

MOLECULAR RHEOSTAT FOR COFACTOR BALANCE

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

[0001] This invention was made with Government support under Grant No. DE-AR0000556, awarded by the Department of Energy. The Government has certain rights in the invention.

CROSS REFERENCE TO RELATED APPLICATIONS

[0002] This application claims priority to U.S. Provisional Application Serial No. 62/409,731, filed October 18, 2016, the disclosures of which are incorporated herein by reference.

INCORPORATION BY REFERENCE OF SEQUENCE LISTING

[0003] Accompanying this filing is a Sequence Listing entitled "Sequence_ST25.txt", created on October 18, 2017 and having 56,906 bytes of data, machine formatted on IBM-PC, MS-Windows operating system. The sequence listing is hereby incorporated by reference in its entirety for all purposes.

TECHNICAL FIELD

[0004] The disclosure provides engineered pathways for chemical production using a molecular rheostat for ATP balance.

BACKGROUND

[0005] Over the past decades there has been a keen interest in engineering cellular metabolism for the production of "green" chemicals that could ween us off of our reliance on petrochemicals. One method is to perform a desired biochemical conversions with purified enzymes or cell extracts. Cell free metabolic systems have many advantages over *in vivo* efforts such as continuous product production, ease of product removal, near 100% yields, and no cell toxicity issues.

[0006] Building cell free pathways that can economically sustain high flux for long periods of time without the metabolic regulatory systems that exist in cells requires new design principles, a field referred to as "synthetic biochemistry". A key consideration in synthetic biochemistry system design is the generation, regulation and recycling of high energy cofactors such as ATP, NADH and NADPH. Generally high energy cofactors are generated in a catabolic or breakdown phase (e.g. glycolysis), then utilized and regenerated in an anabolic or build phase where the

desired chemicals are constructed. The simplest way to design synthetic biochemistry systems is to demand perfect stoichiometry, so that if two ATP are generated in the breakdown phase, then two ATP are utilized in the build phase. Stoichiometric systems can allow flux through the pathway for a period of time, but the second law of thermodynamics dictates that they will eventually wind down as ATP is hydrolyzed or NADH is oxidized by undesired side reactions.

SUMMARY

[0007] The disclosure provides a recombinant, artificial or engineered metabolic pathway comprising a plurality of enzymatic steps that converts a substrate to a product, wherein the pathway comprises a non-naturally occurring molecular rheostat system the alternates between or simultaneously uses a first cofactor pathway for the production of a metabolite and a second cofactor pathway for the production of the metabolite depending upon cofactor availability. In one embodiment, the pathway comprises: (a) a first enzymatic step that converts a first metabolite to a second metabolite using a first co-factor; (b) a second enzymatic step that converts the first metabolite to the second metabolite using a first co-factor and second co-factor or second co-factor; wherein the first enzymatic step is active when the second co-factor level is low and wherein the second enzymatic step is active when the second co-factor level is high. In another or further embodiment, the first cofactor is an oxidizing/reducing co-factors and the second cofactor is P_i . In still another embodiment of any of the foregoing embodiments, the oxidizing/reducing co-factors are $NAD^+/NADH$, $NADP^+/NADPH$ or $FAD^+/FADH$. In still another embodiment of any of the foregoing embodiments, the first cofactor comprises $NADP^+/NADPH$. In still another embodiment of any of the foregoing embodiments, the metabolic pathway comprises the conversion of glyceraldehyde-3-phosphate to 3-phosphoglycerate. In still another embodiment of any of the foregoing embodiments, the metabolic pathway produces a metabolite selected from the group consisting of isobutanol, 3-methyl-1-butanol, leucine, and valine. In still another embodiment of any of the foregoing embodiments, the pathway comprises the conversion of glyceraldehyde-3-phosphate to 1,3-

bisphosphoglycerate and 1,3-bisphosphoglycerate to 3-phosphoglycerate. In still another embodiment of any of the foregoing embodiments, the pathway comprises (i) an enzyme that converts glyceraldehyde-3-phosphate (G3P) and NADP⁺ to 3-phosphoglycerate (3PG) and NADPH; and (ii) an enzyme that converts glyceraldehyde-3-phosphate (G3P), NADP⁺ and free phosphate (Pi) to 1,3-bisphosphoglycerate (1,3BPG) and (iii) an enzyme that converts 1,3 bisphosphoglycerate (1,3BPG) and ADP to 3-phosphoglycerate and ATP. In still another embodiment of any of the foregoing embodiments, the enzyme of (i) comprises a NADP-dependent glyceraldehyde-3-phosphate dehydrogenase (GapN). In still another embodiment of any of the foregoing embodiments, the GapN is obtained from *S. mutans*. In still another embodiment of any of the foregoing embodiments, the enzyme of (ii) comprises a mutant glyceraldehyde-3-phosphate dehydrogenase (mGap) that comprises D34A/L35R/T36K mutations relative to SEQ ID NO:6. In still another embodiment of any of the foregoing embodiments, the enzyme of (ii) comprises a mutant glyceraldehyde-3-phosphate dehydrogenase (mGap) that has a sequence that is at least 95% identical to SEQ ID NO:6 and comprises D34A/L35R/T36K mutations. In still another embodiment of any of the foregoing embodiments, the enzyme of (iii) comprises enzyme commission number (EC number) EC 2.7.2.3. In still another embodiment of any of the foregoing embodiments, the enzyme of (iii) is a phosphoglycerate kinase. In still another embodiment of any of the foregoing embodiments, the phosphoglycerate kinase is a Pgk from *G. stearothermophilus*. In still another embodiment of any of the foregoing embodiments, the enzyme of (iii) has a sequence that is at least 95% identical to SEQ ID NO:7 and has phosphoglycerate kinase activity. In still another embodiment of any of the foregoing embodiments, the molecular rheostat comprise the enzymes of (i) a NADP-dependent glyceraldehyde-3-phosphate dehydrogenase (GapN), (ii) a mutant glyceraldehyde-3-phosphate dehydrogenase that utilizes NADP⁺ and (iii) a phosphoglycerate kinase. In still another embodiment of any of the foregoing embodiments, the pathway comprises (i) a polypeptide that catalyzes the production of glucose-6-phosphate (G6P) from glucose; (ii) a polypeptide that catalyzes the production of Fructose-6-phosphate (F6P) from

glucose-6-phosphate (G6P); (iii) a polypeptide that catalyzes the conversion/phosphorylation of fructose-6-phosphate (F6P) to fructose-1,6-phosphate; (iv) a polypeptide that converts fructose-1,6-phosphate to two glyceraldehyde-3-phosphates (G3P); (v) a molecular rheostat comprising (a) an enzyme that converts glyceraldehyde-3-phosphate (G3P) and NADP⁺ to 3-phosphoglycerate (3PG) and NADPH and (b) an enzyme that converts glyceraldehyde-3-phosphate (G3P), NADP⁺ and free phosphate (Pi) to 1,3-bisphosphoglycerate (1,3BPG) and (c) an enzyme that converts 1,3-bisphosphoglycerate (1,3BPG) and ADP to 3-phosphoglycerate (3PG) and ATP; (vi) a polypeptide that converts 3-phosphoglycerate (3PG) to 2-phosphoglycerate (2PG); (vii) a polypeptide that converts 2-phosphoglycerate (2PG) to phosphoenolpyruvate (PEP); (viii) a polypeptide that converts phosphoenolpyruvate (PEP) to pyruvate; (ix) a polypeptide that converts pyruvate to acetolactate; (x) a polypeptide that converts acetolactate and NADPH to 2,3 dihydroxy-3-methyl butanoate and NADP⁺; (xi) a polypeptide that converts 2,3 dihydroxy-3-methyl butanoate to 3-methyl-2-oxobutanoate; (xii) a polypeptide that converts 3-methyl-2-oxobutanoate to isobutanal and (xiii) a polypeptide that converts isobutanal and NADPH to isobutanol and NADP⁺. In still another embodiment of any of the foregoing embodiments, wherein the pathway is in a cell-free system. In still another embodiment of any of the foregoing embodiments, wherein the polypeptides are present in a cell-free system.

[0008] The disclosure also provides a recombinant polypeptide comprising a sequence that is at least 95% identical to SEQ ID NO:6 and comprises D34A/L35R/T36K mutations and has glyceraldehyde-3-phosphate dehydrogenase activity.

[0009]

[0010] The disclosure provides a molecular rheostat switch that allows a metabolic system to preferentially proceed down one of two pathways depending upon cofactor balance. For example, in one embodiment, the pathway proceeds down an enzyme path that doesn't produce ATP or one that does produce ATP depending upon the amount of free phosphate (Pi) in the system. The choice is regulated by free phosphate which is needed by the mGAP enzyme. Free phosphate

is a proxy for the amount of ATP hydrolyzed to ADP in the system. Effectively the flow down the ATP generating pathway is turned up or down depending on the Pi concentration. The biochemical pathway can be used to produced various chemical and biofuels from a carbon source (e.g., glucose).

[0011] The details of one or more embodiments of the disclosure are set forth in the accompanying drawings and the description below. Other features, objects, and advantages will be apparent from the description and drawings, and from the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

[0012] The accompanying drawings, which are incorporated into and constitute a part of this specification, illustrate one or more embodiments of the disclosure and, together with the detailed description, serve to explain the principles and implementations of the invention.

[0013] **Figure 1** provides a diagram of an *in vitro* pathway from glucose to isobutanol. The gapDH M6 and PGK scavenge inorganic phosphate and remake ATP that has been hydrolyzed in the system.

[0014] **Figure 2A-B** shows results of the stoichiometric pathway from glucose to isobutanol. (A) Time course production from the stoichiometric pathway using a fully purified system. The initial time course production had a high amount of ATPase contamination and produced 11.96 ± 1.57 g/L. The second time course had a lower amount of ATPase activity which increased the isobutanol production to 14.26 ± 0.57 g/L. (B) Histogram of isobutanol production from the stoichiometric pathway after 48 hours after NADPH or ATP supplementation at 24hours.

[0015] **Figure 3A-B** shows a design of the "molecular rheostat" at glyceraldehyde-3-phosphate dehydrogenase. (A) Schematic of the molecular rheostat in glycolysis. (B) Model of the gapDH M6 cyrstal structure.

[0016] **Figure 4A-D** shows a Copasi model of the rheostat pathway with ATPase activity modeled (A-B) and a Copasi model of the stoichiometric pathway with ATPase activity modeled (C-D). The initial conditions are set with 4mM inorganic phosphate, gapDH M6/PGK activity held constant, and ATP hydrolysis was increased

until the reaction died out. The reaction dies at an ATP hydrolysis to gapDH M6 ratio anything higher than 5:1.

[0017] **Figure 5A-C** shows the final production of isobutanol.

(A) Shows a time course of the isobutanol production, glucose consumption, and ATP in the system using a stoichiometric pathway.

(B) Shows a time course of the isobutanol production, glucose consumption and ATP in the ATP rheostat reaction. This reaction created a steady state of ATP at 600uM and produced 2x as much isobutanol as the stoichiometric pathway. (C) Is a 24 hour histogram of isobutanol production from the stoichiometric system (gapN only), too much ATP production system (gapDH M6 only), and the rheostat system (both gapN and GapDH M6).

[0018] **Figure 6A-B** provide detailed schematic of the stoichiometric pathway and rheostat pathway.

[0019] **Figure 7** provides a Caposi Model for hexokinase and the top of glycolysis in the stoichiometric system.

DETAILED DESCRIPTION

[0020] As used herein and in the appended claims, the singular forms "a," "and," and "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to "a polynucleotide" includes a plurality of such polynucleotides and reference to "the enzyme" includes reference to one or more enzymes, and so forth.

[0021] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this disclosure belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice of the disclosed methods and compositions, the exemplary methods, devices and materials are described herein.

[0022] Also, the use of "or" means "and/or" unless stated otherwise. Similarly, "comprise," "comprises," "comprising" "include," "includes," and "including" are interchangeable and not intended to be limiting.

[0023] It is to be further understood that where descriptions of various embodiments use the term "comprising," those skilled in the art would understand that in some specific instances, an

embodiment can be alternatively described using language "consisting essentially of" or "consisting of."

[0024] Any publications discussed above and throughout the text are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the inventors are not entitled to antedate such disclosure by virtue of prior disclosure.

[0025] As used herein, an "activity" of an enzyme is a measure of its ability to catalyze a reaction resulting in a metabolite, *i.e.*, to "function", and may be expressed as the rate at which the metabolite of the reaction is produced. For example, enzyme activity can be represented as the amount of metabolite produced per unit of time or per unit of enzyme (*e.g.*, concentration or weight), or in terms of affinity or dissociation constants.

[0026] The term "biosynthetic pathway", also referred to as "metabolic pathway", refers to a set of anabolic or catabolic biochemical reactions for converting (transmuting) one chemical species into another. Gene products belong to the same "metabolic pathway" if they, in parallel or in series, act on the same substrate, produce the same product, or act on or produce a metabolic intermediate (*i.e.*, metabolite) between the same substrate and metabolite end product. The disclosure provides *in vitro* biosynthetic pathways comprising a molecular rheostat which can optionally include a metabolic purge valve for the production of a desired product or intermediate. The disclosure also provides recombinant microorganism having a metabolically engineered pathway comprising a molecular rheostat and may further comprise a metabolic purge valve for the production of a desired product or intermediate.

