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(54) Title: PRODUCTION OF BUTANOL FROM CARBON MONOXIDE BY A RECOMBINANT MICROORGANISM

(57) Abstract: The invention relates, inter alia, to novel genetically modified microorganisms capable of using CO to produce 1-butanol and/or a precursor thereof, novel methyltranferases and nucleic acids encoding same, methods for producing genetically modified microorganisms using said novel methyltransferases, and methods of producing 1-butanol and/or a precursor thereof by microbial fermentation.

Production Of Butanol From Carbon Monoxide By A Recombinant Microorganism

FIELD

The present invention relates to methods for the production of biofuels by microbial fermentation and genetically modified micro-organisms suitable for use in such methods.

BACKGROUND

Butanol is an important bulk chemical with a wide range of industrial uses that has worldwide production of 4.5-5.5 million tonnes per annum. It is used as a precursor for the production of acrylate and methacrylate esters (used in coatings, plastics, textiles, adhesives, etc), glycol ethers (coatings, electronics) and butyl acetate (paints, ink, coatings, synthetic fruit flavoring) as well as butylamines (production of pesticides and pharmaceuticals) and amine resins. It also has direct use as a solvent (in ink, dyes, etc), an extractant (for the production of drugs and natural substances such as alkaloids, antibiotics, hormones, and vitamins), and in deicing fluids, cosmetics and chromatography.

Butanol also has potential as a second generation biofuel, and in this context is referred to as Biobutanol (Köpke & Dürre, 2010). It has similar properties to gasoline and superior properties to ethanol. Specifically, it has increased mileage due to higher energy density, it can be mixed with gasoline in any concentration (while ethanol can only be blended up to 85%) and is not hygroscopic or corrosive.

Biofuels for transportation are attractive replacements for gasoline and are rapidly penetrating fuel markets as low concentration blends. Biofuels, derived from natural plant sources, are more environmentally sustainable than those derived from fossil resources (such as gasoline), their use allowing a reduction in the levels of so-called fossil carbon dioxide (CO_2) gas that is released into the atmosphere as a result of fuel combustion. In addition, biofuels can be produced locally in many geographies, and can act to reduce dependence on imported fossil energy resources.

The vast majority of biofuels are produced via traditional yeast-based fermentation processes that use crop derived carbohydrates as the main carbon source and are known as first generation biofuels. However, these crops are required for food and many crops also require high agricultural inputs in the form of fertilizers. These limitations mean that first generation biofuels are considered unsustainable and the greenhouse gas reductions that can be achieved are limited. The aim of second generation biofuels is the sustainable use of non-food parts of current crops or other industrial waste to reduce greenhouse gas emissions and reduce dependency on fossil fuels.

Recent 1-butanol production has been mainly by oxo synthesis (Weißermel & Arpe, 2003). Petrochemicals including crude oil are cracked to form propylene which is used during oxo synthesis. However the synthesis process requires use of non-renewable resources as well as suffering from being expensive and non-specific in the products formed.

Butanol can also be produced through biological production methods, the most common being the Acetone-Butanol-Ethanol (ABE) fermentation which has been used industrially since 1913 (Köpke & Dürre, 2010). This method has the unwanted by-product of acetone which is usually produced at about half the volume of butanol which therefore substantially reduces the yield. Additionally, this method of fermentation is limited by the toxicity of butanol to the micro-organism which results in growth being almost completely inhibited at such low butanol concentrations as 1.5% (Köpke and Dürre 2010). Furthermore ABE fermentation uses sugar from corn, starch, cassava and sugar cane as a feedstock. This results in the undesirable use of arable land to produce fuel rather than food. It can also exacerbate problems related to deforestation and desertification.

Only a few organisms are known to naturally produce butanol and none of these produce butanol at a high yield from abundant sources (such as carbon monoxide - CO). Two organisms known to naturally produce butanol from CO are *Butyribacterium methylotrophicum* (which synthesises only traces of butanol (Heiskanen et al, 2007)), and *Clostridium carboxidivorans* (which produces low yields of 1-butanol as a by-product to the main fermentation products ethanol and acetate (Liou et al, 2005)).

A number of organisms have been genetically modified to produce 1-butanol including *E. coli, Bacillus subtilis, Saccharomyces cerevisiae, Pseudomonas putida, or Lactobacillus brevis.* However all of these organisms still rely on sugar as feedstock (Köpke & Dürre, 2010). Despite over 250 Clostridium species being known, only a few are genetically accessible. There is no natural competence (uptake of extracellular DNA from the cell's environment) known in Clostridia and electrotransformation or conjugation are the only methods available for transformation. These issues present significant difficulties in effectively transforming Clostridia species. Most Clostridia have one or more restriction/methylation systems to protect against foreign and phage DNA which means that transformation is particularly difficult and unpredictable.

Bibliographic details of the publications referred to herein are collected at the end of the description.

It is an object of the invention to overcome one or more disadvantages of the prior art, or to at least provide the public with a useful alternative to known technologies.

SUMMARY OF INVENTION

In accordance with the invention, it has been discovered that a genetically modified microorganism is capable of using CO to produce 1-butanol or a precursor thereof as the main fermentation product.

In a first aspect, the invention provides a carboxydotrophic acetogenic recombinant microorganism which produces 1-butanol and/or a precursor thereof as the main fermentation product.

In a related aspect, the invention provides an acetogenic recombinant microorganism which is capable of producing 1-butanol and/or a precursor thereof by fermentation from a substrate comprising CO at a concentration of greater than approximately 1mM or 0.075g/l per litre of fermentation broth.

Preferably, the microorganism comprises exogenous nucleic acids adapted to express one or more enzymes in the butanol biosynthesis pathway.

In one embodiment, the one or more enzymes are chosen from the group consisting:

Thiolase
3-hydroxybutyryl-CoA dehydrogenase
Crotonase/crotonyl-CoA hydratase
Butyryl-CoA dehydrogenase
Electron Transfer Flavoprotein A
Electron Transfer Flavoprotein B

Preferably, the microorganism comprises one or more exogenous nucleic acids encoding one or more of the enzymes.

Preferably, the one or more nucleic acids encoding the one or more enzymes is chosen from the nucleic acids SEQ ID NO. 1 to SEQ ID NO. 6 or functionally equivalent variants thereof.

Preferably, the microorganism comprises one or more exogenous nucleic acids encoding each of Thiolase, 3-hydroxybutyryl-CoA dehydrogenase, Crotonase, Butyryl-CoA dehydrogenase, Electron Transfer Flavoprotein A and Electron Transfer Flavoprotein B.

Preferably, the microorganism comprises a plasmid encoding one or more of, or preferably each of, Thiolase, 3-hydroxybutyryl-CoA dehydrogenase, Crotonase, Butyryl-CoA dehydrogenase, Electron Transfer Flavoprotein A and Electron Transfer Flavoprotein B.

In one embodiment, the microorganism comprises one or more exogenous nucleic acids encoding each of the enzymes thiolase 3-hydroxybutyryl-CoA dehydrogenase, crotonase / crotonyl-CoA hydratase and butyryl-CoA dehydrogenase.

Preferably, the microorganism further comprises an exogenous phosphotransacetylase/acetate kinase promoter. Preferably, the promoter corresponds to SEQ_ID No. 7 or a functionally equivalent variant thereof.

Preferably, the promoter is contained on a construct encoding one or more of the enzymes referred to herein before.

In one embodiment, the microorganism comprises exogenous nucleic acids adapted to express one or more of the enzymes chosen from the group consisting of:
Phosphotransbutyrylase;
butyrate kinase;
ferredoxin dependent aldehyde oxidoreductase;
butyraldehyde dehydrogenase ;
butanol dehydrogenase;
a bifunctional butyraldehyde dehydrogenase and butanol dehydrogenase.

In one embodiment, the microorganism comprises exogenous nucleic acids adapted to express one or more of butyraldehyde dehydrogenase, butanol dehydrogenase and a bifunctional butyraldehyde dehydrogenase/butanol dehydrogenase. Preferably, the microorganism comprises one or more exogenous nucleic acids encoding one or more of butyraldehyde dehydrogenase, butanol dehydrogenase and a bifunctional butyraldehyde dehydrogenase/butanol dehydrogenase.

In one embodiment, the microorganism comprises exogenous nucleic acids adapted to express one or more of Phosphotransbutyrylase, butyrate kinase, ferredoxin dependent aldehyde oxidoreductase, and butanol dehydrogenase. Preferably, the microorganism comprises one or more exogenous nucleic acids encoding one or more of Phosphotransbutyrylase, butyrate kinase, ferredoxin dependent aldehyde oxidoreductase, and butanol dehydrogenase. In particular embodiments, the microorganism comprises exogenous nucleic acids adapted to express each of Phosphotransbutyrylase, butyrate kinase, ferredoxin dependent aldehyde oxidoreductase, and butanol dehydrogenase.

In one embodiment, the one or more nucleic acids encoding the one or more enzymes is chosen from the nucleic acids outlined in tables 7 to 10 herein after and functionally equivalent variants thereof.

In one embodiment, the microorganism comprises one or more nucleic acid adapted to express at least two of the enzymes in the butanol biosynthesis pathway, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, or at least 12 of the enzymes.

In one embodiment, the microorganism comprises one or more nucleic acid adapted to express Thiolase, 3-hydroxybutyryl-CoA dehydrogenase, Crotonase/crotonyl-CoA hydratase, Butyryl-CoA dehydrogenase, Electron Transfer Flavoprotein A, Electron Transfer Flavoprotein B, and one or both of butyraldehyde dehydrogenase and butanol dehydrogenase (or a bifunctional enzyme).

In one embodiment, the microorganism comprises one or more nucleic acid adapted to express Thiolase, 3-hydroxybutyryl-CoA dehydrogenase, Crotonase/crotonyl-CoA hydratase, Butyryl-CoA dehydrogenase, Electron Transfer Flavoprotein A, Electron Transfer Flavoprotein B, and at least one of phosphotransbutyrylase and butyrate kinase and ferredoxin dependent aldehyde oxidoreductase and butanol dehydrogenase.

Preferably, the microorganism is selected from the group of carboxydotrophic acetogenic bacteria. In certain embodiments the microorganism is selected from the group comprising *Clostridium autoethanogenum, Clostridium ljungdahlii, Clostridium ragsdalei, Clostridium carboxidivorans, Clostridium drakei, Clostridium scatologenes, Butyribacterium limosum, Butyribacterium methylotrophicum, Acetobacterium woodii, Alkalibaculum bacchii, Blautia producta, Eubacterium limosum, Moorella thermoacetica, Moorella thermautotrophica, Oxobacter pfennigii*, and *Thermoanaerobacter kiuvi.*

Preferably, the microorganism is *Clostridium autoethanogenum* DSM23693.

In one embodiment, the recombinant microorganism of the invention has the defining characteristics of the microorganism deposited at the DSMZ (Deutsche Sammlung für Mikroorganismen und Zellkulturen GmbH, Braunschweig, Germany) under the accession number DSM24138.

In a second aspect, the invention provides a recombinant methyltransferase gene according to nucleotide SEQ_ID NO 27 or a functionally equivalent variant thereof.

In a third aspect, the invention provides a methyltransferase according to SEQ_ID NO 28 or a functionally equivalent amino acid variant thereof.

