MICROORGANISMS FOR PRODUCING METHACRYLIC ACID AND METHACRYLATE ESTERS AND METHODS RELATED THERETO

BACKGROUND OF THE INVENTION

[001] This application claims the benefit of priority of United States Provisional application serial No. 61/471,078, filed April 1, 2011, and United States Provisional application serial No. 61/571,232, filed June 22, 2011, and United States Provisional application serial No. 61/509,560, filed July 19, 2011, and United States Provisional application serial No. 61/510,054, filed July 20, 2011, and United States Provisional application serial No. 61/512,348, filed July 27, 2011, each of which the entire contents are incorporated herein by reference.

[002] The present invention relates generally to biosynthetic processes, and more specifically to organisms having methacrylic acid biosynthetic capabilities.

[003] Methyl methacrylate (MMA) is an organic compound with the formula $CH_2=C(CH_3)CO_2CH_3$. This colourless liquid is the methyl ester of methacrylic acid (MMA) and is the monomer for the production oZf the transparent plastic polymethyl methacrylate (PMMA).

[004] The principal application of methyl methacrylate is the production of polymethyl methacrylate acrylic plastics. Also, methyl methacrylate is used for the production of the co-polymer methyl methacrylate-butadiene-styrene (MBS), used as a modifier for PVC. Methyl methacrylate polymers and co-polymers are used for waterborne coatings, such as latex paint. Uses are also found in adhesive formulations. Contemporary applications include the use in plates that keep light spread evenly across liquid crystal display (LCD) computer and TV screens. Methyl methacrylate is also used to prepare corrosion casts of anatomical organs, such as coronary arteries of the heart.

[005] Methacrylic acid, or 2-methyl-2-propenoic acid, is a low molecular weight carboxylic acid that occurs naturally in small amounts in the oil of Roman chamomile. It is a corrosive liquid with an acrid unpleasant odor. It is soluble in warm water and miscible with most organic solvents. Methacrylic acid polymerizes readily upon heating or treatment with a catalytic amount of strong acid, such as HCl. The resulting polymer is a ceramic-looking plastic. Methacrylic acid is used industrially in the preparation of its esters, known

collectively as methacrylates, such as methyl methacrylate. The methacrylates have numerous uses, most notably in the manufacture of polymers.

[006] Most commercial producers apply an acetone cyanohydrin (ACH) route to produce methacrylic acid (MAA), with acetone and hydrogen cyanide as raw materials. The intermediate cyanohydrin is converted with sulfuric acid to a sulfate ester of the methacrylamide, hydrolysis of which gives ammonium bisulfate and MAA. Some producers start with an isobutylene or, equivalently, tert-butanol, which is oxidized to methacrolein, and again oxidized to methacrylic acid. MAA is then esterified with methanol to MMA.

[007] The conventional production process, using the acetone cyanohydrin route, involves the conversion of hydrogen cyanide (HCN) and acetone to acetone cyanohydrin, which then undergoes acid assisted hydrolysis and esterification with methanol to give MMA. Difficulties in handling potentially deadly HCN along with the high costs of byproduct disposal (1.2 tons of ammonium bisulfate are formed per ton of MMA) have sparked a great deal of research aimed at cleaner and more economical processes. A number of new processes have been commercialized over the last two decades and many more are close to commercialization. The Asahi "Direct Metha" route, which involves the oxidation of isobutylene to methacrolein, which is then mixed with methanol, oxidized with air, and esterified to MMA, has been described as an economical process.

[008] Other than MMA polymers, the other major product of this industry is crude methacrylic acid, which accounts for about 20 percent of the total production of MMA. Crude MAA is processed into butyl methacrylates and/or "glacial" MAA, which is highly purified crude MAA. Glacial MAA can be used directly as a comonomer in various polymers and is also used to make a variety of small volume methacrylates. On the other hand, MAA can also be converted into MMA via esterification with methanol.

[009] Thus, there exists a need for alternative methods for effectively producing compounds such as methacrylic acid. The present invention satisfies this need and provides related advantages as well.

SUMMARY OF INVENTION

[010] The invention provides a non-naturally occurring microbial organism having a methacrylic acid, methacrylate ester such as methyl methacrylate, 3-hydroxyisobutyrate

and/or 2-hydroxyisobutyrate pathway. The microbial organism contains at least one exogenous nucleic acid encoding an enzyme in a methacrylic acid pathway. The invention additionally provides a method for producing methacrylic acid, methacrylate ester such as methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate. The method can include culturing methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate producing microbial organism, where the microbial organism expresses at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme in a sufficient amount to produce methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate, under conditions and for a sufficient period of time to produce methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate.

[011] The invention also provides non-naturally occurring microbial organisms containing methacrylate ester or methyl methacrylate pathways comprising at least one exogenous nucleic acid encoding a methacrylate ester or a methyl methacrylate enzyme expressed in a sufficient amount to produce methacrylate ester or methyl methacrylate. The microbial organism contains at least one exogenous nucleic acid encoding an enzyme in the methacrylate ester or methyl methacrylate pathway and at least one exogenous nucleic acid that encodes an enzyme that increases the yields of methacrylate ester or methyl methacrylate by (i) enhancing carbon fixation via the reductive TCA cycle, and/or (ii) accessing additional reducing equivalents from gaseous carbon sources and/or syngas components such as CO, CO_2, and/or H_2. In some aspects, the non-naturally occurring microbial organisms comprise (i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein the at least one exogenous nucleic acid is selected from an ATP-citrate lyase, a citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase; (ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein the at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or (iii) at least one exogenous nucleic acid encodes an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof. The invention additionally provides methods of using such microbial organisms to produce methacrylate ester or methyl methacrylate, by culturing a non-naturally occurring microbial organism containing methacrylate ester or methyl methacrylate pathways under conditions and for a sufficient period of time to produce methacrylate ester or methyl methacrylate.

BRIEF DESCRIPTION OF THE DRAWINGS

[012] Figure 1 shows exemplary pathways to methacrylic acid from pyruvate and acetyl-CoA, and aconitate. The enzymes are A. citramalate synthase, B. citramalate dehydratase (citraconate forming), C. citraconate decarboxylase, D. citramalyl-CoA lyase, E. citramalyl-CoA transferase, synthetase or hydrolase, F. citramalate dehydratase (mesaconate forming), G. citraconate isomerase, H. mesaconate decarboxylase, I. aconitate decarboxylase, J. itaconate isomerase, K. citramalyl-CoA dehydratase and L. itaconyl-CoA transferase, synthetase or hydrolase.

[013] Figure 2 shows exemplary pathways from methacrylate to methacrylate esters. Methacrylate can be formed from the pathways depicted in Figure 1 or other methacrylate pathways such as those described in WO 2009/135074 and U.S. publication 2009/0275096. Methacrylyl-CoA can be formed from methacrylate via a methacrylyl-CoA transferase or a methacrylyl-CoA synthetase. Methacrylate esters can be formed from methacrylyl-CoA and an alcohol in the presence of an alcohol transferase enzyme. Methacrylate esters can also be formed directly from methacrylate and an alcohol by a methacrylate ester-forming enzyme or by chemical conversion (for example, heating in the presence of a dehydrating agent such as an acid). R denotes any organic functional group including, but not limited to, a methyl, ethyl, n-propyl, n-butyl, i-propyl, sec-butyl, and tert-butyl, pentyl, or hexyl functional group. For example, if R denotes a methyl-group, R-OH denotes methanol and the product of the pathway is methylmethacrylate.

[014] Figure 3 shows an exemplary metabolic pathway from succinyl-CoA to MMA via 3-hydroxyisobutyrate.

[015] Figure 4 shows an exemplary succinyl-CoA to MAA pathway via 3-amino-2-methylpropionate. The "lumped reaction" (steps 2-3) is catalyzed by 1) methylmalonyl-CoA epimerase and 2) methylmalonyl-CoA reductase.

[016] Figure 5 shows an exemplary 4-hydroxybutyryl-CoA to MAA pathway that proceeds via 3-hydroxyisobutyrate or methacrylyl-CoA. Step 2 can be catalyzed by three alternative enzymes: 3-hydroxyisobutyryl-CoA synthetase, 3-hydroxyisobutyryl-CoA hydrolase or 3-hydroxyisobutyryl-CoA transferase. Similarly, step 5 can be catalyzed by three alternative enzymes: methacrylyl-CoA synthetase, methacrylyl -CoA hydrolase or methacrylyl-CoA transferase.

[017] Figure 6 shows an exemplary alpha-ketoglutarate to MAA pathway via threo-3-methylaspartate.

[018] Figure 7 shows an exemplary alpha-ketoglutarate to MAA pathway via 2-hydroxyglutarate.

[019] Figure 8 shows exemplary metabolic pathways for the conversion of acetyl-CoA or 4-hydroxybutyryl-CoA into MAA or 2-hydroxyisobutyrate.

[020] Figure 9 shows an exemplary pathway from acetyl-CoA to MAA.

[021] Figure 10 shows an exemplary pyruvate to acrylyl-CoA to MAA pathway.

[022] Figure 11 shows an exemplary 2-ketovalerate to MAA pathway. 2-Ketoisovalerate can be produced either from valine or pyruvate. An exemplary set of enzymes for pyruvate conversion to 2-ketoisovalerate is comprised of acetolactate synthase, acetohydroxy acid isomeroreductase, and dihydroxyacid dehydratase.

[023] Figure 12 shows the reverse TCA cycle for fixation of CO_2 on carbohydrates as substrates. The enzymatic transformations are carried out by the enzymes as shown.

[024] Figure 13 shows the pathway for the reverse TCA cycle coupled with carbon monoxide dehydrogenase and hydrogenase for the conversion of syngas to acetyl-CoA.

[025] Figure 14 shows Western blots of 10 micrograms ACS90 (lane 1), ACS91 (lane2), Mta98/99 (lanes 3 and 4) cell extracts with size standards (lane 5) and controls of *M. thermoacetica* CODH (Moth_1202/1203) or Mtr (Moth_1197) proteins (50, 150, 250, 350, 450, 500, 750, 900, and 1000 ng).

[026] Figure 15 shows CO oxidation assay results. Cells (*M. thermoacetica* or *E. coli* with the CODH/ACS operon; ACS90 or ACS91 or empty vector: pZA33S) were grown and extracts prepared. Assays were performed at 55oC at various times on the day the extracts were prepared. Reduction of methylviologen was followed at 578 nm over a 120 sec time course.

[027] Figure 16A shows the pathways for the biosynthesis of methacrylic acid and 3-hydroxyisobutyric acid. The enzymatic transformations shown are carried out by the following enzymes: (1) hydrogenase, (2) carbon monoxide dehydrogenase, (3) succinyl-CoA

transferase, succinyl-CoA synthetase, (4) methylmalonyl-CoA mutase, (5) methylmalonyl-CoA epimerase, (6) methylmalonyl-CoA reductase, (7) methylmalonate semialdehyde reductase and (8) 3-hydroxyisobutyrate dehydratase.

[028] Figure 16B shows the pathway for biosynthesis of methacrylic acid from glucose via a 4-hydroxybutyryl-CoA intermediate. The enzymatic transformations are carried out by the enzymes: (1) hydrogenase, (2) carbon monoxide dehydrogenase, (3) succinyl-CoA transferase, succinyl-CoA synthetase, (4) succinyl-CoA reductase (aldehyde forming), (5) 4-hydroxybutyrate dehydrogenase, (6) 4-hydroxybutyrate kinase, (7) phosphotrans-4-hydroxybutyrylase, (8) succinate reductase, (9) succinyl-CoA reductase (alcohol forming), (10) 4-hydroxybutyryl-CoA synthetase, 4-hydroxybutyryl-CoA transferase, (11) 4-hydroxybutyryl-CoA mutase, (12) 3-hydroxyisobutyryl-CoA synthetase, transferase or hydrolase, (13) 3-hydroxyisobutyrate dehydratase, (14) 3-hydroxyisobutyryl-CoA dehydratase, (15) methacrylyl-CoA synthetase, transferase or hydrolase.

[029] Figure 16C shows the flux distribution showing an enhanced maximum theoretical yield of methacrylic acid on glucose when carbon is routed via the reductive TCA cycle. The enzymatic transformations are carried out by: (1) ATP-citrate lyase; citrate lyase, acetyl-CoA synthetase; or citrate lyase, acetate kinse, phosphotransacetylase, (2) malate dehydrogenase, (3) fumarase, (4) fumarate reductase, (5) succinyl-CoA synthetase or transferase, (6) alpha-ketoglutarate:ferridoxin oxidoreductase, (7) isocitrate dehydrogenase, (8) aconitase, (9) pyruvate:ferridoxin oxidoreductase; pyruvate oxidase, acetyl-CoA synthetase; or pyruvate oxidase, acetate kinase, phosphotransacetylase, (10) acetoacetyl-CoA thiolase, (11) acetoacetyl-CoA reductase, (12) 3-hydroxybutyryl-CoA mutase, (13) 2-hydroxybutyryl-CoA dehydratase, (14) methacrylyl-CoA synthetase, transferase or hydrolase, (15) 2-hydroxyisobutyryl-CoA synthetase, transferase or hydrolase.

[030] Figure 16D shows the flux distribution showing an enhanced maximum theoretical yield of methacrylic acid on glucose via citramalate when carbon is routed via the reductive TCA cycle. The enzymatic transformations are carried out by (1) ATP-citrate lyase; citrate lyase, acetyl-CoA synthetase; or citrate lyase, acetate kinse, phosphotransacetylase, (2) malate dehydrogenase, (3) fumarase, (4) fumarate reductase, (5) succinyl-CoA synthetase or transferase, (6) alpha-ketoglutarate:ferridoxin oxidoreductase, (7) isocitrate dehydrogenase, (8) aconitase, (9) pyruvate:ferridoxin oxidoreductase; pyruvate

oxidase, acetate kinase, phosphotransacetylase, (10) citramalate synthase, (11) citramalate dehydratase and (12) citraconate decarboxylase.

[031] Figure 16E shows pathways for biosynthesis of methacrylic acid from acetyl-CoA and pyruvate. The enzymatic transformations are carried out by the enzymes as shown. Enzymes are (1) citramalate synthase, (2) citramalate dehydratase (citraconate forming), (3) citraconate decarboxylase, (4) citramalyl-CoA lyase, (5) citramalyl-CoA transferase, synthetase or hyrolase, (6) citramalate dehydratase (mesaconate forming), (7) citraconate isomerase, (8) mesaconate decarboxylase, (9) aconitate decarboxylase, (10) itaconate isomerase, (11) itaconyl-CoA transferase or synthetase and (12) itaconyl-CoA hydratase.

[032] Figures 17A and 17B show exemplary pathways. The enzymatic transformations are carried out by the enzymes as shown. Figure 17A shows the pathways for fixation of CO_2 to succinyl-CoA using the reductive TCA cycle. Figure 17B shows exemplary pathways for the biosynthesis of 3-hydroxyisobutric acid and methacrylic acid from succinyl-CoA; the enzymatic transformations shown are carried out by the following enzymes: A. Methylmalonyl-CoA mutase, B. Methylmalonyl-CoA epimerase, C. Methylmalonyl-CoA reductase, D. Methylmalonate semialdehyde reductase, E. 3-Hydroxyisobutyrate dehydratase.

[033] Figures 18A and 18B show exemplary pathways. The enzymatic transformations are carried out by the enzymes as shown. Figure 18A shows the pathways for fixation of CO_2 to succinate using the reductive TCA cycle. Figure 18B shows exemplary pathways for the biosynthesis of 3-hydroxyisobutyric acid and methacrylic acid from succinate; the enzymatic transformations shown are carried out by the following enzymes: A. 3-Hydroxyisobutyryl-CoA dehydratase, B. Methacrylyl-CoA synthetase, transferase or hydrolase, C. Succinyl-CoA transferase or synthetase, D. Succinyl-CoA reductase (aldehyde forming), E. 4-Hydroxybutyrate dehydrogenase, F. 4-Hydroxybutyrate kinase, G. Phosphotrans-4-hydroxybutyrylase, H. Succinate reductase, I. Succinyl-CoA reductase (alcohol forming), J. 4-Hydroxybutyryl-CoA synthetase or transferase, K. 4-Hydroxybutyryl-CoA mutase, L. 3-Hydroxyisobutyryl-CoA synthetase, transferase or hydrolase, M. 3-Hydroxyisobutyrate dehydratase.

[034] Figures 19A and 19B show exemplary pathways. Figure 19A shows the pathways for fixation of CO_2 to acetyl-CoA and pyruvate using the reductive TCA cycle. Figure 19B shows exemplary pathways for the biosynthesis of methacrylate from acetyl-CoA and

pyruvate; the enzymatic transformations shown are carried out by the following enzymes: 1. Citramalate synthase, 2. Citramalate dehydratase (citraconate forming), 3. Citraconate decarboxylase, 4. Citramalyl-CoA lyase, 5. Citramalyl-CoA transferase, synthetase or hydrolase, 6. Citramalate dehydratase (mesaconate forming), 7. Citraconate isomerase, 8. Mesaconate decarboxylase, 9. Aconitate decarboxylase, 10. Itaconate isomerase, 11. Itaconyl-CoA transferase or synthetase, 12. Itaconyl-CoA hydratase.

[035] Figures 20A and 20B show exemplary pathways. Figure 20A shows the pathways for fixation of CO_2 to acetyl-CoA using the reductive TCA cycle. Figure 20B shows exemplary pathways for the biosynthesis of methacrylic acid and 2-hydroxyisobutyric acid from acetyl-CoA.

[036] Figures 21A and 21B show exemplary pathways. Figure 21A shows the pathways for fixation of CO2 to acetyl-CoA using the reductive TCA cycle. Figure 21B shows exemplary pathways for the biosynthesis of methacrylic acid and 3-hydroxyisobutyric acid from acetyl-CoA; the enzymatic transformations shown are carried out by the following enzymes: 1) Acetoacetyl-CoA thiolase (AtoB), 2) 3-Hydroxybutyryl-CoA dehydrogenase (Hbd), 3) Crotonase (Crt), 4) Crotonyl-CoA hydratase (4-Budh), 5) 4-hydroxybutyryl-CoA mutase, 6) 3-hydroxyisobutyryl-CoA hydrolase, synthetase, or transferase, 7) 3-hydroxyisobutyric acid dehydratase, 8) 3-hydroxyisobutyryl-CoA dehydratase, 9) methacrylyl-CoA hydrolase, synthetase, or transferase.

[037] Figure 22A shows the nucleotide sequence (SEQ ID NO:1) of carboxylic acid reductase from *Nocardia iowensis* (GNM_720), and Figure 22B shows the encoded amino acid sequence (SEQ ID NO:2).

[038] Figure 23A shows the nucleotide sequence (SEQ ID NO:3) of phosphpantetheine transferase, which was codon optimized, and Figure 23B shows the encoded amino acid sequence (SEQ ID NO:4).

[039] Figure 24A shows the nucleotide sequence (SEQ ID NO:5) of carboxylic acid reductase from *Mycobacterium smegmatis* mc(2)155 (designated 890), and Figure 24B shows the encoded amino acid sequence (SEQ ID NO:6).

[040] Figure 25A shows the nucleotide sequence (SEQ ID NO:7) of carboxylic acid reductase from *Mycobacterium avium* subspecies paratuberculosis K-10 (designated 891), and Figure 25B shows the encoded amino acid sequence (SEQ ID NO:8).

[041] Figure 26A shows the nucleotide sequence (SEQ ID NO:9) of carboxylic acid reductase from *Mycobacterium marinum* M (designated 892), and Figure 26B shows the encoded amino acid sequence (SEQ ID NO:10).

[042] Figure 27A shows the nucleotide sequence (SEQ ID NO:11) of carboxylic acid reductase designated 891GA, and Figure 27B shows the encoded amino acid sequence (SEQ ID NO:12).

[043] Figure 28 shows an exemplary pathway to a methacrylate ester via 3-hydroxyisobutyrate and/or 3-hydroxyisobutyryl-CoA. R-OH refers to any organic alcohol.

[044] Figure 29 shows an exemplary pathway to a methacrylate ester via 2-hydroxyisobutyrate and/or 2-hydroxyisobutyryl-CoA. R-OH refers to any organic alcohol.

[045] Figure 30 shows an exemplary pathway to an exemplary methacrylate ester, methyl methacrylate.

DETAILED DESCRIPTION OF THE INVENTION

[046] The present invention is directed to the design and production of cells and organisms having biosynthetic production capabilities for methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate. As disclosed herein, metabolic pathways can be designed and recombinantly engineered to achieve the biosynthesis of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate in microbial organisms such as *Escherichia coli* and other cells or organisms. Biosynthetic production of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate is confirmed by construction of strains having the designed metabolic genotype. These metabolically engineered cells or organisms also can be subjected to adaptive evolution to further augment methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate biosynthesis, including under conditions approaching theoretical maximum growth.

[047] Microorganisms for the production of methacrylic acid (MAA) have been previously described (see, for example, WO 2009/135074 and U.S. publication 2009/0275096, which is incorporated herein by reference). The present invention provides additional pathways for engineering microbial organisms for the production of methacrylic acid (MAA). Figure 1 provides exemplary pathways to MAA from acetyl-CoA and pyruvate via intermediate citramalate. Also shown are pathways to MAA from aconitate. In one pathway, acetyl-CoA and pyruvate are first converted to citramalate by citramalate synthase. Dehydration of citramalate can yield either citraconate (Step B) or mesaconate (Step C). Mesaconate and citraconate are interconverted by a cis/trans isomerase in Step G. Decarboxylation of mesaconate (Step H) or citraconate (Step C) yields MAA. In an alternate pathway, citramalate is formed from acetyl-CoA and pyruvate via a citramalyl-CoA intermediate in Steps D and E, catalyzed by citramalyl-CoA lyase and citramalyl-coA hydrolase, transferase or synthetase.

[048] The invention also encompasses pathways from aconitate to MAA. In one pathway, aconitate is first decarboxylated to itaconate by aconitate decarboxylase (Step I). Itaconate is then isomerized to citraconate by itaconate delta-isomerase (Step J). Conversion of citraconate to MAA proceeds either directly by decarboxylation or indirectly via mesaconate. In an alternate pathway, the itaconate intermediate is first converted to itaconyl-CoA by a CoA transferase or synthetase (Step L). Hydration of itaconyl-CoA yields citramalyl-CoA, which can then be converted to MAA as described previously. Additionaly details and embodiments of the exemplary MAA pathways are described herein below.

[049] As used herein, the term "non-naturally occurring" when used in reference to a microbial organism or microorganism of the invention is intended to mean that the microbial organism has at least one genetic alteration not normally found in a naturally occurring strain of the referenced species, including wild-type strains of the referenced species. Genetic alterations include, for example, modifications introducing expressible nucleic acids encoding metabolic polypeptides, other nucleic acid additions, nucleic acid deletions and/or other functional disruption of the microbial organism's genetic material. Such modifications include, for example, coding regions and functional fragments thereof, for heterologous, homologous or both heterologous and homologous polypeptides for the referenced species. Additional modifications include, for example, non-coding regulatory regions in which the modifications alter expression of a gene or operon. Exemplary metabolic polypeptides

include enzymes or proteins within a methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate biosynthetic pathway.

[050] A metabolic modification refers to a biochemical reaction that is altered from its naturally occurring state. Therefore, non-naturally occurring microorganisms can have genetic modifications to nucleic acids encoding metabolic polypeptides, or functional fragments thereof. Exemplary metabolic modifications are disclosed herein.

[051] As used herein, the term "isolated" when used in reference to a microbial organism is intended to mean an organism that is substantially free of at least one component as the referenced microbial organism is found in nature. The term includes a microbial organism that is removed from some or all components as it is found in its natural environment. The term also includes a microbial organism that is removed from some or all components as the microbial organism is found in non-naturally occurring environments. Therefore, an isolated microbial organism is partly or completely separated from other substances as it is found in nature or as it is grown, stored or subsisted in non-naturally occurring environments. Specific examples of isolated microbial organisms include partially pure microbes, substantially pure microbes and microbes cultured in a medium that is non-naturally occurring.

[052] As used herein, the terms "microbial," "microbial organism" or "microorganism" are intended to mean any organism that exists as a microscopic cell that is included within the domains of archaea, bacteria or eukarya. Therefore, the term is intended to encompass prokaryotic or eukaryotic cells or organisms having a microscopic size and includes bacteria, archaea and eubacteria of all species as well as eukaryotic microorganisms such as yeast and fungi. The term also includes cell cultures of any species that can be cultured for the production of a biochemical.

[053] As used herein, "methacrylic acid," having the chemical formula $CH_2=C(CH_3)CO_2$ (see Figure 1) (IUPAC name 2-methyl-2-propenoic acid), is the acid form of methacrylate, and it is understood that methacrylic acid and methacrylate can be used interchangebly throughout to refer to the compound in any of its neutral or ionized forms, including any salt forms thereof. It is understood by those skilled understand that the specific form will depend on the pH.

[054] As used herein, "methacrylate ester," refers to a compound having the chemical formula $CH_2=C(CH_3)COOR$ (see Figures 28 and 29), wherein R is a lower alkyl, that is C1 to C6, branched or straight chain, including, without limitation, methyl, ethyl, n-propyl, n-butyl, i-propyl, sec-butyl, and tert-butyl, pentyl, or hexyl, any of which can be unsaturation thereby being, for example, propenyl, butenyl, pentyl, and hexenyl. Exemplary methacrylate esters include, without limitation, methyl methacrylate, ethyl methacrylate, and n-propyl methacrylate. Methacrylate esters as used herein also include other R groups that are medium to long chain groups, that is C7-C22, wherein the methacrylate esters are derived from fatty alcohols, such as heptyl, octyl, nonyl, decyl, undecyl, lauryl, tridecyl, myristyl, pentadecyl, cetyl, palmitolyl, heptadecyl, stearyl, nonadecyl, arachidyl, heneicosyl, and behenyl alcohols, any one of which can be optionally branched and/or contain unsaturations.

[055] As used herein, the term "CoA" or "coenzyme A" is intended to mean an organic cofactor or prosthetic group (nonprotein portion of an enzyme) whose presence is required for the activity of many enzymes (the apoenzyme) to form an active enzyme system. Coenzyme A functions in certain condensing enzymes, acts in acetyl or other acyl group transfer and in fatty acid synthesis and oxidation, pyruvate oxidation and in other acetylation.

[056] As used herein, the term "substantially anaerobic" when used in reference to a culture or growth condition is intended to mean that the amount of oxygen is less than about 10% of saturation for dissolved oxygen in liquid media. The term also is intended to include sealed chambers of liquid or solid medium maintained with an atmosphere of less than about 1% oxygen.

[057] "Exogenous" as it is used herein is intended to mean that the referenced molecule or the referenced activity is introduced into the host microbial organism. The molecule can be introduced, for example, by introduction of an encoding nucleic acid into the host genetic material such as by integration into a host chromosome or as non-chromosomal genetic material such as a plasmid. Therefore, the term as it is used in reference to expression of an encoding nucleic acid refers to introduction of the encoding nucleic acid in an expressible form into the microbial organism. When used in reference to a biosynthetic activity, the term refers to an activity that is introduced into the host reference organism. The source can be, for example, a homologous or heterologous encoding nucleic acid that expresses the referenced activity following introduction into the host microbial organism. Therefore, the term "endogenous" refers to a referenced molecule or activity that is present in the host.

Similarly, the term when used in reference to expression of an encoding nucleic acid refers to expression of an encoding nucleic acid contained within the microbial organism. The term "heterologous" refers to a molecule or activity derived from a source other than the referenced species whereas "homologous" refers to a molecule or activity derived from the host microbial organism. Accordingly, exogenous expression of an encoding nucleic acid of the invention can utilize either or both a heterologous or homologous encoding nucleic acid.

[058] It is understood that when more than one exogenous nucleic acid is included in a microbial organism that the more than one exogenous nucleic acids refers to the referenced encoding nucleic acid or biosynthetic activity, as discussed above. It is further understood, as disclosed herein, that such more than one exogenous nucleic acids can be introduced into the host microbial organism on separate nucleic acid molecules, on polycistronic nucleic acid molecules, or a combination thereof, and still be considered as more than one exogenous nucleic acid. For example, as disclosed herein a microbial organism can be engineered to express two or more exogenous nucleic acids encoding a desired pathway enzyme or protein. In the case where two exogenous nucleic acids encoding a desired activity are introduced into a host microbial organism, it is understood that the two exogenous nucleic acids can be introduced as a single nucleic acid, for example, on a single plasmid, on separate plasmids, can be integrated into the host chromosome at a single site or multiple sites, and still be considered as two exogenous nucleic acids. Similarly, it is understood that more than two exogenous nucleic acids can be introduced into a host organism in any desired combination, for example, on a single plasmid, on separate plasmids, can be integrated into the host chromosome at a single site or multiple sites, and still be considered as two or more exogenous nucleic acids, for example three exogenous nucleic acids. Thus, the number of referenced exogenous nucleic acids or biosynthetic activities refers to the number of encoding nucleic acids or the number of biosynthetic activities, not the number of separate nucleic acids introduced into the host organism.

[059] The non-naturally occurring microbal organisms of the invention can contain stable genetic alterations, which refers to microorganisms that can be cultured for greater than five generations without loss of the alteration. Generally, stable genetic alterations include modifications that persist greater than 10 generations, particularly stable modifications will persist more than about 25 generations, and more particularly, stable genetic modifications will be greater than 50 generations, including indefinitely.

[060] Those skilled in the art will understand that the genetic alterations, including metabolic modifications exemplified herein, are described with reference to a suitable host organism such as *E. coli* and their corresponding metabolic reactions or a suitable source organism for desired genetic material such as genes for a desired metabolic pathway. However, given the complete genome sequencing of a wide variety of organisms and the high level of skill in the area of genomics, those skilled in the art will readily be able to apply the teachings and guidance provided herein to essentially all other organisms. For example, the *E. coli* metabolic alterations exemplified herein can readily be applied to other species by incorporating the same or analogous encoding nucleic acid from species other than the referenced species. Such genetic alterations include, for example, genetic alterations of species homologs, in general, and in particular, orthologs, paralogs or nonorthologous gene displacements.

[061] An ortholog is a gene or genes that are related by vertical descent and are responsible for substantially the same or identical functions in different organisms. For example, mouse epoxide hydrolase and human epoxide hydrolase can be considered orthologs for the biological function of hydrolysis of epoxides. Genes are related by vertical descent when, for example, they share sequence similarity of sufficient amount to indicate they are homologous, or related by evolution from a common ancestor. Genes can also be considered orthologs if they share three-dimensional structure but not necessarily sequence similarity, of a sufficient amount to indicate that they have evolved from a common ancestor to the extent that the primary sequence similarity is not identifiable. Genes that are orthologous can encode proteins with sequence similarity of about 25% to 100% amino acid sequence identity. Genes encoding proteins sharing an amino acid similarity less that 25% can also be considered to have arisen by vertical descent if their three-dimensional structure also shows similarities. Members of the serine protease family of enzymes, including tissue plasminogen activator and elastase, are considered to have arisen by vertical descent from a common ancestor.

[062] Orthologs include genes or their encoded gene products that through, for example, evolution, have diverged in structure or overall activity. For example, where one species encodes a gene product exhibiting two functions and where such functions have been separated into distinct genes in a second species, the three genes and their corresponding products are considered to be orthologs. For the production of a biochemical product, those

skilled in the art will understand that the orthologous gene harboring the metabolic activity to be introduced or disrupted is to be chosen for construction of the non-naturally occurring microorganism. An example of orthologs exhibiting separable activities is where distinct activities have been separated into distinct gene products between two or more species or within a single species. A specific example is the separation of elastase proteolysis and plasminogen proteolysis, two types of serine protease activity, into distinct molecules as plasminogen activator and elastase. A second example is the separation of mycoplasma 5'-3' exonuclease and *Drosophila* DNA polymerase III activity. The DNA polymerase from the first species can be considered an ortholog to either or both of the exonuclease or the polymerase from the second species and vice versa.

[063] In contrast, paralogs are homologs related by, for example, duplication followed by evolutionary divergence and have similar or common, but not identical functions. Paralogs can originate or derive from, for example, the same species or from a different species. For example, microsomal epoxide hydrolase (epoxide hydrolase I) and soluble epoxide hydrolase (epoxide hydrolase II) can be considered paralogs because they represent two distinct enzymes, co-evolved from a common ancestor, that catalyze distinct reactions and have distinct functions in the same species. Paralogs are proteins from the same species with significant sequence similarity to each other suggesting that they are homologous, or related through co-evolution from a common ancestor. Groups of paralogous protein families include HipA homologs, luciferase genes, peptidases, and others.

[064] A nonorthologous gene displacement is a nonorthologous gene from one species that can substitute for a referenced gene function in a different species. Substitution includes, for example, being able to perform substantially the same or a similar function in the species of origin compared to the referenced function in the different species. Although generally, a nonorthologous gene displacement will be identifiable as structurally related to a known gene encoding the referenced function, less structurally related but functionally similar genes and their corresponding gene products nevertheless will still fall within the meaning of the term as it is used herein. Functional similarity requires, for example, at least some structural similarity in the active site or binding region of a nonorthologous gene product compared to a gene encoding the function sought to be substituted. Therefore, a nonorthologous gene includes, for example, a paralog or an unrelated gene.

[065] Therefore, in identifying and constructing the non-naturally occurring microbial organisms of the invention having methacrylic acid biosynthetic capability, those skilled in the art will understand with applying the teaching and guidance provided herein to a particular species that the identification of metabolic modifications can include identification and inclusion or inactivation of orthologs. To the extent that paralogs and/or nonorthologous gene displacements are present in the referenced microorganism that encode an enzyme catalyzing a similar or substantially similar metabolic reaction, those skilled in the art also can utilize these evolutionally related genes.

[066] Orthologs, paralogs and nonorthologous gene displacements can be determined by methods well known to those skilled in the art. For example, inspection of nucleic acid or amino acid sequences for two polypeptides will reveal sequence identity and similarities between the compared sequences. Based on such similarities, one skilled in the art can determine if the similarity is sufficiently high to indicate the proteins are related through evolution from a common ancestor. Algorithms well known to those skilled in the art, such as Align, BLAST, Clustal W and others compare and determine a raw sequence similarity or identity, and also determine the presence or significance of gaps in the sequence which can be assigned a weight or score. Such algorithms also are known in the art and are similarly applicable for determining nucleotide sequence similarity or identity. Parameters for sufficient similarity to determine relatedness are computed based on well known methods for calculating statistical similarity, or the chance of finding a similar match in a random polypeptide, and the significance of the match determined. A computer comparison of two or more sequences can, if desired, also be optimized visually by those skilled in the art. Related gene products or proteins can be expected to have a high similarity, for example, 25% to 100% sequence identity. Proteins that are unrelated can have an identity which is essentially the same as would be expected to occur by chance, if a database of sufficient size is scanned (about 5%). Sequences between 5% and 24% may or may not represent sufficient homology to conclude that the compared sequences are related. Additional statistical analysis to determine the significance of such matches given the size of the data set can be carried out to determine the relevance of these sequences.

[067] Exemplary parameters for determining relatedness of two or more sequences using the BLAST algorithm, for example, can be as set forth below. Briefly, amino acid sequence alignments can be performed using BLASTP version 2.0.8 (Jan-05-1999) and the

following parameters: Matrix: 0 BLOSUM62; gap open: 11; gap extension: 1; x_dropoff: 50; expect: 10.0; wordsize: 3; filter: on. Nucleic acid sequence alignments can be performed using BLASTN version 2.0.6 (Sept-16-1998) and the following parameters: Match: 1; mismatch: -2; gap open: 5; gap extension: 2; x_dropoff: 50; expect: 10.0; wordsize: 11; filter: off. Those skilled in the art will know what modifications can be made to the above parameters to either increase or decrease the stringency of the comparison, for example, and determine the relatedness of two or more sequences.

[068] In one embodiment, the invention provides a non-naturally occurring microbial organism having a methacrylate ester pathway comprising at least one exogenous nucleic acid encoding a methacrylate ester pathway enzyme expressed in a sufficient amount to produce a methacrylate ester, where the methacrylate ester pathway comprises an alcohol transferase or an ester-forming enzyme, and a dehydratase. In a particular embodiment, the microbial organism comprises two exogenous nucleic acids each encoding a methacrylate ester pathway enzyme. For example, the two exogenous nucleic acids can encode an alcohol transferase and a dehydratase or alternatively an ester-forming enzyme and a dehydratase. In a particular embodiment, the at least one exogenous nucleic acid can be a heterologous nucleic acid. In another embodiment, the non-naturally occurring microbial organism can be in a substantially anaerobic culture medium. The invention additionally provides a method for producing methacrylate ester, comprising culturing the non-naturally occurring microbial organism disclosed herein having a methacrylate ester pathway under conditions and for a sufficient period of time to produce methacrylate ester.

[069] The invention additionally provides a non-naturally occurring microbial organism having a methyl methacrylate pathway comprising at least one exogenous nucleic acid encoding a methyl methacrylate pathway enzyme expressed in a sufficient amount to produce a methyl methacrylate, the methyl methacrylate pathway comprising an alcohol transferase or an ester-forming enzyme, and a dehydratase. In a further embodiment, the microbial organism can comprise two exogenous nucleic acids each encoding a methyl methacrylate pathway enzyme. In a particular embodiment, the two exogenous nucleic acids can encode an alcohol transferase and a dehydratase or alternatively an ester-forming enzyme and a dehydratase. In another embodiment, the at least one exogenous nucleic acid can a heterologous nucleic acid. In another embodiment, the non-naturally occurring microbial organism can be in a substantially anaerobic culture medium. The invenion also provides a

method for producing methyl methacrylate by culturing a non-naturally occurring microbial organism having a methyl methacrylate pathway under conditions and for a sufficient period of time to produce methyl methacrylate.

[070] In one embodiment, the invention provides a non-naturally occurring microbial organism, comprising a microbial organism having a methacrylate ester pathway comprising at least one exogenous nucleic acid encoding a methacrylate ester pathway enzyme expressed in a sufficient amount to produce a methacrylate ester, said methacrylate ester pathway comprising an alcohol transferase or an ester-forming enzyme, and a dehydratase. In one aspect, the non-naturally occurring microbial organism comprises two exogenous nucleic acids each encoding a methacrylate ester pathway enzyme. In one aspect, the two exogenous nucleic acids encode an alcohol transferase and a dehydratase or alternatively an ester-forming enzyme and a dehydratase. In another aspect, the at least one exogenous nucleic acid is a heterologous nucleic acid. In another aspect, the non-naturally occurring microbial organism is in a substantially anaerobic culture medium.

[071] In one embodiment, the invention provides a non-naturally occurring microbial organism, wherein said dehydratase converts a 3-hydroxyisobutyrate ester or a 2-hydroxyisobutyrate ester to said methacrylate ester. In one embodiment, the invention provides a non-naturally occurring microbial organism, wherein said alcohol transferase coverts 3-hydroxyisobutyryl-CoA to a 3-hydroxyisobutyrate ester or 2-hydroxyisobutyryl-CoA to 2-hydroxyisobutyrate ester.

[072] In one embodiment, the invention provides a non-naturally occurring microbial organism, wherein said microbial organism further comprises a methacyrlate ester pathway comprising at least one exogenous nucleic acid encoding a methacrylate ester pathway enzyme expressed in a sufficient amount to produce a methacrylate ester, said methacrylate ester pathway comprising a pathway selected from: (a) a 3-hydroxyisobutyrate-CoA transferase or a 3-hydroxyisobutyrate-CoA synthetase; an alcohol transferase; and a dehydratase; (b) a 3-hydroxyisobutyrate ester-forming enzyme and a dehydratasedehydratase; (c) a 2-hydroxyisobutyrate-CoA transferase or a 2-hydroxyisobutyrate-CoA synthetase; an alcohol transferase; and a dehydratase; or (d) a 2-hydroxyisobutyrate ester-forming enzyme and a dehydratase. In one aspect, the invention provides a method for producing methacrylate ester by culturing the non-naturally occurring microbial organism as disclosed herein under conditions and for a sufficient period of time to produce methacrylate ester.

[073] In one embodiment, the invention provides a non-naturally occurring microbial organism, comprising a microbial organism having a methyl methacrylate pathway comprising at least one exogenous nucleic acid encoding a methyl methacrylate pathway enzyme expressed in a sufficient amount to produce a methyl methacrylate, said methyl methacrylate pathway comprising an alcohol transferase or an ester-forming enzyme, and a dehydratase. In one aspect, the microbial organism comprises two exogenous nucleic acids each encoding a methyl methacrylate pathway enzyme. In another aspect, the two exogenous nucleic acids encode an alcohol transferase and a dehydratase or alternatively an ester-forming enzyme and a dehydratase. In another aspect, the at least one exogenous nucleic acid is a heterologous nucleic acid. In another aspect, the non-naturally occurring microbial organism is in a substantially anaerobic culture medium.

[074] In one embodiment, the invention provides a method for producing methyl methacrylate, comprising culturing the non-naturally occurring microbial organism as described herein under conditions and for a sufficient period of time to produce methyl methacrylate.

[075] In one embodiment, the invention provides a method for producing a methacrylate ester comprising, culturing a non-naturally occurring microbial organism under conditions and for a sufficient period of time to produce a 3-hydroxyisobutyrate ester, wherein said non-naturally occurring microbial organism comprises an exogenous nucleic acid encoding an alcohol transferase or a 3-hydroxyisobutyrate ester-forming enzyme expressed in a sufficient amount to produce a 3-hydroxyisobutyrate ester, and chemically dehydrating said 3-hydroxyisobutyrate ester to produce a methacrylate ester.

[076] In one embodiment, the invention provides a method for producing a methacrylate ester comprising, culturing a non-naturally occurring microbial organism under conditions and for a sufficient period of time to produce a 2-hydroxyisobutyrate ester, wherein said non-naturally occurring microbial organism comprises an exogenous nucleic acid encoding an alcohol transferase or a 2-hydroxyisobutyrate ester-forming enzyme expressed in a sufficient amount to produce a 2-hydroxyisobutyrate ester, and chemically dehydrating said 2-hydroxyisobutyrate ester to produce a methacrylate ester.

[077] In one embodiment, the invention provides a method for producing methyl methacrylate comprising, culturing a non-naturally occurring microbial organism under

conditions and for a sufficient period of time to produce methyl-3-hydroxyisobutyrate, wherein said non-naturally occurring microbial organism comprises an exogenous nucleic acid encoding an alcohol transferase or an ester-forming enzyme expressed in a sufficient amount to produce methyl-3-hydroxyisobutyrate, and chemically dehydrating said methyl-3-hydroxyisobutyrate to produce methyl methacrylate.

[078] In one aspect of the above methods, the exogenous nucleic acid is a heterologous nucleic acid. In another aspect of the above methods, the non-naturally occurring microbial organism is in a substantially anaerobic culture medium.

[079] In one embodiment, the invention provides a method wherein said microbial organism further comprises a 3-hydroxyisobutyrate ester pathway comprising at least one exogenous nucleic acid encoding a 3-hydroxyisobutyrate ester pathway enzyme expressed in a sufficient amount to produce a 3-hydroxyisobutyrate ester, said 3-hydroxyisobutyrate ester pathway comprising a pathway selected from: (a) a 3-hydroxyisobutyrate-CoA transferase or a 3-hydroxyisobutyrate-CoA synthetase; and an alcohol transferase; or (b) a 3-hydroxyisobutyrate ester-forming enzyme. In another embodiment, the ivnetion provides a method wherein said microbial organism further comprises a 2-hydroxyisobutyrate ester pathway comprising at least one exogenous nucleic acid encoding a 2-hydroxyisobutyrate ester pathway enzyme expressed in a sufficient amount to produce a 2-hydroxyisobutyrate ester, said 2-hydroxyisobutyrate ester pathway comprising a pathway selected from: (a) a 2-hydroxyisobutyrate-CoA transferase or a 2-hydroxyisobutyrate-CoA synthetase; and an alcohol transferase; or (b) a 2-hydroxyisobutyrate ester-forming enzyme.

[080] As disclosed herein, the invention provides non-naturally occurring microbial organisms having a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid. Exemplary pathways include, but are not limited to, the pathways disclosed in Figure 1. Exemplary methacrylic acid pathways include, for example, the pathways corresponding to the enzymes shown in Figure 1 as follows and as discussed below in more detail: pathway (1) A/B/C; pathway (2) A/B/G/H; pathway (3) A/F/G/C; pathway (4) A/F/H; pathway (5) D/E/B/C; pathway (6) D/E/B/G/H; pathway (7) D/E/F/H; pathway (8) D/E/F/G/C; pathway (9) I/J/C; pathway (10) I/J/G/H; pathway (11) I/L/K/E/B/C; pathway (12) I/L/K/E/B/G/H; pathway (13) I/L/K/E/F/H; and pathway (14) I/L/K/E/F/G/C.

[081] In a particular embodiment, the invention provides a non-naturally occurring microbial organism, comprising a microbial organism having a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising citramalate synthase (A), citramalate dehydratase (citraconate forming) (B), and citraconate decarboxylase (C)(Figure 1, pathway (1) A/B/C). As disclosed herein, the microbial organism can comprise more than one exogenous nucleic acid encoding a methacrylic acid pathway enzyme, including up to all enzymes in a pathway, for example, three exogenous nucleic acids encode citramalate synthase, citramalate dehydratase (citraconate forming), and citraconate decarboxylase.

[082] In a particular embodiment, MAA producing non-naturally occurring microbial organism of the invention can have at least one exogenous nucleic acid that is a heterologous nucleic acid. In another embodiment the non-naturally occurring microbial organism producing MAA can be in a substantially anaerobic culture medium.

[083] In another embodiment, the invention provides a non-naturally occurring microbial organism comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising citramalate synthase (A), citramalate dehydratase (citraconate forming) (B), citraconate isomerase (G), and mesaconate decarboxylase (H)(Figure 1, pathway (2) A/B/G/H). In still another embodiment, the invention provides a non-naturally occurring microbial organism, comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising citramalate synthase (A), citramalate dehydratase (mesaconate forming) (F) citraconate isomerase (G), and citraconate decarboxylase (C)(Figure 1, pathway (3) A/F/G/C).

[084] In a further embodiment, the invention provides a non-naturally occurring microbial organism, comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising citramalate synthase (A), citramalate dehydratase (mesaconate forming) (F), and mesaconate decarboxylase (H)(Figure 1, pathway (4) A/F/H). In yet a further embodiment, the invention

provides a non-naturally occurring microbial organism, comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising citramalyl-CoA lyase (D), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (citraconate forming) (B), and citraconate decarboxylase (C)(Figure 1, pathway (5) D/E/B/C).

[085] In an additional embodiment, the invention provides a non-naturally occurring microbial organism, comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising citramalyl-CoA lyase (D), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (citraconate forming) (B), citraconate isomerase (G), and mesaconate decarboxylase (H)(Figure 1, pathway (6) D/E/B/G/H). In still another embodiment, the invention provides a non-naturally occurring microbial organism, comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising citramalyl-CoA lyase (D), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (mesaconate forming) (F), and mesaconate decarboxylase (H)(Figure 1, pathway (7) D/E/F/H).

[086] In another embodiment, the invention provides a non-naturally occurring microbial organism, comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising citramalyl-CoA lyase (D), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (mesaconate forming) (F), citraconate isomerase (G), and citraconate decarboxylase (C)(Figure 1, pathway (8) D/E/F/G/C). Additionally, the invention provides a non-naturally occurring microbial organism, comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising aconitate decarboxylase (I), itaconate isomerase (J), and citraconate decarboxylase (C)(Figure 1, pathway (9) I/J/C).

[087] In yet a further embodiment, the invention provides a non-naturally occurring microbial organism, comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising aconitate decarboxylase (I), itaconate isomerase (J), citraconate isomerase (G), and mesaconate decarboxylase (H)(Figure 1, pathway (10) I/J/G/H). In an additional embodiment, the invention provides a non-naturally occurring microbial organism, comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising aconitate decarboxylase (I), itaconyl-CoA transferase, synthetase or hydrolase (L), citramalyl-CoA dehydratase (K), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (citraconate forming) (B), and citraconate decarboxylase (C)(Figure 1, pathway (11) I/L/K/E/B/C).

[088] The invention also provides a non-naturally occurring microbial organism, comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising aconitate decarboxylase (I), itaconyl-CoA transferase, synthetase or hydrolase (L), citramalyl-CoA dehydratase (K), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (citraconate forming) (B), citraconate isomerase (G), and mesaconate decarboxylase (H)(Figure 1, pathway (12) I/L/K/E/B/G/H). In still a further embodiment, the invention provides a non-naturally occurring microbial organism, comprising a microbial organism having a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising aconitate decarboxylase (I), itaconyl-CoA transferase, synthetase or hydrolase (L), citramalyl-CoA dehydratase (K), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (mesaconate forming) (F), and mesaconate decarboxylase (H)(Figure 1, pathway (13) I/L/K/E/F/H). In an additional embodiment, the invention provides a non-naturally occurring microbial organism, comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising aconitate decarboxylase (I), itaconyl-CoA transferase, synthetase or hydrolase (L), citramalyl-CoA dehydratase (K),

citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (mesaconate forming) (F), citraconate isomerase (G), and citraconate decarboxylase (C)(Figure 1, pathway (14) I/L/K/E/F/G/C).

[089] In an additional embodiment, the invention provides a non-naturally occurring microbial organism having a methacrylic acid pathway, wherein the non-naturally occurring microbial organism comprises at least one exogenous nucleic acid encoding an enzyme or protein that converts a substrate to a product selected from the group consisting of acetyl-CoA and pyruvate to citramalate, citramalate to citraconate, and citraconate to methacrylate; acetyl-CoA and pyruvate to citramalyl-CoA, citramalyl-CoA to citramalate, citramalate to citraconate, and citraconate to methyacrylate; aconitate to itaconate, itaconate to itaconyl-CoA, itaconyl-CoA to citramalyl-CoA, citramalyl-CoA to citramalate, citramalate to mesaconate, mesaconate to methacrylate, and so forth such as the reactions described herein and those substrates and products shown in the exemplary methacrylic acid pathways shown in Figure 1. One skilled in the art will understand that these are merely exemplary and that any of the substrate-product pairs disclosed herein suitable to produce a desired product and for which an appropriate activity is available for the conversion of the substrate to the product can be readily determined by one skilled in the art based on the teachings herein. Thus, the invention provides a non-naturally occurring microbial organism containing at least one exogenous nucleic acid encoding an enzyme or protein, where the enzyme or protein converts the substrates and products of a methacrylic acid pathway, such as that shown in Figure 1. Additionally provided is a methacrylic acid pathway comprising acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, crotonase, 4-hydroxybutyryl-CoA dehydratase (or crotonyl-CoA hydratase, 4-hydroxy), 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA synthetase or 3-hydroxyisobutyryl-CoA hydrolase or 3-hydroxyisobutyryl-CoA transferase, and 3-hydroxyisobutyrate dehydratase (see Example XXII and Figure 21). Also provided is a methacrylic acid pathway comprising acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, crotonase, 4-hydroxybutyryl-CoA dehydratase, 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA dehydratase, and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase (see Example XXII and Figure 21).

[090] While generally described herein as a microbial organism that contains a methacrylic acid pathway, it is understood that the invention additionally provides a non-naturally occurring microbial organism comprising at least one exogenous nucleic acid

encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce an intermediate of a methacrylic acid pathway. For example, as disclosed herein, a methacrylic acid pathway is exemplified in Figure 1. Therefore, in addition to a microbial organism containing a methacrylic acid pathway that produces methacrylic acid, the invention additionally provides a non-naturally occurring microbial organism comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme, where the microbial organism produces a methacrylic acid pathway intermediate, for example, citramalyl-CoA, itaconyl-CoA, itaconate, citraconate, citramalate and mesaconate.

[091] It is understood that any of the pathways disclosed herein, as described in the Examples and exemplified in the pathways of Figures 1-30, can be utilized to generate a non-naturally occurring microbial organism that produces any pathway intermediate or product, as desired. As disclosed herein, such a microbial organism that produces an intermediate can be used in combination with another microbial organism expressing downstream pathway enzymes to produce a desired product. However, it is understood that a non-naturally occurring microbial organism that produces a methacrylic acid pathway intermediate can be utilized to produce the intermediate as a desired product.

[092] This invention is also directed, in part to engineered biosynthetic pathways to improve carbon flux through a central metabolism intermediate en route to methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate. The present invention provides non-naturally occurring microbial organisms having one or more exogenous genes encoding enzymes that can catalyze various enzymatic transformations en route to methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate. In some embodiments, these enzymatic transformations are part of the reductive tricarboxylic acid (RTCA) cycle and are used to improve product yields, including but not limited to, from carbohydrate-based carbon feedstock.

[093] In numerous engineered pathways, realization of maximum product yields based on carbohydrate feedstock is hampered by insufficient reducing equivalents or by loss of reducing equivalents and/or carbon to byproducts. In accordance with some embodiments, the present invention increases the yields of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate by (i) enhancing carbon fixation via the reductive TCA cycle, and/or (ii) accessing additional reducing equivalents from gaseous carbon sources and/or syngas components such as CO, CO_2, and/or H_2. In addition to

syngas, other sources of such gases include, but are not limted to, the atmosphere, either as found in nature or generated.

[094] The CO_2-fixing reductive tricarboxylic acid (RTCA) cycle is an endergenic anabolic pathway of CO_2 assimilation which uses reducing equivalents and ATP (Figure 12). One turn of the RTCA cycle assimilates two moles of CO_2 into one mole of acetyl-CoA, or four moles of CO_2 into one mole of oxaloacetate. This additional availability of acetyl-CoA improves the maximum theoretical yield of product molecules derived from carbohydrate-based carbon feedstock. Exemplary carbohydrates include but are not limited to glucose, sucrose, xylose, arabinose and glycerol.

[095] In some embodiments, the reductive TCA cycle, coupled with carbon monoxide dehydrogenase and/or hydrogenase enzymes, can be employed to allow syngas, CO_2, CO, H_2, and/or other gaseous carbon source utilization by microorganisms. Synthesis gas (syngas), in particular is a mixture of primarily H_2 and CO, sometimes including some amounts of CO_2, that can be obtained via gasification of any organic feedstock, such as coal, coal oil, natural gas, biomass, or waste organic matter. Numerous gasification processes have been developed, and most designs are based on partial oxidation, where limiting oxygen avoids full combustion, of organic materials at high temperatures (500-1500°C) to provide syngas as a 0.5:1-3:1 H_2/CO mixture. In addition to coal, biomass of many types has been used for syngas production and represents an inexpensive and flexible feedstock for the biological production of renewable chemicals and fuels. Carbon dioxide can be provided from the atmosphere or in condensed from, for example, from a tank cylinder, or via sublimation of solid CO_2. Similarly, CO and hydrogen gas can be provided in reagent form and/or mixed in any desired ratio. Other gaseous carbon forms can include, for example, methanol or similar volatile organic solvents.

[096] The components of synthesis gas and/or other carbon sources can provide sufficient CO_2, reducing equivalents, and ATP for the reductive TCA cycle to operate. One turn of the RTCA cycle assimilates two moles of CO_2 into one mole of acetyl-CoA and requires 2 ATP and 4 reducing equivalents. CO and/or H_2 can provide reducing equivalents by means of carbon monoxide dehydrogenase and hydrogenase enzymes, respectively. Reducing equivalents can come in the form of NADH, NADPH, FADH, reduced quinones, reduced ferredoxins, reduced flavodoxins and thioredoxins. The reducing equivalents, particularly NADH, NADPH, and reduced ferredoxin, can serve as cofactors for the RTCA

cycle enzymes, for example, malate dehydrogenase, fumarate reductase, alpha-ketoglutarate:ferredoxin oxidoreductase (alternatively known as 2-oxoglutarate:ferredoxin oxidoreductase, alpha-ketoglutarate synthase, or 2-oxoglutarate synthase), pyruvate:ferredoxin oxidoreductase and isocitrate dehydrogenase. The electrons from these reducing equivalents can alternatively pass through an ion-gradient producing electron transport chain where they are passed to an acceptor such as oxygen, nitrate, oxidized metal ions, protons, or an electrode. The ion-gradient can then be used for ATP generation via an ATP synthase or similar enzyme.

[097] The reductive TCA cycle was first reported in the green sulfur photosynthetic bacterium *Chlorobium limicola* (Evans et al., *Proc. Natl. Acad. Sci. U.S.A.* 55:928-934 (1966)). Similar pathways have been characterized in some prokaryotes (proteobacteria, green sulfur bacteria and thermophillic Knallgas bacteria) and sulfur-dependent archaea (Hugler et al., *J. Bacteriol.* 187:3020-3027 (2005; Hugler et al., *Environ. Microbiol.* 9:81-92 (2007). In some cases, reductive and oxidative (Krebs) TCA cycles are present in the same organism (Hugler et al., *supra* (2007); Siebers et al., *J. Bacteriol.* 186:2179-2194 (2004)). Some methanogens and obligate anaerobes possess incomplete oxidative or reductive TCA cycles that may function to synthesize biosynthetic intermediates (Ekiel et al., *J. Bacteriol.* 162:905-908 (1985); Wood et al., *FEMS Microbiol. Rev.* 28:335-352 (2004)).

[098] The key carbon-fixing enzymes of the reductive TCA cycle are alpha-ketoglutarate:ferredoxin oxidoreductase, pyruvate:ferredoxin oxidoreductase and isocitrate dehydrogenase. Additional carbon may be fixed during the conversion of phosphoenolpyruvate to oxaloacetate by phosphoenolpyruvate carboxylase or phosphoenolpyruvate carboxykinase or by conversion of pyruvate to malate by malic enzyme.

[099] Many of the enzymes in the TCA cycle are reversible and can catalyze reactions in the reductive and oxidative directions. However, some TCA cycle reactions are irreversible *in vivo* and thus different enzymes are used to catalyze these reactions in the directions required for the reverse TCA cycle. These reactions are: (1) conversion of citrate to oxaloacetate and acetyl-CoA, (2) conversion of fumarate to succinate, and (3) conversion of succinyl-CoA to alpha-ketoglutarate. In the TCA cycle, citrate is formed from the condensation of oxaloacetate and acetyl-CoA. The reverse reaction, cleavage of citrate to oxaloacetate and acetyl-CoA, is ATP-dependent and catalyzed by ATP-citrate lyase, or

citryl-CoA synthetase and citryl-CoA lyase. Alternatively, citrate lyase can be coupled to acetyl-CoA synthetase, an acetyl-CoA transferase, or phosphotransacetylase and acetate kinase to form acetyl-CoA and oxaloacetate from citrate. The conversion of succinate to fumarate is catalyzed by succinate dehydrogenase while the reverse reaction is catalyzed by fumarate reductase. In the TCA cycle succinyl-CoA is formed from the $NAD(P)^+$ dependent decarboxylation of alpha-ketoglutarate by the alpha-ketoglutarate dehydrogenase complex. The reverse reaction is catalyzed by alpha-ketoglutarate:ferredoxin oxidoreductase.

[0100] An organism capable of utilizing the reverse tricarboxylic acid cycle to enable production of acetyl-CoA-derived products on 1) CO, 2) CO_2 and H_2, 3) CO and CO_2, 4) synthesis gas comprising CO and H_2, and 5) synthesis gas or other gaseous carbon sources comprising CO, CO_2, and H_2 can include any of the following enzyme activities: ATP-citrate lyase, citrate lyase, aconitase, isocitrate dehydrogenase, alpha-ketoglutarate:ferredoxin oxidoreductase, succinyl-CoA synthetase, succinyl-CoA transferase, fumarate reductase, fumarase, malate dehydrogenase, acetate kinase, phosphotransacetylase, acetyl-CoA synthetase, acetyl-CoA transferase, pyruvate:ferredoxin oxidoreductase, NAD(P)H:ferredoxin oxidoreductase, carbon monoxide dehydrogenase, hydrogenase, and ferredoxin (see Figure 13). Enzyme enzymes and the corresponding genes required for these activities are described herein.

[0101] Carbon from syngas or other gaseous carbon sources can be fixed via the reverse TCA cycle and components thereof. Specifically, the combination of certain carbon gas-utilization pathway components with the pathways for formation of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate from acetyl-CoA results in high yields of these products by providing an efficient mechanism for fixing the carbon present in carbon dioxide, fed exogenously or produced endogenously from CO, into acetyl-CoA.

[0102] In some embodiments, a methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway in a non-naturally occurring microbial organism of the invention can utilize any combination of (1) CO, (2) CO_2, (3) H_2, or mixtures thereof to enhance the yields of biosynthetic steps involving reduction, including addition to driving the reductive TCA cycle.

[0103] In some embodiments a non-naturally occurring microbial organism having an methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway includes at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme. The at least one exogenous nucleic acid is selected from an ATP-citrate lyase, citrate lyase, a fumarate reductase, isocitrate dehydrogenase, aconitase, and an alpha-ketoglutarate:ferredoxin oxidoreductase; and at least one exogenous enzyme selected from a carbon monoxide dehydrogenase, a hydrogenase, a NAD(P)H:ferredoxin oxidoreductase, and a ferredoxin, expressed in a sufficient amount to allow the utilization of (1) CO, (2) CO_2, (3) H_2, (4) CO_2 and H_2, (5) CO and CO_2, (6) CO and H_2, or (7) CO, CO_2, and H_2.

[0104] In some embodiments a method includes culturing a non-naturally occurring microbial organism having a methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway also comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme. The at least one exogenous nucleic acid is selected from an ATP-citrate lyase, citrate lyase, a fumarate reductase, isocitrate dehydrogenase, aconitase, and an alpha-ketoglutarate:ferredoxin oxidoreductase. Additionally, such an organism can also include at least one exogenous enzyme selected from a carbon monoxide dehydrogenase, a hydrogenase, a NAD(P)H:ferredoxin oxidoreductase, and a ferredoxin, expressed in a sufficient amount to allow the utilization of (1) CO, (2) CO_2, (3) H_2, (4) CO_2 and H_2, (5) CO and CO_2, (6) CO and H_2, or (7) CO, CO_2, and H_2 to produce a product.

[0105] In some embodiments a non-naturally occurring microbial organism having an methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway further includes at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme expressed in a sufficient amount to enhance carbon flux through acetyl-CoA. The at least one exogenous nucleic acid is selected from an ATP-citrate lyase, citrate lyase, a fumarate reductase, a pyruvate:ferredoxin oxidoreductase, isocitrate dehydrogenase, aconitase and an alpha-ketoglutarate:ferredoxin oxidoreductase.

[0106] In some embodiments a non-naturally occurring microbial organism having an methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway includes at least one exogenous nucleic acid encoding an enzyme expressed in a sufficient amount to enhance the availability of reducing equivalents in the presence of carbon monoxide and/or hydrogen, thereby increasing the yield of redox-limited products

via carbohydrate-based carbon feedstock. The at least one exogenous nucleic acid is selected from a carbon monoxide dehydrogenase, a hydrogenase, an NAD(P)H:ferredoxin oxidoreductase, and a ferredoxin. In some embodiments, the present invention provides a method for enhancing the availability of reducing equivalents in the presence of carbon monoxide or hydrogen thereby increasing the yield of redox-limited products via carbohydrate-based carbon feedstock, such as sugars or gaseous carbon sources, the method includes culturing this non-naturally occurring microbial organism under conditions and for a sufficient period of time to produce methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate.

[0107] In some embodiments, the non-naturally occurring microbial organism having an methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway includes two exogenous nucleic acids each encoding a reductive TCA pathway enzyme. In some embodiments, the non-naturally occurring microbial organism having an methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway includes three exogenous nucleic acids each encoding a reductive TCA pathway enzyme. In some embodiments, the non-naturally occurring microbial organism includes three exogenous nucleic acids encoding an ATP-citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase. In some embodiments, the non-naturally occurring microbial organism includes three exogenous nucleic acids encoding a citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase. In some embodiments, the non-naturally occurring microbial organism includes four exogenous nucleic acids encoding a pyruvate:ferredoxin oxidoreductase; a phosphoenolpyruvate carboxylase or a phosphoenolpyruvate carboxykinase, a CO dehydrogenase; and an H_2 hydrogenase. In some embodiments, the non-naturally occurring microbial organism includes two exogenous nucleic acids encoding a CO dehydrogenase and an H_2 hydrogenase.

[0108] In some embodiments, the non-naturally occurring microbial organisms having an methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway further include an exogenous nucleic acid encoding an enzyme selected from a pyruvate:ferredoxin oxidoreductase, an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, an acetate

kinase, a phosphotransacetylase, an acetyl-CoA synthetase, an NAD(P)H:ferredoxin oxidoreductase, and combinations thereof.

[0109] In some embodiments, the non-naturally occurring microbial organism having an methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway further includes an exogenous nucleic acid encoding an enzyme selected from carbon monoxide dehydrogenase, acetyl-CoA synthase, ferredoxin, NAD(P)H:ferredoxin oxidoreductase and combinations thereof.

[0110] In some embodiments, the non-naturally occurring microbial organism having an methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway utilizes a carbon feedstock selected from (1) CO, (2) CO_2, (3) CO_2 and H_2, (4) CO and H_2, or (5) CO, CO_2, and H_2. In some embodiments, the non-naturally occurring microbial organism having an methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway utilizes hydrogen for reducing equivalents. In some embodiments, the non-naturally occurring microbial organism having an methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway utilizes CO for reducing equivalents. In some embodiments, the non-naturally occurring microbial organism having an methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway utilizes combinations of CO and hydrogen for reducing equivalents.

[0111] In some embodiments, the non-naturally occurring microbial organism having an methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway further includes one or more nucleic acids encoding an enzyme selected from a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a pyruvate carboxylase, and a malic enzyme.

[0112] In some embodiments, the non-naturally occurring microbial organism having an methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway further includes one or more nucleic acids encoding an enzyme selected from a malate dehydrogenase, a fumarase, a fumarate reductase, a succinyl-CoA synthetase, and a succinyl-CoA transferase.

[0113] In some embodiments, the non-naturally occurring microbial organism having an methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate

pathway can have or optionally further includes at least one exogenous nucleic acid encoding a citrate lyase, an ATP-citrate lyase, a citryl-CoA synthetase, a citryl-CoA lyase an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, an acetate kinase, a phosphotransacetylase, an acetyl-CoA synthetase, and a ferredoxin.

[0114] It is understood by those skilled in the art that the pathways described herein for increasing product yield can be combined with any of the pathways disclosed herein, including those pathways depicted in the figures. One skilled in the art will understand that, depending on the pathway to a desired product and the precursors and intermediates of that pathway, a particular pathway for improving product yield, as discussed herein and in the examples, or combination of such pathways, can be used in combination with a pathway to a desired product to increase the yield of that product or a pathway intermediate.

[0115] The invention also provides a non-naturally occurring microbial organism, comprising a microbial organism having a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid; said non-naturally occurring microbial organism further comprising: (i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from an ATP-citrate lyase, citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase, or optionally isocitrate dehydrogenase, aconitase, citryl-CoA synthetase or citryl-CoA lyase; (ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or (iii) at least one exogenous nucleic acid encodes an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof; wherein said methacrylic acid pathway comprises a pathway selected from: (a) citramalate synthase, citramalate dehydratase (citraconate forming), and citraconate decarboxylase; (b) citramalate synthase, citramalate dehydratase (citraconate forming), citraconate isomerase, and mesaconate decarboxylase; (c) citramalate synthase, citramalate dehydratase (mesaconate forming), citraconate isomerase, and citraconate decarboxylase; (d) citramalate synthase, citramalate dehydratase (mesaconate

forming), and mesaconate decarboxylase; (e) citramalyl-CoA lyase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (citraconate forming), and citraconate decarboxylase; (f) citramalyl-CoA lyase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (citraconate forming), citraconate isomerase, and mesaconate decarboxylase; (g) citramalyl-CoA lyase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (mesaconate forming), and mesaconate decarboxylase; (h) citramalyl-CoA lyase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (mesaconate forming), citraconate isomerase, and citraconate decarboxylase; (i) aconitate decarboxylase, itaconate isomerase, and citraconate decarboxylase; (j) aconitate decarboxylase, itaconate isomerase, citraconate isomerase, and mesaconate decarboxylase; (k) aconitate decarboxylase, itaconyl-CoA transferase, synthetase or hydrolase, citramalyl-CoA dehydratase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (citraconate forming), and citraconate decarboxylase; (l) aconitate decarboxylase, itaconyl-CoA transferase, synthetase or hydrolase, citramalyl-CoA dehydratase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (citraconate forming), citraconate isomerase, and mesaconate decarboxylase; (m) aconitate decarboxylase, itaconyl-CoA transferase, synthetase or hydrolase, citramalyl-CoA dehydratase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (mesaconate forming), and mesaconate decarboxylase;(n) aconitate decarboxylase, itaconyl-CoA transferase, synthetase or hydrolase, citramalyl-CoA dehydratase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (mesaconate forming), citraconate isomerase, and citraconate decarboxylase; (o) 3-hydroxyisobutyrate dehydratase; (p) methylmalonyl-CoA mutase, methylmalonyl-CoA reductase, 3-hydroxyisobutyrate dehydrogenase, and 3-hydroxyisobutyrate dehydratase; (q) methylmalonyl-CoA mutase, methylmalonyl-CoA epimerase, methylmalonyl-CoA reductase, 3-hydroxyisobutyrate dehydrogenase, and 3-hydroxyisobutyrate dehydratase; (r) methylmalonyl-CoA mutase, alcohol/aldehyde dehydrogenase, and 3-hydroxyisobutyrate dehydratase; (s) methylmalonyl-CoA mutase, methylmalonyl-CoA epimerase, alcohol/aldehyde dehydrogenase, and 3-hydroxyisobutyrate dehydratase; (t) methylmalonyl-CoA mutase, methylmalonyl-CoA reductase, 3-amino-2-methylpropionate transaminase, and 3-amino-2-methylpropionate ammonia lyase; (u) methylmalonyl-CoA mutase, methylmalonyl-CoA epimerase, methylmalonyl-CoA reductase, 3-amino-2-methylpropionate transaminase, and 3-amino-2-methylpropionate ammonia lyase; (v) 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA synthetase or 3-hydroxyisobutyryl-CoA hydrolase or 3-

hydroxyisobutyryl-CoA transferase, and 3-hydroxyisobutyrate dehydratase; (w) aspartate aminotransferase, glutamate mutase, 3-methylaspartase, and mesaconate decarboxylase; (x) alpha-ketoglutarate reductase, 2-hydroxyglutamate mutase, 3-methylmalate dehydratase, and mesaconate decarboxylase; (y) acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, 3-hydroxybutyryl-CoA mutase, 2-hydroxyisobutyryl-CoA dehydratase, and methacrylyl-CoA transferase or methacrylyl-CoA hydrolase or methacrylyl-CoA synthetase; (z) acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, 3-hydroxybutyryl-CoA mutase, 2-hydroxyisobutyryl-CoA dehydratase, enoyl-CoA hydratase, and 3-hydroxyisobutyryl-CoA hydrolase or 3-hydroxyisobutyryl-CoA synthetase or 3-hydroxyisobutyryl-CoA transferase, and 3-hydroxyisobutyrate dehydratase; (aa) 4-hydroxybutyryl-CoA dehydratase, vinylacetyl-CoA Δ-isomerase, crotonase, 3-hydroxybutyryl-CoA mutase, 2-hydroxyisobutyryl-CoA dehydratase, and any of methacrylyl-CoA hydrolase or methacrylyl-CoA synthetase or methacrylyl-CoA transferase; (bb) 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA dehydratase, and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase; (cc) acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, crotonase, butyryl-CoA dehydrogenase, isobutyryl-CoA mutase, isobutyryl-CoA dehydrogenase, and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase; (dd) lactate dehydrogenase, lactate-CoA transferase, lactoyl-CoA dehydratase, acyl-CoA dehydrogenase, propionyl-CoA carboxylase, methylmalonyl-CoA reductase, 3-hydroxyisobutyrate dehydrogenase, and 3-hydroxyisobutyrate dehydratase; (ee) valine aminotransferase, 2-ketoisovalerate dehydrogenase, isobutyryl-CoA dehydrogenase, and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase; (ff) valine aminotransferase, 2-ketoisovalerate dehydrogenase, isobutyryl-CoA dehydrogenase, methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase, acetolactate synthase, acetohydroxy acid isomeroreductase and dihydroxy-acid dehydratase; (gg) acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, crotonase, 4-hydroxybutyryl-CoA dehydratase, 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA synthetase or 3-hydroxyisobutyryl-CoA hydrolase or 3-hydroxyisobutyryl-CoA transferase, and 3-hydroxyisobutyrate dehydratase; and (hh) acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, crotonase, 4-hydroxybutyryl-CoA dehydratase, 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA dehydratase, and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase.

