]
36	P_826540	71905267	C-8 sterol isomerase, putative [Trypanosoma brucei]
37	AAZ10498	70800589	C-8 sterol isomerase, putative [Trypanosoma brucei]
38	AAX80634	62360216	C-8 sterol isomerase, putative [Trypanosoma brucei]
39	P_758081	71006989	C-8 sterol isomerase [Ustilago maydis 521]
40	EAK82388	46097155	ERG2_USTMA C-8 sterol isomerase (Delta-8--delta-7 sterol isomerase) [Ustilago maydis 521]
41	P32360	416961	C-8 sterol isomerase (Delta-8--delta-7 sterol isomerase)
42	CAA78959	2967	C-8 sterol isomerase [Ustilago maydis]
43	P_567070	58259315	C-8 sterol isomerase [Cryptococcus neoformans var. neoformans JEC21]
44	AAW41251	57223207	C-8 sterol isomerase, putative [Cryptococcus neoformans var.

			neoformans JEC21]
45	EAL23045	50260386	hypothetical protein CNBA8120 [Cryptococcus neoformans var. neoformans B-3501A]
46	P_821186	71658920	C-8 sterol isomerase [Trypanosoma cruzi strain CL Brener]
47	EAN99335	70886558	C-8 sterol isomerase, putative [Trypanosoma cruzi]
48	AAQ18796	33439494	C-8 sterol isomerase [Trypanosoma cruzi]
49	P_847879	73536920	C-8 sterol isomerase-like protein [Leishmania major strain Friedl
50	AAZ09671	70799755	C-8 sterol isomerase-like protein [Leishmania major strain Friedl

Table 93. Examples of ERG3-like polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	BAA33730	3721884	sterol-C5-desaturase [Mus musculus]
2	BAE32506	74178504	unnamed protein product [Mus musculus]
3	AAH24132	18848246	Sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog cerevisae) [Mus musculus]
4	NP_766357	27777693	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog [Mus musculus]
5	BAC36944	26346591	unnamed protein product [Mus musculus]
6	BAC31666	26335931	unnamed protein product [Mus musculus]
7	AAH81704	51859106	Sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog cerevisae) [Rattus norvegicus
8	NP_446094	25742651	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog [Rattus norvegicus]
9	BAB19798	11990472	sterol C5-desaturase [Rattus norvegicus]
10	XP_853004	73955000	PREDICTED: similar to sterol-C5-desaturase-like [Canis familia
11	XP_508825	55637121	PREDICTED: similar to delta7-sterol-C5-desaturase [Pan troglodytes]
12	NP_001...	68160945	sterol-C5-desaturase-like [Homo sapiens]
13	NP_008849	68160941	sterol-C5-desaturase-like [Homo sapiens]
14	BAD96861	62897843	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal) like variant [Homo sapiens]
15	BAD96406	62896931	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal) like variant [Homo sapiens]
16	AAH50427	30046554	Sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal) like [Homo sapiens]
17	AAH12333	15147389	Sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal) like [Homo sapiens]
18	AAF00544	6003685	delta7-sterol-C5-desaturase [Homo sapiens]
19	BAB68218	15637108	sterol C5 desaturase [Homo sapiens]
20	O75845	6174975	Lathosterol oxidase (Lathosterol 5-desaturase) (Delta-7-sterol 5-desaturase) (C-5 sterol desatur
21	BAA33729	3721882	sterol-C5-desaturase [Homo sapiens]
22	XP_001...	1.09E+08	PREDICTED: sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like isoform 2 [Macaca
23	AAH78055	50416254	Sc5d-prov protein [Xenopus laevis]
24	NP_001...	52219112	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog [Danio rerio]
25	AAH81395	51859008	Sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog cerevisae) [Danio rerio]
26	BAA18970	1906796	fungal sterol-C5-desaturase homolog [Homo sapiens]
27	XP_001...	1.09E+08	PREDICTED: sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like isoform 1 [Macaca
28	XP_793331	72159211	PREDICTED: similar to sterol-C5-desaturase (fungal ERG3, delt 5-desaturase) homolog [Strongyloc
29	NP_001...	78369462	hypothetical protein LOC525154 [Bos taurus]
30	AAI03339	74353920	Similar to sterol-C5-desaturase-like [Bos taurus]
31	CAF90498	47207599	unnamed protein product [Tetraodon nigroviridis]

Table 91. Examples of ERG27 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	Q12452	60392263	3-keto-steroid reductase

2	CAA97664	1360483	unnamed protein product [Saccharomyces cerevisiae]
3	AAB67544	1256850	Ylr100wp [Saccharomyces cerevisiae]
4	Q6FIV3	62286920	3-keto-steroid reductase
5	P_449841	50294860	hypothetical protein CAGL0M11506g [Candida glabrata CBS13
6	CAG62821	49529155	unnamed protein product [Candida glabrata CBS138]
7	Q6CJC2	62286919	3-keto-steroid reductase
8	P_455967	50311871	unnamed protein product [Kluyveromyces lactis]
9	CAG98675	49645103	unnamed protein product [Kluyveromyces lactis NRRL Y-1140]
10	Q74ZZ0	62286926	3-keto-steroid reductase
11	P_986733	45201163	AGR068Wp [Eremothecium gossypii]
12	AAS54557	44985946	AGR068Wp [Ashbya gossypii ATCC 10895]
13	Q6BNP0	62286917	3-keto-steroid reductase
14	P_460180	50423199	hypothetical protein DEHA0E21263g [Debaryomyces hansenii C
15	CAG88453	49655848	unnamed protein product [Debaryomyces hansenii CBS767]
16	Q874K0	62286935	3-keto-steroid reductase
17	AAN28009	29465858	3-keto reductase [Candida albicans]
18	P_717865	68476112	3-keto sterol reductase [Candida albicans SC5314]
19	P_717931	68475981	3-keto sterol reductase [Candida albicans SC5314]
20	EAK98982	46439667	hypothetical protein CaO19.3240 [Candida albicans SC5314]
21	EAK98915	46439599	hypothetical protein CaO19.10750 [Candida albicans SC5314]
22	Q6CE88	62286918	3-keto-steroid reductase
23	P_501024	50547109	hypothetical protein [Yarrowia lipolytica]
24	CAG83277	49646890	unnamed protein product [Yarrowia lipolytica CLIB122]
25	P_595440	19112232	3-keto sterol reductase [Schizosaccharomyces pombe 972h-]
26	CAA21246	3738145	SPBC1709.07 [Schizosaccharomyces pombe]
27	BAA13878	1749642	unnamed protein product [Schizosaccharomyces pombe]
28	P_751680	70993666	3-ketosteroid reductase [Aspergillus fumigatus Af293]
29	EAL89642	66849314	3-ketosteroid reductase [Aspergillus fumigatus Af293]
30	P_958799	85091228	hypothetical protein [Neurospora crassa OR74A]
31	EAA29563	28920185	hypothetical protein [Neurospora crassa]
32	BAE58171	83768032	unnamed protein product [Aspergillus oryzae]
33	EAQ85086	88177618	hypothetical protein CHGG_09100 [Chaetomium globosum CBS 148
34	EAT86025	111064905	hypothetical protein SNOG_06194 [Phaeosphaeria nodorum SN1
35	P_663189	67538830	hypothetical protein AN5585.2 [Aspergillus nidulans FGSC A4]
36	EAA62228	40743038	hypothetical protein AN5585.2 [Aspergillus nidulans FGSC A4]
37	EAS36221	90306590	hypothetical protein CIMG_01575 [Coccidioides immitis RS]
38	AAO64345	29150686	3-ketosteroid reductase [Botryotinia fuckeliana]
39	P_796770	72131681	PREDICTED: similar to hydroxysteroid (17-beta) dehydrogenase
40	P_793145	72086766	PREDICTED: similar to hydroxysteroid (17-beta) dehydrogenase
41	P_570518	58266724	3-keto sterol reductase [Cryptococcus neoformans var. neofor
42	AAW43211	57226751	3-keto sterol reductase, putative [Cryptococcus neoformans v
43	EAL21279	50258592	hypothetical protein CNBD3330 [Cryptococcus neoformans var.
44	AAI00220	71681260	Unknown (protein for MGC:114978) [Xenopus laevis]
45	BAE06843	70720928	hypothetical protein [Epichloe festucae]
46	P_001...	62859081	hydroxysteroid (17-beta) dehydrogenase 7 [Xenopus tropicalis
47	P_851698	74006237	PREDICTED: similar to hydroxysteroid (17-beta) dehydrogenase
48	CAC88119	18077845	17beta-hydroxysteroid dehydrogenase type 7 [Mus musculus]
49	AAH11464	15079256	Hsd17b7 protein [Mus musculus]
50	P_034606	87162470	hydroxysteroid (17-beta) dehydrogenase 7 [Mus musculus]
51	BAC25918	26390565	unnamed protein product [Mus musculus]
52	BAC34124	26340924	unnamed protein product [Mus musculus]

53	O88736	8134403	3-keto-steroid reductase (Estradiol 17-beta-dehydrogenase 7)
54	CAA75742	3319971	17-beta-hydroxysteroid dehydrogenase type 7 [Mus musculus]
55	P_695820	68440091	PREDICTED: similar to Hydroxysteroid (17-beta) dehydrogenas
56	P_058931	8393576	hydroxysteroid (17-beta) dehydrogenase 7 [Rattus norvegicus]
57	Q62904	8134405	3-keto-steroid reductase (Estradiol 17-beta-dehydrogenase 7)
58	AAC52623	1397235	ovarian-specific protein
59	BAC37061	26346825	unnamed protein product [Mus musculus]
60	AAM21211	20385196	17-beta-hydroxysteroid dehydrogenase type 7 [Mus musculus]
61	P_363377	39951321	hypothetical protein MG01303.4 [Magnaporthe grisea 70-15]
62	P_581467	76611932	PREDICTED: similar to hydroxysteroid (17-beta) dehydrogenase
63	CAC88111	18077843	17beta hydroxysteroid dehydrogenase [Homo sapiens]
64	AAX42032	61361334	hydroxysteroid (17-beta) dehydrogenase 7 [synthetic construc
65	AAX42031	61361326	hydroxysteroid (17-beta) dehydrogenase 7 [synthetic construc
66	CAI13457	55959848	hydroxysteroid (17-beta) dehydrogenase 7 [Homo sapiens]
67	CAI15947	55959770	hydroxysteroid (17-beta) dehydrogenase 7 [Homo sapiens]
68	AAH65246	40807207	Hydroxysteroid (17-beta) dehydrogenase 7 [Homo sapiens]
69	AAQ89321	37183042	HSD17B7 [Homo sapiens]
70	AAP35738	30582989	hydroxysteroid (17-beta) dehydrogenase 7 [Homo sapiens]
71	AAH07068	13937918	Hydroxysteroid (17-beta) dehydrogenase 7 [Homo sapiens]
72	CAC20418	12053691	17beta-hydroxysteroid dehydrogenase type 7 [Homo sapiens]
73	P56937	8134404	3-keto-steroid reductase (Estradiol 17-beta-dehydrogenase 7)
74	P_057455	7705421	hydroxysteroid (17-beta) dehydrogenase 7 [Homo sapiens]
75	AAF09266	6721095	17 beta-hydroxysteroid dehydrogenase type VII [Homo sapiens]
76	ABB72853	82400271	17-beta hydroxysteroid dehydrogenase 7 [Macaca fascicularis]
77	AAX29487	60653587	hydroxysteroid (17-beta) dehydrogenase 7 [synthetic construc
78	AAP36180	30583863	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 7 [synth
79	AAF14537	6502988	17beta-hydroxysteroid dehydrogenase type 7 [Homo sapiens]
80	AAK20950	13383374	17-beta-hydroxysteroid dehydrogenase type 7 [Oryctolagus cun
81	AAP97275	33150794	ovarian-specific protein; OSP [Homo sapiens]
82	P_422210	50750970	PREDICTED: similar to Estradiol 17 beta-dehydrogenase 7 (17-

Table 95. Examples of ERG26 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	AAT93045	51013503	YGL001C [Saccharomyces cerevisiae]
2	P53199	1723793	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating
3	CAA96701	1322447	unnamed protein product [Saccharomyces cerevisiae]
4	P_446390	50287923	unnamed protein product [Candida glabrata]
5	CAG59317	49525698	unnamed protein product [Candida glabrata CBS138]
6	P_453025	50306127	unnamed protein product [Kluyveromyces lactis]
7	CAH01876	49642158	unnamed protein product [Kluyveromyces lactis NRRL Y-1140]
8	CAC38016	13940379	putative C-3 sterol dehydrogenase [Zygosaccharomyces rouxii]
9	P_985548	45198519	AFR001Wp [Eremothecium gossypii]
10	AAS53372	44984470	AFR001Wp [Ashbya gossypii ATCC 10895]
11	P_458178	50419307	hypothetical protein DEHA0C12463g [Debaryomyces hansenii CBS767]
12	CAG86252	49653844	unnamed protein product [Debaryomyces hansenii CBS767]
13	P_715564	68481045	C-3 sterol dehydrogenase/C-4 decarboxylase [Candida albicans SC53
14	P_715620	68480934	C-3 sterol dehydrogenase/C-4 decarboxylase [Candida albicans SC53
15	EAK96601	46437251	hypothetical protein CaO19.10427 [Candida albicans SC5314]
16	EAK96542	46437191	hypothetical protein CaO19.2909 [Candida albicans SC5314]
17	AAK69617	14582743	C-3 sterol dehydrogenase/C-4 decarboxylase [Candida albicans]
18	P_502124	50549307	hypothetical protein [Yarrowia lipolytica]
19	CAG82444	49647991	unnamed protein product [Yarrowia lipolytica CLIB122]
20	P_596741	19113533	hypothetical protein SPBC3F6.02c [Schizosaccharomyces pombe 972h-
21	CAA17691	2924499	SPBC3F6.02c [Schizosaccharomyces pombe]
22	AAQ88129	37039511	C-3 sterol dehydrogenase [Cryptococcus neoformans var. grubii I
23	P_381379	46108642	hypothetical protein FG01203.1 [Gibberella zeae PH-1]
24	EAA67667	42544824	hypothetical protein FG01203.1 [Gibberella zeae PH-1]
25	EAQ90884	88183416	conserved hypothetical protein [Chaetomium globosum CBS 148
26	P_640712	66813066	3beta-hydroxysteroid dehydrogenase [Dictyostelium discoideum AX4]
27	EAL66725	60468723	3beta-hydroxysteroid dehydrogenase [Dictyostelium discoideum AX4]
28	EAT77489	111056369	hypothetical protein SNOG_15264 [Phaeosphaeria nodorum SN1
29	P_965466	85118539	hypothetical protein [Neurospora crassa OR74A]
30	CAE76518	38567226	related to C-3 sterol dehydrogenase (C-4 decarboxylase) [Neuros
31	EAA36230	28927275	hypothetical protein [Neurospora crassa]
32	P_420279	50745878	PREDICTED: similar to NAD(P) dependent steroid dehydrogena like
33	P_001...	78369400	hypothetical protein LOC616694 [Bos taurus]
34	AAI03390	73586574	Similar to NAD(P) dependent steroid dehydrogenase-like [Bos ta
35	P_001...	62859757	hypothetical protein LOC550044 [Xenopus tropicalis]
36	AAH88699	56788986	LOC496236 protein [Xenopus laevis]
37	P_538199	74008671	PREDICTED: similar to NAD(P) dependent steroid dehydrogena like
38	P_853073	74008673	PREDICTED: similar to NAD(P) dependent steroid dehydrogena like
39	AAH52834	31127258	NAD(P) dependent steroid dehydrogenase-like [Mus musculus]
40	P_001...	109132673	PREDICTED: similar to NAD(P) dependent steroid dehydrogena like
41	P_001...	109132671	PREDICTED: similar to NAD(P) dependent steroid dehydrogena

			like
42	P_001...	57164113	NAD(P) dependent steroid dehydrogenase-like [Rattus norvegicu
43	AAH87626	56388600	NAD(P) dependent steroid dehydrogenase-like [Rattus norvegicu
44	BAE24522	74187675	unnamed protein product [Mus musculus]
45	P_035071	31982437	NAD(P) dependent steroid dehydrogenase-like [Mus musculus]
46	Q9R1J0	8473695	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating
47	CAA15948	7619723	NAD(P)H steroid dehydrogenase [Mus musculus]
48	AAD38448	5052206	putative NAD(P)H steroid dehydrogenase [Mus musculus]
49	AAH19945	18043286	NAD(P) dependent steroid dehydrogenase-like [Mus musculus]
50	AAH07816	14043700	NAD(P) dependent steroid dehydrogenase-like [Homo sapiens]
51	AAH00245	12652969	NAD(P) dependent steroid dehydrogenase-like [Homo sapiens]
52	Q15738	8488997	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating (H
53	P_057006	8393516	NAD(P) dependent steroid dehydrogenase-like [Homo sapiens]
54	AAC50558	4457237	H105e3 [Homo sapiens]
55	CAF99107	47222951	unnamed protein product [Tetraodon nigroviridis]
56	P_756075	71002788	C-3 sterol dehydrogenase/C-4 decarboxylase [Aspergillus fumiga
57	EAL94037	66853713	C-3 sterol dehydrogenase/C-4 decarboxylase [Aspergillus fumiga
58	P_567299	58259773	C-3 sterol dehydrogenase (C-4 sterol decarboxylase) [Cryptococc
59	AAW45782	57229349	C-3 sterol dehydrogenase (C-4 sterol decarboxylase), putative [C
60	EAL18383	50255650	hypothetical protein CNBJ3060 [Cryptococcus neoformans var. neofo
61	P_001...	62955325	hypothetical protein LOC550369 [Danio rerio]
62	AAH93332	62204675	Zgc:112474 [Danio rerio]
63	EAS37011	90307380	hypothetical protein CIMG_02365 [Coccidioides immitis RS]
64	P_755836	71002310	C-3 sterol dehydrogenase/C-4 decarboxylase [Aspergillus fumiga
65	EAL93798	66853474	C-3 sterol dehydrogenase/C-4 decarboxylase [Aspergillus fumiga
66	CAH90815	55728130	hypothetical protein [Pongo pygmaeus]
67	P_760274	71020087	hypothetical protein UM04127.1 [Ustilago maydis 521]
68	EAK85155	46099922	hypothetical protein UM04127.1 [Ustilago maydis 521]
69	P_680844	67901176	hypothetical protein AN7575.2 [Aspergillus nidulans FGSC A4]
70	EAA62155	40742965	hypothetical protein AN7575.2 [Aspergillus nidulans FGSC A4]
71	AAZ14936	70906332	putative sterol dehydrogenase [Coprinellus disseminatus]

Table 96. Examples of ERG25 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	AAS56153	45269545	YGR060W [Saccharomyces cerevisiae]
2	XP_448420	50291975	unnamed protein product [Candida glabrata]
3	XP_451890	50303885	unnamed protein product [Kluyveromyces lactis]
4	NP_986119	45199090	AFR572Wp [Eremothecium gossypii]
5	XP_456861	50409318	hypothetical protein DEHA0A12661g [Debaryomyces hansenii CBS767]
6	XP_713420	68485318	C-4 sterol methyl oxidase [Candida albicans SC5314]
7	XP_461658	50426123	hypothetical protein DEHA0G03124g [Debaryomyces hansenii CBS767]
8	XP_505281	50555746	hypothetical protein [Yarrowia lipolytica]
9	XP_722703	68466442	putative C-4 sterol methyl oxidase [Candida albicans SC5314]
10	XP_722849	68466149	putative C-4 sterol methyl oxidase [Candida albicans SC5314]
11	ABF84061	107785180	C-4 sterol methyl oxidase [Chaetomium globosum]
12	Q9UUH4	28558117	C-4 methylsterol oxidase (Methylsterol monooxygenase)
13	XP_962240	85106720	hypothetical protein [Neurospora crassa OR74A]
14	EAT84680	111063560	hypothetical protein SNOG_08404 [Phaeosphaeria nodorum SN1
15	XP_746668	70982279	hypothetical protein Afu4g04820 [Aspergillus fumigatus Af293]
16	XP_390006	46136629	hypothetical protein FG09830.1 [Gibberella zeae PH-1]
17	BAE65381	83775259	unnamed protein product [Aspergillus oryzae]
18	XP_360827	39942580	hypothetical protein MG03370.4 [Magnaporthe grisea 70-15]
19	ABA70590	77377695	hypothetical protein [Penicillium chrysogenum]
20	XP_369331	39975881	hypothetical protein MG06133.4 [Magnaporthe grisea 70-15]
21	EAS29762	90300131	hypothetical protein CIMG_08508 [Coccidioides immitis RS]
22	XP_762027	71023595	hypothetical protein UM05880.1 [Ustilago maydis 521]
23	XP_569526	58264740	C-4 methyl sterol oxidase [Cryptococcus neoformans var. neoformans JEC21]
24	EAQ88125	88180657	hypothetical protein CHGG_04744 [Chaetomium globosum CBS 148.51]
25	BAE66491	83776372	unnamed protein product [Aspergillus oryzae]
26	XP_746962	70982869	c-4 methyl sterol oxidase [Aspergillus fumigatus Af293]
27	XP_682176	67903840	hypothetical protein AN8907.2 [Aspergillus nidulans FGSC A4]
28	XP_664577	67541619	hypothetical protein AN6973.2 [Aspergillus nidulans FGSC A4]
29	XP_646277	66825845	hypothetical protein DDBDRAFT_0190553 [Dictyostelium discoideum AX4]
30	NP_998917	47523336	sterol-C4-methyl oxidase-like protein [Sus scrofa]
31	AAI07880	79160074	Sterol-C4-methyl oxidase-like [Homo sapiens]
32	BAE01921	67971158	unnamed protein product [Macaca fascicularis]
33	XP_001...	109076099	PREDICTED: sterol-C4-methyl oxidase-like isoform 3 [Macaca mulatta]
34	XP_580615	61871492	PREDICTED: similar to C-4 methylsterol oxidase (Methylsterol monooxygenase) isoform 1 [Bos taurus]
35	CAC24471	12311696	hypothetical protein [Candida albicans]
36	BAE30143	74185334	unnamed protein product [Mus musculus]
37	XP_532714	57096891	PREDICTED: similar to C-4 methylsterol oxidase (Methylsterol monooxygenase) isoform 1 [Canis familiaris]
38	CAF92153	47211304	unnamed protein product [Tetraodon nigroviridis]
39	AAH63155	38649308	Sterol-C4-methyl oxidase-like [Rattus norvegicus]
40	NP_001...	57530155	sterol-C4-methyl oxidase-like [Gallus gallus]
41	NP_998518	47087009	sterol-C4-methyl oxidase-like [Danio rerio]
42	NP_563789	18390767	SMO2-2; C-4 methylsterol oxidase [Arabidopsis thaliana]
43	AAI21457	111309060	Unknown (protein for MGC:146461) [Xenopus tropicalis]

44	AAM64821	21592871	putative C-4 sterol methyl oxidase [Arabidopsis thaliana]
45	AAF79571	8778563	F22G5.23 [Arabidopsis thaliana]
46	AAO13795	27448145	putative sterol 4-alpha-methyl-oxidase [Gossypium arboreum]
47	AAO48604	28864263	ERG25 [Clavispora lusitaniae]
48	AAQ83692	34978966	C-4 sterol methyl oxidase 2 [Nicotiana benthamiana]
49	ABD97153	90658509	C-4 methyl sterol oxidase [Cryptococcus neoformans var. neoformans]
50	ABD97146	90658495	C-4 methyl sterol oxidase [Cryptococcus neoformans var. grubii]
51	ABD97147	90658497	C-4 methyl sterol oxidase [Cryptococcus neoformans var. grubii]
52	ABD97134	90658471	C-4 methyl sterol oxidase [Cryptococcus neoformans var. neoformans]
53	AAL82576	27447203	putative sterol 4-alpha-methyl-oxidase [Zea mays]
54	NP_850133	30684225	SMO2-1; C-4 methylsterol oxidase [Arabidopsis thaliana]
55	NP_973559	42570971	SMO2-1; C-4 methylsterol oxidase [Arabidopsis thaliana]
56	AAL32287	16973432	sterol 4-alpha-methyl-oxidase [Arabidopsis thaliana]
57	ABE83226	92875070	Sterol desaturase [Medicago truncatula]
58	BAF28920	113645779	Os11g0707600 [Oryza sativa (japonica cultivar-group)]
59	BAF20592	113610214	Os07g0101500 [Oryza sativa (japonica cultivar-group)]
60	XP_787442	72077919	PREDICTED: similar to C-4 methylsterol oxidase (Methylsterol monooxygenase) [Strongylocentrotus purpuratus]
61	AAM64359	21592408	putative C-4 sterol methyl oxidase [Arabidopsis thaliana]
62	NP_973777	42571373	SMO2-2; C-4 methylsterol oxidase [Arabidopsis thaliana]
63	NP_001...	62865628	sterol-C4-methyl oxidase-like isoform 2 [Homo sapiens]
64	AAX95419	62733302	4-alpha-methyl-sterol C4-methyl-oxidase [Oryza sativa (japonica cultivar-group)]
65	XP_883875	76638226	PREDICTED: similar to C-4 methylsterol oxidase (Methylsterol monooxygenase) isoform 3 [Bos taurus]
66	ABE87434	92884635	Sterol desaturase [Medicago truncatula]
67	XP_641553	66814748	hypothetical protein DDBDRAFT_0205936 [Dictyostelium discoideum AX4]
68	AAM65428	21593461	putative C-4 sterol methyl oxidase [Arabidopsis thaliana]
69	NP_567669	18416002	SMO1-3 (STEROL 4-ALPHA METHYL OXIDASE); catalytic [Arabidopsis thaliana]
70	AAM64961	21593012	putative C-4 sterol methyl oxidase [Arabidopsis thaliana]
71	AAN18115	23308291	At4g12110/F16J13_180 [Arabidopsis thaliana]
72	AAK61361	27446631	putative sterol 4-alpha-methyl-oxidase [Arabidopsis thaliana]
73	BAF01201	110738551	hypothetical protein [Arabidopsis thaliana]
74	AAQ13424	33337546	sterol-4-methyl-oxidase [Arabidopsis thaliana]
75	BAF27120	113639815	Os10g0545200 [Oryza sativa (japonica cultivar-group)]
76	CAB78254	7267912	putative C-4 sterol methyl oxidase [Arabidopsis thaliana]
77	AAQ94118	37591406	sterol-4-alpha methyl oxidase [Arabidopsis thaliana]
78	AAQ83691	34978964	C-4 sterol methyl oxidase 1 [Nicotiana benthamiana]
79	ABD65536	89266491	sterol-C4-methyl oxidase-like [Ictalurus punctatus]
80	BAC57961	28804511	putative C-4 sterol methyl oxidase [Aster tripolium]

Table 97. Examples of ERG24 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	AAB30203	545906	sterol delta 14 reductase; Erg24p [Saccharomyces cerevisiae]
2	XP_447380	50289897	hypothetical protein CAGL0I02970g [Candida glabrata CBS138]
3	XP_452744	50305569	unnamed protein product [Kluyveromyces lactis]
4	NP_985893	45198864	AFR346Wp [Eremothecium gossypii]
5	XP_710670	68491033	sterol C-14 reductase [Candida albicans SC5314]
6	XP_458371	50419687	hypothetical protein DEHA0C16984g [Debaryomyces hansenii

			CBS767]
7	XP_501260	50547581	hypothetical protein [Yarrowia lipolytica]
8	XP_566548	58258271	C-14 sterol reductase [Cryptococcus neoformans var. neoformans JEC21]
9	NP_596767	19113559	hypothetical protein SPBC16G5.18 [Schizosaccharomyces pombe 972h-]
10	EAL23454	50260804	hypothetical protein CNBA1040 [Cryptococcus neoformans var. neoformans B-3501A]
11	XP_759786	71019111	hypothetical protein UM03639.1 [Ustilago maydis 521]
12	XP_386782	46124457	ER24_FUSSO Delta(14)-sterol reductase (C-14 sterol reductase) (Sterol C14-reductase) [Gibberella zeae PH-1]
13	P78575	6015106	Delta(14)-sterol reductase (C-14 sterol reductase) (Sterol C14-reductase)
14	Q01447	3929349	Delta(14)-sterol reductase (C-14 sterol reductase) (Sterol C14-reductase)

Table 98. Examples of ERG11 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	AAA34546	171354	lanosterol 14-demethylase cytochrome P450
2	AAA34547	171356	lanosterol 14-demethylase cytochrome P450
3	AAY59417	66967944	14alpha-demethylase [Candida glabrata]
4	XP_454109	50308217	unnamed protein product [Kluyveromyces lactis]
5	Q759W0	51701328	Cytochrome P450 51 (CYPLI) (P450-LIA1) (Sterol 14-alpha demethylase) (Lanosterol 14-alpha demethylase) (P450-14DM)
6	AAB32679	912807	cytochrome P-450 lanosterol-alpha-demethylase; P450-L1A1 [Candida glabrata]
7	AAX39316	61189834	lanosterol 14 alpha demethylase [Candida tropicalis]
8	AAF00598	6006769	cytochrome P450 lanosterol 14-alpha demethylase [Candida albicans]
9	XP_716761	68478280	lanosterol 14-alpha-demethylase [Candida albicans SC5314]
10	XP_460143	50423125	hypothetical protein DEHA0E20383g [Debaryomyces hansenii CBS767]
11	ABC41921	83728463	cytochrome P450 lanosterol 14 alpha demethylase [Candida albicans]
12	AAX39315	61189832	lanosterol 14 alpha demethylase [Candida tropicalis]
13	O4CK51	65689	lanosterol 14alpha-demethylase (EC 1.14.14.-) cytochrome P450 - yeast (Candida albicans)
14	XP_716822	68478161	lanosterol 14-alpha-demethylase [Candida albicans SC5314]
15	AAF00603	6006774	cytochrome P450 lanosterol 14-alpha demethylase [Candida albicans]
16	AAF00600	6006771	cytochrome P450 lanosterol 14-alpha demethylase [Candida albicans]
17	BAB03401	9558446	CYP51 variant 3 [Candida albicans]
18	AAK57519	14280372	lanosterol 14-alpha demethylase Erg11p [Candida dubliniensis]
19	AAF00602	6006773	cytochrome P450 lanosterol 14-alpha demethylase [Candida albicans]
20	AAF00601	6006772	cytochrome P450 lanosterol 14-alpha demethylase [Candida albicans]
21	BAB03400	9558444	CYP51 variant 2 [Candida albicans]
22	AAO83898	29378393	cytochrome P-450 lanosterol-alpha-demethylase [Issatchenkia orientalis]
23	AAW50593	57341382	Erg11p [Candida albicans]
24	AAW50592	57341380	Erg11p [Candida albicans]
25	XP_500518	50545962	hypothetical protein [Yarrowia lipolytica]
26	BAC16517	23263326	cytochrome P-450 lanosterol 14alpha-demethylase [Candida albicans]
27	BAC16520	23263332	cytochrome P-450 lanosterol 14alpha-demethylase [Candida albicans]
28	BAC16518	23263328	cytochrome P-450 lanosterol 14alpha-demethylase [Candida albicans]
29	BAC16519	23263330	cytochrome P-450 lanosterol 14alpha-demethylase [Candida albicans]
30	Q02315	2493385	Cytochrome P450 51 (CYPLI) (P450-LIA1) (Sterol 14-alpha demethylase) (Lanosterol 14-alpha demethylase) (P450-14DM)
31	AAO38776	28395121	lanosterol 14 alpha demethylase; ERG11 [Pneumocystis carinii]
32	ABG91757	110816094	sterol 14alpha-demethylase [Pneumocystis carinii]
33	BAE60239	83770104	unnamed protein product [Aspergillus oryzae]
34	XP_749134	70987441	14-alpha sterol demethylase Cyp51B [Aspergillus fumigatus Af2
35	XP_659505	67522889	hypothetical protein AN1901.2 [Aspergillus nidulans FGSC A4]