[0027] As used herein a "cofactor" generally refers to a chemical compound or metabolite that is required for a protein's biological activity. The proteins are commonly enzymes, and cofactors assist in biochemical transformations. Cofactors include, but are not limited to, one or more inorganic ions, or a complex organic or metalloorganic molecule sometimes referred to as a coenzyme; most of which are derived from vitamins and from required organic nutrients in small amounts. Some enzymes or enzyme

complexes require several cofactors. For example, the multienzyme complex pyruvate dehydrogenase at the junction of glycolysis and the citric acid cycle requires five organic cofactors and one metal ion: loosely bound thiamine pyrophosphate (TPP), covalently bound lipoamide and flavin adenine dinucleotide (FAD), and the cosubstrates nicotinamide adenine dinucleotide (NAD⁺) and coenzyme A (CoA), and a metal ion (Mg²⁺). Organic cofactors are often vitamins or are made from vitamins. Many contain the nucleotide adenosine monophosphate (AMP) as part of their structures, such as ATP, coenzyme A, FAD, and NAD⁺.

[0028] An "enzyme" means any substance, typically composed wholly or largely of amino acids making up a protein or polypeptide that catalyzes or promotes, more or less specifically, one or more chemical or biochemical reactions.

[0029] The term "expression" with respect to a gene or polynucleotide refers to transcription of the gene or polynucleotide and, as appropriate, translation of the resulting mRNA transcript to a protein or polypeptide. Thus, as will be clear from the context, expression of a protein or polypeptide results from transcription and translation of the open reading frame.

[0030] A "metabolite" refers to any substance produced by metabolism or a substance necessary for or taking part in a particular metabolic process that gives rise to a desired metabolite, chemical, alcohol or ketone. A metabolite can be an organic compound that is a starting material (e.g., a carbohydrate, a sugar phosphate, pyruvate *etc.*), an intermediate in (e.g., acetyl-coA), or an end product (e.g., isobutanol, isoprene or PHB) of metabolism. Metabolites can be used to construct more complex molecules, or they can be broken down into simpler ones. Intermediate metabolites may be synthesized from other metabolites, perhaps used to make more complex substances, or broken down into simpler compounds, often with the release of chemical energy.

[0031] As used herein, the term "metabolically engineered" or "metabolic engineering" involves rational pathway design and assembly of biosynthetic genes, genes associated with operons, and control elements of such polynucleotides, for the production of a

desired metabolite, such as acetyl-CoA, higher alcohols or other chemical, in a microorganism, or in a cell-free system the rational pathway design and assembly of a biosynthetic pathway and co-factors for the production of a desired metabolite. "Metabolically engineered" can further include optimization of metabolic flux by regulation and optimization of transcription, translation, protein stability and protein functionality using genetic engineering and appropriate culture condition including the reduction of, disruption, or knocking out of, a competing metabolic pathway that competes with an intermediate leading to a desired pathway. For example, in a cell free system a host cell expressing one or more enzymes used in the cell-free system can be further engineered to eliminate or remove competing pathway enzymes thereby removing contaminants or enzymes that may be present in a disrupted or cell-free preparation.

[0032] A biosynthetic gene can be heterologous to the host microorganism, either by virtue of being foreign to the host, or being modified by mutagenesis, recombination, and/or association with a heterologous expression control sequence in an endogenous host cell. In one embodiment, where the polynucleotide is xenogenetic to the host organism, the polynucleotide can be codon optimized.

[0033] A "metabolic purge valve" refers to an engineered metabolic pathway that 'purges' excess metabolites and/or co-factors resulting in a recycling of the metabolite or co-factor for use in a primary metabolic pathway, e.g., by oxidizing a reduced cofactor thus "purging an abundance of reduced cofactors" etc.

[0034] A "molecular rheostat" refers to an enzymatic step that is only activated when a co-factor is at a level sufficient to turn-over the enzyme. In the absence of sufficient levels, the pathway proceeds by a secondary enzymatic step. For example, as shown in Figure 1, a molecular rheostat can be made up of two competing pathway branches that eventually transform glyceraldehyde-3 phosphate (G3P) into 3-phosphoglycerate (3PG). One branch reduces a cofactor in the conversion of G3P which is regulated by oxidation/reduction levels, while the other branch generates ATP, while flow through the ATP generating branch is

regulated by P_i levels. The first branch is made up of one enzyme, the non-phosphorylating GapN used in the stoichiometric pathway, which reduces $NADP^+$ to NADPH and converts G3P directly into 3PG without generating ATP. The second pathway is composed of two enzymes, an NADPH specific, phosphorylating glyceraldehyde-3-phosphate dehydrogenase (GapDH) and phosphoglycerate kinase (PGK), that also produces NADPH but first converts G3P into 1,3-bisphosphoglycerate (1,3BPG) followed by 3PG and ATP by the action of PGK. Therefore, the GapDH/PGK branch produces an additional ATP compared to the GapN only branch. The relative flow through the ATP generating branch of the rheostat is controlled by free P_i , which acts as a proxy for the amount of ATP hydrolyzed to ADP and P_i . The function of the rheostat is depicted in the simplest case, where no exogenous P_i is added to the reaction (Fig. 3A, left panel). In this case there is initially no free P_i and there can be no flux through the phosphorylating GAPDH. Thus, in the absence of P_i , all the flux passes through GapN branch. However, when ATP is hydrolyzed to ADP and P_i , the phosphorylating branch is then utilized. Thus, the rheostat senses the depletion of ATP and acts to restore ATP by utilizing the phosphorylating GAPDH branch (Fig. 3A, right panel).

[0035] The term "polynucleotide," "nucleic acid" or "recombinant nucleic acid" refers to polynucleotides such as deoxyribonucleic acid (DNA), and, where appropriate, ribonucleic acid (RNA).

[0036] A "protein" or "polypeptide", which terms are used interchangeably herein, comprises one or more chains of chemical building blocks called amino acids that are linked together by chemical bonds called peptide bonds. A protein or polypeptide can function as an enzyme.

[0037] The term "recombinant microorganism" and "recombinant host cell" are used interchangeably herein and refer to microorganisms that have been genetically modified to express non-expressed or over-express endogenous polynucleotides, or to express non-endogenous sequences, such as those included in a vector. The polynucleotide generally encodes a target enzyme involved in a metabolic pathway for producing a desired metabolite as described

herein, but may also include protein factors necessary for regulation or activity or transcription. Accordingly, recombinant microorganisms described herein have been genetically engineered to express or over-express target enzymes not previously expressed or over-expressed by a parental microorganism. It is understood that the terms "recombinant microorganism" and "recombinant host cell" refer not only to the particular recombinant microorganism but to the progeny or potential progeny of such a microorganism. It should also be understood that the recombinant microorganism can be used as a source of the polypeptide and that the recombinant microorganism need not have the full pathway for the generation of a desired metabolite. Rather, a plurality of recombinant microorganisms each having one or more, but not all, of the polypeptide for a metabolic pathway can be cocultured to produce the desired metabolite or can be disrupted and the cell-free milieu used or the expressed polypeptide isolated from each of the recombinant microorganisms.

[0038] The term "substrate" or "suitable substrate" refers to any substance or compound that is converted or meant to be converted into another compound by the action of an enzyme. The term includes not only a single compound, but also combinations of compounds, such as solutions, mixtures and other materials which contain at least one substrate, or derivatives thereof. Further, the term "substrate" encompasses not only compounds that provide a carbon source suitable for use as a starting material, but also intermediate and end product metabolites used in a pathway as described herein. In addition, a substrate can be an oxidized or reduced co-factor or a factor that is phosphorylated or de-phosphorylated.

[0039] Metabolic engineering and synthetic biology have been employed for the production of high value chemicals but have not been as successful as hoped in meeting the stringent economics of large scale commodity chemical manufacturing. Microbial systems are often hampered by a variety of technical challenges that make it hard to achieve cost competitiveness, including poor yields due to competing pathways; low productivity caused by slow growth rates

or difficulties in pathway optimization; contaminating microbial growth; product toxicity; and expensive product isolation.

[0040] As demonstrated herein, one approach to overcome these difficulties is to perform complex biochemical transformations using mixtures of enzymes in a reaction vessel or flow system rather than within a cell. Building single, dedicated pathways *in vitro* can eliminate side reactions that occur in the cell, so that nearly 100% yields and fast reaction times are possible. *In vitro* biochemical systems also allow for more precise control over optimization and product toxicity problems can be more easily diagnosed and mitigated. Moreover, product extraction can be more facile.

[0041] Traditionally, *in vitro* pathway construction has been relegated to use as a research tool or in applications that require only 1-3 enzymes for the production of chiral compounds and other high value chemicals. Improvements in protein expression and access to stable enzymes have made more complex systems possible. *In vitro* biotransformation systems have been reported in recent years involving systems of over thirty enzymes. One of the first modern studies in this area was an artificial pathway that produced hydrogen from starch. The concept was recently advanced with a creative system that generated hydrogen from cellobiose at nearly 100% yields. In another effort, hyper-thermophilic glycolysis enzymes were heterologously expressed, heat purified, and assembled to convert glucose to n-butanol in 82% yield. In another study, an elegantly simplified non-phosphorylative Entner-Doudoroff pathway from hyper-thermophilic archaea was constructed to produce ethanol and isobutanol in ~55% yields. These pioneering studies illustrate the flexibility of synthetic biochemistry and the potential for high yields.

[0042] Maintaining proper cofactor balance is an essential part of generating flux and providing a driving force through an enzymatic pathway. *In vivo*, the enzymatic specificity for the cofactors NADH/NADPH and/or ADP/ATP are typically used to control the carbon flux through catabolic and anabolic pathways respectively. Organisms typically sense the reduction state of these cofactors and use this information to up-regulate or down-

regulate catabolic and anabolic pathways to cope with environmental changes. *In vitro* systems, however, do not have the myriad of peripheral pathways that facilitate this control. Moreover, the natural anabolic and catabolic specificities for NADH and NADPH complicate *in vitro* biotransformations. Synthetic biochemistry systems have often dealt with these problems by careful considerations of cofactor stoichiometry in pathway design, through the use of expensive sacrificial metabolites, reengineering enzymes so that only a single cofactor type is needed, adding excess cofactors, or constantly adding intermediates to the reaction mix to sustain the process.

[0043] Although the methods, compositions and systems described herein are described with reference to certain metabolic products, the methods, compositions and systems are applicable to a broad range of recombinant biochemical pathways where co-factor recycling is important. In one exemplary engineered pathway the disclosure describes the production of isobutanol (see, e.g., **FIG. 1, 6A** and **6B**).

[0044] The disclosure describes a molecular rheostat system for co-factor balance in *in vitro* pathways for chemical production and *in vivo* systems. For example, the disclosure describes a pathway to convert glucose into isobutanol that maintains sustainable reducing cofactor balance, without the requirement for perfect stoichiometric matching of cofactor generation and usage to carbon usage.

[0045] The disclosure provides a robust node of control to balance the production and consumption of cofactors such as NADPH and NADH and ATP and ADP in a self-regulating and self-balancing manner. This *in vitro* pathway maintains cofactor balance without requiring adherence to stoichiometry in the generation and utilization of cofactors to ensure carbon flux. In part because the system can switch between enzymatic steps based upon co-factor levels, driving the transformation to near completion.

[0046] Ultimately the methods and compositions of the disclosure can be expanded to incorporate the conversion of low cost substrates such as glucose or other sugars into useful chemicals and biofuels.

[0047] The disclosure demonstrates the design and use of a self-regulating synthetic biochemical pathways over the standard stoichiometric design using a cell free enzymatic pathway. In the production of isobutanol, the exemplary pathway described herein, the non-rheostat pathway produced about 12 g/L of isobutanol before the reaction stopped due to ATP depletion. Using the rheostat of the disclosure the system can produce an excess of ATP when needed and improved the final titer to 24 g/L.

[0048] Synthetic biochemistry systems that do not rely of perfect stoichiometry can run longer and are more flexible because cofactor stoichiometry is not constrained. The disclosure also contemplates the use of molecular purge valves in combination with the rheostat of the disclosure. For example, International application publication no. WO2015/153929 and International application No. PCT/US2016/043260 described such purge valve systems (the disclosure of which are incorporated herein by reference). Together, with the ATP regulatory system described here, these synthetic pathways allow for the design of self-sustaining *in vitro* pathways to a myriad of bio-based products that require balancing both NAD(P)/NAD(P)H and ATP individually or at the same time. These self-regulatory nodes, which can control ATP and NAD(P)/NAD(P)H, provides tools and pathways for industrial cell free enzymatic synthesis.

[0049] In one embodiment, a pathway of the disclosure provide parallel enzymatic step that utilize NADP⁺/NADPH in a first pathway at low Pi and a second pathway that utilizes NADP⁺/NADPH and ADP-ATP cycling at higher Pi.