[0116] The invention additionally provides a non-naturally occurring microbial organism having a 2-hydroxyisobutyric acid pathway comprising at least one exogenous nucleic acid encoding a 2-hydroxyisobutyric acid pathway enzyme expressed in a sufficient amount to produce 2-hydroxyisobutyric acid. Such a non-naturally occurring microbial organism can further comprise (i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein the at least one exogenous nucleic acid is selected from an ATP-citrate lyase, citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase, or optionally isocitrate dehydrogenase, aconitase, citryl-CoA synthetase or citryl-CoA lyase; (ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein the at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or (iii) at least one exogenous nucleic acid encodes an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof; wherein the 2-hydroxyisobutyric acid pathway comprises a pathway selected from (a) acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, 3-hydroxybutyryl-CoA mutase, and 2-hydroxyisobutyryl-CoA transferase or 2-hydroxyisobutyryl-CoA hydrolase or 2-hydroxyisobutyryl-CoA synthetase; and (b) 4-hydroxybutyryl-CoA dehydratase, vinylacetyl-CoA Δ-isomerase, crotonase, 3-hydroxybutyryl-CoA mutase, and any of 2-hydroxyisobutyryl-CoA hydrolase or 2-hydroxyisobutyryl-CoA synthetase or 2-hydroxyisobutyryl-CoA transferase (see Figures 16C). The non-naturally occurring microbial organism can compriase two, three, four or five exogenous nucleic acids each encoding a methacrylic acid pathway enzyme, up to all enzymes of the pathway.

[0117] The invention further provides a non-naturally occurring microbial organism comprising a microbial organism having a 3-hydroxyisobutyric acid pathway comprising at least one exogenous nucleic acid encoding a 3-hydroxyisobutyric acid pathway enzyme expressed in a sufficient amount to produce 3-hydroxyisobutyric acid. The non-naturally occurring microbial organism can further comprise (i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from an ATP-citrate lyase, citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase, or optionally isocitrate dehydrogenase, aconitase, citryl-CoA synthetase or citryl-CoA lyase; (ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive

TCA pathway enzyme, wherein the at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or (iii) at least one exogenous nucleic acid encodes an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof; wherein the 3-hydroxyisobutyric acid pathway comprises a pathway selected fromb (a) 4-hydroxybutyryl-CoA mutase; and (b) 4-hydroxybutyryl-CoA mutase and 3-hydroxyisobutyryl-CoA synthetase or 3-hydroxyisobutyryl-CoA hydrolase or 3-hydroxyisobutyryl-CoA transferase (see Figure 16B). The non-naturally occurring microbial organism can comprise two exogenous nucleic acids each encoding a methacrylic acid pathway enzyme.

[0118] The invention also provides a non-naturally occurring microbial organism comprising a microbial organism having a 3-hydroxyisobutyryl-CoA pathway comprising at least one exogenous nucleic acid encoding a 3-hydroxyisobutyric acid pathway enzyme expressed in a sufficient amount to produce 3-hydroxyisobutyric acid. The non-naturally occurring microbial organism can further comprise (i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein the at least one exogenous nucleic acid is selected from an ATP-citrate lyase, citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase, or optionally isocitrate dehydrogenase, aconitase, citryl-CoA synthetase or citryl-CoA lyase; (ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein the at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or (iii) at least one exogenous nucleic acid encodes an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof; wherein the 3-hydroxyisobutyryl-CoA pathway comprises 4-hydroxybutyryl-CoA mutase (see Figure 16B).

[0119] In a further embodiment, the microbial organism comprising (i) further comprises an exogenous nucleic acid encoding an enzyme selected from a pyruvate:ferredoxin oxidoreductase, an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, an acetate kinase, a phosphotransacetylase, an acetyl-CoA synthetase, an NAD(P)H:ferredoxin oxidoreductase, ferredoxin, and combinations thereof; a microbial organism comprising (ii) further comprises

an exogenous nucleic acid encoding an enzyme selected from an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, and combinations thereof.

[0120] Such a microbial organism can comprise two, three, four, five, six or seven exogenous nucleic acids each encoding a methacrylic acid pathway enzyme, up to all of the enzymes of a pathway. For example, the microbial organism can comprises (a) three exogenous nucleic acids encoding citramalate synthase, citramalate dehydratase (citraconate forming), and citraconate decarboxylase; (b) four exogenous nucleic acids encoding citramalate synthase, citramalate dehydratase (citraconate forming), citraconate isomerase, and mesaconate decarboxylase; (c) four exogenous nucleic acids encoding citramalate synthase, citramalate dehydratase (mesaconate forming), citraconate isomerase, and citraconate decarboxylase; (d) three exogenous nucleic acids encoding citramalate synthase, citramalate dehydratase (mesaconate forming), and mesaconate decarboxylase; (e) four exogenous nucleic acids encoding citramalyl-CoA lyase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (citraconate forming), and citraconate decarboxylase; (f) five exogenous nucleic acids encoding citramalyl-CoA lyase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (citraconate forming), citraconate isomerase, and mesaconate decarboxylase; (g) four exogenous nucleic acids encoding citramalyl-CoA lyase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (mesaconate forming), and mesaconate decarboxylase; (h) five exogenous nucleic acids encoding citramalyl-CoA lyase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (mesaconate forming), citraconate isomerase, and citraconate decarboxylase; (i) three exogenous nucleic acids encoding aconitate decarboxylase, itaconate isomerase, and citraconate decarboxylase; (j) four exogenous nucleic acids encoding aconitate decarboxylase, itaconate isomerase, citraconate isomerase, and mesaconate decarboxylase; (k) six exogenous nucleic acids encoding aconitate decarboxylase, itaconyl-CoA transferase, synthetase or hydrolase, citramalyl-CoA dehydratase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (citraconate forming), and citraconate decarboxylase; (l) seven exogenous nucleic acids encoding aconitate decarboxylase, itaconyl-CoA transferase, synthetase or hydrolase, citramalyl-CoA dehydratase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (citraconate forming), citraconate isomerase, and mesaconate decarboxylase; (m) six exogenous nucleic acids encoding aconitate decarboxylase, itaconyl-CoA transferase,

synthetase or hydrolase, citramalyl-CoA dehydratase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (mesaconate forming), and mesaconate decarboxylase; or (n) seven exogenous nucleic acids encoding aconitate decarboxylase, itaconyl-CoA transferase, synthetase or hydrolase, citramalyl-CoA dehydratase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (mesaconate forming), citraconate isomerase, and citraconate decarboxylase; (o) one exogenous nucleic acid encoding 3-hydroxyisobutyrate dehydratase; (p) four exogenous nucleic acids encoding methylmalonyl-CoA mutase, methylmalonyl-CoA reductase, 3-hydroxyisobutyrate dehydrogenase, and 3-hydroxyisobutyrate dehydratase; (q) five exogenous nucleic acids encoding methylmalonyl-CoA mutase, methylmalonyl-CoA epimerase, methylmalonyl-CoA reductase, 3-hydroxyisobutyrate dehydrogenase, and 3-hydroxyisobutyrate dehydratase; (r) three exogenous nucleic acids encoding methylmalonyl-CoA mutase, alcohol/aldehyde dehydrogenase, and 3-hydroxyisobutyrate dehydratase; (s) four exogenous nucleic acids encoding methylmalonyl-CoA mutase, methylmalonyl-CoA epimerase, alcohol/aldehyde dehydrogenase, and 3-hydroxyisobutyrate dehydratase; (t) four exogenous nucleic acids encoding methylmalonyl-CoA mutase, methylmalonyl-CoA reductase, 3-amino-2-methylpropionate transaminase, and 3-amino-2-methylpropionate ammonia lyase; (u) five exogenous nucleic acids encoding methylmalonyl-CoA mutase, methylmalonyl-CoA epimerase, methylmalonyl-CoA reductase, 3-amino-2-methylpropionate transaminase, and 3-amino-2-methylpropionate ammonia lyase; (v) three exogenous nucleic acids encoding 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA synthetase or 3-hydroxyisobutyryl-CoA hydrolase or 3-hydroxyisobutyryl-CoA transferase, and 3-hydroxyisobutyrate dehydratase; (w) four exogenous nucleic acids encoding aspartate aminotransferase, glutamate mutase, 3-methylaspartase, and mesaconate decarboxylase; (x) four exogenous nucleic acids encoding alpha-ketoglutarate reductase, 2-hydroxyglutamate mutase, 3-methylmalate dehydratase, and mesaconate decarboxylase; (y) five exogenous nucleic acids encoding acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, 3-hydroxybutyryl-CoA mutase, 2-hydroxyisobutyryl-CoA dehydratase, and methacrylyl-CoA transferase or methacrylyl-CoA hydrolase or methacrylyl-CoA synthetase; (z) seven exogenous nucleic acids encoding acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, 3-hydroxybutyryl-CoA mutase, 2-hydroxyisobutyryl-CoA dehydratase, enoyl-CoA hydratase, and 3-hydroxyisobutyryl-CoA hydrolase or 3-hydroxyisobutyryl-CoA synthetase or 3-hydroxyisobutyryl-CoA transferase, and 3-hydroxyisobutyrate dehydratase; (aa) six

exogenous nucleic acids encoding 4-hydroxybutyryl-CoA dehydratase, vinylacetyl-CoA Δ-isomerase, crotonase, 3-hydroxybutyryl-CoA mutase, 2-hydroxyisobutyryl-CoA dehydratase, and any of methacrylyl-CoA hydrolase or methacrylyl-CoA synthetase or methacrylyl-CoA transferase; (bb) three exogenous nucleic acids encoding 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA dehydratase, and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase; (cc) acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, crotonase, butyryl-CoA dehydrogenase, isobutyryl-CoA mutase, isobutyryl-CoA dehydrogenase, and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase; (dd) lactate dehydrogenase, lactate-CoA transferase, lactoyl-CoA dehydratase, acyl-CoA dehydrogenase, propionyl-CoA carboxylase, methylmalonyl-CoA reductase, 3-hydroxyisobutyrate dehydrogenase, and 3-hydroxyisobutyrate dehydratase; (ee) valine aminotransferase, 2-ketoisovalerate dehydrogenase, isobutyryl-CoA dehydrogenase, and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase; (ff) valine aminotransferase, 2-ketoisovalerate dehydrogenase, isobutyryl-CoA dehydrogenase, methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase, acetolactate synthase, acetohydroxy acid isomeroreductase and dihydroxy-acid dehydratase; (gg) acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, crotonase, 4-hydroxybutyryl-CoA dehydratase, 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA synthetase or 3-hydroxyisobutyryl-CoA hydrolase or 3-hydroxyisobutyryl-CoA transferase, and 3-hydroxyisobutyrate dehydratase; and (hh) acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, crotonase, 4-hydroxybutyryl-CoA dehydratase, 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA dehydratase, and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase.

[0121] In another embodiment, a microbial organism can comprise two, three, four or five exogenous nucleic acids each encoding enzymes of (i), (ii) or (iii). For example, amicrobial organism comprising (i) can comprise four exogenous nucleic acids encoding ATP-citrate lyase, citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase; amicrobial organism comprising (ii) can comprise five exogenous nucleic acids encoding pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or a microbial organism comprising (iii) can comprise two exogenous nucleic acids encoding CO dehydrogenase and H_2 hydrogenase.

[0122] The invention additionally provides a non-naturally occurring microbial organism comprising a microbial organism having a 2-hydroxyisobutyric acid pathway comprising at least one exogenous nucleic acid encoding a 2-hydroxyisobutyric acid pathway enzyme expressed in a sufficient amount to produce 2-hydroxyisobutyric acid; wherein said 2-hydroxyisobutyric acid pathway enzymes are selected from those shown in Figure 16C; said non-naturally occurring microbial organism further comprising: (i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from an ATP-citrate lyase, citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase, or optionally isocitrate dehydrogenase, aconitase, citryl-CoA synthetase or citryl-CoA lyase; (ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or (iii) at least one exogenous nucleic acid encodes an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof.

[0123] In a further embodiment, the invention provides a non-naturally occurring microbial organism comprising a microbial organism having a 3-hydroxyisobutyric acid pathway comprising at least one exogenous nucleic acid encoding a 3-hydroxyisobutyric acid pathway enzyme expressed in a sufficient amount to produce 3-hydroxyisobutyric acid; wherein said 2-hydroxyisobutyric acid pathway enzymes are selected from those shown in Figure 16B; said non-naturally occurring microbial organism further comprising (i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from an ATP-citrate lyase, citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase, or optionally isocitrate dehydrogenase, aconitase, citryl-CoA synthetase or citryl-CoA lyase; (ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or (iii) at least one exogenous nucleic acid encodes an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof.

[0124] This invention is directed, in part, to improving the theoretical yields of products using syngas or its components, hydrogen, carbon dioxide and carbon monoxide, as a source of reducing equivalents. In numerous engineered pathways, realization of maximum product yields based on carbohydrate feedstock is hampered by insufficient reducing equivalents or by loss of reducing equivalents and/or carbon to byproducts. The theoretical yields of several products on carbohydrate feedstocks increase substantially if hydrogen and/or carbon monoxide can supply sufficient reducing equivalents. For example, the theoretical yields of MAA, 2-hydroxyisobutyrate and 3-hydroxyisobutyrate increase to 2 mol/mol glucose in the presence of H_2.

[0125] Reducing equivalents, or electrons, can be extracted from synthesis gas components such as CO and H_2 using carbon monoxide dehydrogenase (CODH) and hydrogenase enzymes, respectively. The reducing equivalents are then passed to acceptors such as oxidized ferredoxins, oxidized quinones, oxidized cytochromes, NADP+, water, or hydrogen peroxide to form reduced ferredoxin, reduced quinones, reduced cytochromes, NAD(P)H, H_2, or water, respectively. Reduced ferredoxin and NAD(P)H are particularly useful as they can serve as redox carriers for various Wood-Ljungdahl pathway and reductive TCA cycle enzymes.

[0126] Here, we show specific examples of how additional redox availability from CO and/or H_2 can improve the yields of reduced products such as methacrylic acid, 2-hydroxyisobutyrate and 3-hydroxyisobutyrate.

[0127] Methacrylic acid (MAA), 3-hydroxybutyric acid and 2-hydroxyisobutyric acid are exemplary reduced products. The production of MAA through fermentation has a theoretical yield of 1.33 moles MAA per mole of glucose. It is most commonly produced from the acetone cyanohydrin (ACH) route using the raw materials acetone and hydrogen cyanide as raw materials. The intermediate cyanohydrin is converted with sulfuric acid to a sulfate ester of the methacrylamide, hydrolysis of which gives ammonium bisulfate and MAA. Other producers start with an isobutylene or, equivalently, tert-butanol, which is oxidized to methacrolein, and again oxidized to methacrylic acid. MAA is then esterified with methanol to MMA. Methacrylic acid is used industrially in the preparation of its esters, known collectively as methacrylates, such as methyl methacrylate. The methacrylates have numerous uses, most notably in the manufacture of polymers.

$$C_6H_{12}O_6 \rightarrow 1.33\ C_4H_6O_2 + 0.67\ CO_2 + 2\ H_2O$$

[0128] When the combined feedstocks strategy is applied to MAA production, the reducing equivlents generated from syngas can increase the MAA theoretical yield from glucose to 2 mol MAA per mol of glucose with the pathways detailed in Figure 16A and 16B.

$$1\ C_6H_{12}O_6 + 2\ CO_2 + 6\ H_2 \rightarrow 2\ C_4H_6O_2 + 6\ H_2O$$

or

$$1\ C_6H_{12}O_6 + 2\ CO + 4\ H_2 \rightarrow 2\ C_4H_6O_2 + 4\ H_2O$$

[0129] Similarly, the production of 3-hydroxyisobutyric acid through fermentation can be improved by the combined feedstock strategy. The production of 3-hydroxyisobutyric acid through fermentation has a theoretical yield of 1.33 mol 3-hydroxyisobutyric acid per mol of glucose.

$$3\ C_6H_{12}O_6 \rightarrow 4\ C_4H_8O_3 + 2\ CO_2 + 2\ H_2O$$

[0130] When the combined feedstocks strategy is applied to 3-hydroxyisobutyric acid production, the reducing equivlents generated from syngas can increase the 3-hydroxyisobutyric acid theoretical yield from glucose to 2 mol 3-hydroxyisobutyric acid per mol of glucose with the pathways detailed in Figure 16A and 16B.

$$1\ C_6H_{12}O_6 + 2\ CO_2 + 6\ H_2 \rightarrow 2\ C_4H_8O_3 + 4\ H_2O$$

[0131] Similarly, the production of 2-hydroxyisobutyric acid through fermentation can be improved by the combined feedstock strategy. The production of 2-hydroxyisobutyric acid through fermentation has a theoretical yield of 1.33 mol 2-hydroxyisobutyric acid per mol of glucose.

$$3\ C_6H_{12}O_6 \rightarrow 4\ C_4H_8O_3 + 2\ CO_2 + 2\ H_2O$$

[0132] When the combined feedstocks strategy is applied to 3-hydroxyisobutyric acid production, the reducing equivlents generated from syngas can increase the 3-hydroxyisobutyric acid theoretical yield from glucose to 2 mol 2-hydroxyisobutyric acid per mol of glucose with the pathways detailed in Figure 16B.

$$1\ C_6H_{12}O_6 + 2\ CO_2 + 6\ H_2 \rightarrow 2\ C_4H_8O_3 + 4\ H_2O$$

[0133] The invention is also directed in part to increasing carbon flux through the central metabolism intermediate, acetyl-CoA, en route to product molecules by enhancing carbon fixation via the reductive TCA cycle. Exemplary product molecules include methacrylic acid and 2-hydroxyisobutyrate, although given the teachings and guidance provided herein, it will be recognized by one skilled in the art that any product molecule that has acetyl-CoA as a building block can exhibit enhanced production through increased carbon flux through acetyl-CoA. The present invention provides non-naturally occurring microbial organisms having one or more exogenous genes encoding enzymes that can catalyze various enzymatic transformations en route to acetyl-CoA. In some embodiments, these enzymatic transformations are part of the reductive tricarboxylic acid (RTCA) cycle and are used to improve product yields from carbohydrate-based carbon feedstock. In other embodiments, these enzymatic transformations are part of the Wood-Ljungdahl pathway.

[0134] The CO_2-fixing reductive tricarboxylic acid (RTCA) cycle is an endergenic anabolic pathway of CO_2 assimilation which uses NAD(P)H and ATP. One turn of the RTCA cycle assimilates two moles of CO_2 into one mole of acetyl-CoA, or four moles of CO_2 into one mole of oxaloacetate. This additional availability of acetyl-CoA improves the maximum theoretical yield of product molecules derived from carbohydrate-based carbon feedstock. Exemplary carbohydrates include but are not limited to glucose, sucrose, xylose, arabinose and glycerol. Note that the pathways for the exemplary product molecules described herein all proceed through acetyl-CoA.

[0135] The production of MAA from sugars via the pathways shown in Figures 16C, 16D and 16E has a maximum yield of 1 mole MAA per mole glucose consumed, in the absence of reductive TCA cycle activity. The fixation of carbon by the reductive TCA cycle increases the yield of these pathways to the maximum theoretical yield of MAA from sugars. Figures 16C and 16D are exemplary flux distributions showing how additional carbon generated by the reductive TCA cycle increases the yield of methacrylic acid produced by these pathways from 1 mole/mole glucose to 1.33 moles per mole glucose.

$$C_6H_{12}O_6 \rightarrow 1.33\ C_4H_6O_2 + 0.67\ CO_2 + 2\ H_2O$$

[0136] In one embodiment, the invention provides a non-naturally occurring microbial organism, comprising a microbial organism having a methacrylate ester pathway comprising at least one exogenous nucleic acid encoding a methacrylate ester pathway enzyme expressed in a sufficient amount to produce a methacrylate ester; said non-naturally occurring microbial

organism further comprising: (i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from an ATP-citrate lyase, a citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase, or optionally isocitrate dehydrogenase, aconitase, citryl-CoA synthetase or citryl-CoA lyase; (ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H2 hydrogenase; or (iii) at least one exogenous nucleic acid encodes an enzyme selected from a CO dehydrogenase, an H2 hydrogenase, and combinations thereof; wherein said methacrylate ester pathway comprises an alcohol transferase or an ester-forming enzyme, and a dehydratase. In one aspect, the dehydratase converts a 3-hydroxyisobutyrate ester or a 2-hydroxyisobutyrate ester to said methacrylate ester. In one aspect, the alcohol transferase coverts 3-hydroxyisobutyryl-CoA to a 3-hydroxyisobutyrate ester or 2-hydroxyisobutyryl-CoA to 2-hydroxyisobutyrate ester.

[0137] In one embodiment, the invention provides a microbial organism, wherein the microbial organism further comprises a methacyrlate ester pathway comprising at least one exogenous nucleic acid encoding a methacrylate ester pathway enzyme expressed in a sufficient amount to produce a methacrylate ester, said methacrylate ester pathway comprising a pathway selected from: (a) a 3-hydroxyisobutyrate-CoA transferase or a 3-hydroxyisobutyrate-CoA synthetase; an alcohol transferase; and a dehydratase; (b) a 3-hydroxyisobutyrate ester-forming enzyme and a dehydratase; (c) a 2-hydroxyisobutyrate-CoA transferase or a 2-hydroxyisobutyrate-CoA synthetase; an alcohol transferase; and a dehydratase; or (d) a 2-hydroxyisobutyrate ester-forming enzyme and a dehydratase. In another aspect, the microbial organism comprising (i) further comprises an exogenous nucleic acid encoding an enzyme selected from a pyruvate:ferredoxin oxidoreductase, an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, an acetate kinase, a phosphotransacetylase, an acetyl-CoA synthetase, an NAD(P)H:ferredoxin oxidoreductase, ferredoxin, and combinations thereof. In another aspect, the microbial organism comprising (ii) further comprises an exogenous nucleic acid encoding an enzyme selected from an aconitase, an isocitrate dehydrogenase, a

succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, and combinations thereof.

[0138] In one aspect, the microbial organism comprises two exogenous nucleic acids each encoding a methacrylic acid pathway enzyme. In another aspect, the two exogenous nucleic acids encode an alcohol transferase and a dehydratase or alternatively an ester-forming enzyme and a dehydratase.

[0139] In one embodiment the invention provides a non-naturally occurring microbial, wherein said microbial organism comprising (i) comprises four exogenous nucleic acids encoding an ATP-citrate lyase, citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase; wherein said microbial organism comprising (ii) comprises five exogenous nucleic acids encoding a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H2 hydrogenase; or wherein said microbial organism comprising (iii) comprises two exogenous nucleic acids encoding a CO dehydrogenase and an H2 hydrogenase.

[0140] In one embodiment, the invention provide a method for producing a methacrylate ester comprising, culturing the non-naturally occurring microbial organism as described herein under conditions and for a sufficient period of time to produce methacrylate ester.

[0141] The invention is described herein with general reference to the metabolic reaction, reactant or product thereof, or with specific reference to one or more nucleic acids or genes encoding an enzyme associated with or catalyzing, or a protein associated with, the referenced metabolic reaction, reactant or product. Unless otherwise expressly stated herein, those skilled in the art will understand that reference to a reaction also constitutes reference to the reactants and products of the reaction. Similarly, unless otherwise expressly stated herein, reference to a reactant or product also references the reaction, and reference to any of these metabolic constituents also references the gene or genes encoding the enzymes that catalyze or proteins involved in the referenced reaction, reactant or product. Likewise, given the well known fields of metabolic biochemistry, enzymology and genomics, reference herein to a gene or encoding nucleic acid also constitutes a reference to the corresponding encoded enzyme and the reaction it catalyzes or a protein associated with the reaction as well as the reactants and products of the reaction.

[0142] As disclosed herein, the product methacrylic acid, as well as other intermediates, are carboxylic acids, which can occur in various ionized forms, including fully protonated, partially protonated, and fully deprotonated forms. Accordingly, the suffix "-ate," or the acid form, can be used interchangeably to describe both the free acid form as well as any deprotonated form, in particular since the ionized form is known to depend on the pH in which the compound is found. It is understood that carboxylate products or intermediates includes ester forms of carboxylate products or pathway intermediates, such as O-carboxylate and S-carboxylate esters. O- and S-carboxylates can include lower alkyl, that is C1 to C6, branched or straight chain carboxylates. Some such O- or S-carboxylates include, without limitation, methyl, ethyl, n-propyl, n-butyl, i-propyl, sec-butyl, and tert-butyl, pentyl, hexyl O- or S-carboxylates, any of which can further possess an unsaturation, providing for example, propenyl, butenyl, pentyl, and hexenyl O- or S-carboxylates. O-carboxylates can be the product of a biosynthetic pathway. Exemplary O-carboxylates accessed via biosynthetic pathways can include, without limitation, methyl methacrylate, ethyl methacrylate, and n-propyl methacrylate. Other biosynthetically accessible O-carboxylates can include medium to long chain groups, that is C7-C22, O-carboxylate esters derived from fatty alcohols, such heptyl, octyl, nonyl, decyl, undecyl, lauryl, tridecyl, myristyl, pentadecyl, cetyl, palmitolyl, heptadecyl, stearyl, nonadecyl, arachidyl, heneicosyl, and behenyl alcohols, any one of which can be optionally branched and/or contain unsaturations. O-carboxylate esters can also be accessed via a chemical process, such as esterification of a free carboxylic acid product or transesterification of an O- or S-carboxylate. S-carboxylates are exemplified by CoA S-esters, cysteinyl S-esters, alkylthioesters, and various aryl and heteroaryl thioesters. Additionally, the formation of methacrylic acid esters via a methacryl-CoA intermediate has been proposed (WO/2007/039415 and U.S. Patent No. 7,901,915). Methacryl-CoA can be formed from methacrylate using a methacryl-CoA synthetase as described in WO/2007/039415 and U.S. Patent No. 7,901,915 or by applying a methacryl-CoA transferase (see Figure 2 and Example III). A methacrylyl-CoA transferase can transfer a CoA moiety to methacrylate from several CoA donors including, but not limited to, acetyl-CoA, succinyl-CoA, butyryl-CoA, and propionyl-CoA. Methacrylate can be formed from the pathways depicted in Figure 1 or the pathways described in WO/2009/135074 or U.S. publication 2009/0275096. Methacrylyl-CoA can alternatively be produced from 2-hydroxyisobutyryl-CoA, 3-hydroxyisobutyryl-CoA, 3-hydroxyisobutyrate, or isobutyryl-CoA via 2-hydroxyisobutyryl-CoA dehydratase, 3-hydroxyisobutyryl-CoA dehydratase, 3-

hydroxyisobutyrate dehydratase, or isobutyryl-CoA dehydrogenase as described in WO/2009/135074.

[0143] Thus, the invention additionally provides microbial organisms for producing methacrylate esters. Such organisms can comprise a methacrylate ester pathway comprising methacrylyl-CoA transferase. Such a microbial organism can further comprise a methacrylate ester pathway comprising methacrylyl-CoA synthetase and/or alcohol transferase (see Figure 2 and Example III). It is understood that such an organism that produces a methacrylate ester can be engineered to contain a microbial organism containing a methacrylic acid or methacrylyl-CoA pathway, including but not limited to the methacrylic acid pathways disclosed herein (see Examples I and V-XIV and Figures 1-11) or described in WO2009/135074 or U.S. publication 2009/0275096. Thus, any of the disclosed microbial organisms that produce methacrylic acid can further comprise at least one exogenous nucleic acid encoding a methacrylate ester pathway enzyme expressed in a sufficient amount to produce methacrylate ester, the methacrylate ester pathway comprising methacrylyl-CoA synthetase, methacrylyl-CoA transferase and alcohol transferase. Exemplary enzymatic and chemical conversion of methacrylic acid to methacrylate esters is described in Example IV.

[0144] Thus, the invention additionally provides a microbial organism comprising a methacrylate ester pathway and further comprising a methacrylic acid pathway disclosed herein, including the methacrylic acid pathways described in Figures 1 and 3-11 and in Examples I and V-XIV. In a particular embodiment, the microbial organism comprising a methacrylate ester pathway further commprises a methacrylic acid pathway selected from 3-hydroxyisobutyrate dehydratase; methylmalonyl-CoA mutase, methylmalonyl-CoA reductase, 3-hydroxyisobutyrate dehydrogenase, and 3-hydroxyisobutyrate dehydratase; methylmalonyl-CoA mutase, methylmalonyl-CoA epimerase, methylmalonyl-CoA reductase, 3-hydroxyisobutyrate dehydrogenase, and 3-hydroxyisobutyrate dehydratase; methylmalonyl-CoA mutase, alcohol/aldehyde dehydrogenase, and 3-hydroxyisobutyrate dehydratase; methylmalonyl-CoA mutase, methylmalonyl-CoA epimerase, alcohol/aldehyde dehydrogenase, and 3-hydroxyisobutyrate dehydratase; methylmalonyl-CoA mutase, methylmalonyl-CoA reductase, 3-amino-2-methylpropionate transaminase, and 3-amino-2-methylpropionate ammonia lyase; methylmalonyl-CoA mutase, methylmalonyl-CoA epimerase, methylmalonyl-CoA reductase, 3-amino-2-methylpropionate transaminase, and 3-amino-2-methylpropionate ammonia lyase; 4-hydroxybutyryl-CoA mutase, 3-

hydroxyisobutyryl-CoA synthetase or 3-hydroxyisobutyryl-CoA hydrolase or 3-hydroxyisobutyryl-CoA transferase, and 3-hydroxyisobutyrate dehydratase; aspartate aminotransferase, glutamate mutase, 3-methylaspartase, and mesaconate decarboxylase; alpha-ketoglutarate reductase, 2-hydroxyglutamate mutase, 3-methylmalate dehydratase, and mesaconate decarboxylase; acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, 3-hydroxybutyryl-CoA mutase, 2-hydroxyisobutyryl-CoA dehydratase, and methacrylyl-CoA transferase or methacrylyl-CoA hydrolase or methacrylyl-CoA synthetase; acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, 3-hydroxybutyryl-CoA mutase, 2-hydroxyisobutyryl-CoA dehydratase, enoyl-CoA hydratase, and 3-hydroxyisobutyryl-CoA hydrolase or 3-hydroxyisobutyryl-CoA synthetase or 3-hydroxyisobutyryl-CoA transferase, and 3-hydroxyisobutyrate dehydratase; 4-hydroxybutyryl-CoA dehydratase, vinylacetyl-CoA Δ-isomerase, crotonase, 3-hydroxybutyryl-CoA mutase, 2-hydroxyisobutyryl-CoA dehydratase, and any of methacrylyl-CoA hydrolase or methacrylyl-CoA synthetase or methacrylyl-CoA transferase; and 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA dehydratase, and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase (see Examples V-XIV).

[0145] Exemplary non-naturally occurring microbial organisms capable of producing methacrylic acid are disclosed herein. For example, a methacrylic acid pathway is provided in which succinyl-CoA is a precursor (see Examples V-VI, Figures 3 and 4). In one embodiment, a non-naturally occurring microbial organism has a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising methylmalonyl-CoA mutase, methylmalonyl-CoA epimerase, methylmalonyl-CoA reductase, 3-hydroxyisobutyrate dehydrogenase and 3-hydroxyisobutyrate dehydratase (see Examples V and VI and Figure 3). In another embodiment, a non-naturally occurring microbial organism has a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising methylmalonyl-CoA mutase, methylmalonyl-CoA epimerase, alcohol/aldehyde dehydrogenase, and 3-hydroxyisobutyrate dehydratase (see Example V). Additionally, a non-naturally occurring microbial organism can have a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising methylmalonyl-CoA

mutase, methylmalonyl-CoA epimerase, methylmalonyl-CoA reductase, 3-amino-2-methylpropionate transaminase, and 3-amino-2-methylpropionate ammonia lyase (see Examples VI and Figure 4).

[0146] Additionally provided is a non-naturally occurring microbial organism containing a methacrylic acid pathway having 4-hydroxybutyryl-CoA as a precursor. One such embodiment is a non-naturally occurring microbial organism having a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA synthetase or 3-hydroxyisobutyryl-CoA hydrolase or 3-hydroxyisobutyryl-CoA transferase, and 3-hydroxyisobutyrate dehydratase (see Examples VII and Figure 5). Alternatively, the pathway could include 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA dehydratase; and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase.

[0147] Further provided is a non-naturally occurring microbial organism containing a methacrylic acid pathway having alpha-ketoglutarate as a precursor. One such embodiment is a non-naturally occurring microbial organism having a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising aspartate aminotransferase, glutamate mutase, 3-methylaspartase, and mesaconate decarboxylase (see Examples VIII and Figure 6). In yet another embodiment, a non-naturally occurring microbial organism has a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising alpha-ketoglutarate reductase, 2-hydroxyglutamate mutase, 3-methylmalate dehydratase, and mesaconate decarboxylase (see Examples IX and Figure 7).

[0148] In still another embodiment, a non-naturally occurring microbial organism containing a methacrylic acid pathway has acetyl-CoA as a precursor. For example, a non-naturally occurring microbial organism can have a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, 3-hydroxybutyryl-CoA mutase, 2-

hydroxyisobutyryl-CoA dehydratase, and methacrylyl-CoA transferase or methacrylyl-CoA hydrolase or methacrylyl-CoA synthetase (see Examples X and Figure 8). In another embodiment, a non-naturally occurring microbial organism havs a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, 3-hydroxybutyryl-CoA mutase, 2-hydroxyisobutyryl-CoA dehydratase, enoyl-CoA hydratase, and 3-hydroxyisobutyryl-CoA hydrolase or 3-hydroxyisobutyryl-CoA synthetase or 3-hydroxyisobutyryl-CoA transferase, and 3-hydroxyisobutyrate dehydratase (see Example X).

[0149] In further embodiments, non-naturally occurring microbial organisms can contain a methacrylic acid having 4-hydroxybutyryl-CoA as a precursor. For example, a non-naturally occurring microbial organism has a methacrylic acid pathay comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising 4-hydroxybutyryl-CoA dehydratase; vinylacetyl-CoA Δ-isomerase; crotonase; 3-hydroxybutyryl-CoA mutase; 2-hydroxyisobutyryl-CoA dehydratase; and methacrylyl-CoA hydrolase or methacrylyl-CoA synthetase or methacrylyl-CoA transferase (see Example XIV and Figure 8).

[0150] In yet another embodiment, a non-naturally occurring microbial organism has a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, crotonase, butyryl-CoA dehydrogenase, isobutyryl-CoA mutase, isobutyryl-CoA dehydrogenase, and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase (see Example XI and Figure 9).

[0151] Further provided is a non-naturally occurring microbial organism containing a methacrylic acid pathway having pyruvate as a precursor. For example, a non-naturally occurring microbial organism can have a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising lactate dehydrogenase, lactate-CoA transferase, lactoyl-CoA dehydratase, acyl-CoA dehydrogenase, propionyl-CoA carboxylase, methylmalonyl-CoA reductase, 3-

hydroxyisobutyrate dehydrogenase, and 3-hydroxyisobutyrate dehydratase (see Example XII and Figure 10).

[0152] Also provided is a non-naturally occurring microbial organism containing a methacrylic acid pathway having 2-ketoisovalerate as a precursor. For example, a non-naturally occurring microbial organism can have a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising valine aminotransferase, 2-ketoisovalerate dehydrogenase, isobutyryl-CoA dehydrogenase, and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase (see Example XIII and Figure 11). Such a methacrylic acid pathway can further contain valine aminotransferase, which converst valine to 2-ketoisovalerate (Figure 11). In addition, such a methacrylic acid pathway can further contain enzymes that convert pyruvate to 2-ketoisovalerate (Figure 11), such as acetolactate synthase, acetohydroxy acid isomeroreductase and dihydroxy-acid dehydratase (see Example XIII).

[0153] The invention also provides a non-naturally occurring microbial organism having a methacrylate ester pathway comprising at least one exogenous nucleic acid encoding a methacrylate ester pathway enzyme expressed in a sufficient amount to produce a methacrylate ester, the methacrylate ester pathway comprising a methacrylyl-CoA transferase and an alcohol transferase. In a further embodiment, such a methacrylate ester pathway can further comprise methacrylyl-CoA synthetase. In a particular embodiment, the microbial organism having a methacrylate ester pathway can comprise two exogenous nucleic acids encoding methacrylyl-CoA and alcohol transferase. In a still further embodiment, the invention provides a microbial organism having a methacrylate ester pathway can comprise three exogenous nucleic acids encoding methacrylyl-CoA synthetase, methacrylyl-CoA transferase, and alcohol transferase.

[0154] The non-naturally occurring microbial organisms of the invention can be produced by introducing expressible nucleic acids encoding one or more of the enzymes or proteins participating in one or more methacrylic acid biosynthetic pathways. Depending on the host microbial organism chosen for biosynthesis, nucleic acids for some or all of a particular methacrylic acid biosynthetic pathway can be expressed. For example, if a chosen host is deficient in one or more enzymes or proteins for a desired biosynthetic pathway, then expressible nucleic acids for the deficient enzyme(s) or protein(s) are introduced into the host

for subsequent exogenous expression. Alternatively, if the chosen host exhibits endogenous expression of some pathway genes, but is deficient in others, then an encoding nucleic acid is needed for the deficient enzyme(s) or protein(s) to achieve methacrylic acid biosynthesis. Thus, a non-naturally occurring microbial organism of the invention can be produced by introducing exogenous enzyme or protein activities to obtain a desired biosynthetic pathway or a desired biosynthetic pathway can be obtained by introducing one or more exogenous enzyme or protein activities that, together with one or more endogenous enzymes or proteins, produces a desired product such as methacrylic acid.

[0155] Host microbial organisms can be selected from, and the non-naturally occurring microbial organisms generated in, for example, bacteria, yeast, fungus or any of a variety of other microorganisms applicable to fermentation processes. Exemplary bacteria include species selected from *Escherichia coli, Klebsiella oxytoca, Anaerobiospirillum succiniciproducens, Actinobacillus succinogenes, Mannheimia succiniciproducens, Rhizobium etli, Bacillus subtilis, Corynebacterium glutamicum, Gluconobacter oxydans, Zymomonas mobilis, Lactococcus lactis, Lactobacillus plantarum, Streptomyces coelicolor, Clostridium acetobutylicum, Pseudomonas fluorescens*, and *Pseudomonas putida*. Exemplary yeasts or fungi include species selected from *Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces lactis, Kluyveromyces marxianus, Aspergillus terreus, Aspergillus niger*, *Pichia pastoris, Rhizopus arrhizus, Rhizobus oryzae*, *Yarrowia lipolytica*, and the like. *E. coli* is a particularly useful host organisms since it is a well characterized microbial organism suitable for genetic engineering. Other particularly useful host organisms include yeast such as *Saccharomyces cerevisiae*. It is understood that any suitable microbial host organism can be used to introduce metabolic and/or genetic modifications to produce a desired product.

[0156] Depending on the methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate biosynthetic pathway constituents of a selected host microbial organism, the non-naturally occurring microbial organisms of the invention will include at least one exogenously expressed methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway-encoding nucleic acid and up to all encoding nucleic acids for one or more methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate biosynthetic pathways. For example, methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate biosynthesis can be established in a

host deficient in a pathway enzyme or protein through exogenous expression of the corresponding encoding nucleic acid. In a host deficient in all enzymes or proteins of a methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway, exogenous expression of all enzyme or proteins in the pathway can be included, although it is understood that all enzymes or proteins of a pathway can be expressed even if the host contains at least one of the pathway enzymes or proteins. For example, exogenous expression of all enzymes or proteins in a pathway for production of methacrylic acid can be included, such as citramalate synthase (A), citramalate dehydratase (citraconate forming) (B), and citraconate decarboxylase (C)(Figure 1, pathway (1) A/B/C); citramalate synthase (A), citramalate dehydratase (citraconate forming) (B), citraconate isomerase (G), and mesaconate decarboxylase (H)(Figure 1, pathway (2) A/B/G/H); citramalate synthase (A), citramalate dehydratase (mesaconate forming) (F) citraconate isomerase (G), and citraconate decarboxylase (C)(Figure 1, pathway (3) A/F/G/C); citramalate synthase (A), citramalate dehydratase (mesaconate forming) (F), and mesaconate decarboxylase (H)(Figure 1, pathway (4) A/F/H); citramalyl-CoA lyase (D), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (citraconate forming) (B), and citraconate decarboxylase (C)(Figure 1, pathway (5) D/E/B/C); citramalyl-CoA lyase (D), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (citraconate forming) (B), citraconate isomerase (G), and mesaconate decarboxylase (H)(Figure 1, pathway (6) D/E/B/G/H); citramalyl-CoA lyase (D), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (mesaconate forming) (F), and mesaconate decarboxylase (H)(Figure 1, pathway (7) D/E/F/H); citramalyl-CoA lyase (D), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (mesaconate forming) (F), citraconate isomerase (G), and citraconate decarboxylase (C)(Figure 1, pathway (8) D/E/F/G/C); aconitate decarboxylase (I), itaconate isomerase (J), and citraconate decarboxylase (C)(Figure 1, pathway (9) I/J/C); aconitate decarboxylase (I), itaconate isomerase (J), citraconate isomerase (G), and mesaconate decarboxylase (H)(Figure 1, pathway (10) I/J/G/H); aconitate decarboxylase (I), itaconyl-CoA transferase, synthetase or hydrolase (L), citramalyl-CoA dehydratase (K), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (citraconate forming) (B), and citraconate decarboxylase (C)(Figure 1, pathway (11) I/L/K/E/B/C); aconitate decarboxylase (I), itaconyl-CoA transferase, synthetase or hydrolase (L), citramalyl-CoA dehydratase (K), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (citraconate forming) (B), citraconate isomerase (G), and mesaconate decarboxylase (H)(Figure 1, pathway (12) I/L/K/E/B/G/H); aconitate

decarboxylase (I), itaconyl-CoA transferase, synthetase or hydrolase (L), citramalyl-CoA dehydratase (K), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (mesaconate forming) (F), and mesaconate decarboxylase (H)(Figure 1, pathway (13) I/L/K/E/F/H); and aconitate decarboxylase (I), itaconyl-CoA transferase, synthetase or hydrolase (L), citramalyl-CoA dehydratase (K), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (mesaconate forming) (F), citraconate isomerase (G), and citraconate decarboxylase (C)(Figure 1, pathway (14) I/L/K/E/F/G/C).

[0157] Given the teachings and guidance provided herein, those skilled in the art will understand that the number of encoding nucleic acids to introduce in an expressible form will, at least, parallel the methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway deficiencies of the selected host microbial organism. Therefore, a non-naturally occurring microbial organism of the invention can have one, two, three, four, five, six, or seven, depending on the pathway, including up to all nucleic acids encoding the enzymes or proteins constituting a methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate biosynthetic pathway disclosed herein. In some embodiments, the non-naturally occurring microbial organisms also can include other genetic modifications that facilitate or optimize methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate biosynthesis or that confer other useful functions onto the host microbial organism. One such other functionality can include, for example, augmentation of the synthesis of one or more of the methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway precursors such as acetyl-CoA, pyruvate or aconitate.

[0158] Generally, a host microbial organism is selected such that it produces the precursor of a methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway, either as a naturally produced molecule or as an engineered product that either provides *de novo* production of a desired precursor or increased production of a precursor naturally produced by the host microbial organism. For example, aconitate, acetyl-CoA, and pyruvate are produced naturally in a host organism such as *E. coli*. A host organism can be engineered to increase production of a precursor, as disclosed herein. In addition, a microbial organism that has been engineered to produce a desired precursor can be used as a host organism and further engineered to express enzymes or proteins of a

methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway.

[0159] In some embodiments, a non-naturally occurring microbial organism of the invention is generated from a host that contains the enzymatic capability to synthesize methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate. In this specific embodiment it can be useful to increase the synthesis or accumulation of a methacrylic acid , methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway product to, for example, drive methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway reactions toward methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate production. Increased synthesis or accumulation can be accomplished by, for example, overexpression of nucleic acids encoding one or more of the methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway enzymes or proteins described herein. Over expression of the enzyme or enzymes and/or protein or proteins of the methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway can occur, for example, through exogenous expression of the endogenous gene or genes, or through exogenous expression of the heterologous gene or genes. Therefore, naturally occurring organisms can be readily generated to be non-naturally occurring microbial organisms of the invention, for example, producing methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate, through overexpression of one, two, three, four, five, six or seven, depending on the number of enzymes in the pathway, that is, up to all nucleic acids encoding methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate biosynthetic pathway enzymes or proteins. In addition, a non-naturally occurring organism can be generated by mutagenesis of an endogenous gene that results in an increase in activity of an enzyme in the methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate biosynthetic pathway.

[0160] In particularly useful embodiments, exogenous expression of the encoding nucleic acids is employed. Exogenous expression confers the ability to custom tailor the expression and/or regulatory elements to the host and application to achieve a desired expression level that is controlled by the user. However, endogenous expression also can be utilized in other embodiments such as by removing a negative regulatory effector or induction of the gene's promoter when linked to an inducible promoter or other regulatory element. Thus, an

endogenous gene having a naturally occurring inducible promoter can be up-regulated by providing the appropriate inducing agent, or the regulatory region of an endogenous gene can be engineered to incorporate an inducible regulatory element, thereby allowing the regulation of increased expression of an endogenous gene at a desired time. Similarly, an inducible promoter can be included as a regulatory element for an exogenous gene introduced into a non-naturally occurring microbial organism.

[0161] It is understood that, in methods of the invention, any of the one or more exogenous nucleic acids can be introduced into a microbial organism to produce a non-naturally occurring microbial organism of the invention. The nucleic acids can be introduced so as to confer, for example, a methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate biosynthetic pathway onto the microbial organism. Alternatively, encoding nucleic acids can be introduced to produce an intermediate microbial organism having the biosynthetic capability to catalyze some of the required reactions to confer methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate biosynthetic capability. For example, a non-naturally occurring microbial organism having a methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate biosynthetic pathway can comprise at least two exogenous nucleic acids encoding desired enzymes or proteins, such as the combination of citramalate synthase and citraconate decarboxylase; citraconate isomerase and mesaconate decarboxylase; or itaconyl-CoA transferase, synthetase or hydrolase and itaconate isomerase, and the like. Thus, it is understood that any combination of two or more enzymes of a biosynthetic pathway can be included in a non-naturally occurring microbial organism of the invention. Similarly, it is understood that any combination of three or more enzymes of a biosynthetic pathway can be included in a non-naturally occurring microbial organism of the invention, for example, citramalate dehydratase (citraconate forming), citraconate isomerase and mesaconate decarboxylase; citramalyl-CoA lyase, citramalyl-CoA transferase, synthetase or hydrolase and citramalate dehydratase; or aconitate decarboxylase, itaconate isomerase and mesaconate decarboxylase, and so forth, as desired, so long as the combination of enzymes and/or proteins of the desired biosynthetic pathway results in production of the corresponding desired product. Similarly, any combination of four, for example, citramalyl-CoA lyase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (citraconate forming) and mesaconate decarboxylase; aconitate decarboxylase, itaconate isomerase, citraconate isomerasae and mesaconate decarboxylase, and the like, or more

enzymes of a biosynthetic pathway as disclosed herein can be included in a non-naturally occurring microbial organism of the invention, as desired, including up to all enzymes in a pathway, so long as the combination of enzymes of the desired biosynthetic pathway results in production of the corresponding desired product.

[0162] In addition to the biosynthesis of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate as described herein, the non-naturally occurring microbial organisms and methods of the invention also can be utilized in various combinations with each other and with other microbial organisms and methods well known in the art to achieve product biosynthesis by other routes. For example, one alternative to produce methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate other than use of the methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate producers is through addition of another microbial organism capable of converting a methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway intermediate to methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate. One such procedure includes, for example, the fermentation of a microbial organism that produces a methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway intermediate. The methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway intermediate can then be used as a substrate for a second microbial organism that converts the methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway intermediate to methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate. The methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway intermediate can be added directly to another culture of the second organism or the original culture of the methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway intermediate producers can be depleted of these microbial organisms by, for example, cell separation, and then subsequent addition of the second organism to the fermentation broth can be utilized to produce the final product without intermediate purification steps.

[0163] In other embodiments, the non-naturally occurring microbial organisms and methods of the invention can be assembled in a wide variety of subpathways to achieve biosynthesis of, for example, methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate

and/or 2-hydroxyisobutyrate. In these embodiments, biosynthetic pathways for a desired product of the invention can be segregated into different microbial organisms, and the different microbial organisms can be co-cultured to produce the final product. In such a biosynthetic scheme, the product of one microbial organism is the substrate for a second microbial organism until the final product is synthesized. For example, the biosynthesis of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate can be accomplished by constructing a microbial organism that contains biosynthetic pathways for conversion of one pathway intermediate to another pathway intermediate or the product. Alternatively, methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate also can be biosynthetically produced from microbial organisms through co-culture or co-fermentation using two organisms in the same vessel, where the first microbial organism produces a methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate intermediate and the second microbial organism converts the intermediate to methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate.

[0164] Given the teachings and guidance provided herein, those skilled in the art will understand that a wide variety of combinations and permutations exist for the non-naturally occurring microbial organisms and methods of the invention together with other microbial organisms, with the co-culture of other non-naturally occurring microbial organisms having subpathways and with combinations of other chemical and/or biochemical procedures well known in the art to produce methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate.

[0165] Sources of encoding nucleic acids for a methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway enzyme or protein can include, for example, any species where the encoded gene product is capable of catalyzing the referenced reaction. Such species include both prokaryotic and eukaryotic organisms including, but not limited to, bacteria, including archaea and eubacteria, and eukaryotes, including yeast, plant, insect, animal, and mammal, including human. Exemplary species for such sources include, for example, *Escherichia* species, including *Escherichia coli, Escherichia fergusonii, Methanocaldococcus jannaschii, Leptospira interrrogans, Geobacter sulfurreducens, Chloroflexus aurantiacus, Roseiflexus sp. RS-1, Chloroflexus aggregans, Achromobacter xylosoxydans, Clostrdia* species, includingi *Clostridium kluyveri, Clostridium symbiosum,*

Clostridium acetobutylicum, Clostridium saccharoperbutylacetonicum, Clostridium ljungdahlii, Trichomonas vaginalis G3, Trypanosoma brucei, Acidaminococcus fermentans, Fusobacterium species, including *Fusobacterium nucleatum, Fusobacterium mortiferum, Corynebacterium glutamicum, Rattus norvegicus, Homo sapiens, Saccharomyces* species, including *Saccharomyces cerevisiae, Apsergillus* species, including *Aspergillus terreus, Aspergillus oryzae, Aspergillus niger, Gibberella zeae, Pichia stipitis, Mycobacterium* species, including *Mycobacterium smegmatis, Mycobacterium avium,* including *subsp. pratuberculosis, Salinispora arenicola Pseudomonas* species, including *Pseudomonas sp. CF600, Pseudomonas putida, Pseudomonas fluorescens, Pseudomonas aeruginosa, Ralstonia* species, including *Ralstonia eutropha, Ralstonia eutropha JMP134, Ralstonia eutropha H16, Ralstonia pickettii, Lactobacillus plantarum, Klebsiella oxytoca, Bacillus* species, including *Bacillus subtilis, Bacillus pumilus, Bacillus megaterium, Pedicoccus pentosaceus, Chlorofexus* species, including *Chloroflexus aurantiacus, Chloroflexus aggregans, Rhodobacter sphaeroides, Methanocaldococcus jannaschii, Leptospira interrrogans, Candida maltosa, Salmonella* species, including *Salmonella enterica serovar Typhimurium, Shewanella* species, including *Shewanella oneidensis, Shewanella sp.* MR-4, *Alcaligenes faecalis, Geobacillus stearothermophilus, Serratia marcescens, Vibrio cholerae, Eubacterium barkeri, Bacteroides capillosus, Archaeoglobus fulgidus, Archaeoglobus fulgidus, Haloarcula marismortui, Pyrobaculum aerophilum str. IM2, Rhizobium* species, including *Rhizobium leguminosarum*, as well as other exemplary species disclosed herein or available as source organisms for corresponding genes. However, with the complete genome sequence available for now more than 550 species (with more than half of these available on public databases such as the NCBI), including 395 microorganism genomes and a variety of yeast, fungi, plant, and mammalian genomes, the identification of genes encoding the requisite methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate biosynthetic activity for one or more genes in related or distant species, including for example, homologues, orthologs, paralogs and nonorthologous gene displacements of known genes, and the interchange of genetic alterations between organisms is routine and well known in the art. Accordingly, the metabolic alterations allowing biosynthesis of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate described herein with reference to a particular organism such as *E. coli* can be readily applied to other microorganisms, including prokaryotic and eukaryotic organisms alike. Given the teachings and guidance provided herein, those skilled in the art

will know that a metabolic alteration exemplified in one organism can be applied equally to other organisms.

[0166] In some instances, such as when an alternative methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate biosynthetic pathway exists in an unrelated species, methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate biosynthesis can be conferred onto the host species by, for example, exogenous expression of a paralog or paralogs from the unrelated species that catalyzes a similar, yet non-identical metabolic reaction to replace the referenced reaction. Because certain differences among metabolic networks exist between different organisms, those skilled in the art will understand that the actual gene usage between different organisms may differ. However, given the teachings and guidance provided herein, those skilled in the art also will understand that the teachings and methods of the invention can be applied to all microbial organisms using the cognate metabolic alterations to those exemplified herein to construct a microbial organism in a species of interest that will synthesize methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate.

[0167] Methods for constructing and testing the expression levels of a non-naturally occurring methacrylic acid-, methacrylate ester-, 3-hydroxyisobutyrate- and/or 2-hydroxyisobutyrate- producing host can be performed, for example, by recombinant and detection methods well known in the art. Such methods can be found described in, for example, Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Third Ed., Cold Spring Harbor Laboratory, New York (2001); and Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley and Sons, Baltimore, MD (1999).

[0168] Exogenous nucleic acid sequences involved in a pathway for production of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate can be introduced stably or transiently into a host cell using techniques well known in the art including, but not limited to, conjugation, electroporation, chemical transformation, transduction, transfection, and ultrasound transformation. For exogenous expression in *E. co*li or other prokaryotic cells, some nucleic acid sequences in the genes or cDNAs of eukaryotic nucleic acids can encode targeting signals such as an N-terminal mitochondrial or other targeting signal, which can be removed before transformation into prokaryotic host cells, if desired. For example, removal of a mitochondrial leader sequence led to increased expression in *E. coli* (Hoffmeister et al., *J. Biol. Chem.* 280:4329-4338 (2005)). For

exogenous expression in yeast or other eukaryotic cells, genes can be expressed in the cytosol without the addition of leader sequence, or can be targeted to mitochondrion or other organelles, or targeted for secretion, by the addition of a suitable targeting sequence such as a mitochondrial targeting or secretion signal suitable for the host cells. Thus, it is understood that appropriate modifications to a nucleic acid sequence to remove or include a targeting sequence can be incorporated into an exogenous nucleic acid sequence to impart desirable properties. Furthermore, genes can be subjected to codon optimization with techniques well known in the art to achieve optimized expression of the proteins.

[0169] An expression vector or vectors can be constructed to include one or more methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate biosynthetic pathway encoding nucleic acids as exemplified herein operably linked to expression control sequences functional in the host organism. Expression vectors applicable for use in the microbial host organisms of the invention include, for example, plasmids, phage vectors, viral vectors, episomes and artificial chromosomes, including vectors and selection sequences or markers operable for stable integration into a host chromosome. Additionally, the expression vectors can include one or more selectable marker genes and appropriate expression control sequences. Selectable marker genes also can be included that, for example, provide resistance to antibiotics or toxins, complement auxotrophic deficiencies, or supply critical nutrients not in the culture media. Expression control sequences can include constitutive and inducible promoters, transcription enhancers, transcription terminators, and the like which are well known in the art. When two or more exogenous encoding nucleic acids are to be co-expressed, both nucleic acids can be inserted, for example, into a single expression vector or in separate expression vectors. For single vector expression, the encoding nucleic acids can be operationally linked to one common expression control sequence or linked to different expression control sequences, such as one inducible promoter and one constitutive promoter. The transformation of exogenous nucleic acid sequences involved in a metabolic or synthetic pathway can be confirmed using methods well known in the art. Such methods include, for example, nucleic acid analysis such as Northern blots or polymerase chain reaction (PCR) amplification of mRNA, or immunoblotting for expression of gene products, or other suitable analytical methods to test the expression of an introduced nucleic acid sequence or its corresponding gene product. It is understood by those skilled in the art that the exogenous nucleic acid is expressed in a sufficient amount to produce the desired product, and it is further understood that expression levels can be

optimized to obtain sufficient expression using methods well known in the art and as disclosed herein.

[0170] The invention additionally provides methods of producing methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate using the microbial organisms of the invention comprising a methacrylic acid pathway. In a particular embodiment, the invention provides a method for producing methacrylic acid by culturing a non-naturally occurring microbial organism, comprising a microbial organism having a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising citramalate synthase (A), citramalate dehydratase (citraconate forming) (B), and citraconate decarboxylase (C)(Figure 1, pathway (1) A/B/C), under conditions and for a sufficient period of time to produce methacrylic acid. As disclosed herein, the microbial organism can comprise more than one exogenous nucleic acid encoding a methacrylic acid pathway enzyme, including up to all enzymes in a pathway, for example, three exogenous nucleic acids encode citramalate synthase, citramalate dehydratase (citraconate forming), and citraconate decarboxylase.

[0171] In a particular embodiment, MAA producing non-naturally occurring microbial organism of the invention can have at least one exogenous nucleic acid that is a heterologous nucleic acid. In another embodiment the non-naturally occurring microbial organism producing MAA can be in a substantially anaerobic culture medium.

[0172] In another embodiment, the invention provides a method for producing methacrylic acid by culturing a non-naturally occurring microbial organism comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising citramalate synthase (A), citramalate dehydratase (citraconate forming) (B), citraconate isomerase (G), and mesaconate decarboxylase (H)(Figure 1, pathway (2) A/B/G/H), under conditions and for a sufficient period of time to produce methacrylic acid. In still another embodiment, the invention provides a method for producing methacrylic acid by culturing a non-naturally occurring microbial organism, comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising

citramalate synthase (A), citramalate dehydratase (mesaconate forming) (F) citraconate isomerase (G), and citraconate decarboxylase (C)(Figure 1, pathway (3) A/F/G/C), under conditions and for a sufficient period of time to produce methacrylic acid.

[0173] In a further embodiment, the invention provides a method for producing methacrylic acid by culturing a non-naturally occurring microbial organism, comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising citramalate synthase (A), citramalate dehydratase (mesaconate forming) (F), and mesaconate decarboxylase (H)(Figure 1, pathway (4) A/F/H), under conditions and for a sufficient period of time to produce methacrylic acid. In yet a further embodiment, the invention provides a method for producing methacylic acid by culturing a non-naturally occurring microbial organism, comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising citramalyl-CoA lyase (D), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (citraconate forming) (B), and citraconate decarboxylase (C)(Figure 1, pathway (5) D/E/B/C), under conditions and for a sufficient period of time to produce methacrylic acid.

[0174] In an additional embodiment, the invention provides a method for producing methacrylic acid by culturing a non-naturally occurring microbial organism, comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising citramalyl-CoA lyase (D), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (citraconate forming) (B), citraconate isomerase (G), and mesaconate decarboxylase (H)(Figure 1, pathway (6) D/E/B/G/H), under conditions and for a sufficient period of time to produce methacrylic acid. In still another embodiment, the invention provides a method for producing methacrylic acid by culturing a non-naturally occurring microbial organism, comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising citramalyl-CoA lyase (D), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (mesaconate forming) (F), and mesaconate

decarboxylase (H)(Figure 1, pathway (7) D/E/F/H), under conditions and for a sufficient period of time to produce methacrylic acid.

[0175] In another embodiment, the invention provides a method for producing methacrylic acid by culturing a non-naturally occurring microbial organism, comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising citramalyl-CoA lyase (D), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (mesaconate forming) (F), citraconate isomerase (G), and citraconate decarboxylase (C)(Figure 1, pathway (8) D/E/F/G/C), under conditions and for a sufficient period of time to produce methacrylic acid. Additionally, the invention provides a method for producing methacrylic acid by culturing a non-naturally occurring microbial organism, comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising aconitate decarboxylase (I), itaconate isomerase (J), and citraconate decarboxylase (C)(Figure 1, pathway (9) I/J/C), under conditions and for a sufficient period of time to produce methacrylic acid.

[0176] In yet a further embodiment, the invention provides a method for producing methacrylic acid by culturing a non-naturally occurring microbial organism, comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising aconitate decarboxylase (I), itaconate isomerase (J), citraconate isomerase (G), and mesaconate decarboxylase (H)(Figure 1, pathway (10) I/J/G/H), under conditions and for a sufficient period of time to produce methacrylic acid. In an additional embodiment, the invention provides a method for producing methacrylic acid by culturing a non-naturally occurring microbial organism, comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising aconitate decarboxylase (I), itaconyl-CoA transferase, synthetase or hydrolase (L), citramalyl-CoA dehydratase (K), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (citraconate

forming) (B), and citraconate decarboxylase (C)(Figure 1, pathway (11) I/L/K/E/B/C), under conditions and for a sufficient period of time to produce methacrylic acid.

[0177] The invention also provides a method for producing methacrylic acid by culturing a non-naturally occurring microbial organism, comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising aconitate decarboxylase (I), itaconyl-CoA transferase, synthetase or hydrolase (L), citramalyl-CoA dehydratase (K), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (citraconate forming) (B), citraconate isomerase (G), and mesaconate decarboxylase (H)(Figure 1, pathway (12) I/L/K/E/B/G/H), under conditions and for a sufficient period of time to produce methacrylic acid. In still a further embodiment, the invention provides a method for producing methacrylic acid by culturing a non-naturally occurring microbial organism, comprising a microbial organism having a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising aconitate decarboxylase (I), itaconyl-CoA transferase, synthetase or hydrolase (L), citramalyl-CoA dehydratase (K), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (mesaconate forming) (F), and mesaconate decarboxylase (H)(Figure 1, pathway (13) I/L/K/E/F/H), under conditions and for a sufficient period of time to produce methacrylic acid. In an additional embodiment, the invention provides a method for producing methacrylic acid by culturing a non-naturally occurring microbial organism, comprising a methacrylic acid pathway comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, the methacrylic acid pathway comprising aconitate decarboxylase (I), itaconyl-CoA transferase, synthetase or hydrolase (L), citramalyl-CoA dehydratase (K), citramalyl-CoA transferase, synthetase or hydrolase (E), citramalate dehydratase (mesaconate forming) (F), citraconate isomerase (G), and citraconate decarboxylase (C)(Figure 1, pathway (14) I/L/K/E/F/G/C), under conditions and for a sufficient period of time to produce methacrylic acid.

[0178] The invention also provides a method for producing a methacrylate ester by culturing a non-naturally occurring microbial organism under conditions and for a sufficient period of time to produce a 3-hydroxyisobutyrate ester, wherein the non-naturally occurring

microbial organism includes an exogenous nucleic acid encoding an alcohol transferase or a 3-hydroxyisobutyrate ester-forming enzyme expressed in a sufficient amount to produce a 3-hydroxyisobutyrate ester, and chemically dehydrating the 3-hydroxyisobutyrate ester to produce a methacrylate ester as exemplified in Figure 28 and Figure 30, steps 6 and 7. In another embodiment, the invention provides a method for producing methyl methacrylate by culturing a non-naturally occurring microbial organism under conditions and for a sufficient period of time to produce methyl-3-hydroxyisobutyrate, wherein the non-naturally occurring microbial organism includes an exogenous nucleic acid encoding an alcohol transferase or an ester-forming enzyme expressed in a sufficient amount to produce methyl-3-hydroxyisobutyrate, and chemically dehydrating said methyl-3-hydroxyisobutyrate to produce methyl methacrylate as exemplified in Figure 30, steps 6 and 7. In some aspects of the invention, the methods for producing a methacrylate ester or methyl methacrylate as disclosed herein futher include that the non-naturally occurring microbial organism includes at least one exogenous nucleic acid encoding 3-hydroxyisobutyryl-CoA pathway enzymes as described in Figures 1-11 and 28-30 or any combination thereof. In some aspects, the invention provides that the exogenous nucleic acid is a heterologous nucleic acid. In some aspects, the invention provides that the non-naturally occurring microbial organism is in a substantially anaerobic culture medium.

[0179] In one embodiment, the invention provides a non-naturally occurring microbial organism, comprising a microbial organism having a methyl methacrylate pathway comprising at least one exogenous nucleic acid encoding a methyl methacrylate pathway enzyme expressed in a sufficient amount to produce methyl methacrylate; said non-naturally occurring microbial organism further comprising: (i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from an ATP-citrate lyase, a citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase, or optionally isocitrate dehydrogenase, aconitase, citryl-CoA synthetase or citryl-CoA lyase; (ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or (iii) at least one exogenous nucleic acid encodes an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof; wherein said methyl methacrylate pathway

comprises an alcohol transferase or an ester-forming enzyme, and a dehydratase. In another aspect, the invention provides a method wherein the microbial organism comprising (i) further comprises an exogenous nucleic acid encoding an enzyme selected from a pyruvate:ferredoxin oxidoreductase, an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, an acetate kinase, a phosphotransacetylase, an acetyl-CoA synthetase, an NAD(P)H:ferredoxin oxidoreductase, ferredoxin, and combinations thereof. In another aspect, the invention provides a method wherein the microbial organism comprising (ii) further comprises an exogenous nucleic acid encoding an enzyme selected from an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, and combinations thereof. In one aspect, the microbial organism comprises two exogenous nucleic acids each encoding a methyl methacrylate enzyme. In a further aspect, the two exogenous nucleic acids encode an alcohol transferase and a dehydratase or alternatively a ester-forming enzyme and a dehydratase.

[0180] In one embodiment, the invention provides a method, wherein the microbial organism comprising (i) comprises four exogenous nucleic acids encoding an ATP-citrate lyase, citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase; wherein said microbial organism comprising (ii) comprises five exogenous nucleic acids encoding a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or wherein said microbial organism comprising (iii) comprises two exogenous nucleic acids encoding a CO dehydrogenase and an H_2 hydrogenase.

[0181] In one embodiment, the invention provides a method for producing methyl methacrylate comprising, culturing the non-naturally occurring microbial organism as disclosed herein under conditions and for a sufficient period of time to produce methyl methacrylate.

[0182] In another embodiment, the invention provides a method for producing a methacrylate ester comprising, culturing a non-naturally occurring microbial organism under conditions and for a sufficient period of time to produce a 3-hydroxyisobutyrate ester, wherein said non-naturally occurring microbial organism comprises an exogenous nucleic acid encoding an alcohol transferase or a 3-hydroxyisobutyrate ester-forming enzyme expressed in a sufficient amount to produce a 3-hydroxyisobutyrate ester and said non-

naturally occurring microbial organism further comprising: (i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from an ATP-citrate lyase, a citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase, or optionally isocitrate dehydrogenase, aconitase, citryl-CoA synthetase or citryl-CoA lyase; (ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or (iii) at least one exogenous nucleic acid encoding an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof, and chemically dehydrating said 3-hydroxyisobutyrate ester to produce a methacrylate ester. In another embodiment, the invention provides a method for producing a methacrylate ester comprising, culturing a non-naturally occurring microbial organism under conditions and for a sufficient period of time to produce a 2-hydroxyisobutyrate ester, wherein said non-naturally occurring microbial organism comprises an exogenous nucleic acid encoding an alcohol transferase or a 2-hydroxyisobutyrate ester-forming enzyme expressed in a sufficient amount to produce a 2-hydroxy isobutyrate ester and said non-naturally occurring microbial organism further comprising: (i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from an ATP-citrate lyase, a citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase, or optionally isocitrate dehydrogenase, aconitase, citryl-CoA synthetase or citryl-CoA lyase; (ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or (iii) at least one exogenous nucleic acid encoding an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof, and chemically dehydrating said 2-hydroxy isobutyrate ester to produce a methacrylate ester. In yet another embodiment, the invention provides a method for producing methyl methacrylate comprising, culturing a non-naturally occurring microbial organism under conditions and for a sufficient period of time to produce methyl-3-hydroxyisobutyrate, wherein said non-naturally occurring microbial organism comprises an exogenous nucleic acid encoding an alcohol transferase or an ester-forming enzyme expressed in a sufficient

amount to produce methyl-3-hydroxyisobutyrate and said non-naturally occurring microbial organism further comprising: (i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from an ATP-citrate lyase, a citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase, or optionally isocitrate dehydrogenase, aconitase, citryl-CoA synthetase or citryl-CoA lyase; (ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or (iii) at least one exogenous nucleic acid encoding an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof, and chemically dehydrating said methyl-3-hydroxyisobutyrate to produce methyl methacrylate. In one aspect of the above methods, at least one of said exogenous nucleic acids is a heterologous nucleic acid. In another aspect of the above methods, the non-naturally occurring microbial organism is in a substantially anaerobic culture medium.

[0183] In one embodiment, the invention provides a method as disclosed above and herein, wherein said microbial organism comprising (i) further comprises an exogenous nucleic acid encoding an enzyme selected from a pyruvate:ferredoxin oxidoreductase, an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, an acetate kinase, a phosphotransacetylase, an acetyl-CoA synthetase, an NAD(P)H:ferredoxin oxidoreductase, ferredoxin, and combinations thereof. In another embodiment, the invention provides a method as disclosed above and herein, wherein said microbial organism comprising (ii) further comprises an exogenous nucleic acid encoding an enzyme selected from an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, and combinations thereof. In yet another embodiment, the invention provides a method as disclosed above and herein, wherein said microbial organism comprising (i) comprises four exogenous nucleic acids encoding an ATP-citrate lyase, citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase; wherein said microbial organism comprising (ii) comprises five exogenous nucleic acids encoding a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or

wherein said microbial organism comprising (iii) comprises two exogenous nucleic acids encoding a CO dehydrogenase and an H_2 hydrogenase.

[0184] In one aspect, the methods disclosed herein can further a microbial organism comprising a 3-hydroxyisobutyrate ester pathway comprising at least one exogenous nucleic acid encoding a 3-hydroxyisobutyrate ester pathway enzyme expressed in a sufficient amount to produce a 3-hydroxyisobutyrate ester, said 3-hydroxyisobutyrate ester pathway comprising a pathway selected from: (a) a 3-hydroxyisobutyrate-CoA transferase or a 3-hydroxyisobutyrate-CoA synthetase; and an alcohol transferase; or (b) 3-hydroxyisobutyrate ester-forming enzyme. In one aspect, the methods disclosed herein can further a microbial organism comprising a 2-hydroxyisobutyrate ester pathway comprising at least one exogenous nucleic acid encoding a 2-hydroxyisobutyrate ester pathway enzyme expressed in a sufficient amount to produce a 2-hydroxyisobutyrate ester, said 2-hydroxyisobutyrate ester pathway comprising a pathway selected from: (a) a 2-hydroxyisobutyrate-CoA transferase or a 2-hydroxyisobutyrate-CoA synthetase; and an alcohol transferase; or (b) a 2-hydroxyisobutyrate ester-forming enzyme.

[0185] Suitable purification and/or assays to test for the production of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate can be performed using well known methods. Suitable replicates such as triplicate cultures can be grown for each engineered strain to be tested. For example, product and byproduct formation in the engineered production host can be monitored. The final product and intermediates, and other organic compounds, can be analyzed by methods such as HPLC (High Performance Liquid Chromatography), GC-MS (Gas Chromatography-Mass Spectroscopy) and LC-MS (Liquid Chromatography-Mass Spectroscopy) or other suitable analytical methods using routine procedures well known in the art. The release of product in the fermentation broth can also be tested with the culture supernatant. Byproducts and residual glucose can be quantified by HPLC using, for example, a refractive index detector for glucose and alcohols, and a UV detector for organic acids (Lin et al., *Biotechnol. Bioeng.* 90:775-779 (2005)), or other suitable assay and detection methods well known in the art. The individual enzyme or protein activities from the exogenous DNA sequences can also be assayed using methods well known in the art. For example, citramalate synthase activity can be assayed by monitoring the production of CoA over time in a solution of purified protein, acetyl-CoA, pyruvate and buffer (Atsumi et al., AEM74:7802-7808 (2008)).

[0186] The methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate can be separated from other components in the culture using a variety of methods well known in the art. Such separation methods include, for example, extraction procedures as well as methods that include continuous liquid-liquid extraction, pervaporation, membrane filtration, membrane separation, reverse osmosis, electrodialysis, distillation, crystallization, centrifugation, extractive filtration, ion exchange chromatography, size exclusion chromatography, adsorption chromatography, and ultrafiltration. All of the above methods are well known in the art.

[0187] Any of the non-naturally occurring microbial organisms described herein can be cultured to produce and/or secrete the biosynthetic products of the invention. For example, the methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate producers can be cultured for the biosynthetic production of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate.