In a related aspect the invention provides a recombinant microorganism comprising a methyltransferase gene according to the second aspect. The methyltransferase gene may be present on a nucleic acid construct or integrated into the genome of the microorganism.

In a fourth aspect, the invention provides a nucleic acid comprising SEQ_ID No 1 to 6, or functionally equivalent variants thereof, in any order.

Preferably, the nucleic acid comprises SEQ_ID No 1 to 6 in the order shown in figure 2.

Preferably, the nucleic acid further comprises a phosphotransacetylase/acetate kinase promoter. Preferably, the promoter corresponds to SEQ_ID No. 7 or a functionally equivalent variant thereof.

In a fifth aspect, the invention provides an expression construct comprising one or more nucleic acid sequences wherein the construct, when expressed in an acetogenic microorganism, results in 1-butanol and/or a precursor thereof being produced as the main fermentation product.

Preferably, the one or more nucleic acid sequences encode one or more enzymes that are part of the 1-butanol biosynthesis pathway.

Preferably, the nucleic acids are selected from nucleic acids encoding thiolase, 3-hydroxybutyryl-CoA dehydrogenase, crotonase, butyryl-CoA dehydrogenase, electron transfer flavoprotein A and/or electron transfer flavoprotein B.

Preferably, the one or more nucleic acid sequences are selected from SEQ_ID NO. 1 to SEQ_ID NO. 6 or functionally equivalent variants thereof.

In one embodiment, the nucleic acids are further selected from nucleic acids encoding Phosphotransbutyrylase, butyrate kinase, ferredoxin dependent aldehyde oxidoreductase, butyraldehyde dehydrogenase, butanol dehydrogenase, and a bifunctional butyraldehyde dehydrogenase/butanol dehydrogenase.

In one embodiment, the nucleic acids are selected from the group of nucleic acids outlined in tables 7 to 10 herein after and functionally equivalent variants thereof.

In one embodiment, the expression construct encodes at least 2 enzymes in the butanol biosynthesis pathway, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11 or at least 12 of the enzymes.

Preferably, the expression construct further comprises a phosphotransacetylase/acetate kinase operon promoter. In another embodiment, the expression construct comprises another highly active promoter such as the promoter of the pyruvate:ferredoxin oxidoreductase (SEQ_ID No. 48), the Wood-Ljungdahl gene cluster (SEQ_ID No 47), Rnf operon (SEQ_ID No 49) or the ATP synthase operon (SEQ_ID No 50). Preferably, the phosphotransacetylase/acetate kinase operon promoter corresponds to SEQ_ID No. 7 or a functionally equivalent variant thereof.

In a sixth aspect, the invention provides a methylation construct comprising a methyltransferase gene as described herein.

In a seventh aspect, the invention provides a composition comprising the expression construct of the fifth aspect and the methylation construct of the sixth aspect.

Preferably, the composition is able to produce a recombinant microorganism which produces 1-butanol and/or a precursor thereof as the main fermentation product.

In an eighth aspect, the invention provides a method of producing a recombinant microorganism comprising:

a. introduction into a shuttle microorganism of (i) an expression construct and (ii) a methylation construct according to the sixth aspect comprising a methyltransferase gene;
b. expression of the methyltransferase gene;
c. isolation of one or more constructs from the shuttle microorganism; and,
d. introduction of at least the expression construct into a destination microorganism;

wherein the expression construct comprises one or more genes encoding enzymes to be expressed in the destination microorganism.

In one embodiment, expression of the methyltransferase gene in step b. is constitutive. In another embodiment, expression of the methyltransferase gene in step b. is induced.

In one embodiment, both the methylation construct and the expression construct are isolated in step C. In another embodiment, the expression construct is isolated in step C.

In one embodiment, only the expression construct is introduced into the destination microorganism. In another embodiment, both the expression construct and the methylation construct are introduced into the destination microorganism.

Preferably, the expression construct is as defined in the fifth aspect.

Preferably, the recombinant microorganism produces 1-butanol and/or a precursor thereof as the main fermentation product.

In a related aspect, the invention provides a method of producing a recombinant microorganism comprising:

a. methylation of an expression construct *in vitro* by a methyltransferase according to SEQ_ID No 28 or a functionally equivalent variant thereof
b. introduction of an expression construct into a destination microorganism;

wherein the expression construct comprises one or more genes encoding enzymes to be expressed in the destination microorganism.

Preferably, the expression construct is as defined in the fifth aspect.

Preferably, the recombinant microorganism produces 1-butanol and/or a precursor thereof as the main fermentation product.

Preferably, the methyltransferase is produced by expressing a methyltransferase gene, preferably according to SEQ_ID No 27 or a functionally equivalent variant thereof, in a microorganism and isolating the methyltransferase enzyme.

In a further related aspect, the invention provides a method of producing a recombinant microorganism comprising:

a. introduction into the genome of a shuttle microorganism of a methyltransferase gene, preferably according to SEQ_ID No 27 or a functionally equivalent variant thereof
b. introduction of an expression construct into the shuttle microorganism
c. isolation of one or more constructs from the shuttle microorganism; and,
d. introduction of at least the expression construct into a destination microorganism;

wherein the expression construct comprises one or more genes encoding enzymes to be expressed in the destination microorganism.

Preferably, the expression construct is as defined in the fifth aspect.

Preferably, the recombinant microorganism produces 1-butanol and/or a precursor thereof as the main fermentation product.

In a further related aspect, the invention provides a method of producing a recombinant microorganism comprising:

a. methylation of an expression construct in accordance with the fifth aspect *in vitro* by a methyltransferase
b. introduction of the expression construct into a destination microorganism.

Preferably, the methyltransferase is encoded by a methyltransferase gene as defined in the second aspect or a methyltransferase as defined in the third aspect.

Preferably, the recombinant microorganism produces 1-butanol and/or a precursor thereof as the main fermentation product.

In a ninth aspect, the invention provides a method of producing a recombinant microorganism comprising:

a. introduction of (i) an expression construct according to the fifth aspect and (ii) a methylation construct comprising a methyltransferase gene into a shuttle microorganism;
b. expression of the methyltransferase gene;
c. isolation of one or more constructs from the shuttle microorganism; and
d. introduction of at least the expression construct into a destination microorganism;

wherein the expression construct comprises one or more genes encoding enzymes to be expressed in the destination microorganism.

In one embodiment, expression of the methyltransferase gene in step b. is constitutive. In another embodiment, expression of the methyltransferase gene in step b. is induced.

In one embodiment, both the methylation construct and the expression construct are isolated in step C. In another embodiment, the expression construct is isolated in step C.

In one embodiment, only the expression construct is introduced into the destination microorganism. In another embodiment, both the expression construct and the methylation construct are introduced into the destination microorganism.

Preferably, the recombinant microorganism produces 1-butanol and/or a precursor thereof as the main fermentation product.

In a tenth aspect, the invention provides a method of producing a recombinant microorganism that produces 1-butanol or a precursor thereof as the main fermentation product comprising:

a. Introduction of (i) an expression construct and (ii) a methylation construct comprising a methyltransferase gene into a shuttle microorganism;
b. expression of the methyltransferase gene;
c. isolation of one or more constructs from the shuttle microorganism; and,
d. introduction of at least the expression construct into a destination microorganism;

wherein the expression construct comprises one or more genes encoding enzymes to be expressed in the destination microorganism.

In one embodiment, expression of the methyltransferase gene in step b. is constitutive. In another embodiment, expression of the methyltransferase gene in step b. is induced.

In one embodiment, both the methylation construct and the expression construct are isolated in step C. In another embodiment, the expression construct is isolated in step C.

In one embodiment, only the expression construct is introduced into the destination microorganism. In another embodiment, both the expression construct and the methylation construct are introduced into the destination microorganism.

Preferably, the expression construct is as defined in the fifth aspect.

Preferably, the methylation construct is as defined in the sixth aspect.

In an eleventh aspect, the invention provides a method of production of 1-butanol and/or a precursor thereof by microbial fermentation comprising fermenting a substrate using a recombinant microorganism.

Preferably, 1-butanol and/or a precursor thereof is the main fermentation product.

Preferably, the recombinant microorganism is as described in any one of the eighth to the tenth aspects.

Preferably, 1-butanol and/or a precursor thereof is produced in a yield of from approximately 0.075 grams per litre of fermentation broth (g/l) to approximately 20g/l. In one embodiment, the yield is from approximately 0.15g/l to approximately 1.54g/l. In other embodiments, the yield is approximately 10g/l, approximately 5g/l, or approximately 2g/l. Preferably, the yield of 1-butanol is up to the limit at which butanol becomes toxic to the surrounding media.

Preferably, the substrate comprises CO. Preferably, the substrate is a gaeous substrate comprising CO. In one embodiment, the substrate comprises an industrial waste gas. In certain embodiments, the gas is steel mill waste gas or syngas.

In one embodiment, the substrate will typically contain a major proportion of CO, such as at least about 20% to about 100% CO by volume, from 20% to 70% CO by volume, from 30% to 60% CO by volume, and from 40% to 55% CO by volume. In particular embodiments, the substrate comprises about 25%, or about 30%, or about 35%, or about 40%, or about 45%, or about 50% CO, or about 55% CO, or about 60% CO by volume.

While it is not necessary for the substrate to contain any hydrogen, the presence of H_2 should not be detrimental to product formation in accordance with methods of the invention. In particular embodiments, the presence of hydrogen results in an improved overall efficiency of alcohol production. For example, in particular embodiments, the substrate may comprise an approx 2:1, or 1:1, or 1:2 ratio of H2:CO. In one embodiment the substrate comprises about 30% or less H_2 by volume, 20% or less H_2 by volume, about 15% or less H_2 by volume or about 10% or less H_2 by volume. In other embodiments, the substrate stream comprises low concentrations of H2, for example, less than 5%, or less than 4%, or less than 3%, or less than 2%, or less than 1%, or is substantially hydrogen free. The substrate may also contain some CO_2 for example, such as about 1% to about 80% CO_2 by volume, or 1% to about 30% CO_2 by volume.

Preferably, the precursor produced by the method of any of the preceding aspects is converted to 1-butanol in the presence of phosphotransbutyrylase, butyrate kinase, ferredoxin dependent aldehyde oxidoreductase, and butanol dehydrogenase.

Preferably, the microorganism produces phosphotransbutyrylase, butyrate kinase, ferredoxin dependent aldehyde oxidoreductase, and butanol dehydrogenase both before and after introduction of an exogenous nucleic acid.

Preferably, the precursor produced by the method of any of the preceding aspects is converted to 1-butanol in the presence of butyraldehyde dehydrogenase, butanol dehydrogenase and/or a bifunctional butyraldehyde dehydrogenase/butanol dehydrogenase.

Preferably, the microorganism produces butyraldehyde dehydrogenase, butanol dehydrogenase and/or a bifunctional butyraldehyde dehyrogenase/butanol deydrogenase before and after introduction of an exogenous nucleic acid.

In a twelfth aspect, the invention provides 1-butanol or a precursor thereof when produced by the method of the eleventh aspect.

In a thirteenth aspect, the invention provides a shuttle microorganism comprising a methylation construct as defined herein.

Preferably, the shuttle microorganism further comprises an expression construct as defined herein.

Preferably, the shuttle microorganism is *E.coli, Bacillus subtillis* or *Lactococcus lactis*.

