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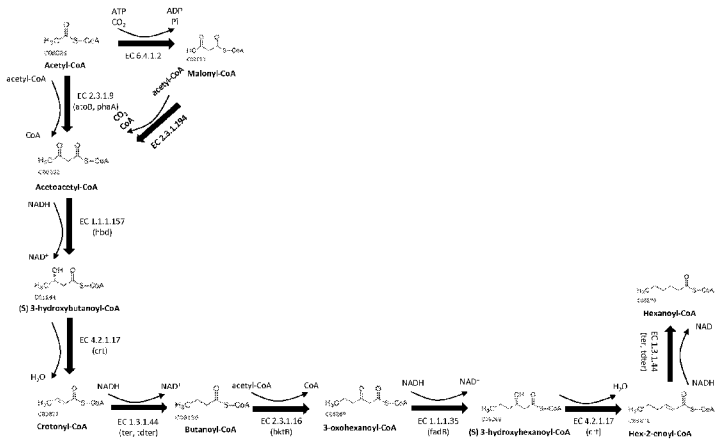
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(54) Title: METHODS OF PRODUCING 6-CARBON CHEMICALS VIA CoA-DEPENDENT CARBON CHAIN ELONGATION ASSOCIATED WITH CARBON STORAGE

FIGURE 1



(57) **Abstract:** This document describes biochemical pathways for producing adipic acid, caprolactam, 6-aminohexanoic acid, hexamethylenediamine or 1,6-hexanediol by forming two terminal functional groups, comprised of carboxyl, amine or hydroxyl groups, in a C6 aliphatic backbone substrate. These pathways, metabolic engineering and cultivation strategies described herein rely on CoA-dependent elongation enzymes or analogues enzymes associated with the carbon storage pathways from polyhydroxyalkanoate accumulating bacteria.

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METHODS OF PRODUCING 6-CARBON CHEMICALS VIA CoA-DEPENDENT CARBON CHAIN ELONGATION ASSOCIATED WITH CARBON STORAGE

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims priority to U.S. Application Serial No. 61/576,401, filed December 16, 2011. The disclosure of the application is incorporated by reference in its entirety.

TECHNICAL FIELD

This invention relates to methods for biosynthesizing adipic acid, 6-aminohexanoic acid, hexamethylenediamine, caprolactam, and 1,6-hexanediol using one or more isolated enzymes such as β-ketothiolases, dehydrogenases, reductases, hydratases, monooxygenases, ω-hydroxylases and transaminases or using recombinant host cells expressing one or more such enzymes.

BACKGROUND

Nylons are polyamides that are generally synthesized by the condensation polymerisation of a diamine with a dicarboxylic acid. Similarly, nylons may be produced by the condensation polymerisation of lactams. A ubiquitous nylon is nylon 6,6, which is produced by reaction of hexamethylenediamine (HMD) and adipic acid. Nylon 6 is produced by a ring opening polymerisation of caprolactam. Therefore, adipic acid, hexamethylenediamine and caprolactam are important intermediates in the production of nylons (Anton & Baird, Polyamides Fibers, Encyclopedia of Polymer Science and Technology, 2001).

Industrially, adipic acid and caprolactam are produced via air oxidation of cyclohexane. The air oxidation of cyclohexane produces, in a series of steps, a mixture of cyclohexanone (K) and cyclohexanol (A), designated as KA oil. Nitric acid oxidation of KA oil produces adipic acid (Musser, Adipic acid, Ullmann's Encyclopedia of Industrial Chemistry, 2000). Caprolactam is produced from cyclohexanone via its oxime and subsequent acid rearrangement (Fuchs, Kieczka and Moran, Caprolactam, Ullmann's Encyclopedia of Industrial Chemistry, 2000)

Industrially, hexamethylenediamine (HMD) is produced by hydrocyanation of C6 building block to adiponitrile, followed by hydrogenation to HMD (Herzog and

Smiley, Hexamethylenediamine, Ullmann's Encyclopedia of Industrial Chemistry, 2012).

Given a reliance on petrochemical feedstocks; biotechnology offers an alternative approach via biocatalysis. Biocatalysis is the use of biological catalysts, such as enzymes, to perform biochemical transformations of organic compounds.

Both bioderived feedstocks and petrochemical feedstocks are viable starting materils for the biocatalysis processes.

Accordingly, against this background, it is clear that there is a need for sustainable methods for producing adipic acid, caprolactam, 6-aminohexanoic acid, hexamethylenediamine and 1,6-hexanediol (hereafter "C6 building blocks") wherein the methods are biocatalyst based (Jang et al, Biotechnology & Bioengineering, 2012, 109(10), 2437 - 2459).

However, no wild-type prokaryote or eukaryote naturally overproduces or excretes C6 building blocks to the extracellular environment. Nevertheless, the metabolism of adipic acid and caprolactam has been reported (Ramsay et al, Appl. Environ. Microbiol, 1986, 52(1), 152 - 156; and Kulkarni and Kanekar, Current Microbiology, 1998, 37, 191 - 194).

The dicarboxylic acid, adipic acid, is converted efficiently as a carbon source by a number of bacteria and yeasts via β-oxidation into central metabolites. β-oxidation of adipate to 3-oxoadipate faciliates further catabolism via, for example, the ortho-cleavage pathway associated with aromatic substrate degradation. The catabolism of 3-oxoadipyl-CoA to acetyl-CoA and succinyl-CoA by several bacteria and fungi has been characterised comprehensively (Harwood and Parales, Annual Review of Microbiology, 1996, 50, 553 - 590). Both adipate and 6-aminohexanoate are intermediates in the catabolism of caprolactam, finally degraded via 3-oxoadipyl-CoA to central metabolites.

Potential metabolic pathways have been suggested for producing adipic acid from biomass-sugar: (1) biochemically from glucose to cis,cis muconic acid via the ortho-cleavage aromatic degradation pathway, followed by chemical catalysis to adipic acid; (2) a reversible adipic acid degradation pathway via the condensation of succinyl-CoA and acetyl-CoA and (3) combining β-oxidation, a fatty acid synthase and ω-oxidation. However, no information using these strategies has been reported (Jang et al, Biotechnology & Bioengineering, 2012, 109(10), 2437 - 2459).

The optimality principle states that microorganisms regulate their biochemical networks to support maximum biomass growth. Beyond the need for expressing heterologous pathways in a host organism, directing carbon flux towards C6 building blocks that serve as carbon sources rather than as biomass growth constituents, contradicts the optimality principle. For example, transferring the 1-butanol pathway from Clostridium species into other production strains has often fallen short by an order of magnitude compared to the production performance of native producers (Shen et al, Appl. Environ. Microbiol, 201 1, 77(9), 2905 - 2915).

The efficient synthesis of the six carbon aliphatic backbone precursor is a key consideration in synthesizing C6 building blocks prior to forming terminal functional groups, such as carboxyl, amine or hydroxyl groups, on the C6 aliphatic backbone.

SUMMARY

This document is based at least in part on the discovery that it is possible to construct biochemical pathways for producing a six carbon chain aliphatic backbone precursor, in which two functional groups, e.g., carboxyl, amine or hydroxyl, can be formed, leading to the synthesis of one or more of adipic acid, 6-aminohexanoic acid, hexamethylenediamine, caprolactam, and 1,6-hexanediol (hereafter "C6 building blocks"). These pathways, metabolic engineering, and cultivation strategies described herein rely on CoA-dependent elongation enzymes or homologs thereof associated with the carbon storage pathways from polyhydroxyalkanoate accumulating bacteria such as *Cupriavidus necator.*

In the face of the optimality principle, it surprisingly has been discovered that appropriate non-natural pathways, feedstocks, host microorganisms, attenuation strategies to the host's biochemical network, and cultivation strategies may be combined to efficiently produce C6 building blocks.

In some embodiments, the C6 aliphatic backbone for conversion to a C6 building block can be formed from acetyl-CoA via two cycles of CoA-dependent carbon chain elongation using either NADH or NADPH dependent enzymes. See FIG. 1 and FIG. 2.

In some embodiments, the enzyme in the CoA-dependent carbon chain elongation pathway generating the C6 aliphatic backbone catalyzes irreversible enzymatic steps.

In some embodiments, the terminal carboxyl groups can be enzymatically formed using an *acyl-CoA hydrolase,* an *aldehyde dehydrogenase,* a *6-oxohexanoate dehydrogenase* or a *cytochrome P450/oi-hydroxylase.* See FIG. 3 and FIG. 4.

In some embodiments, the terminal amine groups can be enzymatically formed using an ω-*transaminase* or a *diamine transaminase.* See FIG. 5 and FIG. 6.

In some embodiments, the terminal hydroxyl group can be enzymatically formed using a *cytochrome P450,* a *monooxygenase,* or an *alcohol dehydrogenase.* See FIG. 7 and FIG. 8.

In one aspect, this document features a method for biosynthesizing one or more products selected from the group consisting of adipic acid, 6-aminohexanoic acid, hexamethylenediamine, caprolactam, and 1,6-hexanediol. The method includes enzymatically synthesizing a six carbon chain aliphatic backbone (e.g., hexanoyl-CoA) and enzymatically forming, in one or more steps, two terminal functional groups selected from the group consisting of carboxyl, amine, and hydroxyl groups in the backbone to directly produce the product or producing the product in a subsequent step. The two terminal functional groups can be the same or can be different.

Hexanoyl-CoA can be enzymatically synthesized from acetyl-CoA via two cycles of CoA-dependent carbon chain elongation using either NADH or NADPH dependent enzymes. Hexanoyl-CoA can be formed by conversion of hex-2-enoyl-CoA by an *enoyl-CoA reductase* classified under EC 1.3.1.44, EC 1.3.1.38, or EC 1.3.1.8 such as the gene product of *ter* or *tdter.* Hex-2-enoyl-CoA can be formed by conversion of (S) 3-hydroxyhexanoyl-CoA by a *trans-2-enoyl-CoA hydratase* classified under EC 4.2.1.17 or by conversion of (R) 3-hydroxyhexanoyl-CoA by a *trans-2-enoyl-CoA hydratase* classified under EC 4.2.1.119. The *trans-2-enoyl-CoA hydratase* can be the gene product of *crt.* (S) 3-hydroxyhexanoyl-CoA can be formed by conversion of 3-oxohexanoyl-CoA by a *3-hydroxyacyl-CoA dehydrogenase* classified under EC 1.1.1.35 such as the *3-hydroxyacyl-CoA dehydrogenase* encoded by *fadB.* The 3-oxohexanoyl-CoA can be formed by conversion of butanoyl-CoA by an *acetyl-CoA C-acyltransferase* classified under EC 2.3.1.16 such as that encoded by *bktB.* Butanoyl-CoA can be formed by conversion of crotonyl-CoA by an *enoyl-CoA reductase* classified under EC 1.3.1.44, EC 1.3.1.38, or EC 1.3.1.8. Crotonyl-CoA can be formed by conversion of (S) 3-hydroxybutanoyl-CoA by a *trans-2-enoyl-CoA*

hydratase classified under EC 4.2.1.17. The (S) 3-hydroxybutanoyl-CoA can be formed by conversion of acetoacetyl-CoA by a *3-hydroxybutyryl-CoA dehydrogenase* classified under EC 1.1.1.157 such as a *3-hydroxybutyryl-CoA dehydrogenase* is encoded by *hbd.* The acetoacetyl-CoA can be formed by conversion of acetyl-CoA by an *acetyl-CoA C-acyltransferase* classified under EC 2.3.1.9 such as that encoded by *atoB* or *phaA.* The acetoacetyl-CoA can be formed by conversion of malonyl-CoA by an *acetoacetyl-CoA synthase* classified under EC 2.3. 1. 194. The malonyl-CoA can be formed by conversion of acetyl-CoA by an *acetyl-CoA carboxylase* classified under EC 6.4. 1.2. The *trans-2-enoyl-CoA hydratase* can be the gene product *oiphaJ.*

The (R) 3-hydroxyhexanoyl-CoA can be formed by conversion of 3-oxohexanoyl-CoA by a *3-oxoacyl-CoA reductase* classified under EC 1.1.1.100 such as that encoded by *fabG.* The crotonyl-CoA can be formed by conversion of (R) 3-hydroxybutanoyl-CoA by a trans-2-enoyl-CoA hydratase classified under EC 4.2.1.1 19. (R) 3-hydroxybutanoyl-CoA can be formed by conversion of acetoacetyl-CoA by an *acetoacyl-CoA reductase* classified under EC 1.1.1.36 such as that encoded by *phaB.*

In any of the methods described herein, the method can include producing hexanoate by forming a first terminal carboxyl group in hexanoyl CoA using an *acyl-CoA hydrolase* and an *aldehyde dehydrogenase,* or *a thioesterase.* The *acyl-CoA hydrolase* or *thioesterase* can be encoded by *YciA, tesB* or *Acotl 3.*

Hexanoate can be produced by forming a first terminal carboxyl group in hexanal by an *aldehyde dehydrogenase* classified under EC 1.2.1.4. Hexanal can be formed by conversion of hexanoyl-CoA by a *butanal dehydrogenase* classified under EC 1.2.1.57.