[0050] The disclosure provides pathways that can be developed *in vitro* in a number of ways. For example, the desired enzymes can be cloned/engineered into a microorganism or cell, expressed and then purified from the culture. In another example, the enzymes can be expressed, the cells disrupted and a disrupted preparation used in the pathways of the disclosure. In another embodiment, the enzymes can be purified and tethered to a substrate in a system (e.g., in a microfluidic system) for use in the metabolic pathway. In yet another embodiment, thermophilic enzymes having the desired activity can be cloned, expressed and the cell or preparations

therefrom heated to a temperature wherein the desired enzymes remain active while undesired enzymes are denatured. In yet another embodiment, the enzymes can be commercially purchased and mixed as appropriate. In all of the foregoing embodiments, the system would be combined with the necessary substrates and cofactors (e.g., NAD⁺, NADP⁺, FAD⁺, AMP, ADP, ATP and the like).

[0051] Accordingly, the disclosure provides "engineered" or "modified" microorganisms that are produced via the introduction of genetic material into a host or parental microorganism of choice thereby modifying or altering the cellular physiology and biochemistry of the microorganism. Through the introduction of genetic material the parental microorganism acquires new properties, e.g. the ability to produce a new, or greater quantities of, an intracellular metabolite. The genetic material introduced into the parental microorganism contains gene(s), or parts of gene(s), coding for one or more of the enzymes involved in a biosynthetic pathway and include gene(s), or parts of gene(s), coding for one or more of the enzymes involved in a molecular rheostat alone or in combination with metabolic purge valve, the pathway(s) useful for the production of a desired metabolite (e.g., isobutanol), and may also include additional elements for the expression and/or regulation of expression of these genes, e.g. promoter sequences.

[0052] An engineered or modified microorganism can also include in the alternative or in addition to the introduction of a genetic material into a host or parental microorganism, the disruption, deletion or knocking out of a gene or polynucleotide to alter the cellular physiology and biochemistry of the microorganism. Through the reduction, disruption or knocking out of a gene or polynucleotide the microorganism acquires new or improved properties (e.g., the ability to produce a new or greater quantities of an intracellular metabolite, improve the flux of a metabolite down a desired pathway, and/or reduce the production of undesirable by-products). For example, it may be desirable to engineer an organism to express a desired set for enzymes in a metabolic pathway while eliminating enzymes of competing pathways. This engineering can be applicable for both *in vitro* (where upon

disruption or purification undesirable enzymes are not present) or *in vivo*.

[0053] A "native" or "wild-type" protein, enzyme, polynucleotide, gene, or cell, means a protein, enzyme, polynucleotide, gene, or cell that occurs in nature.

[0054] A "parental microorganism" refers to a cell used to generate a recombinant microorganism. The term "parental microorganism" describes, in one embodiment, a cell that occurs in nature, *i.e.* a "wild-type" cell that has not been genetically modified. The term "parental microorganism" further describes a cell that serves as the "parent" for further engineering. In this latter embodiment, the cell may have been genetically engineered, but serves as a source for further genetic engineering.

[0055] For example, a wild-type microorganism can be genetically modified to express or over express a first target enzyme such as a NADH-pyruvate dehydrogenase. This microorganism can act as a parental microorganism in the generation of a microorganism modified to express or over-express a second target enzyme. As used herein, "express" or "over express" refers to the phenotypic expression of a desired gene product. In one embodiment, a naturally occurring gene in the organism can be engineered such that it is linked to a heterologous promoter or regulatory domain, wherein the regulatory domain causes expression of the gene, thereby modifying its normal expression relative to the wild-type organism. Alternatively, the organism can be engineered to remove or reduce a repressor function on the gene, thereby modifying its expression. In yet another embodiment, a cassette comprising the gene sequence operably linked to a desired expression control/regulatory element is engineered in to the microorganism.

[0056] Accordingly, a parental microorganism functions as a reference cell for successive genetic modification events. Each modification event can be accomplished by introducing one or more nucleic acid molecules in to the reference cell. The introduction facilitates the expression or over-expression of one or more target enzyme or the reduction or elimination of one or more target enzymes. It is understood that the term "facilitates" encompasses

the activation of endogenous polynucleotides encoding a target enzyme through genetic modification of e.g., a promoter sequence in a parental microorganism. It is further understood that the term "facilitates" encompasses the introduction of exogenous polynucleotides encoding a target enzyme in to a parental microorganism.

[0057] Polynucleotides that encode enzymes useful for generating metabolites including homologs, variants, fragments, related fusion proteins, or functional equivalents thereof, are used in recombinant nucleic acid molecules that direct the expression of such polypeptides in appropriate host cells, such as bacterial or yeast cells.

[0058] It is understood that a polynucleotide described herein include "genes" and that the nucleic acid molecules described above include "vectors" or "plasmids." Accordingly, the term "gene", also called a "structural gene" refers to a polynucleotide that codes for a particular polypeptide comprising a sequence of amino acids, which comprise all or part of one or more proteins or enzymes, and may include regulatory (non-transcribed) DNA sequences, such as promoter region or expression control elements, which determine, for example, the conditions under which the gene is expressed. The transcribed region of the gene may include untranslated regions, including introns, 5'-untranslated region (UTR), and 3'-UTR, as well as the coding sequence.

[0059] Those of skill in the art will recognize that, due to the degenerate nature of the genetic code, a variety of codons differing in their nucleotide sequences can be used to encode a given amino acid. A particular polynucleotide or gene sequence encoding a biosynthetic enzyme or polypeptide described above are referenced herein merely to illustrate an embodiment of the disclosure, and the disclosure includes polynucleotides of any sequence that encode a polypeptide comprising the same amino acid sequence of the polypeptides and proteins of the enzymes utilized in the methods of the disclosure. In similar fashion, a polypeptide can typically tolerate one or more amino acid substitutions, deletions, and insertions in its amino acid sequence without loss or significant loss of a desired activity. The

disclosure includes such polypeptides with alternate amino acid sequences, and the amino acid sequences encoded by the DNA sequences shown herein merely illustrate exemplary embodiments of the disclosure.

[0060] The disclosure provides polynucleotides in the form of recombinant DNA expression vectors or plasmids, as described in more detail elsewhere herein, that encode one or more target enzymes. Generally, such vectors can either replicate in the cytoplasm of the host microorganism or integrate into the chromosomal DNA of the host microorganism. In either case, the vector can be a stable vector (*i.e.*, the vector remains present over many cell divisions, even if only with selective pressure) or a transient vector (*i.e.*, the vector is gradually lost by host microorganisms with increasing numbers of cell divisions). The disclosure provides DNA molecules in isolated (*i.e.*, not pure, but existing in a preparation in an abundance and/or concentration not found in nature) and purified (*i.e.*, substantially free of contaminating materials or substantially free of materials with which the corresponding DNA would be found in nature) form.

[0061] A polynucleotide of the disclosure can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques and those procedures described in the Examples section below. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

[0062] It is also understood that an isolated polynucleotide molecule encoding a polypeptide homologous to the enzymes described herein can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence encoding the particular polypeptide, such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into the polynucleotide by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. In contrast to those

positions where it may be desirable to make a non-conservative amino acid substitution, in some positions it is preferable to make conservative amino acid substitutions.

[0063] As will be understood by those of skill in the art, it can be advantageous to modify a coding sequence to enhance its expression in a particular host. The genetic code is redundant with 64 possible codons, but most organisms typically use a subset of these codons. The codons that are utilized most often in a species are called optimal codons, and those not utilized very often are classified as rare or low-usage codons. Codons can be substituted to reflect the preferred codon usage of the host, a process sometimes called "codon optimization" or "controlling for species codon bias."

[0064] Optimized coding sequences containing codons preferred by a particular prokaryotic or eukaryotic host (see also, Murray et al. (1989) Nucl. Acids Res. 17:477-508) can be prepared, for example, to increase the rate of translation or to produce recombinant RNA transcripts having desirable properties, such as a longer half-life, as compared with transcripts produced from a non-optimized sequence. Translation stop codons can also be modified to reflect host preference. For example, typical stop codons for *S. cerevisiae* and mammals are UAA and UGA, respectively. The typical stop codon for monocotyledonous plants is UGA, whereas insects and *E. coli* commonly use UAA as the stop codon (Dalphin et al. (1996) Nucl. Acids Res. 24: 216-218). Methodology for optimizing a nucleotide sequence for expression in a plant is provided, for example, in U.S. Pat. No. 6,015,891, and the references cited therein.

[0065] "Transformation" refers to the process by which a vector is introduced into a host cell. Transformation (or transduction, or transfection), can be achieved by any one of a number of means including electroporation, microinjection, biolistics (or particle bombardment-mediated delivery), or agrobacterium mediated transformation.

[0066] A "vector" generally refers to a polynucleotide that can be propagated and/or transferred between organisms, cells, or cellular components. Vectors include viruses, bacteriophage, pro-

viruses, plasmids, phagemids, transposons, and artificial chromosomes such as YACs (yeast artificial chromosomes), BACs (bacterial artificial chromosomes), and PLACs (plant artificial chromosomes), and the like, that are "episomes," that is, that replicate autonomously or can integrate into a chromosome of a host cell. A vector can also be a naked RNA polynucleotide, a naked DNA polynucleotide, a polynucleotide composed of both DNA and RNA within the same strand, a poly-lysine-conjugated DNA or RNA, a peptide-conjugated DNA or RNA, a liposome-conjugated DNA, or the like, that are not episomal in nature, or it can be an organism which comprises one or more of the above polynucleotide constructs such as an agrobacterium or a bacterium.

[0067] The various components of an expression vector can vary widely, depending on the intended use of the vector and the host cell(s) in which the vector is intended to replicate or drive expression. Expression vector components suitable for the expression of genes and maintenance of vectors in *E. coli*, yeast, *Streptomyces*, and other commonly used cells are widely known and commercially available. For example, suitable promoters for inclusion in the expression vectors of the disclosure include those that function in eukaryotic or prokaryotic host microorganisms. Promoters can comprise regulatory sequences that allow for regulation of expression relative to the growth of the host microorganism or that cause the expression of a gene to be turned on or off in response to a chemical or physical stimulus. For *E. coli* and certain other bacterial host cells, promoters derived from genes for biosynthetic enzymes, antibiotic-resistance conferring enzymes, and phage proteins can be used and include, for example, the galactose, lactose (lac), maltose, tryptophan (trp), beta-lactamase (bla), bacteriophage lambda PL, and T5 promoters. In addition, synthetic promoters, such as the tac promoter (U.S. Pat. No. 4,551,433, which is incorporated herein by reference in its entirety), can also be used. For *E. coli* expression vectors, it is useful to include an *E. coli* origin of replication, such as from pUC, p1P, p1, and pBR.

[0068] Thus, recombinant expression vectors contain at least one expression system, which, in turn, is composed of at least a

portion of a gene coding sequences operably linked to a promoter and optionally termination sequences that operate to effect expression of the coding sequence in compatible host cells. The host cells are modified by transformation with the recombinant DNA expression vectors of the disclosure to contain the expression system sequences either as extrachromosomal elements or integrated into the chromosome.

[0069] In addition, and as mentioned above, homologs of enzymes useful for generating metabolites are encompassed by the microorganisms and methods provided herein. The term "homologs" used with respect to an original enzyme or gene of a first family or species refers to distinct enzymes or genes of a second family or species which are determined by functional, structural or genomic analyses to be an enzyme or gene of the second family or species which corresponds to the original enzyme or gene of the first family or species. Most often, homologs will have functional, structural or genomic similarities. Techniques are known by which homologs of an enzyme or gene can readily be cloned using genetic probes and PCR. Identity of cloned sequences as homolog can be confirmed using functional assays and/or by genomic mapping of the genes.

[0070] A protein has "homology" or is "homologous" to a second protein if the nucleic acid sequence that encodes the protein has a similar sequence to the nucleic acid sequence that encodes the second protein. Alternatively, a protein has homology to a second protein if the two proteins have "similar" amino acid sequences. (Thus, the term "homologous proteins" is defined to mean that the two proteins have similar amino acid sequences).

[0071] As used herein, two proteins (or a region of the proteins) are substantially homologous when the amino acid sequences have at least about 30%, 40%, 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity. To determine the percent identity of two amino acid sequences, or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in one or both of a first and a second amino acid or nucleic acid sequence for optimal alignment and non-homologous

sequences can be disregarded for comparison purposes). In one embodiment, the length of a reference sequence aligned for comparison purposes is at least 30%, typically at least 40%, more typically at least 50%, even more typically at least 60%, and even more typically at least 70%, 80%, 90%, 100% of the length of the reference sequence. The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position (as used herein amino acid or nucleic acid "identity" is equivalent to amino acid or nucleic acid "homology"). The percent identity between the two sequences is a function of the number of identical positions shared by the sequences, taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences.

[0072] When "homologous" is used in reference to proteins or peptides, it is recognized that residue positions that are not identical often differ by conservative amino acid substitutions. A "conservative amino acid substitution" is one in which an amino acid residue is substituted by another amino acid residue having a side chain (R group) with similar chemical properties (e.g., charge or hydrophobicity). In general, a conservative amino acid substitution will not substantially change the functional properties of a protein. In cases where two or more amino acid sequences differ from each other by conservative substitutions, the percent sequence identity or degree of homology may be adjusted upwards to correct for the conservative nature of the substitution. Means for making this adjustment are well known to those of skill in the art (see, e.g., Pearson et al., 1994, hereby incorporated herein by reference).

[0073] In some instances "isozymes" can be used that carry out the same functional conversion/reaction, but which are so dissimilar in structure that they are typically determined to not be "homologous".