Preferably, the methylation construct of any of the previous aspects comprises a *lac* promoter and the methyltransferase gene and is induced by Isopropyl-β-D-thio-galactoside (IPTG). Expression of the methyltransferase could also be controlled by other inducible promoter systems such as *ara*, *tet*, or T7.

In a fourteenth aspect, the invention provides a nucleic acid having a sequence chosen from the group consisting of SEQ_ID NOs 8 to 13.

In a fifteenth aspect, the invention provides a nucleic acid having a sequence chosen from the group consisting of SEQ_ID NOs 16 to 23.

In a sixteenth aspect, the invention provides a nucleic acid comprising at least the nucleic acid sequence of SEQ ID No. 7 or a functionally equivalent variant thereof, a nucleic acid construct or vector comprising same, and microorganisms comprising said nucleic acid or nucleic acid construct or vector.

In a seventeenth aspect, the invention provides a nucleic acid which encodes a methyltransferase according to SEQ_ID No 28.

In an eighteenth aspect, the invention provides a nucleic acid comprising a nucleic acid encoding a polypeptide having the amino acid sequence of a polypeptide chosen from the group listed in tables 7 to 10 herein after and functionally equivalent variants of any one or more thereof.

In a nineteenth aspect, the invention provides a nucleic acid comprising a nucleic acid chosen from the group listed in tables 7 to 10 herein after and functionally equivalent variants of any one or more thereof.

In a twentieth aspect, the invention provides constructs and microorganisms comprising a nucleic acid of the eighteenth or nineteenth aspects of the invention.

In a twenty first aspect, the invention provides a nucleic acid having a sequence chosen from the group consisting of SEQ_ID NOs 32 to 38 and 123 to 135.

In a twenty second aspect, the invention provides a polypeptide comprising the amino acid sequence of a polypeptide chosen from the group listed in tables 7 to 10 herein after and functionally equivalent variants of any one or more thereof.

In a further aspect, the invention provides an acetogenic recombinant microorganism which comprises at least one exogenous nucleic acid encoding (a) an electron transport flavoprotein and (b) at least one enzyme selected from the group consisting of Thiolase, 3-hydroxybutyryl-CoA dehydrogenase, Crotonase/crotonyl-CoA hydratase, Butyryl-CoA dehydrogenase, Phosphotransbutyrylase, butyrate kinase and ferredoxin dependent aldehyde oxidoreductase; and which does not include an exogenous nucleic acid encoding a bifunctional butyraldehyde/butanol dehydrogenase; and produces 1-butanol as the main fermentation product during fermentation of a gaseous substrate comprising carbon monoxide wherein the recombinant microorganism is selected from the group consisting of: *Clostridium autoethanogenum, Clostridium ljungdahlii,* *Clostridium ragsdalei, Clostridium carboxidivorans, Clostridium drakei, Clostridium scatalogenes, Clostridium aceticum, Clostridium formicoaceticum, Clostridium coskatii.*

In a further aspect, the invention provides a method for the production of 1-butanol by microbial fermentation of a gaseous substrate comprising CO using a recombinant microorganism of the first aspect.

The invention may also be said broadly to consist in the parts, elements and features referred to or indicated in the specification of the application, individually or collectively, in any or all combinations of two or more of said parts, elements or features, and where specific integers are mentioned herein which have known equivalents in the art to which the invention relates, such known equivalents are deemed to be incorporated herein as if individually set forth.

BRIEF DESCRIPTION OF THE FIGURES

These and other aspects of the present invention, which should be considered in all its novel aspects, will become apparent from the following description, which is given by way of example only, with reference to the accompanying figures, in which:

Figure 1 shows the butanol biosynthesis pathway from CO.

Figure 2 shows an exemplary expression plasmid encoding genes involved in 1-butanol biosynthesis.

Figure 3 shows sequencing results of pMTL85245-thlA-crt-hbd which demonstrate that the 1-butanol biosynthesis genes found on the expression plasmid were free of mutations.

Figure 4a, 4b and 4c show a nucleotide alignment of the *C. autoethanogenum* (CAU), *C. ljungdahlii* (CLJ), *C. ragsdalei* (CRA) and the designed methyltransferase (DMT) genes.

Figure 4d shows an amino acid alignment of the methyltransferases from *C. autoethanogenum* (CAU1+2), *C. ljungdahlii* (CLJ), *C. ragsdalei* (CRA1+2) and the designed methyltransferase (DMT).

Figure 5 shows an exemplary methylation plasmid of the invention

Figure 6 shows an agarose gel electrophoresis image of isolated plasmid DNA. Lane 1, 6, 11, 16, 21 and 26 show 100 bp Plus DNA Ladder. Lane 2-5 shows PCR with original methylated plasmid mix as template in the following order: *ermB, ColE1, thlA, crt.* Lane 7-10, 12-15, 17-20, 22-25 and 27-30 show PCR with isolated plasmids from 4 different clones as template, each in the following order *ermB, ColE1, thlA, crt.* Lane 32-35 shows plasmid prep from 4 different clones. Lane 36 shows plasmid prep from original *C. autoethanogenum* DSM23693.

Figure 7 shows HPLC results showing 1-butanol production with *C. autoethanogenum* harboring butanol plasmid pMTL85245-thlA-crt-hbd.

Figure 8 shows an analysis of expression of over 200 genes during a typical fermentation with *Clostridium autoethanogenum* at standard conditions using real-time PCR to identify appropriate promoter regions for the expression of heterologous genes.

Figure 9 shows the sequence for SEQ_ID No 1, 2 and 3.

Figure 10 shows the sequence for SEQ_ID No 4, 5 and 6.

Figure 11 shows the sequence for promoter regions encoded by SEQ_ID No 7, 47, 48, 49 and 50.

Figure 12 shows the sequence for SEQ_ID No 14

Figure 13 shows the sequence for SEQ_ID No 15

Figure 14 shows the sequence for SEQ_ID No 24 and 25

Figure 15 shows the sequence for SEQ_ID No 26

Figure 16 shows the sequence for SEQ_ID No 27

Figure 17 shows the sequence for SEQ_ID No 28

Figure 18 shows the sequence for SEQ_ID No 29

Figure 19 shows the 16s rRNA gene of *C. autoethanogenum* (Y18178, GI:7271109)

Figures 20 and 21 show the sequence for SEQ_ID No 31

Figure 22 shows Seq. ID 39: Nucleotide acid sequence of bifunctional butanol/ butyraldehyde dehydrogenase of *C. autoethanogenum*

Figure 23 shows Seq. ID 40: Nucleotide acid sequence of bifunctional butanol/ butyraldehyde dehydrogenase of *C. autoethanogenum*

Figure 24 shows Seq. ID 41: Nucleotide acid sequence of butyraldehyde dehydrogenase of *C. autoethanogenum*; and, Seq. ID 42: Amino acid sequence of butyraldehyde dehydrogenase of *C. autoethanogenum*

Figure 25 shows Seq. ID 43: Nucleotide acid sequence of butyraldehyde dehydrogenase of *C. autoethanogenum*; and, Seq. ID 44: Amino acid sequence of butyraldehyde dehydrogenase of *C. autoethanogenum*

Figure 26 shows Seq. ID 45: Nucleotide acid sequence of butyraldehyde dehydrogenase of *C. autoethanogenum*

Figure 27 shows Seq. ID 46: Amino acid sequence of butyraldehyde dehydrogenase of *C. autoethanogenum*; and, Seq. ID 119: Nucleotide acid sequence of butanol dehydrogenase of *C. autoethanogenum*

Figure 28 shows Seq. ID 120: Amino acid sequence of butanol dehydrogenase of *C. autoethanogenum*; and Seq. ID 121: Nucleotide acid sequence of butanol dehydrogenase of *C. autoethanogenum.*

Figure 29 shows Seq. ID 122: Amino acid sequence of butanol dehydrogenase of *C. autoethanogenum*; and, Seq. ID 51: Nucleotide acid sequence of butanol dehydrogenase of *C. autoethanogenum.*

Figure 30 shows Seq. ID 52: Amino acid sequence of butanol dehydrogenase of *C. autoethanogenum*; and, Seq. ID 53: Nucleotide acid sequence of butanol dehydrogenase of *C. autoethanogenum*

Figure 31 shows Seq. ID 54: Amino acid sequence of butanol dehydrogenase of *C. autoethanogenum*; and, Seq. ID 55: Nucleotide acid sequence of butanol dehydrogenase of *C. autoethanogenum*

Figure 32 shows Seq. ID 56: Amino acid sequence of butanol dehydrogenase of *C. autoethanogenum*; and, Seq. ID 57: Nucleotide acid sequence of butanol dehydrogenase of *C. autoethanogenum.*

Figure 33 shows Seq. ID 58: Amino acid sequence of butanol dehydrogenase of *C. autoethanogenum*; and Seq. ID 59: Nucleotide sequence of phosphate acetyl/butyryl transferase from *C. autoethanogenum*; and Seq. ID 60: Amino acid sequence of phosphate acetyl/butyryl transferase from *C. autoethanogenum.*

Figure 34 shows Seq. ID 61: Nucleotide sequence of acetate/butyrate kinase from *C. autoethanogenum*; and Seq. ID 62: Amino acid sequence of acetate/butyrate kinase from *C. autoethanogenum.*

Figure 35 shows Seq. ID 63: Nucleotide sequence of aldehyde:ferredoxin oxidoreductase from *C. autoethanogenum*; and Seq. ID 64: Amino acid sequence of aldehyde:ferredoxin oxidoreductase from *C. autoethanogenum*.

Figure 36 shows Seq. ID 65: Nucleotide sequence of aldehyde:ferredoxin oxidoreductase from *C. autoethanogenum*; and Seq. ID 66: Amino acid sequence of aldehyde:ferredoxin oxidoreductase from *C. autoethanogenum*.

Figure 37 shows Seq. ID 67: Nucleotide acid sequence of bifunctional butanol/ butyraldehyde dehydrogenase of *C. ljungdahlii*

Figure 38 shows Seq. ID 68: Amino acid sequence of bifunctional butanol/ butyraldehyde dehydrogenase of *C. ljungdahlii*

Figure 39 shows Seq. ID 69: Nucleotide acid sequence of bifunctional butanol/ butyraldehyde dehydrogenase of *C. ljungdahlii*

Figure 40 shows Seq. ID 70: Amino acid sequence of bifunctional butanol/ butyraldehyde dehydrogenase of *C. ljungdahlii*; and Seq. ID 71: Nucleotide acid sequence of butyraldehyde dehydrogenase of *C. ljungdahlii*.

Figure 41 shows Seq. ID 72: Amino acid sequence of butyraldehyde dehydrogenase of *C. ljungdahlii*; and Seq. ID 73: Nucleotide acid sequence of butyraldehyde dehydrogenase of *C. ljungdahlii*; and Seq. ID 74: Amino acid sequence of butyraldehyde dehydrogenase of *C. ljungdahlii*.

Figure 42 shows Seq. ID 75: Nucleotide acid sequence of butanol dehydrogenase of *C. ljungdahlii*; and Seq. ID 76: Amino acid sequence of butanol dehydrogenase of *C. ljungdahlii*; and Seq. ID 77: Nucleotide acid sequence of butanol dehydrogenase of *C. ljungdahlii*.