In any of the methods described herein, the methods can include converting hexanoate to adipic acid, 6-aminohexanoic acid, hexamethylenediamine, ε caprolactam or 1,6 hexanediol with one or more enzymatic conversions, wherein one of the enzymatic conversions introduces the second terminal functional group. The method can include converting hexanoate to 6-hydroxyhexanoate using a cytochrome P450/ ω-hydroxylase such as from the family CYP153 such as CYP152A6. 6-hydroxyhexanoate can be converted to adipate semialdehyde using (i) an *alcohol dehydrogenase* such as encoded by *YMR318C,* (ii) a *6-hydroxyhexanoate*

dehydrogenase such as that encoded by ChnD, or (iii) a *cytochrome P450/* ω -*hydroxylase.*

In any of the methods described herein, adipic acid can be produced by forming the second terminal functional group in adipate semialdehyde using (i) an *aldehyde dehydrogenase* classified under EC 1.2.1.3, (ii) a *6-oxohexanoate dehydrogenase* classified under EC 1.2.1.63 such as that encoded by *ChnE* or iii) a *cytochrome P450/* ω *-hydroxylase.*

In any of the methods described herein, 6-aminohexanoic acid can be produced by forming the second terminal functional group in adipate semialdehyde using an ω*-transaminase* classified under EC 2.61.18, EC 2.6.1.19 or EC 2.6.1.48.

In any of the methods described herein, caprolactam can be produced from 6-aminohexanoic acid using a *lactamase* classified under EC 3.5.2.-. The amide bond associated with caprolactam is the result of first having a terminal carboxyl group and terminal amine group to form the bond. 6-aminohexanoic acid can be converted to 6-aminohexanal using a *carboxylate reductase* classified under EC 1.2.99.6 such as that encoded by *car* alongside the gene product of *npt,* or *GriC & GriD.*

In any of the methods described herein, hexamethylenediamine can be produced by forming a second terminal functional group in 6-aminohexanal using a *diamine transaminase* classified under EC 2.6.1.29 or EC 2.6.1.82.

In any of the methods described herein, 1,6 hexandiol can be produced by forming the second terminal functional group in 6-hydroxyhexanal using an *alcohol dehydrogenase* classified under EC 1.1.1.-(1,2,21, 184).

In some embodiments, the biological feedstock is, includes, or derives from, monosaccharides, disaccharides, lignocellulose, hemicellulose, cellulose, lignin such as levulinic acid and furfural, lignin, triglycerides such as glycerol and fatty acids, agricultural waste or municipal waste.

In some embodiments, the non-biological feedstock is or derives from natural gas, syngas, CO2/H2, methanol, ethanol, non-volatile residue (NVR) or a caustic wash waste stream from cyclohexane oxidation processes.

In some embodiments, the host microorganism is a prokaryote. For example, the prokaryote can be from the bacterial genus *Escherichia* such as *Escherichia coli*; from the bacterial genus *Clostridia* such as *Clostridium ljungdahlii, Clostridium*

autoethanogenum or *Clostridium kluyveri;* from the bacterial genus *Corynebacteria* such as *Corynebacterium glutamicum;* from the bacterial genus *Cupriavidus* such as *Cupriavidus necator* or *Cupriavidus metallidurans;* from the bacterial genus *Pseudomonas* such as *Pseudomonas fluorescens, Pseudomonas putida* or *Pseudomonas oleavorans;* from the bacterial genus *Delftia* such as *Delftia acidovorans;* from the bacterial genus *Bacillus* such as *Bacillus subtillis;* from the bacterial genus *Lactobacillus* such as *Lactobacillus delbrueckii;* or from the bacterial genus *Lactococcus* such as *Lactococcus lactis.* Such prokaryotes also can be sources of genes for constructing recombinant host cells described herein that are capable of producing C6 building blocks.

In some embodiments, the host microorganism is a eukaryote (e.g., a fungus such as a yeast). For example, the eukaryote can be from the fungal genus *Aspergillus* such as *Aspergillus niger;* from the yeast genus *Saccharomyces* such as *Saccharomyces cerevisiae;* from the yeast genus *Pichia* such as *Pichia pastoris;* from the yeast genus *Yarrowia* such as *Yarrowia lipolytica;* from the yeast genus *Issatchenkia* such as *Issathenkia orientalis;* from the yeast genus *Debaryomyces* such as *Debaryomyces hansenii;* from the yeast genus *Arxula* such as *Arxula adenoinivorans;* or from the yeast genus *Kluyveromyces* such as *Kluyveromyces lactis.* Such eukaryotes also can be sources of genes for constructing recombinant host cells described herein that are capable of producing C6 building blocks.

In some embodiments, the host microorganism's tolerance to high concentrations of one or more C6 building blocks is improved through continuous cultivation in a selective environment.

In some embodiments, the host microorganism's biochemical network is attenuated or augmented to (1) ensure the intracellular availability of acetyl-CoA, (2) create an NADH or NADPH imbalance that may only be balanced via the formation of one or more C6 building blocks, (3) prevent degradation of central metabolites, central precursors leading to and including C6 building blocks and (4) ensure efficient efflux from the cell.

In some embodiments, a non-cyclical cultivation strategy is used to achieve anaerobic, micro-aerobic, or aerobic cultivation conditions.

In some embodiments, a cyclical cultivation strategy is used to alternate between anaerobic and aerobic cultivation conditions.

In some embodiments, the cultivation strategy includes limiting nutrients, such as limiting nitrogen, phosphate or oxygen.

In some embodiments, one or more C6 building blocks are produced by a single type of microorganism, e.g., a recombinant host containing one or more exogenous nucleic acids, using a non-cyclical or cyclical fermentation strategy.

In some embodiments, one or more C6 building blocks are produced by co-culturing more than one type of microorganism, e.g., two or more different recombinant hosts, with each host containing a particular set of exogenous nucleic acids, using a non-cyclical or cyclical fermentation strategy.

In some embodiments, one or more C6 building blocks are produced by successive fermentations, where the broth or centrate from the preceding fermentation is fed to a succession of fermentations as a source of feedstock, central metabolite or central precursor ; finally producing the C6 building block.

This document also features a recombinant host comprising at least one exogenous nucleic acid encoding, for example, one or more of a*formate dehydrogenase, enoyl-CoA reductase, trans-2-enoyl-CoA hydratase, 3-hydroxybutyryl-CoA dehydrogenase, acetyl-CoA C-acyltransferase, acetoacyl-CoA reductase, acetyl-CoA synthetase, acetyl-CoA carboxylase,* a *malic* enzyme, *puridine nucleotide transhydrogenase, glyceraldehydeSP-dehydrogenase, acyl-CoA hydrolase, aldehyde dehydrogenase, thioesterase, cytochrome P450/ ω-hydroxylase, alcohol dehydrogenase, 6-hydroxyhexanoate dehydrogenase, 6-oxohexanoate dehydrogenase, diamine transaminase, propionyl-CoA synthetase,* and a *carboxylate reductase,* wherein said host comprises one or more deficiencies, for example, in *glucose-6-phosphate isomerase, acetate kinase,* an enzyme degrading pyruvate to lactate, enzymes mediating the degradation of phophoenolpyruvate to succinate, *alcohol dehydrogenase, pyruvate decarboxylase, 2-oxoacid decarboxylase, triose phosphate isomerase,* a *glutamate dehydrogenase.*

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention pertains. Although methods and materials similar or equivalent to those described herein can be used to practice the invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of

conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

The details of one or more embodiments of the invention are set forth in the accompanying drawings and the description below. Other features, objects, and advantages of the invention will be apparent from the description and drawings, and from the claims. The word "comprising" in the claims may be replaced by "consisting essentially of or with "consisting of," according to standard practice in patent law.

DESCRIPTION OF DRAWINGS

FIG. 1 is a schematic of an exemplary biochemical pathway leading to hexanoyl-CoA using NADH-dependent enzymes and with acetyl-CoA as a central metabolite.

FIG. 2 is a schematic of an exemplary biochemical pathway leading to hexanoyl-CoA using NADPH-dependent enzymes and with acetyl-CoA as a central metabolite.

FIG. 3 is a schematic of exemplary biochemical pathways leading to hexanoate using hexanoyl-CoA as a central metabolite.

FIG. 4 is a schematic of exemplary biochemical pathways leading to adipic acid using hexanoate as a central precursor.

FIG. 5 is a schematic of exemplary biochemical pathways leading to 6-aminhexanoate using hexanoate as a central precursor.

FIG. 6 is a schematic of an exemplary biochemical pathway leading to hexamethylenediamine using 6-aminhexanoate as a central precursor.

FIG. 7 is a schematic of an exemplary biochemical pathway leading to 6-hydroxyhexanoate using hexanoate as a central precursor.

FIG. 8 is a schematic of an exemplary biochemical pathway leading to 1,6-hexanediol using 6-hydroxyhexanoate as a central precursor.

DETAILED DESCRIPTION

In general, this document provides enzymes, non-natural pathways, cultivation strategies, feedstocks, host microorganisms and attenuations to the host's biochemical network, which generates a six carbon chain aliphatic backbone from central metabolites into which two terminal functional groups may be formed leading to the

synthesis of adipic acid, caprolactam, 6-aminohexanoic acid, hexamethylenediamine or 1,6-hexanediol (referred to as "C6 building blocks" herein). As used herein, the term "central precursor" is used to denote a key metabolite in a pathway leading to the synthesis of C6 building blocks. The term "central metabolite" is used herein to denote a metabolite that is produced in all microorganisms to support growth.

As such, host microorganisms described herein can include endogenous pathways that can be manipulated such that one or more C6 building blocks can be produced. In an endogenous pathway, the host microorganism naturally expresses all of the enzymes catalyzing the reactions within the pathway. A host microorganism containing an engineered pathway does not naturally express all of the enzymes catalyzing the reactions within the pathway but has been engineered such that all of the enzymes within the pathway are expressed in the host. Within an engineered pathway, the enzymes can be from a single source, i.e., from one species or genera, or can be from multiple sources, i.e., different species or genera. Nucleic acids encoding the enzymes described herein have been identified from various organisms and are readily available in publicly available databases such as GenBank or EMBL. Engineered hosts can naturally express none or some (e.g., one or more, two or more, three or more, four or more, five or more, or six or more) of the enzymes of the pathways described herein. Endogenous genes of the engineered hosts also can be disrupted to prevent the formation of undesirable metabolites or prevent the loss of intermediates in the pathway through other enzymes acting on such intermediates. Engineered hosts can be referred to as recombinant hosts or recombinant host cells. Thus, as described herein recombinant hosts can include nucleic acids encoding one or more of a β-*ketothiolases*, *dehydrogenases*, *reductases*, *hydratases*, *monooxygenases*, ω-*hydroxylase* or *transaminases* as described in more detail below.

In addition, the production of C6 building blocks can be performed *in vitro* using the isolated enzymes described herein, using a lysate (e.g., a cell lysate) from a host microorganism as a source of the enzymes, or using a plurality of lysates from different host microorganisms as the source of the enzymes.

The reactions of the pathways described herein can be performed in one or more host strains (a) naturally expressing one or more relevant enzymes,(b) genetically engineered to express one or more relevant enzymes, or (c) naturally

expressing one or more relevant enzymes and genetically engineered to express one or more relevant enzymes. Alternatively, relevant enzymes can be extracted from of the above types of host cells and used in a purified or semi-purified form. Moreover, such extracts include lysates (e.g. cell lysates) that can be used as sources of relevant enzymes. In the methods provided by the document, all the steps can be performed in host cells, all the steps can be performed using extracted enzymes, or some of the steps can be performed in cells and others can be performed using extracted enzymes.

4.1 Enzymes generating the C6 aliphatic backbone for conversion to C6 building blocks

As depicted in FIG. 1 and FIG. 2, the C6 aliphatic backbone for conversion to C6 building blocks can be formed from acetyl-CoA via two cycles of CoA-dependent carbon chain elongation using either NADH or NADPH dependent enzymes. In some embodiments, a CoA-dependent carbon chain elongation cycle comprises an *acetyl-CoA C-acyltransferase,* which converts acetyl-CoA to acetoacetyl-CoA and converts butanoyl-CoA to 3-oxohexanoyl-CoA, or an *acetyl-CoA carboxylase,* which converts acetyl-CoA to malonyl-CoA & an *acetoacetyl-CoA synthase,* which converts malonyl-CoA to acetoacetyl-CoA, a *3-hydroxybutyrl-CoA dehydrogenase,* which converts acetoacetyl-CoA to 3-hydroxybutanoyl CoA or *3-oxoacyl-CoA reductase/3-hydroxyacyl-CoA dehydrogenase,* which converts 3-oxohexanoyl-CoA to 3-hydroxyhexanoyl-CoA, an *enoyl-CoA hydratase,* which converts 3-hydroxybutanoyl-CoA to crotonyl-CoA and converts 3-hydroxyhexanoyl-CoA to hex-2-enoyl-CoA, and a *trans-2-enoyl-CoA reductase,* which converts crotonyl-CoA to butanoyl-CoA and converts hex-2-enoyl-CoA to hexanoyl-CoA.