[0188] For the production of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate, the recombinant strains are cultured in a medium with carbon source and other essential nutrients. It is sometimes desirable and can be highly desirable to maintain anaerobic conditions in the fermenter to reduce the cost of the overall process. Such conditions can be obtained, for example, by first sparging the medium with nitrogen and then sealing the flasks with a septum and crimp-cap. For strains where growth is not observed anaerobically, microaerobic or substantially anaerobic conditions can be applied by perforating the septum with a small hole for limited aeration. Exemplary anaerobic conditions have been described previously and are well-known in the art. Exemplary aerobic and anaerobic conditions are described, for example, in United State publication 2009/0047719, filed August 10, 2007. Fermentations can be performed in a batch, fed-batch or continuous manner, as disclosed herein.

[0189] If desired, the pH of the medium can be maintained at a desired pH, in particular neutral pH, such as a pH of around 7 by addition of a base, such as NaOH or other bases, or acid, as needed to maintain the culture medium at a desirable pH. The growth rate can be determined by measuring optical density using a spectrophotometer (600 nm), and the glucose uptake rate by monitoring carbon source depletion over time.

[0190] The growth medium can include, for example, any carbohydrate source which can supply a source of carbon to the non-naturally occurring microorganism. Such sources include, for example, sugars such as glucose, xylose, arabinose, galactose, mannose, fructose, sucrose and starch. Other sources of carbohydrate include, for example, renewable feedstocks and biomass. Exemplary types of biomasses that can be used as feedstocks in the methods of the invention include cellulosic biomass, hemicellulosic biomass and lignin feedstocks or portions of feedstocks. Such biomass feedstocks contain, for example, carbohydrate substrates useful as carbon sources such as glucose, xylose, arabinose, galactose, mannose, fructose and starch. Given the teachings and guidance provided herein, those skilled in the art will understand that renewable feedstocks and biomass other than those exemplified above also can be used for culturing the microbial organisms of the invention for the production of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate.

[0191] In some embodiments, the present invention provides methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate or a methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate intermediate that has a carbon-12, carbon-13, and carbon-14 ratio that reflects an atmospheric carbon uptake source. In some such embodiments, the uptake source is CO_2. In some embodiments, In some embodiments, the present invention provides methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate or a methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate intermediate that has a carbon-12, carbon-13, and carbon-14 ratio that reflects petroleum-based carbon uptake source. In some embodiments, the present invention provides methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate or a methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate intermediate that has a carbon-12, carbon-13, and carbon-14 ratio that is obtained by a combination of an atmospheric carbon uptake source with a petroleum-based uptake source. Such combination of uptake sources is one means by which the carbon-12, carbon-13, and carbon-14 ratio can be varied.

[0192] In addition to renewable feedstocks such as those exemplified above and herein, the methacrylic acid methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate microbial organisms of the invention also can be modified for growth on syngas as its source of carbon. In this specific embodiment, one or more proteins or enzymes

are expressed in the methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate producing organisms to provide a metabolic pathway for utilization of syngas or other gaseous carbon source.

[0193] Synthesis gas, also known as syngas or producer gas, is the major product of gasification of coal and of carbonaceous materials such as biomass materials, including agricultural crops and residues. Syngas is a mixture primarily of H_2 and CO and can be obtained from the gasification of any organic feedstock, including but not limited to coal, coal oil, natural gas, biomass, and waste organic matter. Gasification is generally carried out under a high fuel to oxygen ratio. Although largely H_2 and CO, syngas can also include CO_2 and other gases in smaller quantities. Thus, synthesis gas provides a cost effective source of gaseous carbon such as CO and, additionally, CO_2.

[0194] The Wood-Ljungdahl pathway catalyzes the conversion of CO and H_2 to acetyl-CoA and other products such as acetate. Organisms capable of utilizing CO and syngas also generally have the capability of utilizing CO_2 and CO_2/H_2 mixtures through the same basic set of enzymes and transformations encompassed by the Wood-Ljungdahl pathway. H_2-dependent conversion of CO_2 to acetate by microorganisms was recognized long before it was revealed that CO also could be used by the same organisms and that the same pathways were involved. Many acetogens have been shown to grow in the presence of CO_2 and produce compounds such as acetate as long as hydrogen is present to supply the necessary reducing equivalents (see for example, Drake, *Acetogenesis*, pp. 3-60 Chapman and Hall, New York, (1994)). This can be summarized by the following equation:

$$2\ CO_2 + 4\ H_2 + n\ ADP + n\ Pi \rightarrow CH_3COOH + 2\ H_2O + n\ ATP$$

Hence, non-naturally occurring microorganisms possessing the Wood-Ljungdahl pathway can utilize CO_2 and H_2 mixtures as well for the production of acetyl-CoA and other desired products.

[0195] The Wood-Ljungdahl pathway is well known in the art and consists of 12 reactions which can be separated into two branches: (1) methyl branch and (2) carbonyl branch. The methyl branch converts syngas to methyl-tetrahydrofolate (methyl-THF) whereas the carbonyl branch converts methyl-THF to acetyl-CoA. The reactions in the methyl branch are catalyzed in order by the following enzymes or proteins: ferredoxin oxidoreductase, formate dehydrogenase, formyltetrahydrofolate synthetase,

methenyltetrahydrofolate cyclodehydratase, methylenetetrahydrofolate dehydrogenase and methylenetetrahydrofolate reductase. The reactions in the carbonyl branch are catalyzed in order by the following enzymes or proteins: methyltetrahydrofolate:corrinoid protein methyltransferase (for example, AcsE), corrinoid iron-sulfur protein, nickel-protein assembly protein (for example, AcsF), ferredoxin, acetyl-CoA synthase, carbon monoxide dehydrogenase and nickel-protein assembly protein (for example, CooC). Following the teachings and guidance provided herein for introducing a sufficient number of encoding nucleic acids to generate a methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway, those skilled in the art will understand that the same engineering design also can be performed with respect to introducing at least the nucleic acids encoding the Wood-Ljungdahl enzymes or proteins absent in the host organism. Therefore, introduction of one or more encoding nucleic acids into the microbial organisms of the invention such that the modified organism contains the complete Wood-Ljungdahl pathway will confer syngas utilization ability.

[0196] Additionally, the reductive (reverse) tricarboxylic acid cycle is and/or hydrogenase activities can also be used for the conversion of CO, CO_2 and/or H_2 to acetyl-CoA and other products such as acetate. Organisms capable of fixing carbon via the reductive TCA pathway can utilize one or more of the following enzymes: ATP citrate-lyase, citrate lyase, aconitase, isocitrate dehydrogenase, alpha-ketoglutarate:ferredoxin oxidoreductase, succinyl-CoA synthetase, succinyl-CoA transferase, fumarate reductase, fumarase, malate dehydrogenase, NAD(P)H:ferredoxin oxidoreductase, carbon monoxide dehydrogenase, and hydrogenase. Specifically, the reducing equivalents extracted from CO and/or H_2 by carbon monoxide dehydrogenase and hydrogenase are utilized to fix CO_2 via the reductive TCA cycle into acetyl-CoA or acetate. Acetate can be converted to acetyl-CoA by enzymes such as acetyl-CoA transferase, acetate kinase/phosphotransacetylase, and acetyl-CoA synthetase. Acetyl-CoA can be converted to methacrylic acid precursors, , methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate. for example, glyceraldehyde-3-phosphate, phosphoenolpyruvate, and pyruvate, by pyruvate:ferredoxin oxidoreductase and the enzymes of gluconeogenesis. Following the teachings and guidance provided herein for introducing a sufficient number of encoding nucleic acids to generate a methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway, those skilled in the art will understand that the same engineering design also can be performed with respect to introducing at least the nucleic acids encoding the reductive TCA

pathway enzymes or proteins absent in the host organism. Therefore, introduction of one or more encoding nucleic acids into the microbial organisms of the invention such that the modified organism contains the complete reductive TCA pathway will confer syngas utilization ability.

[0197] Accordingly, given the teachings and guidance provided herein, those skilled in the art will understand that a non-naturally occurring microbial organism can be produced that secretes the biosynthesized compounds of the invention when grown on a carbon source such as a carbohydrate. Such compounds include, for example, methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate and any of the intermediate metabolites in the methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway. All that is required is to engineer in one or more of the required enzyme or protein activities to achieve biosynthesis of the desired compound or intermediate including, for example, inclusion of some or all of the methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate biosynthetic pathways. Accordingly, the invention provides a non-naturally occurring microbial organism that produces and/or secretes methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate when grown on a carbohydrate or other carbon source and produces and/or secretes any of the intermediate metabolites shown in the methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway when grown on a carbohydrate or other carbon source. The methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate producing microbial organisms of the invention can initiate synthesis from an intermediate, for example, citramalyl-CoA, itaconyl-CoA, itaconate, citramalate, mesaconate or citraconate.

[0198] The non-naturally occurring microbial organisms of the invention are constructed using methods well known in the art as exemplified herein to exogenously express at least one nucleic acid encoding a methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway enzyme or protein in sufficient amounts to produce methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate. It is understood that the microbial organisms of the invention are cultured under conditions sufficient to produce methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate. Following the teachings and guidance provided herein, the non-naturally occurring microbial organisms of the invention can achieve biosynthesis of methacrylic acid,

methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate resulting in intracellular concentrations between about 0.1-200 mM or more. Generally, the intracellular concentration of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate is between about 3-150 mM, particularly between about 5-125 mM and more particularly between about 8-100 mM, including about 10 mM, 20 mM, 50 mM, 80 mM, or more. Intracellular concentrations between and above each of these exemplary ranges also can be achieved from the non-naturally occurring microbial organisms of the invention.

[0199] In some embodiments, culture conditions include anaerobic or substantially anaerobic growth or maintenance conditions. Exemplary anaerobic conditions have been described previously and are well known in the art. Exemplary anaerobic conditions for fermentation processes are described herein and are described, for example, in U.S. publication 2009/0047719, filed August 10, 2007. Any of these conditions can be employed with the non-naturally occurring microbial organisms as well as other anaerobic conditions well known in the art. Under such anaerobic or substantially anaerobic conditions, the methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate producers can synthesize methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate at intracellular concentrations of 5-10 mM or more as well as all other concentrations exemplified herein. It is understood that, even though the above description refers to intracellular concentrations, methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate producing microbial organisms can produce methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate intracellularly and/or secrete the product into the culture medium.

[0200] In addition to the culturing and fermentation conditions disclosed herein, growth condition for achieving biosynthesis of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate can include the addition of an osmoprotectant to the culturing conditions. In certain embodiments, the non-naturally occurring microbial organisms of the invention can be sustained, cultured or fermented as described herein in the presence of an osmoprotectant. Briefly, an osmoprotectant refers to a compound that acts as an osmolyte and helps a microbial organism as described herein survive osmotic stress. Osmoprotectants include, but are not limited to, betaines, amino acids, and the sugar trehalose. Non-limiting examples of such are glycine betaine, praline

betaine, dimethylthetin, dimethylslfonioproprionate, 3-dimethylsulfonio-2-methylproprionate, pipecolic acid, dimethylsulfonioacetate, choline, L-carnitine and ectoine. In one aspect, the osmoprotectant is glycine betaine. It is understood to one of ordinary skill in the art that the amount and type of osmoprotectant suitable for protecting a microbial organism described herein from osmotic stress will depend on the microbial organism used. The amount of osmoprotectant in the culturing conditions can be, for example, no more than about 0.1 mM, no more than about 0.5 mM, no more than about 1.0 mM, no more than about 1.5 mM, no more than about 2.0 mM, no more than about 2.5 mM, no more than about 3.0 mM, no more than about 5.0 mM, no more than about 7.0 mM, no more than about 10mM, no more than about 50mM, no more than about 100mM or no more than about 500mM.

[0201] In some embodiments, the carbon feedstock and other cellular uptake sources such as phosphate, ammonia, sulfate, chloride and other halogens can be chosen to alter the isotopic distribution of the atoms present in methacrylic acid, methacrylate este, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate or any methacrylic acid, methacrylate este, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway intermediate. The various carbon feedstock and other uptake sources enumerated above will be referred to herein, collectively, as "uptake sources." Uptake sources can provide isotopic enrichment for any atom present in the product methacrylic acid, methacrylate este, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway intermediate, or for side products generated in reactions diverging away from a methacrylic acid, methacrylate este, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway. Isotopic enrichment can be achieved for any target atom including, for example, carbon, hydrogen, oxygen, nitrogen, sulfur, phosphorus, chloride or other halogens.

[0202] In some embodiments, the uptake sources can be selected to alter the carbon-12, carbon-13, and carbon-14 ratios. In some embodiments, the uptake sources can be selected to alter the oxygen-16, oxygen-17, and oxygen-18 ratios. In some embodiments, the uptake sources can be selected to alter the hydrogen, deuterium, and tritium ratios. In some embodiments, the uptake sources can be selected to alter the nitrogen-14 and nitrogen-15 ratios. In some embodiments, the uptake sources can be selected to alter the sulfur-32, sulfur-33, sulfur-34, and sulfur-35 ratios. In some embodiments, the uptake sources can be selected to alter the phosphorus-31, phosphorus-32, and phosphorus-33 ratios. In some embodiments,

the uptake sources can be selected to alter the chlorine-35, chlorine-36, and chlorine-37 ratios.

[0203] In some embodiments, the isotopic ratio of a target atom can be varied to a desired ratio by selecting one or more uptake sources. An uptake source can be derived from a natural source, as found in nature, or from a man-made source, and one skilled in the art can select a natural source, a man-made source, or a combination thereof, to achieve a desired isotopic ratio of a target atom. An example of a man-made uptake source includes, for example, an uptake source that is at least partially derived from a chemical synthetic reaction. Such isotopically enriched uptake sources can be purchased commercially or prepared in the laboratory and/or optionally mixed with a natural source of the uptake source to achieve a desired isotopic ratio. In some embodiments, a target atom isotopic ratio of an uptake source can be achieved by selecting a desired origin of the uptake source as found in nature. For example, as discussed herein, a natural source can be a biobased derived from or synthesized by a biological organism or a source such as petroleum-based products or the atmosphere. In some such embodiments, a source of carbon, for example, can be selected from a fossil fuel-derived carbon source, which can be depleted of carbon-14, or an environmental or atmospheric carbon source, such as CO_2, which can possess a larger amount of carbon-14 than its petroleum-derived counterpart.

[0204] The unstable carbon isotope carbon-14 or radiocarbon makes up for roughly 1 in 10^{12} carbon atoms in the earth's atmosphere and has a half-life of about 5700 years. The stock of carbon is replenished in the upper atmosphere by a nuclear reaction involving cosmic rays and ordinary nitrogen (^{14}N). Fossil fuels contain no carbon-14, as it decayed long ago. Burning of fossil fuels lowers the atmospheric carbon-14 fraction, the so-called "Suess effect".

[0205] Methods of determining the isotopic ratios of atoms in a compound are well known to those skilled in the art. Isotopic enrichment is readily assessed by mass spectrometry using techniques known in the art such as accelerated mass spectrometry (AMS), Stable Isotope Ratio Mass Spectrometry (SIRMS) and Site-Specific Natural Isotopic Fractionation by Nuclear Magnetic Resonance (SNIF-NMR). Such mass spectral techniques can be integrated with separation techniques such as liquid chromatography (LC), high performance liquid chromatography (HPLC) and/or gas chromatography, and the like.

[0206] In the case of carbon, ASTM D6866 was developed in the United States as a standardized analytical method for determining the biobased content of solid, liquid, and gaseous samples using radiocarbon dating by the American Society for Testing and Materials (ASTM) International. The standard is based on the use of radiocarbon dating for the determination of a product's biobased content. ASTM D6866 was first published in 2004, and the current active version of the standard is ASTM D6866-11 (effective April 1, 2011). Radiocarbon dating techniques are well known to those skilled in the art, including those described herein.

[0207] The biobased content of a compound is estimated by the ratio of carbon-14 (^{14}C) to carbon-12 (^{12}C). Specifically, the Fraction Modern (Fm) is computed from the expression: Fm = (S-B)/(M-B), where B, S and M represent the $^{14}C/^{12}C$ ratios of the blank, the sample and the modern reference, respectively. Fraction Modern is a measurement of the deviation of the $^{14}C/^{12}C$ ratio of a sample from "Modern." Modern is defined as 95% of the radiocarbon concentration (in AD 1950) of National Bureau of Standards (NBS) Oxalic Acid I (i.e., standard resference materials (SRM) 4990b) normalized to $\delta^{13}C_{VPDB}$=-19 per mil(Olsson, *The use of Oxalic acid as a Standard*. In, Radiocarbon Variations and Absolute Chronology, Nobel Symposium, 12th Proc., John Wiley & Sons, New York (1970)). Mass spectrometry results, for example, measured by ASM, are calculated using the internationally agreed upon definition of 0.95 times the specific activity of NBS Oxalic Acid I (SRM 4990b) normalized to $\delta^{13}C_{VPDB}$=-19 per mil. This is equivalent to an absolute (AD 1950) $^{14}C/^{12}C$ ratio of $1.176 \pm 0.010 \times 10^{-12}$ (Karlen et al., *Arkiv Geofysik*, 4:465-471 (1968)). The standard calculations take into account the differential uptake of one istope with respect to another, for example, the preferential uptake in biological systems of C^{12} over C^{13} over C^{14}, and these corrections are reflected as a Fm corrected for δ^{13}.

[0208] An oxalic acid standard (SRM 4990b or HOx 1) was made from a crop of 1955 sugar beet. Although there were 1000 lbs made, this oxalic acid standard is no longer commercially available. The Oxalic Acid II standard (HOx 2; N.I.S.T designation SRM 4990 C) was made from a crop of 1977 French beet molasses. In the early 1980's, a group of 12 laboratories measured the ratios of the two standards. The ratio of the activity of Oxalic acid II to 1 is 1.2933±0.001 (the weighted mean). The isotopic ratio of HOx II is -17.8 per mille. ASTM D6866-11 suggests use of the available Oxalic Acid II standard SRM 4990 C (Hox2) for the modern standard (see discussion of original vs. currently available oxalic acid

standards in Mann, *Radiocarbon*, 25(2):519-527 (1983)). A Fm = 0% represents the entire lack of carbon-14 atoms in a material, thus indicating a fossil (for example, petroleum based) carbon source. A Fm = 100%, after correction for the post-1950 injection of carbon-14 into the atmosphere from nuclear bomb testing, indicates an entirely modern carbon source. As described herein, such a "modern" source includes biobased sources.

[0209] As described in ASTM D6866, the percent modern carbon (pMC) can be greater than 100% because of the continuing but diminishing effects of the 1950s nuclear testing programs, which resulted in a considerable enrichment of carbon-14 in the atmosphere as described in ASTM D6866-11. Because all sample carbon-14 activities are referenced to a "pre-bomb" standard, and because nearly all new biobased products are produced in a post-bomb environment, all pMC values (after correction for isotopic fraction) must be multiplied by 0.95 (as of 2010) to better reflect the true biobased content of the sample. A biobased content that is greater than 103% suggests that either an analytical error has occurred, or that the source of biobased carbon is more than several years old.

[0210] ASTM D6866 quantifies the biobased content relative to the material's total organic content and does not consider the inorganic carbon and other non-carbon containing substances present. For example, a product that is 50% starch-based material and 50% water would be considered to have a Biobased Content = 100% (50% organic content that is 100% biobased) based on ASTM D6866. In another example, a product that is 50% starch-based material, 25% petroleum-based, and 25% water would have a Biobased Content = 66.7% (75% organic content but only 50% of the product is biobased). In another example, a product that is 50% organic carbon and is a petroleum-based product would be considered to have a Biobased Content = 0% (50% organic carbon but from fossil sources). Thus, based on the well known methods and known standards for determining the biobased content of a compound or material, one skilled in the art can readily determine the biobased content and/or prepared downstream products that utilize of the invention having a desired biobased content.

[0211] Applications of carbon-14 dating techniques to quantify bio-based content of materials are known in the art (Currie et al., *Nuclear Instruments and Methods in Physics Research B,* 172:281-287 (2000)). For example, carbon-14 dating has been used to quantify bio-based content in terephthalate-containing materials (Colonna et al., *Green Chemistry*, 13:2543-2548 (2011)). Notably, polypropylene terephthalate (PPT) polymers derived from

renewable 1,3-propanediol and petroleum-derived terephthalic acid resulted in Fm values near 30% (i.e., since 3/11 of the polymeric carbon derives from renewable 1,3-propanediol and 8/11 from the fossil end member terephthalic acid) (Currie et al., *supra*, 2000). In contrast, polybutylene terephthalate polymer derived from both renewable 1,4-butanediol and renewable terephthalic acid resulted in bio-based content exceeding 90% (Colonna et al., *supra*, 2011).

[0212] Accordingly, in some embodiments, the present invention provides methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate or a methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway intermediate that has a carbon-12, carbon-13, and carbon-14 ratio that reflects an atmospheric carbon, also referred to as environmental carbon, uptake source. For example, in some aspects the methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate or a methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate intermediate can have an Fm value of at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98% or as much as 100%. In some such embodiments, the uptake source is CO_2. In some embodiments, the present invention provides methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate or a methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate intermediate that has a carbon-12, carbon-13, and carbon-14 ratio that reflects petroleum-based carbon uptake source. In this aspect, the methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate or a methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate intermediate can have an Fm value of less than 95%, less than 90%, less than 85%, less than 80%, less than 75%, less than 70%, less than 65%, less than 60%, less than 55%, less than 50%, less than 45%, less than 40%, less than 35%, less than 30%, less than 25%, less than 20%, less than 15%, less than 10%, less than 5%, less than 2% or less than 1%. In some embodiments, the present invention provides methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate or a methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate intermediate that has a carbon-12, carbon-

13, and carbon-14 ratio that is obtained by a combination of an atmospheric carbon uptake source with a petroleum-based uptake source. Using such a combination of uptake sources is one way by which the carbon-12, carbon-13, and carbon-14 ratio can be varied, and the respective ratios would refelect the proportions of the uptake sources.

[0213] Further, the present invention relates to the biologically produced methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate or methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate intermediate as disclosed herein, and to the products derived therefrom, wherein the methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate or a methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate intermediate has a carbon-12, carbon-13, and carbon-14 isotope ratio of about the same value as the CO_2 that occurs in the environment. For example, in some aspects the invention provides bioderived methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate or a bioderived methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate intermediate having a carbon-12 versus carbon-13 versus carbon-14 isotope ratio of about the same value as the CO_2 that occurs in the environment, or any of the other ratios disclosed herein. It is understood, as disclosed herein, that a product can have a carbon-12 versus carbon-13 versus carbon-14 isotope ratio of about the same value as the CO_2 that occurs in the environment, or any of the ratios disclosed herein, wherein the product is generated from bioderived methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate or a bioderived methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate intermediate as disclosed herein, wherein the bioderived product is chemically modified to generate a final product. Methods of chemically modifying a bioderived product of methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate, or an intermediate thereof, to generate a desired product are well known to those skilled in the art, as described herein. The invention further provides polymers, including polymethyl methacrylate (PMMA), acrylic plastics, and co-polymers, such as the co-polymer methyl methacrylate-butadiene-styrene (MBS), and the like, having a carbon-12 versus carbon-13 versus carbon-14 isotope ratio of about the same value as the CO_2 that occurs in the environment, wherein the polymers, including polymethyl methacrylate, acrylic plastics and

the co-polymer methyl methacrylate-butadiene-styrene (MBS), are generated directly from or in combination with bioderived methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate or a bioderived methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate intermediate as disclosed herein.

[0214] Methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate are chemicals used in commercial and industrial applications. Non-limiting examples of such applications include production of polymers, including polymethyl methacrylate (PMMA), also referred to as acrylic glass, Lucite™ or Plexiglas™, acrylic plastics and co-polymers, such as the co-polymer methyl methacrylate-butadiene-styrene (MBS). Moreover, methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate are also used as raw materials in the production of a wide range of products including polymers, including polymethyl methacrylate acrylic plastics and the co-polymer methyl methacrylate-butadiene-styrene (MBS). Accordingly, in some embodiments, the invention provides biobased polymers, including polymethyl methacrylate, acrylic plastics, and co-polymers, including methyl methacrylate-butadiene-styrene (MBS), comprising one or more bioderived methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate or bioderived methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate intermediate produced by a non-naturally occurring microorganism of the invention or produced using a method disclosed herein. Such polymers, including polymethyl methacrylate, acrylic plastics, and co-polymers, including methyl methacrylate-butadiene-styrene, can have a mixture of bioderived and petroleum based precursors, in desired ratios as described above.

[0215] As used herein, the term "bioderived" means derived from or synthesized by a biological organism and can be considered a renewable resource since it can be generated by a biological organism. Such a biological organism, in particular the microbial organisms of the invention disclosed herein, can utilize feedstock or biomass, such as, sugars or carbohydrates obtained from an agricultural, plant, bacterial, or animal source. Alternatively, the biological organism can utilize atmospheric carbon As used herein, the term "biobased" means a product as described above that is composed, in whole or in part, of a bioderived compound of the invention. A biobased or bioderived product is in contrast to a petroleum

derived product, wherein such a product is derived from or synthesized from petroleum or a petrochemical feedstock.

[0216] In some embodiments, the invention provides polymers, including polymethyl methacrylate acrylic plastics and the co-polymer methyl methacrylate-butadiene-styrene (MBS), comprising bioderived methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate or bioderived methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate intermediate, wherein the bioderived methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate or bioderived methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate intermediate includes all or part of the methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate or methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate intermediate used in the production of polymers, including polymethyl methacrylate acrylic plastics and the co-polymer methyl methacrylate-butadiene-styrene (MBS). Thus, in some aspects, the invention provides a biobased polymers, including polymethyl methacrylate acrylic plastics and the co-polymer methyl methacrylate-butadiene-styrene (MBS), comprising at least 2%, at least 3%, at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98% or 100% bioderived methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate or bioderived methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate intermediate as disclosed herein. Additionally, in some aspects, the invention provides a biobased polymers, including polymethyl methacrylate acrylic plastics and the co-polymer methyl methacrylate-butadiene-styrene (MBS), wherein the methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate or methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate intermediate used in its production is a combination of bioderived and petroleum derived methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate or methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate intermediate. For example, a biobased polymers, including polymethyl methacrylate acrylic plastics and the co-polymer methyl methacrylate-butadiene-styrene (MBS), can be produced using 50%

bioderived methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate and 50% petroleum derived methacrylic acid, methacrylate ester such as methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate, or other desired ratios such as 60%/40%, 70%/30%, 80%/20%, 90%/10%, 95%/5%, 100%/0%, 40%/60%, 30%/70%, 20%/80%, 10%/90% of bioderived/petroleum deried precursors, so long as at least a portion of the product comprises a bioderived product produced by the microbial organisms disclosed herein. It is understood that methods for producing polymers, including polymethyl methacrylate acrylic plastics and the co-polymer methyl methacrylate-butadiene-styrene (MBS), using the bioderived methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate or bioderived methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate intermediate of the invention are well known in the art.

[0217] The culture conditions can include, for example, liquid culture procedures as well as fermentation and other large scale culture procedures. As described herein, particularly useful yields of the biosynthetic products of the invention can be obtained under anaerobic or substantially anaerobic culture conditions.

[0218] As described herein, one exemplary growth condition for achieving biosynthesis of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate includes anaerobic culture or fermentation conditions. In certain embodiments, the non-naturally occurring microbial organisms of the invention can be sustained, cultured or fermented under anaerobic or substantially anaerobic conditions. Briefly, anaerobic conditions refers to an environment devoid of oxygen. Substantially anaerobic conditions include, for example, a culture, batch fermentation or continuous fermentation such that the dissolved oxygen concentration in the medium remains between 0 and 10% of saturation. Substantially anaerobic conditions also includes growing or resting cells in liquid medium or on solid agar inside a sealed chamber maintained with an atmosphere of less than 1% oxygen. The percent of oxygen can be maintained by, for example, sparging the culture with an N_2/CO_2 mixture or other suitable non-oxygen gas or gases.

[0219] The culture conditions described herein can be scaled up and grown continuously for manufacturing of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate. Exemplary growth procedures include, for example, fed-batch fermentation and batch separation; fed-batch fermentation and continuous separation, or

continuous fermentation and continuous separation. All of these processes are well known in the art. Fermentation procedures are particularly useful for the biosynthetic production of commercial quantities of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate. Generally, and as with non-continuous culture procedures, the continuous and/or near-continuous production of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate will include culturing a non-naturally occurring methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate producing organism of the invention in sufficient nutrients and medium to sustain and/or nearly sustain growth in an exponential phase. Continuous culture under such conditions can include, for example, growth for 1 day, 2, 3, 4, 5, 6 or 7 days or more. Additionally, continuous culture can include longer time periods of 1 week, 2, 3, 4 or 5 or more weeks and up to several months. Alternatively, organisms of the invention can be cultured for hours, if suitable for a particular application. It is to be understood that the continuous and/or near-continuous culture conditions also can include all time intervals in between these exemplary periods. It is further understood that the time of culturing the microbial organism of the invention is for a sufficient period of time to produce a sufficient amount of product for a desired purpose.

[0220] Fermentation procedures are well known in the art. Briefly, fermentation for the biosynthetic production of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate can be utilized in, for example, fed-batch fermentation and batch separation; fed-batch fermentation and continuous separation, or continuous fermentation and continuous separation. Examples of batch and continuous fermentation procedures are well known in the art.

[0221] In addition to the above fermentation procedures using the methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate, 3-hydroxyisobutyrate ester, 2-hydroxyisobutyrate and/or 2-hydroxyisobutyrate ester producers of the invention for continuous production of substantial quantities of methacrylic acid, methacrylate ester, methyl methacrylate, 3-hydroxyisobutyrate, 3-hydroxyisobutyrate ester, 2-hydroxyisobutyrate and/or 2-hydroxyisobutyrate ester producers also can be, for example, simultaneously subjected to chemical synthesis procedures to convert the product to other compounds or the product can be separated from the fermentation culture and sequentially subjected to chemical or enzymatic conversion to convert the product to other compounds, if

desired. For example, in some embodiments, the invention provides chemical dehydration of a 3-hydroxyisobutyrate ester such as methyl-3-hydroxyisobutyrate or a 2-hydroxyisobutyrate ester such as methyl-2-hydroxyisobutyrate to a methacrylate ester such as methyl methacrylate. It is understood that methods and chemical compounds for catylyzing the dehydration of such compounds are well known in the art.

[0222] 3-hydroxyisobutyrate esters and 2-hydroxyisobutyrate esters can be chemically dehydrated with formation of methacrylate esters, starting with pure 3-hydroxyisobutyrate or 2-hydroxyisobutyrate isolated from the fermentation solution or starting with aqueous or organic solutions of 3-hydroxyisobutyrate ester or 2-hydroxyisobutyrate ester, isolated in work up of the fermentation solution. Such solutions of 3-hydroxyisobutyrate ester or 2-hydroxyisobutyrate ester can also be concentrated before the dehydration step, for example by means of distillation, optionally in the presence of a suitable entrainer.

[0223] The dehydration reaction can be carried out in liquid phase or in the gas phase. The dehydration reaction can be carried out in the presence of a catalyst, the nature of the catalyst employed depending on whether a gas-phase or a liquid-phase reaction is carried out.

[0224] Suitable dehydration catalysts include both acidic catalysts and alkaline catalysts. Acidic catalysts, in particular can exhibit a decreased tendency to form oligomers. The dehydration catalyst can be employed as a homogeneous catalyst, a heterogeneous catalyst, or combinations thereof. Heterogeneous catalysts can be used in conjunction with a suitable support material. Such a support can itself be acidic or alkaline and provide the acidic or alkaline dehydration catalyst or a catalyst can be applied to an inert support.

[0225] Suitable supports which serve as dehydration catalysts include natural or synthetic silicates such as mordenite, montmorillonite, acidic zeolites; supports which are coated with monobasic, dibasic or polybasic inorganic acids, such as phosphoric acid, or with acidic salts of inorganic acids, such as oxides or silicates, for example Al2O3 , TiO2; oxides and mixed oxides such as γ-Al2O3 and ZnO—Al2O3 mixed oxides of heteropolyacids. Alkaline substances which act both as dehydration catalyst and as a support a support material include alkali, alkaline earth, lanthanum, lanthoids or a combinations thereof as their oxides. A further class of materials that can effect dehydration are ion exchangers which can be used in either alkaline or acidic form.

[0226] Suitable homogeneous dehydration catalysts include inorganic acids, such as phosphorus-containing acids such as phosphoric acid. Inorganic acids can be immobilized on the support material by immersion or impregnation.

[0227] In some embodiments, dehydration reaction is carried out in the gas phase using conventional apparatuses known in the art, for example tubular reactors, shell-and-tube heat exchangers and reactors which comprise thermoplates as heat exchangers. In some embodiments, gas-phase dehydration can utilize isolated 3-hydroxyisobutyrate esters or solutions of the ester, the ester being introduced into a reactor with fixed-bed catalysts. Thermal dehydration in the liquid phase can be carried out in a temperature range of between 200 °C and 350 °C, and in some embodiments between 250 and 300° C.

[0228] To generate better producers, metabolic modeling can be utilized to optimize growth conditions. Modeling can also be used to design gene knockouts that additionally optimize utilization of the pathway (see, for example, U.S. patent publications US 2002/0012939, US 2003/0224363, US 2004/0029149, US 2004/0072723, US 2003/0059792, US 2002/0168654 and US 2004/0009466, and U.S. Patent No. 7,127,379). Modeling analysis allows reliable predictions of the effects on cell growth of shifting the metabolism towards more efficient production of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate.

[0229] One computational method for identifying and designing metabolic alterations favoring biosynthesis of a desired product is the OptKnock computational framework (Burgard et al., *Biotechnol. Bioeng.* 84:647-657 (2003)). OptKnock is a metabolic modeling and simulation program that suggests gene deletion or disruption strategies that result in genetically stable microorganisms which overproduce the target product. Specifically, the framework examines the complete metabolic and/or biochemical network of a microorganism in order to suggest genetic manipulations that force the desired biochemical to become an obligatory byproduct of cell growth. By coupling biochemical production with cell growth through strategically placed gene deletions or other functional gene disruption, the growth selection pressures imposed on the engineered strains after long periods of time in a bioreactor lead to improvements in performance as a result of the compulsory growth-coupled biochemical production. Lastly, when gene deletions are constructed there is a negligible possibility of the designed strains reverting to their wild-type states because the genes selected by OptKnock are to be completely removed from the genome. Therefore, this

computational methodology can be used to either identify alternative pathways that lead to biosynthesis of a desired product or used in connection with the non-naturally occurring microbial organisms for further optimization of biosynthesis of a desired product.

[0230] Briefly, OptKnock is a term used herein to refer to a computational method and system for modeling cellular metabolism. The OptKnock program relates to a framework of models and methods that incorporate particular constraints into flux balance analysis (FBA) models. These constraints include, for example, qualitative kinetic information, qualitative regulatory information, and/or DNA microarray experimental data. OptKnock also computes solutions to various metabolic problems by, for example, tightening the flux boundaries derived through flux balance models and subsequently probing the performance limits of metabolic networks in the presence of gene additions or deletions. OptKnock computational framework allows the construction of model formulations that allow an effective query of the performance limits of metabolic networks and provides methods for solving the resulting mixed-integer linear programming problems. The metabolic modeling and simulation methods referred to herein as OptKnock are described in, for example, U.S. publication 2002/0168654, filed January 10, 2002, in International Patent No. PCT/US02/00660, filed January 10, 2002, and U.S. publication 2009/0047719, filed August 10, 2007.

[0231] Another computational method for identifying and designing metabolic alterations favoring biosynthetic production of a product is a metabolic modeling and simulation system termed SimPheny®. This computational method and system is described in, for example, U.S. publication 2003/0233218, filed June 14, 2002, and in International Patent Application No. PCT/US03/18838, filed June 13, 2003. SimPheny® is a computational system that can be used to produce a network model *in silico* and to simulate the flux of mass, energy or charge through the chemical reactions of a biological system to define a solution space that contains any and all possible functionalities of the chemical reactions in the system, thereby determining a range of allowed activities for the biological system. This approach is referred to as constraints-based modeling because the solution space is defined by constraints such as the known stoichiometry of the included reactions as well as reaction thermodynamic and capacity constraints associated with maximum fluxes through reactions. The space defined by these constraints can be interrogated to determine the phenotypic capabilities and behavior of the biological system or of its biochemical components.

[0232] These computational approaches are consistent with biological realities because biological systems are flexible and can reach the same result in many different ways. Biological systems are designed through evolutionary mechanisms that have been restricted by fundamental constraints that all living systems must face. Therefore, constraints-based modeling strategy embraces these general realities. Further, the ability to continuously impose further restrictions on a network model via the tightening of constraints results in a reduction in the size of the solution space, thereby enhancing the precision with which physiological performance or phenotype can be predicted.

[0233] Given the teachings and guidance provided herein, those skilled in the art will be able to apply various computational frameworks for metabolic modeling and simulation to design and implement biosynthesis of a desired compound in host microbial organisms. Such metabolic modeling and simulation methods include, for example, the computational systems exemplified above as SimPheny® and OptKnock. For illustration of the invention, some methods are described herein with reference to the OptKnock computation framework for modeling and simulation. Those skilled in the art will know how to apply the identification, design and implementation of the metabolic alterations using OptKnock to any of such other metabolic modeling and simulation computational frameworks and methods well known in the art.

[0234] The methods described above will provide one set of metabolic reactions to disrupt. Elimination of each reaction within the set or metabolic modification can result in a desired product as an obligatory product during the growth phase of the organism. Because the reactions are known, a solution to the bilevel OptKnock problem also will provide the associated gene or genes encoding one or more enzymes that catalyze each reaction within the set of reactions. Identification of a set of reactions and their corresponding genes encoding the enzymes participating in each reaction is generally an automated process, accomplished through correlation of the reactions with a reaction database having a relationship between enzymes and encoding genes.

[0235] Once identified, the set of reactions that are to be disrupted in order to achieve production of a desired product are implemented in the target cell or organism by functional disruption of at least one gene encoding each metabolic reaction within the set. One particularly useful means to achieve functional disruption of the reaction set is by deletion of each encoding gene. However, in some instances, it can be beneficial to disrupt the reaction

by other genetic aberrations including, for example, mutation, deletion of regulatory regions such as promoters or cis binding sites for regulatory factors, or by truncation of the coding sequence at any of a number of locations. These latter aberrations, resulting in less than total deletion of the gene set can be useful, for example, when rapid assessments of the coupling of a product are desired or when genetic reversion is less likely to occur.

[0236] To identify additional productive solutions to the above described bilevel OptKnock problem which lead to further sets of reactions to disrupt or metabolic modifications that can result in the biosynthesis, including growth-coupled biosynthesis of a desired product, an optimization method, termed integer cuts, can be implemented. This method proceeds by iteratively solving the OptKnock problem exemplified above with the incorporation of an additional constraint referred to as an integer cut at each iteration. Integer cut constraints effectively prevent the solution procedure from choosing the exact same set of reactions identified in any previous iteration that obligatorily couples product biosynthesis to growth. For example, if a previously identified growth-coupled metabolic modification specifies reactions 1, 2, and 3 for disruption, then the following constraint prevents the same reactions from being simultaneously considered in subsequent solutions. The integer cut method is well known in the art and can be found described in, for example, Burgard et al., *Biotechnol. Prog.* 17:791-797 (2001). As with all methods described herein with reference to their use in combination with the OptKnock computational framework for metabolic modeling and simulation, the integer cut method of reducing redundancy in iterative computational analysis also can be applied with other computational frameworks well known in the art including, for example, SimPheny®.

[0237] The methods exemplified herein allow the construction of cells and organisms that biosynthetically produce a desired product, including the obligatory coupling of production of a target biochemical product to growth of the cell or organism engineered to harbor the identified genetic alterations. Therefore, the computational methods described herein allow the identification and implementation of metabolic modifications that are identified by an *in silico* method selected from OptKnock or SimPheny®. The set of metabolic modifications can include, for example, addition of one or more biosynthetic pathway enzymes and/or functional disruption of one or more metabolic reactions including, for example, disruption by gene deletion.

[0238] As discussed above, the OptKnock methodology was developed on the premise that mutant microbial networks can be evolved towards their computationally predicted maximum-growth phenotypes when subjected to long periods of growth selection. In other words, the approach leverages an organism's ability to self-optimize under selective pressures. The OptKnock framework allows for the exhaustive enumeration of gene deletion combinations that force a coupling between biochemical production and cell growth based on network stoichiometry. The identification of optimal gene/reaction knockouts requires the solution of a bilevel optimization problem that chooses the set of active reactions such that an optimal growth solution for the resulting network overproduces the biochemical of interest (Burgard et al., *Biotechnol. Bioeng.* 84:647-657 (2003)).

[0239] An *in silico* stoichiometric model of *E. coli* metabolism can be employed to identify essential genes for metabolic pathways as exemplified previously and described in, for example, U.S. patent publications US 2002/0012939, US 2003/0224363, US 2004/0029149, US 2004/0072723, US 2003/0059792, US 2002/0168654 and US 2004/0009466, and in U.S. Patent No. 7,127,379. As disclosed herein, the OptKnock mathematical framework can be applied to pinpoint gene deletions leading to the growth-coupled production of a desired product. Further, the solution of the bilevel OptKnock problem provides only one set of deletions. To enumerate all meaningful solutions, that is, all sets of knockouts leading to growth-coupled production formation, an optimization technique, termed integer cuts, can be implemented. This entails iteratively solving the OptKnock problem with the incorporation of an additional constraint referred to as an integer cut at each iteration, as discussed above.

[0240] As disclosed herein, a nucleic acid encoding a desired activity of a methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway can be introduced into a host organism. In some cases, it can be desirable to modify an activity of a methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway enzyme or protein to increase production of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate. For example, known mutations that increase the activity of a protein or enzyme can be introduced into an encoding nucleic acid molecule. Additionally, optimization methods can be applied to increase the activity of an enzyme or protein and/or decrease an inhibitory activity, for example, decrease the activity of a negative regulator.

[0241] One such optimization method is directed evolution. Directed evolution is a powerful approach that involves the introduction of mutations targeted to a specific gene in order to improve and/or alter the properties of an enzyme. Improved and/or altered enzymes can be identified through the development and implementation of sensitive high-throughput screening assays that allow the automated screening of many enzyme variants (for example, $>10^4$). Iterative rounds of mutagenesis and screening typically are performed to afford an enzyme with optimized properties. Computational algorithms that can help to identify areas of the gene for mutagenesis also have been developed and can significantly reduce the number of enzyme variants that need to be generated and screened. Numerous directed evolution technologies have been developed (for reviews, see Hibbert et al., *Biomol.Eng* 22:11-19 (2005); Huisman and Lalonde, *In* Biocatalysis in the pharmaceutical and biotechnology industries pgs. 717-742 (2007), Patel (ed.), CRC Press; Otten and Quax. *Biomol.Eng* 22:1-9 (2005).; and Sen et al., *Appl Biochem.Biotechnol* 143:212-223 (2007)) to be effective at creating diverse variant libraries, and these methods have been successfully applied to the improvement of a wide range of properties across many enzyme classes. Enzyme characteristics that have been improved and/or altered by directed evolution technologies include, for example: selectivity/specificity, for conversion of non-natural substrates; temperature stability, for robust high temperature processing; pH stability, for bioprocessing under lower or higher pH conditions; substrate or product tolerance, so that high product titers can be achieved; binding (K_m), including broadening substrate binding to include non-natural substrates; inhibition (K_i), to remove inhibition by products, substrates, or key intermediates; activity (kcat), to increases enzymatic reaction rates to achieve desired flux; expression levels, to increase protein yields and overall pathway flux; oxygen stability, for operation of air sensitive enzymes under aerobic conditions; and anaerobic activity, for operation of an aerobic enzyme in the absence of oxygen.

[0242] Described below in more detail are exemplary methods that have been developed for the mutagenesis and diversification of genes to target desired properties of specific enzymes. Such methods are well known to those skilled in the art. Any of these can be used to alter and/or optimize the activity of a methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate pathway enzyme or protein.

[0243] EpPCR (Pritchard et al., *J Theor.Biol.* 234:497-509 (2005)) introduces random point mutations by reducing the fidelity of DNA polymerase in PCR reactions by the addition

of Mn^{2+} ions, by biasing dNTP concentrations, or by other conditional variations. The five step cloning process to confine the mutagenesis to the target gene of interest involves: 1) error-prone PCR amplification of the gene of interest; 2) restriction enzyme digestion; 3) gel purification of the desired DNA fragment; 4) ligation into a vector; 5) transformation of the gene variants into a suitable host and screening of the library for improved performance. This method can generate multiple mutations in a single gene simultaneously, which can be useful to screen a larger number of potential variants having a desired activity. A high number of mutants can be generated by EpPCR, so a high-throughput screening assay or a selection method, for example, using robotics, is useful to identify those with desirable characteristics.

[0244] Error-prone Rolling Circle Amplification (epRCA) (Fujii et al., *Nucleic Acids Res.* 32:e145 (2004); and Fujii et al., *Nat. Protoc.* 1:2493-2497 (2006)) has many of the same elements as epPCR except a whole circular plasmid is used as the template and random 6-mers with exonuclease resistant thiophosphate linkages on the last 2 nucleotides are used to amplify the plasmid followed by transformation into cells in which the plasmid is re-circularized at tandem repeats. Adjusting the Mn^{2+} concentration can vary the mutation rate somewhat. This technique uses a simple error-prone, single-step method to create a full copy of the plasmid with 3 - 4 mutations/kbp. No restriction enzyme digestion or specific primers are required. Additionally, this method is typically available as a commercially available kit.

[0245] DNA or Family Shuffling (Stemmer, *Proc Natl Acad Sci USA* 91:10747-10751 (1994)); and Stemmer, *Nature* 370:389-391 (1994)) typically involves digestion of two or more variant genes with nucleases such as Dnase I or EndoV to generate a pool of random fragments that are reassembled by cycles of annealing and extension in the presence of DNA polymerase to create a library of chimeric genes. Fragments prime each other and recombination occurs when one copy primes another copy (template switch). This method can be used with >1kbp DNA sequences. In addition to mutational recombinants created by fragment reassembly, this method introduces point mutations in the extension steps at a rate similar to error-prone PCR. The method can be used to remove deleterious, random and neutral mutations.

[0246] Staggered Extension (StEP) (Zhao et al., *Nat. Biotechnol.* 16:258-261 (1998)) entails template priming followed by repeated cycles of 2 step PCR with denaturation and very short duration of annealing/extension (as short as 5 sec). Growing fragments anneal to

different templates and extend further, which is repeated until full-length sequences are made. Template switching means most resulting fragments have multiple parents. Combinations of low-fidelity polymerases (Taq and Mutazyme) reduce error-prone biases because of opposite mutational spectra.

[0247] In Random Priming Recombination (RPR) random sequence primers are used to generate many short DNA fragments complementary to different segments of the template (Shao et al., *Nucleic Acids Res* 26:681-683 (1998)). Base misincorporation and mispriming via epPCR give point mutations. Short DNA fragments prime one another based on homology and are recombined and reassembled into full-length by repeated thermocycling. Removal of templates prior to this step assures low parental recombinants. This method, like most others, can be performed over multiple iterations to evolve distinct properties. This technology avoids sequence bias, is independent of gene length, and requires very little parent DNA for the application.

[0248] In Heteroduplex Recombination linearized plasmid DNA is used to form heteroduplexes that are repaired by mismatch repair (Volkov et al, *Nucleic Acids Res.* 27:e18 (1999); and Volkov et al., *Methods Enzymol.* 328:456-463 (2000)). The mismatch repair step is at least somewhat mutagenic. Heteroduplexes transform more efficiently than linear homoduplexes. This method is suitable for large genes and whole operons.

[0249] Random Chimeragenesis on Transient Templates (RACHITT) (Coco et al., *Nat. Biotechnol.* 19:354-359 (2001)) employs Dnase I fragmentation and size fractionation of single stranded DNA (ssDNA). Homologous fragments are hybridized in the absence of polymerase to a complementary ssDNA scaffold. Any overlapping unhybridized fragment ends are trimmed down by an exonuclease. Gaps between fragments are filled in and then ligated to give a pool of full-length diverse strands hybridized to the scaffold, which contains U to preclude amplification. The scaffold then is destroyed and is replaced by a new strand complementary to the diverse strand by PCR amplification. The method involves one strand (scaffold) that is from only one parent while the priming fragments derive from other genes, and the parent scaffold is selected against. Thus, no reannealing with parental fragments occurs. Overlapping fragments are trimmed with an exonuclease. Otherwise, this is conceptually similar to DNA shuffling and StEP. Therefore, there should be no siblings, few inactives, and no unshuffled parentals. This technique has advantages in that few or no

parental genes are created and many more crossovers can result relative to standard DNA shuffling.

[0250] Recombined Extension on Truncated templates (RETT) entails template switching of unidirectionally growing strands from primers in the presence of unidirectional ssDNA fragments used as a pool of templates (Lee et al., *J. Molec. Catalysis* 26:119-129 (2003)). No DNA endonucleases are used. Unidirectional ssDNA is made by DNA polymerase with random primers or serial deletion with exonuclease. Unidirectional ssDNA are only templates and not primers. Random priming and exonucleases do not introduce sequence bias as true of enzymatic cleavage of DNA shuffling/RACHITT. RETT can be easier to optimize than StEP because it uses normal PCR conditions instead of very short extensions. Recombination occurs as a component of the PCR steps, that is, no direct shuffling. This method can also be more random than StEP due to the absence of pauses.

[0251] In Degenerate Oligonucleotide Gene Shuffling (DOGS) degenerate primers are used to control recombination between molecules; (Bergquist and Gibbs, *Methods Mol.Biol* 352:191-204 (2007); Bergquist et al., *Biomol.Eng* 22:63-72 (2005); Gibbs et al., *Gene* 271:13-20 (2001)) this can be used to control the tendency of other methods such as DNA shuffling to regenerate parental genes. This method can be combined with random mutagenesis (epPCR) of selected gene segments. This can be a good method to block the reformation of parental sequences. No endonucleases are needed. By adjusting input concentrations of segments made, one can bias towards a desired backbone. This method allows DNA shuffling from unrelated parents without restriction enzyme digests and allows a choice of random mutagenesis methods.

[0252] Incremental Truncation for the Creation of Hybrid Enzymes (ITCHY) creates a combinatorial library with 1 base pair deletions of a gene or gene fragment of interest (Ostermeier et al., *Proc. Natl. Acad. Sci. USA* 96:3562-3567 (1999); and Ostermeier et al., *Nat. Biotechnol.* 17:1205-1209 (1999)). Truncations are introduced in opposite direction on pieces of 2 different genes. These are ligated together and the fusions are cloned. This technique does not require homology between the 2 parental genes. When ITCHY is combined with DNA shuffling, the system is called SCRATCHY (see below). A major advantage of both is no need for homology between parental genes; for example, functional fusions between an *E. coli* and a human gene were created via ITCHY. When ITCHY libraries are made, all possible crossovers are captured.

[0253] Thio-Incremental Truncation for the Creation of Hybrid Enzymes (THIO-ITCHY) is similar to ITCHY except that phosphothioate dNTPs are used to generate truncations (Lutz et al., *Nucleic Acids Res* 29:E16 (2001)). Relative to ITCHY, THIO-ITCHY can be easier to optimize, provide more reproducibility, and adjustability.

[0254] SCRATCHY combines two methods for recombining genes, ITCHY and DNA shuffling (Lutz et al., *Proc. Natl. Acad. Sci. USA* 98:11248-11253 (2001)). SCRATCHY combines the best features of ITCHY and DNA shuffling. First, ITCHY is used to create a comprehensive set of fusions between fragments of genes in a DNA homology-independent fashion. This artificial family is then subjected to a DNA-shuffling step to augment the number of crossovers. Computational predictions can be used in optimization. SCRATCHY is more effective than DNA shuffling when sequence identity is below 80%.

[0255] In Random Drift Mutagenesis (RNDM) mutations are made via epPCR followed by screening/selection for those retaining usable activity (Bergquist et al., *Biomol. Eng.* 22:63-72 (2005)). Then, these are used in DOGS to generate recombinants with fusions between multiple active mutants or between active mutants and some other desirable parent. Designed to promote isolation of neutral mutations; its purpose is to screen for retained catalytic activity whether or not this activity is higher or lower than in the original gene. RNDM is usable in high throughput assays when screening is capable of detecting activity above background. RNDM has been used as a front end to DOGS in generating diversity. The technique imposes a requirement for activity prior to shuffling or other subsequent steps; neutral drift libraries are indicated to result in higher/quicker improvements in activity from smaller libraries. Though published using epPCR, this could be applied to other large-scale mutagenesis methods.

[0256] Sequence Saturation Mutagenesis (SeSaM) is a random mutagenesis method that: 1) generates a pool of random length fragments using random incorporation of a phosphothioate nucleotide and cleavage; this pool is used as a template to 2) extend in the presence of "universal" bases such as inosine; 3) replication of an inosine-containing complement gives random base incorporation and, consequently, mutagenesis (Wong et al., *Biotechnol. J.* 3:74-82 (2008); Wong et al., *Nucleic Acids Res.* 32:e26 (2004); and Wong et al., *Anal. Biochem.* 341:187-189 (2005)). Using this technique it can be possible to generate a large library of mutants within 2 to 3 days using simple methods. This technique is non-

directed in comparison to the mutational bias of DNA polymerases. Differences in this approach makes this technique complementary (or an alternative) to epPCR.

[0257] In Synthetic Shuffling, overlapping oligonucleotides are designed to encode "all genetic diversity in targets" and allow a very high diversity for the shuffled progeny (Ness et al., *Nat. Biotechnol.* 20:1251-1255 (2002)). In this technique, one can design the fragments to be shuffled. This aids in increasing the resulting diversity of the progeny. One can design sequence/codon biases to make more distantly related sequences recombine at rates approaching those observed with more closely related sequences. Additionally, the technique does not require physically possessing the template genes.

[0258] Nucleotide Exchange and Excision Technology NexT exploits a combination of dUTP incorporation followed by treatment with uracil DNA glycosylase and then piperidine to perform endpoint DNA fragmentation (Muller et al., *Nucleic Acids Res.* 33:e117 (2005)). The gene is reassembled using internal PCR primer extension with proofreading polymerase. The sizes for shuffling are directly controllable using varying dUPT::dTTP ratios. This is an end point reaction using simple methods for uracil incorporation and cleavage. Other nucleotide analogs, such as 8-oxo-guanine, can be used with this method. Additionally, the technique works well with very short fragments (86 bp) and has a low error rate. The chemical cleavage of DNA used in this technique results in very few unshuffled clones.

[0259] In Sequence Homology-Independent Protein Recombination (SHIPREC), a linker is used to facilitate fusion between two distantly related or unrelated genes. Nuclease treatment is used to generate a range of chimeras between the two genes. These fusions result in libraries of single-crossover hybrids (Sieber et al., *Nat. Biotechnol.* 19:456-460 (2001)). This produces a limited type of shuffling and a separate process is required for mutagenesis. In addition, since no homology is needed, this technique can create a library of chimeras with varying fractions of each of the two unrelated parent genes. SHIPREC was tested with a heme-binding domain of a bacterial CP450 fused to N-terminal regions of a mammalian CP450; this produced mammalian activity in a more soluble enzyme.

[0260] In Gene Site Saturation Mutagenesis™ (GSSM™) the starting materials are a supercoiled dsDNA plasmid containing an insert and two primers which are degenerate at the desired site of mutations (Kretz et al., *Methods Enzymol.* 388:3-11 (2004)). Primers carrying the mutation of interest, anneal to the same sequence on opposite strands of DNA. The

mutation is typically in the middle of the primer and flanked on each side by approximately 20 nucleotides of correct sequence. The sequence in the primer is NNN or NNK (coding) and MNN (noncoding) (N = all 4, K = G, T, M = A, C). After extension, DpnI is used to digest dam-methylated DNA to eliminate the wild-type template. This technique explores all possible amino acid substitutions at a given locus (that is, one codon). The technique facilitates the generation of all possible replacements at a single-site with no nonsense codons and results in equal to near-equal representation of most possible alleles. This technique does not require prior knowledge of the structure, mechanism, or domains of the target enzyme. If followed by shuffling or Gene Reassembly, this technology creates a diverse library of recombinants containing all possible combinations of single-site up-mutations. The usefulness of this technology combination has been demonstrated for the successful evolution of over 50 different enzymes, and also for more than one property in a given enzyme.

[0261] Combinatorial Cassette Mutagenesis (CCM) involves the use of short oligonucleotide cassettes to replace limited regions with a large number of possible amino acid sequence alterations (Reidhaar-Olson et al. *Methods Enzymol.* 208:564-586 (1991); and Reidhaar-Olson et al. *Science* 241:53-57 (1988)). Simultaneous substitutions at two or three sites are possible using this technique. Additionally, the method tests a large multiplicity of possible sequence changes at a limited range of sites. This technique has been used to explore the information content of the lambda repressor DNA-binding domain.

[0262] Combinatorial Multiple Cassette Mutagenesis (CMCM) is essentially similar to CCM except it is employed as part of a larger program: 1) use of epPCR at high mutation rate to 2) identify hot spots and hot regions and then 3) extension by CMCM to cover a defined region of protein sequence space (Reetz et al., *Angew. Chem. Int. Ed Engl.* 40:3589-3591 (2001)). As with CCM, this method can test virtually all possible alterations over a target region. If used along with methods to create random mutations and shuffled genes, it provides an excellent means of generating diverse, shuffled proteins. This approach was successful in increasing, by 51-fold, the enantioselectivity of an enzyme.

[0263] In the Mutator Strains technique, conditional *ts* mutator plasmids allow increases of 20 to 4000-X in random and natural mutation frequency during selection and block accumulation of deleterious mutations when selection is not required (Selifonova et al., *Appl. Environ. Microbiol.* 67:3645-3649 (2001)). This technology is based on a plasmid-derived *mutD5* gene, which encodes a mutant subunit of DNA polymerase III. This subunit binds to

endogenous DNA polymerase III and compromises the proofreading ability of polymerase III in any strain that harbors the plasmid. A broad-spectrum of base substitutions and frameshift mutations occur. In order for effective use, the mutator plasmid should be removed once the desired phenotype is achieved; this is accomplished through a temperature sensitive (ts) origin of replication, which allows for plasmid curing at 41°C. It should be noted that mutator strains have been explored for quite some time (see Low et al., *J. Mol. Biol.* 260:359-3680 (1996)). In this technique, very high spontaneous mutation rates are observed. The conditional property minimizes non-desired background mutations. This technology could be combined with adaptive evolution to enhance mutagenesis rates and more rapidly achieve desired phenotypes.

[0264] Look-Through Mutagenesis (LTM) is a multidimensional mutagenesis method that assesses and optimizes combinatorial mutations of selected amino acids (Rajpal et al., *Proc. Natl. Acad. Sci. USA* 102:8466-8471 (2005)). Rather than saturating each site with all possible amino acid changes, a set of nine is chosen to cover the range of amino acid R-group chemistry. Fewer changes per site allows multiple sites to be subjected to this type of mutagenesis. A >800-fold increase in binding affinity for an antibody from low nanomolar to picomolar has been achieved through this method. This is a rational approach to minimize the number of random combinations and can increase the ability to find improved traits by greatly decreasing the numbers of clones to be screened. This has been applied to antibody engineering, specifically to increase the binding affinity and/or reduce dissociation. The technique can be combined with either screens or selections.

[0265] Gene Reassembly is a DNA shuffling method that can be applied to multiple genes at one time or to create a large library of chimeras (multiple mutations) of a single gene (Tunable GeneReassembly™ (TGR™) Technology supplied by Verenium Corporation). Typically this technology is used in combination with ultra-high-throughput screening to query the represented sequence space for desired improvements. This technique allows multiple gene recombination independent of homology. The exact number and position of cross-over events can be pre-determined using fragments designed via bioinformatic analysis. This technology leads to a very high level of diversity with virtually no parental gene reformation and a low level of inactive genes. Combined with GSSM™, a large range of mutations can be tested for improved activity. The method allows "blending" and "fine tuning" of DNA shuffling, for example, codon usage can be optimized.

[0266] *In Silico* Protein Design Automation (PDA) is an optimization algorithm that anchors the structurally defined protein backbone possessing a particular fold, and searches sequence space for amino acid substitutions that can stabilize the fold and overall protein energetics (Hayes et al., *Proc. Natl. Acad. Sci. USA* 99:15926-15931 (2002)). This technology uses *in silico* structure-based entropy predictions in order to search for structural tolerance toward protein amino acid variations. Statistical mechanics is applied to calculate coupling interactions at each position. Structural tolerance toward amino acid substitution is a measure of coupling. Ultimately, this technology is designed to yield desired modifications of protein properties while maintaining the integrity of structural characteristics. The method computationally assesses and allows filtering of a very large number of possible sequence variants (10^{50}). The choice of sequence variants to test is related to predictions based on the most favorable thermodynamics. Ostensibly only stability or properties that are linked to stability can be effectively addressed with this technology. The method has been successfully used in some therapeutic proteins, especially in engineering immunoglobulins. *In silico* predictions avoid testing extraordinarily large numbers of potential variants. Predictions based on existing three-dimensional structures are more likely to succeed than predictions based on hypothetical structures. This technology can readily predict and allow targeted screening of multiple simultaneous mutations, something not possible with purely experimental technologies due to exponential increases in numbers.

[0267] Iterative Saturation Mutagenesis (ISM) involves: 1) using knowledge of structure/function to choose a likely site for enzyme improvement; 2) performing saturation mutagenesis at chosen site using a mutagenesis method such as Stratagene QuikChange (Stratagene; San Diego CA); 3) screening/selecting for desired properties; and 4) using improved clone(s), start over at another site and continue repeating until a desired activity is achieved (Reetz et al., *Nat. Protoc.* 2:891-903 (2007); and Reetz et al., *Angew. Chem. Int. Ed Engl.* 45:7745-7751 (2006)). This is a proven methodology, which assures all possible replacements at a given position are made for screening/selection.

[0268] Any of the aforementioned methods for mutagenesis can be used alone or in any combination. Additionally, any one or combination of the directed evolution methods can be used in conjunction with adaptive evolution techniques, as described herein.

EXAMPLE I
Exemplary Methacrylic Acid Pathway Enzymes

[0269] This example describes exemplary pathways for production of methacrylic acid.

[0270] Figure 1 depicts exemplary pathways to MAA from acetyl-CoA and pyruvate via intermediate citramalate. Also shown are pathways to MAA from aconitate. In one pathway acetyl-CoA and pyruvate are first converted to citramalate by citramalate synthase. Dehydration of citramalate can yield either citraconate (Step B) or mesaconate (Step C). Mesaconate and citraconate are interconverted by a cis/trans isomerase in Step G. Decarboxylation of mesaconate (Step H) or citraconate (Step C) yields MAA. In an alternate pathway, citramalate is formed from acetyl-CoA and pyruvate via a citramalyl-CoA intermediate in Steps D and E, catalyzed by citramalyl-CoA lyase and citramalyl-coA hydrolase, transferase or synthetase.

[0271] Also exemplified are pathways from aconitate to MAA. In one pathway, aconitate is first decarboxylated to itaconate by aconitate decarboxylase (Step I). Itaconate is then isomerized to citraconate by itaconate delta-isomerase (Step J). Conversion of citraconate to MAA proceeds either directly by decarboxylation or indirectly via mesaconate. In an alternate pathway, the itaconate intermediate is first converted to itaconyl-CoA by a CoA transferase or synthetase (Step L). Hydration of itaconyl-CoA yields citramalyl-CoA, which can then be converted to MAA as described above and shown in Figure 1.

[0272] Table 1 shows enzyme classes that can perform the steps depicted in Figure 1. Exemplary enzymes are described in further detail below.

Table 1. Enzyme classes for the enzymes shown in Figure 1.

Label	Function	Step
2.3.1.a	Synthase	A
2.8.3.a	Coenzyme-A transferase	E, L
3.1.2.a	Thiolester hydrolase (CoA specific)	E
4.1.1.a	Decarboxylase	C, H, J
4.1.3.a	Lyase	D
4.2.1.a	Dehydratase	B, F, K
5.2.1.a	Cis/trans isomerase	G
5.3.3.a	Delta-Isomerase	I
6.2.1.a	Acid-thiol ligase	E, L

[0273] EC 2.3.1.a Synthase (Step A). Citramalate synthase (EC 2.3.1.182) catalyzes the conversion of acetyl-CoA and pyruvate to citramalate and coenzyme A. The enzyme participates in the threonine-independent pathway of isoleucine biosynthesis found in archaea such as *Methanocaldococcus jannaschii* (Howell et al., *J Bacteriol.* 181:331-333 (1999)), *Leptospira interrrogans* (Xu et al., *J Bacteriol.* 186:5400-5409 (2004)) and *Geobacter sulfurreducens* (Risso et al., *J Bacteriol.* 190:2266-2274 (2008)). This enzyme operates in the synthetic direction *in vivo*, is highly specific for pyruvate as a substrate, and is typically inhibited by isoleucine. A recombinant citramalate synthase from *M. jannaschii* developed by directed evolution is highly active and lacks inhibition by isoleucine (Atsumi et al., *Appl Environ Microbiol* 74:7802-7808 (2008)). Citramalate synthase activity was also demonstrated in the citramalate cycle acetate assimilation pathway of *Rhodospirillum rubrum*, although the gene associated with this activity was not been identified (Berg et al., *Mikrobiologiia* 78:22-31 (2009)).

Gene	GenBank	GI Number	Organism
CimA	Q58787.1	2492795	*Methanocaldococcus jannaschii*
CimA	ABK13749.1	116664671	*Leptospira interrrogans*
CimA	ADI84633.1	298505910	*Geobacter sulfurreducens*

[0274] EC 2.8.3.a CoA transferase (Step E). CoA transferases catalyze the reversible transfer of a CoA moiety from one molecule to another. Two transformations in Figure 1 utilize a CoA transferase: conversion of citramalyl-CoA to citramalate (Step E) and activation of itaconate to itaconyl-CoA (Step L). Citramalyl-CoA transferase (EC 2.8.3.7 and 2.8.3.11) in Step E of Figure 1 transfers a CoA moiety from citramalyl-CoA to a donor. A citramalate:succinyl-CoA transferase enzyme is active in the 3-hydroxypropionate cycle of glyoxylate assimilation. The enzyme is encoded by *sst* in *Chloroflexus aurantiacus,* where it is located upstream of the gene encoding citramalyl-CoA lyase (Friedmann et al., *J Bacteriol.* 188:6460-6468 (2006)). This enzyme was cloned, heterologously expressed and characterized in *E. coli*. The enzyme is also active as an itaconate:succinyl-CoA transferase. Similar enzymes are found in *Roseiflexus* sp. RS-1 and *Chloroflexus aggregans* by sequence identity and proximity to the citramalyl-CoA lyase gene. A CoA transferase characterized in *Pseudomonas* sp. B2aba exhibits both citramlayl-CoA transferase and itaconyl-CoA transferase activities, allowing the organism to grow on both itaconate and citramalate (Cooper et al., *Biochem.J* 91:82-91 (1964)). The gene associated with this enzyme has not been identified. Citramalyl-CoA transferase activity was also detected in cell extracts of

Achromobacter xylosoxydans, which efficiently converts itaconate to citramalate (He et al., *J Biosci Bioeng.* 89:388-391 (2000)). The associated gene is not known, but the gene bears the highest protein sequence similarity *Sst*.

Gene	GenBank	GI Number	Organism
Sst	YP_001635864.1	163847820	*Chloroflexus aurantiacus*
RoseRS_0050	YP_001274443.1	148654238	*Roseiflexus* sp. RS-1
Cagg_3093	YP_002464387.1	219849954	*Chloroflexus aggregans*
AXYL_05983	YP_003981992.1	311109139	*Achromobacter xylosoxydans*

[0275] Additional candidate enzymes for catalyzing these transformations include the gene products of *cat1*, *cat2*, and *cat3* of *Clostridium kluyveri,* which have been shown to exhibit succinyl-CoA, 4-hydroxybutyryl-CoA, and butyryl-CoA transferase activity, respectively (Seedorf et al., *Proc.Natl.Acad.Sci USA* 105:2128-2133 (2008); Sohling et al., *J Bacteriol.* 178:871-880 (1996)). Similar CoA transferase activities are also present in *Trichomonas vaginalis* (van Grinsven et al., *J.Biol.Chem.* 283:1411-1418 (2008)) and *Trypanosoma brucei* (Riviere et al., *J.Biol.Chem.* 279:45337-45346 (2004)).

Protein	GenBank ID	GI Number	Organism
cat1	P38946.1	729048	*Clostridium kluyveri*
cat2	P38942.2	172046066	*Clostridium kluyveri*
cat3	EDK35586.1	146349050	*Clostridium kluyveri*
TVAG_395550	XP_001330176	123975034	*Trichomonas vaginalis G3*
Tb11.02.0290	XP_828352	71754875	*Trypanosoma brucei*

[0276] The glutaconyl-CoA-transferase (EC 2.8.3.12) enzyme from anaerobic bacterium *Acidaminococcus fermentans* reacts with glutaconyl-CoA and 3-butenoyl-CoA (Mack et al., *Eur.J.Biochem.* 226:41-51 (1994)), substrates similar in structure to 2,3-dehydroadipyl-CoA. The genes encoding this enzyme are *gctA* and *gctB*. This enzyme has reduced but detectable activity with other CoA derivatives including glutaryl-CoA, 2-hydroxyglutaryl-CoA, adipyl-CoA, crotonyl-CoA and acrylyl-CoA (Buckel et al., *Eur.J Biochem.* 118:315-321 (1981)). The enzyme has been cloned and expressed in *E. coli* (Mack et al., *Eur.J.Biochem.* 226:41-51 (1994)). Glutaconate CoA-transferase activity has also been detected in *Clostridium sporosphaeroides* and *Clostridium symbiosum*. Additional glutaconate CoA-transferase enzymes can be inferred by homology to the *Acidaminococcus fermentans* protein sequence.

Protein	GenBank ID	GI Number	Organism
gctA	CAA57199.1	559392	*Acidaminococcus fermentans*
gctB	CAA57200.1	559393	*Acidaminococcus fermentans*
gctA	ACJ24333.1	212292816	*Clostridium symbiosum*
gctB	ACJ24326.1	212292808	*Clostridium symbiosum*
gctA	NP_603109.1	19703547	*Fusobacterium nucleatum*
gctB	NP_603110.1	19703548	*Fusobacterium nucleatum*

[0277] A CoA transferase that can utilize acetyl-CoA as the CoA donor is acetoacetyl-CoA transferase, encoded by the *E. coli atoA* (alpha subunit) and *atoD* (beta subunit) genes (Korolev et al., *Acta Crystallogr.D.Biol.Crystallogr.* 58:2116-2121 (2002); Vanderwinkel et al., *Biochem.Biophys.Res.Commun.* 33:902-908 (1968)). This enzyme has a broad substrate range (Sramek et al., *Arch.Biochem.Biophys.* 171:14-26 (1975)) and has been shown to transfer the CoA moiety to acetate from a variety of branched and linear acyl-CoA substrates, including isobutyrate (Matthies et al., *Appl Environ.Microbiol* 58:1435-1439 (1992)), valerate (Vanderwinkel et al., *Biochem.Biophys.Res.Commun.* 33:902-908 (1968)) and butanoate (Vanderwinkel et al., *Biochem.Biophys.Res.Commun.* 33:902-908 (1968)). This enzyme is induced at the transcriptional level by acetoacetate, so modification of regulatory control can be useful for engineering this enzyme into a pathway (Pauli et al., *Eur.J Biochem.* 29:553-562 (1972)). Similar enzymes exist in *Corynebacterium glutamicum* ATCC 13032 (Duncan et al., *Appl.Environ.Microbiol* 68:5186-5190 (2002)), *Clostridium acetobutylicum* (Cary et al., *Appl.Environ.Microbiol* 56:1576-1583 (1990); Wiesenborn et al., *Appl.Environ.Microbiol* 55:323-329 (1989)), and *Clostridium saccharoperbutylacetonicum* (Kosaka et al., *Biosci.Biotechnol Biochem.* 71:58-68 (2007)).