[0074] A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue

having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). The following six groups each contain amino acids that are conservative substitutions for one another: 1) Serine (S), Threonine (T); 2) Aspartic Acid (D), Glutamic Acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Alanine (A), Valine (V), and 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W).

[0075] Sequence homology for polypeptides, which can also be referred to as percent sequence identity, is typically measured using sequence analysis software. See, e.g., the Sequence Analysis Software Package of the Genetics Computer Group (GCG), University of Wisconsin Biotechnology Center, 910 University Avenue, Madison, Wis. 53705. Protein analysis software matches similar sequences using measure of homology assigned to various substitutions, deletions and other modifications, including conservative amino acid substitutions. For instance, GCG contains programs such as "Gap" and "Bestfit" which can be used with default parameters to determine sequence homology or sequence identity between closely related polypeptides, such as homologous polypeptides from different species of organisms or between a wild type protein and a mutein thereof. See, e.g., GCG Version 6.1.

[0076] A typical algorithm used comparing a molecule sequence to a database containing a large number of sequences from different organisms is the computer program BLAST (Altschul, 1990; Gish, 1993; Madden, 1996; Altschul, 1997; Zhang, 1997), especially blastp or tblastn (Altschul, 1997). Typical parameters for BLASTp are: Expectation value: 10 (default); Filter: seg (default); Cost to open a gap: 11 (default); Cost to extend a gap: 1 (default); Max.

alignments: 100 (default); Word size: 11 (default); No. of descriptions: 100 (default); Penalty Matrix: BLOSUM62.

[0077] When searching a database containing sequences from a large number of different organisms, it is typical to compare amino acid sequences. Database searching using amino acid sequences can be measured by algorithms other than blastp known in the art. For instance, polypeptide sequences can be compared using FASTA, a program in GCG Version 6.1. FASTA provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences (Pearson, 1990, hereby incorporated herein by reference). For example, percent sequence identity between amino acid sequences can be determined using FASTA with its default parameters (a word size of 2 and the PAM250 scoring matrix), as provided in GCG Version 6.1, hereby incorporated herein by reference.

[0078] In certain embodiments, a metabolic pathway converts a carbon source to a desired intermediate or end product. For example, a carbon source can be converted to pyruvate, which can be metabolized to acetyl-CoA or to isobutanol. Suitable carbon sources can be sugars. For example, a carbon source can be a biomass derived sugar. A "biomass derived sugar" includes, but is not limited to, molecules such as glucose, sucrose, mannose, xylose, and arabinose. The term biomass derived sugar encompasses suitable carbon substrates of 1 to 7 carbons ordinarily used by microorganisms, such as 3-7 carbon sugars, including but not limited to glucose, lactose, sorbose, fructose, idose, galactose and mannose all in either D or L form, or a combination of 3-7 carbon sugars, such as glucose and fructose, and/or 6 carbon sugar acids including, but not limited to, 2-keto-L-gulonic acid, idonic acid (IA), gluconic acid (GA), 6-phosphogluconate, 2-keto-D-gluconic acid (2 KDG), 5-keto-D-gluconic acid, 2-ketogluconatephosphate, 2,5-diketo-L-gulonic acid, 2,3-L-diketogulonic acid, dehydroascorbic acid, erythorbic acid (EA) and D-mannonic acid.

[0079] Cellulosic and lignocellulosic feedstocks and wastes, such as agricultural residues, wood, forestry wastes, sludge from paper manufacture, and municipal and industrial solid wastes,

provide a potentially large renewable feedstock for the production of chemicals, plastics, fuels and feeds. Cellulosic and lignocellulosic feedstocks and wastes, composed of carbohydrate polymers comprising cellulose, hemicellulose, and lignin can be generally treated by a variety of chemical, mechanical and enzymatic means to release primarily hexose and pentose sugars. These sugars can then be "fed" into a pathway to produce pyruvate as further described herein.

[0080] The disclosure provides accession numbers for various genes, homologs and variants useful in the generation of recombinant microorganism described herein. It is to be understood that homologs and variants described herein are exemplary and non-limiting. Additional homologs, variants and sequences are available to those of skill in the art using various databases including, for example, the National Center for Biotechnology Information (NCBI) access to which is available on the World-Wide-Web.

[0081] Culture conditions suitable for the growth and maintenance of a recombinant microorganism provided herein are known in the art.

[0082] It is understood that a range of microorganisms can be engineered to express one or more enzymes of the disclosure. It is also understood that various microorganisms can act as "sources" for genetic material encoding target enzymes suitable for use in a recombinant microorganism provided herein.

[0083] The term "microorganism" includes prokaryotic and eukaryotic microbial species from the Domains Archaea, Bacteria and Eucarya, the latter including yeast and filamentous fungi, protozoa, algae, or higher Protista. The terms "microbial cells" and "microbes" are used interchangeably with the term microorganism.

[0084] The term "prokaryotes" is art recognized and refers to cells which contain no nucleus or other cell organelles. The prokaryotes are generally classified in one of two domains, the Bacteria and the Archaea. The definitive difference between organisms of the Archaea and Bacteria domains is based on

fundamental differences in the nucleotide base sequence in the 16S ribosomal RNA.

[0085] The term "Archaea" refers to a categorization of organisms of the division Mendosicutes, typically found in unusual environments and distinguished from the rest of the procaryotes by several criteria, including the number of ribosomal proteins and the lack of muramic acid in cell walls. On the basis of ssrRNA analysis, the Archaea consist of two phylogenetically-distinct groups: Crenarchaeota and Euryarchaeota. On the basis of their physiology, the Archaea can be organized into three types: methanogens (procaryotes that produce methane); extreme halophiles (procaryotes that live at very high concentrations of salt ([NaCl])); and extreme (hyper) thermophilus (procaryotes that live at very high temperatures). Besides the unifying archaeal features that distinguish them from Bacteria (*i.e.*, no murein in cell wall, ester-linked membrane lipids, *etc.*), these procaryotes exhibit unique structural or biochemical attributes which adapt them to their particular habitats. The Crenarchaeota consists mainly of hyperthermophilic sulfur-dependent procaryotes and the Euryarchaeota contains the methanogens and extreme halophiles.

[0086] "Bacteria", or "eubacteria", refers to a domain of procaryotic organisms. Bacteria include at least 11 distinct groups as follows: (1) Gram-positive (gram+) bacteria, of which there are two major subdivisions: (1) high G+C group (Actinomycetes, Mycobacteria, Micrococcus, others) (2) low G+C group (Bacillus, Clostridia, Lactobacillus, Staphylococci, Streptococci, Mycoplasmas); (2) Proteobacteria, *e.g.*, Purple photosynthetic +non-photosynthetic Gram-negative bacteria (includes most "common" Gram-negative bacteria); (3) Cyanobacteria, *e.g.*, oxygenic phototrophs; (4) Spirochetes and related species; (5) Planctomyces; (6) Bacteroides, Flavobacteria; (7) Chlamydia; (8) Green sulfur bacteria; (9) Green non-sulfur bacteria (also anaerobic phototrophs); (10) *Radioresistant micrococci* and relatives; and (11) Thermotoga and *Thermosipho thermophiles*.

[0087] "Gram-negative bacteria" include cocci, nonenteric rods, and enteric rods. The genera of Gram-negative bacteria include, for example, Neisseria, Spirillum, Pasteurella, Brucella, Yersinia,

Francisella, Haemophilus, Bordetella, Escherichia, Salmonella, Shigella, Klebsiella, Proteus, Vibrio, Pseudomonas, Bacteroides, Acetobacter, Aerobacter, Agrobacterium, Azotobacter, Spirilla, Serratia, Vibrio, Rhizobium, Chlamydia, Rickettsia, Treponema, and Fusobacterium.

[0088] "Gram positive bacteria" include cocci, nonsporulating rods, and sporulating rods. The genera of gram positive bacteria include, for example, Actinomyces, Bacillus, Clostridium, Corynebacterium, Erysipelothrix, Lactobacillus, Listeria, Mycobacterium, Myxococcus, Nocardia, Staphylococcus, Streptococcus, and Streptomyces.

[0089] The disclosure provides a molecular rheostat for controlling ATP levels in an *in vitro* or *in vivo* system that comprises the metabolite conversion of glyceraldehyde-3-phosphate to 3-phosphoglycerate. The molecular rheostat the expression or over expression of heterologous polynucleotide or over-expression of native polynucleotides, or an enzymatic *in vitro* system comprising (i) an enzyme that converts glyceraldehyde-3-phosphate (G3P) and NADP⁺ to 3-phosphoglycerate (3PG) and NADPH and (ii) an enzyme that converts glyceraldehyde-3-phosphate (G3P), NADP⁺ and free phosphate (Pi) to 1,3-bisphosphoglycerate (1,3BPG) and (iii) an enzyme that converts 1,3 bisphosphoglycerate (1,3BPG) and ADP to 3-phosphoglycerate and ATP. In one embodiment, the enzyme of (i) comprises a NADP-dependent glyceraldehyde-3-phosphate dehydrogenase (GapN). In a further embodiment, the GapN is obtained from *S. mutans*. In another embodiment, the enzyme of (ii) comprises a mutant glyceraldehyde-3-phosphate dehydrogenase (mGap) that comprises D34A/L35R/T36K mutations relative to wild-type (SEQ ID NO:6). In another embodiment, the enzyme of (iii) comprises enzyme commission number (EC number) EC 2.7.2.3. In a further embodiment, the enzyme is a phosphoglycerate kinase. In still another embodiment, the phosphoglycerate kinase is a Pgk from *G. stearothermophilus*. In another embodiment, the molecular rheostat comprise the enzymes of a NADP-dependent glyceraldehyde-3-phosphate dehydrogenase (GapN), a mutant glyceraldehyde-3-phosphate dehydrogenase that utilizes NADP⁺ and a phosphoglycerate kinase.

[0090] In another embodiment, the disclosure demonstrates the production of isobutanol using a molecular rheostat. The pathway comprises the expression or over expression of one or more heterologous polynucleotide or over-expression of one or more native polynucleotides, or an enzymatic *in vitro* system comprising (i) a polypeptide that catalyzes the production of glucose-6-phosphate (G6P) from glucose; (ii) a polypeptide that catalyzes the production of Fructose-6-phosphate (F6P) from glucose-6-phosphate (G6P); (iii) a polypeptide the catalyzes the conversion/phosphorylation of fructose-6-phosphate (F6P) to fructose-1,6-phosphate (iv) a polypeptide that converts fructose-1,6-phosphate to two glyceraldehyde-3-phosphates (G3P); (v) a molecular rheostat comprising (a) an enzyme that converts glyceraldehyde-3-phosphate (G3P) and NADP⁺ to 3-phosphoglycerate (3PG) and NADPH and (b) an enzyme that converts glyceraldehyde-3-phosphate (G3P), NADP⁺ and free phosphate (Pi) to 1,3-bisphosphoglycerate (1,3BPG) and (c) an enzyme that converts 1,3-bisphosphoglycerate (1,3BPG) and ADP to 3-phosphoglycerate (3PG) and ATP; (vi) a polypeptide that converts 3-phosphoglycerate (3PG) to 2-phosphoglycerate (2PG); (vii) a polypeptide that converts 2-phosphoglycerate (2PG) to phosphoenolpyruvate (PEP); (viii) a polypeptide that converts phosphoenolpyruvate (PEP) to pyruvate; (ix) a polypeptide that converts pyruvate to acetolactate; (x) a polypeptide that converts acetolactate and NADPH to 2,3 dihydroxy-3-methyl butanoate and NADP⁺; (xi) a polypeptide that converts 2,3 dihydroxy-3-methyl butanoate to 3-methyl-2-oxobutanoate; (xii) a polypeptide that converts 3-methyl-2-oxobutanoate to isobutanol and (xiii) a polypeptide that converts isobutanol to isobutanol.

[0091] It will be recognized by one of skill in the art that the various metabolites identified above can serve as substrate for other catabolic or anabolic pathways.