In some embodiments, an *acetyl-CoA C-acyltransferase* may be classified under EC 2.3.1.9, such as the gene product *oiatoB* or *phaA,* or classified under EC 2.3.1.16, such as the gene product *oibktB.*

The β-*ketothiolase* encoded by *atoB or phaA* accepts acetyl-CoA as substrates, forming butanoyl-CoA (Haywood et al, FEMS Microbiology Letters, 1988, 52, 91-96; Slater et al, Journal of Bacteriology, 1998, 180(8), 1979 - 1987).

The β-*ketothiolase* encoded by *bktB* from *Cupriavidus necator* accepts acetyl-CoA and butanoyl-CoA as substrates, forming the CoA-activated C6 aliphatic

backbone (Haywood et al, FEMS Microbiology Letters, 1988, 52, 91-96; Slater et al, Journal of Bacteriology, 1998, 180(8), 1979 - 1987).

In some embodiments, an *acetyl-CoA carboxylase* may be classified under EC 6.4.1.2.

Conversion of acetyl-CoA to malonyl-CoA by *acetyl-CoA carboxylase* has been shown to increase the rate of fatty acid synthesis (Davis et al, The Journal of Biological Chemistry, 2000, 275(37), 28593 - 28598).

In some embodiments, an *acetoacetyl-CoA synthase* may be classified under EC 2.3.1.194.

It has been demonstrated that *acetoacetyl-CoA synthase* may be used as an irreversible substitute for the gene product of *phaA* in the carbon chain elongation associated with polyhydroxybutyrate synthesis (Matsumoto et al, Biosci. Biotechnol. Biochem., 201 1, 75(2), 364 - 366).

In some embodiments, a *3-hydroxyacyl-CoA dehydrogenase* may be classified under EC 1.1.1.35, such as the gene product *oifadB,* or a *3-hydroxybutyryl-CoA dehydrogenase* may be classified under EC 1.1.1.157, such as the gene product of *hbd,* or an *acetoacetyl-CoA reductase* may be classified under EC 1.1.1.36, such as the gene product *oiphaB* (Liu & Chen, Appl. Microbiol. Biotechnol, 2007, 76(5), 1153 - 1159; Shen *et al, Appl. Environ. Microbiol,* 201 1, 77(9), 2905 - 2915; Budde et al, Journal of Bacteriology, 2010, 192(20), 5319 - 5328).

In some embodiments, a *3-oxoacyl-CoA reductase* may be classified under EC 1.1.1.100, such as the gene product *oifabG* (Budde et al, Journal of Bacteriology, 2010, 192(20), 5319 - 5328; Nomura et al, Appl. Environ. Microbiol, 2005, 71(8), 4297 - 4306) .

In some embodiments, an *enoyl-CoA hydratase* may be classified under EC 4.2.1.17, such as the gene product of *crt,* or classed under EC 4.2.1.1 19, such as the gene product of *phaJ* (Shen *et* αI., ΑppI. *Environ. Microbiol,* 201 1, 77(9), 2905 - 2915; Fukui et al, Journal of Bacteriology, 1998, 180(3), 667 - 673).

In some embodiments, a *trans-2-enoyl-CoA reductase* may be classified under EC 1.3.1.38, EC 1.3.1.8 or EC 1.3.1.44, such as the gene product offer or *tdter* (Nishimaki et al, J. Biochem., 1984, 95, 13 15 - 1321; Shen *et al, Appl. Environ.*

Microbiol, 2011, 77(9), 2905 - 2915); Bond-Watts *et al*, *Biochemistry*, 2012, 51, 6827 - 6837).

4.2 Enzymes generating the terminal carboxyl groups in the biosynthesis of C6 Building Blocks

As depicted in FIG. 3 and FIG. 4, the terminal carboxyl groups can be enzymatically formed using an *acyl-CoA hydrolase*, an *aldehyde dehydrogenase*, a *6-oxohexanoate dehydrogenase* or a *cytochrome P450/ co-hydroxylase*.

In some embodiments, the first terminal carboxyl group leading to the synthesis of a C6 building block is enzymatically formed in hexanoyl-CoA by an *acyl-CoA hydrolase* or *thioesterase* classified under EC 3.1.2.-, resulting in the production of hexanoate. The *acyl-CoA hydrolase* or *thioesterase* can be the gene product of *YciA, tesB* o*xAcot13* (Cantu et al., Protein Science, 2010, 19, 1281 - 1295; Zhuang et al., Biochemistry, 2008, 47(9), 2789 - 2796; Naggert et al., Journal of Biological Chemistry, 1991, 266(17), 11044 - 11050).

In some embodiments, the first terminal carboxyl group leading to the synthesis of a C6 building block is enzymatically formed in hexanal by an *aldehyde dehydrogenase* classified under EC 1.2.1.4 (Ho & Weiner, Journal of Bacteriology, 2005, 187(3), 1067 - 1073), resulting in the production of hexanoate.

In some embodiments, the second terminal carboxyl group leading to the synthesis of adipic acid is enzymatically formed in adipate semilaldehyde by an *aldehyde dehydrogenase* classified under EC 1.2.1.3 (Guerrillot & Vandecasteele, Eur. J. Biochem., 1977, 81, 185 - 192).

In some embodiments, the second terminal carboxyl group leading to the synthesis of adipic acid is enzymatically formed in adipate semialdehyde by a *6-oxohexanoate dehydrogenase* classified under EC 1.2.1.63, such as the gene product of *ChnE* (Iwaki et al., Appl. Environ. Microbiol., 1999, 65(11), 5158 - 5162).

In some embodiments, the second terminal carboxyl group leading to the synthesis of adipic acid is enzymatically formed in adipate semilaldehyde by a *cytochrome P450* (Sanders et al., Journal of Lipid Research, 2005, 46(5), 1001-1008; Sanders et al., The FASEB Journal, 2008, 22(6), 2064 - 2071).

The utility of ω-oxidation in introducing carboxyl groups into alkanes has been demonstrated in the yeast *Candida tropicalis*, leading to the synthesis of adipic acid (Okuhara et al, Agr. Boil. Chem., 1971, 35(9), 1376 - 1380).

4.3 Enzymes generating the terminal amine groups in the biosynthesis of C6 Building Blocks

As depicted in FIG. 5 and FIG. 6, terminal amine groups can be enzymatically formed using a ω-*transaminase* or a *diamine transaminase.*

In some embodiments, the first terminal amine group leading to the synthesis of 6-aminohexanoic acid is enzymatically formed in adipate semialdehyde by a ω-*transaminase* classified under EC 2.6.1.18, such as obtained from *Vibriofluvialis* or *Chromobacterium violaceum*, or classified under EC 2.6.1.19, such as obtained from *Streptomyces griseus*, or classified under 2.6.1.48, such as obtained from *Clostridium viride.*

The reversible ω-*transaminase* from *Chromobacterium violaceum* has demonstrated activity accepting 6-aminohexanoic acid as amino donor, thus forming the first terminal amine group in adipate seminaldehyde (Kaulmann et al., Enzyme and Microbial Technology, 2007, 41, 628 - 637).

The reversible *4-aminobubyrate:2-oxoglutarate transaminase* from *Streptomyces griseus* has demonstrated activity for the conversion of 6-aminohexanoate to adipate semialdehyde (Yonaha et al., Eur. J. Biochem., 1985, 146, 101 - 106).

The reversible *5-aminovalerate transaminase* from *Clostridium viride* has demonstrated activity for the conversion of 6-aminohexanoate to adipate semialdehyde (Barker et al., The Journal of Biological Chemistry, 1987, 262(19), 8994 - 9003).

In some embodiments, the second terminal amine group leading to the synthesis of hexamethylenediamine is enzymatically formed in 6-aminohexanal by a *diamine transaminase* classified under EC 2.6.1.29 or classified under EC 2.6.1.82, such as the gene product of *YgjG.*

The gene product of *ygjG* accepts a broad range of diamine carbon chain length substrates, such as putrescine, cadaverine and spermidine (Samsonova et al., BMC Microbiology, 2003, 3:2)

The *diamine transaminase* from *E.coli* strain B has demonstrated activity for 1,5 diaminopentane and 1,7 diaminoheptane, with 1,6 diaminohexane (HMD) expected to be active (Kim, The Journal of Chemistry, 1963, 239(3), 783 - 786).

4.4 Enzymes generating the terminal hydroxyl groups in the biosynthesis of C6 Building Blocks

As depicted in FIG. 7 and FIG. 8, the terminal hydroxyl group can be enzymatically forming using a *cytochrome P450,* a *monooxygenase* or an *alcohol dehydrogenase.*

In some embodiments, the first terminal hydroxyl group leading to the synthesis of C6 building blocks is enzymatically formed in hexanoate by a *monooxygenase,* a *cytochrome P450* or a ω-*hydroxylase* such as from the CYP153 family such as CYP153A6 (Van Beilen & Funhoff, Current Opinion in Biotechnology, 2005, 16, 308 - 314; Koch et al., Appl. Environ. Microbiol., 2009, 75(2), 337-344; Nieder and Shapiro, Journal of Bacteriology, 1975, 122(1), 93 - 98).

The substrate specificity of terminal ω-*hydroxylase* has been broadened successfully (Koch et al., Appl. Environ. Microbiol., 2009, 75(2), 337-344). Although,

In some embodiments, the second terminal hydroxyl group leading to the synthesis of 1,6 hexanediol is enzymatically formed in 6-hydroxyhexanal by an *alcohol dehydrogenase* classified under EC 1.1.1.- (e.g., 1, 2, 21, or 184). Although non-terminal hydroxylation is observed *in vitro* for CYP153A6, in vivo only 1-hydroxylation occurs (Funhoff et al., Journal of Bacteriology, 2006, 188(14), 5220 - 5227).

4.5 Biochemical pathways

4.5.1 Pathways to hexanoyl-CoA as precursor leading to central precursors to C6 Building Blocks

In some embodiments, hexanoyl-CoA is synthesized from the central metabolite, acetyl-CoA, by conversion of acetyl-CoA to acetoacetyl-CoA by *acetoacetyl-CoA thiolase* (EC 2.3.1.9), such as the gene product *oiatoB* or *phaA,* or by *acetyl-CoA carboxylase* (EC 6.4.1.2) & *acetoacetyl-CoA synthase* (EC 2.3.1.194) via malonyl-CoA; followed by conversion of acetoacetyl-CoA to (S) 3-hydroxybutanoyl-CoA by a *3-hydroxybutyryl-CoA dehydrogenase* (EC 1.1.1.157) such as the gene product of *hbd*; followed by conversion of (S) 3-hydroxybutanoyl-

CoA to crotonyl-CoA by *enoyl-CoA hydratase* (EC 4.2.1.17) such as the gene product of **crt;** followed by conversion of crotonyl-CoA to butanoyl-CoA by *trans-2-enoyl-CoA reductase* (EC 1.3.1.44) such as the gene product offer; followed by conversion of butanoyl-CoA to 3-oxo-hexanoyl-CoA by *acetyl-CoA C-acyltransferase* (EC 2.3.1.16) such as the gene product of *bktB*; followed by conversion of 3-oxo-hexanoyl-CoA to (S) 3-hydroxyhexanoyl-CoA by *3-hydroxyacyl-CoA dehydrogenase* (EC 1.1.1.35) such as the gene product of *fabB*; followed by conversion of (S) 3-hydroxyhexanoyl-CoA to hex-2-enoyl-CoA by *enoyl-CoA hydratase* (EC 4.2.1.17) such as the gene product of **crt;** followed by conversion of hex-2-enoyl-CoA to hexanoyl-CoA by *trans-2-enoyl-CoA reductase* (EC 1.3.1.44) such as the gene product offer or *tdter*. See FIG. 1.

In some embodiments, hexanoyl-CoA is synthesized from the central metabolite, acetyl-CoA, by conversion of acetyl-CoA to acetoacetyl-CoA by *acetoacetyl-CoA thiolase* (EC 2.3.1.9) , such as the gene product *oiatoB* or *phaA,* or by *acetyl-CoA carboxylase* (EC 6.4.1.2) & *acetoacetyl-CoA synthase* (EC 2.3.1.194) via malonyl-CoA; followed by conversion of acetoacetyl-CoA to **(R)** 3-hydroxybutanoyl-CoA by a *3-acetoacetyl-CoA reductase* (EC 1.1.1.36) such as the gene product of *phaB*; followed by conversion of **(R)** 3-hydroxybutanoyl-CoA to crotonyl-CoA by *enoyl-CoA hydratase* (EC 4.2.1.119) such as the gene product of *phaJ;* followed by conversion of crotonyl-CoA to butanoyl-CoA by *trans-2-enoyl-CoA reductase* (EC 1.3.1.38); followed by conversion of butanoyl-CoA to 3-oxo-hexanoyl-CoA by *acetyl-CoA C-acyltransferase* (EC 2.3.1.16) such as the gene product *oibktB;* followed by conversion of 3-oxo-hexanoyl-CoA to **(R)** 3-hydroxyhexanoyl-CoA by *3-oxoacyl-CoA reductase* (EC 1.1.1.100) such as the gene product *oifabG;* followed by conversion of **(R)** 3-hydroxyhexanoyl-CoA to hex-2-enoyl-CoA by *enoyl-CoA hydratase* (EC 4.2. 1. 119) such as the gene product *oiphaJ;* followed by conversion of hex-2-enoyl-CoA to hexanoyl-CoA by *trans-2-enoyl-CoA reductase* (EC 1.3.1.38). See FIG. 2.