Gene	Accession No.	GI Number	Organism
atoA	P76459.1	2492994	*Escherichia coli*
atoD	P76458.1	2492990	*Escherichia coli*
actA	YP_226809.1	62391407	*Corynebacterium glutamicum*
cg0592	YP_224801.1	62389399	*Corynebacterium glutamicum*
ctfA	NP_149326.1	15004866	*Clostridium acetobutylicum*
ctfB	NP_149327.1	15004867	*Clostridium acetobutylicum*
ctfA	AAP42564.1	31075384	*Clostridium saccharoperbutylacetonicum*
ctfB	AAP42565.1	31075385	*Clostridium saccharoperbutylacetonicum*

[0278] EC 3.2.1.a CoA hydrolase (Step E). Enzymes in the 3.1.2 family hydrolyze acyl-CoA molecules to their corresponding acids. Several CoA hydrolases with broad substrate

ranges are suitable candidates for exhibiting citramalyl-CoA hydrolase activity. For example, the enzyme encoded by *acot12* from *Rattus norvegicus* brain (Robinson et al., *Biochem.Biophys.Res.Commun.* 71:959-965 (1976)) can react with butyryl-CoA, hexanoyl-CoA and malonyl-CoA. The human dicarboxylic acid thioesterase, encoded by *acot8,* exhibits activity on glutaryl-CoA, adipyl-CoA, suberyl-CoA, sebacyl-CoA, and dodecanedioyl-CoA (Westin et al., *J.Biol.Chem.* 280:38125-38132 (2005)). The closest *E. coli* homolog to this enzyme, *tesB*, can also hydrolyze a range of CoA thiolesters (Naggert et al., *J Biol Chem* 266:11044-11050 (1991)). A similar enzyme has also been characterized in the rat liver (Deana R., *Biochem Int* 26:767-773 (1992)). Additional enzymes with hydrolase activity in *E. coli* include *ybgC*, *paaI*, and *ybdB* (Kuznetsova, et al., FEMS Microbiol Rev, 2005, 29(2):263-279; Song et al., J Biol Chem, 2006, 281(16):11028-38). Though its sequence has not been reported, the enzyme from the mitochondrion of the pea leaf has a broad substrate specificity, with demonstrated activity on acetyl-CoA, propionyl-CoA, butyryl-CoA, palmitoyl-CoA, oleoyl-CoA, succinyl-CoA, and crotonyl-CoA (Zeiher et al., *Plant.Physiol.* 94:20-27 (1990)). The acetyl-CoA hydrolase, *ACH1*, from *S. cerevisiae* represents another candidate hydrolase (Buu et al., *J.Biol.Chem.* 278:17203-17209 (2003)) .

Gene name	GenBank ID	GI Number	Organism
acot12	NP_570103.1	18543355	*Rattus norvegicus*
tesB	NP_414986	16128437	*Escherichia coli*
acot8	CAA15502	3191970	*Homo sapiens*
acot8	NP_570112	51036669	*Rattus norvegicus*
tesA	NP_415027	16128478	*Escherichia coli*
ybgC	NP_415264	16128711	*Escherichia coli*
paaI	NP_415914	16129357	*Escherichia coli*
ybdB	NP_415129	16128580	*Escherichia coli*
ACH1	NP_009538	6319456	*Saccharomyces cerevisiae*

[0279] Yet another candidate hydrolase is the glutaconate CoA-transferase from *Acidaminococcus fermentans*. This enzyme was transformed by site-directed mutagenesis into an acyl-CoA hydrolase with activity on glutaryl-CoA, acetyl-CoA and 3-butenoyl-CoA (Mack et al., *FEBS.Lett.* 405:209-212 (1997)). This indicates that the enzymes encoding succinyl-CoA:3-ketoacid-CoA transferases and acetoacetyl-CoA:acetyl-CoA transferases can also serve as candidates for this reaction step, with appropriate mutations introduced to change their function as described above.

Gene	GenBank	GI Number	Organism
gctA	CAA57199	559392	*Acidaminococcus fermentans*
gctB	CAA57200	559393	*Acidaminococcus fermentans*

[0280] EC 4.1.1.a Decarboxylase (Steps C, H, J). The final step of MAA in Figure 1 is the decarboxylation of either mesaconate or citraconate. Although enzymes with citraconate or mesaconate decarboxylase activity have not been identified to date, suitable enzyme candidates include aconitate decarboxylase (EC 4.1.1.6), which catalyzes the conversion of aconitate to itaconate, 4-oxalocrotonate decarboxylase (EC 4.1.1.77), which catalyzes the conversion of 4-oxalocrotonate to 2-oxopentenoate, and enzymes in the cinnamate decarboxylase family (EC 4.1.1.-). Aconitate decarboxylase (EC 4.1.1.6) catalyzes the final step in itaconate biosynthesis in a strain of *Candida* and also in the filamentous fungus *Aspergillus terreus* (Bonnarme et al. *J Bacteriol.* 177:3573-3578 (1995); Willke and Vorlop, *Appl Microbiol. Biotechnol* 56:289-295 (2001)). A cis-aconitate decarboxylase (CAD) (EC 4.1.16) has been purified and characterized from *Aspergillus terreus* (Dwiarti et al., *J. Biosci. Bioeng.* 94(1): 29-33 (2002)). Recently, the gene has been cloned and functionally characterized (Kanamasa et al., *Appl.Microbiol Biotechnol* 80:223-229 (2008)) and (WO/2009/014437). Several close homologs of CAD are listed below (EP 2017344A1; WO 2009/014437 A1). The gene and protein sequence of CAD were reported previously (EP 2017344 A1; WO 2009/014437 A1), along with several close homologs listed below.

Gene	GenBank	GI Number	Organism
CAD	XP_001209273	115385453	*Aspergillus terreus*
	XP_001217495	115402837	*Aspergillus terreus*
	XP_001209946	115386810	*Aspergillus terreus*
	BAE66063	83775944	*Aspergillus oryzae*
	XP_001393934	145242722	*Aspergillus niger*
	XP_391316	46139251	*Gibberella zeae*
	XP_001389415	145230213	*Aspergillus niger*
	XP_001383451	126133853	*Pichia stipitis*
	YP_891060	118473159	*Mycobacterium smegmatis*
	NP_961187	41408351	*Mycobacterium avium subsp. pratuberculosis*
	YP_880968	118466464	*Mycobacterium avium*
	ZP_01648681	119882410	*Salinispora arenicola*

[0281] 4-Oxalocronate decarboxylase catalyzes the decarboxylation of 4-oxalocrotonate to 2-oxopentanoate. This enzyme has been isolated from numerous organisms and

characterized. Genes encoding this enzyme include *dmpH* and *dmpE* in *Pseudomonas sp. (strain 600)* (Shingler et al., 174:711-724 (1992)), *xylII* and *xylIII* from *Pseudomonas putida* (Kato et al., *Arch.Microbiol* 168:457-463 (1997); Stanley et al., *Biochemistry* 39:3514 (2000); Lian et al., *J.Am.Chem.Soc.* 116:10403-10411 (1994)) and *Reut_B5691* and *Reut_B5692* from *Ralstonia eutropha JMP134* (Hughes et al., 158:79-83 (1984)). The genes encoding the enzyme from *Pseudomonas sp. (strain 600)* have been cloned and expressed in *E. coli* (Shingler et al., *J. Bacteriol.* 174:711-724 (1992)). The 4-oxalocrotonate decarboxylase encoded by *xylI* in *Pseudomonas putida* functions in a complex with vinylpyruvate hydratase. A recombinant form of this enzyme devoid of the hydratase activity and retaining wild type decarboxylase activity has been characterized (Stanley et al., *Biochem.* 39:718-26 (2000)). A similar enzyme is found in *Ralstonia pickettii* (formerly *Pseudomonas pickettii*) (Kukor et al., *J Bacteriol.* 173:4587-94 (1991)).

Gene	GenBank	GI Number	Organism
dmpH	CAA43228.1	45685	*Pseudomonas sp. CF600*
dmpE	CAA43225.1	45682	*Pseudomonas sp. CF600*
xylII	YP_709328.1	111116444	*Pseudomonas putida*
xylIII	YP_709353.1	111116469	*Pseudomonas putida*
Reut_B5691	YP_299880.1	73539513	*Ralstonia eutropha JMP134*
Reut_B5692	YP_299881.1	73539514	*Ralstonia eutropha JMP134*
xylI	P49155.1	1351446	*Pseudomonas putida*
tbuI	YP_002983475.1	241665116	*Ralstonia pickettii*

[0282] Finally, a class of decarboxylases has been characterized that catalyze the conversion of cinnamate (phenylacrylate) and substituted cinnamate derivatives to their corresponding styrene derivatives. These enzymes are common in a variety of organisms and specific genes encoding these enzymes that have been cloned and expressed in *E. coli* include: *pad 1* from *Saccharomyces cerevisae* (Clausen et al., *Gene* 142:107-112 (1994)), *pdc* from *Lactobacillus plantarum* (Barthelmebs et al., 67:1063-1069 (2001); Qi et al., *Metab Eng* 9:268-276 (2007); Rodriguez et al., *J.Agric.Food Chem.* 56:3068-3072 (2008)), *pofK* (*pad*) from *Klebsiella oxytoca* (Uchiyama et al., *Biosci.Biotechnol.Biochem.* 72:116-123 (2008); Hashidoko et al., *Biosci.Biotech.Biochem.* 58:217-218 (1994)) , *Pedicoccus pentosaceus* (Barthelmebs et al., 67:1063-1069 (2001)), and *padC* from *Bacillus subtilis* and *Bacillus pumilus* (Shingler et al., 174:711-724 (1992)). A ferulic acid decarboxylase from *Pseudomonas fluorescens* also has been purified and characterized (Huang et al., *J.Bacteriol.* 176:5912-5918 (1994)). Enzymes in this class are stable and do not require either exogenous

or internally bound co-factors, thus making these enzymes ideally suitable for biotransformations (Sariaslani, *Annu.Rev.Microbiol.* 61:51-69 (2007)).

Gene name	**GenBankID**	**GI Number**	**Organism**
pad1	BAG32372.1	188496949	*Saccharomyces cerevisae*
pdc	AAC45282.1	1762616	*Lactobacillus plantarum*
pofK (pad)	BAF65031.1	149941607	*Klebsiella oxytoca*
padC	AAC46254.1	2394282	*Bacillus subtilis*
pad	CAC16793.1	11322457	*Pedicoccus pentosaceus*
pad	CAC18719.1	11691810	*Bacillus pumilus*

[0283] Another suitable enzyme is sorbic acid decarboxylase which converts sorbic acid to 1,3-pentadiene. Sorbic acid decarboxylation by *Aspergillus niger* requires three genes: *padA1*, *ohbA1*, and *sdrA* (Plumridge et al. *Fung. Genet. Bio*, 47:683-692 (2010). *PadA1* is annotated as a phenylacrylic acid decarboxylase, *ohbA1* is a putative 4-hydroxybenzoic acid decarboxylase, and *sdrA* is a sorbic acid decarboxylase regulator. Additional species have also been shown to decarboxylate sorbic acid including several fungal and yeast species (Kinderlerler and Hatton, *Food Addit Contam.*, 7(5):657-69 (1990); Casas et al., *Int J Food Micro.*, 94(1):93-96 (2004); Pinches and Apps, *Int. J. Food Microbiol.* 116: 182–185 (2007)). For example, *Aspergillus oryzae* and *Neosartorya fischeri* have been shown to decarboxylate sorbic acid and have close homologs to *padA1*, *ohbA1*, and *sdrA*.

Gene name	GenBankID	GI Number	Organism
padA1	XP_001390532.1	145235767	*Aspergillus niger*
ohbA1	XP_001390534.1	145235771	*Aspergillus niger*
sdrA	XP_001390533.1	145235769	*Aspergillus niger*
padA1	XP_001818651.1	169768362	*Aspergillus oryzae*
ohbA1	XP_001818650.1	169768360	*Aspergillus oryzae*
sdrA	XP_001818649.1	169768358	*Aspergillus oryzae*
padA1	XP_001261423.1	119482790	*Neosartorya fischeri*
ohbA1	XP_001261424.1	119482792	*Neosartorya fischeri*
sdrA	XP_001261422.1	119482788	*Neosartorya fischeri*

[0284] Each of the decarboxylases listed above represents a possible suitable enzyme for decarboxylating mesaconate or citraconate. If the desired activity or productivity of the enzyme is not observed in the desired conversions, the decarboxylase enzymes can be evolved using known protein engineering methods to achieve the required performance. Importantly, it was shown through the use of chimeric enzymes that the C-terminal region of decarboxylases appears to be responsible for substrate specificity (Barthelmebs et al., AEM 67, 1063-1069 (2001)). Accordingly, directed evolution experiments to broaden the specificity of decarboxylases in order to gain activity with mesaconate or citraconate can be focused on the C-terminal region of these enzymes.

[0285] EC 4.1.3.a Lyase (Step D). Citramalyl-CoA lyase (EC 4.1.3.25) converts acetyl-CoA and pyruvate to citramalyl-CoA, shown in Step D of Figure 1. This enzyme participates in the 3-hydroxypropionate (3-HP) cycle of glyoxylate assimilation, where it acts in the citramalyl-CoA degrading direction. The enzyme is encoded by the *ccl* gene in the green nonsulfur phototrophic bacterium *Chloroflexus aurantiacus* (Friedmann et al., *J Bacteriol.* 189:2906-2914 (2007)), where it is located downstream of a gene encoding citramalyl-CoA transferase. The *ccl* gene was cloned and heterologously expressed in *E. coli*. Similar gene clusters are found in *Roseiflexus* sp. RS-1 and *Chloroflexus aggregans*, although the enzymes have not been characterized to date. The 3-HP cycle is also active in *Rhodobacter sphaeroides*, whose genome encodes a protein with high sequence similarity to the ccl gene product (Filatova et al., *Mikrobiologiia* 74:319-328 (2005)). The citramalyl-CoA lyase from a *Bacillus* sp. was shown to be reversible, although the associated gene has not been identified to date (Sasaki et al., *J Biochem.* 73:599-608 (1973)).

Gene	**GenBank**	**GI Number**	**Organism**
Caur_2265	YP_001635863.1	163847819	*Chloroflexus aurantiacus*
RoseRS_0049	YP_001274442.1	148654237	*Roseiflexus* sp. RS-1
Cagg_3093	YP_002464386.1	219849953	*Chloroflexus aggregans*
Rsph17029_1172	YP_001043054.1	126461940	*Rhodobacter sphaeroides*

[0286] EC 4.2.1.a Dehydratase (Steps B, F). The dehydration of citramalate to citraconate in Step B of Figure 1 is catalyzed by an enzyme with citramalate dehydratase (citraconate forming) activity (EC 4.2.1.35). This enzyme, along with citramalate synthase, participates in the threonine-independent isoleucine biosynthesis pathway characterized in *Methanocaldococcus jannaschii* and *Leptospira interrrogans*. The dehydration of citramalate in these organisms catalyzed by isopropylmalate isomerase (IPMI), which catalyzes both the

dehydration of citramalate to citraconate and the subsequent trans-addition of water to citraconate to form methylmalate (Xu et al., *J Bacteriol.* 186:5400-5409 (2004); Drevland et al., *J Bacteriol.* 189:4391-4400 (2007)). The *M. jannaschii* homoaconitase (EC 4.2.1.114) encoded by *hacAB* is also a suitable candidate, and mutants of this enzyme with altered substrate specificity and isopropylmalate isomerase activity have been characterized (Jeyakanthan et al., *Biochemistry* 49:2687-2696 (2010)). The *L. interrogans* IPMI genes were cloned into *E. coli*, where they were able to complement strains deficient in native aconitase activity when expressed together (Xu et al., *J Bacteriol.* 186:5400-5409 (2004)). Citramalate dehydratase has also been characterized in *Pseudomonas putida,* where it participates in 3,5-xylenol degradation. The genes encoding the enzymes of this pathway, including citramalate dehydratase, are located on the transmissible plasmid pRA500, and they have been cloned into *E. coli* (Jain, Appl. Microbiol. Biotechnol., 45:502-508 (1996)). Citraconate is also a substrate of the *Saccharomyces cerevisiae* 3-isopropylmalate dehydratase (EC 4.2.1.33) enzyme encoded by *LEU1* (Kohlhaw, *Methods Enzymol.* 166:423-429 (1988)). The 3-isopropylmalate dehydratase *LEU1* of *Candida maltosa* exhibits higher activity on citraconate than the native substrate (Bode, R. and Birnbaum, D., J. Basic Microbiol. 31:21-26 (1991)). Attenuation or selective inhibition of the citraconate to methylmalate hydration activity may be required to increase accumulation of the citraconate intermediate.

Gene	GenBank	GI Number	Organism
LeuC	P81291.1	3219823	*Methanocaldococcus jannaschii*
LeuD	Q58673.1	3122345	*Methanocaldococcus jannaschii*
hacA	Q58409.1	3122347	*Methanocaldococcus jannaschii*
hacB	Q58667.1	3122344	*Methanocaldococcus jannaschii*
LeuC	NP_712276.1	24214795	*Leptospira interrrogans*
LeuD	NP_712277.1	24214796	*Leptospira interrrogans*
LEU1	AAB19612.1	234318	*Saccharomyces cerevisiae*
cmLEU1	AAB03335.1	1399939	*Candida maltosa*

[0287] Another suitable citramalate dehydratase candidate is the 2-methylcitrate dehydratase enzymes that form cis-2-methylaconitate (EC 4.2.1.79) and *trans*-2-methylaconitate (EC 4.2.1.117). The 2-methylcitrate *cis*-dehydratase of *E. coli* encoded by *prpD* is active on citramalate as a substrate (Blank et al., *Microbiology* 148:133-146 (2002)).

Neither citraconate nor mesaconate were active as substrates, indicating that PrpD is strictly a dehydratase enzyme rather than an isomerase. The PrpD enzyme of *Salmonella enterica serovar Typhimurium* has also been characterized, but activity on citramalate has not been demonstrated (Horswill et al., *Biochemistry* 40:4703-4713 (2001)). The 2-methylcitrate dehydratase enzymes of *Shewanella oneidensis* encoded by *acnB* and *acnD* are also candidates (Grimek et al., *J Bacteriol.* 186:454-462 (2004)). The AcnD enzyme requires a cofactor encoded by *prpF* to function *in vivo*. Crystal structure studies of PrpF in complex with aconitate show that the enzyme functions as a cis/trans isomerase, interconverting the cis/trans isomers of aconitate and 2-methylaconitate (Garvey et al., *Protein Sci* 16:1274-1284 (2007)). An additional candidate from *S. oneidensis* is a predicted isopropylmalate isomerase encoded by *leuCD*.

Gene	GenBank	GI Number	Organism
prpD	AAC73437.1	1786528	*Escherichia coli*
prpD	AAC44816.1	1648968	*Salmonella enterica serovar Typhimurium*
acnB	NP_716069.1	24372027	*Shewanella oneidensis*
acnD	AAN53428.1	24345782	*Shewanella oneidensis*
prpF	AAN53427.1	24345781	*Shewanella oneidensis*
leuC	NP_719761.1	24375718	*Shewanella oneidensis*
leuD	NP_719760.1	24375717	*Shewanella oneidensis*

[0288] The dehydration of citramalate to mesaconate in Step F is catalyzed by citramalate dehydratase (mesaconate forming, EC 4.2.1.34), also called 2-methylmalate dehydratase or mesaconase. This enzyme has been only partially characterized in *Clostridium tetanomorphum*, and gene candidates are not available to date. The activity has also been demonstrated in cell extracts of *Rhodospirillum rubrum*, where it participates in the citramalate cycle of acetate utilization (Berg and Ivanovskii, *Mikrobiologiia* 78:22-31 (2009)), although the associated gene has not been identified.

[0289] Itaconyl-CoA is converted to citramalyl-CoA (Step K of Figure 1) by itaconyl-CoA hydratase (EC 4.2.1.56), an enzyme that participates in itaconate assimilation pathways in organisms such as *Pseudomonas* sp. B2aba (Cooper and Kornberg, *Biochem.J* 91:82-91 (1964)), *Achromobacter xylosoxydans* (He et al., *J Biosci Bioeng.* 89:388-391 (2000)) and *Pseudomonas fluorescens* (Nagai, J., J. Biochem, 53:181-7 (1963)). This enzyme activity has not been associated with a gene to date.

[0290] EC 5.2.1.a Cis/trans isomerase (Step G). The cis/trans isomerization of mesaconate and citraconate is catalyzed by an enzyme with citraconate isomerase activity. Suitable candidates include aconitate isomerase (EC 5.3.3.7), maleate *cis,trans*-isomerase (EC 5.2.1.1), maleylacetone *cis,trans*-isomerase and *cis,trans*-isomerase of unsaturated fatty acids (Cti).

[0291] Aconitate isomerase interconverts *cis*- and *trans*-aconitate. The aconitate isomerase of *Shewanella oneidensis*, encoded by *prpF*, interconverts the cis/trans isomers of aconitate and 2-methylaconitate (Garvey et al., *Protein Sci* 16:1274-1284 (2007)). This enzyme operates in complex with the methylcitrate dehydratase, AcnD. Aconitate isomerase activity was detected in many gram-negative bacteria including *Pseudomonas fluorescens* and *Pseudomonas putida*, but not in gram-positive bacteria (Watanabe et al., *Curr Microbiol* 35:97-102 (1997)). Purified enzyme from *Pseudomonas putida* has been characterized (Klinman et al., *Biochemistry* 10:2253-2259 (1971)). Aconitate isomerase enzymes have also been studied in plants, but the genes have not been identified to date (Thompson et al., *Anal.Biochem.* 184:39-47 (1990)). Some predicted proteins with high sequence homology to the *prpF* protein are listed below.

Gene	GenBank	GI Number	Organism
prpF	AAN53427.1	24345781	*Shewanella oneidensis*
prpF	PP_2337	26989061	*Pseudomonas putida*
Pfl01_1767	YP_347499.1	77457994	*Pseudomonas fluorescens*
Reut_A1811	YP_296020.1	73541500	*Ralstonia eutropha*

[0292] Therefore, the addition of a *cis,trans* isomerase may help to improve the yield of terepthalic acid. Enzymes for similar isomeric conversions include maleate *cis,trans*-isomerase (EC 5.2.1.1), maleylacetone *cis-trans*-isomerase (EC 5.2.1.2), and *cis,trans*-isomerase of unsaturated fatty acids (Cti).

[0293] Maleate *cis,trans*-isomerase (EC 5.2.1.1) catalyzes the conversion of maleic acid in cis formation to fumarate in trans formation (Scher et al., *J Biol.Chem.* 244:1878-1882 (1969)). The *Alcalidgenes faecalis maiA* gene product has been cloned and characterized (Hatakeyama et al., *Biochem.Biophys.Res.Commun.* 239:74-79 (1997)). Other maleate *cis,trans*-isomerases are available in *Serratia marcescens* (Hatakeyama et al., *Biosci.Biotechnol Biochem.* 64:1477-1485 (2000)), *Ralstonia eutropha* and *Geobacillus stearothermophilus*.

Gene	GenBank	GI Number	Organism
maiA	BAA23002	2575787	*Alcaligenes faecalis*
maiA	YP_725437	113866948	*Ralstonia eutropha H16*
maiA	BAA77296	4760466	*Geobacillus stearothermophilus*
maiA	BAA96747.1	8570038	*Serratia marcescens*

[0294] Maleylacetone *cis,trans*-isomerase (EC 5.2.1.2) catalyzes the conversion of 4-maleyl-acetoacetate to 4-fumaryl-acetyacetate, a cis to trans conversion. This enzyme is encoded by *maiA* in *Pseudomonas aeruginosa* (Fernandez-Canon et al., *J Biol.Chem.* 273:329-337 (1998)) and *Vibrio cholera* (Seltzer, *J Biol.Chem.* 248:215-222 (1973)). A similar enzyme was identified by sequence homology in *E. coli O157*.

Gene	GenBank	GI Number	Organism
maiA	NP_250697	15597203	*Pseudomonas aeruginosa*
maiA	NP_230991	15641359	*Vibrio cholerae*
maiA	EDU73766	189355347	*Escherichia coli O157*

[0295] The *cti* gene product catalyzes the conversion of *cis*- unsaturated fatty acids (UFA) to *trans*- UFA. The enzyme has been characterized in *P. putida* (Junker et al., *J Bacteriol.* 181:5693-5700 (1999)). Similar enzymes are found in *Shewanella* sp. MR-4 and *Vibrio cholerae*.

Gene	GenBank	GI Number	Organism
cti	AAD41252	5257178	*Pseudomonas putida*
cti	YP_732637	113968844	*Shewanella* sp. MR-4
cti	ZP_04395785	229506276	*Vibrio cholerae*

[0296] EC 5.3.3.a Delta-isomerase (Steps I). The conversion of itaconate to citraconate is catalyzed by itaconate delta-isomerase. An enzyme with this activity is the methylitaconate delta-isomerase (EC 5.3.3.6) of *Eubacterium barkeri* (Velarde et al., *J Mol Biol* 391:609-620 (2009)). This enzyme was heterologously expressed and characterized in *E. coli*. Homologs with high protein sequence similarity are listed below.

Gene	GenBank	GI Number	Organism
mii	Q0QLE6.1	122953534	*Eubacterium barkeri*
FMAG_01516	ZP_04567526.1	237737045	*Fusobacterium mortiferum*
BACCAP_02290	ZP_02036679.1	154498301	*Bacteroides capillosus*
CLJU_c30450	YP_003781195.1	300856211	*Clostridium ljungdahlii*
BMD_3790	YP_003598973.1	295705898	*Bacillus megaterium*
EFER_3666	YP_002384731.1	218550940	*Escherichia fergusonii*

[0297] EC 6.2.1 CoA synthetase (Step E). The conversion of citramalyl-CoA to citramalate (Figure 1, Step E) and itaconate to itaconyl-CoA (Figure 1, Step L) can be catalyzed by a CoA acid-thiol ligase or CoA synthetase in the 6.2.1 family of enzymes. A succinyl-CoA synthetase enzyme with itaconyl-CoA synthetase (EC 6.2.1.4) activity was characterized in *Pseudomonas* sp. B2aba, but the gene has not been identified (Cooper and Kornberg, *Biochem.J* 91:82-91 (1964)). Additional CoA ligase enzyme candidates include succinyl-CoA synthetase (EC 6.3.1.4), acetyl-CoA synthetase (EC 6.2.1.13), acyl-CoA ligase and malonyl-CoA synthetase (EC 6.3.4.9). Several enzymes with broad substrate ranges have been described in the literature. ADP-forming acetyl-CoA synthetase (ACD, EC 6.2.1.13) is an enzyme that couples the conversion of acyl-CoA esters to their corresponding acids with the concomitant synthesis of ATP. ACD I from *Archaeoglobus fulgidus*, encoded by *AF1211*, was shown to operate on a variety of linear and branched-chain substrates including isobutyrate, isopentanoate, and fumarate (Musfeldt et al., *J Bacteriol.* 184:636-644 (2002)). A second reversible ACD in *Archaeoglobus fulgidus*, encoded by *AF1983*, was also shown to have a broad substrate range with high activity on cyclic compounds phenylacetate and indoleacetate (Musfeldt and Schonheit, *J Bacteriol.* 184:636-644 (2002)). The enzyme from *Haloarcula marismortui* (annotated as a succinyl-CoA synthetase) accepts propionate, butyrate, and branched-chain acids (isovalerate and isobutyrate) as substrates, and was shown to operate in the forward and reverse directions (Brasen et al., *Arch.Microbiol* 182:277-287 (2004)). The ACD encoded by *PAE3250* from hyperthermophilic crenarchaeon *Pyrobaculum aerophilum* showed the broadest substrate range of all characterized ACDs, reacting with acetyl-CoA, isobutyryl-CoA (preferred substrate) and phenylacetyl-CoA (Brasen and Schonheit, *Arch.Microbiol* 182:277-287 (2004)). Directed evolution or engineering can be used to modify this enzyme to operate at the physiological temperature of the host organism. The enzymes from *A. fulgidus*, *H. marismortui* and *P. aerophilum* have all been cloned, functionally expressed, and characterized in *E. coli* (Brasen and Schonheit, *Arch.Microbiol* 182:277-287 (2004); Musfeldt and Schonheit, *J Bacteriol.* 184:636-644 (2002)). The acyl-CoA ligase from *Pseudomonas putida* encoded by *paaF* has been demonstrated to work on several aliphatic substrates including acetic, propionic, butyric, valeric, hexanoic, heptanoic, and octanoic acids and on aromatic compounds such as phenylacetic and phenoxyacetic acids (Fernandez-Valverde et al., *Appl.Environ.Microbiol.* 59:1149-1154 (1993)). A related enzyme, malonyl CoA synthetase (6.3.4.9) from *Rhizobium leguminosarum* can convert several diacids, namely, ethyl-, propyl-, allyl-, isopropyl-,

dimethyl-, cyclopropyl-, cyclopropylmethylene-, cyclobutyl-, and benzyl-malonate into their corresponding monothioesters (Pohl et al., *J.Am.Chem.Soc.* 123:5822-5823 (2001)). Additional candidates are the succinyl-CoA synthetase enzymes encoded by *sucCD* in *E. coli* and *LSC12* in *S. cerevisiae,* which naturally catalyze the formation of succinyl-CoA from succinate with the concomitant consumption of one ATP, a reaction which is reversible *in vivo* (Buck et al., *Biochemistry* 24:6245-6252 (1985)).

Protein	GenBank ID	GI Number	Organism
AF1211	NP_070039.1	11498810	*Archaeoglobus fulgidus*
AF1983	NP_070807.1	11499565	*Archaeoglobus fulgidus*
scs	YP_135572.1	55377722	*Haloarcula marismortui*
PAE3250	NP_560604.1	18313937	*Pyrobaculum aerophilum* str. IM2
paaF	AAC24333.2	22711873	*Pseudomonas putida*
matB	AAC83455.1	3982573	*Rhizobium leguminosarum*
sucC	NP_415256.1	16128703	*Escherichia coli*
sucD	AAC73823.1	1786949	*Escherichia coli*
LSC1	NP_014785	6324716	*Saccharomyces cerevisiae*
LSC2	NP_011760	6321683	*Saccharomyces cerevisiae*

EXAMPLE II
Preparation of a MAA Producing Microbial Organism Having an Actyl-CoA to MAA Pathway

[0298] This example describes the generation of a microbial organism capable of producing MAA from acetyl-CoA and pyruvate. This exemplary pathway is shown in Steps A/B/C of Figure 1.

[0299] *Escherichia coli* is used as a target organism to engineer a MAA-producing pathway from acetyl-CoA and pyruvate as shown in Figure 1 in steps A, B and C. *E. coli* provides a good host for generating a non-naturally occurring microorganism capable of producing MAA. *E. coli* is amenable to genetic manipulation and is known to be capable of producing various products, like ethanol, acetic acid, formic acid, lactic acid, succinic acid and 1,4-butanediol, effectively under anaerobic or microaerobic conditions.

[0300] To generate an *E. coli* strain engineered to produce MAA from acetyl-CoA, nucleic acids encoding the enzymes utilized in the pathway of Figure 1, described previously, are expressed in *E. coli* using well known molecular biology techniques (see, for example,

Sambrook et al, *Molecular Cloning: A Laboratory Manual*, Third Ed. (2001); Ausubel et al, Current Protocols in Molecular Biology (1999)). In particular, an *E. coli* strain is engineered to produce MAA from acetyl-CoA via the route outlined in Figure 1 (Steps A/B/C). Genes encoding enzymes to transform acetyl-CoA to MAA are assembled onto vectors. In particular, the genes *cimA (*Q58787.1), *leuCD* (P81291.1 and Q58673.1) and *cad* (XP_001209273), encoding citramalate synthase, citramalate dehydratase and citraconate decarboxylase, respectively, are cloned into the pZE13 vector (Expressys, Ruelzheim, Germany), under the control of the PA1/lacO promoter. The plasmid is then transformed into the host strain *E. coli* MG1655 containing $lacI^Q$, which allows inducible expression by addition of isopropyl-beta-D-1-thiogalactopyranoside (IPTG). The resulting strain expresses the proteins and enzymes required for synthesis of MAA from acetyl-CoA.

[0301] The resulting genetically engineered organism is cultured in glucose containing medium following procedures well known in the art (see, for example, Sambrook et al., *supra*, 2001). The expression of MAA pathway genes is corroborated using methods well known in the art for determining polypeptide expression or enzymatic activity, including for example, Northern blots, PCR amplification of mRNA and immunoblotting. Enzymatic activities of the expressed enzymes are confirmed using assays specific for the individually activities. The ability of the engineered *E. coli* strain to produce MAA is confirmed using HPLC, gas chromatography-mass spectrometry (GCMS) or liquid chromatography-mass spectrometry (LCMS).

[0302] Microbial strains engineered to have a functional MAA synthesis pathway are further augmented by optimization for efficient utilization of the pathway. Briefly, the engineered strain is assessed to determine whether any of the exogenous genes are expressed at a rate limiting level. Expression is increased for any enzymes expressed at low levels that can limit the flux through the pathway by, for example, introduction of additional gene copy numbers or codon optimization. Strategies are also applied to alter activity, regulation and/or expression of MAA pathway enzymes, such as mutagenesis and/or directed evolution.

[0303] To generate better producers, metabolic modeling is utilized to optimize growth conditions. Modeling is also used to design optional gene knockouts that additionally optimize utilization of the pathway (see, for example, U.S. patent publications US 2002/0012939, US 2003/0224363, US 2004/0029149, US 2004/0072723, US 2003/0059792, US 2002/0168654 and US 2004/0009466, and in U.S. Patent No. 7,127,379). Modeling

analysis allows reliable predictions of the effects on cell growth of shifting the metabolism towards more efficient production of MAA. One modeling method is the bilevel optimization approach, OptKnock (Burgard et al., *Biotechnol. Bioengineer.* 84:647-657 (2003)), which is applied to select gene knockouts that collectively result in better production of MAA. Adaptive evolution also can be used to generate better producers of, for example, the citraconate intermediate or the MAA product. Adaptive evolution is performed to improve tolerance, growth and production characteristics (Fong and Palsson, *Nat. Genet.* 36:1056-1058 (2004); Alper et al., *Science* 314:1565-1568 (2006)). Based on the results, subsequent rounds of modeling, genetic engineering and adaptive evolution can be applied to the MAA producer to further increase production.

[0304] For large-scale production of MAA, the above MAA pathway-containing organism is cultured in a fermenter using a medium known in the art to support growth of the organism under anaerobic conditions. Fermentations are performed in either a batch, fed-batch or continuous manner. Anaerobic conditions are maintained by first sparging the medium with nitrogen and then sealing culture vessel (e.g., flasks can be sealed with a septum and crimp-cap). Microaerobic conditions also can be utilized by providing a small hole for limited aeration. The pH of the medium is maintained at a pH of 7 by addition of an acid, such as H_2SO_4. The growth rate is determined by measuring optical density using a spectrophotometer (600 nm), and the glucose uptake rate by monitoring carbon source depletion over time. Byproducts such as undesirable alcohols, organic acids, and residual glucose can be quantified by HPLC (Shimadzu) with an HPX-087 column (BioRad), using a refractive index detector for glucose and alcohols, and a UV detector for organic acids, Lin et al., *Biotechnol. Bioeng.*, 775-779 (2005).

EXAMPLE III
Exemplary Enzymes for the Formation of Methacrylate Esters from Methacrylate and Alcohols

[0305] This example describes enzymes for an exemplary pathway for production of methacrylate esters.

[0306] Figure 2 depicts an exemplary pathway from MAA and alcohols to methacrylate esters. A methacrylyl-CoA synthetase or methacrylyl-CoA transferase can be applied to form methacrylyl-CoA from methacrylate. Enzymes with alcohol transferase activity can be applied to form methacrylate esters from methacrylyl-CoA and alcohols.

[0307] The conversion of methacrylate to methacrylyl-CoA can be catalyzed by a CoA acid-thiol ligase or CoA synthetase in the 6.2.1 family of enzymes. Exemplary enzymes with this activity are provided in Example I. Alternatively, conversion of methacrylate to methacrylyl-CoA can be catalyzed by a transferase enzyme in the 2.8.3 family of enzymes. CoA transferases catalyze the transfer of a CoA moiety from one molecule to another. Exemplary enzymes with this activity are provided in Example I.

[0308] Formation of methacrylate esters from methacrylyl-CoA and alcohols is catalyzed by enzymes having alcohol transferase activity. Several enzymes with alcohol transferase activity were demonstrated in Examples 1-10 of United States Patent No. 7,901,915. These include Novozyme 435 (immobilized lipase B from *Candida antarctica,* Sigma), Lipase C2 from *Candida cylindracea* (Alphamerix Ltd), lipase from *Pseudomonas fluorescens* (Alphamerix Ltd), L-aminoacylase ex *Aspergillus* spp., and protease ex *Aspergillus oryzae*. Such enzymes were shown to form methyl acrylate and ethyl acrylate from acrylyl-CoA and methanol or ethanol, respectively. Such transferase enzymes can therefore be used to form methacrylate esters.

[0309] Other suitable enzymes include the lipase encoded by *calB* from *Candida antarctica* (Efe et al., *Biotechnol.Bioeng.* 99:1392-1406 (2008)) and the *EstF1* esterase from *Pseudomonas fluorescens* (Khalameyzer et al., *Appl.Environ.Microbiol.* 65:477-482 (1999)). Lipase enzymes encoded by *lipB* from *Pseudomonas fluorescens* and *estA* from *Bacillus subtilis* may also catalyze this transformation. The *B. subtilis* and *P. fluorescens* genes encode triacylglycerol lipase enzymes which have been cloned and characterized in *E. coli* (Dartois et al., *Biochim.Biophys.Acta* 1131:253-260 (1992); Tan et al., *Appl.Environ.Microbiol.* 58:1402-1407 (1992)).

Gene	Accession No.	GI No.	Organism
calB	P41365.1	1170790	*Candida antarctica*
EstF1	AAC36352.1	3641341	*Pseudomonas fluorescens*
lipB	P41773.1	1170792	*Pseudomonas fluorescens*
estA	P37957.1	7676155	*Bacillus subtilis*

[0310] Additional candidate genes that encode enzymes for forming methacrylate esters from methacrylyl-CoA and alcohols include the *Acinetobacter* sp. ADP1 *atfA* encoding a bifunctional enzyme with both wax ester synthase (WS) and acyl-CoA: diacylglycerol

acyltransferase (DGAT) activities (Kalscheuer et al. AJ Biol Chem 2003, 278: 8075-8082.); the *Simmondsia chinensis* gene AAD38041 encoding a enzyme required for the accumulation of waxes in jojoba seeds (Lardizabal et al. Plant Physiology 2000, 122: 645-655.); the *Alcanivorax borkumensis atfAl* and *atfA2* encoding bifunctional WS/DGAT enzymes (Kalscheuer et al. J Bacteriol 2007, 189: 918-928.); *ths Fragaria x ananassa AAT* encoding an alcohol acetyltransferasae (Noichinda et al. FoodSci Technol Res 1999, 5: 239-242.); the *Rosa hybrid cultivar AATl* encoding an alcohol acetyltransferase (Guterman et al. Plant MoI Biol 2006, 60: 555-563.); the *Saccharomyces cerevisiae ATFl* and *ATF2* encoding alcohol acetyltransferases (Mason et al. Yeast 2000, 16: 1287-1298.); and Ws1 and Ws2 from *Marinobacter hydrocarbonoclasticus* (Holtzapple,E. and Schmidt-Dannert,C., J. Bacteriol. 189 (10), 3804-3812, 2007). The carboxylesterase from Lactococcus lactis, encoded by estA, catalyzes the formation of esters from acetyl-CoA and alcohols such as ethanol and methanethiol (Nardi et al. J. Appl. Microbiol. 93:994-1002 (2002)). The alcohol O-acetyltransferase from *Saccharomyces uvarum* converts a wide range of alcohol substrates including branched-chain alcohols to their corresponding acetate esters (Yoshioka and Hashimoto, Agricul and Biol Chem, 45:2183-2191 (1981). The protein sequences of the enzymes encoded by these genes are provided below.

Gene	**GenBank ID**	**GI Number**	**Organism**
atfA	Q8GGG1	81478805	*Acinetobacter sp. ADP1*
AF149919.1:13..1071	AAD38041	5020219	*Simmondsia chinensis*
atfAl	YP694462	110835603	*Alcanivorax borkumensis SK2*
atfA2	YP693524	110834665	*Alcanivorax borkumensis SK2*
AAT	AAG13130.1	10121328	*Fragaria x ananassa*
AATl	Q5I6B5	75105208	*Rosa hybrid cultivar*
ATFl	P40353	2506980	*Saccharomyces cerevisiae*
ATF2	P53296	1723729	*Saccharomyces cerevisiae*
Ws2	ABO21021.1	126567232	*Marinobacter hydrocarbonoclasticus*
Ws1	ABO21020.1	126567230	*Marinobacter hydrocarbonoclasticus*
EstA	AAF62859.1	7453516	*Lactococcus lactis*

EXAMPLE IV
Exemplary Enzymes for the Formation of Methacrylate Esters from Methacrylate and Alcohols

[0311] This example describes enzymes for an exemplary pathway for production of methacrylate esters.

[0312] Figure 2 depicts an exemplary pathway from MAA and alcohols to methacrylate esters. Methacrylate esters can be produced chemically, for example, by heating methacrylate in the presence of an alcohol or multiple alcohols in the presence of a dehydrating agent such as an acid catalyst. Enzymes with methacrylate ester-forming activity can also be applied to form methacrylate esters directly from methacrylate and alcohols. Genes encoding such enzymes can be expressed in an organism containing a methacrylate synthesis pathway. Several such organisms containing methacrylate synthesis pathways are disclosed herein and in WO/2009/135074. The methacrylate ester-forming enzymes can be targeted to the cytosol to enable intracellular conversion of alcohols and methacrylate to methacrylate esters. Alternatively, the methacrylate ester-forming enzymes can be secreted into the fermentation medium to enable extracellular conversion of alcohols and methacrylate to methacrylate esters. Another option is to add methacrylate ester-forming enzymes to a mixture containing methacrylate and alcohols, such as a fermentation broth. Several enzymes with methacrylate-ester forming activity are described below.

[0313] The amidase from *Brevibacterium* sp. R312 (EC 3.5.1.4) is a likely enzyme with methacrylate ester-forming activity. This enzyme was shown to hydrolyze ethylacrylate (Thiery et al., J. Gen. Microbiol., 132:2205-8, 1986; Soubrier et al., Gene, 116:99-104,1992). The microsomal epoxide hydrolase from *Rattus norvegicus* (EC 3.3.2.9) has activity on hydrolyzing glycidyl methacrylate and is another suitable enzyme (Guengerich et al., Rev. Biochem. Toxicol. 4:5-30, 1982). The protein sequences of these genes are provided below.

Gene	GenBank ID	GI Number	Organism
amiE	JC1174	98711	*Brevibacterium* sp.
Eph-1	P07687.1	123928	*Rattus norvegicus*

[0314] Additional genes encoding potential methacrylate ester-forming enzymes include the *Acinetobacter* sp. ADPl *atfA* encoding a bifunctional enzyme with both wax ester synthase (WS) and acyl-CoA: diacylglycerol acyltransferase (DGAT) activities (Kalscheuer

et al. AJ Biol Chem 2003, 278: 8075-8082.); the *Simmondsia chinensis* gene AAD38041 encoding a enzyme required for the accumulation of waxes in jojoba seeds (Lardizabal et al. Plant Physiology 2000, 122: 645-655.); the *Alcanivorax borkumensis atfAl* and *atfA2* encoding bifunctional WS/DGAT enzymes (Kalscheuer et al. J Bacteriol 2007, 189: 918-928.); *ths Fragaria x ananassa AAT* encoding an alcohol acetyltransferasae (Noichinda et al. FoodSci Technol Res 1999, 5: 239-242.); the *Rosa hybrid cultivar AATl* encoding an alcohol acetyltransferase (Guterman et al. Plant MoI Biol 2006, 60: 555-563.); and the *Saccharomyces cerevisiae ATFl* and *ATF2* encoding alcohol acetyltransferases (Mason et al. Yeast 2000, 16: 1287-1298.); and Ws1 and Ws2 from *Marinobacter hydrocarbonoclasticus* (Holtzapple,E. and Schmidt-Dannert,C., J. Bacteriol. 189 (10), 3804-3812, 2007). The carboxylesterase from *Lactococcus lactis*, encoded by *estA*, catalyzes the formation of esters from acetyl-CoA and alcohols such as ethanol and methanethiol (Nardi et al. *J. Appl. Microbiol.* 93:994-1002 (2002)). The alcohol O-acetyltransferase from *Saccharomyces uvarum* converts a wide range of alcohol substrates including branched-chain alcohols to their corresponding acetate esters (Yoshioka and Hashimoto, *Agricul and Biol Chem*, 45:2183-2191 (1981). The gene associated with this activity has not been identified to date. The protein sequences of the enzymes encoded by these genes are provided below.

Gene	GenBank ID	GI Number	Organism
atfA	Q8GGG1	81478805	*Acinetobacter sp. ADP1*
AF149919.1:13..1071	AAD38041	5020219	*Simmondsia chinensis*
atfAl	YP694462	110835603	*Alcanivorax borkumensis SK2*
atfA2	YP693524	110834665	*Alcanivorax borkumensis SK2*
AAT	AAG13130.1	10121328	*Fragaria x ananassa*
AATl	Q5I6B5	75105208	*Rosa hybrid cultivar*
ATFl	P40353	2506980	*Saccharomyces cerevisiae*
ATF2	P53296	1723729	*Saccharomyces cerevisiae*
Ws2	ABO21021.1	126567232	*Marinobacter hydrocarbonoclasticus*
Ws1	ABO21020.1	126567230	*Marinobacter hydrocarbonoclasticus*
EstA	AAF62859.1	7453516	*Lactococcus lactis*

[0315] The *Homo sapiens* paraoxonase enzymes PON1, *PON1 (G3C9),* and PON3 (EC 3.1.8.1) possess both arylesterase and organophosphatase activities and also may possess methacrylate ester-forming activity. PON1 has a common polymorphic site at residue 192, glutamine (R) or arginine (Q), that results in qualitative differences. For example, the R

isozyme has a higher esterase activity on GBL than the S isozyme (Billecke et al., *Drug Metab Dispos.* 28:1335-1342 (2000)). In *H. sapiens* cells, PON1 resides on high-density lipoprotein (HDL) particles, and its activity and stability require this environment. Wild type and recombinant PON1 enzymes have been functionally expressed in other organisms (Rochu et al., *Biochem.Soc.Trans.* 35:1616-1620 (2007); Martin et al., *Appl.Environ.Microbiol.* (2009)). A directed evolution study of PON1 yielded several mutant enzymes with improved solubility and catalytic properties in *E. coli* (nucleotide accession numbers AY499188-AY499199) (Aharoni et al., *Proc.Natl.Acad.Sci.U.S.A* 101:482-487 (2004)). One recombinant variant from this study, G3C9 (Aharoni et al., *Proc.Natl.Acad.Sci.U.S.A* 101:482-487 (2004)), was recently used in an integrated bioprocess for the pH-dependent production of 4-valerolactone from levulinate (Martin et al., *Appl.Environ.Microbiol.* (2009)). Human PON3 is yet another suitable enzyme that may possess methacrylate ester-forming activity (Draganov et al., *J.Lipid Res.* 46:1239-1247 (2005)).

Gene	Accession No.	GI No.	Organism
PON1	NP_000437.3	19923106	*Homo sapiens*
PON1 (G3C9)	AAR95986.1	40850544	*Synthetic variant*
PON3	NP_000931.1	29788996	*Homo sapiens*

[0316] Additionally, the *Candida antarctica* lipase B is another suitable candidate enzyme with methacrylate ester-forming activity (Efe et al., *Biotechnol.Bioeng.* 99:1392-1406 (2008)). The esterase from *Pseudomonas fluorescens*, encoded by *EstF1*, is yet another suitable enzyme (Khalameyzer et al., *Appl.Environ.Microbiol.* 65:477-482 (1999)). Other lipase enzymes from organisms such as *Pseudomonas fluorescens* and *Bacillus subtilis* may also catalyze this transformation. The *B. subtilis* and *P. fluorescens* genes encode triacylglycerol lipase enzymes which have been cloned and characterized in *E. coli* (Dartois et al., *Biochim.Biophys.Acta* 1131:253-260 (1992); Tan et al., *Appl.Environ.Microbiol.* 58:1402-1407 (1992)).

Gene	Accession No.	GI No.	Organism
calB	P41365.1	1170790	*Candida antarctica*
EstF1	AAC36352.1	3641341	*Pseudomonas fluorescens*
lipB	P41773.1	1170792	*Pseudomonas fluorescens*
estA	P37957.1	7676155	*Bacillus subtilis*

[0317] Formation of methacrylate esters may also be catalyzed by enzymes in the 3.1.1 family that act on carboxylic ester bonds molecules for the interconversion between cyclic lactones and the open chain hydroxycarboxylic acids. The L-lactonase from *Fusarium proliferatum* ECU2002 exhibits lactonase and esterase activities on a variety of lactone substrates (Zhang et al., *Appl.Microbiol.Biotechnol.* 75:1087-1094 (2007)). The 1,4-lactone hydroxyacylhydrolase (EC 3.1.1.25), also known as 1,4-lactonase or gamma-lactonase, is specific for 1,4-lactones with 4-8 carbon atoms. The gamma lactonase in human blood and rat liver microsomes was purified (Fishbein et al., *J Biol Chem* 241:4835-4841 (1966)) and the lactonase activity was activated and stabilized by calcium ions (Fishbein et al., *J Biol Chem* 241:4842-4847 (1966)). The optimal lactonase activities were observed at pH 6.0, whereas high pH resulted in hydrolytic activities (Fishbein and Bessman, *J Biol Chem* 241:4842-4847 (1966)). Genes from *Xanthomonas campestris*, *Aspergillus niger* and *Fusarium oxysporum* have been annotated as 1,4-lactonase and can be utilized to catalyze the transformation of 4-hydroxybutyrate to GBL (Zhang et al., *Appl Microbiol Biotechnol* 75:1087-1094 (2007)).

Gene	Accession No.	GI No.	Organism
EU596535.1:1..1206	ACC61057.1	183238971	*Fusarium proliferatum*
xccb100_2516	YP_001903921.1	188991911	*Xanthomonas campestris*
An16g06620	CAK46996.1	134083519	*Aspergillus niger*
BAA34062	BAA34062.1	3810873	*Fusarium oxysporum*

EXAMPLE V
Pathway for Conversion of Succinyl-CoA to MAA via 3-Hydroxyisobutyrate

[0318] This example describes an exemplary MAA synthesis pathway from succinyl-CoA to methacrylic acid via 3-hydroxyisobutyrate.

[0319] One exemplary pathway for MAA synthesis proceeds from succinyl-CoA (see Figure 3). This pathway uses at least three and at most five enzymatic steps to form MAA from succinyl-CoA. In this pathway (see Figure 3), succinyl-CoA is first converted to (R)-methylmalonyl-CoA, which is potentially converted to (S)-methylmalonyl-CoA by an epimerase. Either the (R)- or (S)-stereoisomer of methylmalonyl-CoA is then reduced to (R)- or (S)-3-hydroxyisobutyrate, respectively, by either a pair of enzymes (as shown in Figure 3) or a single enzyme that exhibits acyl-CoA reductase and alcohol dehydrogenase activities. The pathway from succinyl-CoA to 3-hydroxyisobutyrate has also been described in WO 2007/141208. In the final step, 3-hydroxyisobutyrate is dehydrated to form MAA.

[0320] Successfully engineering this pathway involves identifying an appropriate set of enzymes with sufficient activity and specificity. This entails identifying an appropriate set of enzymes, cloning their corresponding genes into a production host, optimizing fermentation conditions, and assaying for product formation following fermentation. To engineer a production host for the production of methacrylic acid, one or more exogenous DNA sequence(s) are expressed in microorganisms. In addition, the microorganisms can have endogenous gene(s) functionally deleted. These modifications allow the production of methacrylic acid using renewable feedstock.

[0321] Below and herein are described a number of biochemically characterized candidate genes capable of encoding enzymes that catalyze each step of the desired pathway. Although described using *E. coli* as a host organism to engineer the pathway, essentially any suitable host organism can be used. Specifically listed are genes that are native to *E. coli* as well as genes in other organisms that can be applied to catalyze the appropriate transformations when properly cloned and expressed.

[0322] Referring to Figure 3, step 1 involves methylmalonyl-CoA mutase (EC 5.4.99.2). In the first step, succinyl-CoA is converted into methylmalonyl-CoA by methylmalonyl-CoA mutase (MCM). Methylmalonyl-CoA mutase is a cobalamin-dependent enzyme that converts succinyl-CoA to methylmalonyl-CoA. In *E. coli*, the reversible adenosylcobalamin-dependant mutase participates in a three-step pathway leading to the conversion of succinate to propionate (Haller et al., *Biochemistry* 39:4622-4629 (2000)). Overexpression of the MCM gene candidate along with the deletion of *YgfG* can be used to prevent the decarboxylation of methylmalonyl-CoA to propionyl-CoA and to maximize the methylmalonyl-CoA available for MAA synthesis. MCM is encoded by genes *scpA* in *Escherichia coli* (Bobik and Rasche, *Anal. Bioanal. Chem.* 375:344-349 (2003); Haller et al., *Biochemistry* 39:4622-4629 (2000)) and *mutA* in *Homo sapiens* (Padovani and Banerjee, *Biochemistry* 45:9300-9306 (2006)). In several other organisms MCM contains alpha and beta subunits and is encoded by two genes. Exemplary gene candidates encoding the two-subunit protein are *Propionibacterium fredenreichii sp. shermani mutA* and *mutB* (Korotkova and Lidstrom, *J. Biol. Chem.* 279:13652-13658 (2004)), *Methylobacterium extorquens mcmA* and *mcmB* (Korotkova and Lidstrom, *supra*, 2004), and *Ralstonia eutropha sbm1* and *sbm2* (Peplinski et al., *Appl. Microbiol. Biotech.* 88:1145-59 (2010)). Additional enzyme

candidates identified based on high homology to the E. coli spcA gene product are also listed below.

Protein	GenBank ID	GI Number	Organism
scpA	NP_417392.1	16130818	*Escherichia coli K12*
mutA	P22033.3	67469281	*Homo sapiens*
mutA	P11652.3	127549	*Propionibacterium fredenreichii sp. shermanii*
mutB	P11653.3	127550	*Propionibacterium fredenreichii sp. shermanii*
mcmA	Q84FZ1	75486201	*Methylobacterium extorquens*
mcmB	Q6TMA2	75493131	*Methylobacterium extorquens*
Sbm1	YP_724799.1	113866310	*Ralstonia eutropha H16*
Sbm2	YP_726418.1	113867929	*Ralstonia eutropha H16*
sbm	NP_838397.1	30064226	*Shigella flexneri*
SARI_04585	ABX24358.1	160867735	*Salmonella enterica*
YfreA_01000861	ZP_00830776.1	77975240	*Yersinia frederiksenii*

[0323] These sequences can be used to identify homologue proteins in GenBank or other databases through sequence similarity searches (for example, BLASTp). The resulting homologue proteins and their corresponding gene sequences provide additional exogenous DNA sequences for transformation into *E. coli* or other suitable host microorganisms to generate production hosts. Additional gene candidates include the following, which were identified based on high homology to the *E. coli spcA* gene product.

[0324] There further exists evidence that genes adjacent to the methylmalonyl-CoA mutase catalytic genes contribute to maximum activity. For example, it has been demonstrated that the *meaB* gene from *M. extorquens* forms a complex with methylmalonyl-CoA mutase, stimulates *in vitro* mutase activity, and possibly protects it from irreversible inactivation (Korotkova and Lidstrom, *J. Biol. Chem.* 279:13652-13658 (2004)). The *M. extorquens meaB* gene product is highly similar to the product of the *E. coli argK* gene (BLASTp: 45% identity, e-value: 4e-67), which is adjacent to *scpA* on the chromosome. No sequence for a *meaB* homolog in *P. freudenreichii* is catalogued in GenBank. However, the *Propionibacterium acnes* KPA171202 gene product, YP_055310.1, is 51% identical to the *M. extorquens meaB* protein and its gene is also adjacent to the methylmalonyl-CoA mutase gene on the chromosome. A similar gene is encoded by H16_B1839 of *Ralstonia eutropha H16*.

Gene	GenBank ID	GI Number	Organism
argK	AAC75955.1	1789285	*Escherichia coli K12*
PPA0597	YP_055310.1	50842083	*Propionibacterium acnes*
KPA171202	2QM8_B	158430328	*Methylobacterium extorquens*
H16_B1839	YP_841351.1	116695775	*Ralstonia eutropha H16*

[0325] *E. coli* can synthesize adenosylcobalamin, a necessary cofactor for this reaction, only when supplied with the intermediates cobinamide or cobalamin (Lawrence and Roth. *J. Bacteriol.* 177:6371-6380 (1995); Lawrence and Roth, *Genetics* 142:11-24 (1996)). Alternatively, the ability to synthesize cobalamins *de novo* has been conferred upon *E. coli* following the expression of heterologous genes (Raux et al., *J. Bacteriol.* 178:753-767 (1996)).

[0326] Referring to Figure 3, step 2 involves methylmalonyl-CoA epimerase (EC 5.1.99.1). The second enzyme in the pathway, methylmalonyl-CoA epimerase (MMCE), interconverts (R)-methylmalonyl-CoA and (S)-methylmalonyl-CoA. MMCE is an essential enzyme in the breakdown of odd-numbered fatty acids and of the amino acids valine, isoleucine, and methionine. Methylmalonyl-CoA epimerase activity is not believed to be encoded in the *E. coli* genome (Boynton et al., *J. Bacteriol.*178:3015-3024 (1996)), but is present in other organisms such as *Homo sapiens* (*YqjC*) (Fuller and Leadlay,. *Biochem. J.* 213:643-650 (1983)), *Rattus norvegicus* (*Mcee*) (Bobik and Rasche, *J. Biol. Chem.* 276:37194-37198 (2001)), *Propionibacterium shermanii* (AF454511) (Fuller. and Leadlay, *Biochem. J.* 213:643-650 (1983); Haller et al., *Biochemistry* 39:4622-4629 (2000); McCarthy et al.,. *Structure* 9:637-646.2001)) and *Caenorhabditis elegans* (*mmce*) (Kuhnl et al., *FEBS J.* 272:1465-1477 (2005)). An additional gene candidate, AE016877 in *Bacillus cereus*, has high sequence homology to other characterized enzymes. This enzymatic step may or may not be necessary depending upon the stereospecificity of the enzyme or enzymes used for the conversion of methylmalonyl-CoA to 3-hydroxyisobutyrate (steps 3-4 in Figure 3). These genes/proteins are described below.

Gene	GenBank ID	GI Number	Organism
YqjC	NP_390273	255767522	*Bacillus subtilis*
MCEE	Q96PE7.1	50401130	*Homo sapiens*
Mcee_predicted	NP_001099811.1	157821869	*Rattus norvegicus*
AF454511	AAL57846.1	18042135	*Propionibacterium fredenreichii sp. shermanii*

Gene	GenBank ID	GI Number	Organism
mmce	AAT92095.1	51011368	*Caenorhabditis elegans*
AE016877	AAP08811.1	29895524	*Bacillus cereus ATCC 14579*

[0327] Referring to Figure 3, step 3 involves methylmalonyl-CoA reductase (EC 1.2.1.-). As shown in Figure 3, the reduction of methylmalonyl-CoA to its corresponding alcohol, 3-hydroxyisobutyrate, can proceed by two enzymatic steps. The first step, conversion of methylmalonyl-CoA to methylmalonic semialdehyde, is accomplished by a CoA-dependent aldehyde dehydrogenase. An enzyme encoded by a malonyl-CoA reductase gene from *Sulfolobus tokodaii* (Alber et. al., *J. Bacteriol.* 188(24):8551–8559 (2006)), has been shown to catalyze the conversion of methylmalonyl-CoA to its corresponding aldehyde (WO2007141208). A similar enzyme exists in *Metallosphaera sedula* (Alber et. al., *J. Bacteriol.* 188(24):8551–8559 (2006)). Several additional CoA dehydrogenases are capable also of reducing an acyl-CoA to its corresponding aldehyde. The reduction of methylmalonyl-CoA to its corresponding aldehyde, methylmalonate semialdehyde, is catalyzed by a CoA-dependent aldehyde dehydrogenase. Exemplary enzymes include fatty acyl-CoA reductase, succinyl-CoA reductase (EC 1.2.1.76), acetyl-CoA reductase and butyryl-CoA reductase. Exemplary fatty acyl-CoA reductase enzymes are encoded by *acr1* of *Acinetobacter calcoaceticus* (Reiser and Somerville. *J. Bacteriol.* 179:2969-2975 (1997)), and *Acinetobacter sp. M-1* fatty acyl-CoA reductase (Ishige et al., *Appl. Environ. Microbiol.* 68:1192-1195 (2002)). Also known is a CoA- and NADP- dependent succinate semialdehyde dehydrogenase (also referred to as succinyl-CoA reductase) encoded by the *sucD* gene in *Clostridium kluyver*i (Sohling and Gottschalk, *J. Bacteriol.* 178:871-880 (1996); Sohling and Gottschalk, *J. Bacteriol.* 178:871-880 (1996)) and *sucD* of *P. gingivalis* (Takahashi, *J. Bacteriol* 182:4704-4710 (2000)). Additional succinyl-CoA reductase enzymes participate in the 3-hydroxypropionate/4-hydroxybutyrate cycle of thermophilic archaea including *Metallosphaera sedula* (Berg et al., *Science* 318:1782-1786 (2007)) and *Thermoproteus neutrophilus* (Ramos-Vera et al., *J Bacteriol*, 191:4286-4297 (2009)). The *M. sedula* enzyme, encoded by *Msed_0709*, is strictly NADPH-dependent and also has malonyl-CoA reductase activity. The *T. neutrophilus* enzyme is active with both NADPH and NADH. The enzyme acylating acetaldehyde dehydrogenase in *Pseudomonas sp*, encoded by *bphG*, is also a good candidate as it has been demonstrated to oxidize and acylate acetaldehyde, propionaldehyde, butyraldehyde, formaldehyde and the branched-chain compound isobutyraldehyde (Powlowski et al., *J. Bacteriol.* 175:377-385 (1993)). In

addition to reducing acetyl-CoA to ethanol, the enzyme encoded by *adhE* in *Leuconostoc mesenteroides* has been shown to oxidize the branched chain compound isobutyraldehyde to isobutyryl-CoA (Kazahaya, *J. Gen. Appl. Microbiol.* 18:43-55 (1972); and Koo et al., *Biotechnol Lett.* 27:505-510 (2005)). Butyraldehyde dehydrogenase catalyzes a similar reaction, conversion of butyryl-CoA to butyraldehyde, in solventogenic organisms such as *Clostridium saccharoperbutylacetonicum* (Kosaka et al., *Biosci Biotechnol Biochem.*, 71:58-68 (2007)).

Protein	**GenBank ID**	**GI Number**	**Organism**
acr1	YP_047869.1	50086359	*Acinetobacter calcoaceticus*
acr1	AAC45217	1684886	*Acinetobacter baylyi*
acr1	BAB85476.1	18857901	*Acinetobacter sp. Strain M-1*
MSED_0709	YP_001190808.1	146303492	*Metallosphaera sedula*
Tneu_0421			*Thermoproteus neutrophilus*
sucD	P38947.1	172046062	*Clostridium kluyveri*
sucD	NP_904963.1	34540484	*Porphyromonas gingivalis*
bphG	BAA03892.1	425213	*Pseudomonas sp*
adhE	AAV66076.1	55818563	*Leuconostoc mesenteroides*
bld	AAP42563.1	31075383	*Clostridium saccharoperbutylacetonicum*

[0328] An additional enzyme type that converts an acyl-CoA to its corresponding aldehyde is malonyl-CoA reductase which transforms malonyl-CoA to malonic semialdehyde. Malonyl-CoA reductase is a key enzyme in autotrophic carbon fixation via the 3-hydroxypropionate cycle in thermoacidophilic archaeal bacteria (Berg, *Science* 318:1782-1786 (2007); and Thauer, *Science* 318:1732-1733 (2007)). The enzyme utilizes NADPH as a cofactor and has been characterized in *Metallosphaera* and *Sulfolobus sp.* (Alber et al., *J. Bacteriol.* 188:8551-8559 (2006); and Hugler, *J. Bacteriol.* 184:2404-2410 (2002)). The enzyme is encoded by *Msed_0709* in *Metallosphaera sedula* (Alber et al., *J. Bacteriol.* 188:8551-8559 (2006); and Berg, *Science* 318:1782-1786 (2007)). A gene encoding a malonyl-CoA reductase from *Sulfolobus tokodaii* was cloned and heterologously expressed in *E. coli* (Alber et al., *J. Bacteriol* 188:8551-8559 (2006). This enzyme has also been shown to catalyze the conversion of methylmalonyl-CoA to its corresponding aldehyde (WO2007141208 (2007)). Although the aldehyde dehydrogenase functionality of these enzymes is similar to the bifunctional dehydrogenase from *Chloroflexus aurantiacus*, there is little sequence similarity. Both malonyl-CoA reductase enzyme candidates have high

sequence similarity to aspartate-semialdehyde dehydrogenase, an enzyme catalyzing the reduction and concurrent dephosphorylation of aspartyl-4-phosphate to aspartate semialdehyde. Additional gene candidates can be found by sequence homology to proteins in other organisms including *Sulfolobus solfataricus* and *Sulfolobus acidocaldarius* and have been listed below. Yet another candidate for CoA-acylating aldehyde dehydrogenase is the *ald* gene from *Clostridium beijerinckii* (Toth, *Appl. Environ. Microbiol.* 65:4973-4980 (1999). This enzyme has been reported to reduce acetyl-CoA and butyryl-CoA to their corresponding aldehydes. This gene is very similar to *eutE* that encodes acetaldehyde dehydrogenase of *Salmonella typhimurium* and *E. coli* (Toth, *Appl. Environ. Microbiol.* 65:4973-4980 (1999).

Gene	GenBank ID	GI Number	Organism
Msed_0709	YP_001190808.1	146303492	*Metallosphaera sedula*
mcr	NP_378167.1	15922498	*Sulfolobus tokodaii*
asd-2	NP_343563.1	15898958	*Sulfolobus solfataricus*
Saci_2370	YP_256941.1	70608071	*Sulfolobus acidocaldarius*
Ald	AAT66436	49473535	*Clostridium beijerinckii*
eutE	AAA80209	687645	*Salmonella typhimurium*
eutE	P77445	2498347	*Escherichia coli*

[0329] A bifunctional enzyme with acyl-CoA reductase and alcohol dehydrogenase activity can directly convert methylmalonyl-CoA to 3-hydroxyisobutyrate. Exemplary bifunctional oxidoreductases that convert an acyl-CoA to alcohol include those that transform substrates such as acetyl-CoA to ethanol (for example, *adhE* from *E. coli* (Kessler et al., *FEBS.Lett.* 281:59-63 (1991))) and butyryl-CoA to butanol (for example, *adhE2* from *C. acetobutylicum* (Fontaine et al., *J.Bacteriol.* 184:821-830 (2002)). The *C. acetobutylicum* enzymes encoded by *bdh* I and *bdh* II (Walter, et al., *J. Bacteriol.* 174:7149-7158 (1992)), reduce acetyl-CoA and butyryl-CoA to ethanol and butanol, respectively. In addition to reducing acetyl-CoA to ethanol, the enzyme encoded by *adhE* in *Leuconostoc mesenteroides* has been shown to oxide the branched chain compound isobutyraldehyde to isobutyryl-CoA (Kazahaya et al., *J.Gen.Appl.Microbiol.* 18:43-55 (1972); Koo et al., *Biotechnol Lett,* 27:505-510 (2005)). Another exemplary enzyme can convert malonyl-CoA to 3-HP. An NADPH-dependent enzyme with this activity has characterized in *Chloroflexus aurantiacus* where it participates in the 3-hydroxypropionate cycle (Hugler et al., *J Bacteriol*, 184:2404-2410 (2002); Strauss et al., *Eur J Biochem*, 215:633-643 (1993)). This enzyme, with a mass of 300

kDa, is highly substrate-specific and shows little sequence similarity to other known oxidoreductases (Hugler et al., *supra*). No enzymes in other organisms have been shown to catalyze this specific reaction; however there is bioinformatic evidence that other organisms may have similar pathways (Klatt et al., *Env Microbiol*, 9:2067-2078 (2007)). Enzyme candidates in other organisms including *Roseiflexus castenholzii*, *Erythrobacter sp. NAP1* and marine gamma proteobacterium HTCC2080 can be inferred by sequence similarity.

Protein	**GenBank ID**	**GI Number**	**Organism**
adhE	NP_415757.1	16129202	*Escherichia coli*
adhE2	AAK09379.1	12958626	*Clostridium acetobutylicum*
adhE	AAV66076.1	55818563	*Leuconostoc mesenteroides*
bdh I	NP_349892.1	15896543	*Clostridium acetobutylicum*
bdh II	NP_349891.1	15896542	*Clostridium acetobutylicum*
mcr	AAS20429.1	42561982	*Chloroflexus aurantiacus*
Rcas_2929	YP_001433009.1	156742880	*Roseiflexus castenholzii*
NAP1_02720	ZP_01039179.1	85708113	*Erythrobacter sp. NAP1*
MGP2080_00535	ZP_01626393.1	119504313	*marine gamma proteobacterium HTCC2080*

[0330] Referring to Figure 3, step 4 involves 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31). 3-hydroxyisobutyrate dehydrogenase catalyzes the reversible oxidation of 3-hydroxyisobutyrate to methylmalonate semialdehyde. The reduction of methylmalonate semialdehyde to 3-hydroxyisobutyrate is catalyzed by methylmalonate semialdehyde reductase or 3-hydroxyisobutyrate dehydrogenase. This enzyme participates in valine, leucine and isoleucine degradation and has been identified in bacteria, eukaryotes, and mammals. The enzyme encoded by *P84067* from *Thermus thermophilus* HB8 has been structurally characterized (Lokanath et al., *J. Mol. Biol.* 352:905-917 (2005)). The reversibility of the human 3-hydroxyisobutyrate dehydrogenase was demonstrated using isotopically-labeled substrate (Manning and Pollitt, *Biochem. J.* 231:481-484 (1985)). Additional genes encoding this enzyme include *3hidh* in *Homo sapiens* (Hawes et al., *Methods Enzymol.* 324:218-228 (2000)) and *Oryctolagus cuniculus* (Chowdhury et al., *Biosci. Biotechnol. Biochem.* 60:2043-2047 (1996); Hawes et al., *Methods Enzymol.* 324:218-228 (2000)), *mmsb* in *Pseudomonas aeruginosa*, and *dhat* in *Pseudomonas putida* (Aberhart and Hsu.. *J Chem.Soc.[Perkin 1]* 6:1404-1406 (1979); Chowdhury et al., *Biosci. Biotechnol. Biochem.* 67:438-441 (2003); Chowdhury et al., *Biosci. Biotechnol. Biochem.* 60:2043-2047 (1996)). Several 3-hydroxyisobutyrate dehydrogenase enzymes have been characterized in

the reductive direction, including *mmsB* from *Pseudomonas aeruginosa* (Gokarn et al., US Patent 7,393,676 (2008)) and *mmsB* from *Pseudomonas putida*.

PROTEIN	GENBANK ID	GI NUMBER	ORGANISM
P84067	P84067	75345323	*Thermus thermophilus*
3hidh	P31937.2	12643395	*Homo sapiens*
3hidh	P32185.1	416872	*Oryctolagus cuniculus*
mmsB	NP_746775.1	26991350	*Pseudomonas putida*
mmsB	P28811.1	127211	*Pseudomonas aeruginosa*
dhat	Q59477.1	2842618	*Pseudomonas putida*

[0331] Referring to Figure 3, as an alternative, steps 3 and 4 can involve a combined Alcohol/Aldehyde dehydrogenase (EC 1.2.1.-). Methylmalonyl-CoA can be reduced to 3-hydroxyisobutyrate in one step by a multifunctional enzyme with dual acyl-CoA reductase and alcohol dehydrogenase activity. Although the direct conversion of methylmalonyl-CoA to 3-hydroxyisobutyrate has not been reported, this reaction is similar to the common conversions such as acetyl-CoA to ethanol and butyryl-CoA to butanol, which are catalyzed by CoA-dependant enzymes with both alcohol and aldehyde dehydrogenase activities. Gene candidates include the *E. coli adhE* (Kessler et al., *FEBS Lett.* 281:59-63 (1991)) and *C. acetobutylicum bdh* I and *bdh* II (Walter, et al., *J. Bacteriol.* 174:7149-7158 (1992)), which can reduce acetyl-CoA and butyryl-CoA to ethanol and butanol, respectively. In addition to reducing acetyl-CoA to ethanol, the enzyme encoded by *adhE* in *Leuconostoc mesenteroides* has been shown to oxide the branched chain compound isobutyraldehyde to isobutyryl-CoA (Kazahaya et al., *J. Gen. Appl. Microbiol.* 18:43-55 (1972); Koo et al., *Biotechnol. Lett.* 27:505-510 (2005)). An additional candidate enzyme for converting methylmalonyl-CoA directly to 3-hydroxyisobutyrate is encoded by a malonyl-CoA reductase from *Chloroflexus aurantiacus* (Hügler, et al., *J. Bacteriol.* 184(9):2404-2410 (2002).