36	XP_681552	67902592	hypothetical protein AN8283.2 [Aspergillus nidulans FGSC A4]
37	AAK73659	14861413	14-alpha sterol demethylase [Aspergillus fumigatus]
38	XP_752137	70994720	14-alpha sterol demethylase Cyp51A [Aspergillus fumigatus Af2
39	BAE57417	83767278	unnamed protein product [Aspergillus oryzae]
40	AAF79204	8778097	cytochrome P450 sterol 14 alpha-demethylase [Emericella nidula
41	CAE18091	33300264	eburicol 14 alpha demethylase [Blumeria graminis]
42	EAS28723	90299092	cytochrome P450 51 [Coccidioides immitis RS]
43	CAE18094	33300270	eburicol 14 alpha demethylase [Blumeria graminis]
44	CAC85624	33300256	eburicol 14alpha demethylase [Blumeria graminis f. sp. tritici]
45	CAE18095	33300272	eburicol 14 alpha demethylase [Blumeria graminis]
46	CAE17515	33284834	eburicol 14 alpha demethylase [Blumeria graminis f. sp. tritici]
47	AAU43734	52352491	eburicol 14 alpha-demethylase [Mycosphaerella graminicola]
48	EAS35219	90305588	cytochrome P450 51 [Coccidioides immitis RS]
49	CAE18102	33300286	eburicol 14 alpha demethylase [Blumeria graminis]
50	CAE18103	33300288	eburicol 14 alpha demethylase [Blumeria graminis]
51	CAE18105	33300292	eburicol 14 alpha demethylase [Blumeria graminis]
52	NP_592990	19113902	hypothetical protein SPAC13A11.02c [Schizosaccharomyces por 972h-]
53	CAE18100	33300282	eburicol 14 alpha demethylase [Blumeria graminis]
54	AAP79601	32330152	eburicol 14alpha-demethylase [Mycosphaerella graminicola]
55	AAC97606	4049645	eburicol 14alpha demethylase; CYP51; cytochrome P450 sterol 1 demethylase [Blumeria graminis f. sp. hordei]
56	CAE18099	33300280	eburicol 14 alpha demethylase [Blumeria graminis]
57	BAE63554	83773427	unnamed protein product [Aspergillus oryzae]
58	XP_381176	46108236	hypothetical protein FG01000.1 [Gibberella zeae PH-1]
59	AAF85983	9230788	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
60	AAP81934	32441730	eburicol 14 alpha-demethylase [Mycosphaerella graminicola]
61	XP_362183	39945292	hypothetical protein MG04628.4 [Magnaporthe grisea 70-15]
62	AAP12370	30314338	lanosterol 14 alpha-demethylase; 14 alpha lanosterol demethylase [Cryptococcus neoformans var. grubii]
63	AAF74756	8347731	eburicol 14-alpha demethylase [Mycosphaerella graminicola]
64	AAF76464	8570176	14 alpha-demethylase [Venturia inaequalis]
65	XP_566464	58258103	sterol 14-demethylase [Cryptococcus neoformans var. neoforman JEC21]
66	EAQ93417	88185949	conserved hypothetical protein [Chaetomium globosum CBS 148.51]
67	AAL79180	18766932	eburicol 14 alpha-demethylase [Monilinia fructicola]
68	AAU01157	51341094	lanosterol 14-alpha-demethylase [Coccidioides posadasii]
69	CAD27793	19572745	cytochrome P-450 14DM [Penicillium digitatum]
70	XP_384268	46116500	hypothetical protein FG04092.1 [Gibberella zeae PH-1]
71	AAG18433	10505323	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
72	AAK26391	13445823	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
73	AAG18431	10505318	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
74	AAK26386	13445813	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
75	AAD55135	5881952	eburicol 14-alpha demethylase; cytochrome P450 sterol 14-alpha demethylase; Erg11 [Uncinula necator]
76	AAK26389	13445819	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
77	CAC85409	15864613	euburicol 14 alpha-demethylase [Venturia nashicola]
78	BAB03659	9664027	cytochrome P-450 14DM [Penicillium digitatum]
79	AAG18435	10505329	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
80	AAG18434	10505326	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
81	AAU01158	51341096	lanosterol 14-alpha-demethylase [Ajellomyces capsulatus]

82	AAK26387	13445815	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
83	AAG18432	10505321	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
84	AAK26388	13445817	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
85	XP_391200	46139019	hypothetical protein FG11024.1 [Gibberella zeae PH-1]
86	AAK26390	13445821	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
87	O14442	14916976	Cytochrome P450 51 (CYPLI) (P450-LIA1) (Sterol 14-alpha demethylase) (Eburicol 14-alpha-demethylase) (P450-14DM)
88	AAG18438	10505336	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
89	XP_759809	71019157	sterol 14-alpha demethylase [Ustilago maydis 521]
90	AAF18468	6581118	eburicol 14 alpha-demethylase [Tapesia acuformis]
91	AAG18436	10505331	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
92	AAC49801	5733843	eburicol 14-alpha demethylase [Uncinula necator]
93	ABE01107	90823211	14alpha demethylase [Blumeriella jaapii]
94	AAG18437	10505334	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
95	CAD27792	19572743	cytochrome P-450 14DM [Penicillium digitatum]
96	XP_964049	85111674	hypothetical protein [Neurospora crassa OR74A]
97	AAF18469	11178694	eburicol 14 alpha-demethylase [Tapesia yallundae]
98	Q12664	2493386	Cytochrome P450 51 (CYPLI) (P450-LIA1) (Sterol 14-alpha demethylase) (Eburicol 14-alpha-demethylase) (P450-14DM)
99	AAG44832	12006321	eburicol 14-alpha demethylase [Tapesia yallundae]
100	AAG44831	12006319	eburicol 14-alpha demethylase [Tapesia yallundae]
101	AAN28927	23505745	sterol 14 alpha-demethylase ERG11 [Leptosphaeria maculans]
102	XP_361987	39944900	hypothetical protein MG04432.4 [Magnaporthe grisea 70-15]
103	EAT88907	111067787	hypothetical protein SNOG_03702 [Phaeosphaeria nodorum SN1
104	AAU01160	51341100	lanosterol 14-alpha-demethylase [Phanerochaete chrysosporium]
105	AAC23550	3220152	cytochrome P450 L1A1 demethylase [Pichia anomala]
106	AAU01159	51341098	lanosterol 14-alpha-demethylase [Coprinopsis cinerea]
107	Q9UVC3	12229768	Cytochrome P450 51 (CYPLI) (P450-LIA1) (Sterol 14-alpha demethylase) (Lanosterol 14-alpha demethylase) (P450-14DM)
108	AAQ88128	37039509	cytochrome P450 lanosterol 14a-demethylase [Cryptococcus neoformans var. grubii H99]
109	NP_064394	71061451	cytochrome P450, family 51 [Mus musculus]
110	EAL24154	51094909	cytochrome P450, family 51, subfamily A, polypeptide 1 [Homo sapiens]
111	Q16850	3915660	Cytochrome P450 51A1 (CYPLI) (P450LI) (Sterol 14-alpha demethylase) (Lanosterol 14-alpha demethylase) (LDM) (P450-14DM) (P45014DM)
112	NP_999597	47523914	cytochrome P450 51 [Sus scrofa]
113	BAC27231	26326975	unnamed protein product [Mus musculus]
114	Q5RE72	83287777	Cytochrome P450 51A1 (CYPLI) (P450LI) (Sterol 14-alpha demethylase) (Lanosterol 14-alpha demethylase) (LDM) (P450-14DM) (P45014DM)
115	Q4PJW3	75075066	Cytochrome P450 51A1 (CYPLI) (P450LI) (Sterol 14-alpha demethylase) (Lanosterol 14-alpha demethylase) (LDM) (P450-14DM) (P45014DM)
116	AAF74562	8347236	lanosterol 14-alpha-demethylase [Mus musculus]
117	AAC50951	1698484	lanosterol 14-alpha demethylase [Homo sapiens]
118	XP_532457	57095976	PREDICTED: similar to Cytochrome P450 51A1 (CYPLI) (P450 (Sterol 14-alpha demethylase) (Lanosterol 14-alpha demethylase) (LDM) (P450-14DM) (P45014DM) isoform 1 [Canis familiaris]
119	AAF73986	8215679	lanosterol 14-alpha-demethylase [Mus musculus]
120	AAH81210	51703589	MGC84806 protein [Xenopus laevis]
121	AAA87074	699396	lanosterol 14-alpha-demethylase

122	XP_418650	50732469	PREDICTED: similar to lanosterol 14-demethylase [Gallus gallu
123	BAE01508	67970330	unnamed protein product [Macaca fascicularis]
124	AAR89624	40748287	14-alpha demethylase [Fundulus heteroclitus]
125	NP_001...	50053648	cytochrome P450, family 51 [Strongylocentrotus purpuratus]
126	AAR89625	40748289	14-alpha demethylase [Danio rerio]
127	NP_001...	99028936	cytochrome P450, family 51 [Danio rerio]
128	CAJ81841	89268132	cytochrome P450, family 51, subfamily A, polypeptide 1 [Xenop tropicalis]
129	AAR89626	40748291	14-alpha demethylase [Abudefduf saxatilis]

Table 99. Examples of ERG4 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	AAD13895	4261595	Unknown [Saccharomyces cerevisiae]
2	AAT93224	51013861	YGL012W [Saccharomyces cerevisiae]
3	AAY42962	66270055	C24 sterol reductase [Candida glabrata]
4	XP_451223	50302575	unnamed protein product [Kluyveromyces lactis]
5	NP_986579	45201009	AGL087Cp [Eremothecium gossypii]
6	XP_456709	50407411	hypothetical protein DEHA0A08888g [Debaryomyces hansenii C
7	XP_717662	68476402	sterol C-24 (28) reductase [Candida albicans SC5314]
8	XP_503021	50551095	hypothetical protein [Yarrowia lipolytica]
9	EAU37607	114195907	Delta(24(24(1)))-sterol reductase [Aspergillus terreus NIH2624]
10	BAE61064	83770931	unnamed protein product [Aspergillus oryzae]
11	NP_594742	19115654	hypothetical protein SPAC20G4.07c [Schizosaccharomyces pomb]
12	CAA45113	5109	sts1+ [Schizosaccharomyces pombe]
13	XP_662788	67538028	hypothetical protein AN5184.2 [Aspergillus nidulans FGSC A4]
14	XP_750461	70991224	c-24(28) sterol reductase [Aspergillus fumigatus Af293]
15	EAS37114	90307483	hypothetical protein CIMG_02468 [Coccidioides immitis RS]
16	XP_365763	39968745	hypothetical protein MG02465.4 [Magnaporthe grisea 70-15]
17	CAC18223	16944336	probable sterol C-24 reductase [Neurospora crassa]
18	XP_961419	85102913	probable sterol C-24 reductase [MIPS] [Neurospora crassa OR74A
19	XP_660288	67524453	hypothetical protein AN2684.2 [Aspergillus nidulans FGSC A4]
20	EAU33849	114192149	Delta(24(24(1)))-sterol reductase [Aspergillus terreus NIH2624]
21	XP_753221	70996933	c-24(28) sterolreductase [Aspergillus fumigatus Af293]
22	BAE59624	83769489	unnamed protein product [Aspergillus oryzae]
23	EAT92432	111071312	predicted protein [Phaeosphaeria nodorum SN15]
24	XP_390179	46136975	hypothetical protein FG10003.1 [Gibberella zeae PH-1]
25	XP_757645	71005958	hypothetical protein UM01498.1 [Ustilago maydis 521]
26	EAS37449	90307818	hypothetical protein CIMG_02803 [Coccidioides immitis RS]
27	NP_820201	29654509	c-24(28) sterol reductase, putative [Coxiella burnetii RSA 493]
28	ZP_012...	94491050	hypothetical protein CburD_01001859 [Coxiella burnetii Dugway 12]
29	AAQ88130	37039513	sterol C-24 reductase [Cryptococcus neoformans var. grubii H99]
30	XP_569697	58265082	delta24(24-1) sterol reductase [Cryptococcus neoformans var. neoformans JEC21]
31	EAQ90721	88183253	hypothetical protein CHGG_02656 [Chaetomium globosum CBS
32	BAE55606	83765463	unnamed protein product [Aspergillus oryzae]
33	CAJ06078	68128884	sterol C-24 reductase, putative [Leishmania major]
34	ABD46555	88601114	sterol C-24 reductase-like protein [Acanthamoeba castellanii]
35	XP_638613	66809779	ERG4/ERG24 ergosterol biosynthesis protein family protein [Dictyostelium discoideum AX4]

Table 100. Examples of NADH kinase polypeptides.

1	XP_504085	50553348	hypothetical protein [Yarrowia lipolytica]
2	XP_001...	126275577	protein involved in oxidative stress [Pichia stipitis CBS 6054]

3	XP_460470	50423771	hypothetical protein DEHA0F02728g [Debaryomyces hansenii CI
4	XP_454815	50309607	unnamed protein product [Kluyveromyces lactis]
5	Q06892	8928263	NADH kinase POS5, mitochondrial precursor
6	XP_719778	68472434	hypothetical protein CaO19_14092 [Candida albicans SC5314]
7	XP_446489	50288121	unnamed protein product [Candida glabrata]
8	CAA59017	668983	POS5 [Saccharomyces cerevisiae]
9	NP_985485	45198456	AFL063Wp [Ashbya gossypii ATCC 10895]
10	XP_001...	119498579	poly(p)/ATP NAD kinase [Neosartorya fischeri NRRL 181]
11	XP_682106	67903700	hypothetical protein AN8837.2 [Aspergillus nidulans FGSC A4]
12	BAE55092	83764948	unnamed protein product [Aspergillus oryzae]
13	NP_594371	19115283	hypothetical protein SPAC323.01c [Schizosaccharomyces pombe
14	EAT76147	111055027	hypothetical protein SNOG_16449 [Phaeosphaeria nodorum SN1
15	XP_760686	71020911	hypothetical protein UM04539.1 [Ustilago maydis 521]
16	XP_001...	115438442	conserved hypothetical protein [Aspergillus terreus NIH2624]
17	XP_382248	46110381	hypothetical protein FG02072.1 [Gibberella zeae PH-1]
18	XP_001...	116198437	hypothetical protein CHGG_07374 [Chaetomium globosum CBS
19	XP_569737	58265162	NADH kinase [Cryptococcus neoformans var. neoformans JEC21
20	XP_754043	70998642	POS5 protein [Aspergillus fumigatus Af293]
21	XP_001...	119182395	hypothetical protein CIMG_06228 [Coccidioides immitis RS]
22	XP_001...	121712620	poly(p)/ATP NAD kinase [Aspergillus clavatus NRRL 1]
23	EAW56155	119576559	NAD kinase, isoform CRA_a [Homo sapiens]
24	BAB14412	10434887	unnamed protein product [Homo sapiens]
25	BAE89891	90080820	unnamed protein product [Macaca fascicularis]
26	XP_001...	108995650	PREDICTED: similar to NAD kinase [Macaca mulatta]
27	AAM01195	20070086	NAD kinase [Homo sapiens]
28	NP_001...	121583899	hypothetical protein LOC562771 [Danio rerio]
29	NP_001...	77735845	NAD kinase [Bos taurus]
30	BAE37946	74227869	unnamed protein product [Mus musculus]
31	CAM16741	123257290	NAD kinase [Mus musculus]
32	NP_619612	20149760	putative inorganic polyphosphate/ATP-NAD kinase [Mus musculu
33	BAE28227	74190892	unnamed protein product [Mus musculus]
34	BAE38227	74225047	unnamed protein product [Mus musculus]
35	XP_848833	73956564	PREDICTED: similar to Putative inorganic polyphosphate/ATP-N kinase (Poly(P)/ATP NAD kinase) isoform 2 [Canis familiaris]
36	EAW56152	119576556	NAD kinase, isoform CRA_b [Homo sapiens]
37	CAG02372	47204918	unnamed protein product [Tetraodon nigroviridis]
38	XP_857358	73956572	PREDICTED: similar to Putative inorganic polyphosphate/ATP-N kinase (Poly(P)/ATP NAD kinase) isoform 7 [Canis familiaris]
39	CAM16742	123257291	NAD kinase [Mus musculus]
40	XP_857444	73956576	PREDICTED: similar to Putative inorganic polyphosphate/ATP-N kinase (Poly(P)/ATP NAD kinase) isoform 8 [Canis familiaris]
41	XP_001...	115935814	PREDICTED: hypothetical protein isoform 2 [Strongylocentrotus purpuratus]
42	XP_645299	66823889	NAD+ kinase family protein [Dictyostelium discoideum AX4]
43	XP_789294	115901710	PREDICTED: hypothetical protein [Strongylocentrotus purpuratu
44	XP_001...	126306655	PREDICTED: hypothetical protein [Monodelphis domestica]
45	AAG44568	12005678	HT029 [Homo sapiens]
46	AAH90019	58477417	Unknown (protein for MGC:109551) [Rattus norvegicus]

47	XP_857322	73956570	PREDICTED: similar to Putative inorganic polyphosphate/ATP-N kinase (Poly(P)/ATP NAD kinase) isoform 6 [Canis familiaris]
48	EAW56154	119576558	NAD kinase, isoform CRA_c [Homo sapiens]
49	AAM13987	20259322	unknown protein [Arabidopsis thaliana]
50	Q56YN3	94717660	NAD(H) kinase 1 (AtNADK-1)
51	Q60E60	94717661	Putative NAD kinase 3
52	NP_001...	71894909	NAD kinase [Gallus gallus]
53	XP_001...	115935816	PREDICTED: hypothetical protein isoform 1 [Strongylocentrotus purpuratus]
54	XP_546709	73956574	PREDICTED: similar to NAD kinase isoform 1 [Canis familiaris]
55	XP_857484	73956578	PREDICTED: similar to Putative inorganic polyphosphate/ATP-N kinase (Poly(P)/ATP NAD kinase) isoform 9 [Canis familiaris]
56	XP_448828	50292791	unnamed protein product [Candida glabrata]
57	Q5JK52	75105828	Probable NAD kinase 1
58	NP_001...	115442329	Os01g0957000 [Oryza sativa (japonica cultivar-group)]
59	NP_188744	42565070	NADK1; NAD+ kinase [Arabidopsis thaliana]
60	XP_001...	125809035	GA17329-PA [Drosophila pseudoobscura]
61	NP_001...	52345700	MGC88972 protein [Xenopus tropicalis]
62	XP_001...	114550602	PREDICTED: hypothetical protein isoform 5 [Pan troglodytes]
63	AAH59316	37589440	MGC68997 protein [Xenopus laevis]
64	NP_001...	115484543	Os11g0191400 [Oryza sativa (japonica cultivar-group)]
65	AAI08527	80479266	MGC130956 protein [Xenopus laevis]
66	EAY80254	125533706	hypothetical protein OsI_034213 [Oryza sativa (indica cultivar-gr
67	EAZ17708	125576486	hypothetical protein OsJ_031917 [Oryza sativa (japonica cultivar-
68	NP_001...	62955137	hypothetical protein LOC550242 [Danio rerio]
69	XP_392018	66523738	PREDICTED: similar to CG33156-PB, isoform B isoform 1 [Apis mellifera]
70	EAU91476	116508581	hypothetical protein CC1G_01965 [Coprinopsis cinerea okayama
71	BAB01450	11994267	unnamed protein product [Arabidopsis thaliana]
72	NP_788348	28573826	CG33156-PC, isoform C [Drosophila melanogaster]
73	NP_788347	28573832	CG33156-PB, isoform B [Drosophila melanogaster]
74	NP_788345	28573828	CG33156-PA, isoform A [Drosophila melanogaster]
75	NP_788346	28573830	CG33156-PE, isoform E [Drosophila melanogaster]
76	XP_455838	50311625	unnamed protein product [Kluyveromyces lactis]
77	XP_857244	73956566	PREDICTED: similar to NAD kinase isoform 4 [Canis familiaris]
78	XP_309524	119113331	ENSANGP00000012587 [Anopheles gambiae str. PEST]
79	Q9C5W3	75169003	NAD kinase 2, chloroplast precursor (AtNADK-2)
80	AAN71432	25012675	RE54276p [Drosophila melanogaster]
81	AAD41416	5263314	Similar to gb|X84260 POS5 gene product from Saccharomyces cerevisiae. EST gb|W43879 comes from this gene. [Arabidopsis t
82	EAT48715	108884490	poly(p)/atp nad kinase [Aedes aegypti]
83	XP_447315	50289767	hypothetical protein CAGL0I01386g [Candida glabrata CBS138]
84	XP_974485	91089195	PREDICTED: similar to CG33156-PE, isoform E [Tribolium cast
85	NP_985908	45198879	AFR361Cp [Ashbya gossypii ATCC 10895]
86	XP_001...	125809033	GA19389-PA [Drosophila pseudoobscura]
87	XP_360075	39941076	hypothetical protein MG05450.4 [Magnaporthe grisea 70-15]
88	XP_629620	66801389	NAD+ kinase family protein [Dictyostelium discoideum AX4]
89	XP_001...	114550592	PREDICTED: NAD kinase isoform 2 [Pan troglodytes]

90	AAT27257	47271174	RH58004p [Drosophila melanogaster]
91	NP_610884	20129957	CG6145-PA, isoform A [Drosophila melanogaster]
92	NP_725315	24653424	CG6145-PB, isoform B [Drosophila melanogaster]
93	XP_365092	39965347	hypothetical protein MG09937.4 [Magnaporthe grisea 70-15]
94	XP_958193	85089965	hypothetical protein [Neurospora crassa OR74A]
95	XP_716634	68478731	hypothetical protein CaO19_7393 [Candida albicans SC5314]
96	BAE62986	83772858	unnamed protein product [Aspergillus oryzae]
97	XP_001...	126133264	NAD kinase associated with ferric reductase [Pichia stipitis CBS 6
98	XP_964420	85112830	hypothetical protein [Neurospora crassa OR74A]
99	XP_001...	119174633	hypothetical protein CIMG_09288 [Coccidioides immitis RS]
100	XP_504332	50553842	hypothetical protein [Yarrowia lipolytica]
101	CAK65780	124400294	unnamed protein product [Paramecium tetraurelia]
102	BAB83863	18181874	ATP-NAD kinase [Saccharomyces cerevisiae]
103	NP_010873	6320794	ATP-NADH kinase; phosophorylates both NAD and NADH; homooctameric structure consisting of 60-kDa subunits; sequence similarity to Utr1p and Pos5p; overexpression complements certai phenotypes [Saccharomyces cerevisiae]
104	XP_381266	46108416	hypothetical protein FG01090.1 [Gibberella zeae PH-1]
105	XP_001...	119478625	NAD+ kinase, putative [Neosartorya fischeri NRRL 181]
106	EAL91328	129558022	NAD+ kinase, putative [Aspergillus fumigatus Af293]
107	XP_362576	39946078	hypothetical protein MG08159.4 [Magnaporthe grisea 70-15]
108	XP_627101	66359846	NAD kinase involved in polyphosphate metabolism [Cryptosporid parvum Iowa II]
109	XP_667126	67611018	inorganic polyphosphate/ATP-NAD kinase [Cryptosporidium hom TU502]
110	AAT92918	51013249	YJR049C [Saccharomyces cerevisiae]
111	XP_001...	115387331	conserved hypothetical protein [Aspergillus terreus NIH2624]
112	CAK73291	124407916	unnamed protein product [Paramecium tetraurelia]
113	XP_001...	116182448	hypothetical protein CHGG_01852 [Chaetomium globosum CBS
114	NP_594181	19115093	hypothetical protein SPAC3H5.11 [Schizosaccharomyces pombe 9
115	BAE62131	83772001	unnamed protein product [Aspergillus oryzae]
116	XP_458264	50419475	hypothetical protein DEHA0C14476g [Debaryomyces hansenii CB
117	EAU91353	116508458	hypothetical protein CC1G_07388 [Coprinopsis cinerea okayama7
118	XP_001...	116206492	hypothetical protein CHGG_02539 [Chaetomium globosum CBS
119	XP_001...	115433294	hypothetical protein ATEG_08163 [Aspergillus terreus NIH2624]
120	XP_680935	67901358	hypothetical protein AN7666.2 [Aspergillus nidulans FGSC A4]
121	CAL52469	116061751	Mitochondrial oxoglutarate/malate carrier proteins (ISS) [Ostreocc tauri]
122	XP_001...	121713904	NAD+ kinase, putative [Aspergillus clavatus NRRL 1]
123	EAT82120	111061000	hypothetical protein SNOG_10726 [Phaeosphaeria nodorum SN15
124	XP_001...	121710930	NAD+ kinase Utr1, putative [Aspergillus clavatus NRRL 1]
125	XP_504486	50554155	hypothetical protein [Yarrowia lipolytica]
126	XP_001...	119497875	NAD+ kinase Utr1, putative [Neosartorya fischeri NRRL 181]
127	XP_573007	58271702	NAD+ kinase [Cryptococcus neoformans var. neoformans JEC21]
128	XP_749271	70988837	utr1 protein [Aspergillus fumigatus Af293]
129	XP_955053	85000669	hypothetical protein TA04160 [Theileria annulata strain Ankara]
130	XP_387326	46125545	hypothetical protein FG07150.1 [Gibberella zeae PH-1]
131	EAT82450	111061330	hypothetical protein SNOG_10115 [Phaeosphaeria nodorum SN15

132	XP_664428	67541308	hypothetical protein AN6824.2 [Aspergillus nidulans FGSC A4]
133	XP_763386	71027485	hypothetical protein TP03_0366 [Theileria parva strain Muguga]
134	CAL57506	116055110	Predicted sugar kinase (ISS) [Ostreococcus tauri]
135	CAG01748	47222781	unnamed protein product [Tetraodon nigroviridis]
136	XP_572857	58271402	hypothetical protein CNI02350 [Cryptococcus neoformans var. neoformans JEC21]
137	XP_753366	70997227	utr1 protein [Aspergillus fumigatus Af293]
138	CAK80963	124415904	unnamed protein product [Paramecium tetraurelia]
139	XP_573006	58271700	NAD+ kinase [Cryptococcus neoformans var. neoformans JEC21]
140	XP_961517	85103418	related to UTR1 (associated with ferric reductase activity) [MIPS] [Neurospora crassa OR74A]
141	XP_001...	118350090	ATP-NAD kinase family protein [Tetrahymena thermophila SB21
142	XP_779743	71081331	hypothetical protein GLP_574_156802_155141 [Giardia lamblia A 50803]
143	AAT11257	47118291	NAD kinase [Holosticha sp. WJC-2003]
144	EAY77288	125529174	hypothetical protein OsI_005135 [Oryza sativa (indica cultivar-gr
145	NP_594232	19115144	hypothetical protein SPAC1B1.02c [Schizosaccharomyces pombe
146	ZP_014...	115380348	probable inorganic polyphosphate/ATP-NAD kinase (Poly(P)/AT kinase) [Stigmatella aurantiaca DW4/3-1]
147	YP_590123	94968075	NAD(+) kinase [Acidobacteria bacterium Ellin345]
148	YP_857489	117621127	probable inorganic polyphosphate/ATP-NAD kinase (Poly(P)/AT kinase) [Aeromonas hydrophila subsp. hydrophila ATCC 7966]
149	YP_633513	108758383	putative inorganic polyphosphate/ATP-NAD kinase [Myxococcus xanthus DK 1622]
150	YP_904229	118603014	NAD(+) kinase [Candidatus Ruthia magnifica str. Cm (Calyptoge magnifica)]
151	XP_001...	119191586	hypothetical protein CIMG_00170 [Coccidioides immitis RS]
152	XP_001...	123475987	ATP-NAD kinase family protein [Trichomonas vaginalis G3]
153	ZP_005...	68549325	NAD(+) kinase [Pelodictyon phaeoclathratiforme BU-1]
154	XP_001...	118363284	ATP-NAD kinase family protein [Tetrahymena thermophila SB21
155	ZP_006...	71481352	NAD(+) kinase [Prosthecochloris vibrioformis DSM 265]
156	ZP_011...	89211745	ATP-NAD/AcoX kinase [Halothermothrix orenii H 168]
157	ZP_013...	110599874	NAD(+) kinase [Geobacter sp. FRC-32]
158	EAZ14886	125573371	hypothetical protein OsJ_004711 [Oryza sativa (japonica cultivar-
159	Q3AAN2	91207626	Probable inorganic polyphosphate/ATP-NAD kinase (Poly(P)/AT kinase)
160	Q6AL12	81641669	Probable inorganic polyphosphate/ATP-NAD kinase (Poly(P)/AT kinase)
161	YP_928312	119775572	NAD(+) kinase [Shewanella amazonensis SB2B]
162	Q97HD7	24418627	Probable inorganic polyphosphate/ATP-NAD kinase (Poly(P)/AT kinase)
163	NP_588005	19075505	hypothetical protein SPCC24B10.02c [Schizosaccharomyces pom 972h-]
164	Q39X41	91207546	Probable inorganic polyphosphate/ATP-NAD kinase (Poly(P)/AT kinase)
165	ZP_016...	121528143	NAD(+) kinase [Ralstonia pickettii 12J]
166	YP_563575	91793924	NAD(+) kinase [Shewanella denitrificans OS217]
167	ZP_014...	114844756	NAD(+) kinase [Thermoanaerobacter ethanolicus X514]
168	ZP_014...	114777948	hypothetical protein SPV1_05984 [Mariprofundus ferrooxydans P
169	AAH24219	46255669	FLJ13052 protein [Homo sapiens]

170	Q4KBJ2	91207437	Probable inorganic polyphosphate/ATP-NAD kinase (Poly(P)/ATI kinase)
171	Q4ZVT9	75502720	Probable inorganic polyphosphate/ATP-NAD kinase (Poly(P)/ATI kinase)
172	ZP_015...	118073231	ATP-NAD/AcoX kinase [Shewanella woodyi ATCC 51908]
173	YP_934084	119898871	probable inorganic polyphosphate/ATP-NAD kinase [Azoarcus sp BH72]
174	ZP_016...	119858632	NAD(+) kinase [Pseudomonas putida W619]
175	EAY56755	124515245	putative sugar kinase [Leptospirillum sp. Group II UBA]
176	NP_276009	15678892	hypothetical protein MTH872 [Methanothermobacter thermautotrc str. Delta H]
177	Q8XW25	24418615	Probable inorganic polyphosphate/ATP-NAD kinase (Poly(P)/ATI kinase)
178	AAN87422	27262282	inorganic polyphosphate/ATP-NAD kinase [Heliobacillus mobilis
179	Q3KE68	91207439	Probable inorganic polyphosphate/ATP-NAD kinase (Poly(P)/ATI kinase)
180	YP_912985	119358341	NAD(+) kinase [Chlorobium phaeobacteroides DSM 266]
181	YP_822395	116620239	NAD(+) kinase [Solibacter usitatus Ellin6076]
182	Q48FT7	91207436	Probable inorganic polyphosphate/ATP-NAD kinase (Poly(P)/ATI kinase)
183	YP_878058	118442965	ATP-NAD kinase, putative [Clostridium novyi NT]
184	NP_717140	28275219	hypothetical protein SO1523 [Shewanella oneidensis MR-1]
185	Q87YK2	34222831	Probable inorganic polyphosphate/ATP-NAD kinase (Poly(P)/ATI kinase)
186	Q8EGS1	34222877	Probable inorganic polyphosphate/ATP-NAD kinase (Poly(P)/ATI kinase)
187	YP_544883	91775127	NAD(+) kinase [Methylobacillus flagellatus KT]
188	ZP_005...	67918021	NAD(+) kinase [Chlorobium limicola DSM 245]
189	YP_901252	118580002	NAD(+) kinase [Pelobacter propionicus DSM 2379]
190	ZP_010...	85712933	NAD kinase [Idiomarina baltica OS145]
191	YP_463943	86157158	NAD(+) kinase [Anaeromyxobacter dehalogenans 2CP-C]
192	ZP_011...	88812327	inorganic polyphosphate/ATP-NAD kinase [Nitrococcus mobilis N
193	ZP_012...	89889540	inorganic polyphosphate/ATP-NAD kinase ppnK [Flavobacteria bacterium BBFL7]
194	ZP_012...	94268824	NAD(+) kinase [delta proteobacterium MLMS-1]
195	YP_607363	104780865	inorganic polyphosphate/ATP-NAD kinase NadK [Pseudomonas entomophila L48]
196	ZP_011...	88935008	ATP-NAD kinase [Geobacter uraniumreducens Rf4]
197	ZP_016...	121534493	NAD(+) kinase [Thermosinus carboxydivorans Nor1]
198	NP_247912	15669107	hypothetical protein MJ0917 [Methanocaldococcus jannaschii DSI 2661]
199	Q8RAC3	24418608	Probable inorganic polyphosphate/ATP-NAD kinase (Poly(P)/ATI kinase)
200	CAJ41952	89267097	ferric reductase [Ustilago hordei]
201	XP_756696	71004060	hypothetical protein UM00549.1 [Ustilago maydis 521]
202	XP_857285	73956568	PREDICTED: similar to NAD kinase isoform 5 [Canis familiaris]
203	AAV31342	54287598	unknown protein [Oryza sativa (japonica cultivar-group)]
204	EAY97893	125552184	hypothetical protein OsI_019126 [Oryza sativa (indica cultivar-grc
205	XP_001...	123471858	ATP-NAD kinase family protein [Trichomonas vaginalis G3]
206	EAZ34164	125594105	hypothetical protein OsJ_017647 [Oryza sativa (japonica cultivar-

207	BAE99495	110743209	hypothetical protein [Arabidopsis thaliana]
208	AAD30577	4836874	Hypothetical protein [Arabidopsis thaliana]
209	NP_001...	115478687	Os09g0345700 [Oryza sativa (japonica cultivar-group)]
210	EAZ08716	125563336	hypothetical protein OsI_029948 [Oryza sativa (indica cultivar-gr
211	EAZ44365	125605329	hypothetical protein OsJ_027848 [Oryza sativa (japonica cultivar-
212	NP_500084	71999610	Y77E11A.2 [Caenorhabditis elegans]
213	CAE68251	39585962	Hypothetical protein CBG13928 [Caenorhabditis briggsae]
214	ZP_009...	82749344	NAD+ kinase [Clostridium beijerincki NCIMB 8052]

Table 101. Examples of DGA1 polypeptides.