4.5.2 Pathways using hexanoyl-CoA as precursor leading to the central precursor hexanoate

In some embodiments, hexanoate is synthesized from the central metabolite, hexanoyl-CoA, by conversion of hexanoyl-CoA to hexanoate by *acyl-CoA hydrolase* or *thioesterase* (EC 3.1.2.-) such as the gene product of *YciA, tesB* or *Acotl3.*

In some embodiments, hexanoate is synthesized from the central metabolite, hexanoyl-CoA, by conversion of hexanoyl-CoA to hexanal by *butanal dehydrogenase* (EC 1.2.1.57); followed by conversion of hexanal to hexanoate by *aldehyde dehydrogenase* (EC 1.2.1.4). See FIG. 3.

The conversion of hexanoyl-CoA to hexanal has been demonstrated for both NADH and NADPH as co-factors (Palosaari and Rogers, Journal of Bacteriology, 1988, 170(7), 2971 - 2976).

4.5.3. Pathways using hexanoate as central precursor to adipic acid

In some embodiments, adipic acid is synthesized from the central precursor, hexanoate, by conversion of hexanoate to 6-hydroxyhexanoate by *monooxygenase* or *cytochrome P450* such as from the CYP153 family such as CYP153A6; followed by conversion of 6-hydroxyhexanoate to adipate semialdehyde by *alcohol dehydrogenase* (EC 1.1.1.2) such as the gene product of YMR318C; followed by conversion of adipate semialdehyde to adipic acid by *6-oxohexanoate dehydrogenase* (EC 1.2.1.63). See FIG. 4.

The *alcohol dehydrogenase* encoded by YMR3 18C has broad substrate specificity, including the oxidation of C6 alcohols.

In some embodiments, adipic acid is synthesized from the central precursor, hexanoate, by conversion of hexanoate to 6-hydroxyhexanoate by *monooxygenase* or *cytochrome P450* such as from the CYP153 family such as CYP153A6; followed by conversion of 6-hydroxyhexanoate to adipate semialdehyde by *6-hydroxyhexanoate dehydrogenase* (EC 1.1.1.258) such as the gene product of *ChnD* (Iwaki et al., Appl. Environ. Microbiol., 1999, 65(11), 5158 - 5162); followed by conversion of adipate semialdehyde to adipic acid by *aldehyde dehydrogenase* (EC 1.2.1.3). See FIG. 4.

In some embodiments, adipic acid is synthesized from the central precursor, hexanoate, by conversion of hexanoate to 6-hydroxyhexanoate by *monooxygenase* or *cytochrome P450* such as from the CYP153 family such as CYP153A6; followed by conversion of 6-hydroxyhexanoate to adipate semialdehyde by *cytochrome P450* (Sanders et al., Journal of Lipid Research, 2005, 46(5), 1001-1008; Sanders et al., The FASEB Journal, 2008, 22(6), 2064 - 2071); followed by conversion of adipate semialdehyde to adipic acid by *cytochrome P450*. See FIG. 4.

4.5.4 Pathway using hexanoate as central precursor to 6-aminohexanoate and e-caprolactam

In some embodiments, 6-aminohexanoate is synthesized from the central precursor, hexanoate, by conversion of hexanoate to 6-hydroxyhexanoate by *monooxygenase* or *cytochrome P450* such as from the CYP153 family such as CYP153A6; followed by conversion of 6-hydroxyhexanoate to adipate semialdehyde by *alcohol dehydrogenase* (EC 1.1.1.2) or *6-hydroxyhexanoate dehydrogenase* (EC 1.1.1.258); followed by conversion of adipate semialdehyde to 6-aminohexanoate by ω-*transaminase* (EC 2.6.1.18, EC 2.6.1.19, EC 2.6.1.48). See FIG. 5.

In some embodiments, e-caprolactam is synthesized from the central precursor, hexanoate, by conversion of hexanoate to 6-hydroxyhexanoate by *monooxygenase* or *cytochrome P450* such as from the CYP153 family such as CYP153A6; followed by conversion of 6-hydroxyhexanoate to adipate semialdehyde by *alcohol dehydrogenase* (EC 1.1.1.2) or *6-hydroxyhexanoate dehydrogenase* (EC 1.1.1.258); followed by conversion of adipate semialdehyde to 6-aminohexanoate by ω-*transaminase* (EC 2.6.1.18, EC 2.6.1.19, EC 2.6.1.48); followed by conversion of 6-aminohexanoate to e-caprolactam by hydrolase (EC 3.5.2.-). See FIG. 5.

4.5.5 Pathway using 6-aminohexanoate as central precursor to hexamethylenediamine

In some embodiments, hexamethylenediamine is synthesized from the central precursor, 6-aminohexanoate, by conversion of 6-aminohexanoate to 6-aminohexanal by *carboxylate reductase* (EC 1.2.99.6) such as the gene product of *car* alongside the gene product of *npt* or the gene product of *GriC & GriD* (Suzuki et al., J. Antibiot., 2007, 60(6), 380 - 387); followed by conversion of 6-aminohexanal to hexamethylenediamine by *diamine transaminase* (EC 2.6.1.29, EC 2.6.1.82). See FIG. 6.

The *carboxylate reductase* encoded by the gene product of *car* and enhancer *npt* has broad substrate specificity, including terminal difunctional C4 and C5 carboxylic acids (Venkitasubramanian et al., Enzyme and Microbial Technology, 2008, 42, 130 — 137).

4.5.6 Pathways using hexanoate as central precursor to 1,6-hexanediol

In some embodiments, 6-hydroxyhexanoate is synthesized from the central precursor, hexanoate, by conversion of hexanoate to 6-hydroxyhexanoate by by *monooxygenase* or *cytochrome P450* such as from the CYP153 family such as CYP153A6. See FIG. 7.

In some embodiments, 1,6 hexanediol is synthesized from the central precursor, 6-hydroxyhexanoate, by conversion of 6-hydroxyhexanoate to 6-hydroxyhexanal by *carboxylate reductase* (EC 1.2.99.6) such as the gene product of *car* alongside the gene product of *npt;* followed by conversion of 6-hydroxyhexanal to 1,6 hexanediol by an *alcohol dehydrogenase* (e.g., EC 1.1.1.1, EC 1.1.1.2, EC 1.1.1.21, or EC 1.1.1.184) (Liu et al., Microbiology, 2009, 155, 2078 - 2085).

4.6 Cultivation strategy

In some embodiments, one or more C6 building blocks are biosynthesized in a recombinant host using anaerobic, aerobic or micro-aerobic cultivation conditions. A non-cyclical or a cyclical cultivation strategy can be used to achieve the desired cultivation conditions. For example, a non-cyclical strategy can be used to achieve anaerobic, aerobic or micro-aerobic cultivation conditions.

In some embodiments, a cyclical cultivation strategy can be used to alternate between anaerobic cultivation conditions and aerobic cultivation conditions.

In some embodiments, the cultivation strategy entails nutrient limitation either via nitrogen, phosphate or oxygen limitation.

In some embodiments, one or more C6 building blocks are produced by a single microorganism via a non-cyclical or cyclical fermentation strategy.

In some embodiments, one or more C6 building blocks are produced by co-culturing more than one microorganism via a non-cyclical or cyclical fermentation strategy.

In some embodiments, one or more C6 building blocks are produced by successive fermentations, where the broth or centrate from the preceding fermentation is fed to a succession of fermentations as feedstock; finally producing the C6 building block.

In some embodiments, a cell retention strategy using, for example, ceramic hollow fiber membranes is employed to achieve and maintain a high cell density during either fed-batch or continuous fermentation.

In some embodiments, the principal carbon source fed to the fermentation in the synthesis of C6 building block derives from biological or non-biological feedstocks.

In some embodiments, the biological feedstock is, includes, or derives from, monosaccharides, disaccharides, lignocellulose, hemicellulose, cellulose, lignin such as levulinic acid and furfural, lignin, triglycerides such as glycerol and fatty acids, agricultural waste or municipal waste.

The efficient catabolism of crude glycerol stemming from the production of biodiesel has been demonstrated in several microorganisms such as *Escherichia coli, Cupriavidus necator, Pseudomonas oleavorans, Pseudomonas putida* and *Yarrowia lipolytica* (Lee *et al., Appl. Biochem. Biotechnol,* 2012, 166, 1801 - 1813; Yang *et al., Biotechnology for Biofuels,* 2012, 5:13; Meijnen *et al, Appl. Microbiol. Biotechnol,* 201 1, 90, 885 - 893).

The efficient catabolism of lignocellulosic-derived levulinic acid has been demonstrated in several organisms such as *Cupriavidus necator* and *Pseudomonas putida* in the synthesis of 3-hydroxy valerate via the precursor propanoyl-CoA (Jaremko and Yu, *Journal of Biotechnology,* 201 1, 155, 201 1, 293 - 298; Martin and Prather, *Journal of Biotechnology,* 2009, 139, 6 1 - 67).

The efficient catabolism of lignin-derived aromatic compounds such benzoate analogues has been demonstrated in several microorganisms such as *Pseudomonas putida, Cupriavidus necator* (Bugg *et al., Current Opinion in Biotechnology,* 20 11, 22, 394 - 400; Perez-Pantoja *et al, FEMS Microbiol. Rev.,* 2008, 32, 736 - 794).

The efficient utilization of agricultural waste, such as olive mill waste water has been demonstrated in several microorganisms, including *Yarrowia lipolytica* (Papanikolaou *et al, Bioresour. Technol,* 2008, 99(7), 2419 - 2428).

The efficient utilization of fermentable sugars such as monosaccharides and disaccharides derived from cellulosic, hemicellulosic, cane and beet molasses, cassava, corn and other argricultural sources has been demonstrated for several microorganism such as *Escherichia coli, Corynebacterium glutamicum* and *Lactobacillus delbrueckii* and *Lactococcus lactis* (see, e.g., Hermann *et al, Journal of Biotechnology,* 2003, 104, 155 - 172; Wee *et al, Food Technol. Biotechnol,* 2006,

44(2), 163 - 172; Ohashi *et al, Journal of Bioscience and Bioengineering,* 1999, 87(5), 647 - 654).

The efficient utilization of furfural, derived from a variety of agricultural lignocellulosic sources, has been demonstrated for *Cupriavidus necator* (Li *et al, Biodegradation,* 2011, 22, 1215 - 1225).

In some embodiments, the non-biological feedstock is or derives from natural gas, syngas, CO2/H2, methanol, ethanol, non-volatile residue (NVR) or a caustic wash waste stream from cyclohexane oxidation processes.

The efficient catabolism of methanol has been demonstrated for the methylotrophic yeast *Pichia pastoris.*

The efficient catabolism of ethanol has been demonstrated for *Clostridium kluyveri* (Seedorf *et al, Proc. Natl. Acad. Sci. USA,* 2008, 105(6) 2128 - 2133).

The efficient catabolism of $C0_2$ and H_2, which may be derived from natural gas and other chemical and petrochemical sources, has been demonstrated for *Cupriavidus necator* (Prybylski *et al., Energy, Sustainability and Society,* 2012, 2:1 1).

The efficient catabolism of syngas has been demonstrated for numerous microorganisms, such as *Clostridium ljungdahlii* and *Clostridium autoethanogenum* (Kopke *et al., Applied and Environmental Microbiology,* 2011, 77(15), 5467 - 5475).

The efficient catabolism of the non-volatile residue waste stream from cyclohexane processes has been demonstrated for numerous microorganisms, such as *Delftia acidovorans* and *Cupriavidus necator* (Ramsay *et al., Applied and Environmental Microbiology,* 1986, 52(1), 152 - 156).

In some embodiments, the host is a prokaryote. For example, the prokaryote can be from the genus *Escherichia* such as *Escherichia coli*; from the genus *Clostridia* such as *Clostridium ljungdahlii, Clostridium autoethanogenum* or *Clostridium kluyveri;* from the genus *Corynebacteria* such as *Corynebacterium glutamicum;* from the genus *Cupriavidus* such as *Cupriavidus necator* or *Cupriavidus metallidurans;* from the genus *Pseudomonas* such as *Pseudomonas fluorescens, Pseudomonas putida* or *Pseudomonas oleavorans;* from the genus *Delftia* such as *Delftia acidovorans;* from the genus *Bacillus* such as *Bacillus subtillis;* from the genus *Lactobacillus* such as *Lactobacillus delbrueckii;* or from the genus *Lactococcus* such as *Lactococcus lactis.* Such prokaryotes also can be a source of genes to construct recombinant host cells described herein that are capable of producing C6 building blocks.

In some embodiments, the host is a eukaryote. For example, the eukaryote can be from the genus *Aspergillus* such as *Aspergillus niger;* from the genus *Saccharomyces* such as *Saccharomyces cerevisiae;* from the genus *Pichia* such as *Pichia pastoris;* or from the genus *Yarrowia* such as *Yarrowia lipolytica;* from the genus *Issatchenkia* such as *Issathenkia orientalis;* from the genus *Debaryomyces* such as *Debaryomyces hansenii;* from the genus *Arxula* such as *Arxula adenoinivorans;* or from the genus *Kluyveromyces* such as *Kluyveromyces lactis.* Such eukaryotes also can be a source of genes to construct recombinant host cells described herein that are capable of producing C6 building blocks.