Protein	GenBank ID	GI Number	Organism
mcr	YP_001636209.1	163848165	*Chloroflexus aurantiacus*
adhE	NP_415757.1	16129202	*Escherichia coli*
bdh I	NP_349892.1	15896543	*Clostridium acetobutylicum*
bdh II	NP_349891.1	15896542	*Clostridium acetobutylicum*
adhE	AAV66076.1	55818563	*Leuconostoc mesenteroides*

[0332] Referring to Figure 3, step 5 involves 3-hydroxyisobutyrate dehydratase (EC 4.2.1.-). The final step involves the dehydration of 3-hydroxyisobutyrate to methacrylic acid. The dehydration of 3-hydroxyisobutyrate to methylacrylic acid is catalyzed by an enzyme with 3-hydroxyisobutyrate dehydratase activity. Although no direct evidence for this specific enzymatic transformation has been identified, most dehydratases catalyze the α,β-elimination of water, which involves activation of the α-hydrogen by an electron-withdrawing carbonyl, carboxylate, or CoA-thiol ester group and removal of the hydroxyl group from the β-position (Buckel and Barker, *J Bacteriol.* 117:1248-1260 (1974); Martins et al, *Proc. Natl. Acad. Sci. USA* 101:15645-15649 (2004)). This is the exact type of transformation proposed for the final step in the methacrylate pathway. In addition, the proposed transformation is highly similar to the 2-(hydroxymethyl)glutarate dehydratase of *Eubacterium barkeri*, which can catalyze the conversion of 2-hydroxymethyl glutarate to 2-methylene glutarate. This enzyme has been studied in the context of nicotinate catabolism and is encoded by *hmd* (Alhapel et al., *Proc. Natl. Acad. Sci. USA* 103:12341-12346 (2006)). Similar enzymes with high sequence homology are found in *Bacteroides capillosus*, *Anaerotruncus colihominis*, and *Natranaerobius thermophilius*. Several enzymes are known to catalyze the alpha, beta elimination of hydroxyl groups. Exemplary enzymes include 2-(hydroxymethyl)glutarate dehydratase (EC 4.2.1.-), fumarase (EC 4.2.1.2), 2-keto-4-pentenoate dehydratase (EC 4.2.1.80), citramalate hydrolyase and dimethylmaleate hydratase.

[0333] 2-(Hydroxymethyl)glutarate dehydratase is a [4Fe-4S]-containing enzyme that dehydrates 2-(hydroxymethyl)glutarate to 2-methylene-glutarate, studied for its role in nicontinate catabolism in *Eubacterium barkeri* (formerly *Clostridium barkeri*) (Alhapel et al., *Proc Natl Acad Sci USA* 103:12341-12346 (2006)). Similar enzymes with high sequence homology are found in *Bacteroides capillosus, Anaerotruncus colihominis*, and *Natranaerobius thermophilius*. These enzymes are also homologous to the α- and β-subunits of [4Fe-4S]-containing bacterial serine dehydratases, for example, *E. coli* enzymes encoded by *tdcG*, *sdhB*, and *sdaA*). An enzyme with similar functionality in *E. barkeri* is dimethylmaleate hydratase, a reversible Fe2+-dependent and oxygen-sensitive enzyme in the aconitase family that hydrates dimethylmaeate to form (2R,3S)-2,3-dimethylmalate. This enzyme is encoded by dmdAB (Alhapel et al., *Proc Natl Acad Sci USA* 103:12341-6 (2006); Kollmann-Koch et al., *Hoppe Seylers.Z.Physiol Chem.* 365:847-857 (1984)).

Protein	GenBank ID	GI Number	Organism
hmd	ABC88407.1	86278275	*Eubacterium barkeri*
BACCAP_02294	ZP_02036683.1	154498305	*Bacteroides capillosus*
ANACOL_02527	ZP_02443222.1	167771169	*Anaerotruncus colihominis*
NtherDRAFT_2368	ZP_02852366.1	169192667	*Natranaerobius thermophilus*
dmdA	ABC88408	86278276	*Eubacterium barkeri*
dmdB	ABC88409	86278277	*Eubacterium barkeri*

[0334] Fumarate hydratase enzymes, which naturally catalyze the reversible hydration of fumarate to malate. Although the ability of fumarate hydratase to react on branched substrates with 3-oxobutanol as a substrate has not been described, a wealth of structural information is available for this enzyme and other researchers have successfully engineered the enzyme to alter activity, inhibition and localization (Weaver, *Acta Crystallogr. D Biol. Crystallogr.* 61:1395-1401 (2005)). *E. coli* has three fumarases: FumA, FumB, and FumC that are regulated by growth conditions. FumB is oxygen sensitive and only active under anaerobic conditions. FumA is active under microanaerobic conditions, and FumC is the only active enzyme in aerobic growth (Tseng et al., *J. Bacteriol.* 183:461-467 (2001); Woods et al., *Biochm. Biophys. Acta* 954:14-26 (1988); Guest et al., *J Gen Microbiol* 131:2971-2984 (1985)). Exemplary enzyme candidates include those encoded by *fumC* from *Escherichia coli* (Estevez et al., *Protein Sci.* 11:1552-1557 (2002); Hong and Lee, *Biotechnol. Bioprocess Eng.* 9:252-255 (2004); Rose and Weaver, *Proc. Natl. Acad. Sci. USA* 101:3393-3397 (2004)), and enzymes found in *Campylobacter jejuni* (Smith et al., *Int. J. Biochem.Cell Biol.* 31:961-975 (1999)), *Thermus thermophilus* (Mizobata et al., *Arch. Biochem. Biophys.* 355:49-55 (1998)), and *Rattus norvegicus* (Kobayashi et al., *J. Biochem.* 89:1923-1931 (1981)). Similar enzymes with high sequence homology include *fum1* from *Arabidopsis thaliana* and *fumC* from *Corynebacterium glutamicum*. The *MmcBC* fumarase from Pelotomaculum thermopropionicum is another class of fumarase with two subunits (Shimoyama et al., *FEMS Microbiol Lett.* 270:207-213 (2007)).

Protein	GenBank ID	GI Number	Organism
fumA	NP_416129.1	16129570	*Escherichia coli*
fumB	NP_418546.1	16131948	*Escherichia coli*
fumC	NP_416128.1	16129569	*Escherichia coli*
fumC	O69294	9789756	*Campylobacter jejuni*
fumC	P84127	75427690	*Thermus thermophilus*
fumH	P14408	120605	*Rattus norvegicus*

Protein	GenBank ID	GI Number	Organism
fum1	P93033	39931311	*Arabidopsis thaliana*
fumC	Q8NRN8	39931596	*Corynebacterium glutamicum*
MmcB	YP_001211906	147677691	*Pelotomaculum thermopropionicum*
MmcC	YP_001211907	147677692	*Pelotomaculum thermopropionicum*

[0335] Dehydration of 4-hydroxy-2-oxovalerate to 2-oxopentenoate is catalyzed by 4-hydroxy-2-oxovalerate hydratase (EC 4.2.1.80). This enzyme participates in aromatic degradation pathways and is typically co-transcribed with a gene encoding an enzyme with 4-hydroxy-2-oxovalerate aldolase activity. Exemplary gene products are encoded by *mhpD* of *E. coli* (Ferrandez et al., *J Bacteriol.* 179:2573-2581 (1997); Pollard et al., *Eur J Biochem.* 251:98-106 (1998)), *todG* and *cmtF* of *Pseudomonas putida* (Lau et al., *Gene* 146:7-13 (1994); Eaton, *J Bacteriol.* 178:1351-1362 (1996)), *cnbE* of *Comamonas* sp. CNB-1 (Ma et al., *Appl Environ Microbiol* 73:4477-4483 (2007)) and mhpD of *Burkholderia xenovorans* (Wang et al., *FEBS J* 272:966-974 (2005)). A closely related enzyme, 2-oxohepta-4-ene-1,7-dioate hydratase, participates in 4-hydroxyphenylacetic acid degradation, where it converts 2-oxo-hept-4-ene-1,7-dioate (OHED) to 2-oxo-4-hydroxy-hepta-1,7-dioate using magnesium as a cofactor (Burks et al., *J.Am.Chem.Soc.* 120: (1998)). OHED hydratase enzyme candidates have been identified and characterized in *E. coli C* (Roper et al., *Gene* 156:47-51 (1995); Izumi et al., *J Mol.Biol.* 370:899-911 (2007)) and *E. coli W* (Prieto et al., *J Bacteriol.* 178:111-120 (1996)). Sequence comparison reveals homologs in a wide range of bacteria, plants and animals. Enzymes with highly similar sequences are contained in *Klebsiella pneumonia* (91% identity, eval = 2e-138) and *Salmonella enterica* (91% identity, eval = 4e-138), among others.

Gene	GenBank Accession No.	GI No.	Organism
mhpD	AAC73453.2	87081722	*Escherichia coli*
cmtF	AAB62293.1	1263188	*Pseudomonas putida*
todG	AAA61942.1	485738	*Pseudomonas putida*
cnbE	YP_001967714.1	190572008	*Comamonas* sp. CNB-1
mhpD	Q13VU0	123358582	*Burkholderia xenovorans*
hpcG	CAA57202.1	556840	*Escherichia coli C*
hpaH	CAA86044.1	757830	*Escherichia coli W*
hpaH	ABR80130.1	150958100	*Klebsiella pneumoniae*
Sari_01896	ABX21779.1	160865156	*Salmonella enterica*

[0336] Another enzyme candidate is citramalate hydrolyase (EC 4.2.1.34), an enzyme that naturally dehydrates 2-methylmalate to mesaconate. This enzyme has been studied in *Methanocaldococcus jannaschii* in the context of the pyruvate pathway to 2-oxobutanoate, where it has been shown to have a broad substrate specificity (Drevland et al., *J Bacteriol.* 189:4391-4400 (2007)). This enzyme activity was also detected in *Clostridium tetanomorphum*, *Morganella morganii, Citrobacter amalonaticus* where it is thought to participate in glutamate degradation (Kato et al., *Arch.Microbiol* 168:457-463 (1997)). The *M. jannaschii* protein sequence does not bear significant homology to genes in these organisms.

Protein	GenBank ID	GI Number	Organism
leuD	Q58673.1	3122345	*Methanocaldococcus jannaschii*

[0337] Dimethylmaleate hydratase (EC 4.2.1.85) is a reversible Fe^{2+}-dependent and oxygen-sensitive enzyme in the aconitase family that hydrates dimethylmaeate to form (2R,3S)-2,3-dimethylmalate. This enzyme is encoded by *dmdAB* in *Eubacterium barkeri* (Alhapel et al., *supra*; Kollmann-Koch et al., *Hoppe Seylers.Z.Physiol Chem.* 365:847-857 (1984)).

Protein	GenBank ID	GI Number	Organism
dmdA	ABC88408	86278276	*Eubacterium barkeri*
dmdB	ABC88409.1	86278277	*Eubacterium barkeri*

[0338] This example describes a biosynthetic pathway for production of MMA from succinyl-CoA.

EXAMPLE VI
Pathway for Conversion of Succinyl-CoA to MAA via 3-Amino-2-Methylpropanoate

[0339] This example describes an exemplary MAA synthesis pathway from succinyl-CoA to MAA via 3-amino-methylpropanoate.

[0340] Another exemplary pathway for MAA biosynthesis proceeds from succinyl-CoA through 3-amino-2-methylpropanoate (see Figure 4). The first three steps of this pathway, involving the conversion of succinyl-CoA to methylmalonate semialdehyde, are identical to the succinyl-CoA to MAA pathway described in Example V (see Figure 3). The pathway

diverges at step 4, where methylmalonate semialdehyde is converted to 3-amino-2-methylpropionate by a transaminase. The final pathway step entails deamination of 3-amino-2-methylpropionate to methacrylic acid.

[0341] Enzyme and gene candidates for catalyzing the first three pathway steps are described in Example V. Gene candidates for steps 4 and 5 are discussed below.

[0342] Referring to Figure 4, step 4 involves 3-amino-2-methylpropionate transaminase (EC 2.6.1.22). 3-amino-2-methylpropionate transaminase catalyzes the transformation from methylmalonate semialdehyde to 3-amino-2-methylpropionate. The enzyme, characterized in *Rattus norvegicus* and *Sus scrofa* and encoded by *Abat*, has been shown to catalyze this transformation in the direction of interest in the pathway (Kakimoto et al., *Biochim. Biophys. Acta* 156:374-380 (1968); Tamaki et al., *Methods Enzymol.* 324:376-389 (2000)). Enzyme candidates in other organisms with high sequence homology to 3-amino-2-methylpropionate transaminase include *Gta-1* in *C. elegans* and *gabT* in *Bacillus subtilus*. Additionally, one of the native GABA aminotransferases in *E. coli*, encoded by gene *gabT*, has been shown to have broad substrate specificity and may utilize 3-amino-2-methylpropionate as a substrate (Liu et al., *Biochemistry* 43:10896-10905 (2004); Schulz et al., *Appl. Environ. Microbiol.* 56:1-6 (1990)).

Protein	GenBank ID	GI Number	Organism
Abat	P50554.3	122065191	*Rattus norvegicus*
Abat	P80147.2	120968	*Sus scrofa*
Gta-1	Q21217.1	6016091	*Caenorhabditis elegans*
gabT	P94427.1	6016090	*Bacillus subtilus*
gabT	P22256.1	16130576	*Escherichia coli K12*

[0343] Referring to Figure 4, step 5 involves 3-amino-2-methylpropionate ammonia lyase (EC 4.3.1.-). In the final step of this pathway, 3-amino-2-methylpropionate is deaminated to methacrylic acid. An enzyme catalyzing this exact transformation has not been demonstrated experimentally; however the native *E. coli* enzyme, aspartate ammonia lyase (EC 4.3.1.1), may be able to catalyze this reaction. Encoded by *aspA* in *E. coli*, aspartate ammonia lyase deaminates asparatate to form fumarate but can also react with alternate substrates aspartatephenylmethylester, asparagine, benzyl-aspartate and malate (Ma et al., *Ann. N.Y.Acad. Sci.* 672:60-65 (1992)). In a separate study, directed evolution was been employed

on this enzyme to alter substrate specificity (Asano et al., *Biomol. Eng.* 22:95-101 (2005)). Genes encoding aspartase in other organisms include *ansB* in *Bacillus subtilus* (Sjostrom et al., *Biochim. Biophys. Acta* 1324:182-190 (1997)) and *aspA* in *Pseudomonas fluorescens* (Takagi et al., *J. Biochem.* 96:545-552 (1984); Takagi et al., *J. Biochem.* 100:697-705 (1986)) and *Serratia marcescens* (Takagi et al., *J. Bacteriol.* 161:1-6 (1985)).

Protein	GenBank ID	GI Number	Organism
aspA	P0AC38.1	90111690	*Escherichia coli K12*
ansB	P26899.1	251757243	*Bacillus subtilus*
aspA	P07346.1	114273	*Pseudomonas fluorescens*
aspA	P33109.1	416661	*Serratia marcescens*

[0344] This example describes an MAA biosynthetic pathway from succinyl-CoA.

EXAMPLE VII
Pathway for Conversion of 4-Hydroxybutyryl-CoA to 3-Hydroxyisobutyric Acid or MAA

[0345] This example describes an exemplary 3-hydroxyisobutyric acid or MAA synthesis pathway from 4-hydroxybutyryl-CoA.

[0346] An additional exemplary pathway entails the conversion of 4HB-CoA to MAA (see Figure 5). In the first step, 4HB-CoA is converted to 3-hydroxyisobutyryl-CoA (3-Hib-CoA) by a methylmutase. 3-Hib-CoA can then be converted to 3-hydroxyisobutyrate by a CoA hydrolase, synthase or transferase. 3-hydroxyisobutyrate can be secreted and recovered as a product or as a final step in the production of methacrylic acid. 3-Hydroxybutyrate can be dehydrated to form methacrylic acid. Alternatively, 3-Hib-CoA can be dehydrated to methacrylyl-CoA which is then converted to MAA by a hydrolase, synthase, or transferase. The enzymes required for converting the tricarboxylic acid cycle intermediates, alpha-ketoglutarate, succinate, or succinyl-CoA, into 4HB-CoA, are well-documented (Burk et al., U.S. application serial No. 12/049,256, filed March 14, 2008; Lutke-Eversloh and Steinbuchel. *FEMS Microbiol. Lett.* 181:63-71 (1999); Sohling and Gottschalk, *Eur. J. Biochem.* 212:121-127 (1993); Sohling and Gottschalk, *J. Bacteriol.* 178:871-880 (1996); Valentin et al., *Eur. J. Biochem.* 227:43-60 (1995); Wolff and Kenealy, *Protein Expr. Purif.* 6:206-212. (1995)).

[0347] Referring to Figure 5, step 1 involves 4-hydroxybutyryl-CoA mutase (EC 5.4.99.-). The conversion of 4HB-CoA to 3-hydroxyisobutyryl-CoA has yet to be demonstrated experimentally. However, two methylmutases, that is, isobutyryl-CoA mutase (ICM) and methylmalonyl-CoA mutase (MCM), which catalyze similar reactions, are good candidates given the structural similarity of their corresponding substrates. Methylmalonyl-CoA mutase is a cobalamin-dependent enzyme that converts succinyl-CoA to methylmalonyl-CoA. This enzyme and suitable gene candidates were discussed in the succinyl-CoA to MAA pathway (see Example V).

[0348] Alternatively, isobutyryl-CoA (ICM, EC 5.4.99.13) could catalyze the proposed transformation. ICM is a cobalamin-dependent methylmutase in the MCM family that reversibly rearranges the carbon backbone of butyryl-CoA into isobutyryl-CoA (Ratnatilleke et al., *J. Biol. Chem.* 274:31679-31685 (1999)). A recent study of a novel ICM in *Methylibium petroleiphilum*, along with previous work, provides evidence that changing a single amino acid near the active site alters the substrate specificity of the enzyme (Ratnatilleke et al., *J. Biol. Chem.* 274:31679-31685 (1999); Rohwerder et al., *Appl. Environ. Microbiol.* 72:4128-4135. (2006)). This indicates that, if a native enzyme is unable to catalyze or exhibits low activity for the conversion of 4HB-CoA to 3HIB-CoA, the enzyme can be rationally engineered to increase this activity. Exemplary ICM genes encoding homodimeric enzymes include *icmA* in *Streptomyces coelicolor A3* (Alhapel et al., *Proc. Natl. Acad. Sci. USA* 103:12341-12346 (2006)) and *Mpe_B0541* in *Methylibium petroleiphilum PM1* (Ratnatilleke et al., *J. Biol. Chem.* 274:31679-31685 (1999); Rohwerder et al., *Appl. Environ. Microbiol.* 72:4128-4135 (2006)). Genes encoding heterodimeric enzymes include *icm* and *icmB* in *Streptomyces cinnamonensis* (Ratnatilleke et al., *J. Biol. Chem.* 274:31679-31685 (1999); Vrijbloed et al., *J. Bacteriol.* 181:5600-5605. (1999); Zerbe-Burkhardt et al., *J. Biol. Chem.* 273:6508-6517 (1998)). Enzymes encoded by *icmA* and *icmB* genes in *Streptomyces avermitilis MA-4680* show high sequence similarity to known ICMs. These genes/proteins are identified below.

Gene	GenBank ID	GI Number	Organism
icmA	CAB40912.1	4585853	*Streptomyces coelicolor A3(2)*
Mpe_B0541	YP_001023546.1	124263076	*Methylibium petroleiphilum PM1*
icm	AAC08713.1	3002492	*Streptomyces cinnamonensis*
icmB	CAB59633.1	6137077	*Streptomyces cinnamonensis*
icmA	NP_824008.1	29829374	*Streptomyces avermitilis*
icmB	NP_824637.1	29830003	*Streptomyces avermitilis*

[0349] Referring to Figure 5, step 2 involves 3-hydroxyisobutyryl-CoA hydrolase (EC 3.1.2.4), synthetase (EC 6.2.1.-) or 3-hydroxyisobutyryl-CoA transferase (EC 2.8.3.-). Step 5 involves methacrylyl-CoA hydrolase, synthetase, or transferase. These transformations can be performed by different classes of enzymes including CoA hydrolases (EC 3.1.2.-), CoA transferases (EC 2.8.3.-), and CoA synthetases (EC 6.1.2.-). As discussed earlier, pathway energetics are most favorable if a CoA transferase or a CoA synthetase is employed to accomplish this transformation (Table 1).

[0350] In the CoA-transferase family, *E. coli* enzyme acyl-CoA:acetate-CoA transferase, also known as acetate-CoA transferase (EC 2.8.3.8), has been shown to transfer the CoA moity to acetate from a variety of branched and linear acyl-CoA substrates, including isobutyrate (Matthies and Schink, *Appl. Environ. Microbiol.* 58:1435-1439 (1992)), valerate (Vanderwinkel et al.,. *Biochem. Biophys. Res. Commun.* 33:902-908 (1968)) and butanoate (Vanderwinkel et al. *supra*, 1968). This enzyme is encoded by *atoA* (alpha subunit) and *atoD* (beta subunit) in *E. coli* sp. K12 (Korolev et al., *Acta Crystallogr. D Biol. Crystallogr.* 58:2116-2121 (2002); Vanderwinkel et al., *supra*, 1968) and *actA* and *cg0592* in *Corynebacterium glutamicum ATCC 13032* (Duncan et al., *Appl. Environ. Microbiol.* 68:5186-5190 (2002)) and represents an ideal candidate to catalyze the desired 3-hydroxyisobutyryl-CoA transferase or methacrylyl-CoA transferase biotransformations shown in Figure 5, steps 2 and 5. Candidate genes by sequence homology include *atoD* and *atoA* in *Escherichia coli* UT189. Similar enzymes also exist in *Clostridium acetobutylicum* and *Clostridium saccharoperbutylacetonicum*.

Gene	GenBank ID	GI Number	Organism
atoA	P76459.1	2492994	*Escherichia coli K12*
atoD	P76458.1	2492990	*Escherichia coli K12*
actA	YP_226809.1	62391407	*Corynebacterium glutamicum ATCC 13032*
cg0592	YP_224801.1	62389399	*Corynebacterium glutamicum ATCC 13032*
atoA	ABE07971.1	91073090	*Escherichia coli UT189*
atoD	ABE07970.1	91073089	*Escherichia coli UT189*
ctfA	NP_149326.1	15004866	*Clostridium acetobutylicum*
ctfB	NP_149327.1	15004867	*Clostridium acetobutylicum*
ctfA	AAP42564.1	31075384	*Clostridium saccharoperbutylacetonicum*

Gene	GenBank ID	GI Number	Organism
ctfB	AAP42565.1	31075385	*Clostridium saccharoperbutylacetonicum*

[0351] Additional exemplary transferase transformations are catalyzed by the gene products of *cat1, cat2*, and *cat3* of *Clostridium kluyveri* which have been shown to exhibit succinyl-CoA, 4-hydroxybutyryl-CoA, and butyryl-CoA acetyltransferase activity, respectively (Sohling and Gottschalk, *J. Bacteriol.* 178(3): 871-880 (1996); Seedorf et al., *Proc. Natl. Acad. Sci. USA*, 105(6):2128-2133 (2008)).

Gene	GenBank ID	GI Number	Organism
cat1	P38946.1	729048	*Clostridium kluyveri*
cat2	P38942.2	172046066	*Clostridium kluyveri*
cat3	EDK35586.1	146349050	*Clostridium kluyveri*

[0352] The glutaconate-CoA-transferase (EC 2.8.3.12) enzyme from anaerobic bacterium *Acidaminococcus fermentans* reacts with diacid glutaconyl-CoA and 3-butenoyl-CoA (Mack and Buckel, *FEBS Lett.* 405:209-212 (1997)). The genes encoding this enzyme are *gctA* and *gctB*. This enzyme has reduced but detectable activity with other CoA derivatives including glutaryl-CoA, 2-hydroxyglutaryl-CoA, adipyl-CoA and acrylyl-CoA (Buckel et al., *Eur. J. Biochem.* 118:315-321 (1981)). The enzyme has been cloned and expressed in *E. coli* (Mack et al., *Eur. J. Biochem.* 226:41-51 (1994)).

Gene	GenBank ID	GI Number	Organism
gctA	CAA57199.1	559392	*Acidaminococcus fermentans*
gctB	CAA57200.1	559393	*Acidaminococcus fermentans*

[0353] Additional enzyme candidates include succinyl-CoA:3-ketoacid CoA transferases which utilize succinate as the CoA acceptor. Exemplary succinyl-CoA:3:ketoacid-CoA transferases are present in *Helicobacter pylori* (Corthesy-Theulaz et al., *J. Biol. Chem.* 272:25659-25667 (1997)) and *Bacillus subtilis* (Stols et al., *Protein Expr. Purif.* 53:396-403 (2007)).

Gene	GenBank ID	GI Number	Organism
HPAG1_0676	YP_627417	108563101	*Helicobacter pylori*
HPAG1_0677	YP_627418	108563102	*Helicobacter pylori*

Gene	GenBank ID	GI Number	Organism
ScoA	NP_391778	16080950	*Bacillus subtilis*
ScoB	NP_391777	16080949	*Bacillus subtilis*

[0354] A candidate ATP synthase is ADP-forming acetyl-CoA synthetase (ACD, EC 6.2.1.13), an enzyme that couples the conversion of acyl-CoA esters to their corresponding acids with the concurrent synthesis of ATP. Although this enzyme has not been shown to react with 3-hydroxyisobutyryl-CoA or methacrylyl-CoA as a substrate, several enzymes with broad substrate specificities have been described in the literature. ACD I from *Archaeoglobus fulgidus*, encoded by AF1211, was shown to operate on a variety of linear and branched-chain substrates including isobutyrate, isopentanoate, and fumarate (Musfeldt and Schonheit,. *J. Bacteriol.* 184:636-644 (2002)). The enzyme from *Haloarcula marismortui* (annotated as a succinyl-CoA synthetase) accepts priopionate, butyrate, and branched-chain acids (isovalerate and isobutyrate) as substrates, and was shown to operate in the forward and reverse directions (Brasen and Schonheit, *Arch. Microbiol.* 182:277-287 (2004)). The ACD encoded by *PAE3250* from hyperthermophilic crenarchaeon *Pyrobaculum aerophilum* showed the broadest substrate range of all characterized ACDs, reacting with acetyl-CoA, isobutyryl-CoA (preferred substrate) and phenylacetyl-CoA (Brasen and Schonheit, *supra*, 2004). However, directed evolution or engineering can be used to modify this enzyme to operate at the physiological temperature of the host organism. The enzymes from *A. fulgidus*, *H. marismortui* and *P. aerophilum* have all been cloned, functionally expressed, and characterized in *E. coli* (Brasen and Schonheit, *supra*, 2004; Musfeldt and Schonheit, *J. Bacteriol.* 184:636-644 (2002)).

Gene	GenBank ID	GI Number	Organism
AF1211	NP_070039.1	11498810	*Archaeoglobus fulgidus DSM 4304*
scs	YP_135572.1	55377722	*Haloarcula marismortui ATCC 43049*
PAE3250	NP_560604.1	18313937	*Pyrobaculum aerophilum str. IM2*

[0355] In the CoA hydrolase family, the enzyme 3-hydroxyisobutyryl-CoA hydrolase is specific for 3-HIBCoA and has been described to efficiently catalyze the desired transformation during valine degradation (Shimomura et al., *J. Biol. Chem.* 269:14248-14253 (1994)). Genes encoding this enzyme include *hibch* of *Rattus norvegicus* (Shimomura et al.,

J. Biol. Chem. 269:14248-14253 (1994); Shimomura et al., *Methods Enzymol.* 324:229-240 (2000)) and *Homo sapiens* (Shimomura et al., *supra*, 2000). Candidate genes by sequence homology include *hibc*h of *Saccharomyces cerevisiae* and *BC_2292* of *Bacillus cereus*.

Gene	GenBank ID	GI Number	Organism
hibch	Q5XIE6.2	146324906	*Rattus norvegicus*
hibch	Q6NVY1.2	146324905	*Homo sapiens*
hibch	P28817.2	2506374	*Saccharomyces cerevisiae*
BC_2292	Q81DR3	29895975	*Bacillus cereus*

[0356] Referring to Figure 5, step 3 involves 3-hydroxyisobutyrate dehydratase (EC 4.2.1.-). The entails dehydration of 3-hydroxyisobutyrate to MAA by 3-hydroxyisobutyrate dehydratase. Gene candidates for this enzyme are described in the succinyl-CoA to MAA pathway (see Example V). Also referring to Figure 5, step 4 involves 3-hydroxyisobutyryl-CoA dehydratase (EC 4.2.1.-). Dehydration of 3-hydroxyisobutyryl-CoA to methacrylyl-CoA can be accomplished by a reversible 3-hydroxyacyl-CoA dehydratase such as crotonase (also called 3-hydroxybutyryl-CoA dehydratase, EC 4.2.1.55) or enoyl-CoA hydratase (also called 3-hydroxyacyl-CoA dehydratase, EC 4.2.1.17). These enzymes are generally reversible (Moskowitz and Merrick, *Biochemistry* 8:2748-2755 (1969); Durre et al., *FEMS Microbiol. Rev.* 17:251-262 (1995)). Exemplary genes encoding crotonase enzymes can be found in *C. acetobutylicum* (Boynton, et al., *J. Bacteriol.* 178(11):3015-3024 (1996)), *C. kluyveri* (Hillmer and Gottschalk, *FEBS Lett.* 21(3):351-354 (1972)), and *Metallosphaera sedula* (Berg et al., *Science* 318(5857) 1782-1786 (2007)) though the sequence of the latter gene is not known. Enoyl-CoA hydratases, which are involved in fatty acid beta-oxidation and/or the metabolism of various amino acids, can also catalyze the hydration of crotonyl-CoA to form 3-hydroxybutyryl-CoA (Agnihotri and Liu, *Bioorg. Med. Chem.* 11(1):9-20 (2003); Roberts et al., *Arch. Microbiol.* 117(1):99-108 (1978); Conrad et al., *J. Bacteriol.* 118(1):103-111 (1974)). The enoyl-CoA hydratases, *phaA* and *phaB*, of *P. putida* are believed to carry out the hydroxylation of double bonds during phenylacetate catabolism (Olivera et al., *Proc. Natl. Acad. Sci. USA* 95:6419-6424 (1998)). The *paaA* and *paaB* from *P. fluorescens* catalyze analogous transformations (Olivera et al., *supra,* 1998). Lastly, a number of *Escherichia coli* genes have been shown to demonstrate enoyl-CoA hydratase functionality including *maoC* (Park and Lee, *J. Bacteriol.* 185:5391-5397 (2003)), *paaF* (Ismail et al., *Eur. J. Biochem.* 270:3047-3054 (2003); Park and Lee, *Appl. Biochem.*

Biotechnol. 113-116:335-346 (2004); Park and Yup, *Biotechnol. Bioeng.* 86:681-686. (2004)), and *paaG* (Ismail et al., *Eur. J. Biochem.* 270:3047-3054 (2003); Park and Lee, *Appl. Biochem. Biotechnol.* 113-116:335-346 (2004); Park and Yup, *Biotechnol. Bioeng.* 86:681-686 (2004)).

Gene	GenBank ID	GI Number	Organism
crt	NP_349318.1	15895969	*Clostridium acetobutylicum*
crt1	YP_001393856	153953091	*Clostridium kluyveri DSM 555*
paaA	NP_745427.1	26990002	*Pseudomonas fluorescens*
paaB	NP_745426.1	26990001	*Pseudomonas fluorescens*
phaA	ABF82233.1	106636093	*Pseudomonas putida*
phaB	ABF82234.1	106636094	*Pseudomonas putida*
maoC	NP_415905.1	16129348	*Escherichia coli*
paaF	NP_415911.1	16129354	*Escherichia coli*
paaG	NP_415912.1	16129355	*Escherichia coli*

[0357] This example describes a biosynthetic pathway for production of 3-hydroxyisobutyric acid or methacrylic acid from 4-hydroxybutyryl-CoA.

EXAMPLE VIII
Pathway for Conversion of Alpha-ketoglutarate to MAA via Threo-3-methylaspartate

[0358] This example describes an exemplary MAA synthesis pathway from alpha-ketoglutarate to threo-3-methylaspartate.

[0359] Another exemplary pathway for MAA biosynthesis proceeds through alpha-ketoglutarate, a metabolite in *E. coli* produced in the TCA cycle (see Figure 6).

[0360] The first step of the pathway, catalyzed by the enzyme aspartate aminotransferase, transfers an amino group from aspartate to alpha-ketoglutarate, forming glutamate and oxaloacetate. The subsequent two steps include rearrangement of the carbon backbone and subsequent deamination to form mesaconate. Enzymes catalyzing these conversions are found in the energy-yielding fermentation of glutamate in soil *Clostridia* and other organisms capable of fermenting amino acids (Buckel and Barker, *J. Bacteriol.* 117:1248-1260 (1974)). The directionality of the pathway in these organisms is in agreement with the direction required for MAA synthesis in the biopathway. The final pathway step entails decarboxylation of mesaconate to yield methacrylic acid.

[0361] Referring to Figure 6, step 1 involves aspartate aminotransferase (EC 2.6.1.1). The first step of the pathway transfers an amino group from aspartate to alpha-ketoglutarate, forming glutamate and oxaloacetate. The genes *aspC* from *Escherichia coli* (Yagi et al., *FEBS Lett.* 100:81-84 (1979); Yagi et al., *Methods Enzymol.* 113:83-89 (1985)), *AAT2* from *Saccharomyces cerevisiae* (Yagi et al., *J. Biochem.* 92:35-43 (1982)) and *ASP5* from *Arabidopsis thaliana* (de la Torre et al., *Plant J.* 46:414-425 (2006); Kwok and Hanson, *J. Exp. Bot.* 55:595-604 (2004); Wilkie and Warren, *Protein Expr. Purif.* 12:381-389 (1998)), encode the enzyme that catalyzes this conversion, aspartate aminotransferase.

Gene	GenBank ID	GI Number	Organism
aspC	NP_415448.1	16128895	*Escherichia coli*
AAT2	P23542.3	1703040	*Saccharomyces cerevisiae*
ASP5	P46248.2	20532373	*Arabidopsis thaliana*

[0362] Referring to Figure 6, step 2 involves glutamate mutase (EC 5.4.99.1). In step 2, the linear carbon chain of glutamate is rearranged to the branched structure of threo-3-methylaspartate. This transformation is catalyzed by glutamate mutase, a cobalamin-dependent enzyme composed of two subunits. Two glutamate mutases, from *Clostridium cochlearium* and *Clostridium tetanomorphum*, have been cloned and functionally expressed in *E. coli* (Holloway and Marsh, *J. Biol. Chem.* 269:20425-20430 (1994); Reitzer et al., *Acta Crystallogr. D Biol. Crystallogr.* 54:1039-1042 (1998)). The genes encoding this two-subunit protein are *glmE* and *glmS* from *Clostridium cochlearium*, *mamA* and *glmE* from *Clostridium tetanomorphum*, and *mutE* and *mut*S from *Clostridium tetani* (Switzer, *Glutamate mutase*, pp. 289-305 Wiley, New York (1982)).

Gene	GenBank ID	GI Number	Organism
glmE	P80077.2	2507035	*Clostridium cochlearium*
glmS	P80078.2	17865765	*Clostridium cochlearium*
mamA	Q05488.1	729588	*Clostridium tetanomorphum*
glmE	Q05509.1	729586	*Clostridium tetanomorphum*
mutE	NP_783086.1	28212142	*Clostridium tetani E88*
mutS	NP_783088.1	28212144	*Clostridium tetani E88*

[0363] Referring to Figure 6, step 3 involves 3-methylaspartase (EC 4.3.1.2). 3-methylaspartase, also referred to as beta-methylaspartase or 3-methylaspartate ammonia-lyase, catalyzes the deamination of threo-3-methylasparatate to mesaconate. The 3-

methylaspartase from *Clostridium tetanomorphum* has been cloned, functionally expressed in *E. coli*, and crystallized (Asuncion et al., *Acta Crystallogr. D Biol. Crystallogr.* 57:731-733 (2001); Asuncion et al., *J. Biol. Chem.* 277:8306-8311 (2002); Botting et al., *Biochemistry* 27:2953-2955 (1988); Goda et al., *Biochemistry* 31:10747-10756 (1992)). In *Citrobacter amalonaticus*, this enzyme is encoded by *BAA28709* (Kato and Asano, *Arch. Microbiol.* 168:457-463 (1997)). 3-methylaspartase has also been crystallized from *E. coli YG1002* (Asano and Kato, *FEMS Microbiol. Lett.* 118:255-258 (1994)), although the protein sequence is not listed in public databases such as GenBank. Sequence homology can be used to identify additional candidate genes, including *CTC_02563* in *C. tetani* and *ECs0761* in *Escherichia coli O157:H7*.

Gene	GenBank ID	GI Number	Organism
MAL	AAB24070.1	259429	*Clostridium tetanomorphum*
BAA28709	BAA28709.1	3184397	*Citrobacter amalonaticus*
CTC_02563	NP_783085.1	28212141	*Clostridium tetani*
ECs0761	BAB34184.1	13360220	*Escherichia coli O157:H7 str. Sakai*

[0364] Referring to Figure 6, step 4 involves mesaconate decarboxylase (EC 4.1.1.-). The final step of the pathway entails the decarboxylation of mesaconate to methacrylic acid. An enzyme catalyzing this exact reaction has not been demonstrated experimentally. However, several enzymes catalyzing highly similar reactions exist. One enzyme with closely related function is aconitate decarboxylase. This enzyme catalyzes the final step in itaconate biosynthesis in a strain of *Candida* and the filamentous fungi *Aspergillus terreus* (Bonnarme et al., *J. Bacteriol.* 177:3573-3578 (1995); Willke and Vorlop, *Appl. Microbiol. Biotechnol.* 56:289-295 (2001)). Although itaconate is a compound of biotechnological interest, no efforts have been made thus far to identify or clone the aconitate decarboxylase gene.

[0365] A second enzyme with similar function is 4-oxalocronate decarboxylase. This enzyme is common in a variety of organisms and the genes encoding the enzyme from *Pseudomonas sp. (strain 600)* have been cloned and expressed in *E. coli* (Shingler et al., *J. Bacteriol.* 174:711-724 (1992)). The methyl group in mesaconate may cause steric hindrance, but this problem could likely be overcome with directed evolution or protein engineering. 4-oxalocronate decarboxylase is composed of two subunits. Genes encoding

this enzyme include *dmpH* and *dmpE* in *Pseudomonas sp.* (*strain 600*) (Shingler et al., *J. Bacteriol.* 174:711-724 (1992)), *xylII* and *xylIII* from *Pseudomonas putida* (Kato and Asano, *Arch. Microbiol.* 168:457-463 (1997); Stanley et al., *Biochemistry* 39:718-726 (2000)), and *Reut_B5691* and *Reut_B5692* from *Ralstonia eutropha JMP134* (Hughes et al., *J. Bacteriol.* 158:79-83 (1984)).

Gene	GenBank ID	GI Number	Organism
dmpH	CAA43228.1	45685	*Pseudomonas sp. CF600*
dmpE	CAA43225.1	45682	*Pseudomonas sp. CF600*
xylII	YP_709328.1	111116444	*Pseudomonas putida*
xylIII	YP_709353.1	111116469	*Pseudomonas putida*
Reut_B5691	YP_299880.1	73539513	*Ralstonia eutropha JMP134*
Reut_B5692	YP_299881.1	73539514	*Ralstonia eutropha JMP134*

[0366] This example describes a biosynthetic pathway for production of MMA from alpha-ketoglutarate.

EXAMPLE IX
Pathway for Conversion of Alpha-ketoglutarate to MAA via 2-Hydroxyglutarate

[0367] This example describes an exemplary MAA synthesis pathway from alph-ketoglutarate to MAA via 2-hydroxyglutarate.

[0368] Another exemplary pathway for MAA biosynthesis has a scheme similar to the pathway described in Example VIII, but it passes through the hydroxylated intermediates 2-hydroxyglutarate and 3-methylmalate (see Figure 7), rather than amine-substituted intermediates (see Figure 6).

[0369] Referring to Figure 7, step 1 involves alpha-ketoglutarate reductase (EC 1.1.99.2). The first step of this pathway entails the reduction of alpha-ketoglutarate to 2-hydroxyglutarate by native enzyme alpha-ketoglutarate reductase. This enzyme is encoded by *serA*, a multifunctional enzyme which also catalyzes the reduction of 3-phosphoglycerate in central metabolism (Zhao and Winkler, *J. Bacteriol.* 178:232-239 (1996)). Genes *L2HGDH* in *Homo sapiens* (Jansen and Wanders, *Biochim. Biophys. Acta* 1225:53-56 (1993)), *FN0487* in *L2hgdh* in *Fusobacterium nucleatum* (Hayashi et al., *J. Nihon Univ. Sch. Dent.* 28:12-21 (1986)), and *L2hgdh_predicted* in *Rattus norvegicus* (Jansen and Wanders, *Biochim. Biophys. Acta* 1225:53-56 (1993)) encode this enzyme. Gene candidates with high sequence homology include *L2hgdh* in *Mus musculus* and *L2HGDH* in *Bos taurus*. At high concentrations, 2-hydroxyglutarate has been shown to feed back on alpha-ketoglutarate

reductase activity by competitive inhibition (Zhao and Winkler, *J. Bacteriol.* 178:232-239. (1996)).

Gene	GenBank ID	GI Number	Organism
serA	CAA01762.1	1247677	*Escherichia coli*
L2HGDH	Q9H9P8.3	317373422	*Homo sapiens*
L2hgdh	NP_663418.1	21703884	*Mus musculus*
L2hgdh_predicted	NP_001101498.1	157820173	*Rattus norvegicus*
L2HGDH	NP_001094560.1	155371911	*Bos taurus*
FN0487	Q8RG31	81763568	*Fusobacterium nucleatum subsp. Nucleatum*

[0370] Referring to Figure 7, step 2 involves 2-hydroxyglutamate mutase (EC 5.4.99.-). In the second step of the pathway, the carbon backbone undergoes rearrangement by a glutamate mutase enzyme. The most common reaction catalyzed by such an enzyme is the conversion of glutamate to threo-3-methylasparate, shown in step 2 of Figure 6. The adenosylcobalamin-dependent glutamate mutase from *Clostridium cochlearium* has also been shown to react with 2-hydroxyglutarate as an alternate substrate (Roymoulik et al., *Biochemistry* 39:10340-10346 (2000)), although the rate of this reaction is two orders of magnitude lower with 2-hydroxyglutarate compared to the rate with native substrate glutamate. Directed evolution of the enzyme can be used to increase glutamate mutase affinity for 2-hydroxyglutarate. GenBank accession numbers of protein sequences encoding glutamate mutases are found in Example VIII, step 2 of the pathway.

[0371] Referring to Figure 7, step 3 involves 3-methylmalate dehydratase (EC 4.2.1.-). In the third step, 3-methylmalate is dehydrated to form mesaconate. Although an enzyme catalyzing this exact transformation has not been described in the literature, several enzymes are able to catalyze a similar reaction. One such enzyme is 2-methylmalate dehydratase, also called citramalate hydrolyase, which converts 2-methylmalate to mesaconate. 2-Methylmalate and 3-methylmalate are closely related, with the only difference in structure being the location of the hydroxyl group. 2-Methylmalate dehydratase activity was detected in *Clostridium tetanomorphum*, *Morganella morganii*, *Citrobacter amalonaticus* in the context of the glutamate degradation VI pathway (Kato and Asano, *Arch. Microbiol.* 168:457-463 (1997)); however the genes encoding this enzyme have not been sequenced to date.

[0372] A second candidate enzyme is fumarate hydratase, which catalyzes the dehydration of malate to fumarate. As described in Example V (step 5), a wealth of structural information is available for this enzyme and other studies have successfully engineered the enzyme to alter activity, inhibition and localization (Weaver, *Acta Crystallogr. D Biol. Crystallogr.* 61:1395-1401 (2005)). Gene candidates are discussed in Example V, step 5 of the pathway.

[0373] Referring to Figure 7, step 4 involves mesaconate decarboxylase (EC 4.1.1.-). The final pathway step involves the decarboxylation of mesaconate to methacrylic acid. This reaction is identical to the final step of the pathway described in Example VIII.

[0374] This example describes a biosynthetic pathway for production of MMA from alpha-ketoglutarate.

EXAMPLE X
Pathway for Conversion of Acetyl-CoA to 2-Hydroxyisobutyric Acid or MAA

[0375] This example describes an exemplary 2-hydroxyisobutyric acid or MAA synthesis pathway from acetyl-CoA.

[0376] MAA biosynthesis can proceed from acetyl-CoA in a minimum of five enzymatic steps (see Figure 8). In this pathway, two molecules of acetyl-CoA are combined to form acetoacetyl-coA, which is then reduced to 3-hydroxybutyryl-CoA. Alternatively, 4-hydroxybutyryl-CoA can be converted to 3-hydroxybutyryl-CoA by way of 4-hydroxybutyryl-CoA dehydratase and crotonase (Martins et al., *Proc. Nat. Acad. Sci. USA* 101(44) 15645-15649 (2004); Jones and Woods, *Microbiol. Rev.* 50:484-524 (1986); Berg et al., *Science* 318(5857) 1782-1786 (2007)). A methylmutase then rearranges the carbon backbone of 3-hydroxybutyryl-CoA to 2-hydroxyisobutyryl-CoA, which is then dehydrated to form methacrylyl-CoA. Alternatively, 2-hydroxyisobutyryl-CoA can be converted to 2-hydroxyisobutyrate, secreted, and recovered as product. The final step converting methacrylyl-CoA to MAA can be performed by a single enzyme (shown in Figure 8) or a series of enzymes.

[0377] Referring to Figure 8, step 1 involves acetoacetyl-CoA thiolase (EC 2.3.1.9). The formation of acetoacetyl-CoA from two acetyl-CoA units is catalyzed by acetyl-CoA thiolase. This enzyme is native to *E. coli*, encoded by gene *atoB*, and typically operates in

the acetoacetate-degrading direction during fatty acid oxidation (Duncombe and Frerman, *Arch. Biochem. Biophys.* 176:159-170 (1976); Frerman and Duncombe, *Biochim. Biophys. Acta* 580:289-297 (1979)). The gene *thlA* from *Clostridium acetobutylicum* was engineered into an isopropanol-producing strain of *E. coli* (Hanai et al., *Appl. Environ. Microbiol.* 73:7814-7818 (2007); Stim-Herndon et al., *Gene* 154:81-85 (1995)). Additional gene candidates include *thl* from *Clostridium pasteurianum* (Meng and Li. Cloning, *Biotechnol. Lett.* 28:1227-1232 (2006)) and *ERG10* from *S. cerevisiae* (Hiser et al, *J Biol Chem* 269:31383-89 (1994)).

Protein	GenBank ID	GI Number	Organism
atoB	NP_416728	16130161	*Escherichia coli*
thlA	NP_349476.1	15896127	*Clostridium acetobutylicum*
thlB	NP_149242.1	15004782	*Clostridium acetobutylicum*
thl	ABA18857.1	75315385	*Clostridium pasteurianum*
ERG10	NP_015297	6325229	*Saccharomyces cerevisiae*

[0378] Referring to Figure 8, step 2 involves acetoacetyl-CoA reductase (EC#: 1.1.1.35). The second step entails the reduction of acetoacetyl-CoA to 3-hydroxybutyryl-CoA by acetoacetyl-CoA reductase. This enzyme participates in the acetyl-CoA fermentation pathway to butyrate in several species of *Clostridia* and has been studied in detail (Jones and Woods, *Microbiol. Rev.* 50:484-524 (1986)). The enzyme from *Clostridium acetobutylicum*, encoded by *hbd*, has been cloned and functionally expressed in *E. coli* (Youngleson et al., *J. Bacteriol.* 171:6800-6807 (1989)). Additionally, subunits of two fatty acid oxidation complexes in *E. coli*, encoded by *fadB* and *fadJ*, function as 3-hydroxyacyl-CoA dehydrogenases (Binstock and Schulz, *Methods Enzymol.* 71 Pt C:403-411 (1981)). Yet other genes demonstrated to reduce acetoacetyl-CoA to 3-hydroxybutyryl-CoA are *phbB* from *Zoogloea ramigera* (Ploux et al., *Eur.J Biochem.* 174:177-182 (1988)) and *phaB* from *Rhodobacter sphaeroides* (Alber et al., *Mol.Microbiol* 61:297-309 (2006)). The former gene is NADPH-dependent, its nucleotide sequence has been determined (Peoples et al., *Mol.Microbiol* 3:349-357 (1989)) and the gene has been expressed in *E. coli*. Substrate specificity studies on the gene led to the conclusion that it could accept 3-oxopropionyl-CoA as a substrate besides acetoacetyl-CoA (Ploux et al., *Eur.J Biochem.* 174:177-182 (1988)). Additional gene candidates include *Hbd1* (C-terminal domain) and *Hbd2* (N-terminal domain) in *Clostridium kluyveri* (Hillmer and Gottschalk, *Biochim. Biophys. Acta* 3334:12-23 (1974)) and *HSD17B10* in *Bos taurus* (Wakil et al., J. Biol. Chem. 207:631-638 (1954)). The

enzyme from *Paracoccus denitrificans* has been functionally expressed and characterized in *E. coli* (Yabutani et al., *FEMS Microbiol Lett.* 133:85-90 (1995)). A number of similar enzymes have been found in other species of *Clostridia* and in *Metallosphaera sedula* (Berg et al., *Science.* 318:1782-1786 (2007)). The enzyme from *Candida tropicalis* is a component of the peroxisomal fatty acid beta-oxidation multifunctional enzyme type 2 (MFE-2). The dehydrogenase B domain of this protein is catalytically active on acetoacetyl-CoA. The domain has been functionally expressed in *E. coli*, a crystal structure is available, and the catalytic mechanism is well-understood (Ylianttila et al., *Biochem Biophys Res Commun* 324:25-30 (2004); Ylianttila et al., *J Mol Biol* 358:1286-1295 (2006)).

Protein	GENBANK ID	GI NUMBER	ORGANISM
fadB	P21177.2	119811	*Escherichia coli*
fadJ	P77399.1	3334437	*Escherichia coli*
Hbd2	EDK34807.1	146348271	*Clostridium kluyveri*
Hbd1	EDK32512.1	146345976	*Clostridium kluyveri*
HSD17B10	O02691.3	3183024	*Bos taurus*
phbB	P23238.1	130017	*Zoogloea ramigera*
phaB	YP_353825.1	77464321	*Rhodobacter sphaeroides*
phaB	BAA08358	675524	*Paracoccus denitrificans*
Hbd	NP_349314.1	15895965	*Clostridium acetobutylicum*
Hbd	AAM14586.1	20162442	*Clostridium beijerinckii*
Msed_1423	YP_001191505	146304189	*Metallosphaera sedula*
Msed_0399	YP_001190500	146303184	*Metallosphaera sedula*
Msed_0389	YP_001190490	146303174	*Metallosphaera sedula*
Msed_1993	YP_001192057	146304741	*Metallosphaera sedula*
Fox2	Q02207	399508	*Candida tropicalis*

[0379] Referring to Figure 8, step 3 involves 3-hydroxybutyryl-CoA mutase (EC 5.4.99.-). In the next step, 3-hydroxybutyryl-CoA is rearranged to form 2-hydroxyisobutyryl-CoA (2-HIBCoA) by 3-hydroxybutyryl-CoA mutase. This enzyme is a novel ICM-like methylmutase recently discovered and characterized in *Methylibium petroleiphilum* (Ratnatilleke et al., J. Biol. Chem. 274:31679-31685 (1999); Rohwerder et al., *Appl. Environ. Microbiol.* 72:4128-4135 (2006)). This enzyme, encoded by *Mpe_B0541* in *Methylibium petroleiphilum PM1*, has high sequence homology to the large subunit of methylmalonyl-CoA mutase in other organisms including *Rsph17029_3657* in *Rhodobacter sphaeroides* and *Xaut_5021* in *Xanthobacter autotrophicus*. As discussed in Example VII (step 1), changes to a single amino acid near the active site alters the substrate specificity of the enzyme

(Ratnatilleke et al., *supra*, 1999; Rohwerder et al., *supra*, 2006), so directed engineering of similar enzymes at this site, such as methylmalonyl-CoA mutase or isobutryryl-CoA mutase described previously, can be used to achieve the desired reactivity.

Gene	GenBank ID	GI Number	Organism
Mpe_B0541	YP_001023546.1	124263076	*Methylibium petroleiphilum PM1*
Rsph17029_3657	YP_001045519.1	126464406	*Rhodobacter sphaeroides*
Xaut_5021	YP_001409455.1	154243882	*Xanthobacter autotrophicus Py2*

[0380] Referring to Figure 8, step 4 involves 2-hydroxyisobutyryl-CoA dehydratase. The dehydration of 2-hydroxyacyl-CoA such as 2-hydroxyisobutyryl-CoA can be catalyzed by a special class of oxygen-sensitive enzymes that dehydrate 2-hydroxyacyl-CoA derivatives via a radical-mechanism (Buckel and Golding, *Annu. Rev. Microbiol.* 60:27-49 (2006); Buckel et al., *Curr. Opin. Chem. Biol.* 8:462-467 (2004); Buckel et al., *Biol. Chem.* 386:951-959 (2005); Kim et al., *FEBS J.* 272:550-561 (2005); Kim et al., *FEMS Microbiol. Rev.* 28:455-468 (2004); Zhang et al., *Microbiology* 145 (Pt 9):2323-2334 (1999)). One example of such an enzyme is the lactyl-CoA dehydratase from *Clostridium propionicum*, which catalyzes the dehydration of lactoyl-CoA to form acryl-CoA (Kuchta and Abeles, *J. Biol. Chem.* 260:13181-13189 (1985); Hofmeister and Buckel, *Eur. J. Biochem.* 206:547-552 (1992)). An additional example is 2-hydroxyglutaryl-CoA dehydratase encoded by *hgdABC* from *Acidaminococcus fermentans* (Muëller and Buckel, *Eur. J. Biochem.* 230:698-704 (1995); Schweiger et al., *Eur. J. Biochem.* 169:441-448 (1987)). Yet another example is the 2-hydroxyisocaproyl-CoA dehydratase from *Clostridium difficile* catalyzed by *hadBC* and activated by *hadI* (Darley et al., *FEBS J.* 272:550–61 (2005)). The corresponding sequences for *A. fermentans* and *C. difficile* can be found as listed below. The sequence of the complete *C. propionicium* lactoyl-CoA dehydratase is not yet listed in publicly available databases. However, the sequence of the beta-subunit corresponds to the GenBank accession number AJ276553 (Selmer et al, *Eur J Biochem*, 269:372-80 (2002)).

Gene	GenBank Accession No.	GI No.	Organism
hgdA	P11569	296439332	*Acidaminococcus fermentans*
hgdB	P11570	296439333	*Acidaminococcus fermentans*
hgdC	P11568	2506909	*Acidaminococcus fermentans*
hadB	YP_001086863	126697966	*Clostridium difficile*
hadC	YP_001086864	126697967	*Clostridium difficile*

hadI	YP_001086862	126697965	*Clostridium difficile*
lcdB	AJ276553	7242547	*Clostridium propionicum*

[0381] Referring to Figure 8, steps 5 or 6 involve a transferase (EC 2.8.3.-), hydrolase (EC 3.1.2.-), or synthetase (EC 6.2.1.-) with activity on a methacrylic acid or 2-hydroxyisobutyric acid, respectively. Direct conversion of methacrylyl-CoA to MAA or 2-hydroxyisobutyryl-CoA to 2-hydrioxyisobutyrate can be accomplished by a CoA transferase, synthetase or hydrolase. As discussed in Example VII, pathway energetics are most favorable if a CoA transferase or a CoA synthetase is employed to accomplish this transformation. In the transferase family, the enzyme acyl-CoA:acetate-CoA transferase, also known as acetate-CoA transferase, is a suitable candidate to catalyze the desired 2-hydroxyisobutyryl-CoA or methacryl-CoA transferase activity due to its broad substrate specificity that includes branched acyl-CoA substrates (Matthies and Schink, *Appl. Environ. Microbiol.* 58:1435-1439 (1992); Vanderwinkel et al., *Biochem. Biophys. Res. Commun.* 33:902-908 (1968)). ADP-forming acetyl-CoA synthetase (ACD) is a promising enzyme in the CoA synthetase family operating on structurally similar branched chain compounds (Brasen and Schonheit, *Arch..Microbiol.* 182:277-287 (2004); Musfeldt and Schonheit, *J. Bacteriol.* 184:636-644 (2002)). In the CoA-hydrolase family, the enzyme 3-hydroxyisobutyryl-CoA hydrolase has been shown to operate on a variety of branched chain acyl-CoA substrates including 3-hydroxyisobutyryl-CoA, methylmalonyl-CoA, and 3-hydroxy-2-methylbutanoyl-CoA (Hawes et al., *Methods Enzymol.* 324:218-228 (2000); Hawes et al., *J. Biol. Chem.* 271:26430-26434 (1996); Shimomura et al., *J. Biol. Chem.* 269:14248-14253 (1994)). Additional exemplary gene candidates for CoA transferases, synthetases, and hydrolases are discussed in Example VII (step 2 and 5).

[0382] Referring to Figure 8, an alternative step 5 involves indirect conversion to MAA. As an alternative to direct conversion of MAA-CoA to MAA, an alternate strategy for converting methacrylyl-CoA into MAA entails a multi-step process in which MAA-CoA is converted to MAA via 3-hydroxyisobutyrate. By this process, MAA-CoA is first converted to 3-hydroxyisobutyryl-CoA, which can subsequently be converted to MAA as described in Example VII.

[0383] The first step of this indirect route entails the conversion of MAA-CoA to 3-hydroxyisobutyryl-CoA (3HIB-CoA) by enoyl-CoA hydratase (EC 4.2.1.17 and 4.2.1.74). In

E. coli, the gene products of *fadA* and *fadB* encode a multienzyme complex involved in fatty acid oxidation that exhibits enoyl-CoA hydratase activity (Nakahigashi and Inokuchi, *Nucleic Acids Research* 18:4937 (1990); Yang, *J. Bacteriol.* 173:7405-7406 (1991); Yang et al., *J. Biol. Chem.* 265:10424-10429 (1990); Yang et al., *Biochemistry* 30:6788-6795 (1991)). Knocking out a negative regulator encoded by *fadR* can be utilized to activate the *fadB* gene product (Sato et al., *J. Biosci. Bioengineer.* 103:38-44 (2007)). The *fadI* and *fadJ* genes encode similar functions and are naturally expressed under anaerobic conditions (Campbell et al., *Mol. Microbiol.* 47:793-805 (2003)).

Gene	GenBank Accession No.	GI No.	Organism
fadA	YP_026272.1	49176430	*Escherichia coli*
fadB	NP_418288.1	16131692	*Escherichia coli*
fadI	NP_416844.1	16130275	*Escherichia coli*
fadJ	NP_416843.1	16130274	*Escherichia coli*
fadR	NP_415705.1	16129150	*Escherichia coli*

[0384] Additional native gene candidates encoding an enoyl-CoA hydratase include *maoC* (Park and Lee, *J. Bacteriol.* 185:5391-5397 (2003)), *paaF* (Ismail et al., *Eur. J. Biochem.* 270:3047-3054 (2003); Park and Lee, *Appl. Biochem. Biotechnol.* 113-116:335-346 (2004); Park and Yup, *Biotechnol. Bioeng.* 86:681-686. (2004)), and *paaG* (Ismail et al., *Eur. J. Biochem.* 270:3047-3054 (2003); Park and Lee, *Appl. Biochem. Biotechnol.* 113-116:335-346 (2004); Park and Yup, *Biotechnol. Bioeng.* 86:681-686 (2004)). Other candidates include *paaA*, *paaB*, and *paaN* from *P. putida* (Olivera et al., *Proc. Natl. Acad. Sci. USA* 95:6419-6424 (1998)) and *P. fluorescens* (Di Gennaro et al., *Arch. Microbiol.* 188:117-125 (2007)). The gene product of *crt* from *C. acetobutylicum* is another candidate (Atsumi et al., *Metab. Eng.* epub Sep 14, 2007; Boynton et al., *J. Bacteriol.* 178:3015-3024 (1996)). The enoyl-CoA hydratase of *Pseudomonas putida*, encoded by ech, catalyzes the conversion of 3-hydroxybutyryl-CoA to crotonyl-CoA (Roberts et al., *Arch.Microbiol* 117:99-108 (1978)). This transformation is also catalyzed by the crt gene product of *Clostridium acetobutylicum*, the crt1 gene product of *C. kluyveri*, and other clostridial organisms Atsumi et al., *Metab Eng* 10:305-311 (2008); Boynton et al., *J Bacteriol.* 178:3015-3024 (1996); Hillmer et al., *FEBS Lett.* 21:351-354 (1972)). Additional enoyl-CoA hydratase candidates are phaA and phaB, of *P. putida*, and paaA and paaB from *P. fluorescens* (Olivera et al., *Proc.Natl.Acad.Sci U.S.A* 95:6419-6424 (1998)).

Gene	GenBank Accession No.	GI No.	Organism
maoC	NP_415905.1	16129348	*Escherichia coli*
paaF	NP_415911.1	16129354	*Escherichia coli*
paaG	NP_415912.1	16129355	*Escherichia coli*
paaN (*phaL*)	NP_745413.1	26989988	*Pseudomonas putida*
paaN	ABF82246.1	106636106	*Pseudomonas fluorescens*
ech	NP_745498.1	26990073	*Pseudomonas putida*
crt	NP_349318.1	15895969	*Clostridium acetobutylicum*
crt1	YP_001393856	153953091	*Clostridium kluyveri*
phaA	NP_745427.1	26990002	*Pseudomonas putida*
phaB	NP_745426.1	26990001	*Pseudomonas putida*
paaA	ABF82233.1	106636093	*Pseudomonas fluorescens*
paaB	ABF82234.1	106636094	*Pseudomonas fluorescens*

[0385] This example describes a biosynthetic pathway for production of 2-hydroxyisobutyrate or MAA from acetyl-CoA.

EXAMPLE XI
Pathway for Conversion of Acetyl-CoA to MAA via Crotonoyl-CoA

[0386] This example describes an exemplary MAA synthetic pathway from acetyl-CoA via crotonoyl-CoA.

[0387] Another route for converting acetyl-CoA to MAA in a minimum of seven enzymatic steps is described (see Figure 9). The yields of this pathway under aerobic and anaerobic conditions are similar to the pathway described in Example X.

[0388] The first two steps of the pathway are identical to steps 1 and 2 in the pathway described in Example X. In the third step, 3-HBCoA is dehydrated to form crotonyl-CoA by a crotonase (EC#: 4.2.1.55). The double bond in crotonyl-CoA is reduced by butyryl-CoA dehydrogenase (EC#: 1.3.99.2). Both of these enzymes, just like the acetoacetyl-CoA reductase, are a part of the acetyl-CoA fermentation pathway to butyrate in *Clostridia* species (Jones and Woods, *Microbiol. Rev.* 50:484-524 (1986)). In the subsequent step, butyryl-CoA is converted into isobutyryl-CoA by isobutyryl-CoA mutase (5.4.99.12), an enzyme that can reversibly convert butyryl-CoA into isobutyryl-CoA. This enzyme has been cloned and sequenced from *Streptomyces cinnamonensis*, and the recombinant enzyme has been characterized in *E. coli* (Ratnatilleke et al., *J. Biol. Chem.* 274:31679-31685 (1999)). The next step in the pathway entails the conversion of isobutyryl-CoA into methacrylyl-CoA via

2-methyl-acylCoA dehydrogenase (EC #: 1.3.99.12). This transformation towards methacrylyl-CoA has been observed in *Streptomyces* species, and the associated enzyme has been isolated and expressed in *E. coli* (Youngleson et al., *J. Bacteriol.* 171:6800-6807 (1989)). In the final step, methacrylyl-CoA is converted to MAA by either a single enzyme or a series of enzymes, as described in Example X (step 5).

[0389] This example describes a biosynthetic pathway for production of MAA from acetyl-CoA.

EXAMPLE XII
Pathway for Conversion of Acrylyl-CoA to MAA

[0390] This example describes an exemplary MAA synthesis pathway from acrylyl-CoA.

[0391] High yields of MAA can be obtained through the acrylyl-CoA pathway (see Figure 10). This pathway requires the activation of lactate to lactoyl-CoA followed by five, or optionally six, more steps for the conversion of this activated CoA molecule into MAA. The MAA yield from glucose using this pathway is 1.28 mol/mol of glucose and oxygen uptake is required for attaining these yields. In the absence of oxygen, the expected yield decreases from 1.28 mol to 1.09 mol/mol glucose consumed. Both the aerobic and anaerobic pathways are energy limited at maximum MAA yield and do not generate any ATP.

[0392] MAA biosynthesis through the acrylyl-CoA pathway first requires the conversion of pyruvate into lactate via lactate dehydrogenase (EC 1.1.1.28), an enzyme native to *E. coli* and many other organisms. The three subsequent steps, converting lactate into propionyl-CoA, are catalyzed by enzymes in pyruvate fermentation pathways in several unrelated bacteria such as *Clostridium propionicum* and *Megasphaera elsdenii* (MetaCyc). Lactate-CoA transferase (EC 2.8.3.1), also known as propionate-CoA transferase, converts lactate into lactoyl-CoA and can use both propionate and lactate as substrates. This enzyme has been purified and characterized (Schweiger et al., *Eur. J. Biochem.* 169:441-448 (1987)). Lactoyl-CoA is dehydrated into acrylyl-CoA using lactoyl-CoA dehydratase (EC 4.2.1.54), an enzyme that has been a subject of numerous studies (Hofmeister and Buckel, *Eur. J. Biochem.* 206:547-552. (1992); Kuchta and Abeles, *J. Biol. Chem.* 260:13181-13189 (1985)). Subsequently, acrylyl-CoA is reduced to propionyl-CoA using the acryloyl-CoA reductase (EC 1.3.2.2, formerly 1.3.99.3) (Hetzel et al., *Eur.J Biochem.* 270:902-910 (2003); Kuchta and Abeles, *supra*, 1985).

[0393] Referring to Figure 10, in step 5, propionyl-CoA is converted into S-methylmalonyl-CoA by propionyl-CoA carboxylase (6.4.1.3). Propionyl-CoA carboxylase has been purified from rat liver (Browner et al., *J. Biol. Chem.* 264:12680-12685 (1989); Kraus et al., *J. Biol. Chem.* 258:7245-7248 (1983)) and has been isolated and characterized from human liver as well (Kalousek et al., *J. Biol. Chem.* 255:60-65 (1980)). Carboxylation of propionyl-CoA into succinyl-CoA via this enzyme has been identified as one of the mechanisms of propionate metabolism in *E. coli* (Evans et al., *Biochem. J.* 291 (Pt 3):927-932 (1993)), but very little is known about the genetics of the pathway.

[0394] The final steps of the pathway entail conversion of methylmalonyl-CoA into MAA (lumped reaction in Figure 10). Enzymes catalyzing these reactions are described in Example V.

[0395] This example describes a biosynthetic pathway for production of MAA from pyruvate.

EXAMPLE XIII
Pathway for Conversion of 2-Ketoisovalerate to MAA

[0396] This example describes an exemplary MAA synthetic pathway from 2-ketoisovalerate.

[0397] The pathway (see Figure 11) exploits multiple steps of the valine degradation route described in several organisms, including *Bacillus subtilis*, *Arabidopsis thaliana*, and several species of *Pseuodomonas* but not known to be present in *E. coli* or in *S. cerevisiae*. In the first step of the valine degradation pathway, valine is converted into 2-ketoisovalerate by branched-chain amino acid aminotransferase (EC 2.6.1.24), an enzyme also native to *E. coli* (Matthies and Schink, *Appl. Environ. Microbiol.* 58:1435-1439 (1992); Rudman and Meister, *J. Biol. Chem.* 200:591-604 (1953)). The subsequent conversion of 2-ketoisovalerate into isobutyryl-CoA, catalyzed by a branched-chain keto-acid dehydrogenase complex (EC 1.2.1.25), is the committing step for MAA biosynthesis via this route. Next, isobutyryl-CoA is converted to methacrylyl-CoA via isobutyryl-CoA dehydrogenase (EC 1.3.99.12). Details for this step are described in Example XI. The final step, conversion of MAA-CoA to MAA, is described in Example V.

[0398] This example describes a biosynthetic pathway for production of MMA from 2-ketoisovalerate.

EXAMPLE XIV
Pathway for Conversion of 4-hydroxybutyryl-CoA to 2-Hydroxyisobutyrate or MAA via 2-Hydroxyisobutyryl-CoA

[0399] This example describes an exemplary 2-hydroxyisobutyrate or MAA synthesis pathway proceeding from 4-hydroxybutyryl-CoA that passes through 2-hydroxyisobutyryl-CoA.

[0400] The pathway first entails the dehydration of 4-hydroxybutyryl-CoA to vinylacetyl-CoA which is subsequently isomerized to crotonoyl-CoA. Crotonyl-CoA is hydrated to form 3-hydroxybutyryl-CoA, which is rearranged into 2-hydroxyisobutyryl-CoA. The final step of the 2-hydroxyisobutyrate pathway involves eliminating the CoA functional group from 2-hydroxyisobutyryl-CoA. The final steps in MAA synthesis involve the dehydration of 2-hydroxyisobutyryl-CoA followed by the removal of the CoA functional group from methacrylyl-CoA. Gene candidates for the first three pathway steps, steps 7, 8, and 9 of Figure 8, are described below. Gene candidates for steps 3, 4, 5, and 6 of Figure 8 are discussed in Example X.

[0401] Referring to Figure 8, steps 7 and 8 are carried out by 4-hydroxybutyryl-CoA dehydratase enzymes. The enzymes from both *Clostridium aminobutyrium* and *C. kluyveri* catalyze the reversible conversion of 4-hydroxybutyryl-CoA to crotonyl-CoA and also possess an intrinsic vinylacetyl-CoA Δ-isomerase activity (Scherf and Buckel, *Eur. J. Biochem.* 215:421-429 (1993); Scherf et al., *Arch. Microbiol.* 161:239-245 (1994)). Both native enzymes have been purified and characterized, including the N-terminal amino acid sequences (Scherf and Buckel, *supra*, 1993; Scherf et al., *supra,* 1994). The *abfD* genes from *C. aminobutyrium* and *C. kluyveri* match exactly with these N-terminal amino acid sequences, thus are encoding the 4-hydroxybutyryl-CoA dehydratases/vinylacetyl-CoA Δ-isomerase. In addition, *abfD* from *Porphyromonas gingivalis* ATCC 33277 is another exemplary 4-hydroxybutyryl-CoA dehydratase that can be identified through homology. The abfD gene product from *Porphyromonas gingivalis* and the Msed_1220 gene product from *Metallosphaera sedula* are closely related by sequence homology to the Clostridial gene products.

Gene	GenBank Accession No.	GI No.	Organism
abfD	YP_001396399.1	153955634	*Clostridium kluyveri DSM 555*
abfD	P55792	84028213	*Clostridium aminobutyricum*
abfD	YP_001928843	188994591	*Porphyromonas gingivalis*

			(ATCC 33277)
Msed_1220	YP_001191305.1	146303989	*Metallosphaera sedula*

[0402] Step 9 of Figure 8 is carried out by a crotonase enzyme. Such enzymes are required for n-butanol formation in some organisms, particularly *Clostridial* species, and also comprise one step of the 3-hydroxypropionate/4-hydroxybutyrate cycle in thermoacidophilic Archaea of the genera *Sulfolobus, Acidianus*, and *Metallosphaera*. Exemplary genes encoding crotonase enzymes can be found in *C. acetobutylicum* (Boynton, et al., *J. Bacteriol.* 178(11):3015-3024 (1996)), *C. kluyveri* (Hillmer and Gottschalk, *FEBS Lett.* 21(3):351-354 (1972)), and *Metallosphaera sedula* (Berg et al., *Science* 318(5857):1782-1786 (2007)) though the sequence of the latter gene is not known. Enoyl-CoA hydratases, which are involved in fatty acid beta-oxidation and/or the metabolism of various amino acids, can also catalyze the hydration of crotonyl-CoA to form 3-hydroxybutyryl-CoA (Agnihotri and Liu, *Bioorg. Med. Chem.* 11(1):9-20 (2003); Roberts et al., *Arch. Microbiol.* 117(1):99-108 (1978); Conrad et al., *J. Bacteriol.* 118(1);103-11 (1974)). The enoyl-CoA hydratases, *phaA* and *phaB*, of *P. putida* are believed to carry out the hydroxylation of double bonds during phenylacetate catabolism (Olivera et al., *Proc Natl Acad Sci USA* 95(11):6419-6424 (1998)). The *paaA* and *paaB* from *P. fluorescens* catalyze analogous transformations (Olivera et al., *supra*, 1998). Lastly, a number of *Escherichia coli* genes have been shown to demonstrate enoyl-CoA hydratase functionality including *maoC* (Park and Lee, *J. Bacteriol.* 185(18):5391-5397 (2003)), *paaF* (Park and Lee, *Biotechnol. Bioeng.* 86(6):681-686 (2004a)); Park and Lee, *Appl. Biochem. Biotechnol.* 113-116: 335-346 (2004b)); Ismail et al. *Eur. J. Biochem.* 270(14):3047-3054 (2003), and *paaG* (Park and Lee, *supra*, 2004; Park and Lee, *supra*, 2004b; Ismail et al., *supra*, 2003).