Row	accession	GI	Description
1	NP_014888	6324819	Dga1p [Saccharomyces cerevisiae].
2	CAG80304	49650569	unnamed protein product [Yarrowia lipolytica CLIB122]
3	AAD45832	5630087	similar to predicted proteins AAB54240 (PID:g2088822) and S67 (PID:g2132925) [Homo sapiens]
4	AAH45058	27924233	Dgat2l1-a protein [Xenopus laevis]
5	AAI00954	71680845	Monoacylglycerol O-acyltransferase 3 [Homo sapiens]
6	AAT78344	50541689	DGAT2 [Bos taurus]
7	AAV35727	54632790	diacylglycerol O-acyltransferase-like protein 2 isoform 1 [Homo s
8	BAC28882	26330304	unnamed protein product [Mus musculus]
9	BAC87534	34536086	unnamed protein product [Homo sapiens]
10	BAE60242	83770107	unnamed protein product [Aspergillus oryzae]
11	CAD38961	21739871	hypothetical protein [Homo sapiens]
12	CAD89266	50058781	TPA: diacylglycerol O-acyltransferase 2 like 3 [Homo sapiens]
13	CAD89267	50058783	TPA: diacylglycerol O-acyltransferase 2 like 4 [Homo sapiens]
14	CAE61732	39585410	Hypothetical protein CBG05683 [Caenorhabditis briggsae]
15	CAE71891	39594313	Hypothetical protein CBG18949 [Caenorhabditis briggsae]
16	CAE72154	39594576	Hypothetical protein CBG19252 [Caenorhabditis briggsae]
17	CAE74669	39580537	Hypothetical protein CBG22470 [Caenorhabditis briggsae]
18	CAE74670	39580538	Hypothetical protein CBG22471 [Caenorhabditis briggsae]
19	CAG02909	47222544	unnamed protein product [Tetraodon nigroviridis]
20	CAH18230	51476480	hypothetical protein [Homo sapiens]
21	CAI41493	123227401	diacylglycerol O-acyltransferase 2-like 3 [Homo sapiens]
22	CAJ05359	68126987	hypothetical protein, conserved [Leishmania major]
23	CAJ81957	89273941	diacylglycerol O-acyltransferase homolog 2 [Xenopus tropicalis]
24	CAL56438	116061050	Acyl-CoA:diacylglycerol acyltransferase (DGAT) (ISS) [Ostreoco tauri]
25	CAM19580	123123023	diacylglycerol O-acyltransferase 2-like 4 [Mus musculus]
26	CAM19588	123123031	diacylglycerol O-acyltransferase 2-like 6 (Dgat2l6) [Mus musculu
27	EAL20089	50257380	hypothetical protein CNBF4150 [Cryptococcus neoformans var. neoformans B-3501A]
28	EAT39311	108875086	diacylglycerol o-acyltransferase [Aedes aegypti]
29	EAT89076	111067956	hypothetical protein SNOG_03871 [Phaeosphaeria nodorum SN15
30	EAU90640	116507745	hypothetical protein CC1G_09880 [Coprinopsis cinerea okayama7
31	EAW50203	119570588	monoacylglycerol O-acyltransferase 3, isoform CRA_a [Homo sap
32	EAW70805	119591211	monoacylglycerol O-acyltransferase 1, isoform CRA_a [Homo sap
33	EAW70806	119591212	monoacylglycerol O-acyltransferase 1, isoform CRA_b [Homo sap
34	EAW74983	119595389	monoacylglycerol O-acyltransferase 2, isoform CRA_b [Homo sap
35	EAW74984	119595390	diacylglycerol O-acyltransferase homolog 2 (mouse), isoform CRA [Homo sapiens]
36	EAW74985	119595391	diacylglycerol O-acyltransferase homolog 2 (mouse), isoform CRA [Homo sapiens]
37	EAX05353	119625758	diacylglycerol O-acyltransferase 2-like 3 [Homo sapiens]
38	NP_001...	54400668	hypothetical protein LOC450063 [Danio rerio]
39	NP_001...	124487273	diacylglycerol O-acyltransferase 2-like 3 [Mus musculus]
40	NP_001...	126158911	hypothetical protein LOC494083 [Danio rerio]

41	NP_080989	18426805	monoacylglycerol O-acyltransferase 1 [Mus musculus]
42	NP_497659	17556144	Y53G8B.2 [Caenorhabditis elegans]
43	NP_504649	17564946	W01A11.2 [Caenorhabditis elegans]
44	NP_505413	17562274	K07B1.4a [Caenorhabditis elegans]
45	NP_507469	17561696	F59A1.10 [Caenorhabditis elegans]
46	NP_587741	63054410	diacylglycerol acyltransferase [Schizosaccharomyces pombe 972h
47	NP_872180	32566955	K07B1.4b [Caenorhabditis elegans]
48	Q08650	74583743	Diacylglycerol O-acyltransferase 1
49	Q28C88	114150035	2-acylglycerol O-acyltransferase 1 (Monoacylglycerol O-acyltrans 1) (Acyl CoA:monoacylglycerol acyltransferase 1) (MGAT1)
50	Q2KHS5	114150033	2-acylglycerol O-acyltransferase 2-A (Monoacylglycerol O-acyltransferase 2-A) (Acyl CoA:monoacylglycerol acyltransferase (MGAT2-A)
51	Q3KPP4	114150034	2-acylglycerol O-acyltransferase 1 (Monoacylglycerol O-acyltrans 1) (Acyl CoA:monoacylglycerol acyltransferase 1) (MGAT1)
52	Q4V9F0	82226123	Diacylglycerol O-acyltransferase 2 (Diglyceride acyltransferase 2)
53	Q5FVP8	81882840	Diacylglycerol O-acyltransferase 2 (Diglyceride acyltransferase 2)
54	Q5M7F4	82179359	2-acylglycerol O-acyltransferase 2-B (Monoacylglycerol O-acyltransferase 2-B) (Acyl CoA:monoacylglycerol acyltransferase (MGAT2-B)
55	Q5M8H5	82179452	2-acylglycerol O-acyltransferase 2 (Monoacylglycerol O-acyltrans 2) (Acyl CoA:monoacylglycerol acyltransferase 2) (MGAT2)
56	Q6E213	74748433	Acyl-CoA wax alcohol acyltransferase 2 (Long-chain-alcohol O-fa acyltransferase 2) (Wax synthase) (hWS) (Multifunctional O-acyltransferase) (Diacylglycerol O-acyltransferase 2-like protein 4 (Diacylglycerol O-acyltransferase candidate 4) (hDC4)
57	Q6PAZ3	82186830	Diacylglycerol O-acyltransferase 2 (Diglyceride acyltransferase 2)
58	Q6ZPD8	74749597	Diacylglycerol O-acyltransferase 2-like protein 6 (Diacylglycerol (acyltransferase candidate 3) (hDC3)
59	Q70VZ7	75045033	2-acylglycerol O-acyltransferase 1 (Monoacylglycerol O-acyltrans 1) (Acyl CoA:monoacylglycerol acyltransferase 1) (MGAT1)
60	Q70VZ8	75045034	Diacylglycerol O-acyltransferase 2 (Diglyceride acyltransferase 2)
61	Q75BY0	74694873	Diacylglycerol O-acyltransferase 1
62	Q80W94	81873317	2-acylglycerol O-acyltransferase 2 (Monoacylglycerol O-acyltrans 2) (Acyl CoA:monoacylglycerol acyltransferase 2) (MGAT2) (Diacylglycerol acyltransferase 2-like protein 5) (Monoacylglycer acyltransferase 1-like)
63	Q86VF5	74727570	2-acylglycerol O-acyltransferase 3 (Monoacylglycerol O-acyltrans 3) (Acyl CoA:monoacylglycerol acyltransferase 3) (MGAT3) (Diacylglycerol acyltransferase 2-like protein 7) (Diacylglycerol O acyltransferase candidate 7) (hDC7)
64	Q91ZV4	81867518	2-acylglycerol O-acyltransferase 1 (Monoacylglycerol O-acyltrans 1) (Acyl CoA:monoacylglycerol acyltransferase 1) (MGAT1) (Diacylglycerol acyltransferase 2-like protein 1)
65	Q96PD6	74717087	2-acylglycerol O-acyltransferase 1 (Monoacylglycerol O-acyltrans 1) (Acyl CoA:monoacylglycerol acyltransferase 1) (MGAT1) (Diacylglycerol acyltransferase 2-like protein 1) (Diacylglycerol C acyltransferase candidate 2) (hDC2)
66	Q96UY1	74623358	Diacylglycerol O-acyltransferase 2B (Diglyceride acyltransferase (MrDGAT2B)
67	Q96UY2	74623359	Diacylglycerol O-acyltransferase 2A (Diglyceride acyltransferase (MrDGAT2A)

68	Q9DCV3	81881828	Diacylglycerol O-acyltransferase 2 (Diglyceride acyltransferase 2
69	T40889	7522384	hypothetical protein SPCC1235.15 - fission yeast (Schizosacchar pombe) (fragment)
70	XP_001...	115388912	hypothetical protein ATEG_02783 [Aspergillus terreus NIH2624]
71	XP_001...	121711189	diacylglycerol o-acyltransferase [Aspergillus clavatus NRRL 1]
72	XP_001...	119176886	hypothetical protein CIMG_07462 [Coccidioides immitis RS]
73	XP_001...	119482526	diacylglycerol o-acyltransferase [Neosartorya fischeri NRRL 181]
74	XP_001...	109107978	PREDICTED: similar to monoacylglycerol O-acyltransferase 2 [M mulatta]
75	XP_001...	109462481	PREDICTED: similar to monoacylglycerol O-acyltransferase 2 [R norvegicus]
76	XP_001...	109101225	PREDICTED: similar to monoacylglycerol O-acyltransferase 1 isc [Macaca mulatta]
77	XP_001...	109101227	PREDICTED: similar to monoacylglycerol O-acyltransferase 1 isc [Macaca mulatta]
78	XP_001...	126338188	PREDICTED: similar to putative monoacylglycerol acyltransferas [Monodelphis domestica]
79	XP_001...	126132896	predicted protein [Pichia stipitis CBS 6054]
80	XP_001...	126327847	PREDICTED: similar to Monoacylglycerol O-acyltransferase 2 [Monodelphis domestica]
81	XP_001...	114583596	PREDICTED: monoacylglycerol O-acyltransferase 1 isoform 1 [P troglodytes]
82	XP_001...	126327845	PREDICTED: similar to Diacylglycerol O-acyltransferase homolc (mouse) [Monodelphis domestica]
83	XP_001...	109487371	PREDICTED: similar to monoacylglycerol O-acyltransferase 1 [R norvegicus]
84	XP_001...	115966304	PREDICTED: similar to putative monoacylglycerol acyltransferas [Strongylocentrotus purpuratus]
85	XP_001...	126343739	PREDICTED: similar to Monoacylglycerol O-acyltransferase 2 [Monodelphis domestica]
86	XP_001...	126342779	PREDICTED: similar to acyl-CoA wax alcohol acyltransferase [Monodelphis domestica]
87	XP_001...	119925522	PREDICTED: similar to Monoacylglycerol O-acyltransferase 2 [B taurus]
88	XP_001...	115736779	PREDICTED: hypothetical protein [Strongylocentrotus purpuratus
89	XP_001...	109512062	PREDICTED: similar to diacylglycerol O-acyltransferase 2-like 3 norvegicus]
90	XP_001...	109131103	PREDICTED: similar to diacylglycerol O-acyltransferase 2-like 3 [Macaca mulatta]
91	XP_001...	126309301	PREDICTED: similar to acyl coenzyme A:monoacylglycerol acyltransferase 3 [Monodelphis domestica]
92	XP_001...	109497161	PREDICTED: similar to monoacylglycerol O-acyltransferase 2 [R norvegicus]
93	XP_001...	94407684	PREDICTED: similar to diacylglycerol O-acyltransferase 2 like 6 musculus]
94	XP_001...	109131095	PREDICTED: similar to diacylglycerol O-acyltransferase 2-like 4 [Macaca mulatta]
95	XP_001...	109066177	PREDICTED: similar to monoacylglycerol O-acyltransferase 3 isc [Macaca mulatta]
96	XP_001...	126342781	PREDICTED: hypothetical protein [Monodelphis domestica]
97	XP_001...	109131101	PREDICTED: similar to diacylglycerol O-acyltransferase 2 like 6 [Macaca mulatta]

98	XP_001...	119499744	diacylglycerol o-acyltransferase [Neosartorya fischeri NRRL 181]
99	XP_001...	109512053	PREDICTED: similar to wax synthase [Rattus norvegicus]
100	XP_228583	109510891	PREDICTED: similar to wax synthase [Rattus norvegicus]
101	XP_315985	118787295	ENSANGP00000024789 [Anopheles gambiae str. PEST]
102	XP_368741	39974701	hypothetical protein MG00503.4 [Magnaporthe grisea 70-15]
103	XP_381525	46108934	hypothetical protein FG01349.1 [Gibberella zeae PH-1]
104	XP_393396	66531974	PREDICTED: similar to monoacylglycerol O-acyltransferase 2 [A mellifera]
105	XP_424082	118085333	PREDICTED: similar to acyl CoA:monoacylglycerol acyltransfer [Gallus gallus]
106	XP_426251	118089278	PREDICTED: hypothetical protein [Gallus gallus]
107	XP_447864	50290863	unnamed protein product [Candida glabrata]
108	XP_455588	50311129	unnamed protein product [Kluyveromyces lactis]
109	XP_458203	50419357	hypothetical protein DEHA0C13101g [Debaryomyces hansenii CI
110	XP_504700	50554583	hypothetical protein [Yarrowia lipolytica]
111	XP_521105	114688993	PREDICTED: diacylglycerol O-acyltransferase 2-like 3 [Pan trogl
112	XP_522112	114639442	PREDICTED: monoacylglycerol O-acyltransferase 2 [Pan troglod
113	XP_522113	114639409	PREDICTED: hypothetical protein [Pan troglodytes]
114	XP_526044	114583594	PREDICTED: monoacylglycerol O-acyltransferase 1 isoform 2 [P troglodytes]
115	XP_527842	114615126	PREDICTED: monoacylglycerol O-acyltransferase 3 isoform 3 [P troglodytes]
116	XP_529027	55663351	PREDICTED: diacylglycerol O-acyltransferase 2-like 4 [Pan trogl
117	XP_542303	73988133	PREDICTED: similar to diacylglycerol O-acyltransferase 2 [Canis familiaris]
118	XP_542304	57102524	PREDICTED: similar to monoacylglycerol O-acyltransferase 2 [C familiaris]
119	XP_545667	74005805	PREDICTED: similar to monoacylglycerol O-acyltransferase 1 [C familiaris]
120	XP_549056	74007688	PREDICTED: similar to diacylglycerol O-acyltransferase 2-like 4 familiaris]
121	XP_549058	74007694	PREDICTED: similar to diacylglycerol O-acyltransferase 2-like 3 familiaris]
122	XP_571234	58268156	diacylglycerol O-acyltransferase [Cryptococcus neoformans var. neoformans JEC21]
123	XP_571236	58268160	diacylglycerol O-acyltransferase [Cryptococcus neoformans var. neoformans JEC21]
124	XP_586669	76679861	PREDICTED: similar to Monoacylglycerol O-acyltransferase 2 [E taurus]
125	XP_608355	119920187	PREDICTED: similar to diacylglycerol O-acyltransferase 2 like 3 taurus]
126	XP_635762	66803881	monoacylglycerol O-acyltransferase [Dictyostelium discoideum A
127	XP_681556	67902600	hypothetical protein AN8287.2 [Aspergillus nidulans FGSC A4]
128	XP_749138	70987450	diacylglycerol acyltransferase type 2A [Aspergillus fumigatus Af2
129	XP_751417	70993138	Diacylglycerol acyltransferase family [Aspergillus fumigatus Af2
130	XP_760084	71019707	hypothetical protein UM03937.1 [Ustilago maydis 521]
131	XP_819169	71664376	diacylglycerol acyltransferase [Trypanosoma cruzi strain CL Bren
132	XP_843764	72386679	diacylglycerol acyltransferase, putative [Trypanosoma brucei]
133	XP_849355	74007692	PREDICTED: similar to diacylglycerol O-acyltransferase 2 like 6 familiaris]

134	XP_850305	73957815	PREDICTED: similar to monoacylglycerol O-acyltransferase 3 [C familiaris]
135	XP_871120	76617458	PREDICTED: similar to acyl CoA:monoacylglycerol acyltransfer [Bos taurus]
136	XP_875499	76654062	PREDICTED: similar to acyl coenzyme A:monoacylglycerol acyltransferase 3 [Bos taurus]
137	XP_965438	85118420	hypothetical protein [Neurospora crassa OR74A]
138	XP_979373	94365281	PREDICTED: similar to monoacylglycerol O-acyltransferase 1 [M musculus]
139	XP_987874	94409141	PREDICTED: similar to diacylglycerol O-acyltransferase 2 like 6 musculus]

Equivalents

[00353] Those skilled in the art will recognize, or be able to understand that the foregoing description and examples are illustrative of practicing the provided invention. Those skilled in the art will be able to ascertain using no more than routine experimentation, many variations of the detail presented herein may be made to the specific embodiments of the invention described herein without departing from the spirit and scope of the present invention.

What is claimed is:

1. A recombinant fungus characterized by:

a. the recombinant fungus is oleaginous in that it can accumulate lipid to at least about 20% of its dry cell weight; and

b. the recombinant fungus produces at least one quinone derived compound, and can accumulate the produced quinone derived compound to at least about 1% of its dry cell weight;

wherein the recombinant fungus comprises at least one modification as compared with a parental fungus, which parental fungus both is not oleaginous and does not accumulate the quinone derived compound to at least about 1% of its dry cell weight, the at least one modification being selected from the group consisting of quinonogenic modifications, oleaginic modifications, and combinations thereof, and

wherein the at least one modification alters oleaginicity of the recombinant fungus, confers to the recombinant fungus oleaginy, confers to the recombinant fungus the ability to produce the at least one quinone derived compound to a level at least about 1% of its dry cell weight, or confers to the recombinant fungus the ability to produce at least one quinone derived compound which the parental fungus does not produce.

2. A recombinant fungus characterized by:

a. the recombinant fungus is oleaginous in that it can accumulate lipid to at least about 20% of its dry cell weight; and

b. the recombinant fungus produces at least one quinone derived compound selected from the group consisting of: a ubiquinone, a vitamin K compound, and a vitamin E compound, and combinations thereof, and can accumulate the produced quinone derived compound to at least about 1% of its dry cell weight;

wherein the recombinant fungus comprises at least one modification as compared with a parental fungus, the at least one modification being selected from the group consisting of quinonogenic modifications, oleaginic modifications, and combinations thereof, and

wherein the at least one modification alters oleaginicity of the recombinant fungus, confers to the recombinant fungus oleaginy, confers to the recombinant fungus the ability to produce the at least one quinone derived compound to a level at least about 1% of its dry cell weight, or confers to the recombinant fungus the ability to produce at least one quinone derived compound which the parental fungus does not naturally produce.

3. A recombinant fungus characterized by:

a. the recombinant fungus is oleaginous in that it can accumulate lipid to at least about 20% of its dry cell weight; and

b. the recombinant fungus produces at least one quinone derived compound, and can accumulate the produced quinone derived compound to at least about 1% of its dry cell weight;

wherein the recombinant fungus is a member of a genus selected from the group consisting of: *Aspergillus*, *Blakeslea*, *Botrytis*, *Candida*, *Cercospora*, *Cryptococcus*, *Cunninghamella*, *Fusarium* (*Gibberella*), *Kluyveromyces*, *Lipomyces*, *Mortierella*, *Mucor*, *Neurospora*, *Penicillium*, *Phycomyces*, *Pichia* (*Hansenula*), *Puccinia*, *Pythium*, *Rhodosporidium*, *Rhodotorula*, *Saccharomyces*, *Sclerotium*, *Trichoderma*, *Trichosporon*, *Xanthophyllomyces* (*Phaffia*), and *Yarrowia*;

or is a species selected from the group consisting of: *Aspergillus terreus*, *Aspergillus nidulans*, *Aspergillus niger*, *Blakeslea trispora*, *Botrytis cinerea*, *Candida japonica*, *Candida pulcherrima*, *Candida revkaufi*, *Candida tropicalis*, *Candida utilis*, *Cercospora nicotianae*, *Cryptococcus curvatus*, *Cunninghamella echinulata*, *Cunninghamella elegans*, *Fusarium fujikuroi* (*Gibberella zeae*), *Kluyveromyces lactis*, *Lipomyces starkeyi*, *Lipomyces lipoferus*, *Mortierella alpina*, *Mortierella ramanniana*, *Mortierella isabellina*, *Mortierella vinacea*, *Mucor circinelloides*, *Neurospora crassa*, *Phycomyces blakesleanus*, *Pichia pastoris*, *Puccinia distincta*, *Pythium irregulare*, *Rhodosporidium toruloides*, *Rhodotorula glutinis*, *Rhodotorula graminis*, *Rhodotorula mucilaginosa*, *Rhodotorula pinicola*, *Rhodotorula gracilis*, *Saccharomyces cerevisiae*, *Sclerotium rolfsii*, *Trichoderma reesei*, *Trichosporon cutaneum*, *Trichosporon pullans*, *Xanthophyllomyces dendrorhous* (*Phaffia rhodozyma*), and *Yarrowia lipolytica*;

wherein the recombinant fungus comprises at least one modification as compared with a parental fungus, the at least one modification being selected from the group consisting of quinonogenic modifications, oleaginic modifications, and combinations thereof, and

wherein the at least one modification alters oleaginicity of the recombinant fungus, confers to the recombinant fungus oleaginy, confers to the recombinant fungus the ability to produce the at least one quinone derived compound to a level at least about 1% of its dry cell weight, or confers to the recombinant fungus the ability to produce at least one quinone derived compound which the parental fungus does not naturally produce.

4. A recombinant fungus characterized by:

a. the recombinant fungus is oleaginous in that it can accumulate lipid to at least about 20% of its dry cell weight; and

b. the recombinant fungus produces at least one quinone derived compound selected from the group consisting of: a ubiquinone, a vitamin K compound, and a vitamin E compound, and combinations thereof, and can accumulate the produced quinone derived compound to at least about 1% of its dry cell weight;

wherein the recombinant fungus is a member of a genus selected from the group consisting of : *Aspergillus*, *Blakeslea*, *Botrytis*, *Candida*, *Cercospora*, *Cryptococcus*, *Cunninghamella*,

Fusarium (*Gibberella*), *Kluyveromyces*, *Lipomyces*, *Mortierella*, *Mucor*, *Neurospora*, *Penicillium*, *Phycomyces*, *Pichia* (*Hansenula*), *Puccinia*, *Pythium*, *Rhodosporidium*, *Rhodotorula*, *Saccharomyces*, *Sclerotium*, *Trichoderma*, *Trichosporon*, *Xanthophyllomyces* (*Phaffia*), and *Yarrowia*;

or is of a species selected from the group consisting of: *Aspergillus terreus*, *Aspergillus nidulans*, *Aspergillus niger*, *Blakeslea trispora*, *Botrytis cinerea*, *Candida japonica*, *Candida pulcherrima*, *Candida revkaufi*, *Candida tropicalis*, *Candida utilis*, *Cercospora nicotianae*, *Cryptococcus curvatus*, *Cunninghamella echinulata*, *Cunninghamella elegans*, *Fusarium fujikuroi* (*Gibberella zeae*), *Kluyveromyces lactis*, *Lipomyces starkeyi*, *Lipomyces lipoferus*, *Mortierella alpina*, *Mortierella ramanniana*, *Mortierella isabellina*, *Mortierella vinacea*, *Mucor circinelloides*, *Neurospora crassa*, *Phycomyces blakesleanus*, *Pichia pastoris*, *Puccinia distincta*, *Pythium irregulare*, *Rhodosporidium toruloides*, *Rhodotorula glutinis*, *Rhodotorula graminis*, *Rhodotorula mucilaginosa*, *Rhodotorula pinicola*, *Rhodotorula gracilis*, *Saccharomyces cerevisiae*, *Sclerotium rolfsii*, *Trichoderma reesei*, *Trichosporon cutaneum*, *Trichosporon pullans*, *Xanthophyllomyces dendrorhous* (*Phaffia rhodozyma*), and *Yarrowia lipolytica*;

wherein the recombinant fungus comprises at least one modification as compared with a parental fungus, the at least one modification being selected from the group consisting of quinonogenic modifications, oleaginic modifications, and combinations thereof, and

wherein the at least one modification alters oleaginicity of the recombinant fungus, confers to the recombinant fungus oleaginy, confers to the recombinant fungus the ability to produce the at least one quinone derived compound to a level at least about 1% of its dry cell weight, or confers to the recombinant fungus the ability to produce at least one quinone derived compound which the parental fungus does not naturally produce.

5. The recombinant fungus of any of claims 1-4 wherein the recombinant fungus is a member of a genus selected from the group consisting of: *Saccharomyces, Xanthophyllomyces (Phaffia),* and *Yarrowia*

6. The recombinant fungus of claim 5 wherein the recombinant fungus is a member of the genus *Saccharomyces*.

7. The recombinant fungus of claim 5 wherein the recombinant fungus is a member of the genus *Xanthophyllomyces (Phaffia)*.

8. The recombinant fungus of claim 5 wherein the recombinant fungus is a member of the genus *Yarrowia*.

9. The recombinant fungus of any of claims 1-4 wherein the recombinant fungus is a species selected from the group consisting of: *Candida utilis, Saccharomyces cerevisiae, Xanthophyllomyces dendrorhous (Phaffia rhodozyma),* and *Yarrowia lipolytica.*

10. The recombinant fungus of claim 9 wherein the recombinant fungus is of the species *Candida utilis.*

11. The recombinant fungus of claim 9 wherein the recombinant fungus is of the species *Saccharomyces cerevisiae.*

12. The recombinant fungus of claim 9 wherein the recombinant fungus is of the species *Xanthophyllomyces dendrorhous (Phaffia rhodozyma).*

13. The recombinant fungus of claim 9 wherein the recombinant fungus is of the species *Yarrowia lipolytica.*

14. The recombinant fungus of any of claims 1-4 wherein the recombinant fungus is a member of a genus selected from the group consisting of : *Aspergillus, Blakeslea, Candida, Cunninghamella, Kluyveromyces, Lipomyces, Mortierella, Pichia (Hansenula), Rhodosporidium, Rhodotorula, Trichoderma,* and *Trichosporon.*

15. The recombinant fungus of any of claims 1-4 wherein the recombinant fungus is a species selected from the group consisting of: *Aspergillus terreus, Aspergillus nidulans, Aspergillus niger, Blakeslea trispora, Candida japonica, Candida pulcherrima, Candida revkaufi, Candida tropicalis, Cunninghamella echinulata, Cunninghamella elegans, Kluyveromyces lactis, Lipomyces starkeyi, Lipomyces lipoferus, Mortierella alpina, Mortierella ramanniana, Mortierella isabellina, Mortierella vinacea, Pichia pastoris, Rhodosporidium toruloides, Rhodotorula glutinis, Trichoderma reesei,* and *Trichosporon pullans.*

16. The recombinant fungus of any of claims 1-4 wherein the recombinant fungus is a member of a genus selected from the group consisting of : *Cercospora, Fusarium (Gibberella), Mucor, Neurospora, Penicillium, Phycomyces, Puccinia,* and *Pythium.*

17. The recombinant fungus of any of claims 1-4 wherein the recombinant fungus is a species selected from the group consisting of: *Cercospora nicotianae, Fusarium fujikuroi (Gibberella zeae), Mucor circinelloides, Neurospora crassa, Phycomyces blakesleanus, Puccinia distincta,*

Pythium irregulare, Rhodotorula graminis, Rhodotorula mucilaginosa, Rhodotorula pinicola, Rhodotorula gracilis, and *Trichosporon cutaneum.*

18. The recombinant fungus of any of claims 1-4 wherein the recombinant fungus is a member of a genus selected from the group consisting of : *Botrytis, Cryptococcus,* and *Sclerotium*

19. The recombinant fungus of any of claims 1-4 wherein the recombinant fungus is a species selected from the group consisting of: *Botrytis cinerea, Cryptococcus curvatus, Sclerotium rolfsii.*

20. The recombinant fungus of any of claims 1-4 wherein the recombinant fungus grows as a single cell.

21. The recombinant fungus of any of claims 1-4 wherein the recombinant fungus is a yeast.

22. The recombinant fungus of any of claims 1-4 wherein the quinone derived compound is a ubiquinone.

23. The recombinant fungus of claim 22 wherein the ubiquinone is CoQ10.

24. The recombinant fungus of claim 22 wherein the ubiquinone is predominantly CoQ10.

25. The recombinant fungus of claim 22 wherein the ubiquinone is a C_{5-9} quinone compound.

26. The recombinant fungus of any of claims 1-4 wherein the quinone derived compound is a vitamin K compound.

27. The recombinant fungus of claim 26 wherein the vitamin K compound is menaquinone.

28. The recombinant fungus of claim 26 wherein the vitamin K compound is phylloquinone.

29. The recombinant fungus of any of claims 1-4 wherein the quinone derived compound is a vitamin E compound.

30. The recombinant fungus of claim 29 wherein the vitamin E compound is a tocopherol.

31. The recombinant fungus of claim 29 wherein the vitamin E compound is a tocotrienol.

32. The recombinant fungus of claim 30 wherein the vitamin E compound is an α-tocopherol.

33. The recombinant fungus of any one of claims 1-32, wherein the parental fungus is oleaginous.

34. The recombinant fungus of any one of claims 1-32 wherein the parental fungus is not oleaginous.

35. The recombinant fungus of any one of claims 1-34 wherein the parental fungus does not naturally produce the at least one quinone derived compound.

36. The recombinant fungus of any one of claims 1-34 wherein the parental fungus naturally produces the at least one quinone derived compound.

37. The recombinant fungus of any one of claims 1-36 wherein the parental fungus does not naturally produce at least one quinone derived compound.

38. The recombinant fungus of any one of claims 1-36 wherein the parental fungus naturally produces at least one quinone derived compound.

39. The recombinant fungus of any one of claims 1-38 wherein the recombinant fungus contains at least one oleaginic modification.

40. The recombinant fungus of claim 39 wherein the at least one oleaginic modification confers oleaginy upon the fungus.

41. The fungus of claim 39 wherein the at least one oleaginic modification alters oleaginicity of the fungus.

42. The recombinant fungus of claim 39 wherein the recombinant fungus further comprises at least one quinonogenic modification wherein the quinonogenic modification confers to the recombinant fungus the ability to produce the at least one quinone derived compound to a level at least about 1% of its dry cell weight or confers to the recombinant fungus the ability to produce at least one quinone derived compound which the parental fungus does not naturally produce.

43. The recombinant fungus of claim 39 wherein the at least one oleaginic modification increases expression or activity of at least one oleaginic polypeptide.

44. The recombinant fungus of claim 39 wherein the at least one oleaginic modification decreases expression or activity of at least one oleaginic polypeptide.

45. The recombinant fungus of claim 39 wherein the at least one oleaginic modification increases expression or activity of at least one oleaginic polypeptide and decreases expression or activity of at least one other oleaginic polypeptide.

46. The recombinant fungus of claim 43 or 44, wherein the at least one oleaginic polypeptide is chosen from acetyl-CoA carboxylase polypeptide, pyruvate decarboxylase polypeptide, isocitrate dehydrogenase polypeptide, ATP-citrate lyase polypeptide, malic enzyme polypeptide, AMP deaminase polypeptide, malate dehydrogenase polypeptide, glucose-6 -phosphate dehydrogenase polypeptide, 6-phosphogluconate dehydrogenase polypeptide, fructose 1, 6 bisphosphatase polypeptide, NADH kinase polypeptide, transhydrogenase polypeptide, acyl-CoA:diacylglycerol acyltransferase polypeptide, phospholipid:diacylglycerol acyltransferase polypeptide, acyl-CoA:cholesterol acyltransferase polypeptide, triglyceride lipase polypeptide, acyl-coenzyme A oxidase polypeptide and combinations thereof.

47. The recombinant fungus of claim 43 or 44 wherein the least one oleaginic polypeptide is chosen from a polypeptide from any one of Tables 1 through 6 or 69-85, 100-101 and combinations thereof.