4.7 Metabolic engineering

The present document provides methods involving less than all the steps described for all the above pathways. Such methods can involve, for example, one, two, three, four, five, six, seven, eight, nine, ten, or more of such steps. Where less than all the steps are included in such a method, the first step can be any one of the steps listed.

Furthermore, recombinant hosts described herein can include any combination of the above enzymes such that one or more of the steps, e.g., one, two, three, four, five, six, seven, eight, nine, ten, or more of such steps, can be performed within a recombinant host. This document provides host cells of any of the genera and species listed and genetically engineered to express one or more (e.g., two, three, four, five, six, seven, eight, nine, 10, eleven, twelve or more) recombinant forms of any of the enzymes recited in the document. Thus, for example, the host cells can contain exogenous nucleic acids encoding enzymes catalyzing one or more of the steps of any of the pathways described herein.

In addition, this document recognizes that where enzymes have been described as accepting CoA-activated substrates, analogous enzyme activities associated with [acp]-bound substrates exist that are not necessarily in the same enzyme class.

Also, this document recognizes that where enzymes have been described accepting (R)-enantiomers of substrate, analogous enzyme activities associated with (S)-enantiomer substrates exist that are not necessarily in the same enzyme class.

This document also recognizes that where an enzyme is shown to accept a particular co-factor, such as NADPH, or co-substrate, such as acetyl-CoA, many enzymes are promiscuous in terms of accepting a number of different co-factors or

co-substrates in catalyzing a particular enzyme activity. Also, this document recognizes that where enzymes have high specificity for e.g., a particular co-factor such as NADH, an enzyme with similar or identical activity that has high specificity for the co-factor NADPH may be in a different enzyme class.

In some embodiments, the enzymes in the pathways outlined in section 4.5 are the result of enzyme engineering via non-direct or rational enzyme design approaches with aims of improving activity, improving specificity, reducing feedback inhibition, reducing repression, improving enzyme solubility, changing stereo-specificity, or changing co-factor specificity.

In some embodiments, the enzymes in the pathways outlined in section 4.5 are gene dosed, i.e., overexpressed, into the resulting genetically modified organism via episomal or chromosomal integration approaches.

In some embodiments, genome-scale system biology techniques such as Flux Balance Analysis are utilized to devise genome scale attenuation or knockout strategies for directing carbon flux to a C6 building block.

Attenuation strategies include, but are not limited to; the use of transposons, homologous recombination (double cross-over approach), mutagenesis, enzyme inhibitors and RNAi interference.

In some embodiments, fluxomic, metabolomic and transcriptomal data are utilized to inform or support genome-scale system biology techniques, thereby devising genome scale attenuation or knockout strategies in directing carbon flux to a C6 building block.

In some embodiments, the host microorganism's tolerance to high concentrations of a C6 building block is improved through continuous cultivation in a selective environment.

In some embodiments, the host microorganism's biochemical network is attenuated or augmented to (1) ensure the intracellular availability of acetyl-CoA, (2) create an NADH or NADPH imbalance that may only be balanced via the formation of C6 building blocks, (3) prevent degradation of central metabolites, central precursors leading to and including C6 building blocks and (4) ensure efficient efflux from the cell.

In some embodiments requiring the intracellular availability of acetyl-CoA for C6 building block synthesis, a *phosphotransacetylase* generating acetate such as *pta* is attenuated (Shen *et al*, Appl. *Environ. Microbiol*, 2011, 77(9), 2905 - 2915).

In some embodiments requiring the intracellular availability of acetyl-CoA for C6 building Block synthesis, a gene in an acetate synthesis pathway encoding an acetate kinase, such as *ack,* is attenuated.

In some embodiments requiring the intracellular availability of acetyl-CoA and NADH for C6 building block synthesis, a gene encoding the degradation of pyruvate to lactate such as *IdhA* is attenuated (Shen *et* αί , Αρρl. *Environ. Microbiol,* 201 1, 77(9), 2905 - 2915).

In some embodiments requiring the intracellular availability of acetyl-CoA and NADH for C6 building block synthesis, genes encoding the degradation of phophoenolpyruvate to succinate such as*frdBC* are attenuated (see, e.g., Shen *et al,* 201 1, *supra).*

In some embodiments requiring the intracellular availability of acetyl-CoA and NADH for C6 building block synthesis, a gene encoding the degradation of acetyl-CoA to ethanol such as the *alcohol dehydrogenase* encoded by *adhE* is attenuated (Shen *et al., 2*0\\, *supra).*

In some embodiments, a gene encoding the degradation of pyruvate to ethanol such as *pyruvate decarboxylase* is attenuated.

In some embodiments, a gene encoding the generation of isobutanol such as a *2-oxoacid decarboxylase* is attenuated.

In some embodiments requiring the intracellular availability of acetyl-CoA for C6 building block synthesis, *acetyl-CoA synthetase* such as the gene product of *acs* is overexpressed in the microorganism (Satoh et al, Journal of Bioscience and Bioengineering, 2003, 95(4), 335 - 341).

In some embodiments, carbon flux is directed into the pentose phosphate cycle by attenuating *glucose-6-phosphate isomerase* (EC 5.3.1.9).

In some embodiments, where pathways require excess NADH co-factor for C6 building block synthesis, a*formate dehydrogenase* gene is overexpressed in the host organism (Shen *et al,* 201 1, *supra).*

In some embodiments, where pathways require excess NADPH co-factor in the synthesis of C6 building block, a puridine nucleotide transhydrogenase gene such as *UdhA* is overexpressed in the host organisms (Brigham *et al, Advanced Biofuels and Bioproducts,* 2012, Chapter 39, 1065 - 1090).

In some embodiments, where pathways require excess NADPH co-factor in the synthesis of C6 building block, a glyceraldehyde-3P-dehydrogenase gene such as *GapNis* overexpressed in the host organisms (Brigham *et al,* 2012, *supra).*

In some embodiments, where pathways require excess NADPH co-factor in the synthesis of C6 building block, a malic enzyme gene such as *maeA* or *maeB* is overexpressed in the host organisms (Brigham *et al,* 2012, *supra).*

In some embodiments, where pathways require excess NADPH co-factor in the synthesis of C6 building block, a glucose-6-phosphate dehydrogenase gene such as *zwfi's* overexpressed in the host organisms (Lim *et al, Journal of Bioscience and Bioengineering,* 2002, 93(6), 543 - 549).

In some embodiments, where pathways require excess NADPH co-factor in the synthesis of C6 building block, a fructose 1,6 diphosphatase gene such as *flip* is overexpressed in the host organisms (Becker *et al, Journal of Biotechnology, 2001,* 132, 99 - 109).

In some embodiments, where pathways require excess NADPH co-factor in the synthesis of C6 building blocks, *triose phosphate isomerase* (EC 5.3.1.1) is attenuated.

In some embodiments, where pathways require excess NADPH co-factor in the synthesis of C6 building blocks, a *glucose dehydrogenase* such as the gene product *oigdh* is overexpressed in the host organism (Satoh et al, Journal of Bioscience and Bioengineering, 2003, 95(4), 335 - 341).

In some embodiments, enzymes facilitating the conversion of NADPH to NADH are attenuated, such as the NADH generation cycle that may be generated via inter-conversion of *glutamate dehydrogenases* in EC 1.4.1.2 (NADH-specific) and EC 1.4.1.4 (NADPH-specific).

In some embodiments, *glutamate dehydrogenases* (EC 1.4.1.3) that utilize both NADH and NADPH are co-factors are attenuated.

In some embodiments, membrane-bound *cytochrome P450lco-hydroxylases* are solubilized via truncation of the N-terminal region that anchors the P450 to the endoplasmic reticulum (Scheller et al., The Journal of Biological Chemistry, 1994, 269(17), 12779 0 12783).

In some embodiments using hosts that naturally accumulate polyhydroxyalkanoates, the *polymer synthase* enzymes can be attenuated in the host strain.

In some embodiments requiring the intracellular availability of butanoyl-CoA for C6 building block synthesis, a *propionyl-CoA synthetase* such as the gene product of PrpE-RS is overexpressed in the microorganism (Rajashekhara & Watanabe, FEBS Letters, 2004, 556, 143 - 147).

In some embodiments, β-oxidation enzymes degrading central metabolites and central precursors leading to and including C6 building blocks are attenuated.

In some embodiments, enzymes activating C6 building blocks via Coenzyme A esterification such as *CoA-ligases* are attenuated.

In some embodiments, the efflux of a C6 building block across the cell membrane to the extracellular media is enhanced or amplified by genetically engineering structural modifications to the cell membrane or increasing any associated transporter activity for a C6 building block.

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

EXAMPLES

Example 1

Genome-scale attenuation strategy for cyclical synthesis of adipic acid from glucose in *Saccharomyces cerevisiae*

Genome-scale Flux Balance Analysis was undertaken using the genome-scale model for *Saccharomyces cerevisiae* designated iMM904 (Mo et al, *BMC Systems Biology*, 2009, 3(37), 1-17).

The IMM904 model was extended by including ω-oxidation pathways as outlined in published work for eukaryotic organisms (Sanders et al., *Journal of Lipid Research*, 2005, 46(5), 1001 - 1008). Furthermore, the β-oxidation reactions in the peroxisome of the iMM904 model were extended and relevant membrane transport reactions were included. The inactivation of a *fumarate reductase* was required during validation of the extended model to align model fluxes with experimental flux data.

The NADH-specific enzymatic reactions outlined in FIG. 1 were incorporated into the model.

Allowance was made for the membrane transport of hexanoic acid and adipic acid to and from the extracellular media.

The stoichiometric balance of NADH in the production of 1-butanol in *E.coli* is far more efficient when overexpressing *formate dehydrogenase* (Shen et al, *Appl.*

Environ. Microbiol, 2011, 77(9), 2905 - 2915). The ïMM904 model includes *formate dehydrogenase,* but lacked *pyruvate formate lyase* activity, which was included into the *Saccharomyces cerevisiae* model.

The co-factor specificity of NAD(H) or NADP(H) dependent enzymes was assessed and where published literature was not unequivocal in terms of specificity, a promiscuous enzyme was assumed.

The metabolic engineering workbench, Optflux, was used to search the solution space associated with the biochemical network for attenuation strategies that (1) produce hexanoate anaerobically from glucose, followed by (2) production of adipate aerobically from the extracellular hexanoate, whilst co-feeding glucose as carbon and energy source.

The optimization trials found four beneficial attenuations; viz. (1) attenuating *glucose-6-phosphate isomerase,* directing flux into the pentose phosphate cycle; (2) attenuating *pyruvate decarboxylase* or *alcohol dehydrogenase,* preventing ethanol production; (3) attenuating *2-oxoacid decarboxylase,* preventing isobutanol production and (4) inactivating β-oxidation, preventing central precursor, central metabolite and adipic acid degradation.

The attenuations in this *S. cerevisiae* mutant using glucose as carbon and energy source, favored the balancing of NADH via the production of hexanoic acid as a means of maximizing biomass growth.

Overexpression of *formate dehydrogenase* in the *S. cerevisiae* mutant eliminated the by-product formation of formate and pyruvate, producing hexanoate with a molar yield of 0.62 [(mol hexanoate)/(mol glucose)].

Cycling from anaerobic to aerobic cultivation, while maintaining a glucose feed rate to match the growth rate under anaerobic conditions, resulted in an overall molar yield of 0.38 [(mol adipate)/(mol total glucose)].

In-silico attenuation of the biochemical network using a validated model determined that a cultivation strategy, cycling between anaerobic and aerobic conditions, produces predominantly adipic acid from the fed glucose.

Example 2

Genome-scale attenuation strategy for micro-aerobic synthesis from glucose using NADH imbalance to direct carbon flux towards adipic acid in *Saccharomyces cerevisiae*

The ïMM904 model outlined in Example 1 was utilized to assess the non-cyclical production of adipic acid using glucose as carbon and energy source under micro-aerobic, substrate oxidation and growth limiting cultivation conditions.

Using the extended ¡MM904 model and the metabolic engineering workbench, Optflux; optimization trials found an optimal attenuation strategy including: (1) attenuating hexanoate transport to the extracellular media; (2) attenuating ethanol excretion to the extracellular media; (3) attenuating *2-hydroxybutyrate oxidoreductase,* preventing 2-hydroxybutyrate production; (4) attenuating *DL gfycerol-3-phosphatase,* preventing glycerol production and (5) attenuating *malate dehydrogenase,* preventing inter-conversion of NADH to NADPH.

The resulting *S. cerevisiae* mutant produces adipate as the most advantageous means of balancing NADH to maximize biomass growth, producing adipate with a molar yield of 0.71 [(mol adipate)/(mol glucose)].

In-silico attenuation of the biochemical network using a validated model determined that a non-cyclical cultivation strategy under micro-aerobic conditions produces predominantly adipic acid from the fed glucose.

Example 3

Genome-scale attenuation strategy for aerobic synthesis from glucose using NADPH imbalance to direct carbon flux towards adipic acid in *Saccharomyces cerevisiae*

The ¡MM904 model outlined in Example 1 was utilized to assess the non-cyclical production of adipic acid using glucose as carbon and energy source under aerobic cultivation and growth limiting conditions.