Gene	**GenBank Accession No.**	**GI No.**	**Organism**
crt	NP_349318.1	15895969	*Clostridium acetobutylicum*
crt1	YP_001393856	153953091	*Clostridium kluyveri DSM 555*
phaA	NP_745427.1	26990002	*Pseudomonas putida*
phaB	NP_745426.1	26990001	*Pseudomonas putida*
paaA	ABF82233.1	106636093	*Pseudomonas fluorescens*
paaB	ABF82234.1	106636094	*Pseudomonas fluorescens*
maoC	NP_415905.1	16129348	*Escherichia coli*
paaF	NP_415911.1	16129354	*Escherichia coli*
paaG	NP_415912.1	16129355	*Escherichia coli*

[0403] This example describes a biosynthesis pathway for 2-hydroxyisobutyrate or methacylic acid from 4-hydroxybutyryl-CoA.

EXAMPLE XV
Exemplary Hydrogenase and CO Dehydrogenase Enzymes for Extracting Reducing Equivalents from Syngas and Exemplary Reductive TCA Cycle Enzymes

[0404] Enzymes of the reductive TCA cycle useful in the non-naturally occurring microbial organisms of the present invention include one or more of ATP-citrate lyase and three CO_2-fixing enzymes: isocitrate dehydrogenase, alpha-ketoglutarate:ferredoxin oxidoreductase, pyruvate:ferredoxin oxidoreductase. The presence of ATP-citrate lyase or citrate lyase and alpha-ketoglutarate:ferredoxin oxidoreductase indicates the presence of an active reductive TCA cycle in an organism. Enzymes for each step of the reductive TCA cycle are shown below and described herein.

[0405] ATP-citrate lyase (ACL, EC 2.3.3.8), also called ATP citrate synthase, catalyzes the ATP-dependent cleavage of citrate to oxaloacetate and acetyl-CoA. ACL is an enzyme of the RTCA cycle that has been studied in green sulfur bacteria *Chlorobium limicola* and *Chlorobium tepidum*. The alpha(4)beta(4) heteromeric enzyme from *Chlorobium limicola* was cloned and characterized in *E. coli* (Kanao et al., *Eur. J. Biochem.* 269:3409-3416 (2002). The *C. limicola* enzyme, encoded by *aclAB*, is irreversible and activity of the enzyme is regulated by the ratio of ADP/ATP. A recombinant ACL from *Chlorobium tepidum* was also expressed in *E. coli* and the holoenzyme was reconstituted *in vitro*, in a study elucidating the role of the alpha and beta subunits in the catalytic mechanism (Kim and Tabita, *J. Bacteriol.* 188:6544-6552 (2006). ACL enzymes have also been identified in *Balnearium lithotrophicum*, *Sulfurihydrogenibium subterraneum* and other members of the bacterial phylum *Aquificae* (Hugler et al., *Environ. Microbiol.* 9:81-92 (2007)). This acitivy has been reported in some fungi as well. Exemplary organisms include *Sordaria macrospora (Nowrousian et al., Curr. Genet. 37:189-93 (2000), Aspergillus nidulans , Yarrowia lipolytica (Hynes and Murray, Eukaryotic Cell, July: 1039-1048, (2010)* and *Aspergillus niger (Meijer et al. J. Ind. Microbiol. Biotechnol. 36:1275-1280 (2009)*. Other candidates can be found based on sequence homology. Information related to these enzymes is tabulated below:

Protein	GenBank ID	GI Number	Organism
aclA	BAB21376.1	12407237	*Chlorobium limicola*
aclB	BAB21375.1	12407235	*Chlorobium limicola*
aclA	AAM72321.1	21647054	*Chlorobium tepidum*
aclB	AAM72322.1	21647055	*Chlorobium tepidum*
aclA	ABI50076.1	114054981	*Balnearium lithotrophicum*
aclB	*ABI*50075.1	114054980	*Balnearium lithotrophicum*
aclA	*ABI50085.1*	*114055*040	*Sulfurihydrogenibium subterraneum*
aclB	ABI50084.1	114055039	*Sulfurihydrogenibium subterraneum*
aclA	AAX76834.1	62199504	*Sulfurimonas denitrificans*
aclB	AAX76835.1	62199506	*Sulfurimonas denitrificans*
acl1	XP_504787.1	50554757	*Yarrowia lipolytica*
acl2	XP_503231.1	50551515	*Yarrowia lipolytica*
SPBC1703.07	NP_596202.1	19112994	*Schizosaccharomyces pombe*
SPAC22A12.16	NP_593246.1	19114158	*Schizosaccharomyces pombe*
acl1	CAB76165.1	7160185	*Sordaria macrospora*
acl2	CAB76164.1	7160184	*Sordaria macrospora*
aclA	CBF86850.1	259487849	*Aspergillus nidulans*
aclB	CBF86848	259487848	*Aspergillus nidulans*

[0406] In some organisms the conversion of citrate to oxaloacetate and acetyl-CoA proceeds through a citryl-CoA intermediate and is catalyzed by two separate enzymes, citryl-CoA synthetase (EC 6.2.1.18) and citryl-CoA lyase (EC 4.1.3.34) (Aoshima, M., *Appl. Microbiol. Biotechnol.* 75:249-255 (2007). Citryl-CoA synthetase catalyzes the activation of citrate to citryl-CoA. The *Hydrogenobacter thermophilus* enzyme is composed of large and small subunits encoded by *ccsA* and *ccsB*, respectively (Aoshima et al., *Mol. Micrbiol.* 52:751-761 (2004)). The citryl-CoA synthetase of *Aquifex aeolicus* is composed of alpha and beta subunits encoded by *sucC1* and *sucD1* (Hugler et al., *Environ. Microbiol.* 9:81-92 (2007)). Citryl-CoA lyase splits citryl-CoA into oxaloacetate and acetyl-CoA. This enzyme is a homotrimer encoded by *ccl* in *Hydrogenobacter thermophilus* (Aoshima et al., *Mol. Microbiol.* 52:763-770 (2004)) and *aq_150* in *Aquifex aeolicus* (Hugler et al., *supra* (2007)). The genes for this mechanism of converting citrate to oxaloacetate and citryl-CoA have also been reported recently in *Chlorobium tepidum* (Eisen et al., PNAS 99(14): 9509-14 (2002).

Protein	GenBank ID	GI Number	Organism
ccsA	BAD17844.1	46849514	*Hydrogenobacter thermophilus*
ccsB	BAD17846.1	46849517	*Hydrogenobacter thermophilus*
sucC1	AAC07285	2983723	*Aquifex aeolicus*
sucD1	AAC07686	2984152	*Aquifex aeolicus*
ccl	BAD17841.1	46849510	*Hydrogenobacter thermophilus*
aq_150	AAC06486	2982866	*Aquifex aeolicus*
CT0380	NP_661284	21673219	*Chlorobium tepidum*
CT0269	NP_661173.1	21673108	*Chlorobium tepidum*
CT1834	AAM73055.1	21647851	*Chlorobium tepidum*

[0407] Oxaloacetate is converted into malate by malate dehydrogenase (EC 1.1.1.37), an enzyme which functions in both the forward and reverse direction. *S. cerevisiae* possesses three copies of malate dehydrogenase, *MDH1* (McAlister-Henn and Thompson, *J. Bacteriol.* 169:5157-5166 (1987), *MDH2* (Minard and McAlister-Henn, *Mol. Cell. Biol.* 11:370-380 (1991); Gibson and McAlister-Henn, *J. Biol. Chem.* 278:25628-25636 (2003)), and *MDH3* (Steffan and McAlister-Henn, *J. Biol. Chem.* 267:24708-24715 (1992)), which localize to the mitochondrion, cytosol, and peroxisome, respectively. *E. coli* is known to have an active malate dehydrogenase encoded by *mdh*.

Protein	GenBank ID	GI Number	Organism
MDH1	NP_012838	6322765	*Saccharomyces cerevisiae*
MDH2	NP_014515	116006499	*Saccharomyces cerevisiae*
MDH3	NP_010205	6320125	*Saccharomyces cerevisiae*
Mdh	NP_417703.1	16131126	*Escherichia coli*

[0408] Fumarate hydratase (EC 4.2.1.2) catalyzes the reversible hydration of fumarate to malate. The three fumarases of *E. coli,* encoded by *fumA*, *fumB* and *fumC*, are regulated under different conditions of oxygen availability. FumB is oxygen sensitive and is active under anaerobic conditions. FumA is active under microanaerobic conditions, and FumC is active under aerobic growth conditions (Tseng et al., *J. Bacteriol.* 183:461-467 (2001);Woods et al., *Biochim. Biophys. Acta* 954:14-26 (1988); Guest et al., *J. Gen. Microbiol.* 131:2971-2984 (1985)). *S. cerevisiae* contains one copy of a fumarase-encoding

gene, *FUM1*, whose product localizes to both the cytosol and mitochondrion (Sass et al., *J. Biol. Chem.* 278:45109-45116 (2003)). Additional fumarase enzymes are found in *Campylobacter jejuni* (Smith et al., *Int. J. Biochem. Cell. Biol.* 31:961-975 (1999)), *Thermus thermophilus* (Mizobata et al., *Arch. Biochem. Biophys.* 355:49-55 (1998)) and *Rattus norvegicus* (Kobayashi et al., *J. Biochem.* 89:1923-1931 (1981)). Similar enzymes with high sequence homology include *fum1* from *Arabidopsis thaliana* and *fumC* from *Corynebacterium glutamicum*. The *MmcBC* fumarase from *Pelotomaculum thermopropionicum* is another class of fumarase with two subunits (Shimoyama et al., *FEMS Microbiol. Lett.* 270:207-213 (2007)).

Protein	GenBank ID	GI Number	Organism
fumA	NP_416129.1	16129570	*Escherichia coli*
fumB	NP_418546.1	16131948	*Escherichia coli*
fumC	NP_416128.1	16129569	*Escherichia coli*
FUM1	NP_015061	6324993	*Saccharomyces cerevisiae*
fumC	Q8NRN8.1	39931596	*Corynebacterium glutamicum*
fumC	O69294.1	9789756	*Campylobacter jejuni*
fumC	P84127	75427690	*Thermus thermophilus*
fumH	P14408.1	120605	*Rattus norvegicus*
MmcB	YP_001211906	147677691	*Pelotomaculum thermopropionicum*
MmcC	YP_001211907	147677692	*Pelotomaculum thermopropionicum*

[0409] Fumarate reductase catalyzes the reduction of fumarate to succinate. The fumarate reductase of *E. coli*, composed of four subunits encoded by *frdABCD,* is membrane-bound and active under anaerobic conditions. The electron donor for this reaction is menaquinone and the two protons produced in this reaction do not contribute to the proton gradient (Iverson et al., *Science* 284:1961-1966 (1999)). The yeast genome encodes two soluble fumarate reductase isozymes encoded by FRDS1 (Enomoto et al., *DNA Res.* 3:263-267 (1996)) and FRDS2 (Muratsubaki et al., *Arch. Biochem. Biophys.* 352:175-181 (1998)), which localize to the cytosol and promitochondrion, respectively, and are used during anaerobic growth on glucose (Arikawa et al., *FEMS Microbiol. Lett.* 165:111-116 (1998)).

Protein	GenBank ID	GI Number	Organism

Protein	GenBank ID	GI Number	Organism
FRDS1	P32614	418423	*Saccharomyces cerevisiae*
FRDS2	NP_012585	6322511	*Saccharomyces cerevisiae*
frdA	NP_418578.1	16131979	*Escherichia coli*
frdB	NP_418577.1	16131978	*Escherichia coli*
frdC	NP_418576.1	16131977	*Escherichia coli*
frdD	NP_418475.1	16131877	*Escherichia coli*

[0410] The ATP-dependent acylation of succinate to succinyl-CoA is catalyzed by succinyl-CoA synthetase (EC 6.2.1.5). The product of the *LSC1* and *LSC2* genes of *S. cerevisiae* and the *sucC* and *sucD* genes of *E. coli* naturally form a succinyl-CoA synthetase complex that catalyzes the formation of succinyl-CoA from succinate with the concomitant consumption of one ATP, a reaction which is reversible *in vivo* (Buck et al., *Biochemistry* 24:6245-6252 (1985)). These proteins are identified below:

Protein	GenBank ID	GI Number	Organism
LSC1	NP_014785	6324716	*Saccharomyces cerevisiae*
LSC2	NP_011760	6321683	*Saccharomyces cerevisiae*
sucC	NP_415256.1	16128703	*Escherichia coli*
sucD	AAC73823.1	1786949	*Escherichia coli*

[0411] Alpha-ketoglutarate:ferredoxin oxidoreductase (EC 1.2.7.3), also known as 2-oxoglutarate synthase or 2-oxoglutarate:ferredoxin oxidoreductase (OFOR), forms alpha-ketoglutarate from CO2 and succinyl-CoA with concurrent consumption of two reduced ferredoxin equivalents. OFOR and pyruvate:ferredoxin oxidoreductase (PFOR) are members of a diverse family of 2-oxoacid:ferredoxin (flavodoxin) oxidoreductases which utilize thiamine pyrophosphate, CoA and iron-sulfur clusters as cofactors and ferredoxin, flavodoxin and FAD as electron carriers *(Adams et al., Archaea. Adv. Protein Chem. 48:101-180 (1996))*. Enzymes in this class are reversible and function in the carboxylation direction in organisms that fix carbon by the RTCA cycle such as *Hydrogenobacter thermophilus*, *Desulfobacter hydrogenophilus* and *Chlorobium species* (Shiba et al. 1985; Evans et al., Proc. Natl. Acad. Scl. U.S.A. 55:92934 (1966); Buchanan, 1971). The two-subunit enzyme from *H. thermophilus*, encoded by *korAB*, has been cloned and expressed in *E. coli* (Yun et al., Biochem. Biophys. Res. Commun. 282:589-594 (2001)). A five subunit OFOR from the

same organism with strict substrate specificity for succinyl-CoA, encoded by *forDABGE*, was recently identified and expressed in *E. coli* (Yun et al. 2002). The kinetics of CO2 fixation of both *H. thermophilus* OFOR enzymes have been characterized (Yamamoto et al., Extremophiles 14:79-85 (2010)). A CO2-fixing OFOR from *Chlorobium thiosulfatophilum* has been purified and characterized but the genes encoding this enzyme have not been identified to date. Enzyme candidates in *Chlorobium* species can be inferred by sequence similarity to the *H. thermophilus* genes. For example, the *Chlorobium limicola* genome encodes two similar proteins. Acetogenic bacteria such as *Moorella thermoacetica* are predicted to encode two OFOR enzymes. The enzyme encoded by *Moth_0034* is predicted to function in the CO2-assimilating direction. The genes associated with this enzyme, *Moth_0034* have not been experimentally validated to date but can be inferred by sequence similarity to known OFOR enzymes.

[0412] OFOR enzymes that function in the decarboxylation direction under physiological conditions can also catalyze the reverse reaction. The OFOR from the thermoacidophilic archaeon *Sulfolobus* sp. strain 7, encoded by ST2300, has been extensively studied (Zhang et al. 1996. A plasmid-based expression system has been developed for efficiently expressing this protein in *E. coli* (Fukuda et al., Eur. J. Biochem. 268:5639-5646 (2001)) and residues involved in substrate specificity were determined (Fukuda and Wakagi, Biochim. Biophys. Acta 1597:74-80 (2002)). The OFOR encoded by *Ape1472/Ape1473* from *Aeropyrum pernix* str. K1 was recently cloned into *E. coli*, characterized, and found to react with 2-oxoglutarate and a broad range of 2-oxoacids (Nishizawa et al., FEBS Lett. 579:2319-2322 (2005)). Another exemplary OFOR is encoded by *oorDABC* in *Helicobacter pylori* (Hughes et al. 1998). An enzyme specific to alpha-ketoglutarate has been reported in *Thauera aromatica* (Dorner and Boll, J, Bacteriol. 184 (14), 3975-83 (2002). A similar enzyme can be found in *Rhodospirillum rubrum* by sequence homology. A two subunit enzyme has also been identified in *Chlorobium tepidum* (Eisen et al., PNAS 99(14): 9509-14 (2002)).

Protein	GenBank ID	GI Number	Organism
korA	BAB21494	12583691	*Hydrogenobacter thermophilus*
korB	BAB21495	12583692	*Hydrogenobacter thermophilus*
forD	BAB62132.1	14970994	*Hydrogenobacter thermophilus*
forA	BAB62133.1	14970995	*Hydrogenobacter thermophilus*
forB	BAB62134.1	14970996	*Hydrogenobacter thermophilus*

forG	BAB62135.1	14970997	*Hydrogenobacter thermophilus*
forE	BAB62136.1	14970998	*Hydrogenobacter thermophilus*
Clim_0204	ACD89303.1	189339900	*Chlorobium limicola*
Clim_0205	ACD89302.1	189339899	*Chlorobium limicola*
Clim_1123	ACD90192.1	189340789	*Chlorobium limicola*
Clim_1124	ACD90193.1	189340790	*Chlorobium limicola*
Moth_1984	YP_430825.1	83590816	*Moorella thermoacetica*
Moth_1985	YP_430826.1	83590817	*Moorella thermoacetica*
Moth_0034	YP_428917.1	83588908	*Moorella thermoacetica*
ST2300	NP_378302.1	15922633	*Sulfolobus* sp. strain 7
Ape1472	BAA80470.1	5105156	*Aeropyrum pernix*
Ape1473	BAA80471.2	116062794	*Aeropyrum pernix*
oorD	NP_207383.1	15645213	*Helicobacter pylori*
oorA	NP_207384.1	15645214	*Helicobacter pylori*
oorB	NP_207385.1	15645215	*Helicobacter pylori*
oorC	NP_207386.1	15645216	*Helicobacter pylori*
CT0163	NP_661069.1	21673004	*Chlorobium tepidum*
CT0162	NP_661068.1	21673003	*Chlorobium tepidum*
korA	CAA12243.2	19571179	*Thauera aromatica*
korB	CAD27440.1	19571178	*Thauera aromatica*
Rru_A2721	YP_427805.1	83594053	*Rhodospirillum rubrum*
Rru_A2722	YP_427806.1	83594054	*Rhodospirillum rubrum*

[0413] Isocitrate dehydrogenase catalyzes the reversible decarboxylation of isocitrate to 2-oxoglutarate coupled to the reduction of $NAD(P)^+$. IDH enzymes in *Saccharomyces cerevisiae* and *Escherichia coli* are encoded by *IDP1* and *icd*, respectively (Haselbeck and McAlister-Henn, *J. Biol. Chem.* 266:2339-2345 (1991); Nimmo, H.G., *Biochem. J.* 234:317-2332 (1986)). The reverse reaction in the reductive TCA cycle, the reductive carboxylation of 2-oxoglutarate to isocitrate, is favored by the NADPH-dependent CO_2-fixing IDH from *Chlorobium limicola* and was functionally expressed in *E. coli* (Kanao et al., *Eur. J. Biochem.* 269:1926-1931 (2002)). A similar enzyme with 95% sequence identity is found in the *C. tepidum* genome in addititon to some other candidates listed below.

Protein	GenBank ID	GI Number	Organism
Icd	ACI84720.1	209772816	*Escherichia coli*
IDP1	AAA34703.1	171749	*Saccharomyces cerevisiae*
Idh	BAC00856.1	21396513	*Chlorobium limicola*
Icd	AAM71597.1	21646271	*Chlorobium tepidum*
icd	NP_952516.1	39996565	*Geobacter sulfurreducens*
icd	YP_393560.	78777245	*Sulfurimonas denitrificans*

[0414] In *H. thermophilus* the reductive carboxylation of 2-oxoglutarate to isocitrate is catalyzed by two enzymes: 2-oxoglutarate carboxylase and oxalosuccinate reductase. 2-Oxoglutarate carboxylase (EC 6.4.1.7) catalyzes the ATP-dependent carboxylation of alpha-ketoglutarate to oxalosuccinate (Aoshima and Igarashi, *Mol. Microbiol*. 62:748-759 (2006)). This enzyme is a large complex composed of two subunits. Biotinylation of the large (A) subunit is required for enzyme function (Aoshima et al., *Mol. Microbiol.* 51:791-798 (2004)). Oxalosuccinate reductase (EC 1.1.1.-) catalyzes the NAD-dependent conversion of oxalosuccinate to D-*threo*-isocitrate. The enzyme is a homodimer encoded by *icd* in *H. thermophilus*. The kinetic parameters of this enzyme indicate that the enzyme only operates in the reductive carboxylation direction *in vivo,* in contrast to isocitrate dehydrogenase enzymes in other organisms (Aoshima and Igarashi, *J. Bacteriol.* 190:2050-2055 (2008)). Based on sequence homology, gene candidates have also been found in *Thiobacillus denitrificans* and *Thermocrinis albus.*

Protein	GenBank ID	GI Number	Organism
cfiA	BAF34932.1	116234991	*Hydrogenobacter thermophilus*
cifB	BAF34931.1	116234990	*Hydrogenobacter thermophilus*
Icd	BAD02487.1	38602676	*Hydrogenobacter thermophilus*
Tbd_1556	YP_315314	74317574	*Thiobacillus denitrificans*
Tbd_1555	YP_315313	74317573	*Thiobacillus denitrificans*
Tbd_0854	YP_314612	74316872	*Thiobacillus denitrificans*
Thal_0268	YP_003473030	289548042	*Thermocrinis albus*
Thal_0267	YP_003473029	289548041	*Thermocrinis albus*
Thal_0646	YP_003473406	289548418	*Thermocrinis albus*

[0415] Aconitase (EC 4.2.1.3) is an iron-sulfur-containing protein catalyzing the reversible isomerization of citrate and iso-citrate via the intermediate *cis*-aconitate. Two

aconitase enzymes are encoded in the *E. coli* genome by *acnA* and *acnB*. AcnB is the main catabolic enzyme, while AcnA is more stable and appears to be active under conditions of oxidative or acid stress (Cunningham et al., *Microbiology* 143 (Pt 12):3795-3805 (1997)). Two isozymes of aconitase in *Salmonella typhimurium* are encoded by *acnA* and *acnB* (Horswill and Escalante-Semerena, *Biochemistry* 40:4703-4713 (2001)). The *S. cerevisiae* aconitase, encoded by *ACO1*, is localized to the mitochondria where it participates in the TCA cycle (Gangloff et al., *Mol. Cell. Biol.* 10:3551-3561 (1990)) and the cytosol where it participates in the glyoxylate shunt (Regev-Rudzki et al., *Mol. Biol. Cell.* 16:4163-4171 (2005)).

Protein	GenBank ID	GI Number	Organism
acnA	AAC7438.1	1787531	*Escherichia coli*
acnB	AAC73229.1	2367097	*Escherichia coli*
acnA	NP_460671.1	16765056	*Salmonella typhimurium*
acnB	NP_459163.1	16763548	*Salmonella typhimurium*
ACO1	AAA34389.1	170982	*Saccharomyces cerevisiae*
HP0779	NP_207572.1	15645398	*Helicobacter pylori 26695*
H16_B0568	CAJ95365.1	113529018	*Ralstonia eutropha*
DesfrDRAFT_3783	ZP_07335307.1	303249064	*Desulfovibrio fructosovorans JJ*
Suden_1040 (acnB)	ABB44318.1	78497778	*Sulfurimonas denitrificans*
Hydth_0755	ADO45152.1	308751669	*Hydrogenobacter thermophilus*
CT0543 (acn)	AAM71785.1	21646475	*Chlorobium tepidum*
Clim_2436	YP_001944436.1	189347907	*Chlorobium limicola*
Clim_0515	ACD89607.1	189340204	*Chlorobium limicola*

[0416] Pyruvate:ferredoxin oxidoreductase (PFOR) catalyzes the reversible oxidation of pyruvate to form acetyl-CoA. The PFOR from *Desulfovibrio africanus* has been cloned and expressed in *E. coli* resulting in an active recombinant enzyme that was stable for several days in the presence of oxygen (Pieulle et al., *J. Bacteriol.* 179:5684-5692 (1997)). Oxygen stability is relatively uncommon in PFORs and is believed to be conferred by a 60 residue extension in the polypeptide chain of the *D. africanus* enzyme. Two cysteine residues in this enzyme form a disulfide bond that prtotects it against inactivation in the form of oxygen. This disulfide bond and the stability in the presence of oxygen has been found in other

Desulfovibrio species also (Vita et al., Biochemistry, 47: 957-64 (2008)). The *M. thermoacetica* PFOR is also well characterized (Menon and Ragsdale, *Biochemistry* 36:8484-8494 (1997)) and was shown to have high activity in the direction of pyruvate synthesis during autotrophic growth (Furdui and Ragsdale, *J. Biol. Chem.* 275:28494-28499 (2000)). Further, *E. coli* possesses an uncharacterized open reading frame, *ydbK*, encoding a protein that is 51% identical to the *M. thermoacetica* PFOR. Evidence for pyruvate oxidoreductase activity in *E. coli* has been described (Blaschkowski et al., *Eur. J. Biochem.* 123:563-569 (1982)). PFORs have also been described in other organisms, including *Rhodobacter capsulatas* (Yakunin and Hallenbeck, Biochimica et Biophysica Acta 1409 (1998) 39-49 (1998)) and *Choloboum tepidum* (Eisen et al., PNAS 99(14): 9509-14 (2002)). The five subunit PFOR from *H. thermophilus*, encoded by *porEDABG*, was cloned into *E. coli* and shown to function in both the decarboxylating and CO_2-assimilating directions (Ikeda et al. 2006; Yamamoto et al., *Extremophiles* 14:79-85 (2010)). Homologs also exist in *C. carboxidivorans P7*. Several additional PFOR enzymes are described in the following review (Ragsdale, S.W., *Chem. Rev.* 103:2333-2346 (2003)). Finally, flavodoxin reductases (e.g., *fqrB* from *Helicobacter pylori* or *Campylobacter jejuni*) (St Maurice et al., *J. Bacteriol.* 189:4764-4773 (2007)) or Rnf-type proteins (Seedorf et al., *Proc. Natl. Acad. Sci. U.S.A.* 105:2128-2133 (2008); and Herrmann, *J. Bacteriol* 190:784-791 (2008)) provide a means to generate NADH or NADPH from the reduced ferredoxin generated by PFOR. These proteins are identified below.

Protein	GenBank ID	GI Number	Organism
DesfrDRAFT_0121	ZP_07331646.1	303245362	*Desulfovibrio fructosovorans JJ*
Por	CAA70873.1	1770208	*Desulfovibrio africanus*
por	YP_012236.1	46581428	*Desulfovibrio vulgaris str. Hildenborough*
Dde_3237	ABB40031.1	78220682	*DesulfoVibrio desulfuricans G20*
Ddes_0298	YP_002478891.1	220903579	*Desulfovibrio desulfuricans subsp. desulfuricans str. ATCC 27774*
Por	YP_428946.1	83588937	*Moorella thermoacetica*
YdbK	NP_415896.1	16129339	*Escherichia coli*

nifJ (CT1628)	NP_662511.1	21674446	*Chlorobium tepidum*
CJE1649	YP_179630.1	57238499	*Campylobacter jejuni*
nifJ	ADE85473.1	294476085	*Rhodobacter capsulatus*
porE	BAA95603.1	7768912	*Hydrogenobacter thermophilus*
porD	BAA95604.1	7768913	*Hydrogenobacter thermophilus*
porA	BAA95605.1	7768914	*Hydrogenobacter thermophilus*
porB	BAA95606.1	776891	*Hydrogenobacter thermophilus*
porG	BAA95607.1	7768916	*Hydrogenobacter thermophilus*
FqrB	YP_001482096.1	157414840	*Campylobacter jejuni*
HP1164	NP_207955.1	15645778	*Helicobacter pylori*
RnfC	EDK33306.1	146346770	*Clostridium kluyveri*
RnfD	EDK33307.1	146346771	*Clostridium kluyveri*
RnfG	EDK33308.1	146346772	*Clostridium kluyveri*
RnfE	EDK33309.1	146346773	*Clostridium kluyveri*
RnfA	EDK33310.1	146346774	*Clostridium kluyveri*
RnfB	EDK33311.1	146346775	*Clostridium kluyveri*

[0417] The conversion of pyruvate into acetyl-CoA can be catalyzed by several other enzymes or their combinations thereof. For example, pyruvate dehydrogenase can transform pyruvate into acetyl-CoA with the concomitant reduction of a molecule of NAD into NADH. It is a multi-enzyme complex that catalyzes a series of partial reactions which results in acylating oxidative decarboxylation of pyruvate. The enzyme comprises of three subunits: the pyruvate decarboxylase (E1), dihydrolipoamide acyltransferase (E2) and dihydrolipoamide dehydrogenase (E3). This enzyme is naturally present in several organisms, including *E. coli* and *S. cerevisiae*. In the *E. coli* enzyme, specific residues in the E1 component are responsible for substrate specificity (Bisswanger, H., J. Biol. Chem. 256:815-82 (1981); Bremer, J., Eur. J. Biochem. 8:535-540 (1969); Gong et al., J. Biol. Chem. 275:13645-13653 (2000)). Enzyme engineering efforts have improved the *E. coli* PDH enzyme activity under anaerobic conditions (Kim et al., J. Bacteriol. 190:3851-3858 (2008); Kim et al., Appl.

Environ. Microbiol. 73:1766-1771 (2007); Zhou et al., Biotechnol. Lett. 30:335-342 (2008)). In contrast to the *E. coli* PDH, the *B. subtilis* complex is active and required for growth under anaerobic conditions (Nakano et al., J. Bacteriol. 179:6749-6755 (1997)). The *Klebsiella pneumoniae* PDH, characterized during growth on glycerol, is also active under anaerobic conditions (5). Crystal structures of the enzyme complex from bovine kidney (18) and the E2 catalytic domain from *Azotobacter vinelandii* are available (4). Yet another enzyme that can catalyze this conversion is pyruvate formate lyase. This enzyme catalyzes the conversion of pyruvate and CoA into acetyl-CoA and formate. Pyruvate formate lyase is a common enzyme in prokaryotic organisms that is used to help modulate anaerobic redox balance. Exemplary enzymes can be found in *Escherichia coli* encoded by *pflB* (Knappe and Sawers, FEMS.Microbiol Rev. 6:383-398 (1990)), *Lactococcus lactis* (Melchiorsen et al., Appl Microbiol Biotechnol 58:338-344 (2002)), and *Streptococcus mutans* (Takahashi-Abbe et al., Oral.Microbiol Immunol. 18:293-297 (2003)). *E. coli* possesses an additional pyruvate formate lyase, encoded by *tdcE*, that catalyzes the conversion of pyruvate or 2-oxobutanoate to acetyl-CoA or propionyl-CoA, respectively (Hesslinger et al., Mol. Microbiol 27:477-492 (1998)). Both *pflB* and *tdcE* from *E. coli* require the presence of pyruvate formate lyase activating enzyme, encoded by *pflA*. Further, a short protein encoded by *yfiD* in *E. coli* can associate with and restore activity to oxygen-cleaved pyruvate formate lyase (Vey et al., Proc.Natl. Acad. Sci. U.S.A. 105:16137-16141 (2008). Note that *pflA* and *pflB* from *E. coli* were expressed in *S. cerevisiae* as a means to increase cytosolic acetyl-CoA for butanol production as described in WO/2008/080124]. Additional pyruvate formate lyase and activating enzyme candidates, encoded by *pfl* and *act*, respectively, are found in *Clostridium pasteurianum* (Weidner et al., J Bacteriol. 178:2440-2444 (1996)).

[0418] Further, different enzymes can be used in combination to convert pyruvate into acetyl-CoA. For example, in *S. cerevisiae*, acetyl-CoA is obtained in the cytosol by first decarboxylating pyruvate to form acetaldehyde; the latter is oxidized to acetate by acetaldehyde dehydrogenase and subsequently activated to form acetyl-CoA by acetyl-CoA synthetase. Acetyl-CoA synthetase is a native enzyme in several other organisms including *E. coli* (Kumari et al., J. Bacteriol. 177:2878-2886 (1995)), *Salmonella enterica* (Starai et al., Microbiology 151:3793-3801 (2005); Starai et al., J. Biol. Chem. 280:26200-26205 (2005)), and *Moorella thermoacetica* (described already). Alternatively, acetate can be activated to form acetyl-CoA by acetate kinase and phosphotransacetylase. Acetate kinase first converts acetate into acetyl-phosphate with the accompanying use of an ATP molecule. Acetyl-

phosphate and CoA are next converted into acetyl-CoA with the release of one phosphate by phosphotransacetylase. Both acetate kinase and phosphotransacetlyase are well-studied enzymes in several *Clostridia* and *Methanosarcina thermophila.*

[0419] Yet another way of converting pyruvate to acetyl-CoA is via pyruvate oxidase. Pyruvate oxidase converts pyruvate into acetate, using ubiquione as the electron acceptor. In *E. coli*, this activity is encoded by *poxB*. *PoxB* has similarity to pyruvate decarboxylase of *S. cerevisiae* and *Zymomonas mobilis*. The enzyme has a thiamin pyrophosphate cofactor (Koland and Gennis, Biochemistry 21:4438-4442 (1982)); O'Brien et al., Biochemistry 16:3105-3109 (1977); O'Brien and Gennis, J. Biol. Chem. 255:3302-3307 (1980)) and a flavin adenine dinucleotide (FAD) cofactor. Acetate can then be converted into acetyl-CoA by either acetyl-CoA synthetase or by acetate kinase and phosphotransacetylase, as described earlier. Some of these enzymes can also catalyze the reverse reaction from acetyl-CoA to pyruvate.

[0420] For enzymes that use reducing equivalents in the form of NADH or NADPH, these reduced carriers can be generated by transferring electrons from reduced ferredoxin. Two enzymes catalyze the reversible transfer of electrons from reduced ferredoxins to $NAD(P)^+$, ferredoxin:NAD^+ oxidoreductase (EC 1.18.1.3) and ferredoxin:$NADP^+$ oxidoreductase (FNR, EC 1.18.1.2). Ferredoxin:$NADP^+$ oxidoreductase (FNR, EC 1.18.1.2) has a noncovalently bound FAD cofactor that facilitates the reversible transfer of electrons from NADPH to low-potential acceptors such as ferredoxins or flavodoxins (Blaschkowski et al., *Eur. J. Biochem.* 123:563-569 (1982); Fujii et al., 1977). The *Helicobacter pylori* FNR, encoded by *HP1164 (fqrB)*, is coupled to the activity of pyruvate:ferredoxin oxidoreductase (PFOR) resulting in the pyruvate-dependent production of NADPH (St et al. 2007). An analogous enzyme is found in *Campylobacter jejuni* (St et al. 2007). A ferredoxin:$NADP^+$ oxidoreductase enzyme is encoded in the *E. coli* genome by *fpr* (Bianchi et al. 1993). Ferredoxin:NAD^+ oxidoreductase utilizes reduced ferredoxin to generate NADH from NAD^+. In several organisms, including *E. coli*, this enzyme is a component of multifunctional dioxygenase enzyme complexes. The ferredoxin:NAD^+ oxidoreductase of *E. coli*, encoded by *hcaD,* is a component of the 3-phenylproppionate dioxygenase system involved in involved in aromatic acid utilization (Diaz et al. 1998). NADH:ferredoxin reductase activity was detected in cell extracts of *Hydrogenobacter thermophilus* strain TK-6, although a gene with this activity has not yet been indicated (Yoon et al. 2006). Finally, the energy-

conserving membrane-associated Rnf-type proteins (Seedorf et al., Proc. Natl. Acad. Sci. U.S.A. 105:2128-2133 (2008); Herrmann et al., *J. Bacteriol.* 190:784-791 (2008)) provide a means to generate NADH or NADPH from reduced ferredoxin. Additional ferredoxin:NAD(P)+ oxidoreductases have been annotated in *Clostridium carboxydivorans* P7.

Protein	GenBank ID	GI Number	Organism
HP1164	NP_207955.1	15645778	*Helicobacter pylori*
RPA3954	CAE29395.1	39650872	*Rhodopseudomonas palustris*
fpr	BAH29712.1	225320633	*Hydrogenobacter thermophilus*
yumC	NP_391091.2	255767736	*Bacillus subtilis*
CJE0663	AAW35824.1	57167045	*Campylobacter jejuni*
fpr	P28861.4	399486	*Escherichia coli*
hcaD	AAC75595.1	1788892	*Escherichia coli*
LOC100282643	NP_001149023.1	226497434	*Zea mays*
RnfC	EDK33306.1	146346770	*Clostridium kluyveri*
RnfD	EDK33307.1	146346771	*Clostridium kluyveri*
RnfG	EDK33308.1	146346772	*Clostridium kluyveri*
RnfE	EDK33309.1	146346773	*Clostridium kluyveri*
RnfA	EDK33310.1	146346774	*Clostridium kluyveri*
RnfB	EDK33311.1	146346775	*Clostridium kluyveri*
CcarbDRAFT_2639	ZP_05392639.1	255525707	*Clostridium carboxidivorans P7*
CcarbDRAFT_2638	ZP_05392638.1	255525706	*Clostridium carboxidivorans P7*
CcarbDRAFT_2636	ZP_05392636.1	255525704	*Clostridium carboxidivorans P7*
CcarbDRAFT_5060	ZP_05395060.1	255528241	*Clostridium carboxidivorans P7*
CcarbDRAFT_2450	ZP_05392450.1	255525514	*Clostridium carboxidivorans P7*
CcarbDRAFT_1084	ZP_05391084.1	255524124	*Clostridium carboxidivorans P7*

[0421] Ferredoxins are small acidic proteins containing one or more iron-sulfur clusters that function as intracellular electron carriers with a low reduction potential. Reduced

ferredoxins donate electrons to Fe-dependent enzymes such as ferredoxin-$NADP^+$ oxidoreductase, pyruvate:ferredoxin oxidoreductase (PFOR) and 2-oxoglutarate:ferredoxin oxidoreductase (OFOR). The *H. thermophilus* gene *fdx1* encodes a [4Fe-4S]-type ferredoxin that is required for the reversible carboxylation of 2-oxoglutarate and pyruvate by OFOR and PFOR, respectively (Yamamoto et al., *Extremophiles* 14:79-85 (2010)). The ferredoxin associated with the *Sulfolobus solfataricus* 2-oxoacid:ferredoxin reductase is a monomeric dicluster [3Fe-4S][4Fe-4S] type ferredoxin (Park et al. 2006). While the gene associated with this protein has not been fully sequenced, the N-terminal domain shares 93% homology with the *zfx* ferredoxin from *S. acidocaldarius*. The *E. coli* genome encodes a soluble ferredoxin of unknown physiological function, *fdx*. Some evidence indicates that this protein can function in iron-sulfur cluster assembly (Takahashi and Nakamura, 1999). Additional ferredoxin proteins have been characterized in *Helicobacter pylori* (Mukhopadhyay et al. 2003) and *Campylobacter jejuni* (van Vliet et al. 2001). A 2Fe-2S ferredoxin from *Clostridium pasteurianum* has been cloned and expressed in *E. coli* (Fujinaga and Meyer, Biochemical and Biophysical Research Communications, 192(3): (1993)). Acetogenic bacteria such as *Moorella thermoacetica*, *Clostridium carboxidivorans P7* and *Rhodospirillum rubrum* are predicted to encode several ferredoxins, listed below.

Protein	**GenBank ID**	**GI Number**	**Organism**
fdx1	BAE02673.1	68163284	*Hydrogenobacter thermophilus*
M11214.1	AAA83524.1	144806	*Clostridium pasteurianum*
Zfx	AAY79867.1	68566938	*Sulfolobus acidocalarius*
Fdx	AAC75578.1	1788874	*Escherichia coli*
hp_0277	AAD07340.1	2313367	*Helicobacter pylori*
fdxA	CAL34484.1	112359698	*Campylobacter jejuni*
Moth_0061	ABC18400.1	83571848	*Moorella thermoacetica*
Moth_1200	ABC19514.1	83572962	*Moorella thermoacetica*
Moth_1888	ABC20188.1	83573636	*Moorella thermoacetica*
Moth_2112	ABC20404.1	83573852	*Moorella thermoacetica*
Moth_1037	ABC19351.1	83572799	*Moorella thermoacetica*
CcarbDRAFT_4383	ZP_05394383.1	255527515	*Clostridium carboxidivorans P7*
CcarbDRAFT_2958	ZP_05392958.1	255526034	*Clostridium carboxidivorans P7*
CcarbDRAFT_2281	ZP_05392281.1	255525342	*Clostridium carboxidivorans P7*
CcarbDRAFT_5296	ZP_05395295.1	255528511	*Clostridium carboxidivorans P7*

CcarbDRAFT_1615	ZP_05391615.1	255524662	*Clostridium carboxidivorans P7*
CcarbDRAFT_1304	ZP_05391304.1	255524347	*Clostridium carboxidivorans P7*
cooF	AAG29808.1	11095245	*Carboxydothermus hydrogenoformans*
fdxN	CAA35699.1	46143	*Rhodobacter capsulatus*
Rru_A2264	ABC23064.1	83576513	*Rhodospirillum rubrum*
Rru_A1916	ABC22716.1	83576165	*Rhodospirillum rubrum*
Rru_A2026	ABC22826.1	83576275	*Rhodospirillum rubrum*
cooF	AAC45122.1	1498747	*Rhodospirillum rubrum*
fdxN	AAA26460.1	152605	*Rhodospirillum rubrum*
Alvin_2884	ADC63789.1	288897953	*Allochromatium vinosum DSM 180*
fdx	YP_002801146.1	226946073	*Azotobacter vinelandii DJ*
CKL_3790	YP_001397146.1	153956381	*Clostridium kluyveri DSM 555*
fer1	NP_949965.1	39937689	*Rhodopseudomonas palustris CGA009*
fdx	CAA12251.1	3724172	*Thauera aromatica*
CHY_2405	YP_361202.1	78044690	*Carboxydothermus hydrogenoformans*
fer	YP_359966.1	78045103	*Carboxydothermus hydrogenoformans*
fer	AAC83945.1	1146198	*Bacillus subtilis*
fdx1	NP_249053.1	15595559	*Pseudomonas aeruginosa PA01*
yfhL	AP_003148.1	89109368	*Escherichia coli K-12*

[0422] Succinyl-CoA transferase catalyzes the conversion of succinyl-CoA to succinate while transferring the CoA moiety to a CoA acceptor molecule. Many transferases have broad specificity and can utilize CoA acceptors as diverse as acetate, succinate, propionate, butyrate, 2-methylacetoacetate, 3-ketohexanoate, 3-ketopentanoate, valerate, crotonate, 3-mercaptopropionate, propionate, vinylacetate, and butyrate, among others.

[0423] The conversion of succinate to succinyl-CoA can be carried by a transferase which does not require the direct consumption of an ATP or GTP. This type of reaction is common in a number of organisms. The conversion of succinate to succinyl-CoA can also be catalyzed by succinyl-CoA:Acetyl-CoA transferase. The gene product of *cat1* of *Clostridium kluyveri* has been shown to exhibit succinyl-CoA: acetyl-CoA transferase activity (Sohling

and Gottschalk, J. Bacteriol. 178:871-880 (1996)). In addition, the activity is present in *Trichomonas vaginalis* (van Grinsven et al. 2008) and *Trypanosoma brucei* (Riviere et al. 2004). The succinyl-CoA:acetate CoA-transferase from *Acetobacter aceti*, encoded by *aarC*, replaces succinyl-CoA synthetase in a variant TCA cycle (Mullins et al. 2008). Similar succinyl-CoA transferase activities are also present in *Trichomonas vaginalis* (van Grinsven et al. 2008), *Trypanosoma brucei* (Riviere et al. 2004) and *Clostridium kluyveri* (Sohling and Gottschalk, 1996c). The beta-ketoadipate:succinyl-CoA transferase encoded by *pcaI* and *pcaJ* in *Pseudomonas putida* is yet another candidate (Kaschabek et al. 2002). The aforementioned proteins are identified below.

Protein	GenBank ID	GI Number	Organism
cat1	P38946.1	729048	*Clostridium kluyveri*
TVAG_395550	XP_001330176	123975034	*Trichomonas vaginalis G3*
Tb11.02.0290	XP_828352	71754875	*Trypanosoma brucei*
pcaI	AAN69545.1	24985644	*Pseudomonas putida*
pcaJ	NP_746082.1	26990657	*Pseudomonas putida*
aarC	ACD85596.1	189233555	*Acetobacter aceti*

[0424] An additional exemplary transferase that converts succinate to succinyl-CoA while converting a 3-ketoacyl-CoA to a 3-ketoacid is succinyl-CoA:3:ketoacid-CoA transferase (EC 2.8.3.5). Exemplary succinyl-CoA:3:ketoacid-CoA transferases are present in *Helicobacter pylori* (Corthesy-Theulaz et al. 1997), *Bacillus subtilis*, and *Homo sapiens* (Fukao et al. 2000; Tanaka et al. 2002). The aforementioned proteins are identified below.

Protein	GenBank ID	GI Number	Organism
HPAG1_0676	YP_627417	108563101	*Helicobacter pylori*
HPAG1_0677	YP_627418	108563102	*Helicobacter pylori*
ScoA	NP_391778	16080950	*Bacillus subtilis*
ScoB	NP_391777	16080949	*Bacillus subtilis*
OXCT1	NP_000427	4557817	*Homo sapiens*
OXCT2	NP_071403	11545841	*Homo sapiens*

[0425] Converting succinate to succinyl-CoA by succinyl-CoA:3:ketoacid-CoA transferase requires the simultaneous conversion of a 3-ketoacyl-CoA such as acetoacetyl-

CoA to a 3-ketoacid such as acetoacetate. Conversion of a 3-ketoacid back to a 3-ketoacyl-CoA can be catalyzed by an acetoacetyl-CoA:acetate:CoA transferase. Acetoacetyl-CoA:acetate:CoA transferase converts acetoacetyl-CoA and acetate to acetoacetate and acetyl-CoA, or vice versa. Exemplary enzymes include the gene products of *atoAD* from *E. coli* (Hanai et al., Appl Environ Microbiol 73:7814-7818 (2007), *ctfAB* from *C. acetobutylicum* (Jojima et al., Appl Microbiol Biotechnol 77:1219-1224 (2008), and *ctfAB* from *Clostridium saccharoperbutylacetonicum* (Kosaka et al., *Biosci.Biotechnol Biochem.* 71:58-68 (2007)) are shown below.

Protein	GenBank ID	GI Number	Organism
AtoA	NP_416726.1	2492994	*Escherichia coli*
AtoD	NP_416725.1	2492990	*Escherichia coli*
CtfA	NP_149326.1	15004866	*Clostridium acetobutylicum*
CtfB	NP_149327.1	15004867	*Clostridium acetobutylicum*
CtfA	AAP42564.1	31075384	*Clostridium saccharoperbutylacetonicum*
CtfB	AAP42565.1	31075385	*Clostridium saccharoperbutylacetonicum*

[0426] Yet another possible CoA acceptor is benzylsuccinate. Succinyl-CoA:(R)-Benzylsuccinate CoA-Transferase functions as part of an anaerobic degradation pathway for toluene in organisms such as *Thauera aromatica* (Leutwein and Heider, *J. Bact.* 183(14) 4288-4295 (2001)). Homologs can be found in *Azoarcus* sp. T, *Aromatoleum aromaticum* EbN1, and *Geobacter metallireducens* GS-15. The aforementioned proteins are identified below.

Protein	GenBank ID	GI Number	Organism
bbsE	AAF89840	9622535	*Thauera aromatic*
Bbsf	AAF89841	9622536	*Thauera aromatic*
bbsE	AAU45405.1	52421824	*Azoarcus sp. T*
bbsF	AAU45406.1	52421825	*Azoarcus sp. T*
bbsE	YP_158075.1	56476486	*Aromatoleum aromaticum EbN1*
bbsF	YP_158074.1	56476485	*Aromatoleum aromaticum EbN1*
Gmet_1521	YP_384480.1	78222733	*Geobacter metallireducens GS-15*
Gmet_1522	YP_384481.1	78222734	*Geobacter metallireducens GS-15*

[0427] Additionally, *ygfH* encodes a propionyl CoA:succinate CoA transferase in *E. coli* (Haller et al., *Biochemistry*, 39(16) 4622-4629). Close homologs can be found in, for example, *Citrobacter youngae* ATCC 29220, *Salmonella enterica* subsp. *arizonae serovar*, and *Yersinia intermedia* ATCC 29909. The aforementioned proteins are identified below.

Protein	GenBank ID	GI Number	Organism
ygfH	NP_417395.1	16130821	*Escherichia coli str. K-12 substr. MG1655*
CIT292_04485	ZP_03838384.1	227334728	*Citrobacter youngae ATCC 29220*
SARI_04582	YP_001573497.1	161506385	*Salmonella enterica subsp. arizonae serovar*
yinte0001_14430	ZP_04635364.1	238791727	*Yersinia intermedia ATCC 29909*

[0428] Citrate lyase (EC 4.1.3.6) catalyzes a series of reactions resulting in the cleavage of citrate to acetate and oxaloacetate. The enzyme is active under anaerobic conditions and is composed of three subunits: an acyl-carrier protein (ACP, gamma), an ACP transferase (alpha), and a acyl lyase (beta). Enzyme activation uses covalent binding and acetylation of an unusual prosthetic group, 2'-(5"-phosphoribosyl)-3-'-dephospho-CoA, which is similar in structure to acetyl-CoA. Acylation is catalyzed by CitC, a citrate lyase synthetase. Two additional proteins, CitG and CitX, are used to convert the apo enzyme into the active holo enzyme (Schneider et al., *Biochemistry* 39:9438-9450 (2000)). Wild type *E. coli* does not have citrate lyase activity; however, mutants deficient in molybdenum cofactor synthesis have an active citrate lyase (Clark, *FEMS Microbiol. Lett.* 55:245-249 (1990)). The *E. coli* enzyme is encoded by *citEFD* and the citrate lyase synthetase is encoded by *citC* (Nilekani and SivaRaman, *Biochemistry* 22:4657-4663 (1983)). The *Leuconostoc mesenteroides* citrate lyase has been cloned, characterized and expressed in *E. coli* (Bekal et al., *J. Bacteriol.* 180:647-654 (1998)). Citrate lyase enzymes have also been identified in enterobacteria that utilize citrate as a carbon and energy source, including *Salmonella typhimurium* and *Klebsiella pneumoniae* (Bott, *Arch. Microbiol.* 167: 78-88 (1997); Bott and Dimroth, *Mol. Microbiol.* 14:347-356 (1994)). The aforementioned proteins are tabulated below.

Protein	**GenBank ID**	**GI Number**	**Organism**
citF	AAC73716.1	1786832	*Escherichia coli*
Cite	AAC73717.2	87081764	*Escherichia coli*
citD	AAC73718.1	1786834	*Escherichia coli*
citC	AAC73719.2	87081765	*Escherichia coli*

Protein	GenBank ID	GI Number	Organism
citG	AAC73714.1	1786830	*Escherichia coli*
citX	AAC73715.1	1786831	*Escherichia coli*
citF	CAA71633.1	2842397	*Leuconostoc mesenteroides*
Cite	CAA71632.1	2842396	*Leuconostoc mesenteroides*
citD	CAA71635.1	2842395	*Leuconostoc mesenteroides*
citC	CAA71636.1	3413797	*Leuconostoc mesenteroides*
citG	CAA71634.1	2842398	*Leuconostoc mesenteroides*
citX	CAA71634.1	2842398	*Leuconostoc mesenteroides*
citF	NP_459613.1	16763998	*Salmonella typhimurium*
cite	AAL19573.1	16419133	*Salmonella typhimurium*
citD	NP_459064.1	16763449	*Salmonella typhimurium*
citC	NP_459616.1	16764001	*Salmonella typhimurium*
citG	NP_459611.1	16763996	*Salmonella typhimurium*
citX	NP_459612.1	16763997	*Salmonella typhimurium*
citF	CAA56217.1	565619	*Klebsiella pneumoniae*
cite	CAA56216.1	565618	*Klebsiella pneumoniae*
citD	CAA56215.1	565617	*Klebsiella pneumoniae*
citC	BAH66541.1	238774045	*Klebsiella pneumoniae*
citG	CAA56218.1	565620	*Klebsiella pneumoniae*
citX	AAL60463.1	18140907	*Klebsiella pneumoniae*

[0429] Acetate kinase (EC 2.7.2.1) catalyzes the reversible ATP-dependent phosphorylation of acetate to acetylphosphate. Exemplary acetate kinase enzymes have been characterized in many organisms including *E. coli*, *Clostridium acetobutylicum* and *Methanosarcina thermophila* (Ingram-Smith et al., *J. Bacteriol.* 187:2386-2394 (2005); Fox and Roseman, *J. Biol. Chem.* 261:13487-13497 (1986); Winzer et al., *Microbioloy* 143 (Pt 10):3279-3286 (1997)). Acetate kinase activity has also been demonstrated in the gene product of *E. coli purT* (Marolewski et al., *Biochemistry* 33:2531-2537 (1994). Some butyrate kinase enzymes (EC 2.7.2.7), for example *buk1* and *buk2* from *Clostridium acetobutylicum,* also accept acetate as a substrate (Hartmanis, M.G., *J. Biol. Chem.* 262:617-621 (1987)).

Protein	GenBank ID	GI Number	Organism
ackA	NP_416799.1	16130231	*Escherichia coli*
Ack	AAB18301.1	1491790	*Clostridium acetobutylicum*
Ack	AAA72042.1	349834	*Methanosarcina thermophila*
purT	AAC74919.1	1788155	*Escherichia coli*

Protein	GenBank ID	GI Number	Organism
buk1	NP_349675	15896326	*Clostridium acetobutylicum*
buk2	Q97II1	20137415	*Clostridium acetobutylicum*

[0430] The formation of acetyl-CoA from acetylphosphate is catalyzed by phosphotransacetylase (EC 2.3.1.8). The *pta* gene from *E. coli* encodes an enzyme that reversibly converts acetyl-CoA into acetyl-phosphate (Suzuki, T., *Biochim. Biophys. Acta* 191:559-569 (969)). Additional acetyltransferase enzymes have been characterized in *Bacillus subtilis* (Rado and Hoch, *Biochim. Biophys. Acta* 321:114-125 (1973), *Clostridium kluyveri* (Stadtman, E., *Methods Enzymol.* 1:5896-599 (1955), and *Thermotoga maritima* (Bock et al., *J. Bacteriol.* 181:1861-1867 (1999)). This reaction is also catalyzed by some phosphotranbutyrylase enzymes (EC 2.3.1.19) including the *ptb* gene products from *Clostridium acetobutylicum* (Wiesenborn et al., *App. Environ. Microbiol.* 55:317-322 (1989); Walter et al., *Gene* 134:107-111 (1993)). Additional *ptb* genes are found in butyrate-producing bacterium L2-50 (Louis et al., *J. Bacteriol.* 186:2099-2106 (2004) and *Bacillus megaterium* (Vazquez et al., *Curr. Microbiol.* 42:345-349 (2001).

Protein	**GenBank ID**	**GI Number**	**Organism**
Pta	NP_416800.1	71152910	*Escherichia coli*
Pta	P39646	730415	*Bacillus subtilis*
Pta	A5N801	146346896	*Clostridium kluyveri*
Pta	Q9X0L4	6685776	*Thermotoga maritima*
Ptb	NP_349676	34540484	*Clostridium acetobutylicum*
Ptb	AAR19757.1	38425288	butyrate-producing bacterium L2-50
Ptb	CAC07932.1	10046659	*Bacillus megaterium*

[0431] The acylation of acetate to acetyl-CoA is catalyzed by enzymes with acetyl-CoA synthetase activity. Two enzymes that catalyze this reaction are AMP-forming acetyl-CoA synthetase (EC 6.2.1.1) and ADP-forming acetyl-CoA synthetase (EC 6.2.1.13). AMP-forming acetyl-CoA synthetase (ACS) is the predominant enzyme for activation of acetate to acetyl-CoA. Exemplary ACS enzymes are found in *E. coli* (Brown et al., *J. Gen. Microbiol.* 102:327-336 (1977)), *Ralstonia eutropha* (Priefert and Steinbuchel, *J. Bacteriol.* 174:6590-6599 (1992)), *Methanothermobacter thermautotrophicus* (Ingram-Smith and Smith, *Archaea* 2:95-107 (2007)), *Salmonella enterica* (Gulick et al., *Biochemistry* 42:2866-2873 (2003)) and

Saccharomyces cerevisiae (Jogl and Tong, *Biochemistry* 43:1425-1431 (2004)). ADP-forming acetyl-CoA synthetases are reversible enzymes with a generally broad substrate range (Musfeldt and Schonheit, *J. Bacteriol*. 184:636-644 (2002)). Two isozymes of ADP-forming acetyl-CoA synthetases are encoded in the *Archaeoglobus fulgidus* genome by are encoded by AF1211 and AF1983 (Musfeldt and Schonheit, *supra* (2002)). The enzyme from *Haloarcula marismortui* (annotated as a succinyl-CoA synthetase) also accepts acetate as a substrate and reversibility of the enzyme was demonstrated (Brasen and Schonheit, *Arch. Microbiol.* 182:277-287 (2004)). The ACD encoded by *PAE3250* from hyperthermophilic crenarchaeon *Pyrobaculum aerophilum* showed the broadest substrate range of all characterized ACDs, reacting with acetate, isobutyryl-CoA (preferred substrate) and phenylacetyl-CoA (Brasen and Schonheit, *supra* (2004)). Directed evolution or engineering can be used to modify this enzyme to operate at the physiological temperature of the host organism. The enzymes from *A. fulgidus*, *H. marismortui* and *P. aerophilum* have all been cloned, functionally expressed, and characterized in *E. coli* (Brasen and Schonheit, *supra* (2004); Musfeldt and Schonheit, *supra* (2002)). Additional candidates include the succinyl-CoA synthetase encoded by *sucCD* in *E. coli* (Buck et al., *Biochemistry* 24:6245-6252 (1985)) and the acyl-CoA ligase from *Pseudomonas putida* (Fernandez-Valverde et al., *Appl. Environ. Microbiol*. 59:1149-1154 (1993)). The aforementioned proteins are tabulated below.

Protein	**GenBank ID**	**GI Number**	**Organism**
acs	AAC77039.1	1790505	*Escherichia coli*
acoE	AAA21945.1	141890	*Ralstonia eutropha*
acs1	ABC87079.1	86169671	*Methanothermobacter thermautotrophicus*
acs1	AAL23099.1	16422835	*Salmonella enterica*
ACS1	Q01574.2	257050994	*Saccharomyces cerevisiae*
AF1211	NP_070039.1	11498810	*Archaeoglobus fulgidus*
AF1983	NP_070807.1	11499565	*Archaeoglobus fulgidus*
scs	YP_135572.1	55377722	*Haloarcula marismortui*
PAE3250	NP_560604.1	18313937	*Pyrobaculum aerophilum* str. IM2
sucC	NP_415256.1	16128703	*Escherichia coli*
sucD	AAC73823.1	1786949	*Escherichia coli*

Protein	GenBank ID	GI Number	Organism
paaF	AAC24333.2	22711873	*Pseudomonas putida*

[0432] The product yields per C-mol of substrate of microbial cells synthesizing reduced fermentation products such as methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate, are limited by insufficient reducing equivalents in the carbohydrate feedstock. Reducing equivalents, or electrons, can be extracted from synthesis gas components such as CO and H_2 using carbon monoxide dehydrogenase (CODH) and hydrogenase enzymes, respectively. The reducing equivalents are then passed to acceptors such as oxidized ferredoxins, oxidized quinones, oxidized cytochromes, NAD(P)+, water, or hydrogen peroxide to form reduced ferredoxin, reduced quinones, reduced cytochromes, NAD(P)H, H_2, or water, respectively. Reduced ferredoxin and NAD(P)H are particularly useful as they can serve as redox carriers for various Wood-Ljungdahl pathway and reductive TCA cycle enzymes.

[0433] Additional redox availability from CO and/or H_2 can improve the yields of reduced products such as methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate. The maximum theoretical yield to produce methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate from glucose is 1.33 mole MAA per mole of glucose under aerobic conditions via the pathways disclosed herein:

$$C_6H_{12}O_6 \rightarrow 1.33\ C_4H_6O_2 + 0.67\ CO_2 + 2\ H_2O$$

[0434] When both feedstocks of sugar and syngas are available, the syngas components CO and H_2 can be utilized to generate reducing equivalents by employing the hydrogenase and CO dehydrogenase. The reducing equivalents generated from syngas components will be utilized to power the glucose to methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate production pathways. Theoretically, all carbons in glucose will be conserved, thus resulting in a maximal theoretical yield to produce methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate from glucose at 2 mol methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate per mol of glucose under either aerobic or anaerobic conditions as described herein.

$$1\ C_6H_{12}O_6 + 2\ CO_2 + 6\ H_2 \rightarrow 2\ C_4H_6O_2 + 6\ H_2O$$

or

$$1\ C_6H_{12}O_6 + 2\ CO + 4\ H_2 \rightarrow 2\ C_4H_6O_2 + 4\ H_2O$$

[0435] As shown in above example, a combined feedstock strategy where syngas is combined with a sugar-based feedstock or other carbon substrate can greatly improve the theoretical yields. In this co-feeding appoach, syngas components H_2 and CO can be utilized by the hydrogenase and CO dehydrogenase to generate reducing equivalents, that can be used to power chemical production pathways in which the carbons from sugar or other carbon substrates will be maximally conserved and the theoretical yields improved. In case of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate production from glucose or sugar, the theoretical yields improve from 1.33 mol methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate per mol of glucose to 2 mol methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate per mol of glucose. Such improvements provide environmental and economic benefits and greatly enhance sustainable chemical production.

[0436] Herein the enzymes and the corresponding genes used for extracting redox from synags components are described. CODH is a reversible enzyme that interconverts CO and CO_2 at the expense or gain of electrons. The natural physiological role of the CODH in ACS/CODH complexes is to convert CO_2 to CO for incorporation into acetyl-CoA by acetyl-CoA synthase. Nevertheless, such CODH enzymes are suitable for the extraction of reducing equivalents from CO due to the reversible nature of such enzymes. Expressing such CODH enzymes in the absence of ACS allows them to operate in the direction opposite to their natural physiological role (i.e., CO oxidation).

[0437] In *M. thermoacetica*, *C. hydrogenoformans*, *C. carboxidivorans P7*, and several other organisms, additional CODH encoding genes are located outside of the ACS/CODH operons. These enzymes provide a means for extracting electrons (or reducing equivalents) from the conversion of carbon monoxide to carbon dioxide. The *M. thermoacetica* gene (Genbank Accession Number: YP_430813) is expressed by itself in an operon and is believed to transfer electrons from CO to an external mediator like ferredoxin in a "Ping-pong" reaction. The reduced mediator then couples to other reduced nicolinamide adenine dinucleotide phosphate (NAD(P)H) carriers or ferredoxin-dependent cellular processes (Ragsdale, *Annals of the New York Academy of Sciences* 1125: 129–136 (2008)). The genes encoding the *C. hydrogenoformans* CODH-II and CooF, a neighboring protein, were cloned and sequenced (Gonzalez and Robb, *FEMS Microbiol Lett.* 191:243-247 (2000)). The

resulting complex was membrane-bound, although cytoplasmic fractions of CODH-II were shown to catalyze the formation of NADPH suggesting an anabolic role (Svetlitchnyi et al., *J Bacteriol.* 183:5134-5144 (2001)). The crystal structure of the CODH-II is also available (Dobbek et al., *Science* 293:1281-1285 (2001)). Similar ACS-free CODH enzymes can be found in a diverse array of organisms including *Geobacter metallireducens* GS-15, *Chlorobium phaeobacteroides* DSM 266, *Clostridium cellulolyticum* H10, *Desulfovibrio desulfuricans* subsp. *desulfuricans* str. ATCC 27774, *Pelobacter carbinolicus* DSM 2380, and *Campylobacter curvus* 525.92.

Protein	GenBank ID	GI Number	Organism
CODH (putative)	YP_430813	83590804	*Moorella thermoacetica*
CODH-II (CooS-II)	YP_358957	78044574	*Carboxydothermus hydrogenoformans*
CooF	YP_358958	78045112	*Carboxydothermus hydrogenoformans*
CODH (putative)	ZP_05390164.1	255523193	*Clostridium carboxidivorans P7*
CcarbDRAFT_0341	ZP_05390341.1	255523371	*Clostridium carboxidivorans P7*
CcarbDRAFT_1756	ZP_05391756.1	255524806	*Clostridium carboxidivorans P7*
CcarbDRAFT_2944	ZP_05392944.1	255526020	*Clostridium carboxidivorans P7*
CODH	YP_384856.1	78223109	*Geobacter metallireducens GS-15*
Cpha266_0148 (cytochrome c)	YP_910642.1	119355998	*Chlorobium phaeobacteroides DSM 266*
Cpha266_0149 (CODH)	YP_910643.1	119355999	*Chlorobium phaeobacteroides DSM 266*
Ccel_0438	YP_002504800.1	220927891	*Clostridium cellulolyticum H10*
Ddes_0382 (CODH)	YP_002478973.1	220903661	*Desulfovibrio desulfuricans subsp. desulfuricans str. ATCC 27774*
Ddes_0381 (CooC)	YP_002478972.1	220903660	*Desulfovibrio desulfuricans subsp. desulfuricans str. ATCC 27774*
Pcar_0057 (CODH)	*YP_355490.1*	*7791767*	*Pelobacter carbinolicus DSM 2380*
Pcar_0058 (CooC)	*YP_355491.1*	*7791766*	*Pelobacter carbinolicus DSM 2380*
Pcar_0058 (HypA)	*YP_355492.1*	*7791765*	*Pelobacter carbinolicus DSM 2380*
CooS (CODH)	*YP_001407343.1*	*154175407*	*Campylobacter curvus 525.92*

[0438] In some cases, hydrogenase encoding genes are located adjacent to a CODH. In *Rhodospirillum rubrum*, the encoded CODH/hydrogenase proteins form a membrane-bound enzyme complex that has been indicated to be a site where energy, in the form of a proton gradient, is generated from the conversion of CO and H_2O to CO_2 and H_2 (Fox et al., *J Bacteriol.* 178:6200-6208 (1996)). The CODH-I of *C. hydrogenoformans* and its adjacent genes have been proposed to catalyze a similar functional role based on their similarity to the *R. rubrum* CODH/hydrogenase gene cluster (Wu et al., *PLoS Genet.* 1:e65 (2005)). The *C. hydrogenoformans* CODH-I was also shown to exhibit intense CO oxidation and CO_2 reduction activities when linked to an electrode (Parkin et al., *J Am.Chem.Soc.* 129:10328-10329 (2007)). The protein sequences of exemplary CODH and hydrogenase genes can be identified by the following GenBank accession numbers.

Protein	GenBank ID	GI Number	Organism
CODH-I (CooS-I)	YP_360644	78043418	*Carboxydothermus hydrogenoformans*
CooF	YP_360645	78044791	*Carboxydothermus hydrogenoformans*
HypA	YP_360646	78044340	*Carboxydothermus hydrogenoformans*
CooH	YP_360647	78043871	*Carboxydothermus hydrogenoformans*
CooU	YP_360648	78044023	*Carboxydothermus hydrogenoformans*
CooX	YP_360649	78043124	*Carboxydothermus hydrogenoformans*
CooL	YP_360650	78043938	*Carboxydothermus hydrogenoformans*
CooK	YP_360651	78044700	*Carboxydothermus hydrogenoformans*
CooM	YP_360652	78043942	*Carboxydothermus hydrogenoformans*
CooC	*YP_360654.1*	78043296	*Carboxydothermus hydrogenoformans*
CooA-1	YP_360655.1	78044021	*Carboxydothermus hydrogenoformans*
CooL	AAC45118	1515468	*Rhodospirillum rubrum*
CooX	AAC45119	1515469	*Rhodospirillum rubrum*
CooU	AAC45120	1515470	*Rhodospirillum rubrum*
CooH	AAC45121	1498746	*Rhodospirillum rubrum*
CooF	AAC45122	1498747	*Rhodospirillum rubrum*

CODH (CooS)	AAC45123	1498748	*Rhodospirillum rubrum*
CooC	AAC45124	1498749	*Rhodospirillum rubrum*
CooT	AAC45125	1498750	*Rhodospirillum rubrum*
CooJ	AAC45126	1498751	*Rhodospirillum rubrum*

[0439] Native to *E. coli* and other enteric bacteria are multiple genes encoding up to four hydrogenases (Sawers, G., *Antonie Van Leeuwenhoek* 66:57-88 (1994); Sawers et al., *J Bacteriol.* 164:1324-1331 (1985); Sawers and Boxer, *Eur.J Biochem.* 156:265-275 (1986); Sawers et al., *J Bacteriol.* 168:398-404 (1986)). Given the multiplicity of enzyme activities, *E. coli* or another host organism can provide sufficient hydrogenase activity to split incoming molecular hydrogen and reduce the corresponding acceptor. *E. coli* possesses two uptake hydrogenases, Hyd-1 and Hyd-2, encoded by the *hyaABCDEF* and *hybOABCDEFG* gene clusters, respectively (Lukey et al., How E. coli is equipped to oxidize hydrogen under different redox conditions, *J Biol Chem* published online Nov 16, 2009). Hyd-1 is oxygen-tolerant, irreversible, and is coupled to quinone reduction via the *hyaC* cytochrome. Hyd-2 is sensitive to O_2, reversible, and transfers electrons to the periplasmic ferredoxin *hybA* which, in turn, reduces a quinone via the *hybB* integral membrane protein. Reduced quinones can serve as the source of electrons for fumarate reductase in the reductive branch of the TCA cycle. Reduced ferredoxins can be used by enzymes such as NAD(P)H:ferredoxin oxidoreductases to generate NADPH or NADH. They can alternatively be used as the electron donor for reactions such as pyruvate ferredoxin oxidoreductase, AKG ferredoxin oxidoreductase, and 5,10-methylene-H4folate reductase.

Protein	GenBank ID	GI Number	Organism
HyaA	AAC74057.1	1787206	*Escherichia coli*
HyaB	AAC74058.1	1787207	*Escherichia coli*
HyaC	AAC74059.1	1787208	*Escherichia coli*
HyaD	AAC74060.1	1787209	*Escherichia coli*
HyaE	AAC74061.1	1787210	*Escherichia coli*
HyaF	AAC74062.1	1787211	*Escherichia coli*

Protein	GenBank ID	GI Number	Organism
HybO	AAC76033.1	1789371	*Escherichia coli*
HybA	AAC76032.1	1789370	*Escherichia coli*
HybB	AAC76031.1	2367183	*Escherichia coli*
HybC	AAC76030.1	1789368	*Escherichia coli*
HybD	AAC76029.1	1789367	*Escherichia coli*

HybE	AAC76028.1	1789366	*Escherichia coli*
HybF	AAC76027.1	1789365	*Escherichia coli*
HybG	AAC76026.1	1789364	*Escherichia coli*

[0440] The hydrogen-lyase systems of *E. coli* include hydrogenase 3, a membrane-bound enzyme complex using ferredoxin as an acceptor, and hydrogenase 4 that also uses a ferredoxin acceptor. Hydrogenase 3 and 4 are encoded by the *hyc* and *hyf* gene clusters, respectively. Hydrogenase 3 has been shown to be a reversible enzyme (Maeda et al., *Appl Microbiol Biotechnol* 76(5):1035-42 (2007)). Hydrogenase activity in *E. coli* is also dependent upon the expression of the *hyp* genes whose corresponding proteins are involved in the assembly of the hydrogenase complexes (Jacobi et al., *Arch.Microbiol* 158:444-451 (1992); Rangarajan et al., *J. Bacteriol.* 190:1447-1458 (2008)).