[0092] Accordingly, the disclosure provides systems and recombinant microorganisms that can produce acetyl-phosphate, pyruvate, glyceraldehyde-3-phosphate, acetyl-CoA and/or other metabolites derived therefrom wherein the system or microorganism comprises a molecular rheostat or a molecular rheostat and a purge valve. For example, the disclosure provides pathways that can

comprise a molecular rheostat and one or more enzyme selected from a glucokinase (Glk or variant of homolog thereof, including a polyphosphate-dependent glucokinase, pfkA), a phosphoketolase (e.g., Fpk, Xpk, or Fpk/Xpk or variant of homolog thereof), a transaldolase (e.g., Tal or variant thereof), a transketolase (e.g., Tkt or variant of homolog thereof), ribose-5-phosphate isomerase (e.g., Rpi or variant of homolog thereof), a ribulose-5-phosphate epimerase (e.g., Rpe or variant of homolog thereof), a triose phosphate isomerase (e.g., Tpi or variant of homolog thereof), a fructose 1,6 bisphosphate aldolase (e.g., Fba or variant of homolog thereof), a phosphoglucosomerase (e.g., Pgi or variant of homolog thereof), an enolase, a decarboxylase (e.g., KivD or homolog), an alcohol dehydrogenase (e.g., an NADPH dependent alcohol dehydrogenase such as YahK or homolog), a phosphoglucosomerase (e.g., Pgi or homolog), a fructose 1,6 bisphosphate isomerase (Fba or homolog thereof), a phosphoglycerate mutase (e.g., Pgi or homolog thereof), a pyruvate kinase (Pyk or homolog thereof), a ketol-acid reductoisomerase (IlvC or homolog thereof), a dihydroxy-acid dehydratase (e.g., IlvD or homolog thereof) and any combination thereof. **Table 1** provides a list of accession number and organism that can be used as source sources of the enzymes:

[0093] **Table 1:** Enzymes and Sources:

Enzyme	Name	Accession number	Source Organism
Sc Hk	Hexokinase	-	<i>S. Cerevisiae</i>
Gt PgiA	Phosphoglucosomerase	ABO68222	<i>G. thermodenitrificans</i> NG80-2
Gs PfkA	Phosphoglucokinase	KOR92562	<i>G. stearothermophilus</i> ATCC12980
Sa FBA	Fructose 1,6 biphosphate aldolase	BAR10119	<i>S. aureus subsp. Aureus</i>
Gs TPI	Triose Phosphate isomerase	KOR95273	<i>G. stearothermophilus</i> ATCC12980
Sm GapN	Non- phosphorylating Glyceraldehyde 3 phosphate dehydrogenase Phosphorylating	NP_J721104	<i>S. mutans</i>
Gs mGapDH	Glyceraldehyde-3- phosphate Dehydrogenase	WP_033015082	<i>G. stearothermophilus</i> ATCC12980
Gs PGK	Phosphoglycerate Kinase	WP_033015089	<i>G. stearothermophilus</i> ATCC12980
Gs PGM	Phosphoglycerate Mutase	KOR95274	<i>G. stearothermophilus</i> ATCC12980
Ec Enolase	Enolase	NP_417259	<i>E. coli K12 sp MG1655</i>
Ec PykF	Pyruvate Kinase	NP_416191	<i>E. coli K12 sp MG1655</i>
Bs Als5	Acetolactate Synthase	NP_391482	<i>B. Subtilis subtilis 168</i>
Ec IlvC	Keto-Acid Reductoisomerase	AKK14493	<i>E. coli K12 sp MG1655</i>
Re IlvD	Dihydroxy-Acid Dehydratase	Q0K4J3	<i>R. eutropha</i>
Uj KivD	Keto-Isovalerate Decarboxylase	CAG34226	<i>L. lactis subsp. Lactis</i>
Ec YahK	Alcohol Dehydrogenase	NC_000913.3	<i>E. coli K12</i>

[0094] The foregoing one or more enzymes can be used in combination with enzymes that catalyze the conversion of glyceraldehyde-3-phosphate to 3-phosphoglycerate with or without an intermediate step of conversion to 1,3-bisphosphoglycerate, wherein the intermediate step is regulated by the level of phosphate.

[0095] In addition, a microorganism may include a disruption, deletion or knockout of expression of an alcohol/acetoaldehyde dehydrogenase that preferentially uses acetyl-coA as a substrate

(e.g. *adhE* gene), as compared to a parental microorganism. In some embodiments, further knockouts may include knockouts in a lactate dehydrogenase (e.g., *ldh*) and *frdBC*. In other embodiments, knockouts or reductions in expression or activity of one or more of *gapA*, *eda*, *edd* and *mgsA* may be performed to remove other glycolysis pathways in the microorganism. Other enzymes that can be knocked out or expression reduced include Fbp, *glpX*, and homologs and variants thereof.

[0096] It will be recognized that subsystems or organism that have one or more (but not all) of the foregoing enzymes can be utilized and then combined with an organism or other subsystems comprising remaining enzymatic members of the pathway.

[0097] As previously noted, the target enzymes described throughout this disclosure generally produce metabolites. In addition, the target enzymes described throughout this disclosure are encoded by polynucleotides.

[0098] Accordingly, in one embodiment, a system or recombinant microorganism provided herein comprises a glucokinase (Glc, polyphosphate-dependent glucokinase or homolog or variant thereof). This expression may be combined with enzymes of the molecular rheostat and may further include additional downstream enzymes for the production of a desired metabolite. The Glc can be derived from *G. stearothermophilus*. In another embodiment, an engineered variant of Glc can be used so long as it has glucokinase activity and can convert glucose to glucose-6-phosphate. Such engineered variants can be obtained by site-directed mutagenesis, directed evolutions and the like. Thus included within the disclosure are polypeptides that are at least 85-99% identical to the sequence of Glc from *E. coli* and having glucokinase activity.

[0099] In another or further embodiment, a system or recombinant microorganism provided herein includes expression of a phosphofructokinase (Pfk, polyphosphate-dependent Pfk or homolog or variants thereof). This expression may be combined with other enzymes in the metabolic pathway for the production of acetyl-phosphate, acetyl-coA or other metabolites derived therefrom. The Pfk can be derived from *G. stearothermophilus*. In another embodiment, an engineered variant of Pfk can be used so long as it

has phosphoglucokinase and/or phosphofructokinase activity and can convert fructose-6 phosphate to fructose-1,6-phosphate. Such engineered variants can be obtained by site-directed mutagenesis, directed evolutions and the like. Thus included within the disclosure are polypeptides that are at least 85-99% identical to a sequence Pfk from *G. stearothermophilus* and having 6-phosphofructokinase activity (e.g., 85-100% identical to SEQ ID NO:1).

[00100] In another embodiment, a system or recombinant microorganism provided herein includes a triose phosphate isomerase. This enzyme may be combined with other enzymes in the metabolic pathway for the production of acetyl-phosphate, pyruvate, acetyl-CoA or other metabolites derived therefrom as described herein above and below. The enzyme produces a metabolite that includes glyceraldehyde-3-phosphate from fructose-1,6-phosphate. The triose phosphate isomerase can be encoded by a *Tpi* gene, polynucleotide or homolog thereof. The *Tpi* gene or polynucleotide can be derived from various microorganisms including *G. stearothermophilus* and *E. coli*.

[00101] In addition to the foregoing, the terms "triose phosphate isomerase" or "Tpi" refer to proteins that are capable of catalyzing the formation of glyceraldehyde-3-phosphate from fructose-1,6-phosphate, and which share at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence identity to SEQ ID NO:2, or at least about 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence similarity, as calculated by NCBI BLAST, using default parameters. Additional homologs include: *G. stearothermophilus* ATCC12980, KOR95273 (SEQ ID NO:2); *Rattus norvegicus* AAA42278.1; *Homo sapiens* AAH17917.1; *Bacillus subtilis* BEST7613 NP_391272.1; *Synechococcus elongatus* PCC 6301 YP_171000.1; and *Salmonella enterica subsp. enterica serovar Typhi str.* AG3 ZP_06540375.1. The sequences associated with the foregoing accession numbers are incorporated herein by reference.

[00102] In another embodiment, a system or recombinant microorganism provided herein includes a fructose 1,6 bisphosphate aldolase. This enzyme may be combined with the expression or over-

expression with other enzymes in the metabolic pathway for the production of acetyl-phosphate, acetyl-CoA or other metabolites derived therefrom as described herein above and below. The enzyme produces a metabolite that includes glyceraldehyde-3-phosphate from fructose 1,6-bisphosphate. The fructose 1,6 bisphosphate aldolase can be encoded by a *Fba* gene, polynucleotide or homolog thereof. The *Fba* gene or polynucleotide can be derived from various microorganisms including *S. aureus*.

[00103] In addition to the foregoing, the terms "fructose 1,6 bisphosphate aldolase" or "Fba" refer to proteins that are capable of catalyzing the formation of glyceraldehyde-3-phosphate from fructose 1,6-bisphosphate, and which share at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence identity to SEQ ID NO:3, or at least about 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence similarity, as calculated by NCBI BLAST, using default parameters. Additional homologs include: *S. aureus subsp. Aureus*, BAR10119 (SEQ ID NO:3); *Synechococcus elongatus* PCC 6301 YP_170823.1; *Vibrio nigrripulchritudo* ATCC 27043 ZP_08732298.1; *Methylobacterium album* BG8 ZP_09865128.1; *Pseudomonas fluorescens* Pf0-1 YP_350990.1; and *Methylobacterium nodulans* ORS 2060 YP_002502325.1. The sequences associated with the foregoing accession numbers are incorporated herein by reference.

[00104] In another embodiment, a system or recombinant microorganism provided herein includes a phosphoglucoisomerase. This enzyme may be combined with the expression or over-expression with other enzymes in the metabolic pathway for the production of acetyl-phosphate, acetyl-CoA or other metabolites derived therefrom as described herein above and below. The enzyme produces a metabolite that includes fructose-phosphate from glucose-6-phosphate. The phosphoglucokinase can be encoded by a *Pgi* gene, polynucleotide or homolog thereof. The *Pgi* gene or polynucleotide can be derived from various microorganisms including *G. thermodenitrificans*.

[00105] In addition to the foregoing, the terms "phosphoglucoisomerase" or "Pgi" refer to proteins that are capable of catalyzing the formation of fructose-6-phosphate from glucose-6-

phosphate, and which share at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence identity to SEQ ID NO:4, or at least about 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence similarity, as calculated by NCBI BLAST, using default parameters.

[00106] In another embodiment, a system or recombinant microorganism provided herein includes a non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase. This enzyme may be combined with the expression or over-expression with other enzymes in the metabolic pathway for the production of acetyl-phosphate, acetyl-CoA or other metabolites derived therefrom as described herein above and below. The enzyme produces a metabolite that includes 3-phosphoglycerate from glyceraldehyde-3-phosphate. The non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase can be encoded by a *GapN* gene, polynucleotide or homolog thereof. The *GapN* gene or polynucleotide can be derived from various microorganisms including *S. mutans*.

[00107] In addition to the foregoing, the terms "non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase " or "GapN" refer to proteins that are capable of catalyzing the formation of 3-phosphoglycerate from glyceraldehyde-3-phosphate, and which share at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence identity to SEQ ID NO:5, or at least about 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence similarity, as calculated by NCBI BLAST, using default parameters.

[00108] In another embodiment, a system or recombinant microorganism provided herein includes a mutant phosphorylating glyceraldehyde-3-phosphate dehydrogenase the preferentially used NADP⁺. This enzyme may be combined with the expression or over-expression with other enzymes in the metabolic pathway for the production of acetyl-phosphate, acetyl-CoA or other metabolites derived therefrom as described herein above and below. The enzyme produces a metabolite that includes 1,3-bisphosphoglycerate from glyceraldehyde-3-phosphate. The mutant phosphorylating glyceraldehyde-3-phosphate dehydrogenase can be encoded by mutated from a *GapDH* gene, polynucleotide or homolog thereof to include

mutations D34A/L35R/T36K. The *GapDH* gene or polynucleotide can be derived from various microorganisms including *G. stearothermophilus*.

[00109] In addition to the foregoing, the terms "mutant phosphorylating glyceraldehyde-3-phosphate dehydrogenase" or "mGap" refer to proteins that are capable of catalyzing the formation of 1,3-bisphosphoglycerate from glyceraldehyde-3-phosphate and NADP⁺ and free phosphate (Pi), and which share at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence identity to SEQ ID NO:6 and includes the mutations D34A/L35R/T36K, or at least about 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence similarity, as calculated by NCBI BLAST, using default parameters.

[00110] In another embodiment, a system or recombinant microorganism provided herein includes a phosphoglycerate kinase. This enzyme may be combined with the expression or over-expression with other enzymes in the metabolic pathway for the production of acetyl-phosphate, acetyl-CoA or other metabolites derived therefrom as described herein above and below. The enzyme produces a metabolite that includes 3-phosphoglycerate from 1,3-bisphosphoglycerate and ADP. The phosphoglycerate kinase can be encoded by a *Pgk* gene, polynucleotide or homolog thereof. The *Pgk* gene or polynucleotide can be derived from various microorganisms including *G. stearothermophilus*.

[00111] In addition to the foregoing, the terms "phosphoglycerate kinase" or "Pgk" refer to proteins that are capable of catalyzing the formation of 3-phosphoglycerate from 1,3-bisphosphoglycerate and ADP, and which share at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence identity to SEQ ID NO:7, or at least about 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence similarity, as calculated by NCBI BLAST, using default parameters.

[00112] In another embodiment, a system or recombinant microorganism provided herein includes a phosphoglycerate mutase. This enzyme may be combined with the expression or over-expression with other enzymes in the metabolic pathway for the production of

acetyl-phosphate, acetyl-CoA or other metabolites derived therefrom as described herein above and below. The enzyme produces a metabolite that includes 2-phosphoglycerate from 3-phosphoglycerate. The phosphoglycerate mutase can be encoded by a *Pgm* gene, polynucleotide or homolog thereof. The *Pgm* gene or polynucleotide can be derived from various microorganisms including *G. stearothermophilus*.

[00113] In addition to the foregoing, the terms "phosphoglycerate mutase" or "Pgm" refer to proteins that are capable of catalyzing the formation of 2-phosphoglycerate from 3-phosphoglycerate, and which share at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence identity to SEQ ID NO:8, or at least about 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence similarity, as calculated by NCBI BLAST, using default parameters.