48. The recombinant fungus of claim 39, wherein the at least one oleaginic modification comprises expression of at least one heterologous oleaginic polypeptide in the fungus.

49. The recombinant fungus of claim 48, wherein the at least one oleaginic modification comprises expression of at least one heterologous gene encoding the at least one heterologous oleaginic polypeptide.

50. The recombinant fungus of claim 48, wherein the at least one heterologous oleaginic polypeptide comprises an animal polypeptide, a mammalian polypeptide, an insect polypeptide, a plant polypeptide, a fungal polypeptide, a yeast polypeptide, an algal polypeptide, a bacterial polypeptide, a cyanobacterial polypeptide, an archaebacterial polypeptide, or a protozoal polypeptide.

51. The recombinant fungus of claim 48, wherein the at least one heterologous oleaginic polypeptide comprises at least two heterologous oleaginic polypeptides.

52. The recombinant fungus of claim 51, wherein the at least two heterologous oleaginic polypeptides are from a single source organism.

53. The recombinant fungus of claim 51, wherein the at least two heterologous oleaginic polypeptides are from at least two different source organisms.

54. The recombinant fungus of any one of claims 1-38 wherein the fungus contains at least one quinonogenic modification.

55. The recombinant fungus of claim 54 wherein the at least one quinonogenic modification confers to the recombinant fungus the ability to produce the at least one quinone derived compound to a level at least about 1% of its dry cell weight.

56. The recombinant fungus of claim 54 wherein the at least one quinonogenic modification confers to the fungus the ability to produce at least one quinone derived compound which the parental fungus does not naturally produce.

57. The recombinant fungus of claim 54 wherein the recombinant fungus further comprises at least one oleaginic modification wherein the oleaginic modification alters oleaginicity of the recombinant fungus or confers to the recombinant fungus oleaginy.

58. The recombinant fungus of claim 54, wherein the at least one quinonogenic modification confers the ability to the recombinant fungus to produce the at least one quinone derived compound to a level selected from the group consisting of at least about 2%, at least about 3%, at least about 5%, and at least about 10% of the recombinant fungus' dry cell weight.

59. The recombinant fungus of claim 54, wherein the at least one quinonogenic modification confers the ability to the recombinant fungus to produce the at least one quinone derived compound such that total quinone derived compound production by the recombinant fungus occurs at a level selected from the group consisting of at least about 2%, at least about 3%, at least about 5%, and at least about 10% of the fungus' dry cell weight.

60. The recombinant fungus of claim 54, wherein the at least one quinonogenic modification increases expression or activity of a quinonogenic polypeptide.

61. The recombinant fungus of claim 54, wherein the at least one quinonogenic modification decreases expression or activity of a quinonogenic polypeptide.

62. The recombinant fungus of claim 54, wherein the at least one quinonogenic modification increases expression or activity of at least one quinonogenic polypeptide and decreases expression or activity of at least one other quinonogenic polypeptide.

63. The recombinant fungus of claim 54, wherein the at least one quinonogenic modification comprises expression of at least one heterologous quinonogenic polypeptide.

64. The recombinant fungus of claim 63 wherein the at least one quinonogenic modification comprises expression of at least one heterologous gene encoding the at least one heterologous quinonogenic polypeptide.

65. The recombinant fungus of claim 60 or 61, wherein the quinonogenic polypeptide is selected from the group consisting of: isoprenoid biosynthesis polypeptides, ubiquinone biosynthesis polypeptides, and ubiquinone biosynthesis competitor polypeptides, and combinations thereof.

66. The recombinant fungus of claim 65, wherein the isoprenoid biosynthesis polypeptides are selected from the group consisting of: acetoacetyl-CoA thiolase polypeptide, HMG-CoA synthase polypeptide, HMG-CoA reductase polypeptide, mevalonate kinase polypeptide, phosphomevalonate kinase polypeptide, mevalonate pyrophosphate decarboxylase polypeptide, IPP isomerase polypeptide, FPP synthase polypeptide, and GGPP synthase polypeptide, and combinations thereof.

67. The recombinant fungus of claim 65, wherein the ubiquinone biosynthesis polypeptides are selected from the group consisting of: polyprenyldiphosphate synthase (e.g. penta-, hexa-, hepta, octa-, nona-, deca-), prenyldiphosphate synthase, PHB-polyprenyltransferase, 4-hydroxybenzoate polyprenyl transferase, O-methyltransferase, a C_{5-9} quinone biosynthesis polypeptide, an isoprenoid biosynthesis polypeptide, any polypeptide having a sequence listed in Tables 23-31, 33, or 35-37, and combinations thereof.

68. The recombinant fungus of claim 65, wherein the ubiquinone biosynthesis competitor polypeptides are selected from the group consisting of squalene synthase polypeptide, anthranilate synthase, chorismate mutase, and combinations thereof.

69. The recombinant fungus of claim 63, wherein the at least one heterologous quinonogenic polypeptide comprises an animal polypeptide, a mammalian polypeptide, an insect polypeptide, a plant polypeptide, a fungal polypeptide, a yeast polypeptide, an algal polypeptide, a bacterial

polypeptide, cyanobacterial polypeptide, an archaebacterial polypeptide, or a protozoal polypeptide.

70. The recombinant fungus of claim 63, wherein the at least one heterologous quinonogenic polypeptide comprises at least two heterologous quinonogenic polypeptides.

71. The recombinant fungus of claim 70, wherein the at least two heterologous quinonogenic polypeptides are from a single source organism.

72. The recombinant fungus of claim 70, wherein the at least two heterologous quinonogenic polypeptides are from at least two different source organisms.

73. A recombinant fungus according to any of the preceding claims wherein the fungus accumulates the produced at least one quinone derived compound to a level selected from the group consisting of: above about 1%, above about 2%, above about 3%, above about 5%, and above about 10% of the fungus' dry cell weight.

74. A recombinant fungus according to any of the preceding claims characterized in that the fungus accumulates lipid in the form of cytoplasmic oil bodies.

75. The recombinant fungus of claim 74 wherein the at least one quinone derived compound accumulates in the cytoplasmic oil bodies.

76. A strain of *Yarrowia lipolytica* comprising one or more modifications selected from the group consisting of an oleaginic modification, a quinonogenic modification, and combinations thereof, such that the strain accumulates from 1% to 15% of its dry cell weight as at least one quinone derived compound.

77. The strain of claim 76 further characterized in that it accumulates from 20% to 50% of its dry cell weight as lipid.

78. The strain of claim 77, wherein the strain accumulates from 20% to 50% of its dry cell weight as lipid in the form of cytoplasmic oil bodies.

79. The strain of claim 76, wherein the strain comprises a quinonogenic modification chosen from:

a. expression of a polypeptide selected from a group consisting of a GGPP synthase polypeptide, a FPP synthase polypeptide, a decaprenyl diphosphate synthase polypeptide, a 4-hydroxybenzoate polyprenyl transferase polypeptide, a DAHP synthase polypeptide, a chorismate lyase polypeptide, a truncated HMG CoA reductase polypeptide, a shikimate pathway polypeptide, a chorismate mutase polypeptide, a chorismate synthase polypeptide, a transketolase polypeptide, and combinations thereof;

b. expression of a heterologous polypeptide selected from the group consisting of an ATP-citrate lyase, an AMP deaminase polypeptide, a cytosolic malic enzyme polypeptide, and combinations thereof;

c. decreased expression or activity of an endogenous polypeptide selected from the group consisting of squalene synthase polypeptide, a prenyldiphosphate synthase polypeptide, and a PHB polyprenyltransferase polypeptide, and combinations thereof;

and combinations thereof.

80. The strain of claim 76, wherein the strain accumulates 1-15% of its dry cell weight as a ubiquinone.

81. The strain of claim 76, wherein the strain comprises a quinonogenic modification chosen from:

a. expression of a polypeptide selected from a group consisting of a GGPP synthase polypeptide, a FPP synthase polypeptide, a decaprenyl diphosphate synthase polypeptide, a 4-hydroxybenzoate polyprenyl transferase polypeptide, a DAHP synthase polypeptide, a chorismate lyase polypeptide, a truncated HMG CoA reductase polypeptide, a shikimate pathway polypeptide, a chorismate mutase polypeptide, a chorismate synthase polypeptide, a transketolase polypeptide, an ATP-citrate lyase polypeptide, an AMP deaminase polypeptide, a cytosolic malic enzyme polypeptide and combinations thereof;

b. expression of a heterologous polypeptide selected from the group consisting of a vitamin K biosynthetic polypeptide, a vitamin E biosynthetic polypeptide, and combinations thereof;

and combinations thereof.

82. The strain of any one of claims 76-81, wherein the strain accumulates 1-15% of its dry cell weight as CoQ10, a C_{5-9} quinone compound, a vitamin K compound, a vitamin E compound, and combinations thereof.

83. The strain of any one of claims 76-81, wherein the at least one quinonogenic modification comprises increased expression of a DAHP synthase polypeptide.

84. The strain of any one of claims 76-81, wherein the at least one quinonogenic modification comprises increased expression of a truncated HMG CoA reductase polypeptide.

85. The strain of any one of claims 76-81, wherein the at least one quinonogenic modification comprises increased expression of a decaprenyl diphosphate synthase polypeptide.

86. The strain of any one of claims 76-81, wherein the at least one quinonogenic modification comprises increased expression of a FPP synthase polypeptide.

87. The strain of any one of claims 76-81, wherein the at least one quinonogenic modification comprises increased expression of a GGPP synthase polypeptide.

88. The strain of any one of claims 76-81, wherein the at least one quinonogenic modification comprises decreased expression of an endogenous squalene synthase polypeptide.

89. The strain of any one of claims 76-81, wherein the at least one quinonogenic modification comprises decreased expression of an endogenous prenyldiphosphate synthase polypeptide.

90. A method of producing a quinone derived compound, the method comprising steps of:

a. cultivating the fungus of any one of the preceding claims under conditions that allow production of the quinone derived compound;

b. and isolating the produced quinone derived compound .

91. The method of claim 90, wherein the step of cultivating comprises cultivating under conditions and for a time sufficient that the quinone derived compound accumulates to a level above at least about 1% of the dry cell weight of the fungus.

92. The method of claim 90, wherein the step of cultivating comprises cultivating under conditions and for a time sufficient that the fungus accumulates lipid bodies to a level above about 20% of its dry cell weight.

93. The method of any one of claims 90-92, wherein the quinone derived compound is selected from the group consisting of a ubiquinone, a vitamin K compound, a vitamin E compound, and combinations thereof.

94. The method of any one of claims 90-92, wherein the step of cultivating comprises growing cells under conditions of excess carbon and limiting non-carbon nutrient.

95. The method of claim 94, wherein the limiting non-carbon nutrient is chosen from nitrogen, phosphate, magnesium, and combinations thereof.

96. The method of claim 94 wherein the limiting non-carbon nutrient comprises nitrogen.

97. The method of claim 94 wherein the carbon:nitrogen ratio is within the range selected from the group consisting of about 200:1, 150:1, 125:1, 100:1, 95:1, 90:1, 85:1, 80:1, 75:1, 70:1, 65:1, 6-:1, 55:1, 50:1, 45:1, 40:1, 35:1, 30:1, 25:1, 20:1, 15:1, and 10:1.

98. The method of claim 94 wherein the carbon:nitrogen ratio is less than about 10:1.

99. The method of any one of claims 90-92, wherein the step of cultivating comprises growing under conditions of controlled dissolved oxygen concentration.

100. The method of claim 99, wherein the step of cultivating comprises modulating feed rate to maintain a specific level of dissolved oxygen.

101. The method of claim 90, wherein the step of cultivating comprises a first phase of growing under conditions of excess carbon and limiting oxygen, followed by a second phase of growing under conditions of excess oxygen and limiting carbon.

102. The method of claim 90, wherein the step of isolating comprises homogenizing cells and subjecting them to extraction.

103. The method of claim 102, wherein the extraction comprises supercritical liquid extraction.

104. The method of claim 102, wherein the extraction comprises solvent extraction.

105. The method of any of claim 90-104, wherein the quinone derived compound accumulates in lipid bodies.

106. The method of claim 105, wherein the lipid bodies are characterized by major components selected from the group consisting of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and combinations thereof.

107. The method of claim 105, wherein the lipid bodies comprise fatty acids, which fatty acids are selected from the group consisting of C16 and C18 fatty acids, and combinations thereof.

108. The method of claim 107, wherein the fatty acids are selected from the group consisting of C16:0, C16:1, C18:0, C18:1, C18:2 and combinations thereof.

109. The method of claim 90, wherein the step of isolating comprises fractionating the cultivation medium to obtain at least one quinone derived compound-enriched fraction.

110. The method of claim 90, wherein: the step of cultivating comprises cultivating the fungus under conditions that allow accumulation of the quinone derived compound in cytoplasmic oil bodies; and the step of isolating comprises isolating oil derived from the cytoplasmic oil bodies.

111. The method of claim 90, wherein the quinone derived compound is chosen from CoQ10, a C_{5-9} quinone compound, and combinations thereof.

112. The method of claim 90, wherein the quinone derived compound comprises CoQ10.

113. The method of claim 90, wherein the step of isolating comprises concentrating the quinone derived compound.

114. The method of claim 113, wherein the step of isolating comprises concentrating the quinone derived compound until it is at least about 5-fold more concentrated.

115. The method of claim 90 or any one of claims 112-114, further comprises a step of chemically modifying the quinone derived compound.

116. The method of claim 115, wherein the step of chemically modifying comprises esterifying or de-esterifying the quinone derived compound.

117. The method of claim 90 or any one of claims 112-114, further comprising a step of combining the quinone derived compound with one or more other agents in a composition.

118. The method of claim 117, wherein the step of combining comprises combing the quinone derived compound with one or more other agents selected from the group consisting of binders, fillers, and combinations thereof.

119. The method of claim 117, wherein the step of combining comprises combining the quinone derived compound with one or more other agents selected from the group consisting of chelating agents, pigments, salts, surfactants, moisturizers, viscosity modifiers, thickeners, emollients, fragrances, preservatives, and combinations thereof.

120. An engineered *Y. lipolytica* strain that produces a ubiquinone, the strain containing one or more quinonogenic modifications selected from the group consisting of:

a. increased expression or activity of a GGPP synthase polypeptide;

b. increased expression or activity of a truncated HMG CoA reductase polypeptide;

c. increased expression or activity of a 4-hydroxybenzoate polyprenyl transferase polypeptide;

d. increased expression or activity of a decaprenyl diphosphate synthase polypeptide;

e. increased expression or activity of a DAHP synthase polypeptide;

f. increased expression or activity of a chorismate lyase polypeptide;

g. increased expression or activity of a shikimate pathway polypeptide;

h. increased expression or activity of a chorismate mutase polypeptide;

i. increased expression or activity of a transketolase polypeptide;

j. increased expression or activity of an FPP synthase polypeptide;

k. increased expression or activity of an IPP isomerase polypeptide;

l. increased expression or activity of an HMG-CoA synthase polypeptide;

m. increased expression or activity of a mevalonate kinase polypeptide;

n. increased expression or activity of a phosphomevalonate kinase polypeptide;

o. increased expression or activity of a mevalonate pyrophosphate decarboxylate polypeptide;

p. increased expression or activity of a cytosolic malic enzyme polypeptide;

q. increased expression or activity of a malate dehydrogenase polypeptide;

r. increased expression or activity of an AMP deaminase polypeptide;

s. increased expression or activity of a glucose 6 phosphate dehydrogenase polypeptide;

t. increased expression or activity of a malate dehydrogenase homolog2 polypeptide;

v. increased expression or activity of a GND1-6-phosphogluconate dehydrogenase polypeptide;

w. increased expression or activity of a isocitrate dehydrogenase polypeptide;

x increased expression or activity of a IDH2-isocitrate dehydrogenase polypeptide;

y. increased expression or activity of a fructose 1,6 bisphosphatase polypeptide;

z. increased expression or activity of an Erg10-acetoacetyl CoA thiolase polypeptide;

aa. increased expression or activity of an ATP citrate lyase subunit 2 polypeptide;

bb. increased expression or activity of an ATP citrate lyase subunit 1 polypeptide;

cc. increased expression or activity of a chorsimate synthase polypeptide

dd. decreased expression or activity of a squalene synthase polypeptide;

ee. decreased expression or activity of a prenyldiphosphate synthase polypeptide; or

ff. decreased expression or activity of a PHB polyprenyltransferase polypeptide; and combinations thereof.

121. The engineered *Y. lipolytica* strain of claim 120, wherein the one or more quinonogenic modifications is selected from the group consisting of:

a. increased expression or activity of a decaprenyl diphosphate synthase polypeptide;

b. increased expression or activity of an 4-hydroxybenzoate polyprenyl polypeptide;

c. increased expression or activity of a GGPP synthase polypeptide;

d. increased expression or activity of an FPP synthase polypeptide;

e. increased expression or activity of an HMG CoA reductase polypeptide;

f. decreased expression or activity of a squalene synthase polypeptide;

g. decreased expression of activity of a prenyldiphosphate synthase polypeptide;

h. increased expression or activity of a DAHP synthase polypeptide;

i. increased expression or activity of a chorismate lyase polypeptide;

j. increased expression or activity of a chorismate synthase polypeptide;

k. increased expression or activity of a chorismate mutase polypeptide

l. increased expression or activity of an ATP-citrate lyase polypeptide;

m. increased expression or activity of an AMP deaminase polypeptide;

n. increased expression or activity of a cytosolic malic enzyme polypeptide; and combinations thereof.

122. The engineered *Y. lipolytica* strain of any one of claims 120-121, wherein the decaprenyl diphosphate synthase polypeptide is a polypeptide from the genus *Silibacter* or *Loktanella*.

123. The engineered *Y. lipolytica* strain of claim 122, wherein the decaprenyl diphosphate synthase polypeptide is a polypeptide from the species *Silibacter pomeroyi* or *Loktanella vestfoldenesis*.

124. The engineered *Y. lipolytica* strain of any one of claims 120-121, wherein the 4-hydroxybenzoate polyprenyl polypeptide is a polypeptide from the genus *Silibacter* or *Bos*.

125. The engineered *Y. lipolytica* strain of claim 124, wherein the 4-hydroxybenzoate polyprenyl polypeptide is a polypeptide from the genus *Silibacter pomeroyi* or *Bos taurus*.

126. The engineered *Y. lipolytica* strain of any one of claims 120-121, wherein the HMG CoA reductase polypeptide is a polypeptide from the genus *Yarrowia*.

127. The engineered *Y. lipolytica* strain of claim 126, wherein the HMG CoA reductase polypeptide is a polypeptide from the species *Yarrowia lipolytica*.

128. The engineered *Y. lipolytica* strain of any one of claims 120-121, wherein the DAHP synthase polypeptide is a polypeptide from the genus *Erwinia*.

129. The engineered *Y. lipolytica* strain of claim 128, wherein the DAHP synthase polypeptide is a polypeptide from the species *Erwinia carotovora*.

130. The engineered *Y. lipolytica* strain of any one of claims 120-121, wherein the chorismate lyase polypeptide is a polypeptide from the genus *Erwinia*.

131. The engineered *Y. lipolytica* strain of claim 130, wherein the chorismate lyase polypeptide is a polypeptide from the species *Erwinia carotovora*.

132. The engineered *Y. lipolytica* strain of any one of claims 120-121, wherein the ATP-citrate lyase polypeptide is a polypeptide from the genus *Neurospora*.

133. The engineered *Y. lipolytica* strain of claim 132, wherein the ATP-citrate lyase polypeptide is a polypeptide from the species *Neurospora crassa*.

134. The engineered *Y. lipolytica* strain of any one of claims 120-121, wherein the AMP deaminase polypeptide is a polypeptide from the genus *Saccharomyces*.

135. The engineered *Y. lipolytica* strain of claim 134, wherein the AMP deaminase polypeptide is a polypeptide from the species *Saccharomyces cerevisiae*.

136. The engineered *Y. lipolytica* strain of any one of claims 120-121, wherein the cytosolic malic enzyme polypeptide is a polypeptide from the genus *Mucor*.

137. The engineered *Y. lipolytica* strain of claim 136, wherein the cytosolic malic enzyme polypeptide is a polypeptide from the species *Mucor circinelloides*.

138. The engineered *Y. lipolytica* strain of any one of claims 120-121, wherein the GGPP synthase polypeptide is a polypeptide from the genus *Yarrowia*.

139. The engineered *Y. lipolytica* strain of claim 138, wherein the GGPP synthase polypeptide is a polypeptide from the species *Yarrowia lipolytica*.

140. The engineered *Y. lipolytica* strain of any one of claims 120-121, wherein the FPP synthase polypeptide is a polypeptide from the genus *Yarrowia*.

141. The engineered *Y. lipolytica* strain of claim 140, wherein the FPP synthase polypeptide is a polypeptide from the species *Yarrowia lipolytica*.

142. The engineered *Y. lipolytica* strain of any one of claims 120-121, wherein the chorismate synthase polypeptide is a polypeptide from the genus *Yarrowia*.

143. The engineered *Y. lipolytica* strain of claim 142, wherein the chorismate synthase polypeptide is a polypeptide from the species *Yarrowia lipolytica*.

144. The engineered *Y. lipolytica* strain of any one of claims 120-121, wherein the ubiquinone comprises CoQ10.

145. The engineered *Y. lipolytica* strain of any one of claims 120-121, wherein the produced ubiquinone accumulates to levels that are greater than at least about 1.0% of the dry weight of the cells.

146. The engineered *Y. lipolytica* strain of any one of claims 120-121, wherein the produced ubiquinone accumulates to levels that are greater than at least about 2.5% of the dry weight of the cells.

147. The engineered *Y. lipolytica* strain of any one of claims 120-121, wherein the produced ubiquinone accumulates to levels that are greater than at least about 5.0% of the dry weight of the cells.

148. The engineered *Y. lipolytica* strain of any one of claims 120-121, further comprising a second quinonogenic modification chosen from the group:

a. increased expression or activity of a vitamin K biosynthesis polypeptide,
b. increased expression or activity of a vitamin E biosynthesis polypeptide,

and combinations thereof.

149. The engineered *Y. lipolytica* strain of claim 148, wherein the strain produces vitamin K.

150. The engineered *Y. lipolytica* strain of claim 149, wherein the produced vitamin K accumulates to levels that are greater than at least about 1.0% of the dry weight of the cells.

151. The engineered *Y. lipolytica* strain of claim 148, wherein the strain produces vitamin E.

152. The engineered *Y. lipolytica* strain of claim 149, wherein the produced vitamin E accumulates to levels that are greater than at least about 1.0% of the dry weight of the cells.

153. The engineered *Y. lipolytica* strain of any one of claims 120-121, wherein a quinone derived compound produced by the strain accumulates in lipid bodies.

154. The engineered *Y. lipolytica* strain of claim 153, wherein the quinone derived compound is selected from the group consisting of: CoQ10, a C_{5-9} quinone compound, a vitamin K compound, and a vitamin E compound, and combinations thereof.

155. The engineered *Y. lipolytica* strain of claim 153, wherein the lipid bodies are characterized by major components selected from the group consisting of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and combinations thereof.

156. The engineered *Y. lipolytica* strain of claim 153, wherein the lipid bodies comprise fatty acids, which fatty acids are selected from the group consisting of C16 and C18 fatty acids, and combinations thereof.

157. The engineered *Y. lipolytica* strain of claim 156, wherein the fatty acids are selected from the group consisting of C16:0, C16:1, C18:0, C18:1, C18:2 and combinations thereof.

158. The engineered *Y. lipolytica* strain of claim 153, wherein the quinone derived compound is characterized by a negligible solubility in water and solubility in oil within the range of about <0.001% - 0.2%; 0.004%-0.15%; 0.005-0.1%; or 0.005-0.5%.

159. An engineered *S. cerevisiae* strain, comprising one or more quinonogenic modifications,

wherein the one or more quinonogenic modifications are selected from the group consisting of:

a. increased expression or activity of a decaprenyl diphosphate synthase polypeptide;
b. increased expression or activity of an 4-hydroxybenzoate polyprenyl polypeptide;
c. increased expression or activity of a GGPP synthase polypeptide;
d. increased expression or activity of an FPP synthase polypeptide;
e. increased expression or activity of an HMG CoA reductase polypeptide;
f. decreased expression or activity of a squalene synthase polypeptide;
g. decreased expression of activity of a prenyldiphosphate synthase polypeptide;
h. increased expression or activity of a DAHP synthase polypeptide;
i. increased expression or activity of a chorismate lyase polypeptide;
j. increased expression or activity of a chorismate synthase polypeptide;
k. increased expression or activity of an ATP-citrate lyase polypeptide;
l. increased expression or activity of an AMP deaminase polypeptide;
m. increased expression or activity of a cytosolic malic enzyme polypeptide; and

combinations thereof.

160. An engineered *Y. lipolytica* strain containing a truncated HMG CoA reductase polypeptide.

161. The engineered *Y. lipolytica* strain of claim 160, wherein the HMG CoA reductase polypeptide is a *Yarrowia* polypeptide.

162. The engineered *Y. lipolytica* strain of claim 160 or 161, wherein the HMG CoA reductase polypeptide is a *Yarrowia lipolytica* polypeptide.

163. The engineered *Y. lipolytica* strain of claim 162, further comprising a second HMG CoA reductase polypeptide from a second organism.

164. An engineered *Y. lipolytica* strain having increased expression or activity of a decaprenyl diphosphate synthase gene.

165. The engineered *Y. lipolytica* strain of claim 164, wherein the decaprenyl diphosphate synthase polypeptide is a *Silibacter* or *Loktanella* polypeptide.

166. The engineered *Y. lipolytica* strain of claim 164 or 165, wherein the decaprenyl diphosphate synthas polypeptide is a *Silibacter pomeroyi* or *Loktanella vestfoldenesis*polypeptide.

167. The engineered *Y. lipolytica* strain of claim 164, further comprising a second decaprenyl diphosphate synthase polypeptide from a second organism.

168. An engineered *Y. lipolytica* strain having decreased expression or activity of a squalene synthase polypeptide.

169. The engineered *Y. lipolytica* strain of claim 168, wherein the squalene synthase polypeptide is an endogenous squalene synthase polypeptide.

170. The engineered *Y. lipolytica* strain of claim 168 or 169, wherein the squalene synthase polypeptide is a polypeptide from an organism of a genus selected from the group consisting of: *Neurospora, Xanthophyllomyces (Phaffia), Aspergillus, Saccharomyces, Mucor, Rhotorula, Candida, Mortierella*, and *Yarrowia*.

171. The engineered *Y. lipolytica* strain of claim 170, wherein the squalene synthase polypeptide is a polypeptide from an organism selected from the group consisting of: *Neurospora crassa, Xanthophyllomyces dendrorhous (Phaffia rhodozyma), Aspergillus niger, Saccharomyces cerevisiae, Mucor circinelloides, Rhotorula glutinis, Candida utilis, Mortierella alpina*, and *Yarrowia lipolytica*.

172. The engineered *Y. lipolytica* strain of claim 168, further comprising a second squalene synthase polypeptide from a second organism.

173. An engineered *Y. lipolytica* strain having increased expression or activity of a 4-hydroxybenzoate polyprenyl polypeptide.

174. The engineered *Y. lipolytica* strain of claim 173, wherein the 4-hydroxybenzoate polyprenyl polypeptide is a polypeptide from the genus *Silibacter* or *Bos*.

175. The engineered *Y. lipolytica* strain of claim 173, wherein the 4-hydroxybenzoate polyprenyl polypeptide is a polypeptide from the genus *Silibacter pomeroyi* or *Bos taurus*.

176. An engineered *Y. lipolytica* strain having increased expression or activity of a DAHP synthase polypeptide.

177. The engineered *Y. lipolytica* strain of claim 176, wherein the DAHP synthase polypeptide is a polypeptide from the genus *Erwinia*.

178. The engineered *Y. lipolytica* strain of claim 176, wherein the DAHP synthase polypeptide is a polypeptide from the species *Erwinia carotovora.*

179. An engineered *Y. lipolytica* strain having increased expression or activity of a chorismate lyase polypeptide.

180. The engineered *Y. lipolytica* strain of claim 179, wherein the chorismate lyase polypeptide is a polypeptide from the genus *Erwinia.*

181. The engineered *Y. lipolytica* strain of claim 179, wherein the chorismate lyase polypeptide is a polypeptide from the species *Erwinia carotovora.*

182. An engineered *Y. lipolytica* strain having increased expression or activity of a ATP-citrate lyase polypeptide.

183. The engineered *Y. lipolytica* strain of claim 182, wherein the ATP-citrate lyase polypeptide is a polypeptide from the genus *Neurospora.*

184. The engineered *Y. lipolytica* strain of claim 182, wherein the ATP-citrate lyase polypeptide is a polypeptide from the species *Neurospora crassa.*

185. An engineered *Y. lipolytica* strain having increased expression or activity of an AMP deaminase polypeptide.

186. The engineered *Y. lipolytica* strain of any claim 185, wherein the AMP deaminase polypeptide is a polypeptide from the genus *Saccharomyces.*

187. The engineered *Y. lipolytica* strain of any claim 185, wherein the AMP deaminase polypeptide is a polypeptide from the species *Saccharomyces cerevisiae.*

188. An engineered *Y. lipolytica* strain having increased expression or activity of a cytosolic malic polypeptide.

189. The engineered *Y. lipolytica* strain of claim 188, wherein the cytosolic malic enzyme polypeptide is a polypeptide from the genus *Mucor.*

190. The engineered *Y. lipolytica* strain of claim 188, wherein the cytosolic malic enzyme polypeptide is a polypeptide from the species *Mucor circinelloides*.

191. An engineered *Y. lipolytica* strain having increased expression or activity of a GGPP synthase polypeptide.

192. The engineered *Y. lipolytica* strain of claim 191, wherein the GGPP synthase polypeptide is a polypeptide from the genus *Yarrowia*.

193. The engineered *Y. lipolytica* strain of claim 191, wherein the GGPP synthase polypeptide is a polypeptide from the species *Yarrowia lipolytica*.

194. An engineered *Y. lipolytica* strain having increased expression or activity of an FPP synthase polypeptide.

195. The engineered *Y. lipolytica* strain of claim 194, wherein the FPP synthase polypeptide is a polypeptide from the genus *Yarrowia*.

196. The engineered *Y. Yarrowia* strain of claim 194, wherein the FPP synthase polypeptide is a polypeptide from the species *Yarrowia lipolytica*.

197. An engineered *Y. lipolytica* strain having increased expression or activity of a chorismate synthase polypeptide.

198. The engineered *Y. lipolytica* strain of claim 197, wherein the chorismate synthase polypeptide is a polypeptide from the genus *Yarrowia*.

199. The engineered *Y. Yarrowia* strain of claim 197, wherein the chorismate synthase polypeptide is a polypeptide from the species *Yarrowia lipolytica*.

200. The engineered *Y. lipolytica* strain of any of claims 160-199, wherein the strain produces a ubiquinone.

201. The engineered *Y. lipolytica* strain of claim 200, wherein the produced ubiquinone accumulates to levels that are greater than at least about 1.0% of the dry weight of the cells.

202. The engineered *Y. lipolytica* strain of claim 200, wherein the produced ubiquinone accumulates in lipid bodies.

203. The engineered *Y. lipolytica* strain of claim 202, wherein the lipid bodies are characterized by major components selected from the group consisting of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and combinations thereof.

204. The engineered *Y. lipolytica* strain of claim 202, wherein the lipid bodies comprise fatty acids, which fatty acids are selected from the group consisting of C16 and C18 fatty acids, and combinations thereof.

205. The engineered *Y. lipolytica* strain of claim 204, wherein the fatty acids are selected from the group consisting of C16:0, C16:1, C18:0, C18:1, C18:2 and combinations thereof.

206. The engineered *Y. lipolytica* strain of claim 200, wherein the ubiquinone is characterized by a negligible solubility in water and solubility in oil within the range of about <0.001% - 0.2%; 0.004%-0.15%; 0.005-0.1%; or 0.005-0.5%.

207. A method of preparing a food or feed additive or a dietary supplement containing a quinone derived compound, the method comprising steps of:

a. cultivating the fungus of any one of claims 1-89, the engineered *Y. lipolytica* strain of any one of claims 120-158 or 160-206, or the engineered *S. cerevisiae* strain of claim 159 under conditions that allow production of the quinone derived compound;

b. isolating the quinone derived compound; and

c. combining the isolated quinone derived compound with one or more other food or feed additive components.

208. A composition comprising:

lipid bodies;

at least one quinone derived compound; and

intact fungal cells.

209. The composition of claim 208, wherein not more than 5%, 4%, 3%, 2%, or 1% of the composition is intact fungal cells.

210. The composition of claim 208, wherein not more than about 5%, 4%, 3%, 2%, or 1% of the composition is water soluble cell components.

211. The composition of claim 208, wherein the quinone derived compound comprises at least about 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or higher of the composition.