The NADH-specific enzymatic reactions outlined in FIG. 1 were replaced by the equivalent NADPH-specific enzymatic reactions outlined in FIG. 2.

Using the extended ¡MM904 model and the metabolic engineering workbench, Optflux; optimization trials found an optimal attenuation strategy including; (1) attenuating *triose phosphate isomerase Iphosphoglucose isomerase,* redirecting flux into the pentose phosphate cycle; (2) preventing the inter-conversion of NADPH to NADH, by attenuating the *NADH-dependent glutamate dehydrogenase* and *proline oxidase.*

The resulting *S. cerevisiae* mutant produces adipate as the most advantageous means of balancing NADPH to maximize biomass growth, producing adipate with a molar yield of 0.4 [(mol adipate)/(mol glucose)].

In-silico attenuation of the biochemical network using a validated model determined that a non-cyclical cultivation strategy under aerobic conditions produces predominantly adipic acid from the fed glucose.

OTHER EMBODIMENTS

It is to be understood that while the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

WHAT IS CLAIMED:

1. A method for biosynthesizing one or more products selected from the group consisting of adipic acid, 6-aminohexanoic acid, hexamethylenediamine, caprolactam, and 1,6-hexanediol, said method comprising enzymatically synthesizing a six carbon chain aliphatic backbone and enzymatically forming, in one or more steps, two terminal functional groups selected from the group consisting of carboxyl, amine, and hydroxyl groups in said backbone to directly produce the product or producing the product in a subsequent step.

2. The method of claim 1, wherein said two terminal functional groups are the same.

3. The method of claim 1, wherein said two terminal functional groups are different.

4. The method of claim 1, where the six carbon chain aliphatic backbone is hexanoyl-CoA.

5. The method of claim 4, wherein hexanoyl-CoA is enzymatically synthesized from acetyl-CoA via two cycles of CoA-dependent carbon chain elongation using either NADH or NADPH dependent enzymes.

6. The method of claim 4 or 5, where hexanoyl-CoA is formed by conversion of hex-2-enoyl-CoA by an enoyl-CoA reductase classified under EC 1.3.1.44, EC 1.3.1.38, or EC 1.3.1.8.

7. The method of claim 6, where said enoyl-CoA reductase is the gene product of ter or tdter.

8. The method of claim 6, where hex-2-enoyl-CoA is formed by conversion of (S) 3-hydroxyhexanoyl-CoA by a trans-2-enoyl-CoA hydratase classified under EC 4.2.1.17 or by conversion of (R) 3-hydroxyhexanoyl-CoA by a trans-2-enoyl-CoA hydratase classified under EC 4.2.1.119.

9. The method of claim 8, where said trans-2-enoyl-CoA hydratase is the gene product of crt.

10. The method of claim 8 or claim 9, where (S) 3-hydroxyhexanoyl-CoA is formed by conversion of 3-oxohexanoyl-CoA by a 3-hydroxyacyl-CoA dehydrogenase classified under EC 1.1.1.35.

11. The method of claim 10, where said 3-hydroxyacyl-CoA dehydrogenase is encoded by fadB.

12. The method of claim 10 or claim 11, wherein 3-oxohexanoyl-CoA is formed by conversion of butanoyl-CoA by an acetyl-CoA C-acyltransferase classified under EC 2.3.1.16.

13. The method of claim 12, wherein said acetyl-CoA C-acyltransferase is encoded by bktB.

14. The method of claim 12 or claim 13, wherein butanoyl-CoA is formed by conversion of crotonyl-CoA by an enoyl-CoA reductase classified under EC 1.3.1.44, EC 1.3.1.38, or EC 1.3.1.8.

15. The method of claim 14, wherein crotonyl-CoA is formed by conversion of (S) 3-hydroxybutanoyl-CoA by a trans-2-enoyl-CoA hydratase classified under EC 4.2.1.17.

16. The method of claim 15, wherein (S) 3-hydroxybutanoyl-CoA is formed by conversion of acetoacetyl-CoA by a 3-hydroxybutyryl-CoA dehydrogenase classified under EC 1.1.1.157.

17. The method of claim 16, wherein said 3-hydroxybutyryl-CoA dehydrogenase is encoded by hbd.

18. The method of claim 16 or claim 17, wherein acetoacetyl-CoA is formed by conversion of acetyl-CoA by an acetyl-CoA C-acyltransferase classified under EC 2.3.1.9.

19. The method of claim 18, wherein said acetyl-CoA C-acyltransferase is encoded by atoB or phaA.

20. The method of claim 18 or claim 19, wherein acetoacetyl-CoA is formed by conversion of malonyl-CoA by an acetoacetyl-CoA synthase classified under EC 2.3.1.194.

21. The method of claim 20, wherein malonyl-CoA is formed by conversion of acetyl-CoA by an acetyl-CoA carboxylase classified under EC 6.4.1.2.

22. The method of claim 8, wherein said trans-2-enoyl-CoA hydratase is the gene product of phaJ.

23. The method of claim 8 or claim 22, wherein (R) 3-hydroxyhexanoyl-CoA is formed by conversion of 3-oxohexanoyl-CoA by a 3-oxoacyl-CoA reductase classified under EC 1.1.1.100.

24. The method of claim 23, wherein said 3-oxoacyl-CoA reductase is encoded by fabG.

25. The method of claim 14, wherein crotonyl-CoA is formed by conversion of (R) 3-hydroxybutanoyl-CoA by a trans-2-enoyl-CoA hydratase classified under EC 4.2.1.1 19.

26. The method of claim 25, wherein (R) 3-hydroxybutanoyl-CoA is formed by conversion of acetoacetyl-CoA by an acetoacyl-CoA reductase classified under EC 1.1.1.36.

27. The method of claim 26, wherein said actetoacyl-CoA reductase is encoded by phaB.

28. The method of any one of claims 1-4, comprising producing hexanoate by forming a first terminal carboxyl group in hexanoyl CoA using an acyl-CoA hydrolase and an aldehyde dehydrogenase, or a thioesterase.

29. The method of claim 28, wherein said acyl-CoA hydrolase or thioesterase is encoded by YciA, tesB or Acotl3.

30. The method of any one of claims 1-4, comprising producing hexanoate by forming a first terminal carboxyl group in hexanal by an aldehyde dehydrogenase classified under EC 1.2.1.4.

31. The method of claim 30, wherein hexanal is formed by conversion of hexanoyl-CoA by a butanal dehydrogenase classified under EC 1.2.1.57.

32. The method of any one of claims 29-31, further comprising converting hexanoate to adipic acid, 6-aminohexanoic acid, hexamethylenediamine, ε caprolactam or 1,6 hexanediol with one or more enzymatic conversions, wherein one of said enzymatic conversions introduces the second terminal functional group.

33. The method of claim 32, comprising converting hexanoate to 6-hydroxyhexanoate using a cytochrome P450/ ω-hydroxylase.

34. The method of claim 33, wherein said cytochrome P450/ ω-hydroxylase is from the family CYP153 such as CYP152A6.

35. The method of claim 33 or claim 34, comprising converting 6-hydroxyhexanoate to adipate semialdehyde using (i) an alcohol dehydrogenase, (ii) a 6-hydroxyhexanoate dehydrogenase or (iii) a cytochrome P450/ ω -hydroxylase.

36. The method of claim 35, wherein said alcohol dehydrogenase is encoded by YMR318C.

37. The method of claim 35 or claim 36, wherein said 6-hydroxyhexanoate dehydrogenase is encoded by ChnD.

38. The method of any one of claims 1-3 or 32, comprising producing adipic acid by forming the second terminal functional group in adipate semialdehyde using (i) an aldehyde dehydrogenase classified under EC 1.2.1.3, (ii) a 6-oxohexanoate dehydrogenase classified under EC 1.2.1.63 or (iii) a cytochrome P450/ω-hydroxylase.

39. The method of claim 38, wherein said 6-oxohexanoate dehydrogenase is encoded by ChnE.

40. The method of claim 32 or 33, comprising producing 6-aminohexanoic acid by forming the second terminal functional group in adipate semialdehyde using an ω-transaminase classified under EC 2.61.18, EC 2.6.1.19 or EC 2.6.1.48.

41. The method of claim 1, 32, or 40, comprising producing e-caprolactam from 6-aminohexanoic acid using a lactamase classified under EC 3.5.2.-.

42. The method of claim 41, comprising converting 6-aminohexanoic acid to 6-aminohexanal using a carboxylate reductase classified under EC 1.2.99.6.

43. The method of claim 1, 32, or 42, comprising producing hexamethylenediamine by forming a second terminal functional group in 6-aminohexanal using a diamine transaminase classified under EC 2.6.1.29 or EC 2.6.1.82.

44. The method of claim 42 or 43, wherein said carboxylate reductase is encoded by car alongside the gene product of npt.

45. The method of claim 42 or 43, wherein said carboxylate reductase is encoded by GriC & GriD.

46. The method of any one of claims 1, 33, or 34, comprising producing 1,6 hexandiol by forming the second terminal functional group in 6-hydroxyhexanal using an alcohol dehydrogenase classified under EC 1.1.1.-(1,2,21, 184).

47. The method of any of the preceding claims, wherein said method is performed using cell lysates comprising said enzymes.

48. The method of any of the preceding claims, wherein said method is performed in a recombinant host.

49. The method of claim 48, wherein said host is cultured under anaerobic, aerobic or micro-aerobic cultivation conditions.

50. The method of claim 48, wherein said host is subjected to a cyclical cultivation strategy to alternate said host between anaerobic cultivation conditions and aerobic cultivation conditions.

51. The method of claim 48, wherein said host is cultured under conditions of nutrient limitation either via nitrogen, phosphate or oxygen limitation.

52. The method of any one of claims 48-51, wherein the C6 building block is produced by a single microorganism strain via a non-cyclical or cyclical fermentation strategy.

53. The method of any one of claims 48-51, wherein the C6 building block is produced by co-culturing two or more microorganism strains via a non-cyclical or cyclical fermentation strategy.

54. The method of any one of claims 48-50, wherein the C6 building block is produced by successive fermentations, wherein the broth or centrate from the preceding fermentation is fed to a succession of fermentations as a source of feedstock, central metabolite, or central precursor; finally producing the C6 building block.

55. The method of any one of claims 48-51, wherein said recombinant host cells are retained in ceramic hollow fiber membranes to maintain a high cell density during fermentation.

56. The method of 49 or 50, wherein the principal carbon source fed to the fermentation derives from biological or non-biological feedstocks.

57. The method of claim 56, wherein the biological feedstock is or derives from monosaccharides, disaccharides, lignocellulose, hemicellulose, cellulose, lignin such as levulinic acid and furfural, lignin, triglycerides such as glycerol and fatty acids, agricultural waste or municipal waste.

58. The method of claim 56, wherein the non-biological feedstock is or derives from natural gas, syngas, C02/H2, methanol, ethanol, non-volatile residue (NVR) or caustic wash waste stream from cyclohexane oxidation processes.

59. The method of claim 49, wherein the host is a prokaryote or a eukaryote.

60. The method of claim 59, wherein the host is a prokaryote from the genus Escherichia such as Escherichia coli; from the genus Clostridia such as Clostridium ljungdahlii, Clostridium autoethanogenum or Clostridium kluyveri; from the genus Corynebacteria such as Corynebacterium glutamicum; from the genus Cupriavidus such as Cupriavidus necator or Cupriavidus metallidurans; from the genus Pseudomonas such as Pseudomonas fluorescens, Pseudomonas putida or Pseudomonas oleavorans; from the genus Delftia such as Delftia acidovorans; from

the genus Bacillus such as Bacillus subtillis; from the genus Lactobacillus such as Lactobacillus delbrueckii; or from the genus Lactococcus such as Lactococcus lactis.

61. The method of claim 59, wherein the host is a eukaryote from the genus Aspergillus such as Aspergillus niger; from the genus Saccharomyces such as Saccharomyces cerevisiae; from the genus Pichia such as Pichia pastoris; from the genus Yarrowia such as Yarrowia lipolytica; from the genus Issatchenkia such as Issathenkia orientalis; from the genus Debaryomyces such as Debaryomyces hansenii; from the genus Arxula such as Arxula adenoinivorans; or from the genus Kluyveromyces such as Kluyveromyces lactis.

62. The method of claim 59, wherein the host's tolerance to high concentrations of a C6 building block is improved through continuous cultivation in a selective environment.

63. The method of claim 59, wherein the host naturally accumulates polyhydroxyalkanoates, and wherein the polymer synthase enzymes are attenuated in the host strain.

64. The method of claim 51, wherein the intracellular concentration of acetyl-CoA for biosynthesis of C6 building blocks is increased in the host by attenuating genes degrading acetyl-CoA.

65. The method of claim 48, wherein an imbalance in NADH is generated that can only be balanced via the formation of a C6 building block.

66. The method of claim 65, wherein a gene encoding a formate dehydrogenase is overexpressed, a gene encoding a pyruvate formate lyase is overexpressed, 2-hydroxybutyrate oxidoreductase activity is attenuated, DL glycerol-3-phosphatase activity is attenuated, and/or malate dehydrogenase activity is attenuated.