Figure 43 shows Seq. ID 78: Amino acid sequence of butanol dehydrogenase of *C. ljungdahlii*; and Seq. ID 79: Nucleotide acid sequence of butanol dehydrogenase of *C. ljungdahlii*; and Seq. ID 80: Amino acid sequence of butanol dehydrogenase of *C. ljungdahlii*.

Figure 44 shows Seq. ID 81: Nucleotide acid sequence of butanol dehydrogenase of *C. ljungdahlii*; and Seq. ID 82: Amino acid sequence of butanol dehydrogenase of *C. ljungdahlii*; and Seq. ID 83: Nucleotide acid sequence of butanol dehydrogenase of *C. ljungdahlii.*

Figure 45 shows Seq. ID 84: Amino acid sequence of butanol dehydrogenase of *C. ljungdahlii*; and Seq. ID 85: Nucleotide sequence of phosphate acetyl/butyryl transferase from *C. ljungdahlii*; and Seq. ID 86: Amino acid sequence of phosphate acetyl/butyryl transferase from *C. ljungdahlii*; and Seq. ID 87: Nucleotide sequence of acetate/butyrate kinase from *C. ljungdahlii*.

Figure 46 shows Seq. ID 88: Amino acid sequence of acetate/butyrate kinase from *C. ljungdahlii*; and Seq. ID 89: Nucleotide sequence of aldehyde:ferredoxin oxidoreductase from *C. ljungdahlii*; and Seq. ID 90: Amino acid sequence of aldehyde:ferredoxin oxidoreductase from *C. ljungdahlii*.

Figure 47 shows Seq. ID 91: Nucleotide sequence of aldehyde:ferredoxin oxidoreductase from *C. ljungdahlii*; and Seq. ID 92: Amino acid sequence of aldehyde:ferredoxin oxidoreductase from *C. ljungdahlii.*

Figure 48 shows Seq. ID 93: Nucleotide Acid sequence of bifunctional butanol/ butyraldehyde dehydrogenase from *C. ragsdalei*

Figure 49 shows Seq. ID 94: Amino Acid sequence of bifunctional butanol/ butyraldehyde dehydrogenase from *C. ragsdalei*

Figure 50 shows Seq. ID 95: Nucleotide Acid sequence of bifunctional butanol/ butyraldehyde dehydrogenase from *C. ragsdalei*.

Figure 51 shows Seq. ID 96: Amino Acid sequence of bifunctional butanol/ butyraldehyde dehydrogenase from *C. ragsdalei*; and Seq. ID 97: Nucleotide Acid sequence of butyraldehyde dehydrogenase from *C. ragsdalei*.

Figure 52 shows Seq. ID 98: Amino Acid sequence of butyraldehyde dehydrogenase from *C. ragsdalei*; Seq. ID 99: Nucleotide Acid sequence of butyraldehyde dehydrogenase from *C. ragsdalei*; and Seq. ID 100: Amino Acid sequence of butyraldehyde dehydrogenase from *C. ragsdalei*.

Figure 53 shows Seq. ID 101: Nucleotide Acid sequence of butanol dehydrogenase from *C. ragsdalei*; and Seq. ID 102: Amino Acid sequence of butanol dehydrogenase from *C. ragsdalei*; and Seq. ID 103: Nucleotide Acid sequence of butanol dehydrogenase from *C. ragsdalei.*

Figure 54 shows Seq. ID 104: Amino Acid sequence of butanol dehydrogenase from *C. ragsdalei*; and Seq. ID 105: Nucleotide Acid sequence of butanol dehydrogenase from *C. ragsdalei*; and Seq. ID 106: Amino Acid sequence of butanol dehydrogenase from *C. ragsdalei*:

Figure 55 shows Seq. ID 107: Nucleotide Acid sequence of butanol dehydrogenase from *C. ragsdalei*; and Seq. ID 108: Amino Acid sequence of butanol dehydrogenase from *C. ragsdalei*; and Seq. ID 109: Nucleotide Acid sequence of butanol dehydrogenase from *C. ragsdalei.*

Figure 56 shows Seq. ID 110: Amino Acid sequence of butanol dehydrogenase from *C. ragsdalei*; and Seq. ID 111: Nucleotide sequence of phosphate acetyl/butyryl transferase from *C. ragsdalei*; and Seq. ID 112: Amino acid sequence of phosphate acetyl/butyryl transferase from *C. ragsdalei*; and Seq. ID 113: Nucleotide sequence of acetate/butyrate kinase from *C. ragsdalei.*

Figure 57 shows Seq. ID 114: Amino acid sequence of acetate/butyrate kinase from *C. ragsdalei*; and Seq. ID 115: Nucleotide sequence of aldehyde:ferredoxin oxidoreductase from *C. ragsdalei*; and Seq. ID 116: Amino acid sequence of aldehyde:ferredoxin oxidoreductase from *C. ragsdalei.*

Figure 58 shows Seq. ID 117: Nucleotide sequence of aldehyde:ferredoxin oxidoreductase from *C. ragsdalei;* and Seq. ID 118: Amino acid sequence of aldehyde:ferredoxin oxidoreductase from *C. ragsdalei.*

Figure 59 shows SEQ ID 136: 16S rRNA gene of Clostridium ljungdahlii (CP001666.1, GI:300433347).

Figure 60 shows Gene expression pattern of (A) bifunctional butanol/butyraldehyde dehydrogenase (Seq ID 39); (B) butyraldehyde dehydrogenase (Seq. ID 41); (C) butyraldehyde dehydrogenase (Seq. ID 45); (D) butanol dehydrogenase (Seq. ID 53); (E) butanol dehydrogenase (Seq. ID 57); (F) phosphate acetyl/butyryl transferase (Seq. ID 57); (G) acetate/butyrate kinase

(Seq. ID 59); (H) aldehyde:ferredoxin oxidoreductase (Seq. ID 63); (OI) aldehyde:ferredoxin oxidoreductase (Seq. ID 65).

DETAILED DESCRIPTION OF THE INVENTION

The following is a description of the present invention, including preferred embodiments thereof, given in general terms. The invention is further elucidated from the disclosure given under the heading "Examples" herein below, which provides experimental data supporting the invention, specific examples of various aspects of the invention, and means of performing the invention.

Among others, the closely related microorganisms *C. autoethanogenum, C. ljungdahlii, and C. ragsdalei* are known to be useful for production of ethanol as biofuel from carbon monoxide. In order to produce 1-butanol as a biofuel from a gaseous substrate, a universal transformation system for these organisms has been developed and production of 1-butanol as the main fermentation product from CO has been demonstrated.

The inventors have found that when particular genes encoding proteins in the 1-butanol biosynthesis pathway (figure 1) were introduced into acetogenic microorganisms, such microorganisms were able to use a gaseous substrate to produce 1-butanol or a precursor thereof as the main fermentation product. Although some unmodified microorganisms are known to produce 1-butanol, the yield of 1-butanol from CO produced by such unmodified microorganisms is very low. As a result, their utility for production of biofuels from gaseous substrates is extremely limited due to their low efficiency and a subsequent lack of commercial viability. *Clostridium autoethanogenum* naturally produces ethanol, acetate, 2,3-butandiol and lactic acid but is not known to produce 1-butanol.

As shown in figure 1, the Wood-Ljungdahl pathway converts CO to acetyl-CoA. This compound may be further converted to 1-butanol in acetogenic microorganisms by the action of the enzymes thiolase, 3-hydroxybutyryl-CoA dehydrogenase, crotonase / crotonyl-CoA hydratase, butyryl-CoA dehydrogenase, butyraldehyde dehydrogenase and butanol dehydrogenase. In a particular embodiment of the invention, the microorganism expresses the first four enzymes which may be encoded by the nucleic acid SEQ_ID Nos 1 to 4 or functionally equivalent variants thereof. The present invention provides a microorganism that facilitates the conversion of acetyl-CoA to 1-butanol by the action of enzymes encoded by recombinant nucleic acids as well as naturally occurring enzymes. The invention also provides for the use of microorganisms expressing other recombinant nucleic acid sequences which encode enzymes at other stages in the Wood-Ljungdahl or butanol biosynthesis pathways. The inventors have also identified a number of novel enzymes and nucleic acids.

Since there is no natural competence (uptake of extracellular DNA from the cell's environment) known in Clostridia and electrotransformation or conjugation are the only methods available for transformation. These issues present significant difficulties in effectively transforming Clostridium species. Additionally, the restriction/methylation systems found in Clostridia protect against foreign and phage DNA and result in their genetic transformation being particularly troublesome. Transformation of several Clostridium strains (*C. acetobutylicum* ATCC824, *C. cellulolyticum* ATCC35319, *C. botulinum* ATCC25765, and *C. difficile* CD3 and CD6) was shown to be only possible if DNA is methylated *in vivo* in *E. coli* or methylated *in vitro* in a specific pattern prior to transformation (Mermelstein et al, 1993; Herbert et al, 2003; Jennert et al, 2000; Davis et al, 2000). However, the determination of the correct methylation pattern is often not possible due to unspecific exonucleases, etc. Additionally, many Clostridium species also possess restriction systems which digest DNA that is methylated at a specific ("wrong") position.

The abovementioned major hurdles have been overcome by the inventors in developing the recombinant microorganisms of the present invention. A novel methylation system comprising a novel methyltransferase gene was developed to circumvent the naturally occurring restriction barriers present in native acetogenic microorganisms. Accordingly, the methylation method and methyltransferase gene of the present invention may be applied to a number of compatible microorganisms that have restriction barriers preventing effective introduction and expression of desirable recombinant nucleic acids in microorganisms.

Definitions

As referred to herein, "precursors of 1-butanol" include butyryl CoA, butyryl-phosphate, butyrate, and butyraldehyde.

As referred to herein, a "fermentation broth" is a culture medium comprising at least a nutrient media and bacterial cells.

As referred to herein, a "shuttle microorganism" is a microorganism in which a methyltransferase enzyme is expressed and is distinct from the destination microorganism.

As referred to herein, a "destination microorganism" is a microorganism in which the genes included on the expression construct are expressed and is distinct from the shuttle microorganism.

As referred to herein, the term "main fermentation product" is intended to mean the one fermentation product which is produced in the highest concentration and/or yield.

The terms "increasing the efficiency", "increased efficiency" and the like, when used in relation to a fermentation process, include, but are not limited to, increasing one or more of the rate of growth of microorganisms catalysing the fermentation, the volume of desired product (such as alcohols) produced per volume of substrate (such as sugar) consumed, the rate of production or level of production of the desired product, and the relative proportion of the desired product produced compared with other by-products of the fermentation.

The phrase "substrate comprising carbon monoxide" and like terms should be understood to include any substrate in which carbon monoxide is available to one or more strains of bacteria for growth and/or fermentation, for example.

The phrase "gaseous substrate comprising carbon monoxide" and like phrases and terms includes any gas which contains a level of carbon monoxide. In certain embodiments the substrate contains at least about 20% to about 100% CO by volume, from 20% to 70% CO by volume, from 30% to 60% CO by volume, and from 40% to 55% CO by volume. In particular embodiments, the substrate comprises about 25%, or about 30%, or about 35%, or about 40%, or about 45%, or about 50% CO, or about 55% CO, or about 60% CO by volume.