[00114] In another embodiment, a system or recombinant microorganism provided herein includes an enolase. This enzyme may be combined with the expression or over-expression with other enzymes in the metabolic pathway for the production of acetyl-phosphate, acetyl-CoA or other metabolites derived therefrom as described herein above and below. The enzyme produces a metabolite that includes phosphoenolpyruvate from 2-phosphoglycerate. The enolase can be encoded by an *enolase* gene, polynucleotide or homolog thereof. The *enolase* gene or polynucleotide can be derived from various microorganisms including *E. coli*.

[00115] In addition to the foregoing, the terms "enolase" refer to proteins that are capable of catalyzing the formation of phosphoenolpyruvate from 2-phosphoglycerate, and which share at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence identity to SEQ ID NO:9, or at least about 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence similarity, as calculated by NCBI BLAST, using default parameters.

[00116] In another embodiment, a system or recombinant microorganism provided herein includes a pyruvate kinase. This enzyme may be combined with the expression or over-expression with other enzymes in the metabolic pathway for the production of

acetyl-phosphate, acetyl-CoA or other metabolites derived therefrom as described herein above and below. The enzyme produces a metabolite that includes pyruvate from phosphoenolpyruvate. The pyruvate kinase can be encoded by a *Pyk* gene, polynucleotide or homolog thereof. The *Pyk* gene or polynucleotide can be derived from various microorganisms including *E. coli*.

[00117] In addition to the foregoing, the terms "pyruvate kinase" or "Pyk" refer to proteins that are capable of catalyzing the formation of pyruvate from phosphoenolpyruvate, and which share at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence identity to SEQ ID NO:10, or at least about 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence similarity, as calculated by NCBI BLAST, using default parameters.

[00118] In another embodiment, a system or recombinant microorganism provided herein includes an acetolactate synthase. This enzyme may be combined with the expression or over-expression with other enzymes in the metabolic pathway for the production of acetyl-phosphate, acetyl-CoA or other metabolites derived therefrom as described herein above and below. The enzyme produces a metabolite that includes acetolactate from pyruvate. The acetolactate synthase can be encoded by a *AlsS* gene, polynucleotide or homolog thereof. The *AlsS* gene or polynucleotide can be derived from various microorganisms including *B. subtilis*. In one aspect, the acetohydroxy acid synthase may be encoded by a polynucleotide derived from the *ilvIH* operon, *ilvBN* operon, *ilvGM* in *E. coli*, or the *alsS* gene from *Bacillus subtilis*, or homologs thereof. The *ilvI* gene of the *ilvIH* operon encodes an acetohydroxyacid synthase large subunit polypeptide and the *ilvH* gene of the *ilvIH* operon encodes an acetohydroxyacid synthase small subunit polypeptide.

[00119] In addition to the foregoing, the terms "acetolactate synthase" or "AlsS" refer to proteins that are capable of catalyzing the formation of pyruvate from phosphoenolpyruvate, and which share at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence identity to SEQ ID NO:11, or at least about 50%, 60%, 70%, 80%, 90%, 95%,

96%, 97%, 98%, 99% or greater sequence similarity, as calculated by NCBI BLAST, using default parameters.

[00120] In another embodiment, a system or recombinant microorganism provided herein includes an acetohydroxy acid isomeroreductase. This enzyme may be combined with the expression or over-expression with other enzymes in the metabolic pathway for the production of acetyl-phosphate, acetyl-CoA or other metabolites derived therefrom as described herein above and below. The enzyme produces a metabolite that includes 2,3 dihydroxy-3-methyl butanoate from acetolactate. The acetohydroxy acid isomeroreductase can be encoded by a *IlvC* gene, polynucleotide or homolog thereof. The *IlvC* gene or polynucleotide can be derived from various microorganisms including *E. coli*. Acetohydroxy acid isomeroreductase is the second enzyme in parallel pathways for the biosynthesis of isoleucine and valine. *IlvC* encodes an acetohydroxy acid isomeroreductase in *E. coli*. Homologs and variants of *ilvC* are known and include, for example, acetohydroxyacid reductoisomerase (*Schizosaccharomyces pombe* 972h-) gi|162312317|ref|NP_001018845.2|(162312317); acetohydroxyacid reductoisomerase (*Schizosaccharomyces pombe*) gi|3116142|emb|CAA18891.1|(3116142); acetohydroxyacid reductoisomerase (*Saccharomyces cerevisiae* YJM789) gi|151940879|gb|EDN59261.1|(151940879); *Ilv5p*: acetohydroxyacid reductoisomerase (*Saccharomyces cerevisiae*) gi|609403|gb|AAB67753.1|(609403); *ACL198Wp* (*Ashbya gossypii* ATCC 10895) gi|45185490|ref|NP_983206.1|(45185490); *ACL198Wp* (*Ashbya gossypii* ATCC 10895) gi|44981208|gb|AAS51030.1|(44981208); acetohydroxy-acid isomeroreductase; *Ilv5x* (*Saccharomyces cerevisiae*) gi|957238|gb|AAB33579.1||bbm|369068|bbs|165406(957238); acetohydroxy-acid isomeroreductase; *Ilv5g* (*Saccharomyces cerevisiae*) gi|957236|gb|AAB33578.1||bbm|369064|bbs|165405(957236); and ketol-acid reductoisomerase (*Schizosaccharomyces pombe*) gi|2696654|dbj|BAA24000.1|(2696654), each sequence associated with the accession number is incorporated herein by reference.

[00121] In addition to the foregoing, the terms "acetohydroxy acid isomeroreductase" or "*IlvC*" refer to proteins that are capable of catalyzing the formation of pyruvate from phosphoenolpyruvate, and which share at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%,

75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence identity to SEQ ID NO:12, or at least about 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence similarity, as calculated by NCBI BLAST, using default parameters.

[00122] In another embodiment, a system or recombinant microorganism provided herein includes dihydroxy-acid dehydratase. This enzyme may be combined with the expression or over-expression with other enzymes in the metabolic pathway for the production of acetyl-phosphate, acetyl-CoA or other metabolites derived therefrom as described herein above and below. The enzyme produces a metabolite that includes 3-methyl-2-oxobutanoate from 2,3 dihydroxy-3-methyl butanoate. The dihydroxy-acid dehydratase can be encoded by a *IlvD* gene, polynucleotide or homolog thereof. The *IlvD* gene or polynucleotide can be derived from various microorganisms including *E. coli*. Dihydroxy-acid dehydratases catalyzes the fourth step in the biosynthesis of isoleucine and valine, the dehydration of 2,3-dihydroxy-isovaleric acid into alpha-ketoisovaleric acid. *IlvD* and *ilv3* encode a dihydroxy-acid dehydratase. Homologs and variants of dihydroxy-acid dehydratases are known and include, for example, *IlvD* (*Mycobacterium leprae*) gi|2104594|emb|CAB08798.1|(2104594); dihydroxy-acid dehydratase (*Tropheryma whipplei* TW08/27) gi|28410848|emb|CAD67234.1|(28410848); dihydroxy-acid dehydratase (*Mycobacterium leprae*) gi|13093837|emb|CAC32140.1|(13093837); dihydroxy-acid dehydratase (*Rhodopirellula baltica* SH 1) gi|32447871|emb|CAD77389.1|(32447871); and putative dihydroxy-acid dehydratase (*Staphylococcus aureus* subsp. aureus MRSA252) gi|49242408|emb|CAG41121.1|(49242408), each sequence associated with the accession numbers are incorporated herein by reference.

[00123] In addition to the foregoing, the terms " dihydroxy-acid dehydratase " or "*IlvD*" refer to proteins that are capable of catalyzing the formation of pyruvate from phosphoenolpyruvate, and which share at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence identity to SEQ ID NO:13, or at least about 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence similarity, as calculated by NCBI BLAST, using default parameters.

[00124] In another embodiment, a system or recombinant microorganism provided herein includes 2-ketoacid decarboxylase (also referred to as a keto-isovalerate decarboxylase). This enzyme may be combined with the expression or over-expression with other enzymes in the metabolic pathway for the production of acetyl-phosphate, acetyl-CoA or other metabolites derived therefrom as described herein above and below. The enzyme produces a metabolite that includes isobutanal from 3-methyl-2-oxobutanoate. The 2-ketoacid decarboxylase can be encoded by a *kivD* gene, polynucleotide or homolog thereof. The *kivD* gene or polynucleotide can be derived from various microorganisms including *L. lactis*. Dihydroxy-acid dehydratases catalyzes the fourth step in the biosynthesis of isoleucine and valine, the dehydration of 2,3-dihydroxy-isovaleric acid into alpha-ketoisovaleric acid. *IlvD* and *ilv3* encode a dihydroxy-acid dehydratase. 2-ketoacid decarboxylases catalyze the conversion of a 2-ketoacid to the respective aldehyde. For example, 2-ketoisovalerate decarboxylase catalyzes the conversion of 2-ketoisovalerate to isobutyraldehyde. A number of 2-ketoacid decarboxylases are known and are exemplified by the *pdC*, *pdC1*, *pdC5*, *pdC6*, *aro10*, *thI3*, *kdcA* and *kivD* genes. Exemplary homologs and variants useful for the conversion of a 2-ketoacid to the respective aldehyde comprise sequences designated by the following accession numbers and identified enzymatic activity:

gi|44921617|gb|AAS49166.1| branched-chain alpha-keto acid decarboxylase (*Lactococcus lactis*); gi|15004729|ref|NP_149189.1| Pyruvate decarboxylase (*Clostridium acetobutylicum* ATCC 824); gi|82749898|ref|YP_415639.1| probable pyruvate decarboxylase (*Staphylococcus aureus* RF122); gi|77961217|ref|ZP_00825060.1| COG3961: Pyruvate decarboxylase and related thiamine pyrophosphate-requiring enzymes (*Yersinia mollaretii* ATCC 43969); gi|71065418|ref|YP_264145.1| putative pyruvate decarboxylase (*Psychrobacter arcticus* 273-4); gi|16761331|ref|NP_456948.1| putative decarboxylase (*Salmonella enterica* subsp. *enterica* serovar Typhi str. CT18); gi|93005792|ref|YP_580229.1| Pyruvate decarboxylase (*Psychrobacter cryohalolentis* K5); gi|23129016|ref|ZP_00110850.1| COG3961: Pyruvate decarboxylase and related thiamine pyrophosphate-requiring enzymes (*Nostoc*

punctiforme PCC 73102); gi|16417060|gb|AAL18557.1|AF354297_1
 pyruvate decarboxylase (*Sarcina ventriculi*);
 gi|15607993|ref|NP_215368.1|PROBABLE PYRUVATE OR INDOLE-3-PYRUVATE
 DECARBOXYLASE PDC (*Mycobacterium tuberculosis* H37Rv);
 gi|41406881|ref|NP_959717.1| Pdc (*Mycobacterium avium* subsp.
 paratuberculosis K-10); gi|91779968|ref|YP_555176.1| putative
 pyruvate decarboxylase (*Burkholderia xenovorans* LB400);
 gi|15828161|ref|NP_302424.1| pyruvate (or indolepyruvate)
 decarboxylase (*Mycobacterium leprae* TN);
 gi|118616174|ref|YP_904506.1| pyruvate or indole-3-pyruvate
 decarboxylase Pdc (*Mycobacterium ulcerans* Agy99);
 gi|67989660|ref|NP_001018185.1| hypothetical protein SPAC3H8.01
 (*Schizosaccharomyces pombe* 972h-);
 gi|21666011|gb|AAM73540.1|AF282847_1 pyruvate decarboxylase PdcB
 (*Rhizopus oryzae*); gi|69291130|ref|ZP_00619161.1| Pyruvate
 decarboxylase:Pyruvate decarboxylase (*Kineococcus radiotolerans*
 SRS30216); gi|66363022|ref|XP_628477.1| pyruvate decarboxylase
 (*Cryptosporidium parvum* Iowa II); gi|70981398|ref|XP_731481.1|
 pyruvate decarboxylase (*Aspergillus fumigatus* Af293);
 gi|121704274|ref|XP_001270401.1| pyruvate decarboxylase, putative
 (*Aspergillus clavatus* NRRL 1); gi|119467089|ref|XP_001257351.1|
 pyruvate decarboxylase, putative (*Neosartorya fischeri* NRRL 181);
 gi|26554143|ref|NP_758077.1| pyruvate decarboxylase (*Mycoplasma*
penetrans HF-2); gi|21666009|gb|AAM73539.1|AF282846_1 pyruvate
 decarboxylase PdcA (*Rhizopus oryzae*) each sequence associated with
 the accession numbers are incorporated herein by reference.

[00125] The 2-keto acid decarboxylase activity can be provided
 by one of the following genes: *PDC6* from *Saccharomyces cerevisiae*,
kivd from *Lactococcus lactis*, and *THI3* *Saccharomyces cerevisiae* (α -
 ketoisocaproate decarboxylase) and *pdc* *Clostridium acetobutylicum*.
 The alcohol dehydrogenase (*Adh*) activity can be provided by *ADH2*
 from *Saccharomyces cerevisiae*.

[00126] In addition to the foregoing, the terms "2-ketoacid
 decarboxylase" or "kivD" refer to proteins that are capable of
 catalyzing the formation of pyruvate from phosphoenolpyruvate, and
 which share at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%,
 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence identity

to SEQ ID NO:14, or at least about 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence similarity, as calculated by NCBI BLAST, using default parameters.