67. The method of claim 65, wherein carbon flux is directed into the pentose phosphate cycle in the host by attenuating a glucose-6-phosphate isomerase classified under EC 5.3. 1.9.

68. The method of claim 64 or 65, wherein a gene encoding an acetate kinase, such as ack, is attenuated in the host.

69. The method of claim 64 or 65, wherein a gene encoding an enzyme that mediates the degradation of pyruvate to lactate such as ldhA is attenuated in the host.

70. The method of claim 64 or 65, wherein genes encoding enzymes mediating the degradation of phophoenolpyruvate to succinate such as frdBC are attenuated in the host.

71. The method of claim 64 or 65, wherein a gene encoding an enzyme mediating the degradation of acetyl-CoA to ethanol such as the alcohol dehydrogenase encoded by adhE is attenuated in the host.

72. The method of claim 64 or 65, wherein a gene encoding an enzyme mediating the degradation of pyruvate to ethanol such as pyruvate decarboxylase is attenuated in the host.

73. The method of claim 64 or 65, wherein a gene encoding an enzyme mediating the generation of isobutanol such as a 2-oxoacid decarboxylase is attenuated in the host

74. The method of claim 48, wherein the intracellular concentration of acetyl-CoA for biosynthesis of a C6 building block is increased in the host by overexpressing genes forming acetyl-CoA.

75. The method of claim 74, wherein an acetyl-CoA synthetase such as the gene product of acs is overexpressed in the host.

76. The method of claim 48, wherein an imbalance in NADPH is generated in the host that can only be balanced via the formation of a C6 building block.

77. The method of claim 76, wherein a puridine nucleotide transhydrogenase gene such as UdhA is overexpressed in the host.

78. The method of claim 76, wherein a glyceraldehyde-3P-dehydrogenase gene such as GapN is overexpressed in the host, a malic enzyme gene such as maeA or maeB is overexpressed in the host, a glucose-6-phosphate dehydrogenase gene such as zwf is overexpressed in the host, a fructose 1,6 diphosphatase gene such as fbp is overexpressed in the host, activity of a triose phosphate isomerase is attenuated in the host, and/or activity of malate dehydrogenase is attenuated.

79. The method of claim 76, wherein membrane-bound cytochrome P450/ω-hydroxylases are solubilized in the host via truncation of the N-terminal region that anchors the P450 to the endoplasmic reticulum.

80. The method of claim 76, wherein a glucose dehydrogenase such as the gene product of gdh is overexpressed in the host.

81. The method of claim 76, wherein enzymes facilitating the conversion of NADPH to NADH are attenuated in the host or transport of hexanoate to the extracellular media is attenuated.

82. The method of claim 76, wherein the NADH generation cycle that may be generated via inter-conversion of glutamate dehydrogenases in EC 1.4.1.2 (NADH-specific) and EC 1.4.1.4 (NADPH-specific) is attenuated in the host.

83. The method of claim 76, wherein a glutamate dehydrogenases (EC 1.4.1.3) that utilize both NADH and NADPH as co-factors is attenuated in the host.

84. The method of claim 48, wherein the degradation of central metabolites leading to the formation of the hexanoyl-CoA is attenuated in the host.

85. The method of claim 84, wherein a propionyl-CoA synthetase such as the gene product of PrpE-RS is overexpressed in the host.

86. The method of claim 84, wherein β-oxidation enzymes degrading central metabolites and central precursors leading to and including C6 building blocks are attenuated in the host.

87. The method of claim 84, wherein enzymes activating C6 building blocks via Coenzyme A esterification such as CoA-ligases are attenuated.

88. The method of claim 48, wherein the efflux of a C6 building block across the cell membrane to the extracellular media is enhanced or amplified by genetically engineering structural modifications to the cell membrane or increasing any associated transporter activity for a C6 building block.

89. A recombinant host comprising at least one exogenous nucleic acid encoding one or more of a formate dehydrogenase, enoyl-CoA reductase, trans-2-enoyl-CoA hydratase, 3-hydroxybutyryl-CoA dehydrogenase, acetyl-CoA C-acyltransferase, acetoacyl-CoA reductase, acetyl-CoA synthetase, acetyl-CoA carboxylase, a malic enzyme, puridine nucleotide transhydrogenase, glyceraldehyde-3P-dehydrogenase, acyl-CoA hydrolase, aldehyde dehydrogenase, thioesterase, cytochrome P450/ ω-hydroxylase, alcohol dehydrogenase, 6-hydroxyhexanoate dehydrogenase, 6-oxohexanoate dehydrogenase, diamine transaminase, propionyl-CoA synthetase, and a carboxylate reductase, wherein said host comprises one or more deficiencies in glucose-6-phosphate isomerase, acetate kinase, an enzyme degrading pyruvate to lactate, enzymes mediating the degradation of phophoenolpyruvate to succinate, alcohol dehydrogenase, pyruvate decarboxylase, 2-oxoacid decarboxylase, triose phosphate isomerase, a glutamate dehydrogenase.

FIGURE 1

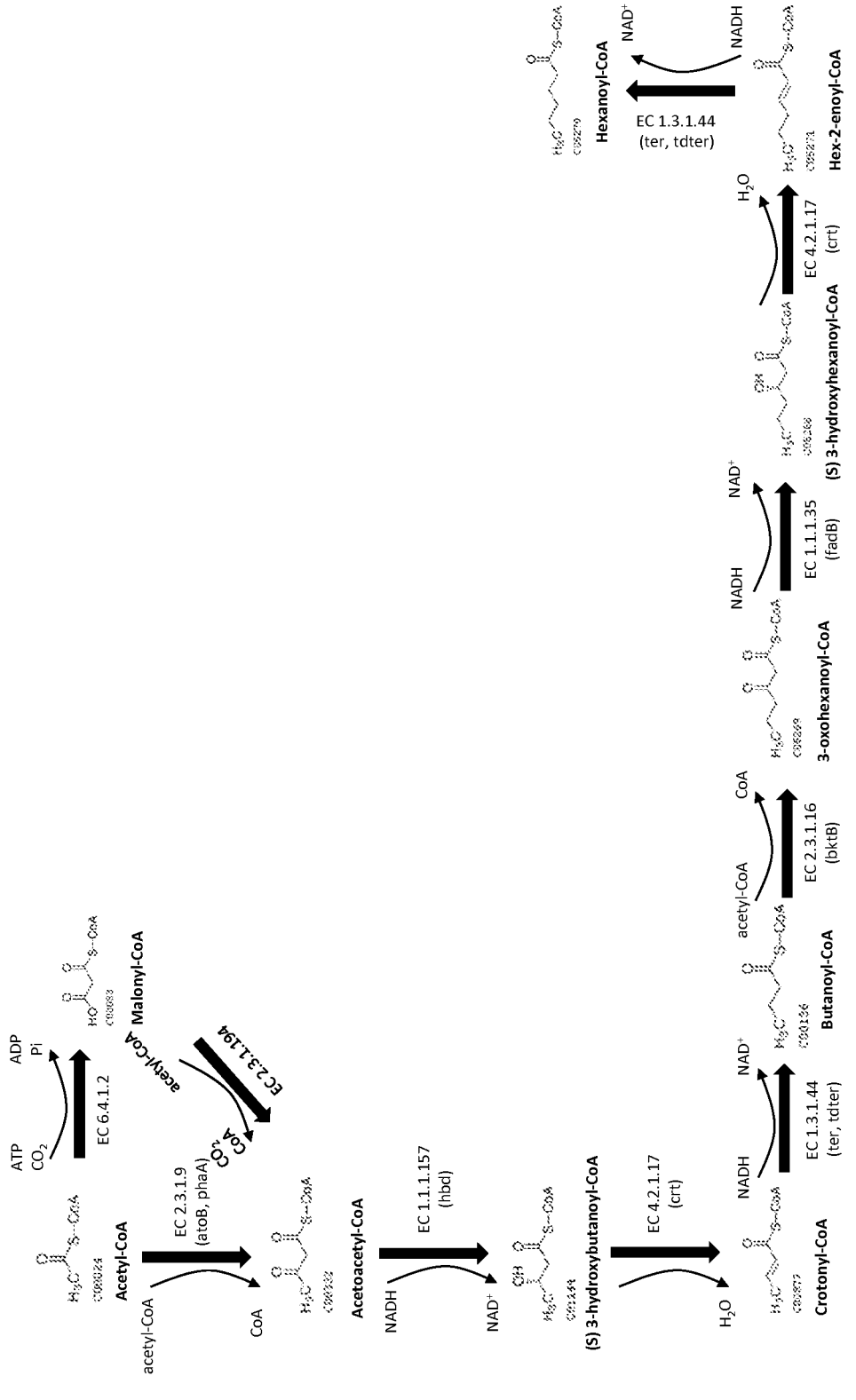

ATP
ADP
Pi
CO_2
EC 6.4.1.2
Malonyl-CoA
acetyl-CoA
EC 2.3.1.9
(atoB, phaA)
CoA
EC 2.3.1.194
CO_2
Acetyl-CoA
acetyl-CoA
Acetoacetyl-CoA
NADH
EC 1.1.1.157
(hbd)
NAD^+
(S) 3-hydroxybutanoyl-CoA
EC 4.2.1.17
(crt)
H_2O
Crotonyl-CoA
NADH
EC 1.3.1.44
(ter, tdter)
NAD^+
Butanoyl-CoA
acetyl-CoA
CoA
EC 2.3.1.16
(bktB)
3-oxohexanoyl-CoA
NADH
EC 1.1.1.35
(fadB)
NAD^+
(S) 3-hydroxyhexanoyl-CoA
H_2O
EC 4.2.1.17
(crt)
Hex-2-enoyl-CoA
EC 1.3.1.44
(ter, tdter)
Hexanoyl-CoA
NAD^+
NADH

FIGURE 2

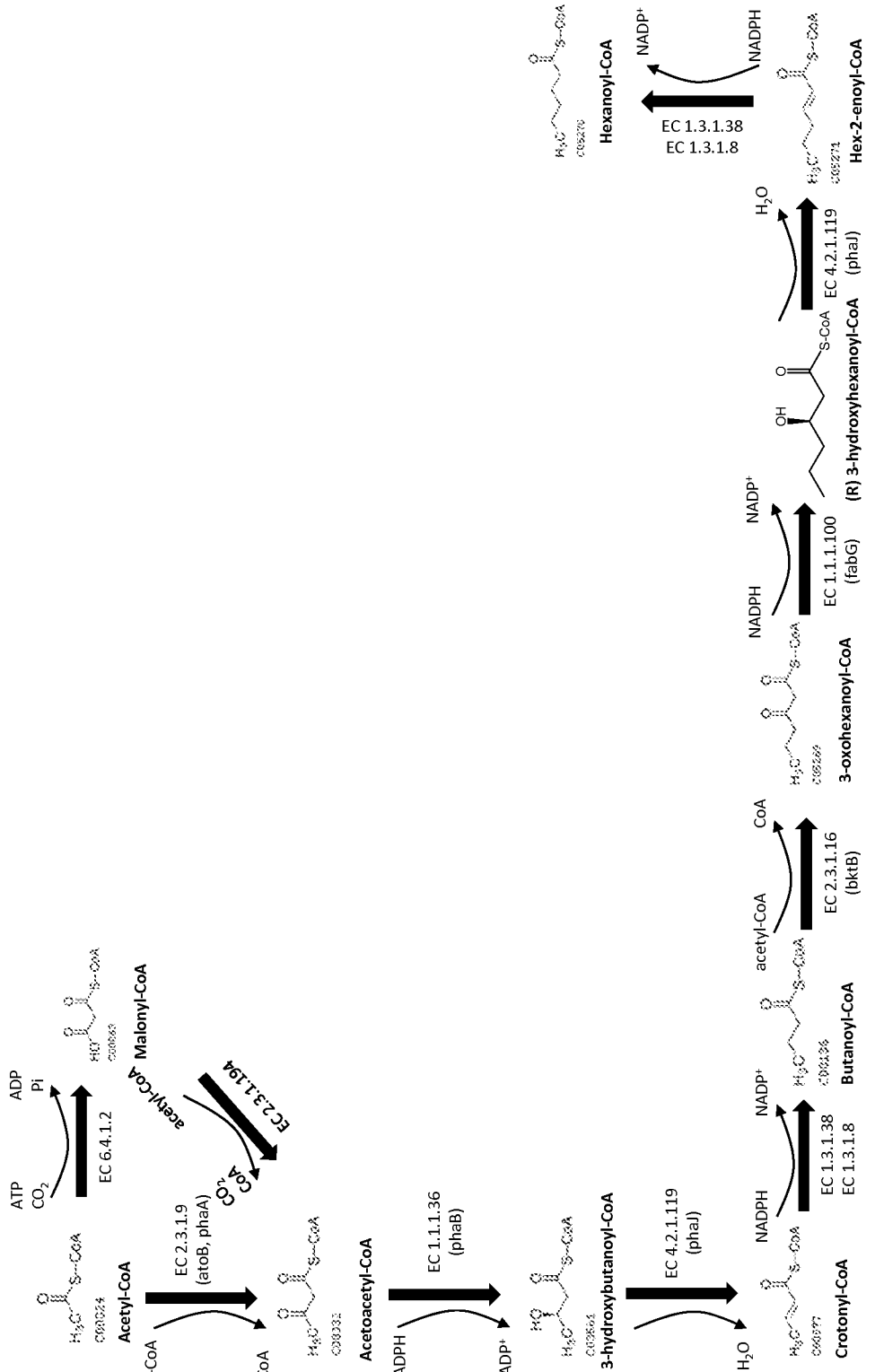

ATP
CO_2
ADP
PI
EC 6.4.1.2
Malonyl-CoA
acetyl-CoA
EC 2.3.1.9
(atoB, phaA)
CoA
Acetyl-CoA
acetyl-CoA
EC 2.3.1.19
CO_2
CoA
Acetoacetyl-CoA
NADPH
EC 1.1.1.36
(phaB)
$NADP^+$
(R) 3-hydroxybutanoyl-CoA
EC 4.2.1.119
(phaJ)
H_2O
Crotonyl-CoA
NADPH
EC 1.3.1.38
EC 1.3.1.8
$NADP^+$
Butanoyl-CoA
acetyl-CoA
EC 2.3.1.16
(bktB)
CoA
3-oxohexanoyl-CoA
NADPH
EC 1.1.1.100
(fabG)
$NADP^+$
(R) 3-hydroxyhexanoyl-CoA
H_2O
EC 4.2.1.119
(phaJ)
Hex-2-enoyl-CoA
NADPH
EC 1.3.1.38
EC 1.3.1.8
$NADP^+$
Hexanoyl-CoA