While it is not necessary for the substrate to contain any hydrogen, the presence of H_2 should not be detrimental to product formation in accordance with methods of the invention. In particular embodiments, the presence of hydrogen results in an improved overall efficiency of alcohol production. For example, in particular embodiments, the substrate may comprise an approx 2:1, or 1:1, or 1:2 ratio of H2:CO. In one embodiment the substrate comprises about 30% or less H_2 by volume, 20% or less H_2 by volume, about 15% or less H_2 by volume or about 10% or less H_2 by volume. In other embodiments, the substrate stream comprises low concentrations of H2, for example, less than 5%, or less than 4%, or less than 3%, or less than 2%, or less than 1%, or is substantially hydrogen free. The substrate may also contain some CO_2 for example, such as about 1% to about 80% CO_2 by volume, or 1% to about 30% CO_2 by volume. In one embodiment the substrate comprises less than or equal to about 20% CO_2 by volume. In particular embodiments the substrate comprises less than or equal to about 15% CO_2 by volume, less than or equal to about 10% CO_2 by volume, less than or equal to about 5% CO_2 by volume or substantially no CO_2.

In the description which follows, embodiments of the invention are described in terms of delivering and fermenting a "gaseous substrate containing CO". However, it should be appreciated that the gaseous substrate may be provided in alternative forms. For example, the gaseous substrate containing CO may be provided dissolved in a liquid. Essentially, a liquid is saturated with a carbon monoxide containing gas and then that liquid is added to the bioreactor. This may be achieved using standard methodology. By way of example, a microbubble dispersion generator (Hensirisak et. al. Scale-up of microbubble dispersion generator for aerobic fermentation; Applied Biochemistry and Biotechnology Volume 101, Number 3 / October, 2002) could be used. By way of further example, the gaseous substrate containing CO may be adsorbed onto a solid support. Such alternative methods are encompassed by use of the term "substrate containing CO" and the like.

In particular embodiments of the invention, the CO-containing gaseous substrate is an industrial off or waste gas. "Industrial waste or off gases" should be taken broadly to include any gases comprising CO produced by an industrial process and include gases produced as a result of ferrous metal products manufacturing, non-ferrous products manufacturing, petroleum refining processes, gasification of coal, gasification of biomass, electric power production, carbon black production, and coke manufacturing. Further examples may be provided elsewhere herein.

Unless the context requires otherwise, the phrases "fermenting", "fermentation process" or "fermentation reaction" and the like, as used herein, are intended to encompass both the growth phase and product biosynthesis phase of the process. As will be described further herein, in some embodiments the bioreactor may comprise a first growth reactor and a second fermentation reactor. As such, the addition of metals or compositions to a fermentation reaction should be understood to include addition to either or both of these reactors.

The term "bioreactor" includes a fermentation device consisting of one or more vessels and/or towers or piping arrangement, which includes the Continuous Stirred Tank Reactor (CSTR), Immobilized Cell Reactor (ICR), Trickle Bed Reactor (TBR), Bubble Column, Gas Lift Fermenter, Static Mixer, or other vessel or other device suitable for gas-liquid contact. As is described herein after, in some embodiments the bioreactor may comprise a first growth reactor and a second fermentation reactor. As such, when referring to the addition of substrate to the bioreactor or fermentation reaction it should be understood to include addition to either or both of these reactors where appropriate.

"Exogenous nucleic acids" are nucleic acids which originate outside of the microorganism to which they are introduced. Exogenous nucleic acids may be derived from any appropriate source, including, but not limited to, the microorganism to which they are to be introduced, strains or species of microorganisms which differ from the organism to which they are to be introduced, or they may be artificially or recombinantly created. In one embodiment, the exogenous nucleic acids represent nucleic acid sequences naturally present within the microorganism to which they are to be introduced, and they are introduced to increase expression of or over-express a particular gene (for example, by increasing the copy number of the sequence (for example a gene)). In another embodiment, the exogenous nucleic acids represent nucleic acid sequences not naturally present within the microorganism to which they are to be introduced and allow for the expression of a product not naturally present within the microorganism or increased expression of a gene native to the microorganism (for example in the case of introduction of a regulatory element such as a promoter). The exogenous nucleic acid may be adapted to integrate into the genome of the microorganism to which it is to be introduced or to remain in an extra-chromosomal state.

It should be appreciated that the invention may be practised using nucleic acids whose sequence varies from the sequences specifically exemplified herein provided they perform substantially the same function. For nucleic acid sequences that encode a protein or peptide this means that the encoded protein or peptide has substantially the same function. For nucleic acid sequences that represent promoter sequences, the variant sequence will have the ability to promote expression of one or more genes. Such nucleic acids may be referred to herein as "functionally equivalent variants". By way of example, functionally equivalent variants of a nucleic acid include allelic variants, fragments of a gene, genes which include mutations (deletion, insertion, nucleotide substitutions and the like) and/or polymorphisms and the like. Homologous genes from other bacteria capable of butyric acid or butanol fermentation may also be considered as examples of functionally equivalent variants of the sequences specifically exemplified herein. These include homologous genes in species such as *Clostridium acetobutylicum, Clostridium beijerinckii, Clostridium tetani, Clostridium pasteurianum, Clostridium kluyveri, Clostridium cellulovorans, Clostridium perfringens, Clostridium botulinum, Clostridium butyricum* strain DSM10702, *Clostridium tyrobutyricum* strain ATCC 25755, *Anaerococcus prevotii* DSM 20548, *Thermoanaerobacter tengcongensis, Brachyspira pilosicoli, Bacillus megaterium, Streptococcus pyogenes* and *Clostridium saccharoperbutylacetonicum* details of which are publicly available on websites such as Genbank or NCBI. The phrase "functionally equivalent variants" should also be taken to include nucleic acids whose sequence varies as a result of codon optimisation for a particular organism. "Functionally equivalent variants" of a nucleic acid herein will preferably have at least approximately 70%, preferably approximately 80%, more preferably approximately 85%, preferably approximately 90%, preferably approximately 95% or greater nucleic acid sequence identity with the nucleic acid identified. In a particular embodiment, the functionally equivalent variant of the thiolase gene as defined herein may be the atoAB gene in *E. coli* (NC_000913.2; atoA = GeneID: 946719; atoB = GeneID: 946727). Functionally equivalent variants of the eftAB gene as defined herein may be found in Tsai and Saier (1995).

It should also be appreciated that the invention may be practised using polypeptides whose sequence varies from the amino acid sequences specifically exemplified herein. These variants may be referred to herein as "functionally equivalent variants". A functionally equivalent variant of a protein or a peptide includes those proteins or peptides that share at least 40%, preferably 50%, preferably 60%, preferably 70%, preferably 75%, preferably 80%, preferably 85%, preferably 90%, preferably 95% or greater amino acid identity with the protein or peptide identified and has substantially the same function as the peptide or protein of interest. Such variants include within their scope fragments of a protein or peptide wherein the fragment comprises a truncated form of the polypeptide wherein deletions may be from 1 to 5, to 10, to 15, to 20, to 25 amino acids, and may extend from residue 1 through 25 at either terminus of the polypeptide, and wherein deletions may be of any length within the region; or may be at an internal location. Functionally equivalent variants of the specific polypeptides herein should also be taken to include polypeptides expressed by homologous genes in other species of bacteria, for example as exemplified in the previous paragraph.

"Substantially the same function" as used herein is intended to mean that the nucleic acid or polypeptide is able to perform the function of the nucleic acid or polypeptide of which it is a variant. For example, a variant of an enzyme of the invention will be able to catalyse the same reaction as that enzyme. However, it should not be taken to mean that the variant has the same level of activity as the polypeptide or nucleic acid of which it is a variant.

One may assess whether a functionally equivalent variant has substantially the same function as the nucleic acid or polypeptide of which it is a variant using any number of known methods. However, by way of example, the methods outlined in Inui et al (2008) may be used to assess enzyme activity.

"Over-express", "over expression" and like terms and phrases when used in relation to the invention should be taken broadly to include any increase in expression of one or more protein as compared to the expression level of the protein of a parental microorganism under the same conditions. It should not be taken to mean that the protein is expressed at any particular level.

A "parental microorganism" is a microorganism used to generate a recombinant microorganism of the invention. The parental microorganism may be one that occurs in nature (ie a wild type microorganism) or one that has been previously modified but which does not express or over-express one or more of the enzymes the subject of the present invention. Accordingly, the recombinant microorganisms of the invention have been modified to express or over-express one or more enzymes that were not expressed or over-expressed in the parental microorganism.

The terms nucleic acid "constructs" or "vectors" and like terms should be taken broadly to include any nucleic acid (including DNA and RNA) suitable for use as a vehicle to transfer genetic material into a cell. The terms should be taken to include plasmids, viruses (including bacteriophage), cosmids and artificial chromosomes. Constructs or vectors may include one or more regulatory elements, an origin of replication, a multicloning site and/or a selectable marker, among other elements, sites and markers. In one particular embodiment, the constructs or vectors are adapted to allow expression of one or more genes encoded by the construct or vector. Nucleic acid constructs or vectors include naked nucleic acids as well as nucleic acids formulated with one or more agents to facilitate delivery to a cell (for example, liposome-conjugated nucleic acid, an organism in which the nucleic acid is contained).

It should be appreciated that nucleic acids of the invention may be in any appropriate form, including RNA, DNA, or cDNA, including double-stranded and single-stranded nucleic acids.

In one aspect the invention provides genetically modified microorganisms capable of using CO to produce 1-butanol and/or a precursor thereof as the main fermentation product. The microorganism is preferably an acetogenic recombinant microorganism which produces 1-butanol and/or a precursor thereof as the main fermentation product. In one particular embodiment, the acetogenic recombinant microorganism is capable of producing 1-butanol or a precursor thereof by fermentation from a substrate comprising CO at a concentration of greater than approximately 1mM or 0.075g/l of butanol per litre of fermentation broth.

In one particular embodiment, the microorganism comprises one or more exogenous nucleic acid adapted to express or over-express one or more enzymes in the butanol biosynthesis pathway. In one embodiment, the microorganism is adapted to express one or more enzyme in the butanol biosynthesis pathway which is not naturally present in the parental microorganism from which it is derived, or to over-express one or more enzyme in the butanol biosynthesis pathway which are naturally present in the parental microorganism.

The microorganism may be adapted to express or over-express the one or more enzymes by any number of recombinant methods including, for example, increasing expression of native genes within the microorganism (for example, by introducing a stronger or constitutive promoter to drive expression of a gene), increasing the copy number of a gene encoding a particular enzyme by introducing exogenous nucleic acids encoding and adapted to express the enzyme, introducing an exogenous nucleic acid encoding and adapted to express an enzyme not naturally present within the parental microorganism.

In certain embodiments, the parental microorganism may be transformed to provide a combination of increased or over-expression of one or more genes native to the parental microorganism and introduction of one or more genes not native to the parental microorganism.

Preferably, the microorganism comprises one or more exogenous nucleic acids encoding one or more of the enzymes chosen from the group consisting: Thiolase; 3-hydroxybutyryl-CoA dehydrogenase; Crotonase/crotonyl-CoA hydratase; Butyryl-CoA dehydrogenase; Electron Transfer Flavoprotein A; and, Electron Transfer Flavoprotein B. In one embodiment, the one or more nucleic acids encoding the one or more enzymes is chosen from the nucleic acids SEQ ID NO. 1 to SEQ ID NO. 6 or functionally equivalent variants thereof.