212. The composition of claim 208, wherein the lipid bodies are characterized by major components selected from the group consisting of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and combinations thereof

213. The composition of claim 208 wherein the lipid bodies comprise fatty acids, which fatty acids are selected from the group consisting of C16 and C18 fatty acids, and combinations thereof.

214. The composition of claim 213 wherein the fatty acids are selected from the group consisting of . C16:0, C16:1, C18:0, C18:1, C18:2 and combinations thereof.

215. The composition of any one of claims 208-214 wherein the quinone derived compound is selected from the group consisting of a ubiquinone, a vitamin K compound, and a vitamin E compound, and combinations thereof.

216. The composition of claim 215, wherein the ubiquinone is selected from the group consisting of CoQ10, a C_{5-9} quinone compound, and combinations thereof.

217. A composition comprising:

an oil suspension comprising:

lipid bodies;

at least one quinone derived compound; and

intact fungal cells; and

a binder or filler.

218. The composition of any of claims 208-217 wherein the at least one quinone derived compound is characterized by negligible solubility in water and solubility in oil within the range of about <0.001% - 0.2%; 0.004%-0.15%; 0.005-0.1%; or 0.005-0.5%.

219. A composition comprising:

an oil suspension comprising:

lipid bodies;

at least one quinone derived compound; and

intact fungal cells; and

one or more other agents selected from the group consisting of chelating agents, pigments, salts, surfactants, moisturizers, viscosity modifiers, thickeners, emollients, fragrances, preservatives, and combinations thereof.

220. The composition of any of claims 208-219, wherein the composition is dried.

221. The composition of claim 220, formulated as a feedstuff.

222. The composition of claim 220 further comprising a binder, a filler, or both.

223. The composition of any one of claims 208-222, wherein the fungals cell are selected from the group consisting of: *Yarrowia, Sacchaomyces, Phaffi, Candida,* and combinations thereof.

224. The composition of claim 223, wherein the fungal cells are *Yarrowia lipolytica.*

225. The composition of claim 223, wherein the fungal cells are *Saccharomyces cerevisiae.*

226. The composition of claim 223, wherein the fungal cells are *Phaffia rhodozyma.*

227. The composition of claim 223, wherein the fungal cells are *Candida utilis.*

228. An isolated quinone derived compound, prepared by a method comprising steps of:

a. cultivating the fungus of any one of any one of claims 1-89, the engineered *Y. lipolytica* strain of any one of claims 120-158 or 160-206, or the engineered *S. cerevisiae* strain of claim 159 under conditions that allow production of a quinone derived compound; and

b. isolating the produced quinone derived compound.

229. The compound of claim 228, wherein the fungus is selected from a genus of the group consisting of: *Yarrowia, Saccharomyces, Phaffia,* and *Candida.*

230. The compound of claim 229, wherein the fungus is *Yarrowia lipolytica.*

231. The compound of claim 229, wherein the fungus is *Saccharomyces cerevisiae.*

232. The compound of claim 229, wherein the fungus is *Phaffia rhodozyma.*

233. The compound of claim 229, wherein the fungus is *Candida utilis*.

234. The compound of claim 228, wherein the step of cultivating comprising cultivating under conditions and for a time sufficient that the quinone derived compound accumulates to a level above at least about 1% of the dry cell weight of the fungus.

235. The compound of claim 228, wherein the step of cultivating comprises cultivating under conditions and for a time sufficient that the fungus accumulates lipid bodies to a level above about 20% of its dry cell weight.

236. The compound of claim 228, wherein the quinone derived compound is selected from the group consisting of a ubiquinone, a vitamin K compound, a vitamin E compound, and combinations thereof.

237. The compound of claim 228, wherein the step of cultivating comprises growing cells under conditions of excess carbon and limiting non-carbon nutrient.

238. The compound of claim 237, wherein the limiting non-carbon nutrient is selected from the group consisting of nitrogen, phosphate, magnesium, and combinations thereof.

239. The compound of claim 237 wherein the limiting non-carbon nutrient comprises nitrogen.

240. The compound of claim 237 wherein the carbon:nitrogen ratio is within the range selected from the group consisting of about 200:1, 150:1, 125:1, 100:1, 95:1, 90:1, 85:1, 80:1, 75:1, 70:1, 65:1, 6-:1, 55:1, 50:1, 45:1, 40:1, 35:1, 30:1, 25:1, 20:1, 15:1, and 10:1.

241. The compound of claim 237 wherein the carbon:nitrogen ratio is less than about 10:1.

242. The compound of claim 228, wherein the step of cultivating comprises growing under conditions of controlled dissolved oxygen concentration.

243. The compound of claim 242, wherein the step of cultivating comprises modulating feed rate to maintain a specific level of dissolved oxygen.

244. The compound of claim 228, wherein the step of cultivating comprises a first phase of growing under conditions of excess carbon and limiting oxygen, followed by a second phase of growing under conditions of excess oxygen and limiting carbon.

245. The compound of claim 228, wherein the step of isolating comprises homogenizing cells and subjecting them to extraction, wherein the extraction comprises supercritical liquid extraction.

246. The compound of claim 245, wherein the extraction comprises solvent extraction.

247. The compound of claim 245, wherein the quinone derived compound accumulates in lipid bodies.

248. The compound of claim 247, wherein the lipid bodies are characterized by major components selected from the group consisting of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and combinations thereof.

249. The compound of claim 247, wherein the lipid bodies comprise fatty acids, which fatty acids are selected from the group consisting of C16 and C18 fatty acids, and combinations thereof.

250. The compound of claim 249, wherein the fatty acids are selected from the group consisting of C16:0, C16:1, C18:0, C18:1, C18:2 and combinations thereof.

251. The compound of claim 228, wherein the step of isolating comprises fractionating the cultivation medium to obtain at least one quinone derived compound- enriched fraction.

252. The compound of claim 228, wherein: the step of cultivating comprises cultivating the fungus under conditions that allow accumulation of the quinone derived compound in cytoplasmic oil bodies; and the step of isolating comprises isolating oil derived from the cytoplasmic oil bodies.

253. The compound of claim 228, wherein the quinone derived compound is selected from the group consisting of:CoQ10, a C_{5-9} quinone compound, and combinations thereof.

254. The compound of claim 228, wherein the quinone derived compound comprises a ubiquinone.

255. The compound of claim 228, wherein the step of isolating comprises concentrating the quinone derived compound.

256. The compound of claim 255, wherein the step of isolating comprises concentrating the quinone derived compound until it is at least about 5-fold more concentrated.

257. The compound of claim 228 wherein the method of preparing further comprises a step of chemically modifying the quinone derived compound.

258. The compound of claim 257, wherein the step of chemically modifying comprises esterifying or de-esterifying the quinone derived compound.

259. A composition comprising the quinone derived compound of any one of claims 228-258, further comprising one or more other agents.

260. The composition of claim 259, wherein the one or more other agents is selected from the group consisting of binders, fillers, and combinations thereof.

261. The composition of claim 259, wherein the one or more other agents is selected from the group consisting of chelating agents, pigments, salts, surfactants, moisturizers, viscosity modifiers, thickeners, emollients, fragrances, preservatives, and combinations thereof.

262. The composition of claim 261, further comprising one or more binders or fillers.

263. The composition of claim 259, wherein the quinone derived compound is a ubiquinone.

264. The composition of any of claims 259-263 wherein the composition is formulated as a feedstuff.

265. A feedstuff comprising:

a quinone derived compound in lipid bodies.

266. The feedstuff of claim 265, wherein the lipid bodies are characterized by major components selected from the group consisting of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and combinations thereof.

267. The feedstuff of claim 265, wherein the lipid bodies comprise fatty acids, which fatty acids are selected from the group consisting of C16 and C18 fatty acids, and combinations thereof.

268. The feedstuff of claim 267, wherein the fatty acids are selected from the group consisting of C16:0, C16:1, C18:0, C18:1, C18:2 and combinations thereof.

269. The feedstuff of any of claims 265-268, wherein the quinone derived compound is characterized by a negligible solubility in water and solubility in oil within the range of about <0.001% - 0.2%; 0.004%-0.15%; 0.005-0.1%; or 0.005-0.5%.

270. A quinone derived compound composition comprising:

a *Y. lipolytica* cell containing at least 1% quinone derived compound by weight.

271. A quinone derived compound composition comprising:

Y lipolytica lipid bodies; and

at least one quinone derived compound ,

where the at least one quinone derived compound is present at a level that is at least 1% by weight of the lipid bodies.

272. The quinone derived compound composition of either claim 270 or claim 271, comprising a quinone derived compound selected from the group consisting of: a ubiquinone, a vitamin K compound, and a vitamin E compound, and combinations thereof.

273. The quinone derived compound composition of claim 272 wherein the ubiquinone is selected from the group consisting of CoQ10, a C_{5-9} quinone compound, and combinations thereof.

274. The quinone derived compound composition of claim 270 or 271, further comprising one or more binders or fillers.

275. The quinone derived compound composition of claim 270 or 271, further comprising one or more chelating agents, pigments, salts, surfactants , moisturizers, viscosity modifiers, thickeners, emollients, fragrances, preservatives, and combinations thereof.

276. The quinone derived compound composition of claim 270 or 271, wherein the composition is formulated as a feedstuff.

277. A method comprising steps of:

a. cultivating the fungus of any one of claims 1-89, the engineered *Y. lipolytica* strain of any one of claims 120-158 or 160-206, or the engineered *S. cerevisiae* strain of claim 159 under conditions that allow production of a quinone derived compound;

b. and isolating the produced quinone derived compound.

278. The method of claim 277 wherein the produced quinone derived compound is a ubiquinone.

279. The method of claim 277 wherein the produced quinone derived compound is CoQ10.

280. The method of claim 277 wherein the produced quinone derived compound is a C_{5-9} quinone compound.

281. The method of claim 277 wherein the produced quinone derived compound is a vitamin K compound.

282. The method of claim 277 wherein the produced quinone derived compound is a vitamin E compound.

283. The method of any of claims 277-282 wherein the step of isolating comprises extracting with an organic or a non-organic solvent.

284. The method of claim 283 wherein the step of isolating comprises extracting with a solvent selected from the group consisting of acetone, supercritical carbon dioxide, chloroform, ethanol, ethyl acetate, heptane, hexane, hexane:ethyl acetate, isopropanol, methanol, methylene chloride, octane, tetrahydrofuran (THF), soybeen oil, rapeseed oil, and combinations thereof.

285. The method of any of claims 277-284 wherein the step of cultivating comprises growing under conditions of limiting nutrient, where the limiting nutrient is selected from the group consisting of carbon, nitrogen, phosphate, magnesium, or combinations thereof.

286. The method of claim 285 wherein the limiting nutrient is selected from the group consisting of nitrogen, phosphate, magnesium, or combinations thereof, and carbon is in excess.

287. The method of claim 286 wherein the limiting nutrient is carbon.

288. The method of claim 286 wherein the limiting nutrient is phosphate and phosphate addition is controlled so that production of canthazanthin as compared with echinenone is altered.

289. The method of any of claim 277-288 wherein the step of cultivating comprises growing under conditions where at least one environmental parameter is controlled for at least a portion of the cultivating.

290. The method of claim 289 wherein the controlled environmental parameter is selected from the group consisting of amount of a particular nutrient, pH, temperature, pressure, oxygen concentration, timing of feeds, content of feeds, and combinations thereof.

291. The method of claim 290 wherein at least one environmental parameter is not controlled during at least a portion of the cultivating.

292. The method of claim 291 wherein the controlled environmental parameter is selected from the group consisting of amount of a particular nutrient, pH, temperature, pressure, oxygen concentration, timing of feeds, content of feeds, and combinations thereof.

293. The method of any of claims 277-292 wherein the step of cultivating comprises cultivating at about 20-40 °C.

294. The method of any of claims 277-292 wherein the step of cultivating comprises cultivating at about 20-30 °C.

295. The method of of any of claims 277-292 wherein the step of cultivating comprises cultivating at about 20, 20.5, 21, 21.5, 22, 22.5, 23, 23.5, 24, 24.5, 25, 25.5, 26, 26.5, 27, 27.5, 28, 28.5, 29, 29.5, 30 °C or above.

296. The method of any of claims 277-294 wherein the step of cultivating comprises cultivating within a pH range of about pH 4-7.5.

297. The method of any of claims 277-294 wherein the step of cultivating comprises cultivating within a pH range of about pH 4-6.5.

298. The method of any of claims 277-294 wherein the step of cultivating comprises cultivating within a pH range of about pH 3.5-7.

299. The method of any of claims 277-294 wherein the step of cultivating comprises cultivating within a pH range of about pH 3.5-4

300. The method of any of claims 277-294 wherein the step of cultivating comprises cultivating within a pH range of about pH, 4-4.5.

301. The method of any of claims 277-294 wherein the step of cultivating comprises cultivating within a pH range of about pH 4.5-5.

302. The method of any of claims 277-294 wherein the step of cultivating comprises cultivating within a pH range of about pH 5-5.5.

303. The method of any of claims 277-294 wherein the step of cultivating comprises cultivating within a pH range of about pH 5.5-6.

304. The method of any of claims 277-294 wherein the step of cultivating comprises cultivating within a pH range of about pH 6-6.5.

305. The method of any of claims 277-294 wherein the step of cultivating comprises cultivating within a pH range of about pH 6.5-7.

306. The method of any of claims 277-294 wherein the step of cultivating comprises cultivating at a pH of about pH 4.0, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5.0, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6.0, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7.0, 7.1, 7.2, 7.3, 7.4, 7.5 or above.

307. The method of any one of claims 277-304 wherein temperature is varied during the culture period.

308. The method of any one of claims 277-306 wherein pH is varied during the culture period.

309. The method of claim 305 or 306 wherein the variation is gradual.

310. The method of claim 305 or 306 wherein the variation is stepwise.

311. The method of claim 305 or 306 wherein the variation is sometimes gradual and sometimes stepwise.

312. The method of any of claims 277-311 wherein the step of cultivating comprises cultivating at an oxygen concentration within the rage of about 5-30%.

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313. The method of any of claims 277-311 wherein the step of cultivating comprises cultivating at an oxygen concentration within the rage of about 5-20%

314. The method of any of claims 277-311 wherein the step of cultivating comprises cultivating at an oxygen concentration within the rage of about 10-25%.

315. The method of any of claims 277-311 wherein the step of cultivating comprises cultivating at an oxygen concentration within the rage of about 10-30%.

316. The method of any of claims 277-311 wherein the step of cultivating comprises cultivating at an oxygen concentration within the rage of about 15-25%

317. The method of any of claims 277-311 wherein the step of cultivating comprises cultivating at an oxygen concentration within the rage of about 15-30%.

318. The method of any of claims 277-311 wherein the step of cultivating comprises cultivating at an oxygen concentration of about 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, or more.

319. The method of any of claims 277-311 wherein the step of cultivating comprises cultivating at an oxygen concentration above about 20%.

320. The method of any of claims 277-292 wherein the step of cultivating comprises cultivating at about pH 5.5 and at a temperature between about 28-30 °C.

321. The method of claim 320 wherein the step of cultivating comprises cultivating at an oxygen concentration above about 20%.

322. The method of any one of claims 277-321 wherein the step of isolating comprises crystallizing the quinone derived compound.

323. The method of claim 322 wherein the step of isolating comprises collecting crystals.

324. The method of claim 323 wherein the step of collecting comprises filtering or centrifuging or both.

325. The method of any one of claims 277-324 further comprising formulating the isolated carotenoid.

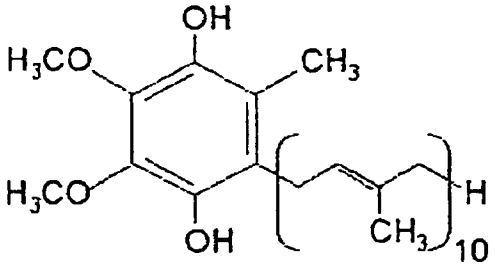
326. The method of claim 324 wherein the step of formulating comprises preparing as a cold-water dispersible powder.

327. The method of claim 326 wherein the step of formulating comprises preparing as a suspension of crystals in oil.

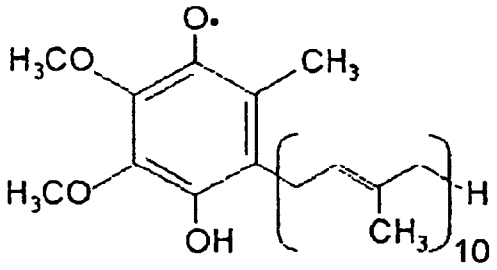
328. The method of claim 327 wherein the oil is vegetable oil.

329. The method of claim 327 or 328 wherein the step of formulating comprises preparing as a 5%-30% w/w suspension of crystals in oil.

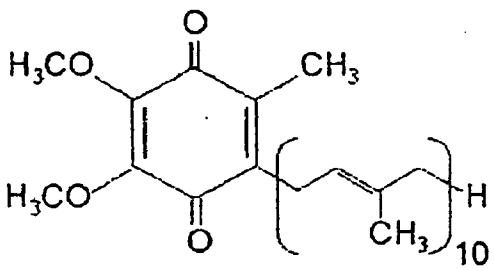
Coenzyme Q_{10}



Ubiquinol ($CoQH_2$)

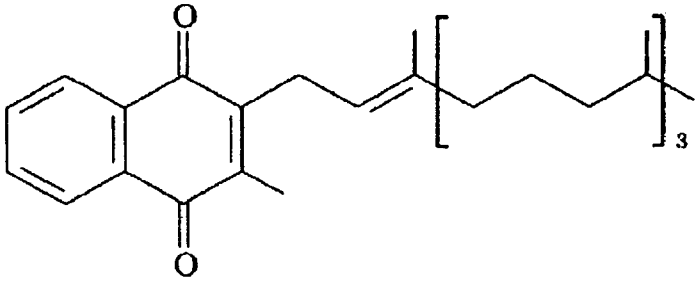


Semiquinone radical ($CoQH\cdot$)

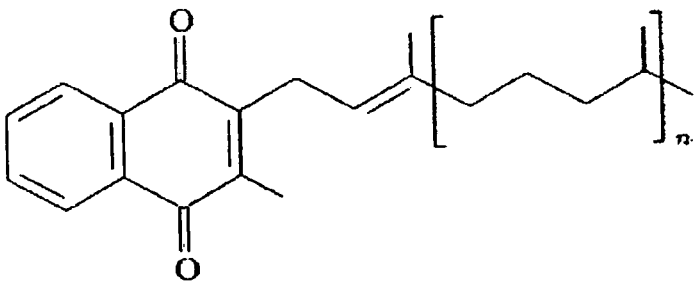


Ubiquinone (CoQ)

FIGURE 1A



PHYLLOQUINONE

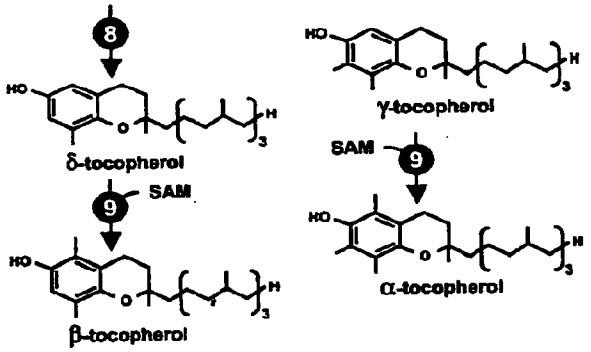


MENAQUINONE

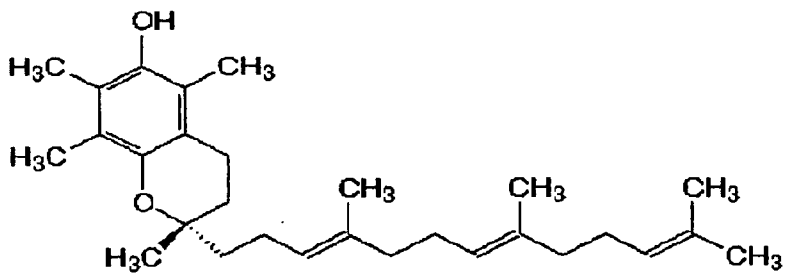
VITAMIN K

FIGURE 1B

Vitamin E - Structures and Chemistry



Tocopherols



Tocotrienol Structure

FIGURE 1C

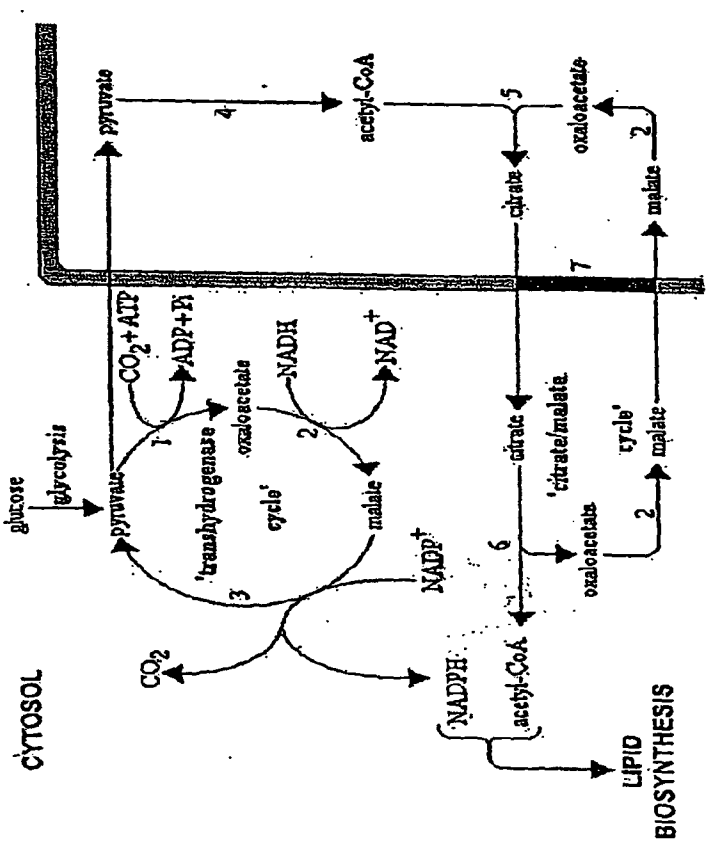

MITOCHONDRION
CYTOSOL
glucose
glycolysis
pyruvate
pyruvate
4
acetyl-CoA
5
oxaloacetate
2
citrate
malate
7
CO_2+ATP
ADP+Pi
oxaloacetate
NADH
NAD^+
1
2
'transhydrogenase
cycle'
malate
3
$NADP^+$
6
citrate
'citrate/malate
cycle'
malate
oxaloacetate
2
CO_2
NADPH
acetyl-CoA
LIPID
BIOSYNTHESIS

FIGURE 2

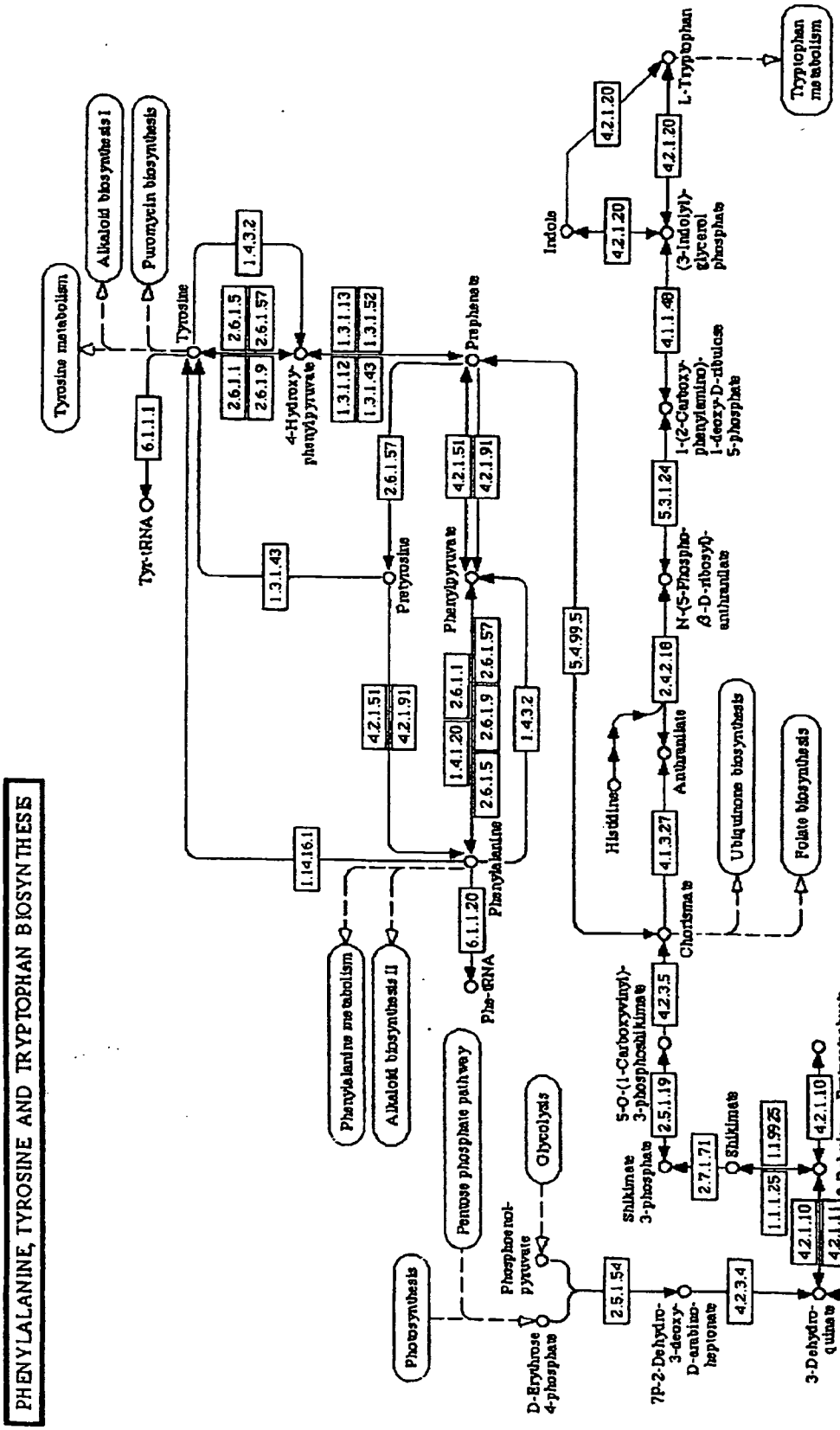

PHENYLALANINE, TYROSINE AND TRYPTOPHAN BIOSYNTHESIS
Tyrosine metabolism
Alkaloid biosynthesis I
Puromycin biosynthesis
Tyrosine
Tyr-tRNA
6.1.1.1
2.6.1.1
2.6.1.5
2.6.1.57
2.6.1.9
1.4.3.2
4-Hydroxy-phenylpyruvate
1.3.1.12
1.3.1.43
1.3.1.13
1.3.1.52
Prephenate
2.6.1.57
Prephenate
4.2.1.51
4.2.1.91
1.3.1.43
Prephenate
Phenylpyruvate
1.4.1.20
2.6.1.1
2.6.1.5
2.6.1.9
2.6.1.57
1.4.3.2
5.4.99.5
1.14.16.1
Phenylalanine
Phenylalanine metabolism
Alkaloid biosynthesis II
6.1.1.20
Phe-tRNA
Histidine
2.4.2.18
N-(5-Phospho-β-D-ribosyl)-anthranilate
5.3.1.24
1-(2-Carboxy-phenylamino)-1-deoxy-D-ribulose 5-phosphate
4.1.1.48
(3-Indolyl)-glycerol phosphate
4.2.1.20
L-Tryptophan
Tryptophan metabolism
Indole
4.2.1.20
Anthranilate
4.1.3.27
Chorismate
4.2.3.5
Ubiquinone biosynthesis
Folate biosynthesis
5-O-(1-Carboxyvinyl)-3-phosphoshikimate
2.5.1.19
Shikimate 3-phosphate
2.7.1.71
Shikimate
1.1.1.25
1.1.99.5
4.2.1.10
Protocatechuate
3-Dehydro-shikimate
4.2.1.11
3-Dehydro-quinate
1.1.1.24
1.1.99.5
Quinate
7P-2-Dehydro-3-deoxy-D-arabino-heptonate
4.2.3.4
2.5.1.54
D-Erythrose 4-phosphate
Phosphoenol-pyruvate
Glycolysis
Pentose phosphate pathway
Photosynthesis

Figure 3

FIGURE 4A

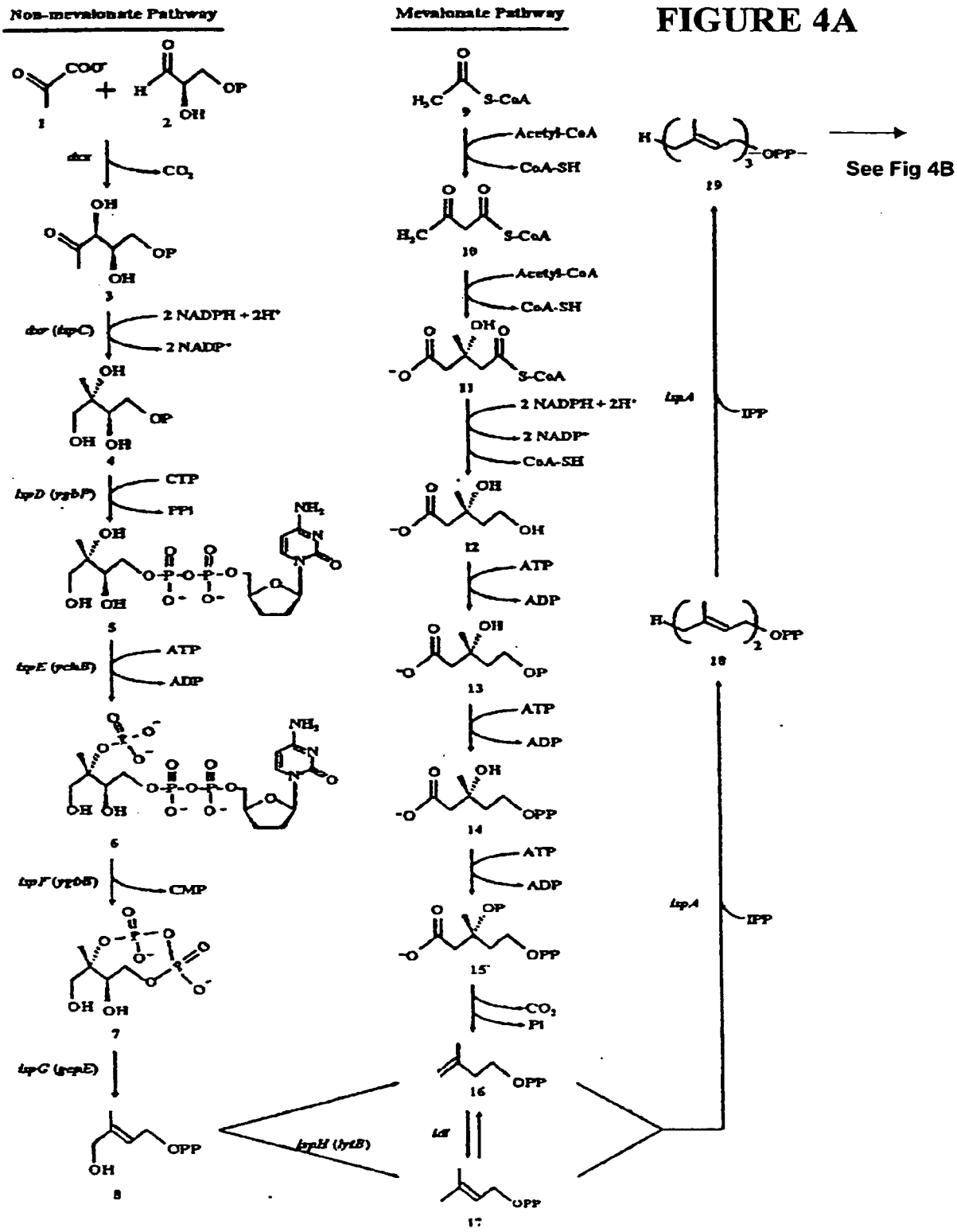

Non-mevalonate Pathway
Mevalonate Pathway
See Fig 4B
Acetyl-CoA
CoA-SH
2 NADPH + 2H+
2 NADP+
ATP
ADP
CTP
PPi
CMP
CO2
Pi
IPP
OPP
S-CoA