FIGURE 3

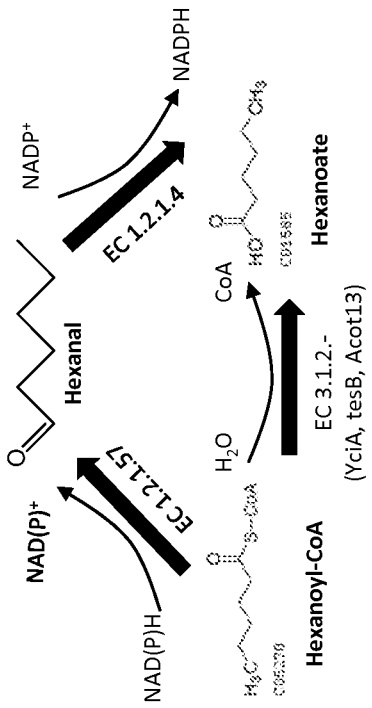

NADP+
NADPH
EC 1.2.1.4
Hexanal
NAD(P)+
EC 1.2.1.57
NAD(P)H
H2O
CoA
Hexanoyl-CoA
EC 3.1.2.-
(YciA, tesB, Acot13)
Hexanoate

FIGURE 4

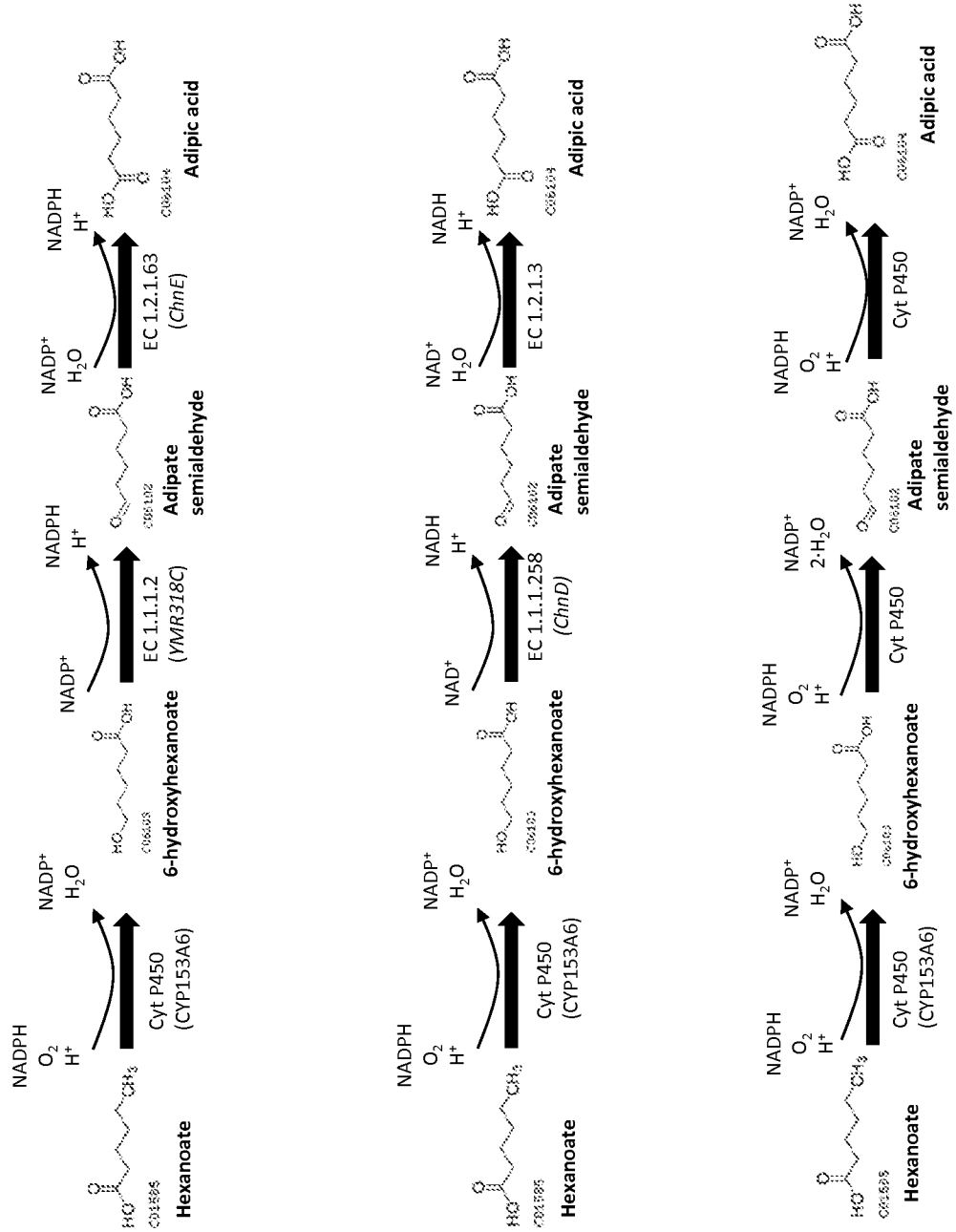

NADPH
O2
H+
NADP+
H2O
Cyt P450
(CYP153A6)
Hexanoate
6-hydroxyhexanoate
NADPH
H+
NADP+
EC 1.1.1.2
(YMR318C)
Adipate
semialdehyde
NADP+
H2O
NADPH
H+
EC 1.2.1.63
(ChnE)
Adipic acid
NADPH
O2
H+
NADP+
H2O
Cyt P450
(CYP153A6)
Hexanoate
6-hydroxyhexanoate
NAD+
NADH
H+
EC 1.1.1.258
(ChnD)
Adipate
semialdehyde
NAD+
H2O
NADH
H+
EC 1.2.1.3
Adipic acid
NADPH
O2
H+
NADP+
H2O
Cyt P450
(CYP153A6)
Hexanoate
6-hydroxyhexanoate
NADPH
O2
H+
NADP+
2·H2O
Cyt P450
Adipate
semialdehyde
NADPH
O2
H+
NADP+
H2O
Cyt P450
Adipic acid

FIGURE 5

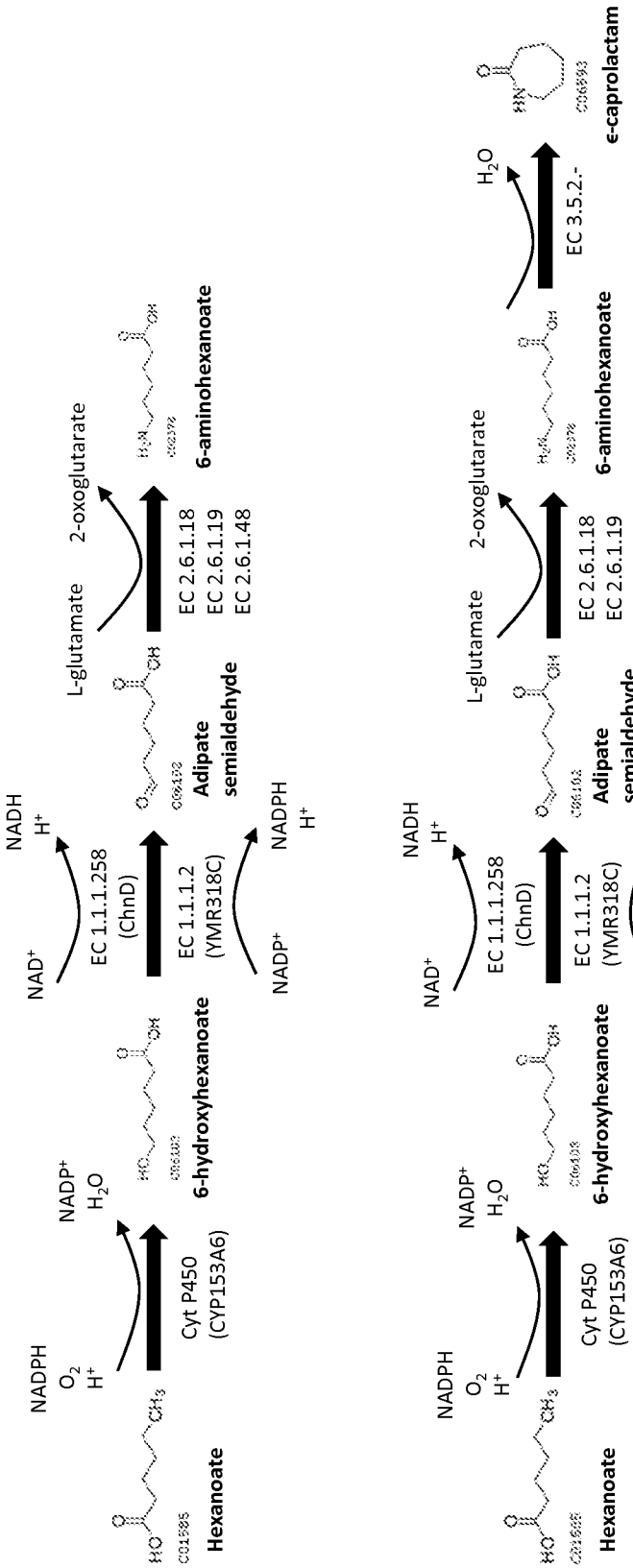

NADPH
O_2
H^+
Cyt P450
(CYP153A6)
Hexanoate
$NADP^+$
H_2O
6-hydroxyhexanoate
NAD^+
EC 1.1.1.258
(ChnD)
NADH
H^+
EC 1.1.1.2
(YMR318C)
Adipate
semialdehyde
$NADP^+$
NADPH
H^+
L-glutamate
2-oxoglutarate
EC 2.6.1.18
EC 2.6.1.19
EC 2.6.1.48
6-aminohexanoate
H_2O
EC 3.5.2.-
ε-caprolactam

FIGURE 6


NADPH
ATP
NADP+
ADP
Pi
6-aminohexanoate
EC 1.2.99.6
(car, npt
GriC, GriD)
6-aminohexanal
L-glutamate
2-oxoglutarate
EC 2.6.1.29
EC 2.6.1.82
Hexamethylenediamine

FIGURE 7

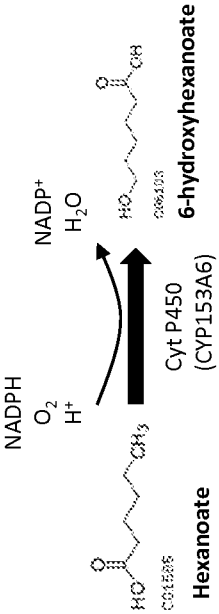
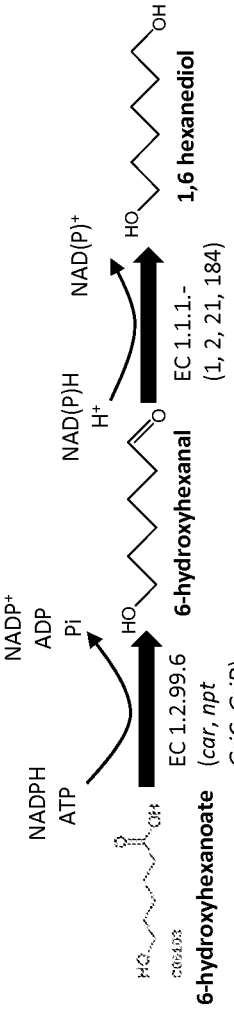

NADPH
O2
H+
NADP+
H2O
Cyt P450
(CYP153A6)
Hexanoate
6-hydroxyhexanoate

FIGURE 8


NADPH
ATP
NADP+
ADP
Pi
NAD(P)H
H+
NAD(P)+
HO
O
OH
6-hydroxyhexanoate
EC 1.2.99.6
(car, npt
GriC, GriD)
6-hydroxyhexanal
EC 1.1.1.-
(1, 2, 21, 184)
1,6 hexanediol