In one embodiment the recombinant microorganism is adapted to express one or more of the genes which encode the enzymes thiolase (IUBMB enzyme nomenclature EC:2.3.1.9) (*thlA*), 3-hydroxybutyryl-CoA dehydrogenase (EC:1.1.1.157) (*hbd*), crotonase / crotonyl-CoA hydratase (EC:1.1.1.157) (*crt* or *cch*) and/or butyryl-CoA dehydrogenase (EC4.2.1.55) (*bcd*). In one embodiment, the microorganism is adapted to express all of these enzymes. In a further embodiment, the genes correspond to one or more of the nucleic acid sequences selected from SEQ_ID Nos 1 to 4 or functionally equivalent variants thereof. The recombinant microorganism of the invention may also contain two electron transferring proteins. In one embodiment, the electron transferring proteins are electron transferring flavoproteins (EC1.3.99.2) (*etfAB*) encoded by SEQ_ID Nos 5 and 6, or functionally equivalent variants thereof. The use of these electron-transferring flavoproteins enhances the efficiency of the microorganism in producing 1-butanol. The flavoproteins provide a stable complex that is required for the activity of Bcd.

In one particular embodiment, the microorganism comprises one or more exogenous nucleic acids encoding each of Thiolase, 3-hydroxybutyryl-CoA dehydrogenase, Crotonase, Butyryl-CoA dehydrogenase, Electron Transfer Flavoprotein A and Electron Transfer Flavoprotein B.

In one embodiment, the microorganism comprises a plasmid encoding one or more of, or preferably each of, Thiolase, 3-hydroxybutyryl-CoA dehydrogenase, Crotonase, Butyryl-CoA dehydrogenase, Electron Transfer Flavoprotein A and Electron Transfer Flavoprotein B.

In one embodiment, the microorganism alternatively or further comprises exogenous nucleic acids adapted to express one or more of the enzymes chosen from the group consisting of: Phosphotransbutyrylase; butyrate kinase; ferredoxin dependent aldehyde oxidoreductase (or in other words aledhyde:ferredoxin oxidoreductase); butyraldehyde dehydrogenase ; butanol dehydrogenase; a bifunctional butyraldehyde dehydrogenase/butanol dehydrogenase.

In one embodiment, the microorganism comprises exogenous nucleic acids adapted to express one or more of butyraldehyde dehydrogenase, butanol dehydrogenase and a bifunctional butyraldehyde dehydrogenase/butanol dehydrogenase. Preferably, the microorganism comprises one or more exogenous nucleic acids encoding one or more of butyraldehyde dehydrogenase, butanol dehydrogenase and a bifunctional butyraldehyde dehydrogenase/butanol dehydrogenase.

In one embodiment, the microorganism comprises exogenous nucleic acids adapted to express one or more of Phosphotransbutyrylase, butyrate kinase, ferredoxin dependent aldehyde oxidoreductase, and butanol dehydrogenase. Preferably, the microorganism comprises one or more exogenous nucleic acids encoding one or more of Phosphotransbutyrylase, butyrate kinase, ferredoxin dependent aldehyde oxidoreductase, and butanol dehydrogenase. In particular embodiments, the microorganism comprises exogenous nucleic acids adapted to express each of Phosphotransbutyrylase, butyrate kinase, ferredoxin dependent aldehyde oxidoreductase, and butanol dehydrogenase.

In one embodiment, the microorganism comprises one or more nucleic acid adapted to express at least two of the enzymes in the 1-butanol biosynthesis pathway, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, or at least 12 of the enzymes.

In one embodiment, the microorganism further comprises an exogenous phosphotransacetylase/acetate kinase promoter, although other promoters may be used. Preferably, the promoter corresponds to SEQ_ID No. 7 or a functionally equivalent variant thereof. Preferably, the promoter is contained on a construct encoding one or more of the enzymes referred to herein before.

Preferably, the parental microorganism is selected from the group of carboxydotrophic acetogenic bacteria. In certain embodiments the microorganism is selected from the group comprising *Clostridium autoethanogenum, Clostridium ljungdahlii, Clostridium ragsdalei, Clostridium carboxidivorans, Clostridium drakei, Clostridium scatologenes, Butyribacterium limosum, Butyribacterium methylotrophicum, Acetobacterium woodii, Alkalibaculum bacchii, Blautia producta, Eubacterium limosum, Moorella thermoacetica, Moorella thermautotrophica, Oxobacter pfennigii*, and *Thermoanaerobacter kiuvi.*

In one particular embodiment, the parental microorganism is selected from the cluster of ethanologenic, acetogenic Clostridia comprising the species *C. autoethanogenum*, *C. ljungdahlii*, and *C. ragsdalei* and related isolates. These include but are not limited to strains *C. autoethanogenum* JAI-1^T (DSM10061) [Abrini J, Naveau H, Nyns E-J: *Clostridium autoethanogenum*, sp. nov., an anaerobic bacterium that produces ethanol from carbon monoxide. Arch Microbiol 1994, 4: 345-351], *C. autoethanogenum* LBS1560 (DSM19630) [Simpson SD, Forster RL, Tran PT, Rowe MJ, Warner IL: Novel bacteria and methods thereof.

International patent 2009, WO/2009/064200], *C. autoethanogenum* LBS1561 (DSM23693), *C. ljungdahlii* PETC^T (DSM13528 = ATCC 55383) [Tanner RS, Miller LM, Yang D: *Clostridium ljungdahlii* sp. nov., an Acetogenic Species in Clostridial rRNA Homology Group I. Int J Syst Bacteriol 1993, 43: 232-236], *C. ljungdahlii* ERI-2 (ATCC 55380) [Gaddy JL: Clostridium stain which produces acetic acid from waste gases. US patent 1997, 5,593,886], *C. ljungdahlii* C-01 (ATCC 55988) [Gaddy JL, Clausen EC, Ko C-W: Microbial process for the preparation of acetic acid as well as solvent for its extraction from the fermentation broth. US patent, 2002, 6,368,819], *C. ljungdahlii* O-52 (ATCC 55989) [Gaddy JL, Clausen EC, Ko C-W: Microbial process for the preparation of acetic acid as well as solvent for its extraction from the fermentation broth. US patent, 2002, 6,368,819], *C. ragsdalei* P11^T (ATCC BAA-622) [Huhnke RL, Lewis RS, Tanner RS: Isolation and Characterization of novel Clostridial Species. International patent 2008, WO 2008/028055], related isolates such as *"C. coskatii"* [Zahn JA, Saxena J, Do Y, Patel M, Fishein S, Datta R, Tobey R: *Clostridium coskatii*, sp. nov., an Anaerobic Bacterium that Produces Ethanol from Synthesis Gas. Poster SIM Annual Meeting and Exhibition, San Francisco, 2010], or mutated strains such as *C. ljungdahlii* OTA-1 (Tirado-Acevedo O. Production of Bioethanol from Synthesis Gas Using *Clostridium ljungdahlii*. PhD thesis, North Carolina State University, 2010). These strains form a subcluster within the Clostridial rRNA cluster I , and their 16S rRNA gene is more than 99% identical with a similar low GC content of around 30%. However, DNA-DNA reassociation and DNA fingerprinting experiments showed that these strains belong to distinct species [Huhnke RL, Lewis RS, Tanner RS: Isolation and Characterization of novel Clostridial Species. International patent 2008, WO 2008/028055].

All species of this cluster have a similar morphology and size (logarithmic growing cells are between 0.5-0.7 x 3-5 µm), are mesophilic (optimal growth temperature between 30-37 °C) and strictly anaerobe [Tanner RS, Miller LM, Yang D: *Clostridium ljungdahlii* sp. nov., an Acetogenic Species in Clostridial rRNA Homology Group I. Int J Syst Bacteriol 1993, 43: 232-236; Abrini J, Naveau H, Nyns E-J: *Clostridium autoethanogenum*, sp. nov., an anaerobic bacterium that produces ethanol from carbon monoxide. Arch Microbiol 1994, 4: 345-351; Huhnke RL, Lewis RS, Tanner RS: Isolation and Characterization of novel Clostridial Species. International patent 2008, WO 2008/028055]. Moreover, they all share the same major phylogenetic traits, such as same pH range (pH 4-7.5, with an optimal initial pH of 5.5-6), strong autotrophic growth on CO containing gases with similar growth rates, and a similar metabolic profile with ethanol and acetic acid as main fermentation end product, and small amounts of 2,3-butanediol and lactic acid formed under certain conditions. [Tanner RS, Miller LM, Yang D: *Clostridium ljungdahlii* sp. nov., an

Acetogenic Species in Clostridial rRNA Homology Group I. Int J Syst Bacteriol 1993, 43: 232-236; Abrini J, Naveau H, Nyns E-J: *Clostridium autoethanogenum*, sp. nov., an anaerobic bacterium that produces ethanol from carbon monoxide. Arch Microbiol 1994, 4: 345-351; Huhnke RL, Lewis RS, Tanner RS: Isolation and Characterization of novel Clostridial Species. International patent 2008, WO 2008/028055]. Indole production was observed with all three species as well. However, the species differentiate in substrate utilization of various sugars (e.g. rhamnose, arabinose), acids (e.g. gluconate, citrate), amino acids (e.g. arginine, histidine), or other substrates (e.g. betaine, butanol). Moreover some of the species were found to be auxotroph to certain vitamins (e.g. thiamine, biotin) while others were not.

In one embodiment, the microorganism produces phosphotransbutyrylase, butyrate kinase, ferredoxin dependent aldehyde oxidoreductase, and butanol dehydrogenase both before and after introduction of an exogenous nucleic acid.

In one embodiment, the microorganism produces butyraldehyde dehydrogenase and/or butanol dehydrogenase both before and after introduction of an exogenous nucleic acid.

In one particular embodiment, the microorganism is *Clostridium autoethanogenum* DSM23693.

In one embodiment, the recombinant microorganism of the invention has the defining characteristics of the microorganism deposited at the DSMZ (Deutsche Sammlung für Mikroorganismen und Zellkulturen GmbH, Braunschweig, Germany) under the accession number DSM24138.

The one or more exogenous nucleic acids may be delivered to a parental microorganism as naked nucleic acids or may be formulated with one or more agents to facilitate the tranformation process (for example, liposome-conjugated nucleic acid, an organism in which the nucleic acid is contained). The one or more nucleic acids may be DNA, RNA, or combinations thereof, as is appropriate.

The microorganisms of the invention may be prepared from a parental microorganism and one or more exogenous nucleic acids using any number of techniques known in the art for producing recombinant microorganisms. By way of example only, transformation (including transduction or transfection) may be achieved by electroporation, conjugation, or chemical and natural competence. Suitable transformation techniques are described for example in Sambrook et al, 1989.

In certain embodiments, due to the restriction systems which are active in the microorganism to be transformed, it is necessary to methylate the nucleic acid to be introduced into the microorganism. This can be done using a variety of techniques, including those described below, and further exemplified in the Examples section herein after.

In another aspect, the invention provides a method of producing a recombinant microorganism comprising the following steps:

a. introduction into a shuttle microorganism of (i) an expression construct and (ii) a methylation construct comprising a methyltransferase gene;

b. expression of the methyltransferase gene;

c. isolation of one or more constructs from the shuttle microorganism; and,

d. introduction of the one or more constructs into a destination microorganism;

wherein the expression construct comprises one or more genes encoding enzymes to be expressed in the destination organism.