Protein	GenBank ID	GI Number	Organism
HycA	NP_417205	16130632	*Escherichia coli*
HycB	NP_417204	16130631	*Escherichia coli*
HycC	NP_417203	16130630	*Escherichia coli*
HycD	NP_417202	16130629	*Escherichia coli*
HycE	NP_417201	16130628	*Escherichia coli*
HycF	NP_417200	16130627	*Escherichia coli*
HycG	NP_417199	16130626	*Escherichia coli*
HycH	NP_417198	16130625	*Escherichia coli*
HycI	NP_417197	16130624	*Escherichia coli*

Protein	GenBank ID	GI Number	Organism
HyfA	NP_416976	90111444	*Escherichia coli*
HyfB	NP_416977	16130407	*Escherichia coli*
HyfC	NP_416978	90111445	*Escherichia coli*
HyfD	NP_416979	16130409	*Escherichia coli*
HyfE	NP_416980	16130410	*Escherichia coli*
HyfF	NP_416981	16130411	*Escherichia coli*
HyfG	NP_416982	16130412	*Escherichia coli*
HyfH	NP_416983	16130413	*Escherichia coli*
HyfI	NP_416984	16130414	*Escherichia coli*

HyfJ	NP_416985	90111446	*Escherichia coli*
HyfR	NP_416986	90111447	*Escherichia coli*

Protein	GenBank ID	GI Number	Organism
HypA	NP_417206	16130633	*Escherichia coli*
HypB	NP_417207	16130634	*Escherichia coli*
HypC	NP_417208	16130635	*Escherichia coli*
HypD	NP_417209	16130636	*Escherichia coli*
HypE	NP_417210	226524740	*Escherichia coli*
HypF	NP_417192	16130619	*Escherichia coli*

[0441] The *M. thermoacetica* hydrogenases are suitable for a host that lacks sufficient endogenous hydrogenase activity. *M. thermoacetica* can grow with CO_2 as the exclusive carbon source indicating that reducing equivalents are extracted from H_2 to enable acetyl-CoA synthesis via the Wood-Ljungdahl pathway (Drake, H. L., *J. Bacteriol.* 150:702-709 (1982); Drake and Daniel, *Res. Microbiol.* 155:869-883 (2004); Kellum and Drake, *J. Bacteriol.* 160:466-469 (1984)) (see Figures 12 and 13). *M. thermoacetica* has homologs to several *hyp*, *hyc*, and *hyf* genes from *E. coli*. The protein sequences encoded for by these genes are identified by the following GenBank accession numbers.

[0442] Proteins in *M. thermoacetica* whose genes are homologous to the *E. coli hyp* genes are shown below.

Protein	GenBank ID	GI Number	Organism
Moth_2175	YP_431007	83590998	*Moorella thermoacetica*
Moth_2176	YP_431008	83590999	*Moorella thermoacetica*
Moth_2177	YP_431009	83591000	*Moorella thermoacetica*
Moth_2178	YP_431010	83591001	*Moorella thermoacetica*
Moth_2179	YP_431011	83591002	*Moorella thermoacetica*
Moth_2180	YP_431012	83591003	*Moorella thermoacetica*
Moth_2181	YP_431013	83591004	*Moorella thermoacetica*

[0443] Proteins in *M. thermoacetica* that are homologous to the *E. coli* Hydrogenase 3 and/or 4 proteins are listed below.

Protein	GenBank ID	GI Number	Organism
Moth_2182	YP_431014	83591005	*Moorella thermoacetica*
Moth_2183	YP_431015	83591006	*Moorella thermoacetica*
Moth_2184	YP_431016	83591007	*Moorella thermoacetica*
Moth_2185	YP_431017	83591008	*Moorella thermoacetica*
Moth_2186	YP_431018	83591009	*Moorella thermoacetica*
Moth_2187	YP_431019	83591010	*Moorella thermoacetica*
Moth_2188	YP_431020	83591011	*Moorella thermoacetica*
Moth_2189	YP_431021	83591012	*Moorella thermoacetica*
Moth_2190	YP_431022	83591013	*Moorella thermoacetica*
Moth_2191	YP_431023	83591014	*Moorella thermoacetica*
Moth_2192	YP_431024	83591015	*Moorella thermoacetica*

[0444] In addition, several gene clusters encoding hydrogenase functionality are present in *M. thermoacetica* and their corresponding protein sequences are provided below.

Protein	GenBank ID	GI Number	Organism
Moth_0439	YP_429313	83589304	*Moorella thermoacetica*
Moth_0440	YP_429314	83589305	*Moorella thermoacetica*
Moth_0441	YP_429315	83589306	*Moorella thermoacetica*
Moth_0442	YP_429316	83589307	*Moorella thermoacetica*
Moth_0809	YP_429670	83589661	*Moorella thermoacetica*
Moth_0810	YP_429671	83589662	*Moorella thermoacetica*
Moth_0811	YP_429672	83589663	*Moorella thermoacetica*
Moth_0812	YP_429673	83589664	*Moorella thermoacetica*
Moth_0814	YP_429674	83589665	*Moorella thermoacetica*
Moth_0815	YP_429675	83589666	*Moorella thermoacetica*
Moth_0816	YP_429676	83589667	*Moorella thermoacetica*
Moth_1193	YP_430050	83590041	*Moorella thermoacetica*
Moth_1194	YP_430051	83590042	*Moorella thermoacetica*
Moth_1195	YP_430052	83590043	*Moorella thermoacetica*
Moth_1196	YP_430053	83590044	*Moorella thermoacetica*
Moth_1717	YP_430562	83590553	*Moorella thermoacetica*
Moth_1718	YP_430563	83590554	*Moorella thermoacetica*
Moth_1719	YP_430564	83590555	*Moorella thermoacetica*

Moth_1883	YP_430726	83590717	*Moorella thermoacetica*
Moth_1884	YP_430727	83590718	*Moorella thermoacetica*
Moth_1885	YP_430728	83590719	*Moorella thermoacetica*
Moth_1886	YP_430729	83590720	*Moorella thermoacetica*
Moth_1887	YP_430730	83590721	*Moorella thermoacetica*
Moth_1888	YP_430731	83590722	*Moorella thermoacetica*
Moth_1452	YP_430305	83590296	*Moorella thermoacetica*
Moth_1453	YP_430306	83590297	*Moorella thermoacetica*
Moth_1454	YP_430307	83590298	*Moorella thermoacetica*

[0445] *Ralstonia eutropha* H16 uses hydrogen as an energy source with oxygen as a terminal electron acceptor. Its membrane-bound uptake [NiFe]-hydrogenase is an ''O2-tolerant'' hydrogenase (Cracknell, et al. Proc Nat Acad Sci, 106(49) 20681-20686 (2009)) that is periplasmically-oriented and connected to the respiratory chain via a b-type cytochrome (Schink and Schlegel, *Biochim. Biophys. Acta*, 567, 315-324 (1979); Bernhard et al., *Eur. J. Biochem*. 248, 179–186 (1997)). *R. eutropha* also contains an O_2-tolerant soluble hydrogenase encoded by the *Hox* operon which is cytoplasmic and directly reduces NAD+ at the expense of hydrogen (Schneider and Schlegel, *Biochim. Biophys. Acta* 452, 66–80 (1976); Burgdorf, *J. Bact*. 187(9) 3122-3132(2005)). Soluble hydrogenase enzymes are additionally present in several other organisms including *Geobacter sulfurreducens* (Coppi, *Microbiology* 151, 1239–1254 (2005)), *Synechocystis* str. PCC 6803 (Germer, *J. Biol. Chem.*, 284(52), 36462–36472 (2009)), and *Thiocapsa roseopersicina* (Rakhely, *Appl. Environ. Microbiol.* 70(2) 722–728 (2004)). The *Synechocystis* enzyme is capable of generating NADPH from hydrogen. Overexpression of both the *Hox* operon from *Synechocystis* str. PCC 6803 and the accessory genes encoded by the *Hyp* operon from *Nostoc* sp. PCC 7120 led to increased hydrogenase activity compared to expression of the *Hox* genes alone (Germer, *J. Biol. Chem.* 284(52), 36462–36472 (2009)).

Protein	GenBank ID	GI Number	Organism
HoxF	NP_942727.1	38637753	*Ralstonia eutropha H16*
HoxU	NP_942728.1	38637754	*Ralstonia eutropha H16*
HoxY	NP_942729.1	38637755	*Ralstonia eutropha H16*
HoxH	NP_942730.1	38637756	*Ralstonia eutropha H16*

HoxW	NP_942731.1	38637757	*Ralstonia eutropha H16*
HoxI	NP_942732.1	38637758	*Ralstonia eutropha H16*
HoxE	NP_953767.1	*39997816*	*Geobacter sulfurreducens*
HoxF	NP_953766.1	*39997815*	*Geobacter sulfurreducens*
HoxU	NP_953765.1	*39997814*	*Geobacter sulfurreducens*
HoxY	NP_953764.1	*39997813*	*Geobacter sulfurreducens*
HoxH	NP_953763.1	*39997812*	*Geobacter sulfurreducens*
GSU2717	NP_953762.1	*39997811*	*Geobacter sulfurreducens*
HoxE	NP_441418.1	16330690	*Synechocystis* str. PCC 6803
HoxF	NP_441417.1	16330689	*Synechocystis* str. PCC 6803
Unknown function	NP_441416.1	16330688	*Synechocystis* str. PCC 6803
HoxU	NP_441415.1	16330687	*Synechocystis* str. PCC 6803
HoxY	NP_441414.1	16330686	*Synechocystis* str. PCC 6803
Unknown function	NP_441413.1	16330685	*Synechocystis* str. PCC 6803
Unknown function	NP_441412.1	16330684	*Synechocystis* str. PCC 6803
HoxH	NP_441411.1	16330683	*Synechocystis* str. PCC 6803
HypF	NP_484737.1	17228189	*Nostoc* sp. PCC 7120
HypC	NP_484738.1	17228190	*Nostoc* sp. PCC 7120
HypD	NP_484739.1	17228191	*Nostoc* sp. PCC 7120
Unknown function	NP_484740.1	17228192	*Nostoc* sp. PCC 7120
HypE	NP_484741.1	17228193	*Nostoc* sp. PCC 7120
HypA	NP_484742.1	17228194	*Nostoc* sp. PCC 7120
HypB	NP_484743.1	17228195	*Nostoc* sp. PCC 7120
Hox1E	AAP50519.1	37787351	*Thiocapsa roseopersicina*

Hox1F	AAP50520.1	37787352	*Thiocapsa roseopersicina*
Hox1U	AAP50521.1	37787353	*Thiocapsa roseopersicina*
Hox1Y	AAP50522.1	37787354	*Thiocapsa roseopersicina*
Hox1H	AAP50523.1	37787355	*Thiocapsa roseopersicina*

[0446] Several enzymes and the corresponding genes used for fixing carbon dioxide to either pyruvate or phosphoenolpyruvate to form the TCA cycle intermediates, oxaloacetate or malate are described below.

[0447] Carboxylation of phosphoenolpyruvate to oxaloacetate is catalyzed by phosphoenolpyruvate carboxylase. Exemplary PEP carboxylase enzymes are encoded by *ppc* in *E. coli* (Kai et al., *Arch. Biochem. Biophys*. 414:170-179 (2003), *ppcA* in *Methylobacterium extorquens AM1* (Arps et al., *J. Bacteriol*. 175:3776-3783 (1993), and *ppc* in *Corynebacterium glutamicum* (Eikmanns et al., *Mol. Gen. Genet*. 218:330-339 (1989).

Protein	GenBank ID	GI Number	Organism
Ppc	NP_418391	16131794	*Escherichia coli*
ppcA	AAB58883	28572162	*Methylobacterium extorquens*
Ppc	ABB53270	80973080	*Corynebacterium glutamicum*

[0448] An alternative enzyme for converting phosphoenolpyruvate to oxaloacetate is PEP carboxykinase, which simultaneously forms an ATP while carboxylating PEP. In most organisms PEP carboxykinase serves a gluconeogenic function and converts oxaloacetate to PEP at the expense of one ATP. *S. cerevisiae* is one such organism whose native PEP carboxykinase, *PCK1*, serves a gluconeogenic role (Valdes-Hevia et al., *FEBS Lett*. 258:313-316 (1989). *E. coli* is another such organism, as the role of PEP carboxykinase in producing oxaloacetate is believed to be minor when compared to PEP carboxylase, which does not form ATP, possibly due to the higher K_m for bicarbonate of PEP carboxykinase (Kim et al., *Appl. Environ. Microbiol.* 70:1238-1241 (2004)). Nevertheless, activity of the native *E. coli* PEP carboxykinase from PEP towards oxaloacetate has been recently demonstrated in *ppc* mutants of *E. coli* K-12 (Kwon et al., *J. Microbiol. Biotechnol.* 16:1448-1452 (2006)). These strains exhibited no growth defects and had increased succinate production at high $NaHCO_3$ concentrations. Mutant strains of *E. coli* can adopt Pck as the dominant CO2-fixing enzyme following adaptive evolution (Zhang et al. 2009). In some organisms, particularly rumen

bacteria, PEP carboxykinase is quite efficient in producing oxaloacetate from PEP and generating ATP. Examples of PEP carboxykinase genes that have been cloned into *E. co*li include those from *Mannheimia succiniciproducens* (Lee et al., *Biotechnol. Bioprocess Eng.* 7:95-99 (2002)), *Anaerobiospirillum succiniciproducens* (Laivenieks et al., *Appl. Environ. Microbiol.* 63:2273-2280 (1997), and *Actinobacillus succinogenes* (Kim et al. *supra*). The PEP carboxykinase enzyme encoded by *Haemophilus influenza* is effective at forming oxaloacetate from PEP.

Protein	GenBank ID	GI Number	Organism
PCK1	NP_013023	6322950	*Saccharomyces cerevisiae*
pck	NP_417862.1	16131280	*Escherichia coli*
pckA	YP_089485.1	52426348	*Mannheimia succiniciproducens*
pckA	O09460.1	3122621	*Anaerobiospirillum succiniciproducens*
pckA	Q6W6X5	75440571	*Actinobacillus succinogenes*
pckA	P43923.1	1172573	*Haemophilus influenza*

[0449] Pyruvate carboxylase (EC 6.4.1.1) directly converts pyruvate to oxaloacetate at the cost of one ATP. Pyruvate carboxylase enzymes are encoded by *PYC1* (Walker et al., *Biochem. Biophys. Res. Commun.* 176:1210-1217 (1991) and *PYC2* (Walker et al., *supra*) in *Saccharomyces cerevisiae*, and *pyc* in *Mycobacterium smegmatis* (Mukhopadhyay and Purwantini, *Biochim. Biophys. Acta* 1475:191-206 (2000)).

Protein	GenBank ID	GI Number	Organism
PYC1	NP_011453	6321376	*Saccharomyces cerevisiae*
PYC2	NP_009777	6319695	*Saccharomyces cerevisiae*
Pyc	YP_890857.1	118470447	*Mycobacterium smegmatis*

[0450] Malic enzyme can be applied to convert CO_2 and pyruvate to malate at the expense of one reducing equivalent. Malic enzymes for this purpose can include, without limitation, malic enzyme (NAD-dependent) and malic enzyme (NADP-dependent). For example, one of the *E. coli* malic enzymes (Takeo, *J. Biochem.* 66:379-387 (1969)) or a similar enzyme with higher activity can be expressed to enable the conversion of pyruvate and CO_2 to malate. By fixing carbon to pyruvate as opposed to PEP, malic enzyme allows

the high-energy phosphate bond from PEP to be conserved by pyruvate kinase whereby ATP is generated in the formation of pyruvate or by the phosphotransferase system for glucose transport. Although malic enzyme is typically assumed to operate in the direction of pyruvate formation from malate, overexpression of the NAD-dependent enzyme, encoded by maeA, has been demonstrated to increase succinate production in *E. coli* while restoring the lethal Δpfl-ΔldhA phenotype under anaerobic conditions by operating in the carbon-fixing direction (Stols and Donnelly, *Appl. Environ. Microbiol.* 63(7) 2695-2701 (1997)). A similar observation was made upon overexpressing the malic enzyme from *Ascaris suum* in *E. coli* (Stols et al., *Appl. Biochem. Biotechnol.* 63-65(1), 153-158 (1997)). The second *E. coli* malic enzyme, encoded by *maeB*, is NADP-dependent and also decarboxylates oxaloacetate and other alpha-keto acids (Iwakura et al., *J. Biochem.* 85(5):1355-65 (1979)).

Protein	GenBank ID	GI Number	Organism
maeA	NP_415996	90111281	*Escherichia coli*
maeB	NP_416958	16130388	*Escherichia coli*
NAD-ME	P27443	126732	*Ascaris suum*

[0451] The enzymes used for converting oxaloacetate (formed from, for example, PEP carboxylase, PEP carboxykinase, or pyruvate carboxylase) or malate (formed from, for example, malic enzyme or malate dehydrogenase) to succinyl-CoA via the reductive branch of the TCA cycle are malate dehydrogenase, fumarate dehydratase (fumarase), fumarate reductase, and succinyl-CoA transferase. The genes for each of the enzymes are described herein above.

[0452] Enzymes, genes and methods for engineering pathways from succinyl-CoA to various products into a microorganism are now known in the art. The additional reducing equivalents obtained from CO and/or H_2, as disclosed herein, improve the yields of methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate when utilizing carbohydrate-based feedstock. For example, methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate can be produced from succinyl-CoA (see Figures). Exemplary enzymes for the conversion succinyl-CoA to methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate include enzymes disclosed herein.

[0453] Enzymes, genes and methods for engineering pathways from glycolysis intermediates to various products into a microorganism are known in the art. The additional reducing equivalents obtained from CO and H_2, as described herein, improve the yields of all these products on carbohydrates. For example, methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate can be produced from the glycolysis intermediate, succinate. Exemplary enzymes for the conversion of succinate to MAA include succinyl-CoA transferase, succinyl-CoA synthetase, succinyl-CoA reductase (aldehyde forming) , 4-hydroxybutyrate dehydrogenase, 4-hydroxybutyrate kinase, phosphotrans-4-hydroxybutyrylase, succinate reductase, succinyl-CoA reductase (alcohol forming), 4-hydroxybutyryl-CoA synthetase, 4-hydroxybutyryl-CoA transferase, 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA synthetase, 3-hydroxyisobutyryl-CoA transferase, 3-hydroxyisobutyryl-CoA hydrolase, 3-hydroxyisobutyrate dehydratase, 3-hydroxyisobutyryl-CoA dehydratase, methacrylyl-CoA synthetase, methacrylyl-CoA transferase and methacrylyl-CoA hydrolase.

EXAMPLE XVI
Methods for Handling CO and Anaerobic Cultures

[0454] This example describes methods used in handling CO and anaerobic cultures.

[0455] A. Handling of CO in small quantities for assays and small cultures. CO is an odorless, colorless and tasteless gas that is a poison. Therefore, cultures and assays that utilized CO required special handling. Several assays, including CO oxidation, acetyl-CoA synthesis, CO concentration using myoglobin, and CO tolerance/utilization in small batch cultures, called for small quantities of the CO gas that were dispensed and handled within a fume hood. Biochemical assays called for saturating very small quantities (<2 mL) of the biochemical assay medium or buffer with CO and then performing the assay. All of the CO handling steps were performed in a fume hood with the sash set at the proper height and blower turned on; CO was dispensed from a compressed gas cylinder and the regulator connected to a Schlenk line. The latter ensures that equal concentrations of CO were dispensed to each of several possible cuvettes or vials. The Schlenk line was set up containing an oxygen scrubber on the input side and an oil pressure release bubbler and vent on the other side. Assay cuvettes were both anaerobic and CO-containing. Threfore, the assay cuvettes were tightly sealed with a rubber stopper and reagents were added or removed using gas-tight needles and syringes. Secondly, small (~50 mL) cultures were grown with

saturating CO in tightly stoppered serum bottles. As with the biochemical assays, the CO-saturated microbial cultures were equilibrated in the fume hood using the Schlenk line setup. Both the biochemical assays and microbial cultures were in portable, sealed containers and in small volumes making for safe handling outside of the fume hood. The compressed CO tank was adjacent to the fume hood.

[0456] Typically, a Schlenk line was used to dispense CO to cuvettes, each vented. Rubber stoppers on the cuvettes were pierced with 19 or 20 gage disposable syringe needles and were vented with the same. An oil bubbler was used with a CO tank and oxygen scrubber. The glass or quartz spectrophotometer cuvettes have a circular hole on top into which a Kontes stopper sleeve, Sz7 774250-0007 was fitted. The CO detector unit was positioned proximal to the fume hood.

[0457] B. Handling of CO in larger quantities fed to large-scale cultures. Fermentation cultures are fed either CO or a mixture of CO and H_2 to simulate syngas as a feedstock in fermentative production. Therefore, quantities of cells ranging from 1 liter to several liters can include the addition of CO gas to increase the dissolved concentration of CO in the medium. In these circumstances, fairly large and continuously administered quantities of CO gas are added to the cultures. At different points, the cultures are harvested or samples removed. Alternatively, cells are harvested with an integrated continuous flow centrifuge that is part of the fermenter.

[0458] The fermentative processes are carried out under anaerobic conditions. In some cases, it is uneconomical to pump oxygen or air into fermenters to ensure adequate oxygen saturation to provide a respiratory environment. In addition, the reducing power generated during anaerobic fermentation may be needed in product formation rather than respiration. Furthermore, many of the enzymes for various pathways are oxygen-sensitive to varying degrees. Classic acetogens such as *M. thermoacetica* are obligate anaerobes and the enzymes in the Wood-Ljungdahl pathway are highly sensitive to irreversible inactivation by molecular oxygen. While there are oxygen-tolerant acetogens, the repertoire of enzymes in the Wood-Ljungdahl pathway might be incompatible in the presence of oxygen because most are metallo-enzymes, key components are ferredoxins, and regulation can divert metabolism away from the Wood-Ljungdahl pathway to maximize energy acquisition. At the same time, cells in culture act as oxygen scavengers that moderate the need for extreme measures in the presence of large cell growth.

[0459] C. Anaerobic chamber and conditions. Exemplary anaerobic chambers are available commercially (see, for example, Vacuum Atmospheres Company, Hawthorne CA; MBraun, Newburyport MA). Conditions included an O_2 concentration of 1 ppm or less and 1 atm pure N_2. In one example, 3 oxygen scrubbers/catalyst regenerators were used, and the chamber included an O_2 electrode (such as Teledyne; City of Industry CA). Nearly all items and reagents were cycled four times in the airlock of the chamber prior to opening the inner chamber door. Reagents with a volume >5mL were sparged with pure N_2 prior to introduction into the chamber. Gloves are changed twice/yr and the catalyst containers were regenerated periodically when the chamber displays increasingly sluggish response to changes in oxygen levels. The chamber's pressure was controlled through one-way valves activated by solenoids. This feature allowed setting the chamber pressure at a level higher than the surroundings to allow transfer of very small tubes through the purge valve.

[0460] The anaerobic chambers achieved levels of O_2 that were consistently very low and were needed for highly oxygen sensitive anaerobic conditions. However, growth and handling of cells does not usually require such precautions. In an alternative anaerobic chamber configuration, platinum or palladium can be used as a catalyst that requires some hydrogen gas in the mix. Instead of using solenoid valves, pressure release can be controlled by a bubbler. Instead of using instrument-based O_2 monitoring, test strips can be used instead.

[0461] D. Anaerobic microbiology. Small cultures were handled as described above for CO handling. In particular, serum or media bottles are fitted with thick rubber stoppers and aluminum crimps are employed to seal the bottle. Medium, such as Terrific Broth, is made in a conventional manner and dispensed to an appropriately sized serum bottle. The bottles are sparged with nitrogen for ~30 min of moderate bubbling. This removes most of the oxygen from the medium and, after this step, each bottle is capped with a rubber stopper (such as Bellco 20 mm septum stoppers; Bellco, Vineland, NJ) and crimp-sealed (Bellco 20 mm). Then the bottles of medium are autoclaved using a slow (liquid) exhaust cycle. At least sometimes a needle can be poked through the stopper to provide exhaust during autoclaving; the needle needs to be removed immediately upon removal from the autoclave. The sterile medium has the remaining medium components, for example buffer or antibiotics, added via syringe and needle. Prior to addition of reducing agents, the bottles are equilibrated for 30 - 60 minutes with nitrogen (or CO depending upon use). A reducing agent such as a 100 x 150

mM sodium sulfide, 200 mM cysteine-HCl is added. This is made by weighing the sodium sulfide into a dry beaker and the cysteine into a serum bottle, bringing both into the anaerobic chamber, dissolving the sodium sulfide into anaerobic water, then adding this to the cysteine in the serum bottle. The bottle is stoppered immediately as the sodium sulfide solution generates hydrogen sulfide gas upon contact with the cysteine. When injecting into the culture, a syringe filter is used to sterilize the solution. Other components are added through syringe needles, such as B12 (10 μM cyanocobalamin), nickel chloride ($NiCl_2$, 20 microM final concentration from a 40 mM stock made in anaerobic water in the chamber and sterilized by autoclaving or by using a syringe filter upon injection into the culture), and ferrous ammonium sulfate (final concentration needed is 100 μM—made as 100-1000x stock solution in anaerobic water in the chamber and sterilized by autoclaving or by using a syringe filter upon injection into the culture). To facilitate faster growth under anaerobic conditions, the 1 liter bottles were inoculated with 50 mL of a preculture grown anaerobically. Induction of the pA1-lacO1 promoter in the vectors was performed by addition of isopropyl β-D-1-thiogalactopyranoside (IPTG) to a final concentration of 0.2 mM and was carried out for about 3 hrs.

[0462] Large cultures can be grown in larger bottles using continuous gas addition while bubbling. A rubber stopper with a metal bubbler is placed in the bottle after medium addition and sparged with nitrogen for 30 minutes or more prior to setting up the rest of the bottle. Each bottle is put together such that a sterile filter will sterilize the gas bubbled in and the hoses on the bottles are compressible with small C clamps. Medium and cells are stirred with magnetic stir bars. Once all medium components and cells are added, the bottles are incubated in an incubator in room air but with continuous nitrogen sparging into the bottles.

EXAMPLE XVIII
CO oxidation (CODH) Assay

[0463] This example describes assay methods for measuring CO oxidation (CO dehydrogenase; CODH).

[0464] The 7 gene CODH/ACS operon of *Moorella thermoacetica* was cloned into *E. coli* expression vectors. The intact ~10 kbp DNA fragment was cloned, and it is likely that some of the genes in this region are expressed from their own endogenous promoters and all contain endogenous ribosomal binding sites. These clones were assayed for CO oxidation, using an assay that quantitatively measures CODH activity. Antisera to the *M. thermoacetica*

gene products was used for Western blots to estimate specific activity. *M. thermoacetica* is Gram positive, and ribosome binding site elements are expected to work well in *E. coli*. This activity, described below in more detail, was estimated to be ~1/50th of the *M. thermoacetica* specific activity. It is possible that CODH activity of recombinant *E. coli* cells could be limited by the fact that *M. thermoacetica* enzymes have temperature optima around 55°C. Therefore, a mesophilic CODH/ACS pathway could be advantageous such as the close relative of *Moorella* that is mesophilic and does have an apparently intact CODH/ACS operon and a Wood-Ljungdahl pathway, *Desulfitobacterium hafniense*. Acetogens as potential host organisms include, but are not limited to, *Rhodospirillum rubrum, Moorella thermoacetica and Desulfitobacterium hafniense.*

[0465] CO oxidation is both the most sensitive and most robust of the CODH/ACS assays. It is likely that an *E. coli*-based syngas using system will ultimately need to be about as anaerobic as *Clostridial* (i.e., *Moorella*) systems, especially for maximal activity. Improvement in CODH should be possible but will ultimately be limited by the solubility of CO gas in water.

[0466] Initially, each of the genes was cloned individually into expression vectors. Combined expression units for multiple subunits/1 complex were generated. Expression in *E. coli* at the protein level was determined. Both combined *M. thermoacetica* CODH/ACS operons and individual expression clones were made.

[0467] CO oxidation assay. This assay is one of the simpler, reliable, and more versatile assays of enzymatic activities within the Wood-Ljungdahl pathway and tests CODH (Seravalli et al., *Biochemistry* 43:3944-3955 (2004)). A typical activity of *M. thermoacetica* CODH specific activity is 500 U at 55°C or ~60U at 25°C. This assay employs reduction of methyl viologen in the presence of CO. This is measured at 578 nm in stoppered, anaerobic, glass cuvettes.

[0468] In more detail, glass rubber stoppered cuvettes were prepared after first washing the cuvette four times in deionized water and one time with acetone. A small amount of vacuum grease was smeared on the top of the rubber gasket. The cuvette was gassed with CO, dried 10 min with a 22 Ga. needle plus an exhaust needle. A volume of 0.98 mlL of reaction buffer (50 mM Hepes, pH 8.5, 2mM dithiothreitol (DTT) was added using a 22 Ga. needle, with exhaust needled, and 100%CO. Methyl viologen (CH_3 viologen) stock was 1 M

in water. Each assay used 20 microliters for 20 mM final concentration. When methyl viologen was added, an 18 Ga needle (partial) was used as a jacket to facilitate use of a Hamilton syringe to withdraw the CH_3 viologen. 4 -5 aliquots were drawn up and discarded to wash and gas equilibrate the syringe. A small amount of sodium dithionite (0.1 M stock) was added when making up the CH_3 viologen stock to slightly reduce the CH_3 viologen. The temperature was equilibrated to 55°C in a heated Olis spectrophotometer (Bogart GA). A blank reaction (CH_3 viologen + buffer) was run first to measure the base rate of CH_3 viologen reduction. Crude *E. coli* cell extracts of ACS90 and ACS91 (CODH-ACS operon of *M. thermoacetica* with and without, respectively, the first *cooC*). 10 microliters of extract were added at a time, mixed and assayed. Reduced CH_3 viologen turns purple. The results of an assay are shown in Table 2.

Table 2. Crude extract CO Oxidation Activities.

ACS90	7.7 mg/ml	ACS91	11.8 mg/ml	
Mta98	9.8 mg/ml	Mta99	11.2 mg/ml	
Extract	**Vol**	**OD/**	**U/ml**	**U/mg**
ACS90	10 microliters	0.073	0.376	0.049
ACS91	10 microliters	0.096	0.494	0.042
Mta99	10 microliters	0.0031	0.016	0.0014
ACS90	10 microliters	0.099	0.51	0.066
Mta99	25 microliters	0.012	0.025	0.0022
ACS91	25 microliters	0.215	0.443	0.037
Mta98	25 microliters	0.019	0.039	0.004
ACS91	10 microliters	0.129	0.66	0.056
Averages				
ACS90	0.057 U/mg			
ACS91	0.045 U/mg			
Mta99	0.0018 U/mg			

[0469] Mta98/Mta99 are *E. coli* MG1655 strains that express methanol methyltransferase genes from *M. thermoacetia* and, therefore, are negative controls for the ACS90 ACS91 *E. coli* strains that contain *M. thermoacetica* CODH operons.

[0470] If ~ 1% of the cellular protein is CODH, then these figures would be approximately 100X less than the 500 U/mg activity of pure *M. thermoacetica* CODH. Actual estimates based on Western blots are 0.5% of the cellular protein, so the activity is about 50X less than for *M. thermoacetica* CODH. Nevertheless, this experiment

demonstrates CO oxidation activity in recombinant *E. coli* with a much smaller amount in the negative controls. The small amount of CO oxidation (CH_3 viologen reduction) seen in the negative controls indicates that *E. coli* may have a limited ability to reduce CH_3 viologen.

[0471] To estimate the final concentrations of CODH and Mtr proteins, SDS-PAGE followed by Western blot analyses were performed on the same cell extracts used in the CO oxidation, ACS, methyltransferase, and corrinoid Fe-S assays. The antisera used were polyclonal to purified *M. thermoacetica* CODH-ACS and Mtr proteins and were visualized using an alkaline phosphatase-linked goat-anti-rabbit secondary antibody. The Westerns were performed and results are shown in Figure 14. The amounts of CODH in ACS90 and ACS91 were estimated at 50 ng by comparison to the control lanes. Expression of CODH-ACS operon genes including 2 CODH subunits and the methyltransferase were confirmed via Western blot analysis. Therefore, the recombinant *E. coli* cells express multiple components of a 7 gene operon. In addition, both the methyltransferase and corrinoid iron sulfur protein were active in the same recombinant *E. coli* cells. These proteins are part of the same operon cloned into the same cells.

[0472] The CO oxidation assays were repeated using extracts of *Moorella thermoacetica* cells for the positive controls. Though CODH activity in *E. coli* ACS90 and ACS91 was measurable, it was at about 130 – 150 X lower than the *M. thermoacetica* control. The results of the assay are shown in Figure 15. Briefly, cells (*M. thermoacetica* or *E. coli* with the CODH/ACS operon; ACS90 or ACS91 or empty vector: pZA33S) were grown and extracts prepared as described above. Assays were performed as described above at 55°C at various times on the day the extracts were prepared. Reduction of methylviologen was followed at 578 nm over a 120 sec time course.

[0473] These results describe the CO oxidation (CODH) assay and results. Recombinant *E. coli* cells expressed CO oxidation activity as measured by the methyl viologen reduction assay.

EXAMPLE XVIII
E. coli CO Tolerance Experiment and CO Concentration Assay (myoglobin assay)

[0474] This example describes the tolerance of *E. coli* for high concentrations of CO.

[0475] To test whether or not *E. coli* can grow anaerobically in the presence of saturating amounts of CO, cultures were set up in 120 ml serum bottles with 50 ml of Terrific Broth

medium (plus reducing solution, $NiCl_2$, $Fe(II)NH_4SO_4$, cyanocobalamin, IPTG, and chloramphenicol) as described above for anaerobic microbiology in small volumes. One half of these bottles were equilibrated with nitrogen gas for 30 min. and one half was equilibrated with CO gas for 30 min. An empty vector (pZA33) was used as a control, and cultures containing the pZA33 empty vector as well as both ACS90 and ACS91 were tested with both N_2 and CO. All were inoculated and grown for 36 hrs with shaking (250 rpm) at 37°C. At the end of the 36 hour period, examination of the flasks showed high amounts of growth in all. The bulk of the observed growth occurred overnight with a long lag.

[0476] Given that all cultures appeared to grow well in the presence of CO, the final CO concentrations were confirmed. This was performed using an assay of the spectral shift of myoglobin upon exposure to CO. Myoglobin reduced with sodium dithionite has an absorbance peak at 435 nm; this peak is shifted to 423 nm with CO. Due to the low wavelength and need to record a whole spectrum from 300 nm on upwards, quartz cuvettes must be used. CO concentration is measured against a standard curve and depends upon the Henry's Law constant for CO of maximum water solubility = 970 micromolar at 20°C and 1 atm.

[0477] For the myoglobin test of CO concentration, cuvettes were washed 10X with water, 1X with acetone, and then stoppered as with the CODH assay. N_2 was blown into the cuvettes for ~10 min. A volume of 1 ml of anaerobic buffer (HEPES, pH 8.0, 2mM DTT) was added to the blank (not equilibrated with CO) with a Hamilton syringe. A volume of 10 microliter myoglobin (~1 mM—can be varied, just need a fairly large amount) and 1 microliter dithionite (20 mM stock) were added. A CO standard curve was made using CO saturated buffer added at 1 microliter increments. Peak height and shift was recorded for each increment. The cultures tested were pZA33/CO, ACS90/CO, and ACS91/CO. Each of these was added in 1 microliter increments to the same cuvette. Midway through the experiment a second cuvette was set up and used. The results are shown in Table 3.

Table 3. Carbon Monoxide Concentrations, 36 hrs.

Strain and Growth Conditions	Final CO concentration (micromolar)
pZA33-CO	930
ACS90-CO	638
	494
	734
	883
ave	**687**
SD	**164**
ACS91-CO	728
	812
	760
	611
ave.	**728**
SD	**85**

[0478] The results shown in Table 3 indicate that the cultures grew whether or not a strain was cultured in the presence of CO or not. These results indicate that *E. coli* can tolerate exposure to CO under anaerobic conditions and that *E. coli* cells expressing the CODH-ACS operon can metabolize some of the CO.

[0479] These results demonstrate that *E. coli* cells, whether expressing CODH/ACS or not, were able to grow in the presence of saturating amounts of CO. Furthermore, these grew equally well as the controls in nitrogen in place of CO. This experiment demonstrated that laboratory strains of *E. coli* are insensitive to CO at the levels achievable in a syngas project performed at normal atmospheric pressure. In addition, preliminary experiments indicated that the recombinant *E. coli* cells expressing CODH/ACS actually consumed some CO, probably by oxidation to carbon dioxide.

EXAMPLE XVIX
Pathways for the Production of MAA and 3-Hydroxyisobutyric Acid from Succinate via Methylmalonyl-CoA

[0480] The reductive TCA cycle improves the yield of methacrylic acid (MAA) when utilizing a carbohydrate-based feedstock. MAA production can be achieved in a recombinant organism by the pathway shown in Figure 16A.

[0481] For example, MAA and/or 3-hydroxyisobutyric acid can be produced from succinate via a methylmalonyl-CoA intermediate as shown in Figure 16A. Exemplary enzymes for the conversion of succinate to MAA or 3-hydroxyisobutyric acid by this route include succinyl-CoA transferase, succinyl-CoA synthetase, methylmalonyl-CoA mutase,

methylmalonyl-CoA epimerase, methylmalonyl-CoA reductase, methylmalonate semialdehyde reductase and 3-hydroxyisobutyrate dehydratase.

[0482] In this pathway, central metabolic intermediates are first channeled into succinate. For formation of succinate, phosphoenolpyruvate (PEP) is converted into oxaloacetate either via PEP carboxykinase or PEP carboxylase. Alternatively, PEP is converted first to pyruvate by pyruvate kinase and then to oxaloacetate by methylmalonyl-CoA carboxytransferase or pyruvate carboxylase. Oxaloacetate is then converted to succinate by means of the reductive TCA cycle.

[0483] Succinate is then activated to succinyl-CoA by a succinyl-CoA transferase or synthetase. Methylmalonyl-CoA mutase then forms methylmalonyl-CoA from succinyl-CoA. Methylmalonyl-CoA is then reduced to methylmalonate semialdehyde. Further reduction of methylmalonate semialdehyde yields 3-hydroxyisobutyric acid, which can be secreted as a product or further transformed to MAA via dehydration.

[0484] Exemplary enzyme candidates for the transformations shown in Figure 16A are described below. Succinyl-CoA transferase and synthetase enzymes were described previously in Example XV (RTCA cycle).

[0485] Methylmalonyl-CoA mutase. Methylmalonyl-CoA mutase is a cobalamin-dependent enzyme that converts succinyl-CoA to methylmalonyl-CoA. In *E. coli*, the reversible adenosylcobalamin-dependant mutase participates in a three-step pathway leading to the conversion of succinate to propionate. Exemplary MCM enzymes are described in Example V.

[0486] Alternatively, isobutyryl-CoA mutase (ICM) could catalyze the proposed transformation. ICM is a cobalamin-dependent methylmutase in the MCM family that reversibly rearranges the carbon backbone of butyryl-CoA into isobutyryl-CoA (Ratnatilleke, *J Biol Chem*. 274:31679-31685 (1999)). Exemplary ICM enzymes are described in Example VII.

[0487] Methylmalonyl-CoA epimerase. Methylmalonyl-CoA epimerase (MMCE) is the enzyme that interconverts (R)-methylmalonyl-CoA and (S)-methylmalonyl-CoA. MMCE is an essential enzyme in the breakdown of odd-numbered fatty acids and of the amino acids valine, isoleucine, and methionine. Exemplary MMCE enzymes are desribed in Example V.

[0488] Methylmalonyl-CoA reductase. The reduction of methylmalonyl-CoA to its corresponding aldehyde, methylmalonate semialdehyde, is catalyzed by a CoA-dependent aldehyde dehydrogenase. Exemplary enzymes are described in Example V.

[0489] Methylmalonate semialdehyde reductase. The reduction of methylmalonate semialdehyde to 3-hydroxyisobutyrate is catalyzed by methylmalonate semialdehyde reductase or 3-hydroxyisobutyrate dehydrogenase. This enzyme participates in valine, leucine and isoleucine degradation and has been identified in bacteria, eukaryotes, and mammals. Exemplary methylmalonate semialdehyde reductase enzymes are described in Example V.

[0490] 3-Hydroxyisobutyrate dehydratase. The dehydration of 3-hydroxyisobutyrate to methylacrylic acid is catalyzed by an enzyme with 3-hydroxyisobutyrate dehydratase activity. Exemplary 3-hydroxyisobutyrate dehydratase enzymes are described in Example V.

[0491] An active reductive TCA cycle improves the yield of the acetyl-CoA derived product methacrylic acid (MAA), as shown in the exemplary pathways of Figure 17. Pathways of the reductive TCA cycle are described herein as well as the conversion of succinyl-CoA to methacrylic acid (see also Figures 3 and 16A and Example V). Figures 17A and 17B show exemplary pathways. The enzymatic transformations are carried out by the enzymes as shown. Figure 17A shows the pathways for fixation of CO_2 to succinyl-CoA using the reductive TCA cycle. Figure 17B shows exemplary pathways for the biosynthesis of 3-hydroxyisobutric acid and methacrylic acid from succinyl-CoA; the enzymatic transformations shown are carried out by the following enzymes: A. Methylmalonyl-CoA mutase, B. Methylmalonyl-CoA epimerase, C. Methylmalonyl-CoA reductase, D. Methylmalonate semialdehyde reductase, E. 3-Hydroxyisobutyrate dehydratase.

EXAMPLE XX
Pathways for the Production of MAA and 3-Hydroxyisobutyric Acid from Succinate via 4-Hydroxybutyryl-CoA

[0492] The reductive TCA cycle improves the yield of methacrylic acid (MAA) when utilizing a carbohydrate-based feedstock. MAA production can be achieved in a recombinant organism by as shown in Figure 16B.

[0493] For example, MAA and/or 3-hydroxyisobutyric acid can be produced from succinate via a 4-hydroxybutyryl-CoA intermediate by a number of alternate routes depicted

in Figure 16B. Exemplary enzymes for these routes include: succinyl-CoA transferase, succinyl-CoA synthetase, succinyl-CoA reductase (aldehyde forming) , 4-hydroxybutyrate dehydrogenase, 4-hydroxybutyrate kinase, phosphotrans-4-hydroxybutyrylase, succinate reductase, succinyl-CoA reductase (alcohol forming), 4-hydroxybutyryl-CoA synthetase, 4-hydroxybutyryl-CoA transferase, 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA synthetase, 3-hydroxyisobutyryl-CoA transferase, 3-hydroxyisobutyryl-CoA hydrolase, 3-hydroxyisobutyrate dehydratase, 3-hydroxyisobutyryl-CoA dehydratase, methacrylyl-CoA synthetase, methacrylyl-CoA transferase and methacrylyl-CoA hydrolase.

[0494] Formation of the 4-hydroxybutyryl-CoA intermediate from succinate proceeds through several routes depicted in Figure16B. Succinate is first converted to succinyl-CoA by a CoA transferase or synthetase. Succinyl-CoA is then converted to succinic semialdehyde by a CoA-dependent aldehyde dehydrogenase. Alternately, succinate is directly converted to succinic semialdehyde by an acid reductase. The succinic semialdehyde intermediate is reduced to 4-hydroxybutyrate (4-HB) by 4-hydroxybutyrate dehydrogenase. A bifunctional aldehyde dehydrogenase/alcohol dehydrogenase directly converts succinyl-CoA to 4-HB. Activation of 4-HB to its acyl-CoA is catalyzed by a CoA transferase or synthetase. Alternatively, 4-HB can be converted into a 4-hydroxybutyryl-phosphate intermediate and subsequently transformed into 4-HB-CoA by a phosphotrans-4-hydroxybutyrylase.

[0495] Isomerization of 4-hydroxybutyryl-CoA to 3-hydroxyisobutyryl-CoA is catalyzed by a 4-HB-CoA methylmutase. Removal of the CoA moiety of 3-hydroxyisobutyryl-CoA yields 3-hydroxyisobutyrate, which can be secreted as a product or further transformed to MAA by dehydration. Dehydration of 3-hydroxyisobutyryl-CoA to methacrylyl-CoA, followed by removal of the CoA moiety by a CoA hydrolase, transferase or synthetase, is another route for MAA formation.

[0496] Exemplary enzyme candidates for the transformations shown in Figures 16A and 16B are described below. Succinyl-CoA transferase and synthetase enzymes were described previously in Example I (RTCA cycle). Methylmalonyl-CoA mutase and methylmalonyl-CoA epimerase were described in Example III. 3-Hydroxyisobutyrate dehydratase enzyme candidates were described in Example III.

[0497] Table 4 shows enzyme classes that can perform the steps depicted in Figure 16B. Exemplary enzymes are described in further detail below.

Table 4. Exemplary enzymes that carry out the steps in Figure 16B.

Label	Function	Step
1.1.1.a	Oxidoreductase (oxo to alcohol)	5
1.1.1.c	CoA reducatse (alcohol forming)	9
1.2.1.b	CoA reductase (aldehyde forming)	4
1.2.1.e	Oxidoreductase (acid to aldehyde)	8
2.3.1.a	Phosphotransacylase	7
2.7.2.a	Kinase	6
2.8.3.a	Coenzyme-A transferase	3,10, 12,15
3.1.2.a	Thiolester hydrolase (CoA specific)	12, 15
4.2.1.a	Dehydratase	13,14
5.4.99.a	Methyl mutase	11
6.2.1.a	Acid-thiol ligase/CoA synthetase	3,10, 12,15

[0498] 1.1.1.a. Enzymes exhibiting 4-hydroxybutyrate dehydrogenase activity (EC 1.1.1.61) reduce succinate semialdehyde to 4-hydroxybutyrate (Step 5 of Figure 16B). Such enzymes have been characterized in *Ralstonia eutropha* (Bravo et al., *J Forens Sci*, 49:379-387 (2004)), *Clostridium kluyveri* (Wolff et al., *Protein Expr.Purif.* 6:206-212 (1995)) and *Arabidopsis thaliana* (Breitkreuz et al., *J Biol Chem*, 278:41552-41556 (2003)). The *A. thaliana* enzyme was cloned and characterized in yeast (Breitkreuz et al., *J.Biol.Chem.* 278:41552-41556 (2003)). Yet another gene is the alcohol dehydrogenase *adhI* from *Geobacillus thermoglucosidasius* (Jeon et al., *J Biotechnol* 135:127-133 (2008)).

PROTEIN	GENBANK ID	GI NUMBER	ORGANISM
4hbd	YP_726053.1	113867564	*Ralstonia eutropha* H16
4hbd	L21902.1	146348486	*Clostridium kluyveri* DSM 555
4hbd	Q94B07	75249805	*Arabidopsis thaliana*
adhI	AAR91477.1	40795502	*Geobacillus thermoglucosidasius*

[0499] 1.1.1.c. A bifunctional enzyme with acyl-CoA reductase and alcohol dehydrogenase activity can directly convert succinyl-CoA to 4-hydroxybutyrate. Exemplary

bifunctional oxidoreductases that convert an acyl-CoA to alcohol include those that transform substrates such as acetyl-CoA to ethanol (for example, *adhE* from *E. coli* (Kessler et al., *FEBS.Lett.* 281:59-63 (1991))) and butyryl-CoA to butanol (for example, *adhE2* from *C. acetobutylicum* (Fontaine et al., *J.Bacteriol.* 184:821-830 (2002))). The *C. acetobutylicum* enzymes encoded by *bdh* I and *bdh* II (Walter, et al., *J. Bacteriol.* 174:7149-7158 (1992)), reduce acetyl-CoA and butyryl-CoA to ethanol and butanol, respectively. In addition to reducing acetyl-CoA to ethanol, the enzyme encoded by *adhE* in *Leuconostoc mesenteroides* has been shown to oxide the branched chain compound isobutyraldehyde to isobutyryl-CoA (Kazahaya et al., *J.Gen.Appl.Microbiol.* 18:43-55 (1972); Koo et al., *Biotechnol Lett,* 27:505-510 (2005)). Another exemplary enzyme can convert malonyl-CoA to 3-HP. An NADPH-dependent enzyme with this activity has characterized in *Chloroflexus aurantiacus* where it participates in the 3-hydroxypropionate cycle (Hugler et al., *J Bacteriol*, 184:2404-2410 (2002); Strauss et al., *Eur J Biochem*, 215:633-643 (1993)). This enzyme, with a mass of 300 kDa, is highly substrate-specific and shows little sequence similarity to other known oxidoreductases (Hugler et al., *supra*). No enzymes in other organisms have been shown to catalyze this specific reaction; however there is bioinformatic evidence that other organisms may have similar pathways (Klatt et al., *Env Microbiol*, 9:2067-2078 (2007)). Enzyme candidates in other organisms including *Roseiflexus castenholzii*, *Erythrobacter sp. NAP1* and marine gamma proteobacterium HTCC2080 can be inferred by sequence similarity.

Protein	**GenBank ID**	**GI Number**	**Organism**
adhE	NP_415757.1	16129202	*Escherichia coli*
adhE2	AAK09379.1	12958626	*Clostridium acetobutylicum*
adhE	AAV66076.1	55818563	*Leuconostoc mesenteroides*
bdh I	NP_349892.1	15896543	*Clostridium acetobutylicum*
bdh II	NP_349891.1	15896542	*Clostridium acetobutylicum*
mcr	AAS20429.1	42561982	*Chloroflexus aurantiacus*
Rcas_2929	YP_001433009.1	156742880	*Roseiflexus castenholzii*
NAP1_02720	ZP_01039179.1	85708113	*Erythrobacter sp. NAP1*
MGP2080_00535	ZP_01626393.1	119504313	*marine gamma proteobacterium HTCC2080*

[0500] Longer chain acyl-CoA molecules can be reduced to their corresponding alcohols by enzymes such as the jojoba (*Simmondsia chinensis*) *FAR* which encodes an alcohol-forming fatty acyl-CoA reductase. Its overexpression in *E. coli* resulted in FAR activity and the accumulation of fatty alcohol (Metz et al., *Plant Physiol*, 122:635-644 (2000)).

Protein	GenBank ID	GI Number	Organism
FAR	AAD38039.1	5020215	*Simmondsia chinensis*

[0501] 1.2.1.b. The reduction of succinyl-CoA to its corresponding aldehyde, succinate semialdehyde, is catalyzed by succinyl-CoA reductase (aldehyde forming). Exemplary enzymes include succinyl-CoA reductase (EC 1.2.1.76), acetyl-CoA reductase, butyryl-CoA reductase and fatty acyl-CoA reductase. Enzymes with succinyl-CoA reductase activity are encoded by *sucD* of *Clostridium kluyveri* (Sohling, *J. Bacteriol.* 178:871-880 (1996)) and *sucD* of *P. gingivalis* (Takahashi, *J. Bacteriol* 182:4704-4710 (2000)). Additional succinyl-CoA reductase enzymes participate in the 3-hydroxypropionate/4-hydroxybutyrate cycle of thermophilic archaea including *Metallosphaera sedula* (Berg et al., *Science* 318:1782-1786 (2007)) and *Thermoproteus neutrophilus* (Ramos-Vera et al., *J Bacteriol*, 191:4286-4297 (2009)). The *M. sedula* enzyme, encoded by *Msed_0709*, is strictly NADPH-dependent and also has malonyl-CoA reductase activity. The *T. neutrophilus* enzyme is active with both NADPH and NADH. The enzyme acylating acetaldehyde dehydrogenase in *Pseudomonas sp*, encoded by *bphG*, is yet another as it has been demonstrated to oxidize and acylate acetaldehyde, propionaldehyde, butyraldehyde, isobutyraldehyde and formaldehyde (Powlowski, *J. Bacteriol.* 175:377-385 (1993)). In addition to reducing acetyl-CoA to ethanol, the enzyme encoded by *adhE* in *Leuconostoc mesenteroides* has been shown to oxidize the branched chain compound isobutyraldehyde to isobutyryl-CoA (Kazahaya, *J. Gen. Appl. Microbiol.* 18:43-55 (1972); and Koo et al., *Biotechnol Lett.* 27:505-510 (2005)). Butyraldehyde dehydrogenase catalyzes a similar reaction, conversion of butyryl-CoA to butyraldehyde, in solventogenic organisms such as *Clostridium saccharoperbutylacetonicum* (Kosaka et al., *Biosci Biotechnol Biochem.*, 71:58-68 (2007)). Exemplary fatty acyl-CoA reductases enzymes are encoded by *acr1* of *Acinetobacter calcoaceticus* (Reiser, *Journal of Bacteriology* 179:2969-2975 (1997)) and *Acinetobacter sp. M-1* (Ishige et al., *Appl. Environ. Microbiol.* 68:1192-1195 (2002)).

Protein	GenBank ID	GI Number	Organism
MSED_0709	YP_001190808.1	146303492	*Metallosphaera sedula*
Tneu_0421			*Thermoproteus neutrophilus*
sucD	P38947.1	172046062	*Clostridium kluyveri*
sucD	NP_904963.1	34540484	*Porphyromonas gingivalis*
bphG	BAA03892.1	425213	*Pseudomonas sp*
adhE	AAV66076.1	55818563	*Leuconostoc mesenteroides*

Protein	GenBank ID	GI Number	Organism
bld	AAP42563.1	31075383	*Clostridium saccharoperbutylacetonicum*
acr1	YP_047869.1	50086359	*Acinetobacter calcoaceticus*
acr1	AAC45217	1684886	*Acinetobacter baylyi*
acr1	BAB85476.1	18857901	*Acinetobacter sp. Strain M-1*

[0502] 1.2.1.e. Direct conversion of succinate to succinate semialdehyde is catalyzed by a carboxylic acid reductase. Exemplary enzymes include carboxylic acid reductase, alpha-aminoadipate reductase and retinoic acid reductase. Carboxylic acid reductase (CAR), found in *Nocardia iowensis,* catalyzes the magnesium, ATP and NADPH-dependent reduction of carboxylic acids to their corresponding aldehydes (Venkitasubramanian et al., *J Biol.Chem.* 282:478-485 (2007)). The natural substrate of this enzyme is benzoate and the enzyme exhibits broad acceptance of aromatic substrates including p-toluate (Venkitasubramanian et al., *Biocatalysis in Pharmaceutical and Biotechnology Industries*. CRC press (2006)). The enzyme from *Nocardia iowensis*, encoded by *car,* was cloned and functionally expressed in *E. coli* (Venkitasubramanian et al., *J Biol.Chem.* 282:478-485 (2007)). CAR requires post-translational activation by a phosphopantetheine transferase (PPTase) that converts the inactive apo-enzyme to the active holo-enzyme (Hansen et al., *Appl.Environ.Microbiol* 75:2765-2774 (2009)). Expression of the *npt* gene, encoding a specific PPTase, product improved activity of the enzyme. An additional enzyme candidate found in *Streptomyces griseus* is encoded by the *griC* and *griD* genes. This enzyme is believed to convert 3-amino-4-hydroxybenzoic acid to 3-amino-4-hydroxybenzaldehyde as deletion of either *griC* or *griD* led to accumulation of extracellular 3-acetylamino-4-hydroxybenzoic acid, a shunt product of 3-amino-4-hydroxybenzoic acid metabolism (Suzuki, et al., *J. Antibiot.* 60(6):380-387 (2007)). Co-expression of *griC* and *griD* with SGR_665, an enzyme similar in sequence to the *Nocardia iowensis npt*, can be beneficial.

Gene	GenBank Accession No.	GI No.	Organism
car	AAR91681.1	40796035	*Nocardia iowensis*
npt	ABI83656.1	114848891	*Nocardia iowensis*
griC	YP_001825755.1	182438036	*Streptomyces griseus*
griD	YP_001825756.1	182438037	*Streptomyces griseus*

[0503] Additional *car* and *npt* genes can be identified based on sequence homology.

Gene name	GI No.	GenBank Accession No.	Organism
fadD9	121638475	YP_978699.1	*Mycobacterium bovis* BCG
BCG_2812c	121638674	YP_978898.1	*Mycobacterium bovis* BCG
nfa20150	54023983	YP_118225.1	*Nocardia farcinica* IFM 10152
nfa40540	54026024	YP_120266.1	*Nocardia farcinica* IFM 10152
SGR_6790	182440583	YP_001828302.1	*Streptomyces griseus* subsp. *griseus* NBRC 13350
SGR_665	182434458	YP_001822177.1	*Streptomyces griseus* subsp. *griseus* NBRC 13350
MSMEG_2956	YP_887275.1	YP_887275.1	*Mycobacterium smegmatis MC2 155*
MSMEG_5739	YP_889972.1	118469671	*Mycobacterium smegmatis MC2 155*
MSMEG_2648	YP_886985.1	118471293	*Mycobacterium smegmatis MC2 155*
MAP1040c	NP_959974.1	41407138	*Mycobacterium avium subsp. paratuberculosis K-10*
MAP2899c	NP_961833.1	41408997	*Mycobacterium avium subsp. paratuberculosis K-10*
MMAR_2117	YP_001850422.1	183982131	*Mycobacterium marinum M*
MMAR_2936	YP_001851230.1	183982939	*Mycobacterium marinum M*
MMAR_1916	YP_001850220.1	183981929	*Mycobacterium marinum M*
TpauDRAFT_33060	ZP_04027864.1	227980601	*Tsukamurella paurometabola DSM 20162*
TpauDRAFT_20920	ZP_04026660.1	ZP_04026660.1	*Tsukamurella paurometabola DSM 20162*
CPCC7001_1320	ZP_05045132.1	254431429	*Cyanobium PCC7001*
DDBDRAFT_0187729	XP_636931.1	66806417	*Dictyostelium discoideum AX4*

[0504] An enzyme with similar characteristics, alpha-aminoadipate reductase (AAR, EC 1.2.1.31), participates in lysine biosynthesis pathways in some fungal species. This enzyme naturally reduces alpha-aminoadipate to alpha-aminoadipate semialdehyde. The carboxyl group is first activated through the ATP-dependent formation of an adenylate that is then reduced by NAD(P)H to yield the aldehyde and AMP. Like CAR, this enzyme utilizes magnesium and requires activation by a PPTase. Enzyme candidates for AAR and its corresponding PPTase are found in *Saccharomyces cerevisiae* (Morris et al., *Gene* 98:141-145 (1991)), *Candida albicans* (Guo et al., *Mol.Genet.Genomics* 269:271-279 (2003)), and *Schizosaccharomyces pombe* (Ford et al., *Curr.Genet.* 28:131-137 (1995)). The AAR from *S. pombe* exhibited significant activity when expressed in *E. coli* (Guo et al., *Yeast* 21:1279-1288 (2004)). The AAR from *Penicillium chrysogenum* accepts S-carboxymethyl-L-cysteine as an alternate substrate, but did not react with adipate, L-glutamate or diaminopimelate (Hijarrubia et al., *J Biol.Chem.* 278:8250-8256 (2003)). The gene encoding the *P. chrysogenum* PPTase has not been identified to date and no high-confidence hits were identified by sequence comparison homology searching.

Gene	GenBank Accession No.	GI No.	Organism
LYS2	AAA34747.1	171867	*Saccharomyces cerevisiae*
LYS5	P50113.1	1708896	*Saccharomyces cerevisiae*
LYS2	AAC02241.1	2853226	*Candida albicans*
LYS5	AAO26020.1	28136195	*Candida albicans*
Lys1p	P40976.3	13124791	*Schizosaccharomyces pombe*
Lys7p	Q10474.1	1723561	*Schizosaccharomyces pombe*
Lys2	CAA74300.1	3282044	*Penicillium chrysogenum*

[0505] 2.3.1.a. An enzyme with phosphotrans-4-hydroxybutyrylase activity is required to convert 4-hydroxybutyryl-phosphate to 4-hydroxybutyryl-CoA. Exemplary phosphate-transferring acyltransferases include phosphotransacetylase (EC 2.3.1.8) and phosphotransbutyrylase (EC 2.3.1.19). The *pta* gene from *E. coli* encodes a phosphotransacetylase that reversibly converts acetyl-CoA into acetyl-phosphate (Suzuki, *Biochim.Biophys.Acta* 191:559-569 (1969)). This enzyme can also utilize propionyl-CoA as a substrate, forming propionate in the process (Hesslinger et al., *Mol.Microbiol* 27:477-492 (1998)). Other phosphate acetyltransferases that exhibit activity on propionyl-CoA are found in *Bacillus subtilis* (Rado et al., *Biochim.Biophys.Acta* 321:114-125 (1973)), *Clostridium kluyveri* (Stadtman, *Methods Enzymol* 1:596-599 (1955)), and *Thermotoga maritima* (Bock et

al., *J Bacteriol.* 181:1861-1867 (1999)). Similarly, the *ptb* gene from *C. acetobutylicum* encodes phosphotransbutyrylase, an enzyme that reversibly converts butyryl-CoA into butyryl-phosphate (Wiesenborn et al., *Appl Environ.Microbiol* 55:317-322 (1989); Walter et al., *Gene* 134:107-111 (1993)). Additional *ptb* genes are found in butyrate-producing bacterium L2-50 (Louis et al., *J.Bacteriol.* 186:2099-2106 (2004)) and *Bacillus megaterium* (Vazquez et al., *Curr.Microbiol* 42:345-349 (2001)).

Protein	GenBank ID	GI Number	Organism
pta	NP_416800.1	71152910	*Escherichia coli*
pta	P39646	730415	*Bacillus subtilis*
pta	A5N801	146346896	*Clostridium kluyveri*
pta	Q9X0L4	6685776	*Thermotoga maritima*
ptb	NP_349676	34540484	*Clostridium acetobutylicum*
ptb	AAR19757.1	38425288	butyrate-producing bacterium L2-50
ptb	CAC07932.1	10046659	*Bacillus megaterium*

[0506] 2.7.2.a. Kinase or phosphotransferase enzymes in the EC class 2.7.2 transform carboxylic acids to phosphonic acids with concurrent hydrolysis of one ATP. Exemplary 4-Hydroxybutyrate kinase enzyme candidates include butyrate kinase (EC 2.7.2.7), isobutyrate kinase (EC 2.7.2.14), aspartokinase (EC 2.7.2.4), acetate kinase (EC 2.7.2.1) and gamma-glutamyl kinase (EC 2.7.2.11). Butyrate kinase catalyzes the reversible conversion of butyryl-phosphate to butyrate during acidogenesis in *Clostridial* species (Cary et al., *Appl Environ Microbiol* 56:1576-1583 (1990)). The *Clostridium acetobutylicum* enzyme is encoded by either of the two *buk* gene products (Huang et al., *J Mol.Microbiol Biotechnol* 2:33-38 (2000)). Other butyrate kinase enzymes are found in *C. butyricum* and *C. tetanomorphum* (Twarog et al., *J Bacteriol.* 86:112-117 (1963)). A related enzyme, isobutyrate kinase from *Thermotoga maritima,* was expressed in *E. coli* and crystallized (Diao et al., *J Bacteriol.* 191:2521-2529 (2009); Diao et al., *Acta Crystallogr.D.Biol.Crystallogr.* 59:1100-1102 (2003)). Aspartokinase catalyzes the ATP-dependent phosphorylation of aspartate and participates in the synthesis of several amino acids. The aspartokinase III enzyme in *E. coli,* encoded by *lysC,* has a broad substrate range and the catalytic residues involved in substrate specificity have been elucidated (Keng et al., *Arch Biochem Biophys* 335:73-81 (1996)). Two additional kinases in *E. coli* are also acetate kinase and gamma-glutamyl kinase. The *E. coli* acetate kinase, encoded by *ackA* (Skarstedt et al., *J.Biol.Chem.* 251:6775-6783 (1976)), phosphorylates propionate in addition to acetate

(Hesslinger et al., *Mol.Microbiol* 27:477-492 (1998)). The *E. coli* gamma-glutamyl kinase, encoded by *proB* (Smith et al., *J.Bacteriol.* 157:545-551 (1984)), phosphorylates the gamma carbonic acid group of glutamate.

Protein	**GenBank ID**	**GI Number**	**Organism**
buk1	NP_349675	15896326	*Clostridium acetobutylicum*
buk2	Q97II1	20137415	*Clostridium acetobutylicum*
buk2	Q9X278.1	6685256	*Thermotoga maritima*
lysC	NP_418448.1	16131850	*Escherichia coli*
ackA	NP_416799.1	16130231	*Escherichia coli*
proB	NP_414777.1	16128228	*Escherichia coli*

[0507] 2.8.3.a. CoA transferases catalyze the reversible transfer of a CoA moiety from one molecule to another. Several transformations in Figure 16B require a CoA transferase activity: succinyl-CoA transferase, 4-hydroxybutyryl-CoA transferse, 3-hydroxyisobutyryl-CoA transferase and methacrylyl-CoA transferase. Enzyme candidates for succinyl-CoA transferase have been described previously herein and are also applicable to this pathway. Additional exemplary CoA transferase enzymes include the gene products of *cat1*, *cat2*, and *cat3* of *Clostridium kluyveri* which have been shown to exhibit succinyl-CoA, 4-hydroxybutyryl-CoA, and butyryl-CoA transferase activity, respectively (Seedorf et al., *Proc.Natl.Acad.Sci U.S.A* 105:2128-2133 (2008); Sohling et al., *J Bacteriol.* 178:871-880 (1996)). Similar CoA transferase activities are also present in *Trichomonas vaginalis* (van Grinsven et al., *J.Biol.Chem.* 283:1411-1418 (2008)) and *Trypanosoma brucei* (Riviere et al., *J.Biol.Chem.* 279:45337-45346 (2004)).

Protein	GenBank ID	GI Number	Organism
cat1	P38946.1	729048	*Clostridium kluyveri*
cat2	P38942.2	172046066	*Clostridium kluyveri*
cat3	EDK35586.1	146349050	*Clostridium kluyveri*
TVAG_395550	XP_001330176	123975034	*Trichomonas vaginalis G3*
Tb11.02.0290	XP_828352	71754875	*Trypanosoma brucei*

[0508] The glutaconyl-CoA-transferase (EC 2.8.3.12) enzyme from anaerobic bacterium *Acidaminococcus fermentans* reacts with glutaconyl-CoA and 3-butenoyl-CoA (Mack et al., 226:41-51 (1994)), substrates similar in structure to 2,3-dehydroadipyl-CoA. The genes encoding this enzyme are *gctA* and *gctB*. This enzyme has reduced but detectable activity

with other CoA derivatives including glutaryl-CoA, 2-hydroxyglutaryl-CoA, adipyl-CoA, crotonyl-CoA and acrylyl-CoA (Buckel et al., *Eur.J Biochem.* 118:315-321 (1981)). The enzyme has been cloned and expressed in *E. coli* (Mack et al., *Eur.J.Biochem.* 226:41-51 (1994)). Glutaconate CoA-transferase activity has also been detected in *Clostridium sporosphaeroides* and *Clostridium symbiosum*. Additional glutaconate CoA-transferase enzymes can be inferred by homology to the *Acidaminococcus fermentans* protein sequence.

Protein	GenBank ID	GI Number	Organism
gctA	CAA57199.1	559392	*Acidaminococcus fermentans*
gctB	CAA57200.1	559393	*Acidaminococcus fermentans*
gctA	ACJ24333.1	212292816	*Clostridium symbiosum*
gctB	ACJ24326.1	212292808	*Clostridium symbiosum*
gctA	NP_603109.1	19703547	*Fusobacterium nucleatum*
gctB	NP_603110.1	19703548	*Fusobacterium nucleatum*

[0509] A CoA transferase that can utilize acetyl-CoA as the CoA donor is acetoacetyl-CoA transferase, encoded by the *E. coli atoA* (alpha subunit) and *atoD* (beta subunit) genes (Korolev et al., *Acta Crystallogr.D.Biol.Crystallogr.* 58:2116-2121 (2002); Vanderwinkel et al., 33:902-908 (1968)). This enzyme has a broad substrate range (Sramek et al., *Arch Biochem Biophys* 171:14-26 (1975)) and has been shown to transfer the CoA moiety to acetate from a variety of branched and linear acyl-CoA substrates, including isobutyrate (Matthies et al., *Appl Environ.Microbiol* 58:1435-1439 (1992)), valerate (Vanderwinkel et al., *Biochem.Biophys.Res.Commun.* 33:902-908 (1968)) and butanoate (Vanderwinkel et al., *Biochem.Biophys.Res.Commun.* 33:902-908 (1968)). This enzyme is induced at the transcriptional level by acetoacetate, so modification of regulatory control may be necessary for engineering this enzyme into a pathway (Pauli et al., *Eur.J Biochem.* 29:553-562 (1972)). Similar enzymes exist in *Corynebacterium glutamicum* ATCC 13032 (Duncan et al., 68:5186-5190 (2002)), *Clostridium acetobutylicum* (Cary et al., *Appl Environ Microbiol* 56:1576-1583 (1990); Wiesenborn et al., *Appl Environ Microbiol* 55:323-329 (1989)), and *Clostridium saccharoperbutylacetonicum* (Kosaka et al., *Biosci.Biotechnol Biochem.* 71:58-68 (2007)).

Gene	GI #	Accession No.	Organism
atoA	2492994	P76459.1	*Escherichia coli*
atoD	2492990	P76458.1	*Escherichia coli*
actA	62391407	YP_226809.1	*Corynebacterium glutamicum*

cg0592	62389399	YP_224801.1	*Corynebacterium glutamicum*
ctfA	15004866	NP_149326.1	*Clostridium acetobutylicum*
ctfB	15004867	NP_149327.1	*Clostridium acetobutylicum*
ctfA	31075384	AAP42564.1	*Clostridium saccharoperbutylacetonicum*
ctfB	31075385	AAP42565.1	*Clostridium saccharoperbutylacetonicum*

[0510] 3.1.2.a. 3-Hydroxyisobutyryl-CoA hydrolase catalyzes the conversion of 3-hydroxyisobutyryl-CoA to 3-hydroxyisobutyrate. This enzyme participates in valine degradation pathways (Shimomura et al., *J Biol Chem.* 269:14248-14253 (1994)). Genes encoding this enzyme include *hibch* of *Rattus norvegicus* (Shimomura et al., *Methods Enzymol.* 324:229-240 (2000)) and *Homo sapiens* (Shimomura et al., *supra*). Similar gene candidates can also be identified by sequence homology, including *hibch* of *Saccharomyces cerevisiae* and *BC_2292* of *Bacillus cereus*.

Gene name	**GenBank Accession #**	**GI#**	**Organism**
hibch	Q5XIE6.2	146324906	*Rattus norvegicus*
hibch	Q6NVY1.2	146324905	*Homo sapiens*
hibch	P28817.2	2506374	*Saccharomyces cerevisiae*
BC_2292	AP09256	29895975	*Bacillus cereus*

[0511] Methylmalonyl-CoA is converted to methylmalonate by methylmalonyl-CoA hydrolase (EC 3.1.2.7). This enzyme, isolated from *Rattus norvegicus* liver, is also active on malonyl-CoA and propionyl-CoA as alternative substrates (Kovachy et al., *J. Biol. Chem.*, 258: 11415-11421 (1983)). The gene associated with this enzyme has not been identified to date. Exemplary CoA hydrolases with broad substrate ranges are suitable candidates, as are the 3-HIB-CoA hydrolase enzymes described above. The enzyme encoded by *acot12* from *Rattus norvegicus* brain (Robinson et al., *Biochem.Biophys.Res.Commun.* 71:959-965 (1976)) can react with butyryl-CoA, hexanoyl-CoA and malonyl-CoA. The human dicarboxylic acid thioesterase, encoded by *acot8,* exhibits activity on glutaryl-CoA, adipyl-CoA, suberyl-CoA, sebacyl-CoA, and dodecanedioyl-CoA (Westin et al., *J.Biol.Chem.* 280:38125-38132 (2005)). The closest *E. coli* homolog to this enzyme, *tesB*, can also hydrolyze a range of CoA thiolesters (Naggert et al., *J Biol Chem* 266:11044-11050 (1991)). A similar enzyme has also been characterized in the rat liver (Deana R., *Biochem Int* 26:767-773 (1992)). Additional enzymes with hydrolase activity in *E. coli* include *ybgC*, *paaI*, and *ybdB* (Kuznetsova, et al., *FEMS Microbiol Rev*, 2005, 29(2):263-279; Song et al., *J Biol Chem*,

2006, 281(16):11028-38). Though its sequence has not been reported, the enzyme from the mitochondrion of the pea leaf has a broad substrate range, with demonstrated activity on acetyl-CoA, propionyl-CoA, butyryl-CoA, palmitoyl-CoA, oleoyl-CoA, succinyl-CoA, and crotonyl-CoA (Zeiher et al., *Plant.Physiol.* 94:20-27 (1990)). The acetyl-CoA hydrolase, *ACH1*, from *S. cerevisiae* represents another candidate hydrolase (Buu et al., *J.Biol.Chem.* 278:17203-17209 (2003)) .

Gene name	GenBank Accession #	GI#	Organism
acot12	NP_570103.1	18543355	*Rattus norvegicus*
tesB	NP_414986	16128437	*Escherichia coli*
acot8	CAA15502	3191970	*Homo sapiens*
acot8	NP_570112	51036669	*Rattus norvegicus*
tesA	NP_415027	16128478	*Escherichia coli*
ybgC	NP_415264	16128711	*Escherichia coli*
paaI	NP_415914	16129357	*Escherichia coli*
ybdB	NP_415129	16128580	*Escherichia coli*
ACH1	NP_009538	6319456	*Saccharomyces cerevisiae*

[0512] Yet another candidate hydrolase is the glutaconate CoA-transferase from *Acidaminococcus fermentans*. This enzyme was transformed by site-directed mutagenesis into an acyl-CoA hydrolase with activity on glutaryl-CoA, acetyl-CoA and 3-butenoyl-CoA (Mack et al., *FEBS.Lett.* 405:209-212 (1997)).This suggests that the enzymes encoding succinyl-CoA:3-ketoacid-CoA transferases and acetoacetyl-CoA:acetyl-CoA transferases may also serve as candidates for this reaction step but would require certain mutations to change their function.