FIGURE 4B

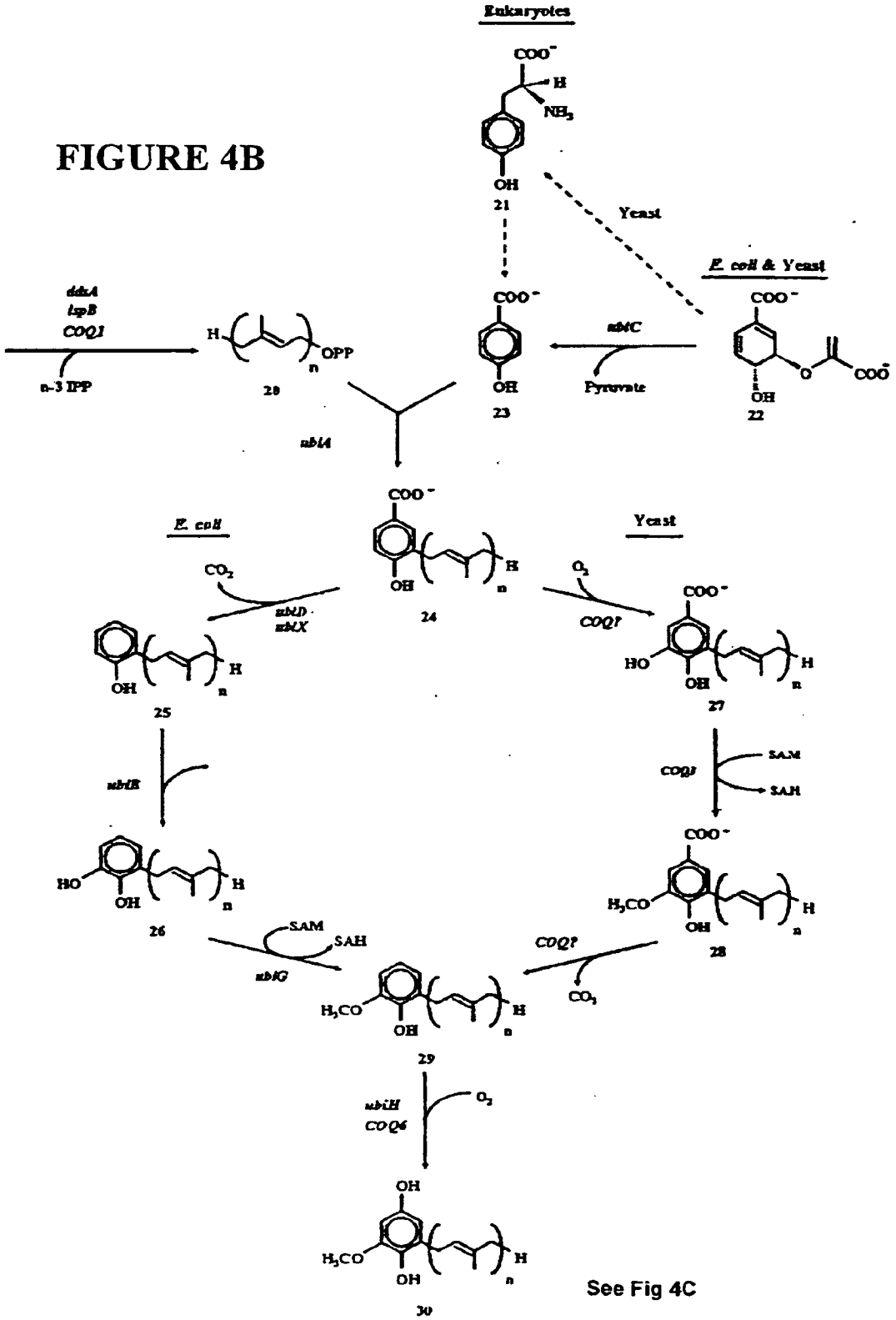
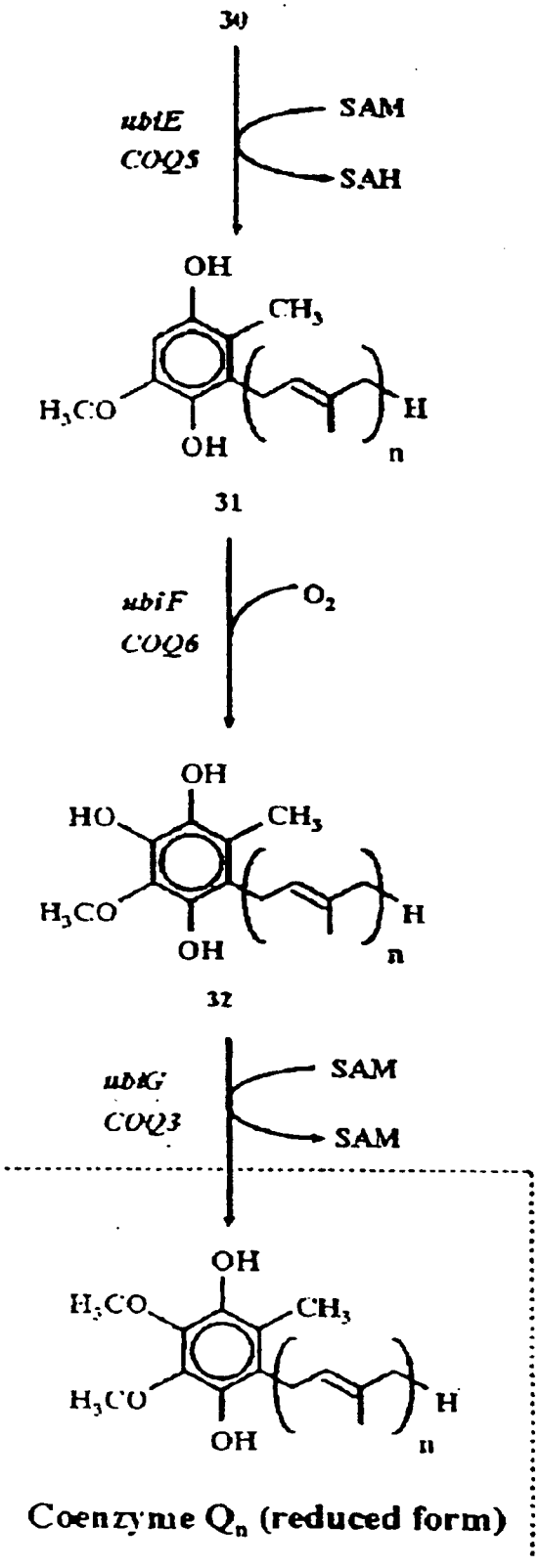

Eukaryotes
Yeast
E. coli & Yeast
ubiC
Pyruvate
ddsA
lspB
COQ1
n-3 IPP
ubiA
E. coli
Yeast
ubiD
ubiX
COQ7
ubiE
COQ3
SAM
SAH
ubiG
COQ7
CO2
ubiH
COQ6
See Fig 4C

FIGURE 4C


30
ubiE
COQ5
SAM
SAH
OH
CH3
H3CO
OH
H
n
31
ubiF
COQ6
O2
OH
HO
CH3
H3CO
OH
H
n
32
ubiG
COQ3
SAM
SAM
OH
H3CO
CH3
H3CO
OH
H
n
Coenzyme Qn (reduced form)

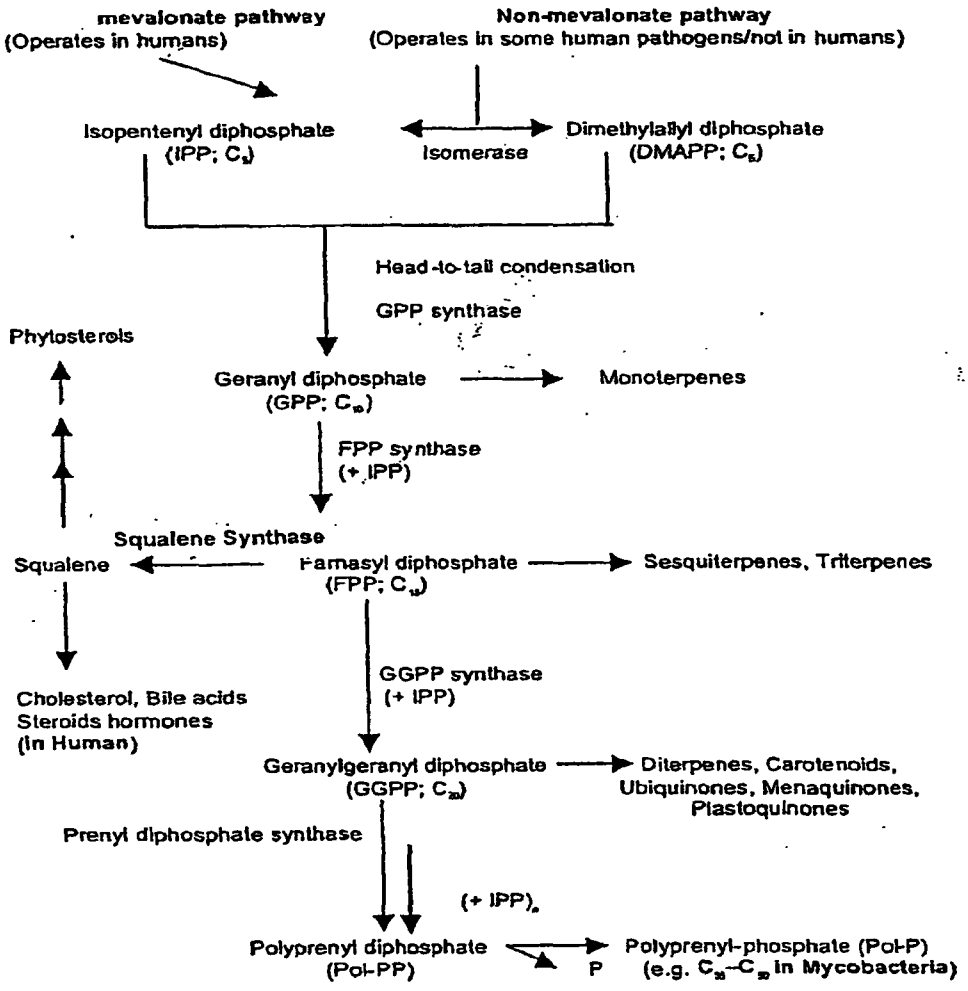

mevalonate pathway
(Operates in humans)
Non-mevalonate pathway
(Operates in some human pathogens/not in humans)
Isopentenyl diphosphate
(IPP; C5)
Isomerase
Dimethylallyl diphosphate
(DMAPP; C5)
Head-to-tail condensation
GPP synthase
Phytosterols
Geranyl diphosphate
(GPP; C10)
Monoterpenes
FPP synthase
(+ IPP)
Squalene Synthase
Squalene
Farnasyl diphosphate
(FPP; C15)
Sesquiterpenes, Triterpenes
GGPP synthase
(+ IPP)
Cholesterol, Bile acids
Steroids hormones
(in Human)
Geranylgeranyl diphosphate
(GGPP; C20)
Diterpenes, Carotenoids,
Ubiquinones, Menaquinones,
Plastoquinones
Prenyl diphosphate synthase
(+ IPP)n
Polyprenyl diphosphate
(Pol-PP)
P
Polyprenyl-phosphate (Pol-P)
(e.g. C35–C55 in Mycobacteria)

FIGURE 5

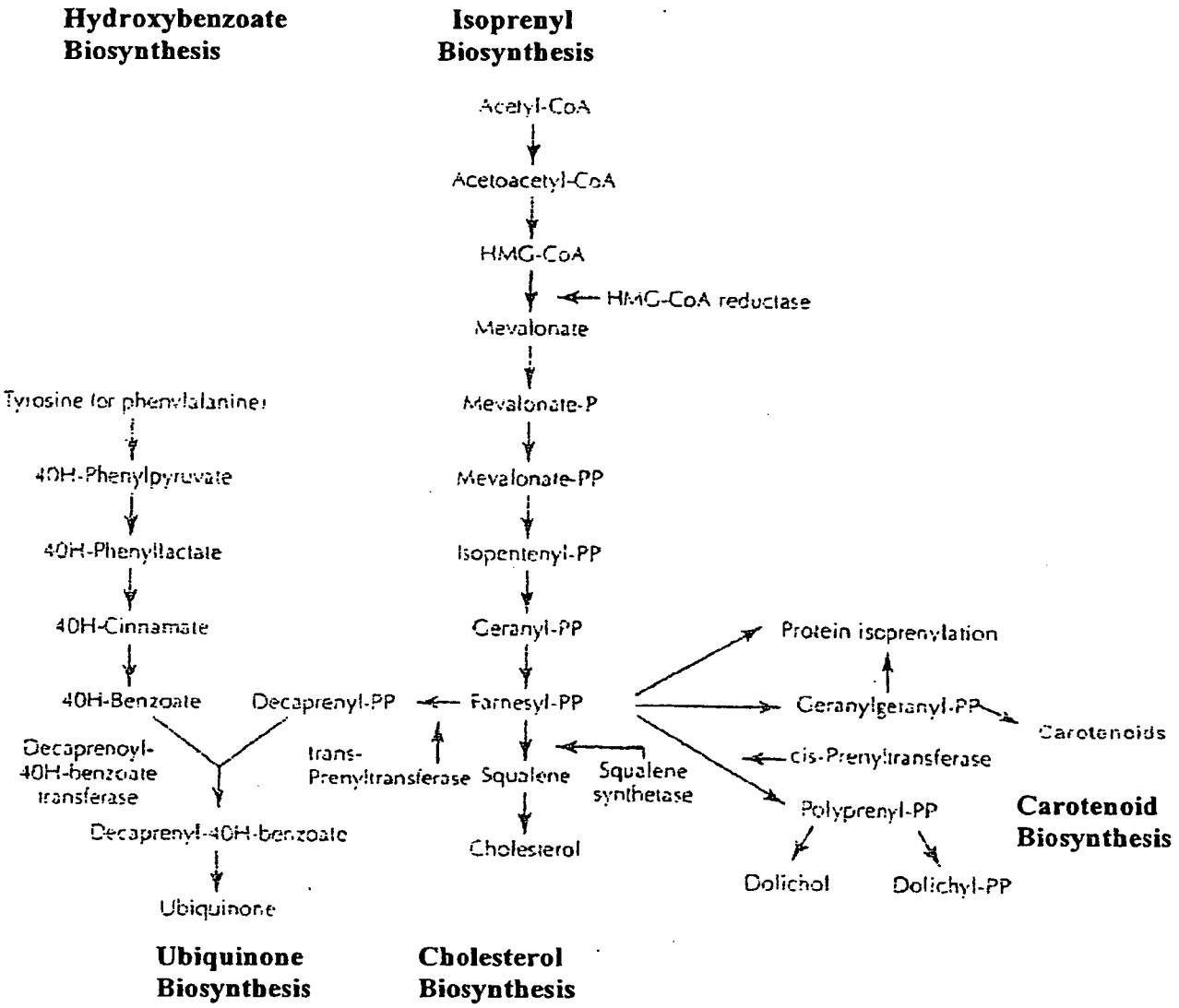

Hydroxybenzoate Biosynthesis
Isoprenyl Biosynthesis
Acetyl-CoA
Acetoacetyl-CoA
HMG-CoA
HMG-CoA reductase
Mevalonate
Tyrosine (or phenylalanine)
Mevalonate-P
40H-Phenylpyruvate
Mevalonate-PP
40H-Phenyllactate
Isopentenyl-PP
40H-Cinnamate
Geranyl-PP
Protein isoprenylation
40H-Benzoate
Decaprenyl-PP
Farnesyl-PP
Geranylgeranyl-PP
Carotenoids
Decaprenoyl-40H-benzoate transferase
trans-Prenyltransferase
Squalene
Squalene synthetase
cis-Prenyltransferase
Polyprenyl-PP
Carotenoid Biosynthesis
Decaprenyl-40H-benzoate
Cholesterol
Dolichol
Dolichyl-PP
Ubiquinone
Ubiquinone Biosynthesis
Cholesterol Biosynthesis

FIGURE 6

FIGURE 7A

Alignment of representative fungal HMG-CoA reductase polypetides.



FIGURE 7B

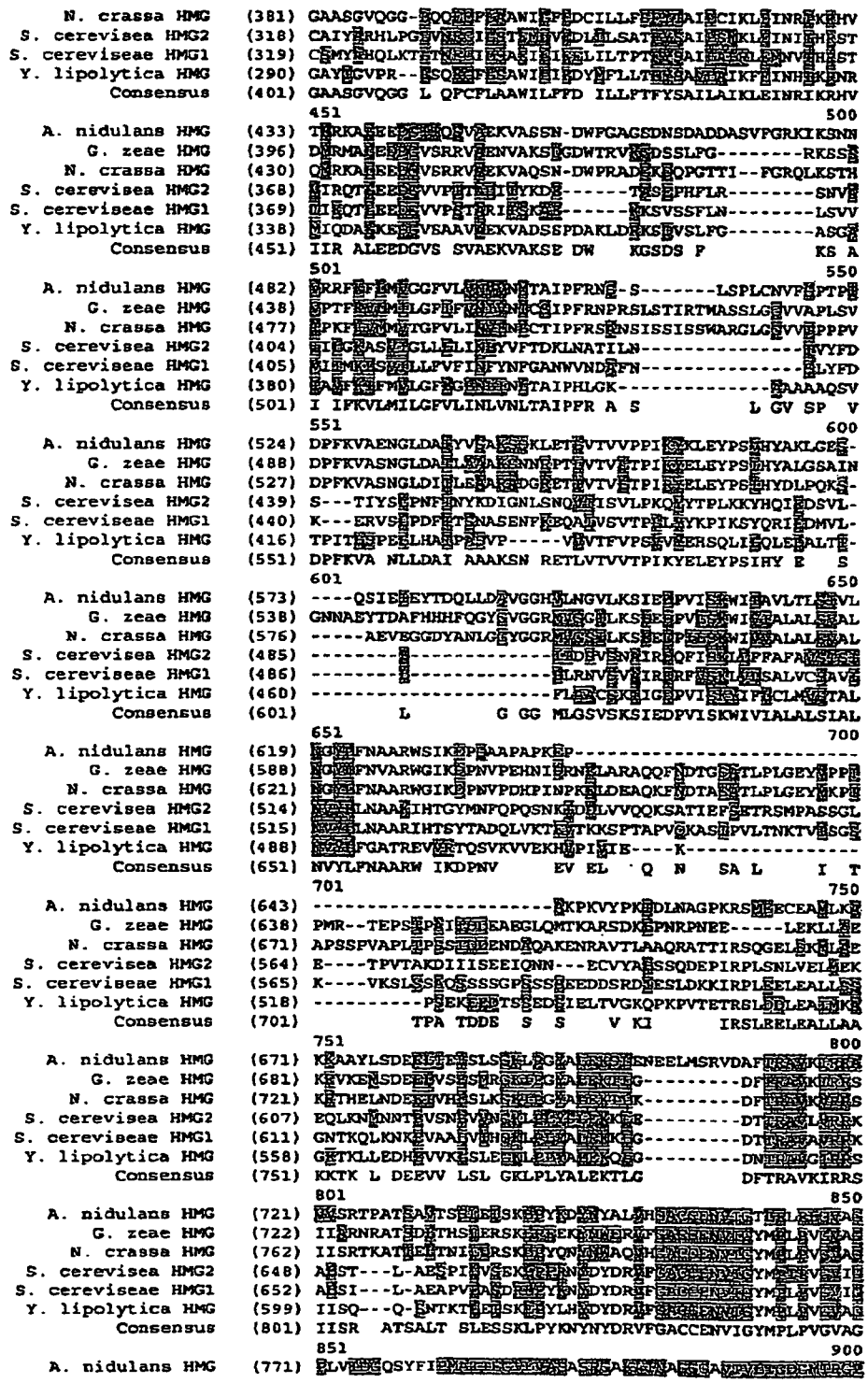

N. crassa HMG (381)
S. cerevisea HMG2 (318)
S. cereviseae HMG1 (319)
Y. lipolytica HMG (290)
Consensus (401)
451
500
A. nidulans HMG (433)
G. zeae HMG (396)
N. crassa HMG (430)
S. cerevisea HMG2 (368)
S. cereviseae HMG1 (369)
Y. lipolytica HMG (338)
Consensus (451)
501
550
A. nidulans HMG (482)
G. zeae HMG (438)
N. crassa HMG (477)
S. cerevisea HMG2 (404)
S. cereviseae HMG1 (405)
Y. lipolytica HMG (380)
Consensus (501)
551
600
A. nidulans HMG (524)
G. zeae HMG (488)
N. crassa HMG (527)
S. cerevisea HMG2 (439)
S. cereviseae HMG1 (440)
Y. lipolytica HMG (416)
Consensus (551)
601
650
A. nidulans HMG (573)
G. zeae HMG (538)
N. crassa HMG (576)
S. cerevisea HMG2 (485)
S. cereviseae HMG1 (486)
Y. lipolytica HMG (460)
Consensus (601)
651
700
A. nidulans HMG (619)
G. zeae HMG (588)
N. crassa HMG (621)
S. cerevisea HMG2 (514)
S. cereviseae HMG1 (515)
Y. lipolytica HMG (488)
Consensus (651)
701
750
A. nidulans HMG (643)
G. zeae HMG (638)
N. crassa HMG (671)
S. cerevisea HMG2 (564)
S. cereviseae HMG1 (565)
Y. lipolytica HMG (518)
Consensus (701)
751
800
A. nidulans HMG (671)
G. zeae HMG (681)
N. crassa HMG (721)
S. cerevisea HMG2 (607)
S. cereviseae HMG1 (611)
Y. lipolytica HMG (558)
Consensus (751)
801
850
A. nidulans HMG (721)
G. zeae HMG (722)
N. crassa HMG (762)
S. cerevisea HMG2 (648)
S. cereviseae HMG1 (652)
Y. lipolytica HMG (599)
Consensus (801)
851
900
A. nidulans HMG (771)

FIGURE 7C

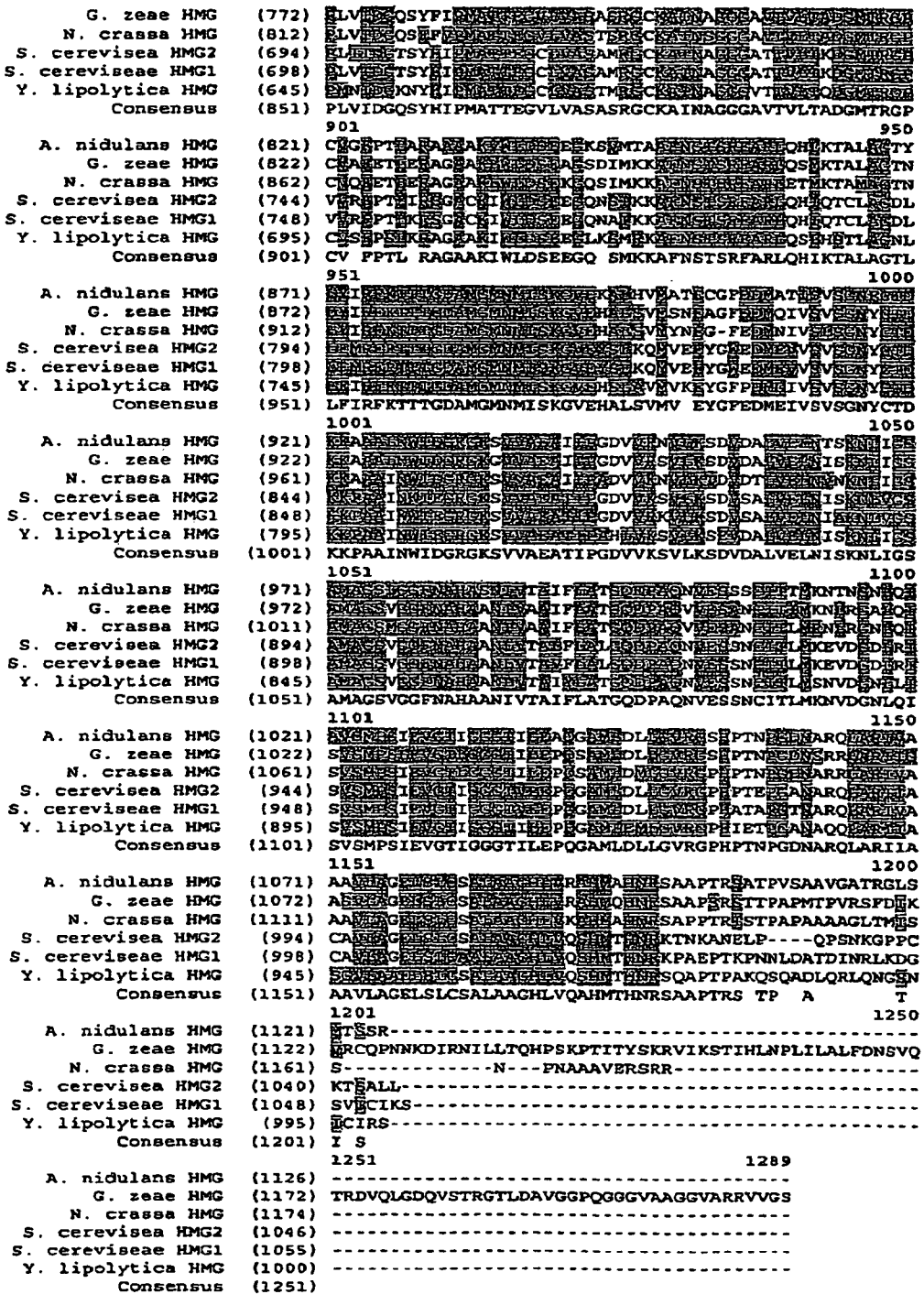
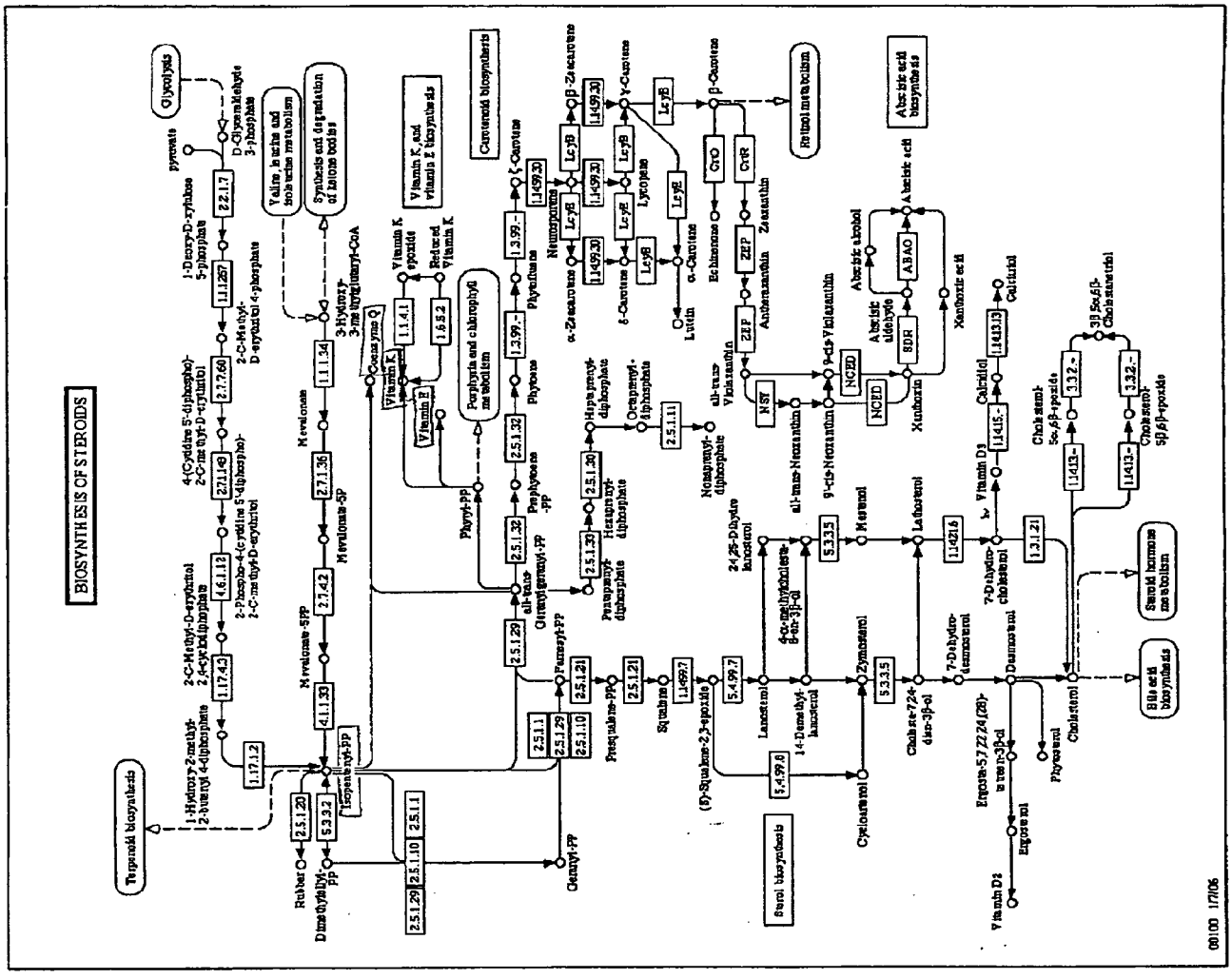

G. zeae HMG (772)
N. crassa HMG (812)
S. cerevisea HMG2 (694)
S. cereviseae HMG1 (698)
Y. lipolytica HMG (645)
Consensus (851) PLVIDGQSYHIPMATTEGVLVASASRGCKAINAGGGAVTVLTADGMTRGP
901 950
A. nidulans HMG (821)
G. zeae HMG (822)
N. crassa HMG (862)
S. cerevisea HMG2 (744)
S. cereviseae HMG1 (748)
Y. lipolytica HMG (695)
Consensus (901) CV FPTL RAGAAKIWLDSEEGQ SMKKAFNSTSRFARLQHIKTALAGTL
951 1000
A. nidulans HMG (871)
G. zeae HMG (872)
N. crassa HMG (912)
S. cerevisea HMG2 (794)
S. cereviseae HMG1 (798)
Y. lipolytica HMG (745)
Consensus (951) LFIRFKTTTGDAMGMNMISKGVEHALSVMV EYGFEDMEIVSVSGNYCTD
1001 1050
A. nidulans HMG (921)
G. zeae HMG (922)
N. crassa HMG (961)
S. cerevisea HMG2 (844)
S. cereviseae HMG1 (848)
Y. lipolytica HMG (795)
Consensus (1001) KKPAAINWIDGRGKSVVAEATIPGDVVKSVLKSDVDALVELNISKNLIGS
1051 1100
A. nidulans HMG (971)
G. zeae HMG (972)
N. crassa HMG (1011)
S. cerevisea HMG2 (894)
S. cereviseae HMG1 (898)
Y. lipolytica HMG (845)
Consensus (1051) AMAGSVGGFNAHAANIVTAIFLATGQDPAQNVESSNCITLMKNVDGNLQI
1101 1150
A. nidulans HMG (1021)
G. zeae HMG (1022)
N. crassa HMG (1061)
S. cerevisea HMG2 (944)
S. cereviseae HMG1 (948)
Y. lipolytica HMG (895)
Consensus (1101) SVSMPSIEVGTIGGGTILEPQGAMLDLLGVRGPHPTNPGDNARQLARIIA
1151 1200
A. nidulans HMG (1071)
G. zeae HMG (1072)
N. crassa HMG (1111)
S. cerevisea HMG2 (994) CA----GPGSGSNNGTMQFTNTMNKTNKANELP----QPSNKGPPC
S. cereviseae HMG1 (998) CA----GPGSGSNNGTMQFTNTMNKPAEPTKPNNLDATDINRLKDG
Y. lipolytica HMG (945)
Consensus (1151) AAVLAGELSLCSALAAGHLVQAHMTHNRSAAPTRS TP A T
1201 1250
A. nidulans HMG (1121)
G. zeae HMG (1122)
N. crassa HMG (1161) S----------N---PNAAAVERSRR----------
S. cerevisea HMG2 (1040) KT-ALL----------
S. cereviseae HMG1 (1048) SV-CIKS----------
Y. lipolytica HMG (995) -CIRS----------
Consensus (1201) I S
1251 1289
A. nidulans HMG (1126) ----------
G. zeae HMG (1172) TRDVQLGDQVSTRGTLDAVGGPQGGGVAAGGVARRVVGS
N. crassa HMG (1174) ----------
S. cerevisea HMG2 (1046) ----------
S. cereviseae HMG1 (1055) ----------
Y. lipolytica HMG (1000) ----------
Consensus (1251)