In one embodiment, the methyltransferase gene of step B is expressed consitutively. In another embodiment, expression of the methyltransferase gene of step B is induced.

The shuttle microorganism is a microorganism, preferably a restriction negative microorganism, that facilitates the methylation of the nucleic acid sequences that make up the expression construct. In a particular embodiment, the shuttle microorganism is a restriction negative *E. coli, Bacillus subtillis or Lactococcus lactis.*

Once the expression construct and the methylation construct are introduced into the shuttle microorganism, the methyltransferase gene present on the methylation construct is expressed. In one embodiment, where expression must be induced, induction may be by any suitable promoter system although in one particular embodiment of the invention, the methylation construct comprises an inducible *lac* promoter (preferably encoded by SEQ_ID NO 28) and is induced by addition of lactose or an analogue thereof, more preferably isopropyl-β-D-thio-galactoside (IPTG). Other suitable promoters include the *ara*, *tet*, or T7 system. In an alternative embodiment of the invention, the methylation construct promoter is a constitutive promoter.

In one embodiment the expression construct promoter is a constitutive promoter that is preferably highly active under appropriate fermentation conditions. However, an inducible promoter could be used. In preferred embodiments, the expression construct promoter is selected from the group comprising phosphotransacetylase/acetate kinase operon promoter, pyruvate:ferredoxin oxidoreductase (SEQ_ID No. 48), the Wood-Ljungdahl gene cluster (SEQ_ID No 47), Rnf operon (SEQ_ID No 49) or the ATP synthase operon ((SEQ_ID No 50). Preferably, the phosphotransacetylase/acetate kinase operon promoter corresponds to SEQ_ID No. 7 or a functionally equivalent variant thereof. Figure 8 shows that expression of genes operably linked to these promoters have a high level of expression in *Clostridium autoethanogenum* under standard conditions.

In a particular embodiment, the methylation construct has an origin of replication specific to the identity of the shuttle microorganism so that any genes present on the methylation construct are expressed in the shuttle microorganism. Preferably, the expression construct has an origin of replication specific to the identity of the destination microorganism so that any genes present on the expression construct are expressed in the destination microorganism.

Expression of the methyltransferase enzyme results in methylation of the genes present on the expression construct. The expression construct may then be isolated from the shuttle microorganism according to any one of a number of known methods. By way of example only, the methodology described in the Examples section described hereinafter may be used to isolate the expression construct.

In one particular embodiment, both constructs are concurrently isolated. The expression construct may be introduced into the destination microorganism using any number of known methods. However, by way of example, the methodology described in the Examples section hereinafter may be used. Since the expression construct is methylated, the nucleic acid sequences present on the expression construct are able to be incorporated into the destination microorganism and successfully expressed.

In a further embodiment, the invention provides a method of producing a recombinant microorganism comprising:

a. methylation of an expression construct *in vitro* by a methyltransferase, preferably according to SEQ_ID No 28 or a functionally equivalent variant thereof; and,
b. introduction of an expression construct, preferably according to the fifth aspect, into a destination microorganism;

wherein the expression construct comprises one or more genes encoding enzymes to be expressed in the destination microorganism.

It is envisaged that a methyltransferase gene of the invention, preferably according to SEQ_ID No 27 or a functionally equivalent variant thereof, may be introduced into a shuttle microorganism and over-expressed. The resulting methyltransferase enzyme may be collected using known methods and used *in vitro* to methylate an expression construct, preferably, the expression construct is as defined in the fifth aspect. The expression construct may then be introduced into the destination microorganism for expression. Preferably, the recombinant microorganism produces 1-butanol and/or a precursor thereof as the main fermentation product.

In a further embodiment, the invention provides a method of producing a recombinant microorganism comprising:

a. introduction into the genome of a shuttle microorganism of a methyltransferase gene, preferably according to SEQ_ID No 27 or a functionally equivalent variant thereof;
b. introduction of an expression construct into the shuttle microorganism;
c. isolation of one or more constructs from the shuttle microorganism; and,
d. introduction of at least the expression construct into a destination microorganism;

wherein the expression construct comprises one or more genes encoding enzymes to be expressed in the destination microorganism.

Standard methods are used for the introduction of a methyltransferase gene, preferably according to SEQ_ID No 27, into the genome of the shuttle microorganism. The methyltransferase may be constitutively expressed by the microorganism and result in the production of a methyltransferase enzyme, preferably according to SEQ_ID No 28 or a functionally equivalent variant thereof. An expression construct is methylated, isolated and introduced into the destination microorganism which preferably, produces 1-butanol and/or a precursor thereof as the main fermentation product.

The invention also includes microorganisms comprising a recombinant methyltransferase gene or methylation construct as herein described.

The present invention also provides a hybrid methyltransferase gene (SEQ_ID NO 28) developed following analysis of methyltransferase nucleic acid sequences and restriction barrier systems from *C. autoethanogenum*, *C. ljungdahlii*, and *C. ragsdalei.*

The methyltransferase gene is expressed in a shuttle microorganism which results in the production of a methyltransferase enzyme which methylates the sequence of the expression construct. The methyltransferase gene may be present on a construct or integrated into the genome of the shuttle microorganism. The hybrid methyltransferase gene is codon optimised for *E. coli* and may be incorporated into a methylation construct (figure 5). The methyltransferase gene may be codon optimised for use in another species of microorganism where appropriate, for example *Bacillus subtillus.* Methods for codon optimisation are standard and would be known to one of skill in the art (Carbone et al, 2003). Also incorporated within the scope of the invention are methyltransferase genes that have at least 70%, preferably 75%, preferably 80%, preferably 85%, preferably 90%, preferably 95% or greater nucleic acid sequence identity to SEQ_ID NO 28 and express a polypeptide which is able to methylate DNA.

It will be appreciated by one of skill in the art that the methylation method and methyltransferase gene will have utility across a range of microorganisms. In one embodiment, the destination microorganism is selected from the group comprising *Clostridium autoethanogenum, Clostridium ljungdahlii, Clostridium ragsdalei, Clostridium carboxidivorans, Clostridium drakei, Clostridium scatologenes, Butyribacterium limosum, Butyribacterium methylotrophicum, Acetobacterium woodii, Alkalibaculum bacchii, Blautia producta, Eubacterium limosum, Moorella thermoacetica, Moorella thermautotrophica, Oxobacter pfennigii*, and *Thermoanaerobacter kiuvi..* In one particular embodiment, the destination microorganism is selected from the group consisting *Clostridium autoethanogenum, Clostridium ljungdahlii* and *Clostridium ragsdalei.* In one particular embodiment the destination microorganism is *Clostridium autoethanogenum* DSM23693.

The invention also provides various nucleic acids or nucleic acid constructs as outlined in aspects 4, 5, 14, 15, 16, 18, 19 and 21 of the invention herein before described.

In another embodiment of the invention, there is an expression construct comprising one or more nucleic acids encoding one or more enzymes chosen from Thiolase, 3-hydroxybutyryl-CoA dehydrogenase, Crotonase, Butyryl-CoA dehydrogenase and an electron transfer protein or a functionally equivalent variant thereof. Preferably, the electron transfer protein is Electron Transfer Flavoprotein A or Electron Transfer Flavoprotein B. In a particular embodiment, both Electron Transfer Flavoprotein A and Electron Transfer Flavoprotein B are included on the expression construct.

Exemplary sequence information for each gene and equivalent enzyme is provided on GenBank as detailed in Table 1 herein after. Skilled persons will readily appreciate alternative genes and enzymes which may be used. In one embodiment, the enzymes are encoded by the nucleic acid SEQ_ID No 1 to 6 which may be present in any order on the construct or in the order shown in figure 2. SEQ_ID Nos 8 to 13 and SEQ_ID Nos 16 to 23 are novel sequences used to clone and sequence the genes referred to in the immediately preceding paragraph.

In order to obtain 1-butanol from a precursor the activity of one or more of butyraldehyde dehydrogenase (EC1.2.1.10), alcohol dehydrogenase (EC 1.1.1.1), phosphotransbutyrylase (EC 2.3.1.19), butyrate kinase (EC 2.7.2.7), aldehyde:ferredoxin oxidoreductase (EC1.2.7.5) and alcohol dehydrogenase (EC 1.1.1.1) may be required. The alcohol dehydrogenase of the invention is a butanol dehydrogenase. In certain embodiments, butyraldehyde dehydrogenase (EC1.2.1.10) and alcohol dehydrogenase (EC 1.1.1.1), or phosphotransbutyrylase (EC 2.3.1.19), butyrate kinase (EC 2.7.2.7), aldehyde:ferredoxin oxidoreductase (EC1.2.7.5) and alcohol dehydrogenase (EC 1.1.1.1), or a combination of both sets of enzymes is required. In one embodiment, the butyraldehyde dehydrogenase and butanol dehydrogenase activity is supplied by a bifunctional butyraldehyde dehydrogenase/butanol dehydrogenase. These various enzymes are shown in the butanol biosynthesis pathway depicted in figure 1. In some microorganisms butyraldehyde dehydrogenase, butanol dehydrogenase, phosphotransbutyrylase, butyrate kinase, and/or aldehyde:ferredoxin oxidoreductase are naturally expressed by the microorganism and therefore catalyse the conversion of butyryl-CoA to 1-butanol.

Accordingly, in one embodiment, the expression construct comprises nucleic acids encoding one or more of phosphotransbutyrylase, butyrate kinase, ferredoxin dependent aldehyde oxidoreductase, butyraldehyde dehydrogenase, butanol dehydrogenase, and a bifunctional butyraldehyde dehydrogenase/butanol dehydrogenase in addition to or in the alternative to one or more of Thiolase, 3-hydroxybutyryl-CoA dehydrogenase, Crotonase, Butyryl-CoA dehydrogenase and an electron transfer protein.

Examples of appropriate enzymes and amino acid and nucleic acid sequence information include, but are not limited to: butyraldehyde dehydrogenase, such as Ald from *C. beijerinckii* (ABR35947, GI:149905114), *C. saccharobutylicum* (CAQ57983, GI:189310620), or *Clostridium saccharoperbutylacetoniucm* (AAP42563, GI:31075383); butanol dehydrogenase, such as BdhB from *C. acetobutylicum* (NP_349891, GI:15896542); bifunctional butyraldehyde/butanol dehydrogenase enzyme, such as AdhE1 from *C. acetobutylicum* (NP_149325, GI:15004865) or AdhE2 from *C. acetobutylicum* (NP_149199, GI:15004739), *C. beijerinckii.* YP_001307449, GI:150015195); a phosphotransbutyrylase such as Ptb from *C. acetobutylicum* (NP_348368); butyrate kinase such as Buk from *C. acetobutylicum* (AAK81015.1); aldehyde:ferredoxin oxidoreductase AOR from *C. acetobutylicum* (NP_348637). Persons of ordinary skill in the art to which the invention relates may readily appreciate alternative examples of appropriate enzymes of use in the invention. The inventors have also identified a number of novel enzymes and genes which may be used in the invention, the details of which are provided herein after in the Examples section (in particular see tables 7 to 10). The invention also encompasses functionally equivalent variants of these enzymes and genes and their use in methods of the invention.