Gene name	GenBank Accession #	GI#	Organism
gctA	CAA57199	559392	*Acidaminococcus fermentans*
gctB	CAA57200	559393	*Acidaminococcus fermentans*

[0513] 4.2.1.a. Two transformations in Figure 16B require dehydratase enzymes. The dehydration of 3-hydroxyisobutyrate to MAA is catalyzed by 3-hydroxyisobutyrate. Enzyme candidates for this transformation are described in Example VII. The dehydration of 3-hydroxyisobutyryl-CoA to methacrylyl-CoA is catalyzed by an enzyme with 3-hydroxyisobutyryl-CoA dehydratase activity. Exemplary enzymes include enoyl-CoA hydratases and crotonases.

[0514] Enoyl-CoA hydratases (EC 4.2.1.17) catalyze the dehydration of a range of 3-hydroxyacyl-CoA substrates (Roberts et al., *Arch.Microbiol* 117:99-108 (1978); Agnihotri et al., *Bioorg.Med.Chem.* 11:9-20 (2003); Conrad et al., *J Bacteriol.* 118:103-111 (1974)). The enoyl-CoA hydratase of *Pseudomonas putida*, encoded by *ech*, catalyzes the conversion of 3-hydroxybutyryl-CoA to crotonyl-CoA (Roberts et al., *Arch.Microbiol* 117:99-108 (1978)). This transformation is also catalyzed by the *crt* gene product of *Clostridium acetobutylicum*, the *crt1* gene product of *C. kluyveri,* and other clostridial organisms Atsumi et al., *Metab Eng* 10:305-311 (2008); Boynton et al., *J Bacteriol.* 178:3015-3024 (1996); Hillmer et al., *FEBS Lett.* 21:351-354 (1972)). Additional enoyl-CoA hydratase candidates are *phaA* and *phaB*, of *P. putida*, and *paaA* and *paaB* from *P. fluorescens* (Olivera et al., *Proc.Natl.Acad.Sci U.S.A* 95:6419-6424 (1998)). The gene product of *pimF* in *Rhodopseudomonas palustris* is predicted to encode an enoyl-CoA hydratase that participates in pimeloyl-CoA degradation (Harrison et al., *Microbiology* 151:727-736 (2005)). Lastly, a number of *Escherichia coli* genes have been shown to demonstrate enoyl-CoA hydratase functionality including *maoC* (Park et al., *J Bacteriol.* 185:5391-5397 (2003)), *paaF* (Ismail et al., *Eur.J Biochem.* 270:3047-3054 (2003); Park et al., *Appl.Biochem.Biotechnol* 113-116:335-346 (2004); Park et al., *Biotechnol Bioeng* 86:681-686 (2004)) and *paaG* (Ismail et al., *Eur.J Biochem.* 270:3047-3054 (2003); Park and Lee, *Appl.Biochem.Biotechnol* 113-116:335-346 (2004); Park and Yup, *Biotechnol Bioeng* 86:681-686 (2004)).

Gene	GenBank Accession No.	GI No.	Organism
ech	NP_745498.1	26990073	*Pseudomonas putida*
crt	NP_349318.1	15895969	*Clostridium acetobutylicum*
crt1	YP_001393856	153953091	*Clostridium kluyveri*
phaA	NP_745427.1	26990002	*Pseudomonas putida*
phaB	NP_745426.1	26990001	*Pseudomonas putida*
paaA	ABF82233.1	106636093	*Pseudomonas fluorescens*
paaB	ABF82234.1	106636094	*Pseudomonas fluorescens*
maoC	NP_415905.1	16129348	*Escherichia coli*
paaF	NP_415911.1	16129354	*Escherichia coli*
paaG	NP_415912.1	16129355	*Escherichia coli*

[0515] Alternatively, the *E. coli* gene products of *fadA* and *fadB* encode a multienzyme complex involved in fatty acid oxidation that exhibits enoyl-CoA hydratase activity (Yang et al., *Biochemistry* 30:6788-6795 (1991); Yang, *J Bacteriol.* 173:7405-7406 (1991);

Nakahigashi et al., *Nucleic Acids Res.* 18:4937 (1990)). Knocking out a negative regulator encoded by *fadR* can be utilized to activate the *fadB* gene product (Sato et al., *J Biosci.Bioeng* 103:38-44 (2007)). The *fadI* and *fadJ* genes encode similar functions and are naturally expressed under anaerobic conditions (Campbell et al., *Mol.Microbiol* 47:793-805 (2003)).

Protein	GenBank ID	GI Number	Organism
fadA	YP_026272.1	49176430	*Escherichia coli*
fadB	NP_418288.1	16131692	*Escherichia coli*
fadI	NP_416844.1	16130275	*Escherichia coli*
fadJ	NP_416843.1	16130274	*Escherichia coli*
fadR	NP_415705.1	16129150	*Escherichia coli*

[0516] 5.4.99.a. 4-Hydroxybutyryl-CoA is rearranged to form 3-hydroxyisobutyryl-CoA by an enzyme with 4-hydroxybutyryl-CoA mutase activity. This activity has not been demonstrated to date. Methylmalonyl-CoA mutase and isobutyryl-CoA mutase catalyze similar transformations. Exemplary methylmalonyl-CoA mutase and isobutyryl-CoA mutase enzyme candidates are described in Examples V and VII.

[0517] 6.2.1.a. The conversion of acyl-CoA substrates to their acid products can be catalyzed by a CoA acid-thiol ligase or CoA synthetase in the 6.2.1 family of enzymes. Enzymes of Figure 16B in this class include succinyl-CoA synthetase, 4-hydroxybutyryl-CoA synthetase, 3-hydroxyisobutyryl-CoA synthetase and methacrylyl-CoA synthetase. Succinyl-CoA synthetase enzyme candidates were described previously. Exemplary enzymes for catalyzing 4-hydroxybutyryl-CoA synthetase, 3-hydroxyisobutyryl-CoA synthetase and methacrylyl-CoA synthetase activities are described herein and below. ADP-forming acetyl-CoA synthetase (ACD, EC 6.2.1.13) is an enzyme that couples the conversion of acyl-CoA esters to their corresponding acids with the concomitant synthesis of ATP. ACD I from *Archaeoglobus fulgidus*, encoded by AF1211, was shown to operate on a variety of linear and branched-chain substrates including isobutyrate, isopentanoate, and fumarate (Musfeldt et al., *J Bacteriol.* 184:636-644 (2002)). A second reversible ACD in *Archaeoglobus fulgidus*, encoded by AF1983, was also shown to have a broad substrate range with high activity on cyclic compounds phenylacetate and indoleacetate (Musfeldt and Schonheit, *J Bacteriol.* 184:636-644 (2002)). The enzyme from *Haloarcula marismortui* (annotated as a succinyl-CoA synthetase) accepts propionate, butyrate, and branched-chain acids (isovalerate and isobutyrate) as substrates, and was shown to operate in the forward and reverse directions

(Brasen et al., *Arch Microbiol* 182:277-287 (2004)). The ACD encoded by *PAE3250* from hyperthermophilic crenarchaeon *Pyrobaculum aerophilum* showed the broadest substrate range of all characterized ACDs, reacting with acetyl-CoA, isobutyryl-CoA (preferred substrate) and phenylacetyl-CoA (Brasen et al, *supra*). Directed evolution or engineering can be used to modify this enzyme to operate at the physiological temperature of the host organism. The enzymes from *A. fulgidus*, *H. marismortui* and *P. aerophilum* have all been cloned, functionally expressed, and characterized in *E. coli* (Brasen and Schonheit, *supra*; Musfeldt and Schonheit, *J Bacteriol.* 184:636-644 (2002)). An additional candidate is succinyl-CoA synthetase, encoded by *sucCD* of *E. coli* and *LSC1* and *LSC2* genes of *Saccharomyces cerevisiae*. These enzymes catalyze the formation of succinyl-CoA from succinate with the concomitant consumption of one ATP in a reaction which is reversible *in vivo* (Buck et al., *Biochemistry* 24:6245-6252 (1985)). The acyl CoA ligase from *Pseudomonas putida* has been demonstrated to work on several aliphatic substrates including acetic, propionic, butyric, valeric, hexanoic, heptanoic, and octanoic acids and on aromatic compounds such as phenylacetic and phenoxyacetic acids (Fernandez-Valverde et al., *Appl.Environ.Microbiol.* 59:1149-1154 (1993)). A related enzyme, malonyl CoA synthetase (6.3.4.9) from *Rhizobium leguminosarum* could convert several diacids, namely, ethyl-, propyl-, allyl-, isopropyl-, dimethyl-, cyclopropyl-, cyclopropylmethylene-, cyclobutyl-, and benzyl-malonate into their corresponding monothioesters (Pohl et al., *J.Am.Chem.Soc.* 123:5822-5823 (2001)).

Protein	**GenBank ID**	**GI Number**	**Organism**
AF1211	NP_070039.1	11498810	*Archaeoglobus fulgidus*
AF1983	NP_070807.1	11499565	*Archaeoglobus fulgidus*
scs	YP_135572.1	55377722	*Haloarcula marismortui*
PAE3250	NP_560604.1	18313937	*Pyrobaculum aerophilum* str. IM2
sucC	NP_415256.1	16128703	*Escherichia coli*
sucD	AAC73823.1	1786949	*Escherichia coli*
LSC1	NP_014785	6324716	*Saccharomyces cerevisiae*
LSC2	NP_011760	6321683	*Saccharomyces cerevisiae*
paaF	AAC24333.2	22711873	*Pseudomonas putida*
matB	AAC83455.1	3982573	*Rhizobium leguminosarum*

[0518] An active reductive TCA cycle improves the yield of the acetyl-CoA derived product methacrylic acid (MAA), as shown in the exemplary pathways of Figure 18.

Pathways of the reductive TCA cycle are described herein as well as the conversion of succinate to 4-hydroxybutyryl-CoA and methacrylic acid (see also Figures 5 and 16B and Example VII). Figures 18A and 18B show exemplary pathways. The enzymatic transformations are carried out by the enzymes as shown. Figure 18A shows the pathways for fixation of CO_2 to succinate using the reductive TCA cycle. Figure 18B shows exemplary pathways for the biosynthesis of 3-hydroxyisobutyric acid and methacrylic acid from succinate; the enzymatic transformations shown are carried out by the following enzymes: A. 3-Hydroxyisobutyryl-CoA dehydratase, B. Methacrylyl-CoA synthetase, transferase or hydrolase, C. Succinyl-CoA transferase or synthetase, D. Succinyl-CoA reductase (aldehyde forming), E. 4-Hydroxybutyrate dehydrogenase, F. 4-Hydroxybutyrate kinase, G. Phosphotrans-4-hydroxybutyrylase, H. Succinate reductase, I. Succinyl-CoA reductase (alcohol forming), J. 4-Hydroxybutyryl-CoA synthetase or transferase, K. 4-Hydroxybutyryl-CoA mutase, L. 3-Hydroxyisobutyryl-CoA synthetase, transferase or hydrolase, M. 3-Hydroxyisobutyrate dehydratase.

Example XXI

Pathways for the Production of MAA and 2-Hydroxyisobutyric acid from Acetyl-CoA

[0519] An active reductive TCA cycle improves the yield of the acetyl-CoA derived product methacrylic acid (MAA), as shown in the flux distribution of Figure 16C. In this pathway, MAA is produced from acetyl-CoA in five enzymatic steps. In the first step, two molecules of acetyl-CoA are combined to form acetoacetyl-CoA. Acetoacetyl-CoA is subsequently reduced to 3-hydroxybutyryl-CoA. A methylmutase then rearranges the carbon backbone of 3-hydroxybutyryl-CoA to 2-hydroxyisobutyryl-CoA, which is then dehydrated to form methacrylyl-CoA. Alternatively, 2-hydroxyisobutyryl-CoA can be converted to 2-hydroxyisobutyrate, secreted, and recovered as product. The final step converting methacrylyl-CoA to MAA can be performed by a single enzyme or a series of enzymes. An alternate strategy for converting methacrylyl-CoA into MAA entails a multi-step process in which MAA-CoA is converted to MAA via 3-hydroxyisobutyrate. By this process, MAA-CoA is first converted to 3-hydroxyisobutyryl-CoA, which can subsequently be converted to 3-hydroxyisobutyrate by 3-hydroxyisobutyryl-CoA transferase, synthetase or hydrolase. 3-Hydroxyisobutyrate can then be converted to MAA biocatalytically via a 3-hydroxyisobutyrate dehdyratase, or secreted and converted to MAA by chemical dehydration.

[0520] Enzyme candidates for each pathway step are described herein. CoA transferase, synthetase and hydrolase enzymes catalyzing the conversion of methacrylyl-CoA to MAA were described above in Example VII. Enzymes describing the indirect conversion of methacrylyl-CoA to 3-hydroxyisobutyrate and methacrylic acid are alsodescribed above.

[0521] Acetoacetyl-CoA thiolase. The formation of acetoacetyl-CoA from two acetyl-CoA units is catalyzed by acetyl-CoA thiolase. Exemplary enzymes are described in Example X.

EXAMPLE XXII
Pathways for the Production of MAA from Pyruvate and Acetyl-CoA

[0522] An active reductive TCA cycle improves the yield of the acetyl-CoA derived product methacrylic acid (MAA). A flux distribution showing this improved yield is shown in Figure 16D.

[0523] Figure 16E (see also Figure 1 and Example I) depicts exemplary pathways to MAA from acetyl-CoA and pyruvate via the intermediate citramalate. Also shown are pathways to MAA from aconitate. In one pathway acetyl-CoA and pyruvate are converted to citramalate by citramalate synthase. Dehydration of citramalate can yield either citraconate or mesaconate. Mesaconate and citraconate are interconverted by a cis/trans isomerase. Decarboxylation of mesaconate or citraconate yields MAA. In an alternate pathway, citramalate is formed from acetyl-CoA and pyruvate via a citramalyl-CoA intermediate, catalyzed by citramalyl-CoA lyase and citramalyl-coA hydrolase, transferase or synthetase. Also shown are pathways from aconitate to MAA. In one pathway, aconitate is first decarboxylated to itaconate by aconitate decarboxylase. Itaconate is then isomerized to citraconate by itaconate delta-isomerase. Conversion of citraconate to MAA proceeds either directly by decarboxylation or indirectly via mesaconate. In an alternate pathway, the itaconate intermediate is first converted to itaconyl-CoA by a CoA transferase or synthetase. Hydration of itaconyl-CoA yields citramalyl-CoA, which can then be converted to MAA as described previously.

[0524] Table 1 as provided in Example I shows enzyme classes that can perform the steps depicted in Figure 16E. Exemplary enzymes are described below and in further detail in Example I.

[0525] EC 2.3.1.a Synthase. Citramalate synthase (EC 2.3.1.182) catalyzes the conversion of acetyl-CoA and pyruvate to citramalate and coenzyme A. Exemplary enzymes are described in Example I.

[0526] EC 2.8.3.a CoA transferase (Step E). CoA transferases catalyze the reversible transfer of a CoA moiety from one molecule to another. Two transformations in Figure 16E utilize a CoA transferase: conversion of citramalyl-CoA to citramalate and activation of itaconate to itaconyl-CoA. Citramalyl-CoA transferase (EC 2.8.3.7 and 2.8.3.11) transfers a CoA moiety from citramalyl-CoA to a donor. A citramalate:succinyl-CoA transferase enzyme is active in the 3-hydroxypropionate cycle of glyoxylate assimilation. Exemplary enzymes are described in Example I.

[0527] EC 3.2.1.a CoA hydrolase. Enzymes in the 3.1.2 family hydrolyze acyl-CoA molecules to their corresponding acids. Several CoA hydrolases with broad substrate ranges are suitable candidates for exhibiting citramalyl-CoA hydrolase activity. Exemplary enzymes are described in Example I.

[0528] EC 4.1.1.a Decarboxylase. The final step of MAA synthesis in Figure 16E is the decarboxylation of either mesaconate or citraconate. Exemplary enzymes are described in Example I.

[0529] EC 4.1.3.a Lyase. Citramalyl-CoA lyase (EC 4.1.3.25) converts acetyl-CoA and pyruvate to citramalyl-CoA. This enzyme participates in the 3-hydroxypropionate (3-HP) cycle of glyoxylate assimilation, where it acts in the citramalyl-CoA degrading direction. Exemplary enzymes are described in Example I.

[0530] EC 4.2.1.a Dehydratase. The dehydration of citramalate to citraconate is catalyzed by an enzyme with citramalate dehydratase (citraconate forming) activity (EC 4.2.1.35). This enzyme, along with citramalate synthase, participates in the threonine-independent isoleucine biosynthesis pathway characterized in *Methanocaldococcus jannaschii* and *Leptospira interrrogans*. The dehydration of citramalate in these organisms catalyzed by isopropylmalate isomerase (IPMI), which catalyzes both the dehydration of citramalate to citraconate and the subsequent trans-addition of water to citraconate to form methylmalate (Xu et al., *J Bacteriol.* 186:5400-5409 (2004); Drevland et al., *J Bacteriol.* 189:4391-4400 (2007)). Exemplary enzymes are described in Example I.

[0531] EC 5.2.1.a Cis/trans isomerase. The cis/trans isomerization of mesaconate and citraconate is catalyzed by an enzyme with citraconate isomerase activity. Suitable candidates include aconitate isomerase (EC 5.3.3.7), maleate *cis,trans*-isomerase (EC 5.2.1.1), maleylacetone *cis,trans*-isomerase and *cis,trans*-isomerase of unsaturated fatty acids (Cti). Aconitate isomerase interconverts *cis*- and *trans*-aconitate. Exemplary enzymes are described in Example I.

[0532] EC 5.3.3.a Delta-isomerase. The conversion of itaconate to citraconate is catalyzed by itaconate delta-isomerase. Exemplary enzymes are described in Example I.

[0533] EC 6.2.1 CoA synthetase. The conversion of citramalyl-CoA to citramalate and itaconate to itaconyl-CoA can be catalyzed by a CoA acid-thiol ligase or CoA synthetase in the 6.2.1 family of enzymes. Exemplary enzymes are described in Example I.

[0534] An active reductive TCA cycle improves the yield of the acetyl-CoA derived product methacrylic acid (MAA), as shown in the exemplary pathways of Figure 19. Pathways of the reductive TCA cycle are described herein as well as the conversion of acetyl-CoA and/or pyruvate via the intermediate citramalate to methacrylic acid (see also Figures 1 and 16E and Example I). Figures 19A and 19B show exemplary pathways. Figure 19A shows the pathways for fixation of CO_2 to acetyl-CoA and pyruvate using the reductive TCA cycle. Figure 19B shows exemplary pathways for the biosynthesis of methacrylate from acetyl-CoA and pyruvate; the enzymatic transformations shown are carried out by the following enzymes: 1. Citramalate synthase, 2. Citramalate dehydratase (citraconate forming), 3. Citraconate decarboxylase, 4. Citramalyl-CoA lyase, 5. Citramalyl-CoA transferase, synthetase or hydrolase, 6. Citramalate dehydratase (mesaconate forming), 7. Citraconate isomerase, 8. Mesaconate decarboxylase, 9. Aconitate decarboxylase, 10. Itaconate isomerase, 11. Itaconyl-CoA transferase or synthetase, 12. Itaconyl-CoA hydratase.

[0535] An active reductive TCA cycle improves the yield of the acetyl-CoA derived product methacrylic acid (MAA), as shown in the exemplary pathways of Figure 20. Pathways of the reductive TCA cycle are described herein as well as the conversion of acetyl-CoA to methacrylic acid or 2-hydroxyisobutyric acid (see also Figures 8 and Example X). Figures 20A and 20B show exemplary pathways. Figure 20A shows the pathways for fixation of CO_2 to acetyl-CoA using the reductive TCA cycle. Figure 20B shows exemplary

pathways for the biosynthesis of methacrylic acid and 2-hydroxyisobutyric acid from acetyl-CoA.

[0536] An active reductive TCA cycle improves the yield of the acetyl-CoA derived product methacrylic acid (MAA), as shown in the exemplary pathways of Figure 21. Pathways of the reductive TCA cycle are described herein as well as the conversion of acetyl-CoA via the intermediate 3-hydroxyisobutyryl-CoA to methacrylic acid (see also Figures 5, 8 and 9 and Examples VII, X, XI and XIV). Figures 21A and 21B show exemplary pathways. Figure 21A shows the pathways for fixation of CO_2 to acetyl-CoA using the reductive TCA cycle. Figure 21B shows exemplary pathways for the biosynthesis of methacrylic acid and 3-hydroxyisobutyric acid from acetyl-CoA; the enzymatic transformations shown are carried out by the following enzymes: 1) Acetoacetyl-CoA thiolase (AtoB), 2) 3-Hydroxybutyryl-CoA dehydrogenase (Hbd), 3) Crotonase (Crt), 4) Crotonyl-CoA hydratase (4-Budh), 5) 4-hydroxybutyryl-CoA mutase, 6) 3-hydroxyisobutyryl-CoA hydrolase, synthetase, or transferase, 7) 3-hydroxyisobutyric acid dehydratase, 8) 3-hydroxyisobutyryl-CoA dehydratase, 9) methacrylyl-CoA hydrolase, synthetase, or transferase. Crotonyl-CoA hydratase, forming 4-hydroxybutyrl-CoA, is the reverse reaction of 4-hydroxybutyrl-CoA dehydratase, which catalyze the reversible conversion of 4-hydroxybutyryl-CoA to crotonyl-CoA (see Example XIV). Thus, in an embodiment of the invention, a methacrylic acid pathway comprises acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, also referred to herein as 3-hydroxybutyryl-CoA dehydrogenase (see Figures 9 and 21), crotonase, 4-hydroxybutyryl-CoA dehydratase, also referred to herein as crotonyl-CoA hydratase, 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA synthetase or 3-hydroxyisobutyryl-CoA hydrolase or 3-hydroxyisobutyryl-CoA transferase, and 3-hydroxyisobutyrate dehydratase. Alternatively, a methacrylic acid pathway comprises acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, crotonase, 4-hydroxybutyryl-CoA dehydratase, 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA dehydratase, and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase (see Figure 21).

EXAMPLE XXIII
Exemplary Carboxylic Acid Reductases

[0537] This example describes the use of carboxylic acid reductases to carry out the conversion of a caroboxylic acid to an aldehyde.

[0538] 1.2.1.e Acid reductase. The conversion of unactivated acids to aldehydes can be carried out by an acid reductase. Examples of such conversions include, but are not limited, the conversion of 4-hydroxybutyrate, succinate, alpha-ketoglutarate, and 4-aminobutyrate to 4-hydroxybutanal, succinate semialdehyde, 2,5-dioxopentanoate, and 4-aminobutanal, respectively. One notable carboxylic acid reductase can be found in *Nocardia iowensis* which catalyzes the magnesium, ATP and NADPH-dependent reduction of carboxylic acids to their corresponding aldehydes (Venkitasubramanian et al., *J. Biol. Chem.* 282:478-485 (2007)). This enzyme is encoded by the *car* gene and was cloned and functionally expressed in *E. coli* (Venkitasubramanian et al., *J. Biol. Chem.* 282:478-485 (2007)). Expression of the *npt* gene product improved activity of the enzyme via post-transcriptional modification. The *npt* gene encodes a specific phosphopantetheine transferase (PPTase) that converts the inactive apo-enzyme to the active holo-enzyme. The natural substrate of this enzyme is vanillic acid, and the enzyme exhibits broad acceptance of aromatic and aliphatic substrates (Venkitasubramanian et al., in *Biocatalysis in the Pharmaceutical and Biotechnology Industires*, ed. R.N. Patel, Chapter 15, pp. 425-440, CRC Press LLC, Boca Raton, FL. (2006)).

Gene	Accession No.	GI No.	Organism
car	AAR91681.1	40796035	*Nocardia iowensis* (sp. NRRL 5646)
npt	ABI83656.1	114848891	*Nocardia iowensis* (sp. NRRL 5646)

[0539] Additional *car* and *npt* genes can be identified based on sequence homology.

Gene	Accession No.	GI No.	Organism
fadD9	YP_978699.1	121638475	*Mycobacterium bovis* BCG
BCG_2812c	YP_978898.1	121638674	*Mycobacterium bovis* BCG
nfa20150	YP_118225.1	54023983	*Nocardia farcinica* IFM 10152
nfa40540	YP_120266.1	54026024	*Nocardia farcinica* IFM 10152
SGR_6790	YP_001828302.1	182440583	*Streptomyces griseus* subsp. griseus NBRC 13350
SGR_665	YP_001822177.1	182434458	*Streptomyces griseus* subsp. griseus NBRC 13350

[0540] An additional enzyme candidate found in *Streptomyces griseus* is encoded by the *griC* and *griD* genes. This enzyme is believed to convert 3-amino-4-hydroxybenzoic acid to 3-amino-4-hydroxybenzaldehyde as deletion of either *griC* or *griD* led to accumulation of extracellular 3-acetylamino-4-hydroxybenzoic acid, a shunt product of 3-amino-4-hydroxybenzoic acid metabolism (Suzuki, et al., *J. Antibiot.* 60(6):380-387 (2007)). Co-expression of *griC* and *griD* with SGR_665, an enzyme similar in sequence to the *Nocardia iowensis npt*, can be beneficial.

Gene	**Accession No.**	**GI No.**	**Organism**
griC	182438036	YP_001825755.1	*Streptomyces griseus* subsp. griseus NBRC 13350
griD	182438037	YP_001825756.1	*Streptomyces griseus* subsp. griseus NBRC 13350
MSMEG_2956	YP_887275.1	YP_887275.1	*Mycobacterium smegmatis MC2 155*
MSMEG_5739	YP_889972.1	118469671	*Mycobacterium smegmatis MC2 155*
MSMEG_2648	YP_886985.1	118471293	*Mycobacterium smegmatis MC2 155*
MAP1040c	NP_959974.1	41407138	*Mycobacterium avium* subsp. *paratuberculosis* K-10
MAP2899c	NP_961833.1	41408997	*Mycobacterium avium* subsp. *paratuberculosis* K-10
MMAR_2117	YP_001850422.1	183982131	*Mycobacterium marinum M*
MMAR_2936	YP_001851230.1	183982939	*Mycobacterium marinum M*
MMAR_1916	YP_001850220.1	183981929	*Mycobacterium marinum M*
TpauDRAFT_33060	ZP_04027864.1	227980601	*Tsukamurella paurometabola DSM 20162*
TpauDRAFT_20920	ZP_04026660.1	227979396	*Tsukamurella paurometabola DSM 20162*
CPCC7001_1320	ZP_05045132.1	254431429	*Cyanobium PCC7001*
DDBDRAFT_0187729	XP_636931.1	66806417	*Dictyostelium discoideum AX4*

[0541] An enzyme with similar characteristics, alpha-aminoadipate reductase (AAR, EC 1.2.1.31), participates in lysine biosynthesis pathways in some fungal species. This enzyme naturally reduces alpha-aminoadipate to alpha-aminoadipate semialdehyde. The carboxyl group is first activated through the ATP-dependent formation of an adenylate that is then reduced by NAD(P)H to yield the aldehyde and AMP. Like CAR, this enzyme utilizes magnesium and requires activation by a PPTase. Enzyme candidates for AAR and its corresponding PPTase are found in *Saccharomyces cerevisiae* (Morris et al., *Gene* 98:141-145 (1991)), *Candida albicans* (Guo et al., *Mol. Genet. Genomics* 269:271-279 (2003)), and *Schizosaccharomyces pombe* (Ford et al., *Curr. Genet.* 28:131-137 (1995)). The AAR from *S. pombe* exhibited significant activity when expressed in *E. coli* (Guo et al., *Yeast* 21:1279-1288 (2004)). The AAR from *Penicillium chrysogenum* accepts S-carboxymethyl-L-cysteine as an alternate substrate, but did not react with adipate, L-glutamate or diaminopimelate (Hijarrubia et al., *J. Biol. Chem.* 278:8250-8256 (2003)). The gene encoding the *P. chrysogenum* PPTase has not been identified to date.

Gene	**Accession No.**	**GI No.**	**Organism**
LYS2	AAA34747.1	171867	*Saccharomyces cerevisiae*
LYS5	P50113.1	1708896	*Saccharomyces cerevisiae*
LYS2	AAC02241.1	2853226	*Candida albicans*
LYS5	AAO26020.1	28136195	*Candida albicans*
Lys1p	P40976.3	13124791	*Schizosaccharomyces pombe*
Lys7p	Q10474.1	1723561	*Schizosaccharomyces pombe*
Lys2	CAA74300.1	3282044	*Penicillium chrysogenum*

[0542] Cloning and Expression of Carboxylic Acid Reductase. *Escherichia coli* is used as a target organism to engineer the pathway for methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate. *E. coli* provides a good host for generating a non-naturally occurring microorganism capable of producing methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate. *E. coli* is amenable to genetic manipulation and is known to be capable of producing various intermediates and products effectively under various oxygenation conditions.

[0543] To generate a microbial organism strain such as an *E. coli* strain engineered to produce methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate], nucleic acids encoding a carboxylic acid reductase and phosphopantetheine transferase are expressed in *E. coli* using well known molecular biology

techniques (see, for example, Sambrook, supra, 2001; Ausubel supra, 1999). In particular, *car* genes from *Nocardia iowensis* (designated 720), *Mycobacterium smegmatis* mc(2)155 (designated 890), *Mycobacterium avium* subspecies *paratuberculosis* K-10 (designated 891) and *Mycobacterium marinum M* (designated 892) were cloned into pZS*13 vectors (Expressys, Ruelzheim, Germany) under control of PA1/lacO promoters. The *npt* (ABI83656.1) gene (i.e., 721) was cloned into the pKJL33S vector, a derivative of the original mini-F plasmid vector PML31 under control of promoters and ribosomal binding sites similar to those used in pZS*13.

[0544] The *car* gene (GNM_720) was cloned by PCR from *Nocardia* genomic DNA. Its nucleic acid and protein sequences are shown in Figures 22A and 22B, respectively. A codon-optimized version of the *npt* gene (GNM_721) was synthesized by GeneArt (Regensburg, Germany). Its nucleic acid and protein sequences are shown in Figures 23A and 23B, respectively. The nucleic acid and protein sequences for the *Mycobacterium smegmatis* mc(2)155 (designated 890), *Mycobacterium avium* subspecies *paratuberculosis* K-10 (designated 891) and *Mycobacterium marinum M* (designated 892) genes and enzymes can be found in Figures 24, 25, and 26, respectively. The plasmids are transformed into a host cell to express the proteins and enzymes required for methacrylic acid, methacrylate ester, 3-hydroxyisobutyrate and/or 2-hydroxyisobutyrate production.

[0545] Additional CAR variants were generated. A codon optimized version of CAR 891 was generated and designated 891GA. The nucleic acid and amino acid sequences of CAR 891GA are shown in Figures 27A and 27B, respectively. Over 2000 CAR variants were generated. In particular, all 20 amino acid combinations were made at positions V295, M296, G297, G391, G421, D413, G414, Y415, G416, and S417, and additional variants were tested as well. Exemplary CAR variants include: E16K; Q95L; L100M; A1011T; K823E; T941S; H15Q; D198E; G446C; S392N; F699L; V883I; F467S; T987S; R12H; V295G; V295A; V295S; V295T; V295C; V295V; V295L; V295I; V295M; V295P; V295F; V295Y; V295W; V295D; V295E; V295N; V295Q; V295H; V295K; V295R; M296G; M296A; M296S; M296T; M296C; M296V; M296L; M296I; M296M; M296P; M296F; M296Y; M296W; M296D; M296E; M296N; M296Q; M296H; M296K; M296R; G297G; G297A; G297S; G297T; G297C; G297V; G297L; G297I; G297M; G297P; G297F; G297Y; G297W; G297D; G297E; G297N; G297Q; G297H; G297K; G297R; G391G; G391A; G391S; G391T; G391C; G391V; G391L; G391I; G391M; G391P; G391F; G391Y; G391W; G391D; G391E;

G391N; G391Q; G391H; G391K; G391R; G421G; G421A; G421S; G421T; G421C; G421V; G421L; G421I G421M; G421P; G421F; G421Y; G421W; G421D; G421E; G421N; G421Q; G421H; G421K; G421R; D413G; D413A; D413S; D413T; D413C; D413V; D413L; D413I; D413M; D413P; D413F; D413Y; D413W; D413D; D413E; D413N; D413Q; D413H; D413K; D413R; G414G; G414A; G414S; G414T; G414C; G414V; G414L; G414I; G414M; G414P; G414F; G414Y; G414W; G414D; G414E; G414N; G414Q; G414H; G414K; G414R; Y415G; Y415A; Y415S; Y415T; Y415C; Y415V; Y415L; Y415I; Y415M; Y415P; Y415F; Y415Y; Y415W; Y415D; Y415E; Y415N; Y415Q; Y415H; Y415K; Y415R; G416G; G416A; G416S; G416T; G416C; G416V; G416L; G416I; G416M; G416P; G416F; G416Y; G416W; G416D; G416E; G416N; G416Q; G416H; G416K; G416R; S417G; S417A; S417S; S417T; S417C; S417V S417L; S417I; S417M; S417P; S417F; S417Y; S417W; S417D; S417E; S417N; S417Q; S417H; S417K; and S417R.

[0546] The CAR variants were screened for activity, and numerous CAR variants were found to exhibit CAR activity.

[0547] This example describes the use of CAR for converting carboxylic acids to aldehydes.

EXAMPLE XXIV

PATHWAY FOR THE CONVERSION OF 4-HYDROXYBUTYRYL-COA TO METHYL METHACRYLATE

[0548] This example describes a pathway for converting 4-hydroxybutyryl-CoA to methyl methacrylate as an exemplary methacrylate ester.

[0549] An exemplary pathway to methyl methacrylate is shown in Figure 30. Briefly, 4-hydroxybutyryl-CoA can be converted to 3-hydroxybutyryl-CoA as described above. 3-Hydroxyisobutyryl-CoA can be converted to 3-hydroxyisobutyrate methyl ester as shown in Figure 30 using an alcohol tranferase, as described above, in particular a methyl transferase (see Example III; see also WO/2007/039415 and U.S. Patent No. 7,901,915). 3-Hydroxyisobutyrate methyl ester can be converted to methyl methacrylate by a dehydratase or by chemical conversion, as described above, for example, for the conversion of methacrylate to methacrylate esters (see Figure 2). Exemplary dehydratases include those described above, for example, in Examples V, VI, X and XII.

[0550] Nucleic acids (especially a DNA) coding for an enzyme capable of effecting the transfer of an alcohol moietyl from an alcohol starting material as defined herein to (meth)acrylyl CoA under removal of the CoA moiety, such as a transferase (EC 2) or hydrolase (EC 3) class of enzymes, e.g. lipase, esterase (such as acetyl choline esterase), transferase (such as choline acetyl transferase), protease or acylase (such as aminoacylase) (including coding for one or more such enzymes).

[0551] An EC group 2 enzyme, that is a transferase includes, for example, transaminases, transamidases, transketolases, transphosphorylases or choline acetyl transferase that are known to catalyse the movement of a chemical group from one compound to another. An EC class 3; hydrolase, which are also capable of catalysing transesterification reactions, include, for example, lipases from *Candida antartica* (CAL B), porcine pancreatic lipase (PPL), *Candid rugosa* (CRL) *Pseudomonas cepacia* (PCL) and the like; esterases such as pig liver esterase (PLE) acetyl choline esterase; also proteases such as subtilisin, protease, for instance from *Aspergillus* spp., *Bacillus* spp., *Rhizopus* spp and other hydrolases such as penicillin amidase or, for example, L-amino acylase can be suitable enzymes to catalyse the transfer.

[0552] These enzymes can be derived from a prokaryote such as a bacterium, a eukaryote or a higher organism, such as lipase from *Candida* spp., esterase or choline acetyl transferase from mammalian cells, and they can be supplied to the reaction as such. Alternatively, it can also be produced biosynthetically from appropriate starting materials derived from biomass.

[0553] While this example describes conversion to methyl methacrylate, it is understood by those skilled in the art that other methacrylate esters can be made using a similar pathway and selecting an appropriate transferase for the desired ester.

EXAMPLE XXV

CONVERSION OF 3-HYDROXYISOBUTYRATE, 2-HYDROXYISOBUTYRATE, 3-HYDROXYISOBUTYRYL-COA OR 2-HYRDOXYISOBUTYRYL-COA TO A METHACRYLATE ESTER

[0554] This example describes the conversion of 3–hydroxyisobutyrate, 2-hydroxyisobutyrate, 3-hydroxyisobutyryl-CoA or 2-hydroxyisobutyryl-CoA to a methacrylate ester.

[0555] Alternative scenarios included herein are:

(1) A. Sugars to 3-hydroxyisobutyryl-CoA (enzymatic, pathways described previously), B. 3-hydroxyisobutyryl-CoA to 3-hydroxyisobutyrate ester by an alcohol transferase, C. 3-hydroxyisobutyrate ester to methacrylate ester by a dehydratase enzyme or chemical conversion

(2) A. Sugars to 2-hydroxyisobutyryl-CoA (enzymatic, pathways described previously), B. 2-hydroxyisobutyryl-CoA to 2-hydroxyisobutyrate ester by an alcohol transferase, C. 2-hydroxyisobutyrate ester to methacrylate ester by a dehydratase enzyme or chemical conversion

(3) A. Sugars to 3-hydroxyisobutyrate (enzymatic, pathway described previously), B. 3-hydroxyisobutyrate to 3-hydroxyisobutyrate ester by a 3-hydroxyisobutyrate ester forming enzyme, C. 3-hydroxyisobutyrate ester to methacrylate ester by a dehydratase enzyme or chemical conversion

(4) A. Sugars to 2-hydroxyisobutyrate (enzymatic, pathway described previously), B. 2-hydroxyisobutyrate to 2-hydroxyisobutyrate ester by a 2-hydroxyisobutyrate ester forming enzyme, C. 2-hydroxyisobutyrate ester to methacrylate ester by a dehydratase enzyme or chemical conversion

(5) A. Exogenous 3-hydroxyisobutyrate supplied to organism (could be a product of another organism (i.e. co-culture or separate fermentation) or could be derived from other sources), B. 3-hydroxyisobutyrate to 2-hydroxyisobutyrate ester by a 3-hydroxyisobutyrate ester forming enzyme, C. 3-hydroxyisobutyrate ester to methacrylate ester by a dehydratase enzyme or chemical conversion

(6) A. Exogenous 3-hydroxyisobutyrate supplied to organism (could be a product of another organism (i.e. co-culture or separate fermentation) or could be derived from other sources), B. 3-hydroxyisobutyrate to 3-hydroxyisobutyryl-CoA by a CoA transferase or synthetase, C. formation of 3-hydroxyisobutyrate ester by an alcohol transferase enzyme, C. 3-hydroxyisobutyrate ester to methacrylate ester by a dehydratase enzyme or chemical conversion

(7) A. Exogenous 2-hydroxyisobutyrate supplied to organism (could be a product of another organism (i.e. co-culture or separate fermentation) or could be

derived from other sources), B. 2-hydroxyisobutyrate to 2-hydroxyisobutyrate ester by a 2-hydroxyisobutyrate ester forming enzyme, C. 2-hydroxyisobutyrate ester to methacrylate ester by a dehydratase enzyme or chemical conversion

(8) A. Exogenous 2-hydroxyisobutyrate supplied to organism (could be a product of another organism (i.e. co-culture or separate fermentation) or could be derived from other sources), B. 2-hydroxyisobutyrate to 2-hydroxyisobutyryl-CoA by a CoA transferase or synthetase, C. formation of 2-hydroxyisobutyrate ester by an alcohol transferase enzyme, C. 2-hydroxyisobutyrate ester to methacrylate ester by a dehydratase enzyme or chemical conversion

[0556] Pathways to methacrylate esters from 3-hydroxybutyrate, 2-hydroxybutyrate, 3-hydroxyisobutyryl-CoA and 2-hydroxyisobutyryl-CoA are shown in Figures 28 and 29. Examplary pathways to these methacrylate ester precursors have been described previously in this application and are shown in Figures 3, 5 and 8. 3-Hydroxybutyrate can be formed from succinyl-CoA by the pathway shown in Figure 3 or from 4-hydroxybutyryl-CoA as shown in Figure 5. 3-Hydroxybutyryl-CoA can be formed from 4-hydroxybutyryl-CoA by the pathway shown in Figure 5. 2-Hydroxyisobutyrate and 2-hydroxybutyryl-CoA can be formed by the pathway described in Figure 8.

[0557] 2-Hydroxyisobutyrate and its CoA ester, 2-hydroxyisobutyryl-CoA, can be interconverted by a 2-hydroxyisobutyryl-CoA transferase or 2-hydroxyisobutyryl-CoA synthetase. Likewise, 3-hydroxyisobutyrate and its CoA ester, 3-hydroxyisobutyryl-CoA, can be interconverted by a 3-hydroxyisobutyryl-CoA transferase or 3-hydroxyisobutyryl-CoA synthetase. Exemplary CoA transferase and synethetase enzymes are described above in Examples I and VII.

[0558] The dehydration of 3-hydroxyisobutyric ester to methacrylic ester can be performed under similar conditions as the dehydration of 3-hyroxyisobutyric acid to methacrylic acid. These reaction conditions are mild (reference: US Patent application 20100068773).

[0559] The chemical dehydration of 2-hydroxyisobutyrate ester to methacrylate ester is analogous to the dehydration of 2-hydroxyisobutyric acid to methacrylic acid, which is disclosed, for example, in U.S. Pat. Nos. 3,666,805 and 5,225,594. In these references, 2-

hydroxyisobutryic acid is dehydrated using metal oxides and hydroxides, ion exchange resins, alumina,silica, amines, phosphines, alkali metal alkoxides or carboxylates, at reaction temperatures typically between 160-250 degrees C. In one method (U.S. Pat. No. 5,225,594), 2-hydroxyisobutyric acid and sodiumhydroxide were reacted at 185 – 195 degrees C under vacuum (300 torr) with stirring, resulting in a 97.1% conversion of 2-hydroxyisobutyric acid, and a 96% yield of methacrylic acid. A similar approach could be applied to dehydrate 2-hydroxyisobutyric ester to methacrylic ester.

[0560] Throughout this application various publications have been referenced. The disclosures of these publications in their entireties, including GenBank and GI number publications, are hereby incorporated by reference in this application in order to more fully describe the state of the art to which this invention pertains. Although the invention has been described with reference to the examples provided above, it should be understood that various modifications can be made without departing from the spirit of the invention.

What is claimed is:

1. A non-naturally occurring microbial organism having a methacrylic acid pathway, said microbial organism comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid, said methacrylic acid pathway comprising a pathway selected from:

(a) citramalate synthase, citramalate dehydratase (citraconate forming), and citraconate decarboxylase;

(b) citramalate synthase, citramalate dehydratase (citraconate forming), citraconate isomerase, and mesaconate decarboxylase;

(c) citramalate synthase, citramalate dehydratase (mesaconate forming), citraconate isomerase, and citraconate decarboxylase;

(d) citramalate synthase, citramalate dehydratase (mesaconate forming), and mesaconate decarboxylase;

(e) citramalyl-CoA lyase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (citraconate forming), and citraconate decarboxylase;

(f) citramalyl-CoA lyase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (citraconate forming), citraconate isomerase, and mesaconate decarboxylase;

(g) citramalyl-CoA lyase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (mesaconate forming), and mesaconate decarboxylase;

(h) citramalyl-CoA lyase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (mesaconate forming), citraconate isomerase, and citraconate decarboxylase;

(i) aconitate decarboxylase, itaconate isomerase, and citraconate decarboxylase;

(j) aconitate decarboxylase, itaconate isomerase, citraconate isomerase, and mesaconate decarboxylase;

(k) aconitate decarboxylase, itaconyl-CoA transferase, synthetase or hydrolase, citramalyl-CoA dehydratase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (citraconate forming), and citraconate decarboxylase;

(l) aconitate decarboxylase, itaconyl-CoA transferase, synthetase or hydrolase, citramalyl-CoA dehydratase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (citraconate forming), citraconate isomerase, and mesaconate decarboxylase;

(m) aconitate decarboxylase, itaconyl-CoA transferase, synthetase or hydrolase, citramalyl-CoA dehydratase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (mesaconate forming), and mesaconate decarboxylase; and

(n) aconitate decarboxylase, itaconyl-CoA transferase, synthetase or hydrolase, citramalyl-CoA dehydratase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (mesaconate forming), citraconate isomerase, and citraconate decarboxylase;

(o) acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, crotonase, 4-hydroxybutyryl-CoA dehydratase, 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA synthetase or 3-hydroxyisobutyryl-CoA hydrolase or 3-hydroxyisobutyryl-CoA transferase, and 3-hydroxyisobutyrate dehydratase; and

(p) acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, crotonase, 4-hydroxybutyryl-CoA dehydratase, 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA dehydratase, and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase.

2. The non-naturally occurring microbial organism of claim 1, wherein said microbial organism comprises two, three, four, five, six or seven exogenous nucleic acids each encoding a methacrylic acid pathway enzyme.

3. The non-naturally occurring microbial organism of claim 2, wherein said microbial organism comprises exogenous nucleic acids encoding each of the enzymes of at least one of the pathways selected from (a)-(p).

4. The non-naturally occurring microbial organism of claim 1, wherein said non-naturally occurring microbial organism further comprises a methacrylate ester pathway comprising at least one exogenous nucleic acid encoding a methacrylate ester pathway enzyme expressed in a sufficient amount to produce a methacrylate ester, said methacrylate ester pathway comprising methacrylyl-CoA synthetase, methacrylyl-CoA transferase, and alcohol transferase.

5. The non-naturally occurring microbial organism of claim 4, wherein said microbial organism comprises two or three exogenous nucleic acids each encoding a methacrylate ester pathway enzyme.

6. The non-naturally occurring microbial organism of claim 4, wherein said three exogenous nucleic acids encode methacrylyl-CoA synthetase, methacrylyl-CoA transferase, and alcohol transferase.

7. A non-naturally occurring microbial organism having a methacrylate ester pathway, said microbial organism comprising at least one exogenous nucleic acid encoding a methacrylate ester pathway enzyme expressed in a sufficient amount to produce a methacrylate ester, said methacrylate ester pathway comprising methacrylyl-CoA transferase.

8. The non-naturally occurring microbial organism of claim 7, wherein the methacrylate ester pathway further comprises methacrylyl-CoA synthetase and alcohol transferase.

9. The non-naturally occurring microbial organism of claim 7, wherein said microbial organism comprises two or three exogenous nucleic acids each encoding a methacrylate ester pathway enzyme.

10. The non-naturally occurring microbial organism of claim 7, wherein said three exogenous nucleic acids encode methacrylyl-CoA synthetase, methacrylyl-CoA transferase and alcohol transferase.

11. The non-naturally occurring microbial organism of claim 7, wherein said non-naturally occurring microbial organism further comprises a methacrylic acid pathway selected from:

(a) citramalate synthase, citramalate dehydratase (citraconate forming), and citraconate decarboxylase;

(b) citramalate synthase, citramalate dehydratase (citraconate forming), citraconate isomerase, and mesaconate decarboxylase;

(c) citramalate synthase, citramalate dehydratase (mesaconate forming), citraconate isomerase, and citraconate decarboxylase;

(d) citramalate synthase, citramalate dehydratase (mesaconate forming), and mesaconate decarboxylase;

(e) citramalyl-CoA lyase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (citraconate forming), and citraconate decarboxylase;

(f) citramalyl-CoA lyase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (citraconate forming), citraconate isomerase, and mesaconate decarboxylase;

(g) citramalyl-CoA lyase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (mesaconate forming), and mesaconate decarboxylase;

(h) citramalyl-CoA lyase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (mesaconate forming), citraconate isomerase, and citraconate decarboxylase;

(i) aconitate decarboxylase, itaconate isomerase, and citraconate decarboxylase;

(j) aconitate decarboxylase, itaconate isomerase, citraconate isomerase, and mesaconate decarboxylase;

(k) aconitate decarboxylase, itaconyl-CoA transferase, synthetase or hydrolase, citramalyl-CoA dehydratase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (citraconate forming), and citraconate decarboxylase;

(l) aconitate decarboxylase, itaconyl-CoA transferase, synthetase or hydrolase, citramalyl-CoA dehydratase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (citraconate forming), citraconate isomerase, and mesaconate decarboxylase;

(m) aconitate decarboxylase, itaconyl-CoA transferase, synthetase or hydrolase, citramalyl-CoA dehydratase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (mesaconate forming), and mesaconate decarboxylase;

(n) aconitate decarboxylase, itaconyl-CoA transferase, synthetase or hydrolase, citramalyl-CoA dehydratase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (mesaconate forming), citraconate isomerase, and citraconate decarboxylase;

(o) 3-hydroxyisobutyrate dehydratase;

(p) methylmalonyl-CoA mutase, methylmalonyl-CoA reductase, 3-hydroxyisobutyrate dehydrogenase, and 3-hydroxyisobutyrate dehydratase;

(q) methylmalonyl-CoA mutase, methylmalonyl-CoA epimerase, methylmalonyl-CoA reductase, 3-hydroxyisobutyrate dehydrogenase, and 3-hydroxyisobutyrate dehydratase;

(r) methylmalonyl-CoA mutase, alcohol/aldehyde dehydrogenase, and 3-hydroxyisobutyrate dehydratase;

(s) methylmalonyl-CoA mutase, methylmalonyl-CoA epimerase, alcohol/aldehyde dehydrogenase, and 3-hydroxyisobutyrate dehydratase;

(t) methylmalonyl-CoA mutase, methylmalonyl-CoA reductase, 3-amino-2-methylpropionate transaminase, and 3-amino-2-methylpropionate ammonia lyase;

(u) methylmalonyl-CoA mutase, methylmalonyl-CoA epimerase, methylmalonyl-CoA reductase, 3-amino-2-methylpropionate transaminase, and 3-amino-2-methylpropionate ammonia lyase;

(v) 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA synthetase or 3-hydroxyisobutyryl-CoA hydrolase or 3-hydroxyisobutyryl-CoA transferase, and 3-hydroxyisobutyrate dehydratase;

(w) aspartate aminotransferase, glutamate mutase, 3-methylaspartase, and mesaconate decarboxylase;

(x) alpha-ketoglutarate reductase, 2-hydroxyglutamate mutase, 3-methylmalate dehydratase, and mesaconate decarboxylase;

(y) acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, 3-hydroxybutyryl-CoA mutase, 2-hydroxyisobutyryl-CoA dehydratase, and methacrylyl-CoA transferase or methacrylyl-CoA hydrolase or methacrylyl-CoA synthetase;

(z) acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, 3-hydroxybutyryl-CoA mutase, 2-hydroxyisobutyryl-CoA dehydratase, enoyl-CoA hydratase, and 3-hydroxyisobutyryl-CoA hydrolase or 3-hydroxyisobutyryl-CoA synthetase or 3-hydroxyisobutyryl-CoA transferase, and 3-hydroxyisobutyrate dehydratase;

(aa) 4-hydroxybutyryl-CoA dehydratase, vinylacetyl-CoA Δ-isomerase, crotonase, 3-hydroxybutyryl-CoA mutase, 2-hydroxyisobutyryl-CoA dehydratase, and any of methacrylyl-CoA hydrolase or methacrylyl-CoA synthetase or methacrylyl-CoA transferase;

(bb) 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA dehydratase, and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase;

(cc) acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, crotonase, butyryl-CoA dehydrogenase, isobutyryl-CoA mutase, isobutyryl-CoA dehydrogenase, and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase;

(dd) lactate dehydrogenase, lactate-CoA transferase, lactoyl-CoA dehydratase, acyl-CoA dehydrogenase, propionyl-CoA carboxylase, methylmalonyl-CoA reductase, 3-hydroxyisobutyrate dehydrogenase, and 3-hydroxyisobutyrate dehydratase;

(ee) valine aminotransferase, 2-ketoisovalerate dehydrogenase, isobutyryl-CoA dehydrogenase, and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase;

(ff) acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, crotonase, 4-hydroxybutyryl-CoA dehydratase, 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA synthetase or 3-hydroxyisobutyryl-CoA hydrolase or 3-hydroxyisobutyryl-CoA transferase, and 3-hydroxyisobutyrate dehydratase; and

(gg) acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, crotonase, 4-hydroxybutyryl-CoA dehydratase, 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA dehydratase, and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase.

12. A non-naturally occurring microbial organism having a methacrylic acid pathway, said microbial organism comprising at least one exogenous nucleic acid encoding a methacrylic acid pathway enzyme expressed in a sufficient amount to produce methacrylic acid; said non-naturally occurring microbial organism further comprising:

(i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from an ATP-citrate lyase, citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase, or optionally isocitrate dehydrogenase, aconitase, citryl-CoA synthetase or citryl-CoA lyase;

(ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or

(iii) at least one exogenous nucleic acid encodes an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof;

wherein said methacrylic acid pathway comprises a pathway selected from:

(a) citramalate synthase, citramalate dehydratase (citraconate forming), and citraconate decarboxylase;

(b) citramalate synthase, citramalate dehydratase (citraconate forming), citraconate isomerase, and mesaconate decarboxylase;

(c) citramalate synthase, citramalate dehydratase (mesaconate forming), citraconate isomerase, and citraconate decarboxylase;

(d) citramalate synthase, citramalate dehydratase (mesaconate forming), and mesaconate decarboxylase;

(e) citramalyl-CoA lyase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (citraconate forming), and citraconate decarboxylase;

(f) citramalyl-CoA lyase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (citraconate forming), citraconate isomerase, and mesaconate decarboxylase;

(g) citramalyl-CoA lyase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (mesaconate forming), and mesaconate decarboxylase;

(h) citramalyl-CoA lyase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (mesaconate forming), citraconate isomerase, and citraconate decarboxylase;

(i) aconitate decarboxylase, itaconate isomerase, and citraconate decarboxylase;

(j) aconitate decarboxylase, itaconate isomerase, citraconate isomerase, and mesaconate decarboxylase;

(k) aconitate decarboxylase, itaconyl-CoA transferase, synthetase or hydrolase, citramalyl-CoA dehydratase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (citraconate forming), and citraconate decarboxylase;

(l) aconitate decarboxylase, itaconyl-CoA transferase, synthetase or hydrolase, citramalyl-CoA dehydratase, citramalyl-CoA transferase, synthetase or hydrolase,

citramalate dehydratase (citraconate forming), citraconate isomerase, and mesaconate decarboxylase;

(m) aconitate decarboxylase, itaconyl-CoA transferase, synthetase or hydrolase, citramalyl-CoA dehydratase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (mesaconate forming), and mesaconate decarboxylase;

(n) aconitate decarboxylase, itaconyl-CoA transferase, synthetase or hydrolase, citramalyl-CoA dehydratase, citramalyl-CoA transferase, synthetase or hydrolase, citramalate dehydratase (mesaconate forming), citraconate isomerase, and citraconate decarboxylase;

(o) 3-hydroxyisobutyrate dehydratase;

(p) methylmalonyl-CoA mutase, methylmalonyl-CoA reductase, 3-hydroxyisobutyrate dehydrogenase, and 3-hydroxyisobutyrate dehydratase;

(q) methylmalonyl-CoA mutase, methylmalonyl-CoA epimerase, methylmalonyl-CoA reductase, 3-hydroxyisobutyrate dehydrogenase, and 3-hydroxyisobutyrate dehydratase;

(r) methylmalonyl-CoA mutase, alcohol/aldehyde dehydrogenase, and 3-hydroxyisobutyrate dehydratase;

(s) methylmalonyl-CoA mutase, methylmalonyl-CoA epimerase, alcohol/aldehyde dehydrogenase, and 3-hydroxyisobutyrate dehydratase;

(t) methylmalonyl-CoA mutase, methylmalonyl-CoA reductase, 3-amino-2-methylpropionate transaminase, and 3-amino-2-methylpropionate ammonia lyase;

(u) methylmalonyl-CoA mutase, methylmalonyl-CoA epimerase, methylmalonyl-CoA reductase, 3-amino-2-methylpropionate transaminase, and 3-amino-2-methylpropionate ammonia lyase;

(v) 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA synthetase or 3-hydroxyisobutyryl-CoA hydrolase or 3-hydroxyisobutyryl-CoA transferase, and 3-hydroxyisobutyrate dehydratase;

(w) aspartate aminotransferase, glutamate mutase, 3-methylaspartase, and mesaconate decarboxylase;

(x) alpha-ketoglutarate reductase, 2-hydroxyglutamate mutase, 3-methylmalate dehydratase, and mesaconate decarboxylase;

(y) acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, 3-hydroxybutyryl-CoA mutase, 2-hydroxyisobutyryl-CoA dehydratase, and methacrylyl-CoA transferase or methacrylyl-CoA hydrolase or methacrylyl-CoA synthetase;

(z) acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, 3-hydroxybutyryl-CoA mutase, 2-hydroxyisobutyryl-CoA dehydratase, enoyl-CoA hydratase, and 3-hydroxyisobutyryl-CoA hydrolase or 3-hydroxyisobutyryl-CoA synthetase or 3-hydroxyisobutyryl-CoA transferase, and 3-hydroxyisobutyrate dehydratase;

(aa) 4-hydroxybutyryl-CoA dehydratase, vinylacetyl-CoA Δ-isomerase, crotonase, 3-hydroxybutyryl-CoA mutase, 2-hydroxyisobutyryl-CoA dehydratase, and any of methacrylyl-CoA hydrolase or methacrylyl-CoA synthetase or methacrylyl-CoA transferase;

(bb) 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA dehydratase, and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase;

(cc) acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, crotonase, butyryl-CoA dehydrogenase, isobutyryl-CoA mutase, isobutyryl-CoA dehydrogenase, and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase;

(dd) lactate dehydrogenase, lactate-CoA transferase, lactoyl-CoA dehydratase, acyl-CoA dehydrogenase, propionyl-CoA carboxylase, methylmalonyl-CoA reductase, 3-hydroxyisobutyrate dehydrogenase, and 3-hydroxyisobutyrate dehydratase;

(ee) valine aminotransferase, 2-ketoisovalerate dehydrogenase, isobutyryl-CoA dehydrogenase, and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase;

(ff) acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, crotonase, 4-hydroxybutyryl-CoA dehydratase, 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA synthetase or 3-hydroxyisobutyryl-CoA hydrolase or 3-hydroxyisobutyryl-CoA transferase, and 3-hydroxyisobutyrate dehydratase; and

(gg) acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, crotonase, 4-hydroxybutyryl-CoA dehydratase, 4-hydroxybutyryl-CoA mutase, 3-hydroxyisobutyryl-CoA dehydratase,

and methacrylyl-CoA synthetase or methacrylyl-CoA hydrolase or methacrylyl-CoA transferase.

13. The non-naturally occurring microbial organism of claim 12, wherein said microbial organism comprises two, three, four, five, six or seven exogenous nucleic acids each encoding a methacrylic acid pathway enzyme.

14. The non-naturally occurring microbial organism of claim 13, wherein said microbial organism comprises exogenous nucleic acids encoding each of the enzymes of at least one of the pathways selected from (a)-(gg).

15. A non-naturally occurring microbial organism having a 2-hydroxyisobutyric acid pathway, said microbial organism comprising at least one exogenous nucleic acid encoding a 2-hydroxyisobutyric acid pathway enzyme expressed in a sufficient amount to produce 2-hydroxyisobutyric acid; said non-naturally occurring microbial organism further comprising:

(i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from an ATP-citrate lyase, citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase, or optionally isocitrate dehydrogenase, aconitase, citryl-CoA synthetase or citryl-CoA lyase;

(ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or

(iii) at least one exogenous nucleic acid encodes an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof;

wherein said 2-hydroxyisobutyric acid pathway comprises a pathway selected from:

(a) acetoacetyl-CoA thiolase, acetoacetyl-CoA reductase, 3-hydroxybutyryl-CoA mutase, and 2-hydroxyisobutyryl-CoA transferase or 2-hydroxyisobutyryl-CoA hydrolase or 2-hydroxyisobutyryl-CoA synthetase; and

(b) 4-hydroxybutyryl-CoA dehydratase, vinylacetyl-CoA Δ-isomerase, crotonase, 3-hydroxybutyryl-CoA mutase, and any of 2-hydroxyisobutyryl-CoA hydrolase or 2-hydroxyisobutyryl-CoA synthetase or 2-hydroxyisobutyryl-CoA transferase.

16. The non-naturally occurring microbial organism of claim 15, wherein said microbial organism comprises two, three, four or five exogenous nucleic acids each encoding a methacrylic acid pathway enzyme.

17. The non-naturally occurring microbial organism of claim 15, wherein said microbial organism comprises exogenous nucleic acids encoding each of the enzymes of at least one of the pathways selected from (a)-(b).

18. A non-naturally occurring microbial organism having a 3-hydroxyisobutyric acid pathway, said microbial organism comprising at least one exogenous nucleic acid encoding a 3-hydroxyisobutyric acid pathway enzyme expressed in a sufficient amount to produce 3-hydroxyisobutyric acid; said non-naturally occurring microbial organism further comprising:

(i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from an ATP-citrate lyase, citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase, or optionally isocitrate dehydrogenase, aconitase, citryl-CoA synthetase or citryl-CoA lyase;

(ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or

(iii) at least one exogenous nucleic acid encodes an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof;

wherein said 3-hydroxyisobutyric acid pathway comprises a pathway selected from:

(a) 4-hydroxybutyryl-CoA mutase; and

(b) 4-hydroxybutyryl-CoA mutase and 3-hydroxyisobutyryl-CoA synthetase or 3-hydroxyisobutyryl-CoA hydrolase or 3-hydroxyisobutyryl-CoA transferase.

19. The non-naturally occurring microbial organism of claim 18, wherein said microbial organism comprises two exogenous nucleic acids each encoding a methacrylic acid pathway enzyme.

20. The non-naturally occurring microbial organism of claim 18, wherein said microbial organism comprises exogenous nucleic acids encoding each of the enzymes of at least one of the pathways selected from (a)-(b).

21. A non-naturally occurring microbial having a 3-hydroxyisobutyryl-CoA pathway, said microbial organism comprising at least one exogenous nucleic acid encoding a 3-hydroxyisobutyric acid pathway enzyme expressed in a sufficient amount to produce 3-hydroxyisobutyric acid; said non-naturally occurring microbial organism further comprising:

(i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from an ATP-citrate lyase, citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase, or optionally isocitrate dehydrogenase, aconitase, citryl-CoA synthetase or citryl-CoA lyase;

(ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or

(iii) at least one exogenous nucleic acid encodes an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof;

wherein said 3-hydroxyisobutyryl-CoA pathway comprises 4-hydroxybutyryl-CoA mutase.

22. A non-naturally occurring microbial organism having a methacrylate ester pathway, said microbial organism comprising comprising at least one exogenous nucleic acid encoding a methacrylate ester pathway enzyme expressed in a sufficient amount to produce a methacrylate ester, said methacrylate ester pathway comprising an alcohol transferase or an ester-forming enzyme, and a dehydratase.

23. The non-naturally occurring microbial organism of claim 22, wherein said microbial organism comprises two exogenous nucleic acids each encoding a methacrylate ester pathway enzyme.

24. The non-naturally occurring microbial organism of claim 22, wherein said two exogenous nucleic acids encode an alcohol transferase and a dehydratase or or an ester-forming enzyme and a dehydratase.

25. The non-naturally occurring microbial organism of claim 22, wherein said dehydratase converts a 3-hydroxyisobutyrate ester or a 2-hydroxyisobutyrate ester to said methacrylate ester; or wherein said alcohol transferase converts 3-hydroxyisobutyryl-CoA to a 3-hydroxyisobutyrate ester or 2-hydroxyisobutyryl-CoA to 2-hydroxyisobutyrate ester.

26. The non-naturally occurring microbial organism of claim 22, wherein said microbial organism comprises a methacrylate ester pathway comprising:

(a) a 3-hydroxyisobutyrate-CoA transferase or a 3-hydroxyisobutyrate-CoA synthetase; an alcohol transferase; and a dehydratase;

(b) a 3-hydroxyisobutyrate ester-forming enzyme and a dehydratase;

(c) a 2-hydroxyisobutyrate-CoA transferase or a 2-hydroxyisobutyrate-CoA synthetase; an alcohol transferase; and a dehydratase; or

(d) a 2-hydroxyisobutyrate ester-forming enzyme and a dehydratase.

27. A non-naturally occurring microbial organism having a methyl methacrylate pathway, said microbial organism comprising at least one exogenous nucleic acid encoding a methyl methacrylate pathway enzyme expressed in a sufficient amount to produce a methyl methacrylate, said methyl methacrylate pathway comprising an alcohol transferase or an ester-forming enzyme, and a dehydratase.

28. The non-naturally occurring microbial organism of claim 27, wherein said microbial organism comprises two exogenous nucleic acids each encoding a methyl methacrylate pathway enzyme.

29. The non-naturally occurring microbial organism of claim 27, wherein said two exogenous nucleic acids encode an alcohol transferase and a dehydratase or an ester-forming enzyme and a dehydratase.

30. The non-naturally ocurring microbial organism of any of claims 7-11 and 21-29, further comprising:

(i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from an ATP-citrate lyase, a citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase, or optionally isocitrate dehydrogenase, aconitase, citryl-CoA synthetase or citryl-CoA lyase;

(ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or

(iii) at least one exogenous nucleic acid encodes an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof.

31. The non-naturally occurring microbial organism of any of claims 12, 15, 18, 21 or 30, wherein said microbial organism comprising (i) further comprises an exogenous nucleic acid encoding an enzyme selected from a pyruvate:ferredoxin oxidoreductase, an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, an acetate kinase, a phosphotransacetylase, an acetyl-CoA synthetase, an NAD(P)H:ferredoxin oxidoreductase, ferredoxin, and combinations thereof.

32. The non-naturally occurring microbial organism of any of claims 12, 15, 18, 21 or 30, wherein said microbial organism comprising (ii) further comprises an exogenous nucleic acid encoding an enzyme selected from an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, and combinations thereof.

33. The non-naturally occurring microbial organism of any of claims 12, 15, 18, 21 or 30, wherein said microbial organism comprises two, three, four or five exogenous nucleic acids each encoding enzymes of (i), (ii) or (iii).

34. The non-naturally occurring microbial orgnaism of any of claims 12, 15, 18, 21 or 30, wherein said microbial organism comprising (i) comprises three exogenous nucleic acids encoding ATP-citrate lyase or citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase;

wherein said microbial organism comprising (ii) comprises four exogenous nucleic acids encoding pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase or a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or

wherein said microbial organism comprising (iii) comprises two exogenous nucleic acids encoding CO dehydrogenase and H_2 hydrogenase.

35. The non-naturally occurring microbial organism of any of claims 1-34, wherein said at least one exogenous nucleic acid is a heterologous nucleic acid, or wherein said non-naturally occurring microbial organism is in a substantially anaerobic culture medium.

36. A method for producing a methacrylate ester comprising, culturing a non-naturally occurring microbial organism under conditions and for a sufficient period of time to produce a 3-hydroxyisobutyrate ester, a 2-hydroxyisobutyrate ester, or methyl-3-hydroxyisobutyrate, wherein said non-naturally occurring microbial organism comprises an exogenous nucleic acid encoding an alcohol transferase; or 3-hydroxyisobutyrate ester-forming enzyme, 2-hydroxyisobutyrate ester-forming enzyme or methyl-3-hydroxyisobutyrate ester-forming enzyme, expressed in a sufficient amount to produce a 3-hydroxyisobutyrate ester, a 2-hydroxyisobutyrate ester or methyl-3-hydroxyisobutyrate, and chemically dehydrating said 3-hydroxyisobutyrate ester or 2-hydroxyisobutyrate ester to produce a methacrylate ester, or chemically dehydrating said methyl-3-hydroxyisobutyrate to produce methyl methacrylate.

37. The method of claim 36, wherein said microbial organism comprises:

a 3-hydroxyisobutyrate ester pathway comprising:

(a) a 3-hydroxyisobutyrate-CoA transferase or a 3-hydroxyisobutyrate-CoA synthetase; and an alcohol transferase; or

(b) 3-hydroxyisobutyrate ester-forming enzyme; or

a 2-hydroxyisobutyrate ester pathway comprising:

(a) a 2-hydroxyisobutyrate-CoA transferase or a 2-hydroxyisobutyrate-CoA synthetase; and an alcohol transferase; or

(b) a 2-hydroxyisobutyrate ester-forming enzyme.

38. A method for producing a methacrylate ester comprising, culturing a non-naturally occurring microbial organism under conditions and for a sufficient period of time to produce a 3-hydroxyisobutyrate ester, a 2-hydroxyisobutyrate ester, or methyl-3-hydroxyisobutyrate,

wherein said non-naturally occurring microbial organism comprises an exogenous nucleic acid encoding an alcohol transferase; or a 3-hydroxyisobutyrate ester-forming enzyme, a 2-hydroxyisobutyrate ester-forming enzyme, or a methyl-3-hydroxyisobutyrate ester-forming enzyme, expressed in a sufficient amount to produce a 3-hydroxyisobutyrate ester, 2-hydroxyisobutyrate ester, or methyl-3-hydroxyisobutyrate, and said non-naturally occurring microbial organism further comprising:

(i) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from an ATP-citrate lyase, a citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase, or optionally isocitrate dehydrogenase, aconitase, citryl-CoA synthetase or citryl-CoA lyase;

(ii) a reductive TCA pathway comprising at least one exogenous nucleic acid encoding a reductive TCA pathway enzyme, wherein said at least one exogenous nucleic acid is selected from a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase, a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or

(iii) at least one exogenous nucleic acid encoding an enzyme selected from a CO dehydrogenase, an H_2 hydrogenase, and combinations thereof, and

chemically dehydrating said 3-hydroxyisobutyrate ester or 2-hydroxy isobutyrate ester to produce a methacrylate ester; or chemically dehydrating said methyl-3-hydroxyisobutyrate to produce methyl methacrylate.

39. The method of claim 38, wherein said microbial organism comprises:

a 3-hydroxyisobutyrate ester pathway comprising:

(a) a 3-hydroxyisobutyrate-CoA transferase or a 3-hydroxyisobutyrate-CoA synthetase; and an alcohol transferase; or

(b) 3-hydroxyisobutyrate ester-forming enzyme; or

a 2-hydroxyisobutyrate ester pathway comprising:

(a) a 2-hydroxyisobutyrate-CoA transferase or a 2-hydroxyisobutyrate-CoA synthetase; and an alcohol transferase; or

(b) a 2-hydroxyisobutyrate ester-forming enzyme.

40. The method of any of claims 38-39, wherein said microbial organism comprising (i) further comprises an exogenous nucleic acid encoding an enzyme selected from a pyruvate:ferredoxin oxidoreductase, an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, an acetate kinase, a phosphotransacetylase, an acetyl-CoA synthetase, an NAD(P)H:ferredoxin oxidoreductase, ferredoxin, and combinations thereof.

41. The method of any of claims 38-39, wherein said microbial organism comprising (ii) further comprises an exogenous nucleic acid encoding an enzyme selected from an aconitase, an isocitrate dehydrogenase, a succinyl-CoA synthetase, a succinyl-CoA transferase, a fumarase, a malate dehydrogenase, and combinations thereof.

42. The method of any of claims 38-39, wherein said microbial organism comprising (i) comprises three exogenous nucleic acids encoding an ATP-citrate lyase or citrate lyase, a fumarate reductase, and an alpha-ketoglutarate:ferredoxin oxidoreductase;

wherein said microbial organism comprising (ii) comprises four exogenous nucleic acids encoding a pyruvate:ferredoxin oxidoreductase, a phosphoenolpyruvate carboxylase or a phosphoenolpyruvate carboxykinase, a CO dehydrogenase, and an H_2 hydrogenase; or

wherein said microbial organism comprising (iii) comprises two exogenous nucleic acids encoding a CO dehydrogenase and an H_2 hydrogenase.

43. A method for producing methacrylic acid, comprising culturing the non-naturally occurring microbial organism of any of claims 1-6, 12-14 or 30-35, under conditions and for a sufficient period of time to produce methacrylic acid.

44. A method for producing a methacrylate ester, comprising culturing the non-naturally occurring microbial organism of any of claims 7-11, 22-29 or 30-35 under conditions and for a sufficient period of time to produce a methacrylate ester.

45. A method for producing 2-hydroxyisobutyric acid, 3-hydroxyisobutyric acid, or 3-hydroxyisobutyryl-CoA, comprising culturing the non-naturally occurring microbial organism of any of claims 15-21 or 30-35 under conditions and for a sufficient period of time to produce 2-hydroxyisobutyric acid, 3-hydroxyisobutyric acid, or 3-hydroxyisobutyryl-CoA.

46. The method of any one of claims 36-45, wherein at least one of said exogenous nucleic acids is a heterologous nucleic acid; or wherein said non-naturally occurring microbial organism is in a substantially anaerobic culture medium.