FIG 8


BIOSYNTHESIS OF STEROIDS
Terpenoid biosynthesis
Glycolysis
pyruvate
Valine, leucine and isoleucine metabolism
Synthesis and degradation of ketone bodies
Vitamin K and vitamin E biosynthesis
Carotenoid biosynthesis
Porphyrin and chlorophyll metabolism
Retinol metabolism
Abietic acid biosynthesis
Bile acid biosynthesis
Steroid hormone metabolism
Steroid biosynthesis
Mevalonate pathway
Isopentenyl-PP
Dimethylallyl-PP
Geranyl-PP
Farnesyl-PP
Squalene
Lanosterol
Cholesterol
Desmosterol
Lathosterol
7-Dehydrocholesterol
Zymosterol
Cholestanol
Phytoene
Phytofluene
Neurosporene
Lycopene
Lutein
Zeaxanthin
Violaxanthin
Neoxanthin
Xanthoxin
Abscisic acid
Abscisic aldehyde
Abscisic alcohol
Calcitriol
Calcidiol
Vitamin D3
Vitamin D2
Ergosterol
Phytosterol
Campesterol
Brassicasterol
Dehydroergosterol
Ergosta-5,7,22,24(28)-tetraen-3β-ol
Cholesta-7,24-dien-3β-ol
Cholesta-5,7,24-trien-3β-ol
(3S,5S,6R)-3,5,6-Trihydroxycholestan-7-one
(3S,5R,6S)-3,5,6-Trihydroxycholestan-7-one
5α,6α-epoxide
5β,6β-epoxide
00100 1/7/06

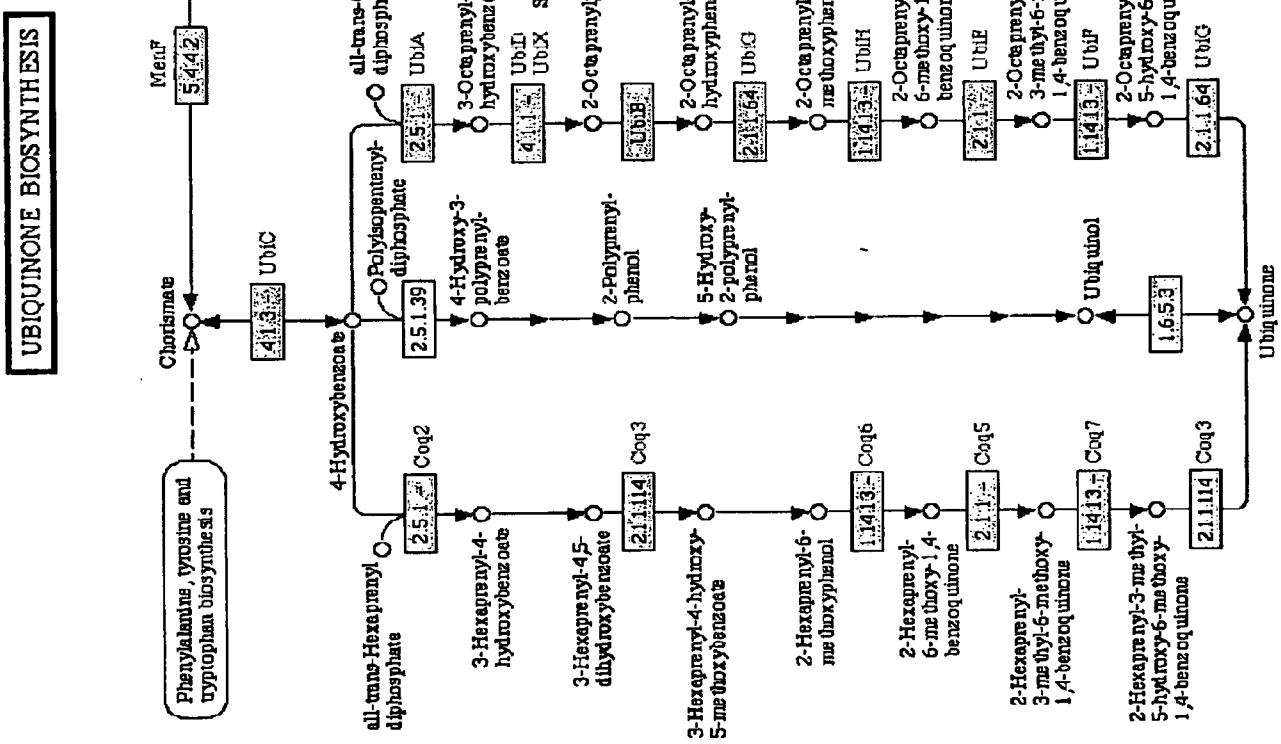
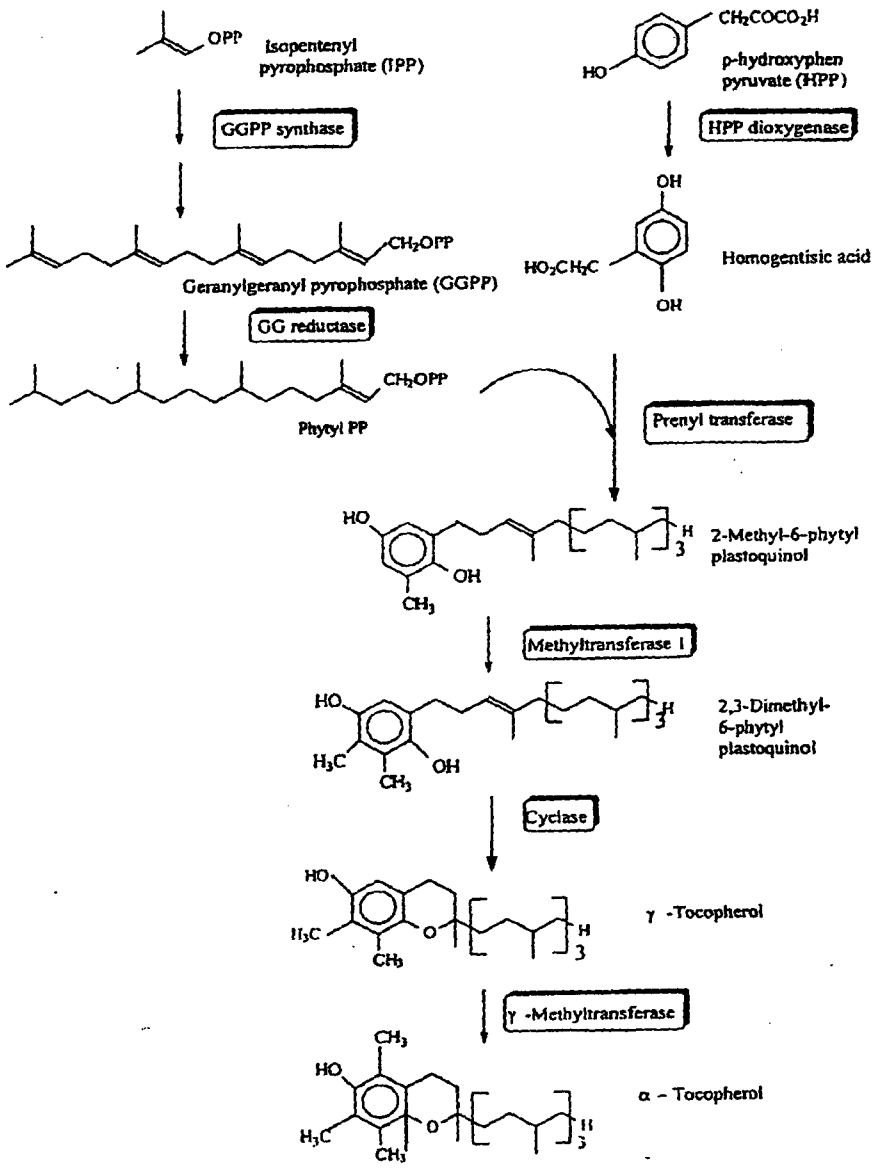

UBIQUINONE BIOSYNTHESIS
Chorismate
MenF
5.4.4.2
Isochorismate
MenD
2.5.1.64
2-Succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate
MenC
4.2.1.-
2-Succinyl-benzoate
MenE
6.2.1.26
2-Succinyl-benzoyl-CoA
MenB
4.1.3.36
1,4-Dihydroxy-2-naphthoyl-CoA
3.1.2.-
1,4-Dihydroxy-2-naphthoate
MenA
2.5.1.-
2-Phytyl-1,4-naphthoquinone
2-Demethyl-menaquinone
UbiE MenG
2.1.1.-
Menaquinone
Phylloquinone
Spirodilactone
UbiC
4.1.3.-
4-Hydroxybenzoate
all-trans-Octaprenyl-diphosphate
UbiA
2.5.1.-
3-Octaprenyl-4-hydroxybenzoate
UbiD UbiX
4.1.1.-
2-Octaprenylphenol
UbiB
2-Octaprenyl-6-hydroxyphenol
UbiG
2.1.1.64
2-Octaprenyl-6-methoxyphenol
UbiH
1.14.13.-
2-Octaprenyl-6-methoxy-1,4-benzoquinone
UbiF
2.1.1.-
2-Octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone
UbiF
1.14.13.-
2-Octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone
UbiG
2.1.1.64
Ubiquinone
Ubiquinol
1.6.5.3
Polyisopentenyl-diphosphate
2.5.1.39
4-Hydroxy-3-polyprenyl-benzoate
2-Polyprenyl-phenol
5-Hydroxy-2-polyprenyl-phenol
Phenylalanine, tyrosine and tryptophan biosynthesis
all-trans-Hexaprenyl diphosphate
Coq2
2.5.1.-
3-Hexaprenyl-4-hydroxybenzoate
Coq3
2.1.1.114
3-Hexaprenyl-4,5-dihydroxybenzoate
3-Hexaprenyl-4-hydroxy-5-methoxybenzoate
2-Hexaprenyl-6-methoxyphenol
Coq6
1.14.13.-
2-Hexaprenyl-6-methoxy-1,4-benzoquinone
Coq5
2.1.1.-
2-Hexaprenyl-3-methyl-6-methoxy-1,4-benzoquinone
Coq7
1.14.13.-
2-Hexaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone
Coq3
2.1.1.114

FIG 10A

PM Bramley et al



Qhvsf 3/ Qbu x bz pgupdpqi f spm
gpsn bujpo HHQQ t zou bt f ;
hf sbozdnf sbozmqzspqi pt qbi bd
t zou bt f - l QQ ejpyzhf obt f ;
p.l zespyzqi f ozmqzsvvbd
ejpyzhf obt f - HH sf evdbt f ;
hf sbozdnf sbozmsf evdbt f - qi zuzmQQ;
qi zuzmqzspqi pt qi bd /

Stage 1. Formation of the homogentisic acid head group
The head group for both tocopherols and plastoquinones, homogentisic acid (HGA), is produced from *p*-hydroxyphenylpyruvic acid (HPP) by the enzyme *p*-hydroxyphenylpyruvic acid dioxygenase (HPPDase). This is a complex enzymic reaction that catalyses the addition of two oxygen atoms, a decarboxylation and rearrangement of the side chain of HPP. It is an irreversible reaction and is the committed step to head group synthesis for all plastid-located quinone compounds.

Stage 2. Addition of a hydrophobic tail to generate 2-methyl-6-phytylplastoquinol
HGA is subject to a prenylation (C20) reaction, coupled to a presumably simultaneous decarboxylation to form the first true tocopherol intermediate, 2-methyl-6-phytylplastoquinol. This step of the pathway is the branch point for commitment to either tocopherols/tocotrienols or plastoquinones (C45 isoprenoid side chain) and is a potential key regulatory step. Geranylgeranyl reductase, the enzyme responsible for the step-wise reduction of geranylgeranyl pyrophosphate (GGPP) to phytyl pyrophosphate (phytyl-PP), has been recently purified from *Arabidopsis* and its cDNA cloned.[52] This enzyme, which is plastid-located, is responsible for the side-chains of the tocopherol, chlorophyll and phylloquinone pathways. The availability of various substrates (GGPP, phytol, solanyl pyrophosphate) and the activity of the en-

FIG 10B

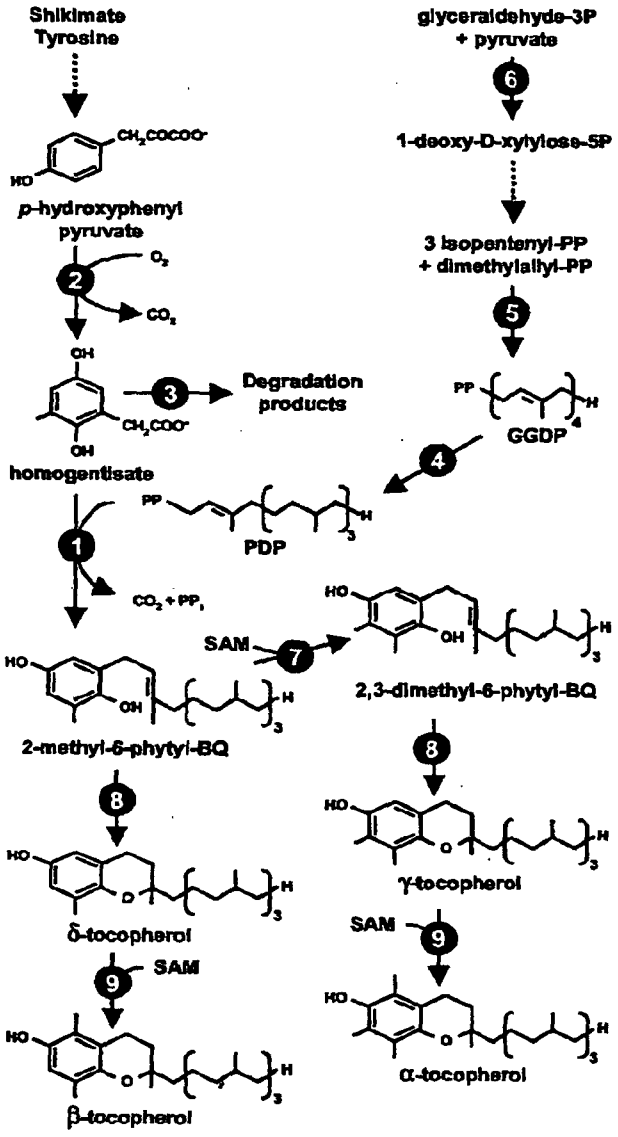


Figure 1. The tocopherol biosynthetic pathway in plants. Dashed arrows represent multiple steps. Enzymes are indicated by circled numbers: 1, HGA phytyltransferase (HPT); 2, *p*-hydroxyphenyl pyruvate dioxygenase (HPPD); 3, HGA dioxygenase; 4, geranylgeranyl diphosphate reductase (GGDR); 5, geranylgeranyl diphosphate synthase (GGPS); 6, 1-deoxy-D-xylulose-5-phosphate synthase (DXPS); 7, 2-methyl-6-phytyl-1,4-benzoquinol methyltransferase (MPBQ); 8, tocopherol cyclase (TC); and 9, γ-tocopherol methyltransferase (γ-TMT).

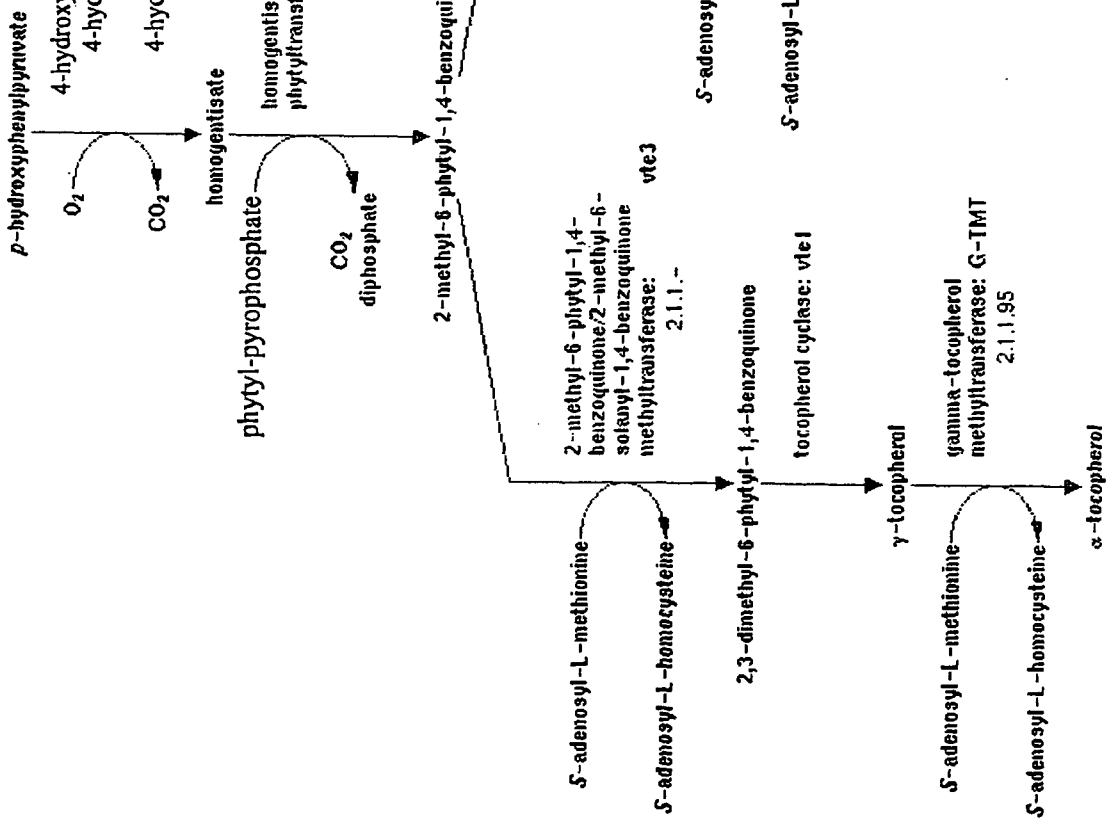
the first prenylquinol intermediate in the pathway and can be methylated to 2,3-dimethyl-6-phytyl-1,4-benzoquinol (DMPBQ) by MPBQ methyltransferase (MPBQ MT; Soll and Schultz, 1979, 1980; Hutson and Threlfall, 1980; Marshall et al., 1985; Soll, 1987; Shintani et al., 2002). Both MPBQ and DMPBQ are substrates for TC to yield the first tocopherols of the pathway, γ-tocopherol and δ-tocopherol, respectively (Stocker et al., 1996; Arango and Heise, 1998; Porfirova et al., 2002). Both γ- and δ-tocopherol can be methylated by γ-TMT to yield α- and β-tocopherol, respectively (D'Harlingue and Camara, 1985; Shintani and DellaPenna, 1998).

Because of the importance of vitamin E in human and plant physiology, the tocopherol biosynthetic pathway has become a focus for plant metabolic engineering. To successfully manipulate the tocopherol content and/or composition of various plant tissues, enzymes with high flux coefficients must be identified in the pathway. This requires the cloning of individual tocopherol biosynthetic enzymes and a detailed understanding of the molecular and biochemical regulation of individual steps of the pathway. In recent years, several genes encoding enzymes directly or indirectly involved in tocopherol biosynthesis have been cloned and overexpressed in plants to test whether they are limiting for tocopherol synthesis in various tissues (Garcia et al., 1997, 1999; Norris et al., 1998; Shintani and DellaPenna, 1998; Collakova and DellaPenna, 2001; Estevez et al., 2001; Schledz et al., 2001; Savidge et al., 2002; Tsegaye et al., 2002).

Precursor feeding studies with safflower (*Carthamus tinctorius*) cell cultures suggested that levels of HGA, PDP, or both might be limiting for flux through the tocopherol biosynthetic pathway (Furuya et al., 1987). HPPD produces HGA from HPP and has been cloned and characterized from a variety of plants (Garcia et al., 1997, 1999; Norris et al., 1998). Overexpression of HPPD in Arabidopsis leaves and seeds resulted in a 10-fold increase in HPPD specific activity but only a 10% to 30% increase in total tocopherol levels (Tsegaye et al., 2002). This result may be attributable to enhanced degradation of HGA in transgenics or to a low flux coefficient of HPPD in the tocopherol pathway (Tsegaye et al., 2002). Plastidic phytol levels may also be limiting for tocopherol synthesis because feeding phytol to safflower cell cultures stimulated tocopherol levels to an even higher extent than HGA (Furuya et al., 1987). Other studies suggest that DXP pathway-derived isopentenyl diphosphate, which is used for the synthesis of phytol and PDP, may limit isoprenoid synthesis in Arabidopsis chloroplasts (Estevez et al., 2001). Constitutive overexpression of the first enzyme of the DXP pathway, DXP synthase (DXPS) in Arabidopsis leaves resulted in elevated levels of several plastidic isoprenoids including tocopherols, which were increased up to 2-fold relative to wild type (Estevez et al., 2001).

Arabidopsis leaves accumulate predominantly α-tocopherol, whereas the major tocopherol present in Arabidopsis seeds is γ-tocopherol (Shintani and DellaPenna, 1998). This difference was shown to be the result of low-seed γ-TMT activity because over-

Fig. 10C


p-hydroxyphenylpyruvate
4-hydroxyphenylpyruvate digoxygenase: pds-1
4-hydroxyphenylpyruvate digoxygenase: AT1G11840
4-hydroxyphenylpyruvate digoxygenase: AT1G67280
1.13.11.27
O2
CO2
homogentisate
phytyl-pyrophosphate
homogentisate phytyltransferase: HPT1
CO2
diphosphate
2-methyl-6-phytyl-1,4-benzoquinone
tocopherol cyclase: vte1
δ-tocopherol
delta-tocopherol methyltransferase: G-TMT 2.1.1.95
S-adenosyl-L-methionine
S-adenosyl-L-homocysteine
β-tocopherol
2-methyl-6-phytyl-1,4-benzoquinone/2-methyl-6-solanyl-1,4-benzoquinone methyltransferase: vte3 2.1.1.-
S-adenosyl-L-methionine
S-adenosyl-L-homocysteine
2,3-dimethyl-6-phytyl-1,4-benzoquinone
tocopherol cyclase: vte1
γ-tocopherol
gamma-tocopherol methyltransferase: G-TMT 2.1.1.95
S-adenosyl-L-methionine
S-adenosyl-L-homocysteine
α-tocopherol

11A

Figure [redacted] *Y. Lipolytica* Genes

1/3

Genbank protein GI number	Genbank protein Accession Number	polypeptide	Y. lipolytica gene	Oligo 1	Oligo 2
50557288	XP_506052	HMG-CoA synthase	YALI0F30481g	MO4890-5'ctctagacacaaaaatgtcgcaaccccagaacgt	MO4891-5'cacgcgtctactgcttgatctcgtact
50546973	XP_500956	Mevalonate Kinase	YALI0B16038g	MO4982-5'cgctagccacaaaaatggactacatcatttcggcgc	MO4983-5'cacgcgtctaatgggtccagggaccga
50552418	XP_503619	Phosphomevalonate kinase	YALI0E06193g	MO4984-5'ctctagacacaaaaatgaccacctattcggctccg	MO4985-5'cggcgcgccctacttgaacccctctcga
50555265	XP_505041	Mevalonate Pyrophosphate Decarboxylase	YALI0F05632g	MO4986-5'ctctagacacaaaaatgatccaccaggcctccacca	MO4987-5'cacgcgtctacttgctgttcttcagag
50555131	XP_504974	IPP Isomerase	YALI0F04015g	MO4988-5'ctctagacacaaaaatgacgacgtcttacagcga	MO4989-5'cacgcgtctacttgatccaccgccgaa
50552378	XP_503599	FPP synthase	YALI0E05753	MO4990-5'ctctagacacaaaaatgtccaaggcgaaattcgaa	MO4991-5'cacgcgtctacttctgtcgcttgtaaa
50553402	XP_504112	Malic Enzyme	YALI0E18634g	MO4992-5'ctctagacacaaaaatgttacgactacgaaccat	MO4993-5'cacgcgtctagtcgtaatcccgcacat

11B

Figure [redacted] *Y. Lipolytica* Genes

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50552824	XP_503822	AMP Deaminase	YALI0E11495g	MO4996- 5'cgctagccacaaaaatgccgcagcaagcaatgga	MO4997- 5'cacgcgtttaaccatgcagccgctcaa
50550873	XP_502909	Malate Dehydrogenase Homolog	YALI0D16753g	MO5000- 5'ctctagacacaaaaatgttccgaacccgagttac	MO5001- 5'cacgcgtttaagggttctgcttgacaa
50550839	XP_502892	Isocitrate Dehydrogenase	YALI0D16247g	MO5004- 5'ctctagacacaaaaatgacacaaacgcacaatct	MO5005- 5'cacgcgtttacatcttgtacgcagggt
50545147	XP_500111	Fructose 1,6 bisphosphatase	YALI0A15972g	MO5008- 5'ctctagacacaaaaatggaagccaaccccgaagt	MO5009- 5'cacgcgttcatttcagaaggtacttct
50552796	XP_503808	Acetoacetyl CoA thiolase	YALI0E11099g	MO4852- 5'ctctagacacaaaaatgcgactcactctgccc	MO4853- 5'cacgcgtctactcgacagaagagaccttc
50554757	XP_504787	ATP citrate lyase subunit 1	YALI0E34793g	MO4741- 5'ttctagacccaaaaatgtctgccaacgagaacatct c	MO4743- 5'aacgcgtctatgatcgagtcttggccttg
50551515	XP_503231	ATP citrate lyase subunit 2	YALI0D24431g	MO4760- 5'ttctagacacaaaaatgtcagcgaaatccattcacg a	MO4861- 5'cacgcgttaaactccgagaggagtgg
50553046	XP_503933	Malate Dehydrogenase	YALI0E14190g	MO4994- 5'ctctagacacaaaagtggttaaagctgtcgttgc	MO4995- 5'cacgcgtttacttggcaggaggagggt

11C

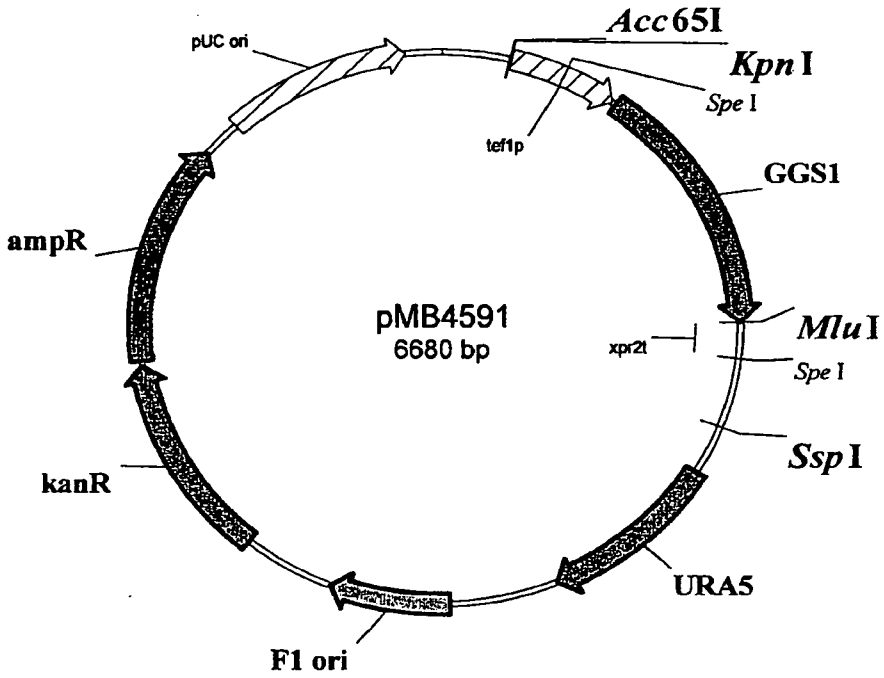
Figure [redacted] *Y. Lipolytica* Genes

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50553728	XP_504275	Glucose 6 Phosphate Dehydrogenase	YALI0E22649g	MO4998- 5'ctctagacacaaaaatgactggcaccttacccaa	MO4999- 5'cacgcgttcacgaggagcccttggtga
50546937	XP_500938	6-phosphogluconate dehydrogenase	YALI0B15598g	MO5002- 5'ctctagacacaaaaatgactgacacttcaaacat	MO5003- 5'cacgcgtttaagcatcgtaagtggaag
50550013	XP_502479	Isocitrate dehydrogenase	YALI0D06303g	MO5006- 5'ctctagacacaaaaatgctcaaccttagaaccgc	MO5007- 5'cacgcgtctacttgagtcgcttgataa

12

Figure [redacted] A. Schematic diagram of certain plasmids used herein



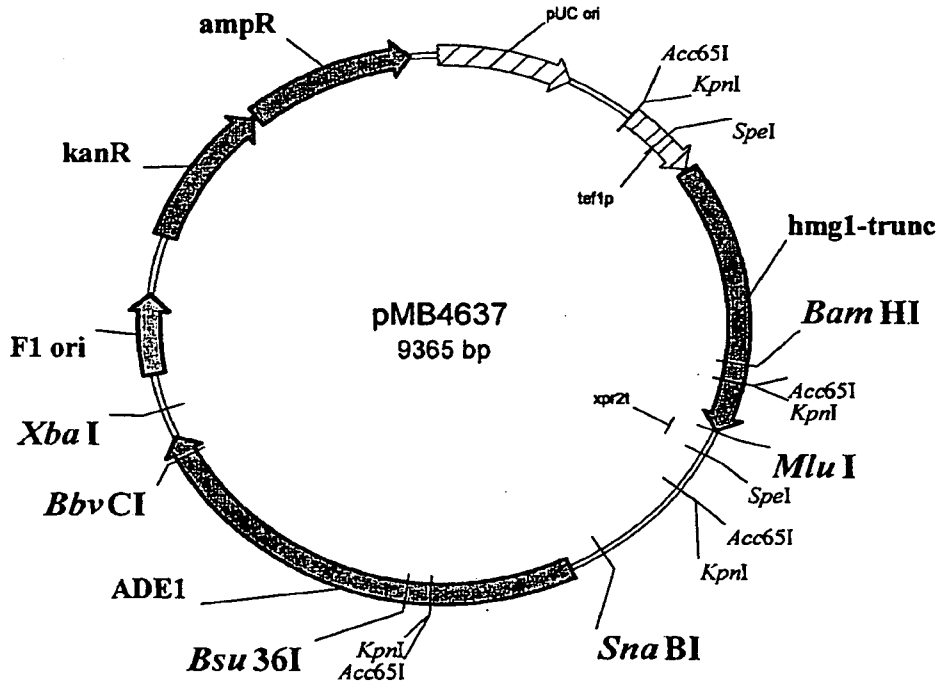
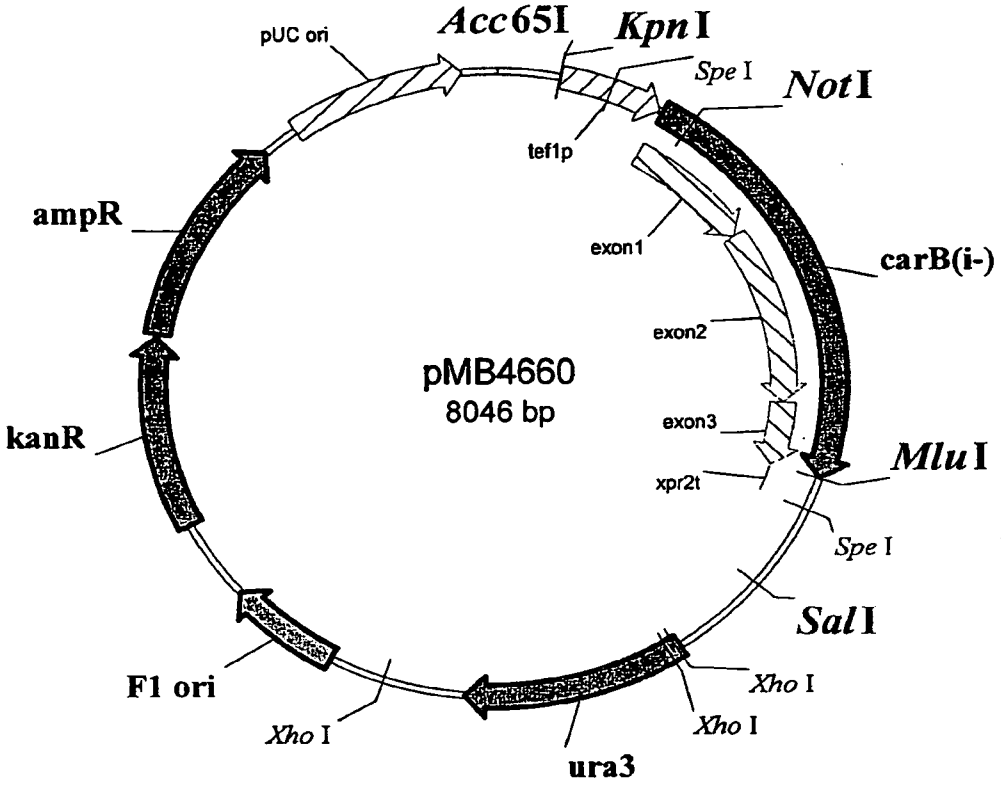
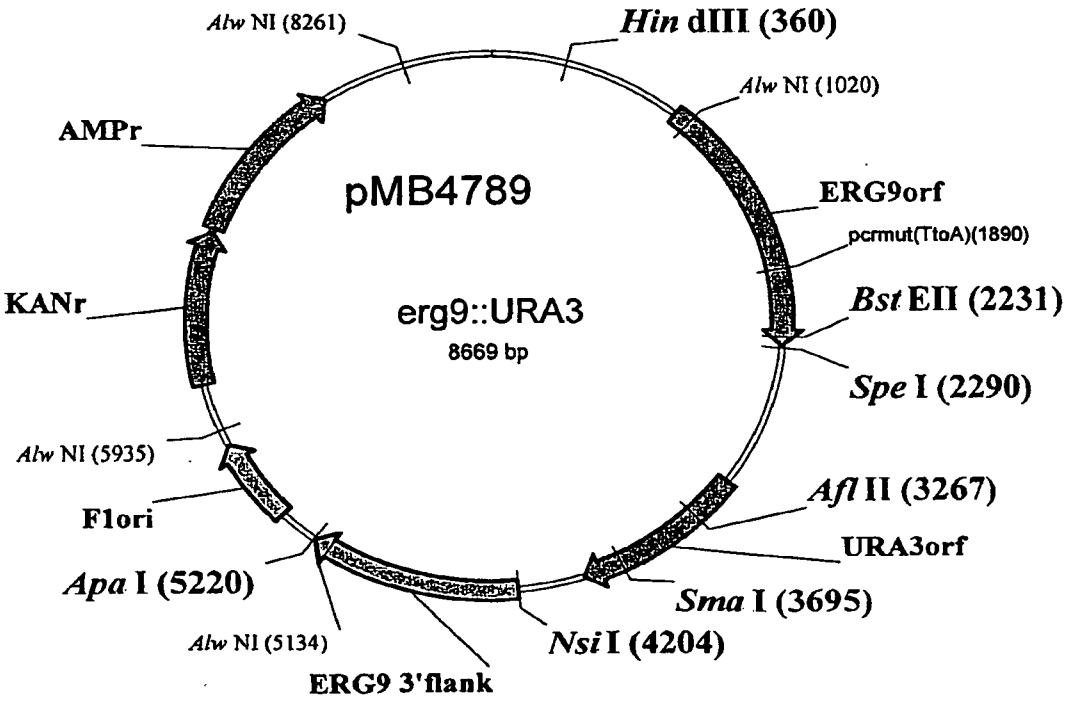