[00127] In another embodiment, a system or recombinant microorganism provided herein includes an alcohol dehydrogenase. This enzyme may be combined with the expression or over-expression with other enzymes in the metabolic pathway for the production of acetyl-phosphate, acetyl-CoA or other metabolites derived therefrom as described herein above and below. The enzyme produces a metabolite that includes isobutanol from isobutanal. The alcohol dehydrogenase can be encoded by a *Yahk* gene, polynucleotide or homolog thereof. The *Yahk* gene or polynucleotide can be derived from various microorganisms including *E. coli*.

[00128] In addition to the foregoing, the terms "alcohol dehydrogenase" or "Yahk" refer to proteins that are capable of catalyzing the formation of pyruvate from phosphoenolpyruvate, and which share at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence identity to SEQ ID NO:15, or at least about 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or greater sequence similarity, as calculated by NCBI BLAST, using default parameters.

[00129] In all of the foregoing embodiments, a system or recombinant microorganism provided herein may include a purge valve. The purge valve includes an enzymatic reaction the vents/removes or otherwise eliminates over abundance of an excessive co-factor in order to maintain system function. For example, in one embodiment, the purge valve includes an NADH-oxidase (NoxE). The NADH oxidase can be encoded by a *NoxE* gene, polynucleotide or homolog thereof. The *NoxE* gene or polynucleotide can be derived from various microorganisms including *L. Lactis* (see, e.g., Accession number YP_007507681).

[00130] As previously discussed, general texts which describe molecular biological techniques useful herein, including the use of vectors, promoters and many other relevant topics, include Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods in Enzymology Volume 152, (Academic Press, Inc., San Diego, Calif.) ("Berger"); Sambrook et al., Molecular Cloning--A Laboratory

Manual, 2d ed., Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., 1989 ("Sambrook") and Current Protocols in Molecular Biology, F. M. Ausubel *et al.*, eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (supplemented through 1999) ("Ausubel"), each of which is incorporated herein by reference in its entirety.

[00131] Examples of protocols sufficient to direct persons of skill through *in vitro* amplification methods, including the polymerase chain reaction (PCR), the ligase chain reaction (LCR), Q β -replicase amplification and other RNA polymerase mediated techniques (e.g., NASBA), e.g., for the production of the homologous nucleic acids of the disclosure are found in Berger, Sambrook, and Ausubel, as well as in Mullis *et al.* (1987) U.S. Pat. No. 4,683,202; Innis *et al.*, eds. (1990) PCR Protocols: A Guide to Methods and Applications (Academic Press Inc. San Diego, Calif.) ("Innis"); Arnheim & Levinson (Oct. 1, 1990) C&EN 36-47; The Journal Of NIH Research (1991) 3: 81-94; Kwok *et al.* (1989) Proc. Natl. Acad. Sci. USA 86: 1173; Guatelli *et al.* (1990) Proc. Nat'l. Acad. Sci. USA 87: 1874; Lomell *et al.* (1989) J. Clin. Chem 35: 1826; Landegren *et al.* (1988) Science 241: 1077-1080; Van Brunt (1990) Biotechnology 8: 291-294; Wu and Wallace (1989) Gene 4:560; Barringer *et al.* (1990) Gene 89:117; and Sooknanan and Malek (1995) Biotechnology 13:563-564.

[00132] Improved methods for cloning *in vitro* amplified nucleic acids are described in Wallace *et al.*, U.S. Pat. No. 5,426,039.

[00133] Improved methods for amplifying large nucleic acids by PCR are summarized in Cheng *et al.* (1994) Nature 369: 684-685 and the references cited therein, in which PCR amplicons of up to 40 kb are generated. One of skill will appreciate that essentially any RNA can be converted into a double stranded DNA suitable for restriction digestion, PCR expansion and sequencing using reverse transcriptase and a polymerase. See, e.g., Ausubel, Sambrook and Berger, all *supra*.

[00134] The invention is illustrated in the following examples, which are provided by way of illustration and are not intended to be limiting.

EXAMPLES

[00135] Miller LB media or Miller LB-agar (BD Difco) was used for growth of bacterial strains in liquid or solid media. *E. coli* BL21Gold(DE3) [B, F⁻, *ompT*, *hsdS_B*, (*r_B*⁻, *m_B*⁻), *dcm*⁺, *Tet^r*, *galλ*, (DE3) *endA Hte*] (Agilent) was used as host for both cloning and expression of recombinant proteins using pET vectors. *E. coli* TOP10(DE3) [F⁻ *mcrA* Δ(*mrr*-*hsdRMS*-*mcrBC*) Ψ80*lacZ*Δ*M15* Δ*lacX74* *nupG* *recA1* *araD139* Δ(*ara-leu*)7697 *galE15* *galK16* *rpsL*(Str^R) *endA1* λ⁻] was used for expression of recombinant proteins from the pBAD/p15A vector. Plasmids pET28a(+) and pET22b(+) were purchased from Novagen. HotStart Taq Mastermix (Denville) was used for gene amplification from genomic or plasmid DNA. *Phusion* DNA polymerase (Finnzymes), Taq DNA ligase (MCLab), and T5 Exonuclease (Epicenter) were purchased separately and used to make the assembly master mix (AMM) used for cloning. ATP, pyruvate, and NAD(P)⁺ were from Sigma.

[00136] Plasmid Construction. The expression plasmids for the enzymes were constructed from the pET28a plasmid backbone using the *NdeI* and *SacI* cut sites to produce constructs with an N-terminal 6xHis tag for purification. *E. coli* BL21-Gold cells were used as the host strain for enzyme expression. All enzymes were expressed in Luria-Bertani (LB) media supplemented with 50 μg/mL kanamycin and were induced with 0.2 mM isopropyl-β-D-1-thiogalactopyranoside added to the culture at the end of log phase growth.

[00137] Enzyme purification. Cells from 0.5 L of culture were harvested by centrifugation and resuspended in 150mM Tris pH 7.5, 100 mM NaCl. The cells were lysed on ice with sonication and the cell debris was removed by 12,000 x g centrifugation at 4 °C. The supernatant was then mixed with 5 mL nickel-nitrilotriacetic acid (NTA) agarose and after 30 minutes, the agarose slurry was loaded onto a gravity column and washed with five column volumes of 100 mM Tris pH 7.5, 100 mM NaCl, 15 mM imidazole. The enzyme was then eluted with 250 mM imidazole, 100 mM Tris pH 7.5. The resulting enzyme was dialyzed into 50 mM Tris pH 7.5, 50 mM NaCl and stored at 4 °C.

[00138] Enzyme activity and optimization. All of the enzymes used in this work were assayed. The enzymes were assayed in 50 mM

tris buffer pH 7.5, 5 mM MgCl, and 5 mM KCl which mirrors the final reaction conditions. The activity of NAD(P)H producing or consuming reactions were monitored at 340nm. The activity of ATP consuming enzymes were monitored using a coupled assay with Zwf and NADP⁺ at 340nm.

[00139] ATPase assays of the enzymes were tested with 5mM PEP, 1mM ATP, 1ul PK/LDH, 0.25 mM NADH and 5 ul of the given enzyme. The ATPase activity was calculated by the decrease in NADH concentration at 340nm.

[00140] **Final isobutanol reaction conditions and analysis.** The optimized self-sustaining reaction for the biotransformation glucose to isobutanol composed of 50 mM Tris pH 7.5, 5 mM MgCl, 5 mM KCl, 2 mM NADP⁺, 4mM ATP, 1mM glutathione, 0.25mM TPP, 0.25mM MnCl, 4 mM Pi, 0.5mM 2,3 BPG, and 660 mM glucose in a final reaction volume of 200 μ L. The reactions were initiated with the addition of glucose, which was left out of the initial mixture. All reactions were performed at room temperature.

[00141] To assay for isobutanol, the reactions were incubated and extracted with 0.3 mL hexanes. 1ul of the hexane layer was applied to a 0.25 micron HP-Innowax column using a HP 5890 Series II gas chromatogram. The GC method used an injection temperature that was held at 50°C for 5 minutes before it was increased to 275°C over 35 minutes. The peak intensities were compared to an authentic standard to assess concentrations.

[00142] **A Stoichiometric Isobutanol Pathway.** A pathway was designed and implemented to make isobutanol with stoichiometric recycling of high energy cofactors. The 2-keto-acid isobutanol build phase employs 2 pyruvate and 2 NADPH, but no ATP, whereas the canonical glycolysis pathway produces 2 pyruvate, 2 NADH and 2 ATP. Thus to make the cofactor use stoichiometric the pathway needed (1) generate 2 NADPH rather than NADH and (2) eliminate net ATP production. With these constraints in mind, the 14 enzyme pathway shown in Figure 1 and 6 was developed in which glyceraldehyde phosphate dehydrogenase (GAPDH) and phosphoglycerate kinase (PGK) are replaced with a non-phosphorylating glyceraldehyde phosphate dehydrogenase (GAPN). The use of GAPN eliminates the production of 2 ATP and generates NADPH rather than NADH. The overall pathway

becomes stoichiometric with respect to the production and consumption of both ATP and NADPH and has an overall theoretical carbon yield of 41%.

[00143] The overall pathway shown in Figure 1 was first modeled using COPASI to identify likely key steps in the pathway. The model revealed that the relative activities of hexokinase and phosphofructokinase were useful for achieving flux through the system. The result makes sense because in glycolysis, hexokinase and phosphofructokinase compete with each other for any available ATP. Therefore, when the relative activity of hexokinase is too high, ATP can be rapidly exhausted in the production glucose-6-phosphate (G6P) leaving insufficient ATP for the phosphofructokinase reaction, ultimately stopping the carbon flux and killing the reaction. With this in mind, initial reactions were set up with hexokinase as the limiting enzyme. Once isobutanol production from glucose was detected, cofactor and enzyme concentrations were systematically optimized, resulting in the production time course seen in **Figure 2A**. The high initial productivity sharply decreased by 18 hours rising to a titer of 161 ± 3 mM isobutanol after 3 days (11.9 ± 0.2 g/L).

[00144] As the pathway is stoichiometrically balanced with respect to ATP production and consumption, it was speculated that the sharp decrease in reaction rate might be due to ATPase activity in the system. Accordingly, ATPase activity was measured in each of the individual enzymes in the pathway and found that the enolase and ilvC enzyme preparations possessed notably higher ATPase levels than the other enzymes in the system. Accordingly, enolase and ilvC were repurified, which reduced contaminating ATPase activity. The stoichiometric reaction was set up again with the repurified enzymes, leading to an improved titer of 192 ± 8 mM isobutanol over the course of three days (14.2 ± 0.6 g/L). Nevertheless, production still decreased after 18 hours.

[00145] Tests were performed to analyze if cofactor depletion remained a problem by initiating the reactions as usual and then adding another bolus of ATP or NADPH after 24 hours (**Figure 2B**). After 48 hours, the reaction supplemented with NADPH showed no change in isobutanol production, but the ATP supplemented reaction

increased isobutanol production by 41% over the control. These results suggest that ATP hydrolysis, whether by ATPase contamination or passive ATP hydrolysis, may be the limiting factor for isobutanol production in this stoichiometric pathway even after multiple attempts to purify away any ATPase contamination.

[00146] Design of an ATP Rheostat. The results so far suggest that ATP depletion is a major problem for the long term sustainability of the stoichiometric reaction system. One way to deal with this problem might be to scrupulously purify all enzymes to eliminate any ATPase activity. But it may never be possible to completely eliminate spontaneous hydrolysis or hydrolysis by imperfect kinase reactions. Moreover, requiring completely pristine enzyme preparations is impractical on a large scale. Thus, a method to restore ATP levels as an intrinsic feature of the system was developed. To this end, a molecular rheostat was used.

[00147] The molecular rheostat (**Figure 3A**) is made up two competing pathway branches that eventually transform glyceraldehyde-3 phosphate (G3P) into 3-phosphoglycerate (3PG). One branch generates ATP, while flow through the ATP generating branch is regulated by P_i levels. The first branch is made up of one enzyme, the non-phosphorylating GapN used in the stoichiometric pathway, which reduces $NADP^+$ to NADPH and converts G3P directly into 3PG without generating ATP. The second pathway is composed of two enzymes, an NADPH specific, phosphorylating glyceraldehyde-3-phosphate dehydrogenase (GapDH) and phosphoglycerate kinase (PGK), that also produces NADPH but first converts G3P into 1,3-bisphosphoglycerate (1,3BPG) followed by 3PG and ATP by the action of PGK. Therefore, the GapDH/PGK branch produces an additional ATP compared to the GapN only branch.

[00148] The relative flow through the ATP generating branch of the rheostat is controlled by free P_i , which acts as a proxy for the amount of ATP hydrolyzed to ADP and P_i . The function of the rheostat is easiest to see in the simplest case, where no exogenous P_i is added to the reaction (**Figure 3A**). In this case there is initially no free P_i and there can be no flux through the phosphorylating GAPDH. Thus, in the absence of P_i , all the flux passes through GapN branch. Only when ATP is hydrolyzed to ADP and

P_i, can the phosphorylating branch be utilized. Thus, the rheostat senses the depletion of ATP and acts to restore ATP by utilizing the phosphorylating GAPDH branch.