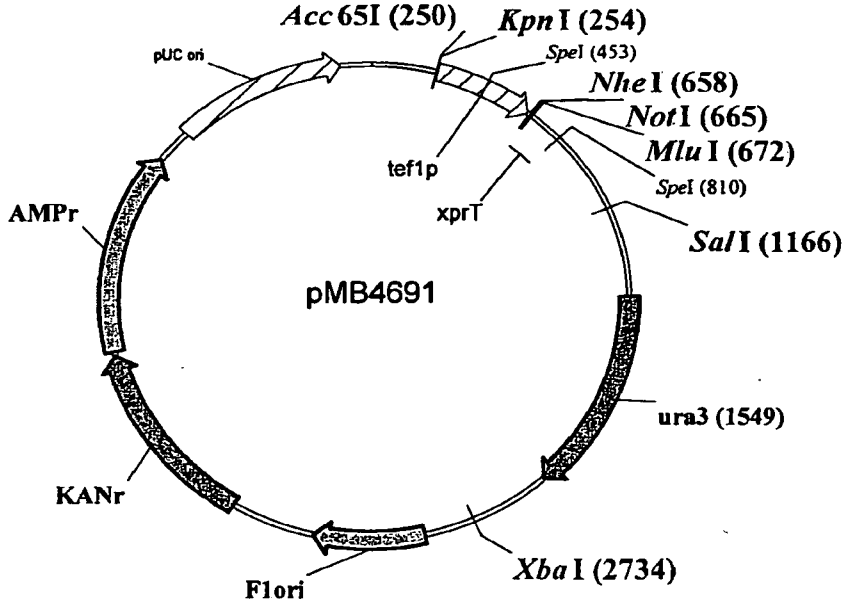
Figure 12B. Schematic diagram of certain plasmids used herein





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Figure [redacted]C. Schematic diagram of certain plasmids used herein



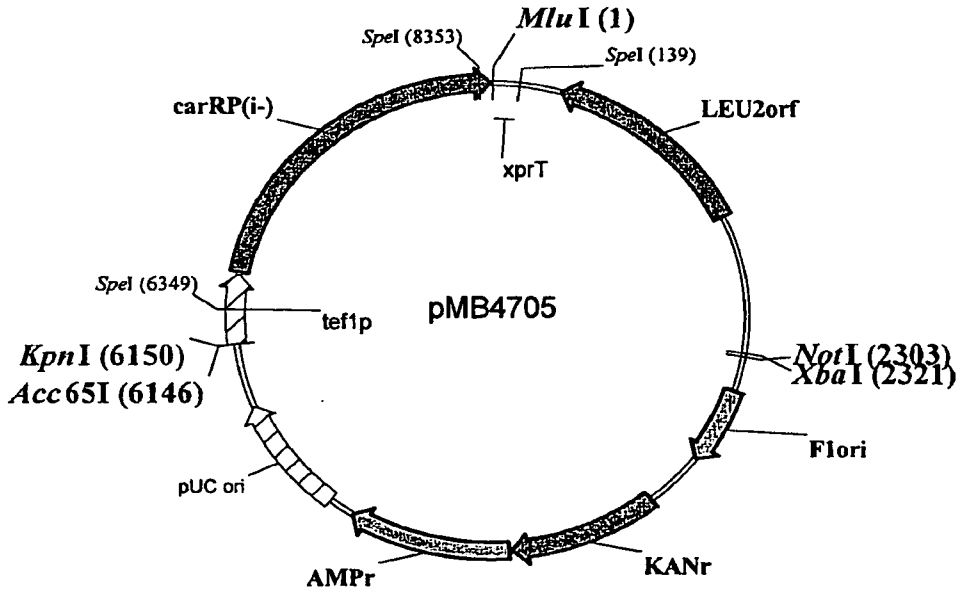


Figure 12 D

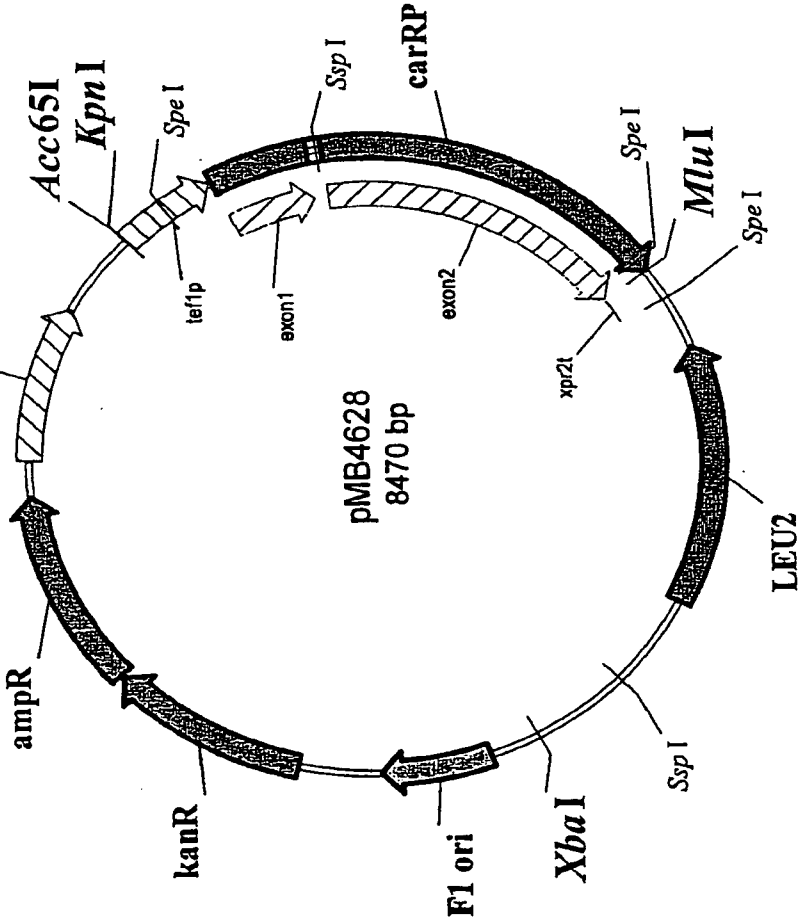

pMB4628
8470 bp
Acc65I
KpnI
Spe I
Ssp I
carRP
Spe I
MluI
Spe I
LEU2
Ssp I
XbaI
F1 ori
kanR
ampR
pUC ori
tef1p
exon1
exon2
xpr2t

Figure 12E

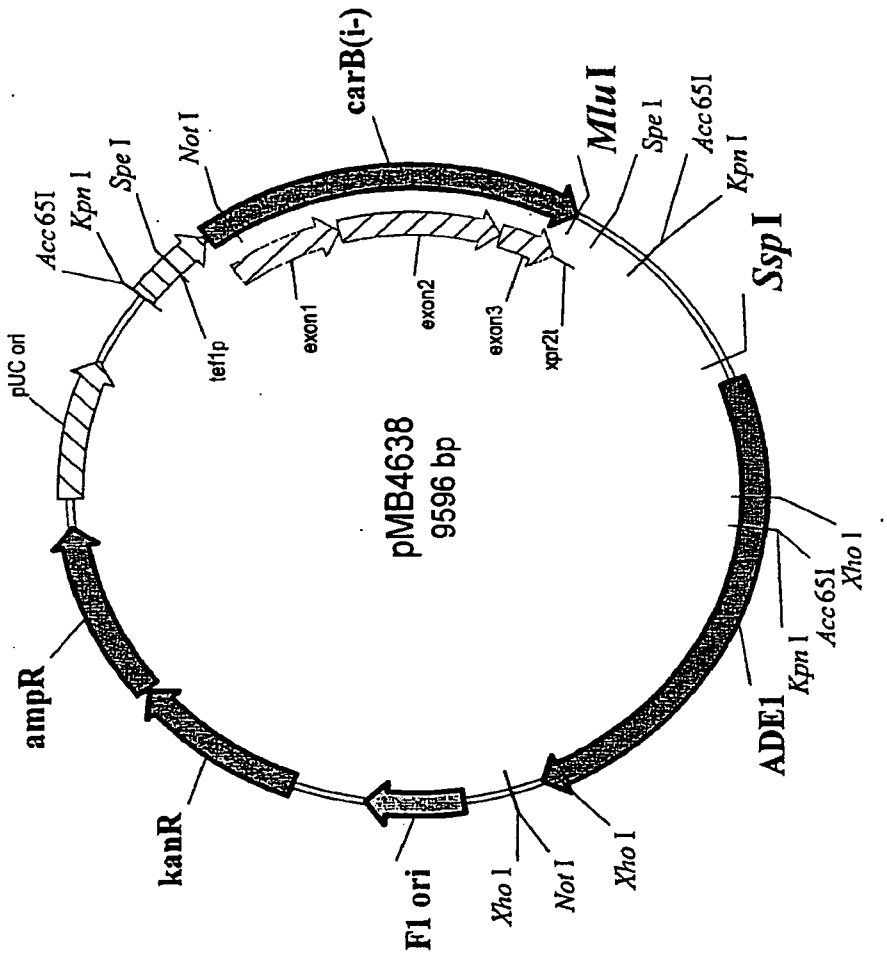

pMB4638
9596 bp
carB(i-)
MluI
Spe I
Acc65I
Kpn I
SspI
ADE1
Kpn I
Acc65I
Xho I
Xho I
Not I
Xho I
F1 ori
kanR
ampR
pUC ori
tef1p
exon1
exon2
exon3
xpr2t
Acc65I
Kpn I
Spe I
Not I

Figure 12F

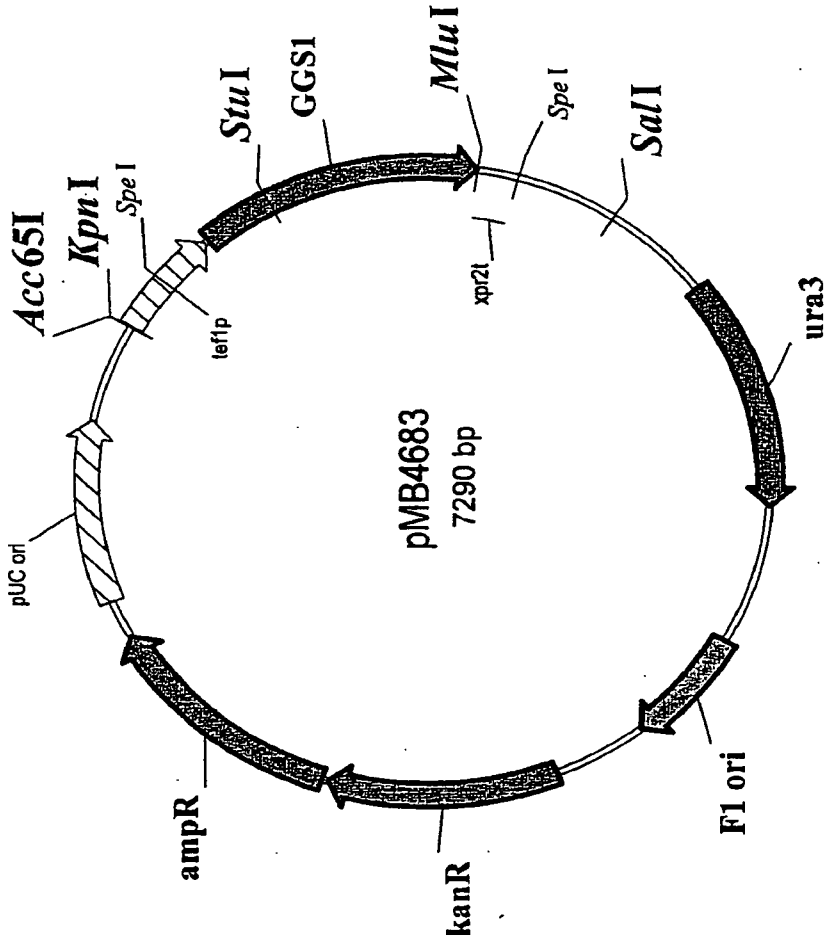

pMB4683
7290 bp
Acc65I
KpnI
Spe I
StuI
GGS1
MluI
Spe I
SalI
ura3
F1 ori
kanR
ampR
pUC ori
tef1p
xpr2t

Figure 12G

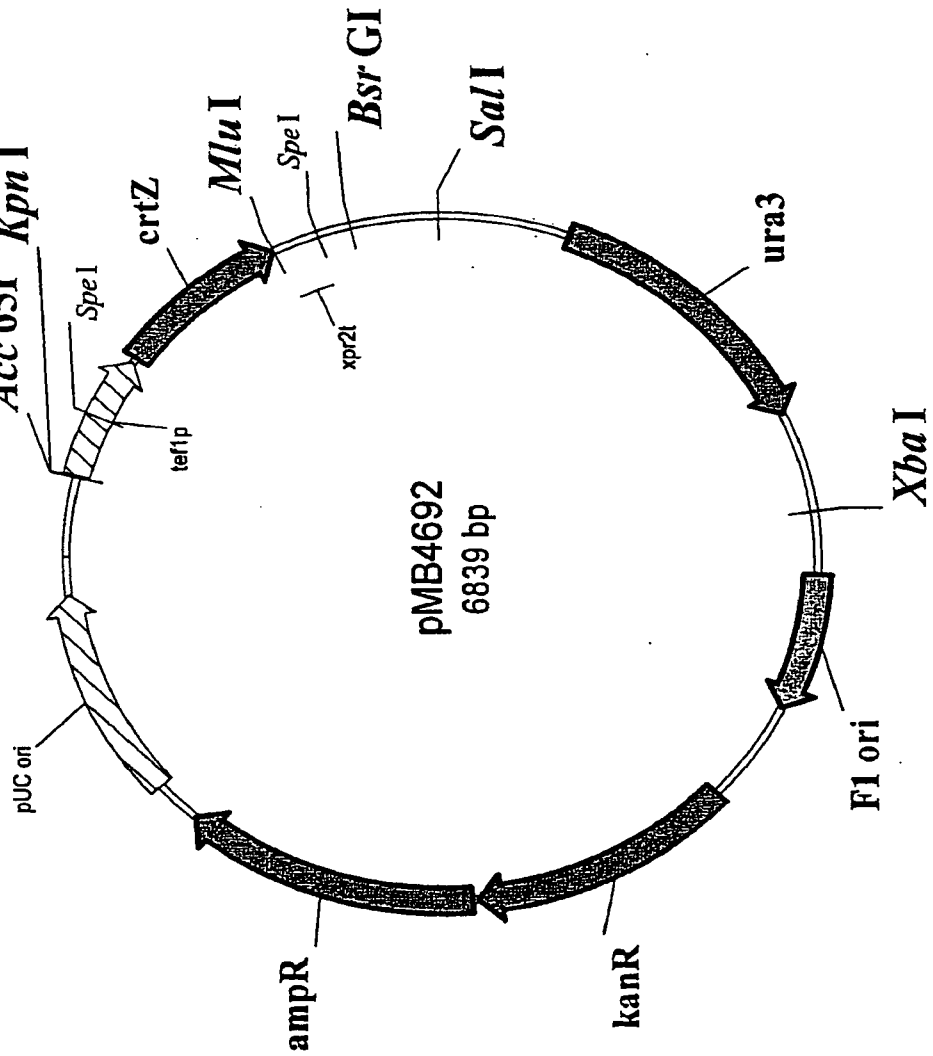

Acc 65I
Kpn I
Spe I
tef1p
crtZ
Mlu I
Spe I
Bsr GI
xpr2t
Sal I
ura3
Xba I
F1 ori
kanR
ampR
pUC ori
pMB4692
6839 bp

Figure 12H

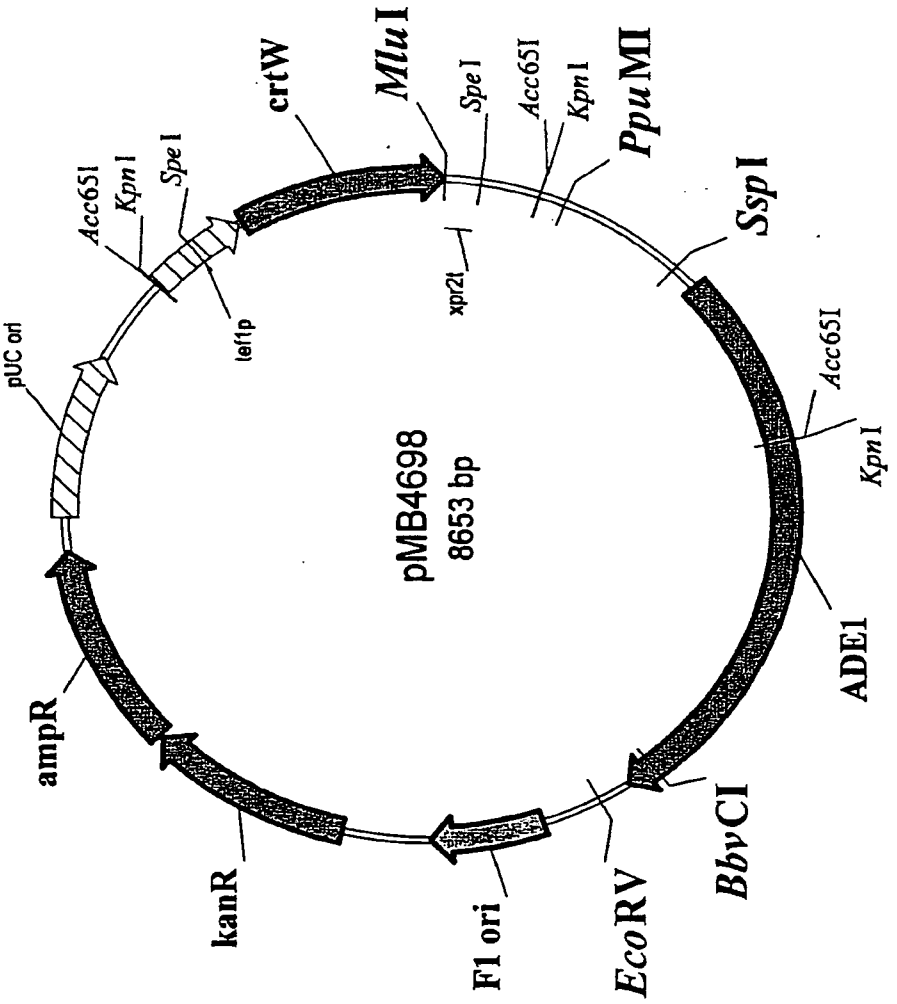

pMB4698
8653 bp
crtW
MluI
SpeI
Acc65I
KpnI
PpuMI
SspI
Acc65I
KpnI
ADE1
BbvCI
EcoRV
F1 ori
kanR
ampR
pUC ori
Acc65I
KpnI
SpeI
lef1p
xpr2t

Figure 12 I

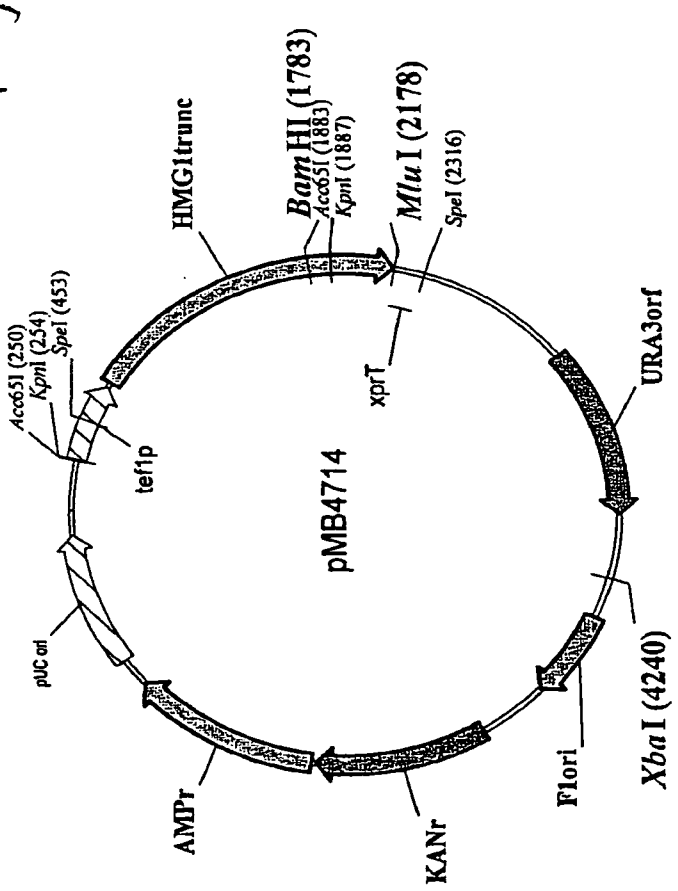

pMB4714
HMG1trunc
BamHI (1783)
Acc65I (1883)
KpnI (1887)
MluI (2178)
SpeI (2316)
xprT
URA3orf
XbaI (4240)
F1ori
KANr
AMPr
pUC ori
tef1p
Acc65I (250)
KpnI (254)
SpeI (453)

Figure 12J

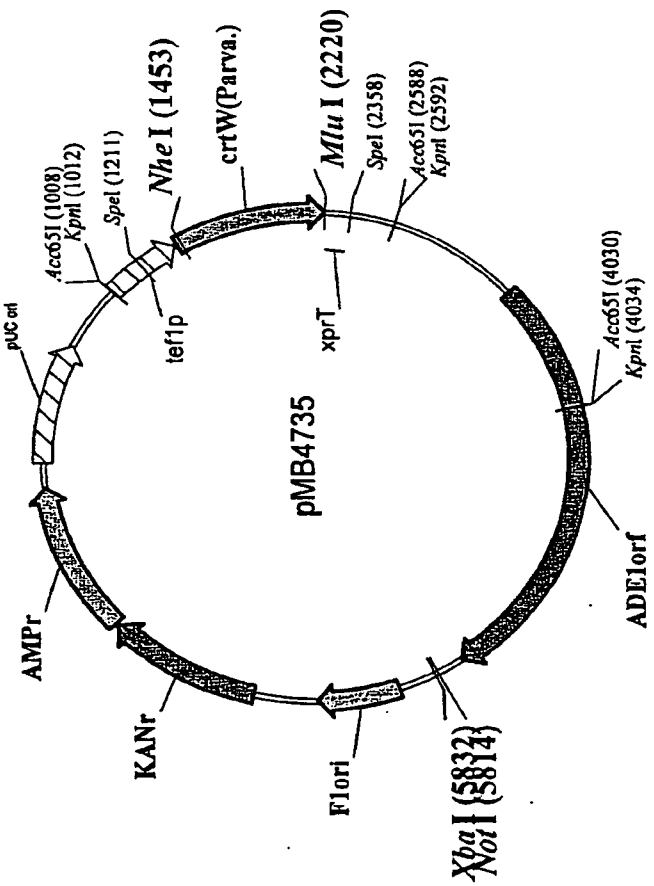

pMB4735
Acc65I (1008)
KpnI (1012)
SpeI (1211)
NheI (1453)
crtW(Parva.)
MluI (2220)
SpeI (2358)
Acc65I (2588)
KpnI (2592)
Acc65I (4030)
KpnI (4034)
ADE1orf
XbaI (5814)
NotI (5832)
F1ori
KANr
AMPr
pUC ori
tef1p
xprT

Figure 12 K

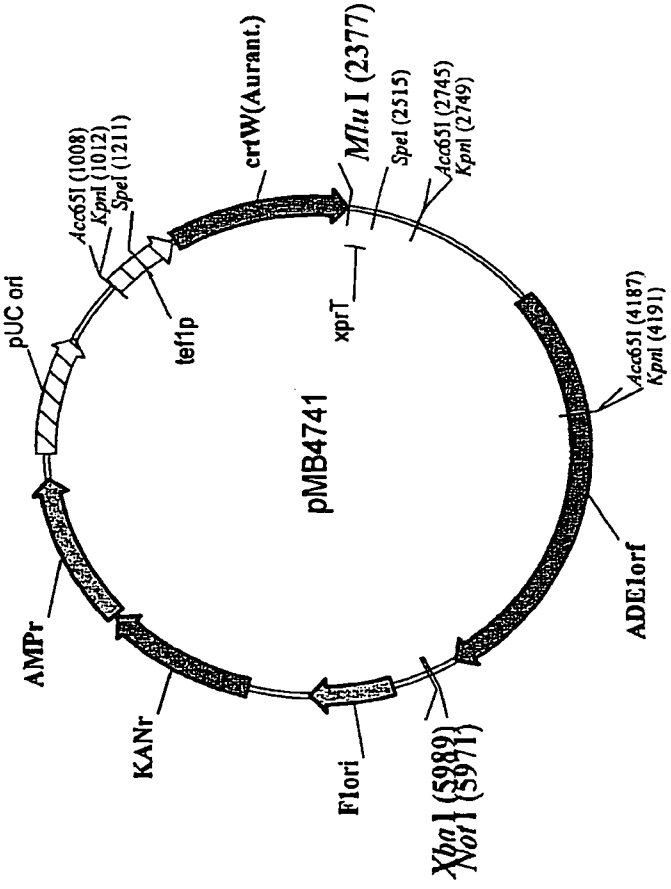

pMB4741
crtW(Aurant.)
MluI (2377)
SpeI (2515)
Acc65I (2745)
KpnI (2749)
xprT
Acc65I (4187)
KpnI (4191)
ADE1orf
XbaI (5989)
NotI (5971)
F1ori
KANr
AMPr
pUC ori
Acc65I (1008)
KpnI (1012)
SpeI (1211)
tef1p

Figure 12L

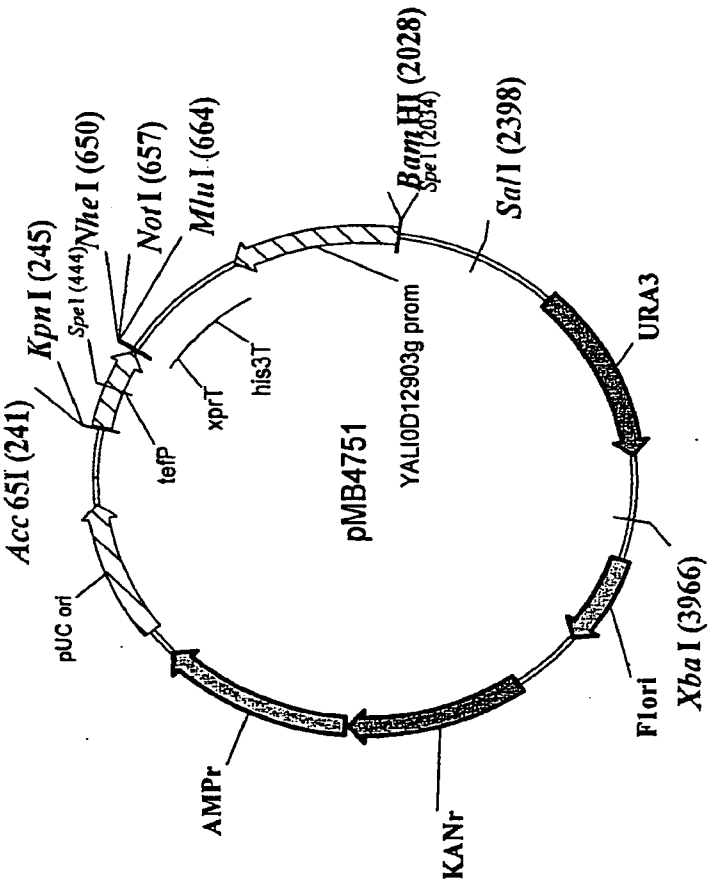
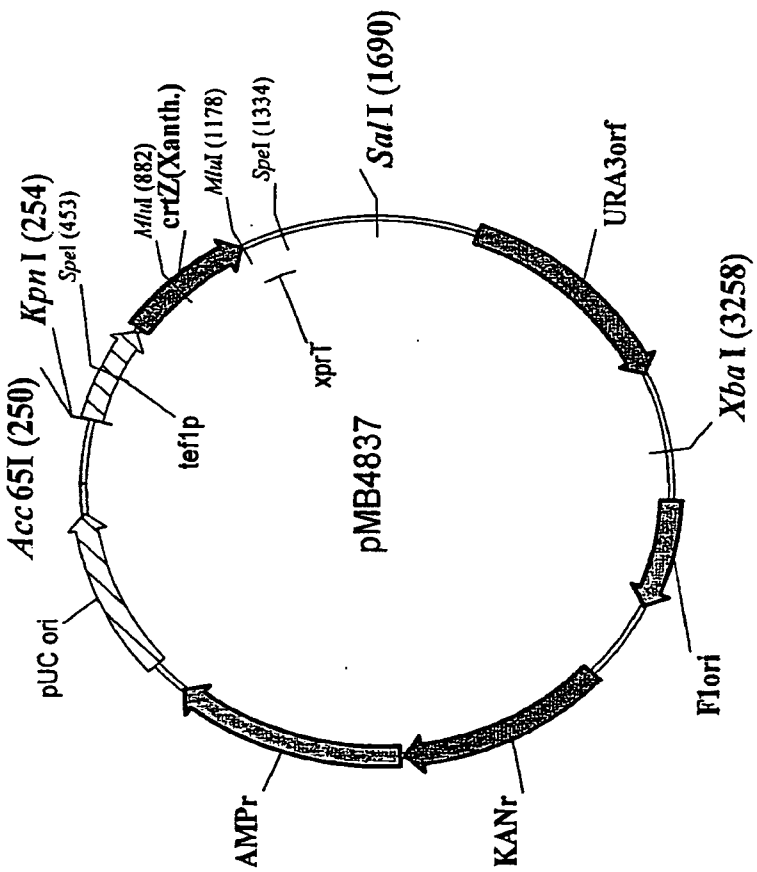

pMB4751
Acc 65I (241)
Kpn I (245)
Spe I (444)
Nhe I (650)
Not I (657)
Mlu I (664)
BamHI (2028)
Spe I (2034)
Sal I (2398)
URA3
F1 ori
Xba I (3966)
KANr
AMPr
pUC ori
tefP
xprT
his3T
YALI0D12903g prom

Figure 12M


pMB4837
Acc 65I (250)
Kpn I (254)
SpeI (453)
MluI (882)
crtZ(Xanth.)
MluI (1178)
SpeI (1334)
SalI (1690)
URA3orf
Xba I (3258)
F1ori
KANr
AMPr
pUC ori
tef1p
xprT