[00149] To explore the effectiveness of this design, a computer model of the overall pathway was made with and without the molecular rheostat system using COPASI (**Figure 4**). As expected, the stoichiometric pathway, relying on GapN only, gradually winds down when any amount of ATP hydrolysis is introduced, much like what was observed experimentally. When this pathway is augmented with GapDH and PGK to complete the molecular rheostat, the reaction reaches a steady state and proceeds to completion. In this model the molecular rheostat reaches a steady state any time the flux through GapDH and PGK is greater than the ATPase activity that is modeled. This autoregulatory function means that the node will operate at a wide range of ATPase activities and that there is no need to perfectly tune and match the system to the specific amount of ATP hydrolysis for the system to reach a steady state. This autoregulatory behavior for ATP production is a key feature for designing easy to use, self-sustaining *in vitro* enzymatic pathways. In addition, modeling this pathway computationally allowed quick tests of the rheostat concept under an array of conditions and determine that increasing P_i, ATP, and hexokinase should result in an increase in the overall reaction rate.

[00150] Engineering Gap M6. To implement the "molecular rheostat" module, GapDH enzyme was engineered that efficiently uses NADP⁺. Both the *E. coli* GapDH (*EcGap*) and *G. stearothermophilus* GapDH (*GsGap*) prefer NAD⁺ over NADP⁺ although the *GsGap* displays a higher basal activity with NADP⁺ than *EcGap* (which is absolutely specific for NAD⁺). Although the cofactor specificity of *GsGap* has adjusted before by sequence-based design, the mutant only slightly preferred NADP⁺ over NAD⁺. To more strongly flip the cofactor specificity of *GsGap* the crystal structure was examined and basic residues introduced into the loop region proximate to the 2'OH of NAD⁺ that may help stabilize binding of a 2' phosphate in NADP⁺. A series of mutations were made altering residues D34, L35, and T36 of SEQ ID NO:6. The kinetics and specificity of the best enzyme, a D34A/L35R/T36K triple mutant (herein referred to as mGap), were

obtained. The wild type GsGap enzyme has only modest activity with NADP⁺, but the triple mutant mGAP showed much improved activity with NADP⁺ at the expense of NAD⁺.

Enzyme	Cofactor	k _{cat} (μM/min/mg)	K _M (mM)	k _{cat} /K _M
gapDH WT	NAD ⁺	21.8 ± 2.6	1.5 ± 0.3	14.5
	NADP ⁺	1.2 ± 0.1	1.6 ± 0.5	2.1
mGapDH	NAD ⁺	0.2 ± 0.04	0.6 ± 0.4	0.4
	NADP ⁺	3.2 ± 0.1	0.3 ± 0.04	11.9

[00151] **Isobutanol production with molecular rheostat.** To implement the molecular rheostat for the production of isobutanol from glucose, the two enzymes mGap and PGK were added to the optimized stoichiometric reaction. To ensure sufficient ATP production through the molecular rheostat, the units of mGap and PGK activity in the reaction were an order of magnitude greater than the aggregate ATPase activity in the reaction. Reactions with and without the molecular rheostat were set up side-by-side over a 72 hour time course and were tested for Isobutanol production, residual glucose and ATP (**Figure 5A-B**). The reaction with the molecular rheostat produced 24.1 ± 1.8 g/L of isobutanol at 91.5% of the theoretical yield with a maximum productivity of 1.4 ± 0.3 g/L/h. This isobutanol production represents a 101.7% improvement over the stoichiometric *in vitro* reaction and is higher than any published *in vivo* isobutanol production without the aid of complex *in situ* isobutanol removal.

[00152] The enzymes and enzyme concentrations in the final preparation pathway (see, e.g., Figure 6A-B) are presented in the following table:

Enzyme	Stock concentration (mg/mL)	Enzyme Activity (uM/min/mg)	Units/mL added to reaction
Sc Hk	2.73	7.2 ± 0.1	0.025
Gt PgiA	5.7	19.2 ± 0.2	1.094
Gs PfkA	8.49	9.6 ± 0.2	3.260
Sa FBA	9.84	21.1 ± 0.3	8.305
Gs TPI	12.75	96.6 ± 5.4	12.317
Sm GapN	16.09	20.6 ± 2.7	9.944
Gs Gap M6	4.47	7.9 ± 0.4	0.177
Gs PGK	6.28	102.3 ± 2.9	3.212
Gs PGM	12.16	97.2 ± 13.0	17.729
Ec Enolase	26.09	82.5 ± 0.1	53.485
Ec PykF	16.39	365.3 ± 37.9	299.363
Bs AlsS	6.22	6.94 ± 1.22	1.727
Ec IlvC	21.43	0.88 ± 0.23	1.509
Re IlvD	11.58	3.4 ± 0.3 ¹	1.575
Ll KivD	6.27	13.39 ± 2.28	0.672
Ec YdhK	2.18	3.64 ± 0.37	0.635

[00153] The molecular rheostat performed as expected and maintain a higher ATP concentration relative to the stoichiometrically balanced reaction. The rheostat reaction held a steady state concentration of ATP of around 600 μ M over 48 hours before the reaction stopped and the ATP concentration dropped. In contrast, the ATP concentration in the stoichiometric reaction steadily dropped throughout the entire run. Over the first 48 hours of both reactions there is a good correlation between the concentration of ATP in the reaction and the isobutanol productivity. Additionally, each component of the rheostat system was tested by leaving them out of the reaction and measuring the isobutanol produced after 24 hours (**Figure 5C**). When either the GapN or mGap/PGK was left out, production of isobutanol was drastically reduced compared to the full molecular rheostat system.

[00154] Although the system containing the molecular rheostat produced a self-sustaining reaction and maintained a steady state of ATP for the first 48 hours, the reaction stopped at the 72 hour time point. In the reaction with the molecular rheostat, a precipitate was noticed that began to form after 24 hours which coincided with a decrease in isobutanol production. Upon

completion of the reaction the precipitate was collected by centrifugation and separated by SDS-PAGE to identify proteins in the precipitate. Hexokinase was identified as the major constituent of the precipitate followed by KivD, and mGap. These results suggested that some of the enzymes were denaturing over time, possibly due to increasing isobutanol concentrations.

[00155] To determine the stability of each system component to isobutanol, each enzyme and cofactor in the pathway was tested for stability in 0%, 4% and 8% (saturating) isobutanol. Hexokinase, GapN, mGap, and IlvC were most susceptible to isobutanol inactivation while most other enzymes and cofactors maintained significant activity at saturating levels of Isobutanol over 30 hours. These results rapidly identify a handful of priority enzymes that could be targeted for stability improvements to improve the overall sustainability of the system.

[00156] A number of embodiments of the invention have been described. Nevertheless, it will be understood that various modifications may be made without departing from the spirit and scope of the invention. Accordingly, other embodiments are within the scope of the following claims.

WHAT IS CLAIMED IS

1. A recombinant, artificial or engineered metabolic pathway comprising a plurality of enzymatic steps that converts a substrate to a product, wherein the pathway comprises a non-naturally occurring molecular rheostat system the alternates between or simultaneously uses a first cofactor pathway for the production of a metabolite and a second cofactor pathway for the production of the metabolite depending upon cofactor availability.
2. A recombinant, artificial or engineered metabolic pathway of claim 1, wherein the pathway comprises:
 - (a) a first enzymatic step that converts a first metabolite to a second metabolite using a first co-factor;
 - (b) a second enzymatic step that converts the first metabolite to the second metabolite using a first co-factor and second co-factor or second co-factor;wherein the first enzymatic step is active when the second co-factor level is low and wherein the second enzymatic step is active when the second co-factor level is high.
3. The recombinant, artificial or engineered pathway of claim 1 or 2, wherein the first cofactor is an oxidizing/reducing co-factors and the second cofactor is P_i .
4. The recombinant, artificial or engineered pathway of claim 3, wherein the oxidizing/reducing co-factors are $NAD^+/NADH$, $NADP^+/NADPH$ or $FAD^+/FADH$.
5. The recombinant, artificial or engineered pathway of any of claim 2-4, wherein the first cofactor comprises $NADP^+/NADPH$.
6. The recombinant, artificial or engineered metabolic pathway of claim 1, wherein the metabolic pathway comprises the conversion of glyceraldehyde-3-phosphate to 3-phosphoglycerate.
7. The recombinant, artificial or engineered metabolic pathway of claim 6, wherein the metabolic pathway produces a metabolite

selected from the group consisting of isobutanol, 3-methyl-1-butanol, leucine, and valine.

8. The recombinant, artificial or engineered metabolic pathway of claim 6, wherein the pathway comprises the conversion of glyceraldehyde-3-phosphate to 1,3-bisphosphoglycerate and 1,3-bisphosphoglycerate to 3-phosphoglycerate.

9. The recombinant artificial or engineered metabolic pathway of any one of claims 6, 7 or 8 comprising (i) an enzyme that converts glyceraldehyde-3-phosphate (G3P) and NADP⁺ to 3-phosphoglycerate (3PG) and NADPH; and (ii) an enzyme that converts glyceraldehyde-3-phosphate (G3P), NADP⁺ and free phosphate (Pi) to 1,3-bisphosphoglycerate (1,3BPG) and (iii) an enzyme that converts 1,3-bisphosphoglycerate (1,3BPG) and ADP to 3-phosphoglycerate and ATP.

10. The recombinant artificial or engineered metabolic pathway of claim 9, wherein the enzyme of (i) comprises a NADP-dependent glyceraldehyde-3-phosphate dehydrogenase (GapN).

11. The recombinant artificial or engineered metabolic pathway of claim 10, wherein the GapN is obtained from *S. mutans*.

12. The recombinant artificial or engineered metabolic pathway of claim 9, wherein the enzyme of (ii) comprises a mutant glyceraldehyde-3-phosphate dehydrogenase (mGap) that comprises D34A/L35R/T36K mutations relative to SEQ ID NO:6.

13. The recombinant artificial or engineered metabolic pathway of claim 9, wherein the enzyme of (ii) comprises a mutant glyceraldehyde-3-phosphate dehydrogenase (mGap) that has a sequence that is at least 95% identical to SEQ ID NO:6 and comprises D34A/L35R/T36K mutations.

14. The recombinant artificial or engineered metabolic pathway of claim 9, wherein the enzyme of (iii) comprises enzyme commission number (EC number) EC 2.7.2.3.

15. The recombinant artificial or engineered metabolic pathway of claim 9, wherein the enzyme of (iii) is a phosphoglycerate kinase.

16. The recombinant artificial or engineered metabolic pathway of claim 15, wherein the phosphoglycerate kinase is a Pgk from *G. stearothermophilus*.

17. The recombinant artificial or engineered metabolic pathway of claim 15, wherein the enzyme of (iii) has a sequence that is at least 95% identical to SEQ ID NO:7 and has phosphoglycerate kinase activity.

18. The recombinant artificial or engineered metabolic pathway of claim 9, wherein the molecular rheostat comprise the enzymes of (i) a NADP-dependent glyceraldehyde-3-phosphate dehydrogenase (GapN), (ii) a mutant glyceraldehyde-3-phosphate dehydrogenase that utilizes NADP⁺ and (iii) a phosphoglycerate kinase.

19. The recombinant artificial or engineered metabolic pathway of claim 1, wherein the pathway comprises:

(i) a polypeptide that catalyzes the production of glucose-6-phosphate (G6P) from glucose;

(ii) a polypeptide that catalyzes the production of Fructose-6-phosphate (F6P) from glucose-6-phosphate (G6P);

(iii) a polypeptide that catalyzes the conversion/phosphorylation of fructose-6-phosphate (F6P) to fructose-1,6-phosphate

(iv) a polypeptide that converts fructose-1,6-phosphate to two glyceraldehyde-3-phosphates (G3P);

(v) a molecular rheostat comprising

(a) an enzyme that converts glyceraldehyde-3-phosphate (G3P) and NADP⁺ to 3-phosphoglycerate (3PG) and NADPH and

(b) an enzyme that converts glyceraldehyde-3-phosphate (G3P), NADP⁺ and free phosphate (Pi) to 1,3-bisphosphoglycerate (1,3BPG) and

- (c) an enzyme that converts 1,3 bisphosphoglycerate (1,3BPG) and ADP to 3-phosphoglycerate (3pG) and ATP;
- (vi) a polypeptide that converts 3-phosphoglycerate (3PG) to 2-phosphoglycerate (2PG);
- (vii) a polypeptide that converts 2-phosphoglycerate (2PG) to phosphoenolpyruvate (PEP);
- (viii) a polypeptide that converts phosphoenolpyruvate (PEP) to pyruvate;
- (ix) a polypeptide that converts pyruvate to acetolactate;
- (x) a polypeptide that converts acetolactate and NADPH to 2,3 dihydroxy-3-methyl butanoate and NADP⁺;
- (xi) a polypeptide that converts 2,3 dihydroxy-3-methyl butanoate to 3-methyl-2-oxobutanoate;
- (xii) a polypeptide that converts 3-methyl-2-oxobutanoate to isobutanal and
- (xiii) a polypeptide that converts isobutanal and NADPH to isobutanol and NADP⁺.

20. The recombinant, artificial or engineered pathway of any one of claims 1, 2, 4, 6, 7, 8, 18 or 19, wherein the pathway is in a cell-free system.

21. A recombinant polypeptide comprising a sequence that is at least 95% identical to SEQ ID NO:6 and comprises D34A/L35R/T36K mutations and has glyceraldehyde-3-phosphate dehydrogenase activity.