The inclusion of one or more of these genes may help avoid co-production of butyrate completely, increasing the efficiency of 1-butanol production. The invention also provides recombinant microorganisms comprising one or more nucleic acids adapted to express or increase expression of one or more of these enzymes.

In one embodiment, the nucleic acid(s) encode an enzyme chosen from the group of enzymes listed in tables 7 to 10 herein after and functional equivalents of any one or more thereof. In a particular embodiment, the nucleic acids are chosen from the group of nucleic acids listed in tables 7 to 10 herein after and functional equivalents of any one or more thereof.

In one embodiment, the expression construct encodes at least 2 enzymes in the butanol biosynthesis pathway, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11 or at least 12 of the enzymes.

Preferably, the expression construct further comprises a suitable promoter as hereinbefore described. In one embodiment the promoter is a phosphotransacetylase/acetate kinase promoter. Preferably, the promoter corresponds to SEQ_ID No. 7 or a functionally equivalent variant thereof.

In a preferred embodiment, the expression construct comprises a nucleic acid encoding all of said enzymes. It will be appreciated by one of skill in the art that the expression construct may comprise nucleic acids encoding alternative electron transferring proteins.

The genes to be expressed in the recombinant microorganism may be assembled in the expression construct under the control of any appropriate promoter. In a particular embodiment, the promoter allows for substantially constitutive expression of the genes under its control. In a particular embodiment, the promoter is a phosphotransacetylase/acetate kinase (SEQ_ID NO 7) promoter. Other promoters which may find use in the invention include those from *C. autoethanogenum* (or *C. ljungdahlii*). The inventors have also identified a number of other promoters that are operably linked to genes that were highly expressed under typical fermentation conditions in *Clostridium autoethanogenum* (figure 8). Analysis of expression of over 200 genes during typical fermentation conditions using real-time PCR identified a number of appropriate promoters. These include pyruvate:ferredoxin oxidoreductase (SEQ_ID No. 48), the Wood-Ljungdahl gene cluster (SEQ_ID No 47), Rnf operon (SEQ_ID No 49) and the ATP synthase operon (SEQ_ID No 50). It will be appreciated by those of skill in the art that other promoters which can direct expression, preferably a high level of expression under appropriate fermentation conditions, would be effective as alternatives to the presently preferred embodiments.

In one embodiment, the invention comprises a construct, recombinant microorganism or a nucleic acid sequence comprising nucleic acid SEQ_ID NOs 1 to 6 in the order shown in figure 2. However, it will be appreciated by one of skill in the art that the invention may still have the desired utility when the nucleic acid sequences are presented in any order and with one or more of the sequences absent.

In another embodiment, the invention comprises a nucleic acid comprising the promoter sequence represented by Seq ID No. 7, or a functionally equivalent variant thereof, construct comprising said promoter and recombinant microorganisms comprising same.

It will be appreciated that an expression construct of the present invention may contain any number of regulatory elements in addition to the promoter as well as additional genes suitable for expression of further proteins if desired. In one embodiment the construct includes one promoter. In another embodiment, the construct includes two or more promoters. In one particular embodiment, the construct includes one promoter for with each gene to be expressed. In one embodiment, the construct includes one or more ribosomal binding sites, preferably a ribosomal binding site for each gene to be expressed.

It will be appreciated by those of skill in the art that the nucleic acid sequences and construct sequences defined herein may contain standard linker nucleotides such as those required for ribosome binding sites and/or restriction sites. Such linker sequences should not be interpreted as being required and do not provide a limitation on the sequences defined.

When the expression construct of the invention is expressed in an acetogenic microorganism, the microorganism produces 1-butanol or a precursor thereof as the main fermentation product. It is envisaged that other genes which encode enzymes catalyzing different steps of the Wood-Ljungdahl or butanol biosynthesis pathways may also be incorporated in the expression construct in order to produce 1-butanol as the main fermentation product.

It is envisaged that the expression construct and the methylation construct as defined above may be combined to provide a composition of matter. Such a composition has particular utility in circumventing restriction barrier mechanisms in a wide variety of microorganisms but in a preferred embodiment, the recombinant microorganism produced by use of the composition produces 1-butanol or a precursor thereof as the main fermentation product.

Nucleic acids and nucleic acid constructs, including expression constructs of the invention, may be constructed using any number of techniques standard in the art. For example, chemical synthesis or recombinant techniques may be used. Such techniques are described, for example, in Sambrook et al (1989). Further exemplary techniques are described in the Examples section herein after. Essentially, the individual genes and regulatory elements will be operably linked to one another such that the genes can be expressed to form the desired proteins. Suitable vectors for use in the invention will be appreciated by those of ordinary skill in the art. However, by way of example, the following vectors may be suitable: pMTL80000 shuttle vectors, pIMP1, pJIR750 and the plasmids exemplified in the Examples section herein after.

To the extent that the invention provides novel nucleic acids and nucleic acid vectors, it also provides nucleic acids which are capable of hybridising to at least a portion of a nucleic acid herein described, a nucleic acid complementary to any one thereof, or a functionally equivalent variant of any one thereof. Such nucleic acids will preferably hybridise to such nucleic acids, a nucleic acid complementary to any one thereof, or a functionally equivalent variant of any one thereof, under stringent hybridisation conditions. "Stringent hybridisation conditions" means that the nucleic acid is capable of hybridising to a target template under standard hybridisation conditions such as those described in Sambrook *et al* (1989). It will be appreciated that the minimal size of such nucleic acids is a size which is capable of forming a stable hybrid between a given nucleic acid and the complementary sequence to which it is designed to hybridise. Accordingly, the size is dependent on the nucleic acid composition and percent homology between the nucleic acid and its complementary sequence, as well as the hybridisation conditions which are utilised (for example, temperature and salt concentrations). In one embodiment, the nucleic acid is at least 10 nucleotides in length, at least 15 nucleotides in length, at least, 20 nucleotides in length, at least 25 nucleotides in length, or at least 30 nucleotides in length.

It should be appreciated that nucleic acids of the invention may be in any appropriate form, including RNA, DNA, or cDNA, including double-stranded and single-stranded nucleic acids.

The invention also provides host organisms, particularly microorganisms, and including viruses, bacteria, and yeast, comprising any one or more of the nucleic acids described herein.

The invention provides a method of production of 1-butanol and/or a precursor thereof by microbial fermentation comprising fermenting a gaseous substrate comprising CO using a recombinant microorganism. In certain embodiments, 1-butanol or a precursor thereof is co-produced with another fermentation product (for example, ethanol). In one embodiment, the 1-butanol or a precursor thereof is the main fermentation product. In one, embodiment, the recombinant microorganism is as herein before described.

In one embodiment, 1-butanol and/or a precursor thereof is produced in a yield of from approximately 0.075 grams per litre of fermentation broth (g/l) to approximately 20g/l. In one embodiment, the yield is from approximately 0.15g/l to approximately 1.54g/l. In other embodiments, the yield is approximately 10g/l, approximately 5g/l, or approximately 2g/l. Preferably, the yield of 1-butanol is up to the limit at which butanol becomes toxic to the bacteria.

Preferably, the fermentation comprises the steps of anaerobically fermenting a substrate in a bioreactor to produce 1-butanol and/or a precursor thereof using recombinant microorganisms as described herein.

Where the precursor of 1-butanol is referred to herein it is envisaged that it may be optionally converted to 1-butanol in the presence of butyraldehyde dehydrogenase, butanol dehydrogenase, a bifunctional butyraldehyde dehydrogenase/butanol dehydrogenase, phosphotransbutyrylase, butyrate kinase, and/or ferredoxin dependent aldehyde oxidoreductase. Preferably, the microorganism produces one or more of these enzymes both before and after introduction of a recombinant nucleic acid.

In an embodiment of the invention, the gaseous substrate fermented by the microorganism is a gaseous substrate containing CO. The gaseous substrate may be a CO-containing waste gas obtained as a by-product of an industrial process, or from some other source such as from automobile exhaust fumes. In certain embodiments, the industrial process is selected from the group consisting of ferrous metal products manufacturing, such as a steel mill, non-ferrous products manufacturing, petroleum refining processes, gasification of coal, electric power production, carbon black production, ammonia production, methanol production and coke manufacturing. In these embodiments, the CO-containing gas may be captured from the industrial process before it is emitted into the atmosphere, using any convenient method. The CO may be a component of syngas (gas comprising carbon monoxide and hydrogen). The CO produced from industrial processes is normally flared off to produce CO_2 and therefore the invention has particular utility in reducing CO_2 greenhouse gas emissions and producing butanol for use as a biofuel. Depending on the composition of the gaseous CO –containing substrate, it may also be desirable to treat it to remove any undesired impurities, such as dust particles before introducing it to the fermentation. For example, the gaseous substrate may be filtered or scrubbed using known methods.

It will be appreciated that for growth of the bacteria and CO-to-1butanol fermentation to occur, in addition to the CO-containing substrate gas, a suitable liquid nutrient medium will need to be fed to the bioreactor. A nutrient medium will contain vitamins and minerals sufficient to permit growth of the micro-organism used. Anaerobic media suitable for fermentation to produce butanol using CO are known in the art. For example, suitable media are described Biebel (2001). In one embodiment of the invention the media is as described in the Examples section herein after.

The fermentation should desirably be carried out under appropriate conditions for the CO-to-butanol fermentation to occur. Reaction conditions that should be considered include pressure, temperature, gas flow rate, liquid flow rate, media pH, media redox potential, agitation rate (if using a continuous stirred tank reactor), inoculum level, maximum gas substrate concentrations to ensure that CO in the liquid phase does not become limiting, and maximum product concentrations to avoid product inhibition.

In addition, it is often desirable to increase the CO concentration of a substrate stream (or CO partial pressure in a gaseous substrate) and thus increase the efficiency of fermentation reactions where CO is a substrate. Operating at increased pressures allows a significant increase in the rate of CO transfer from the gas phase to the liquid phase where it can be taken up by the micro-organism as a carbon source for the production of butanol. This in turn means that the retention time (defined as the liquid volume in the bioreactor divided by the input gas flow rate) can be reduced when bioreactors are maintained at elevated pressure rather than atmospheric pressure. The optimum reaction conditions will depend partly on the particular micro-organism of the invention used. However, in general, it is preferred that the fermentation be performed at pressure higher than ambient pressure. Also, since a given CO-to-butanol conversion rate is in part a function of the substrate retention time, and achieving a desired retention time in turn dictates the required volume of a bioreactor, the use of pressurized systems can greatly reduce the volume of the bioreactor required, and consequently the capital cost of the fermentation equipment. According to examples given in US patent no. 5,593,886, reactor volume can be reduced in linear proportion to increases in reactor operating pressure, i.e. bioreactors operated at 10 atmospheres of pressure need only be one tenth the volume of those operated at 1 atmosphere of pressure.

The benefits of conducting a gas-to-ethanol fermentation at elevated pressures has been described elsewhere. For example, WO 02/08438 describes gas-to-ethanol fermentations performed under pressures of 30 psig and 75 psig, giving ethanol productivities of 150 g/l/day and 369 g/l/day respectively. However, example fermentations performed using similar media and input gas compositions at atmospheric pressure were found to produce between 10 and 20 times less ethanol per litre per day.

The composition of gas streams used to feed a fermentation reaction can have a significant impact on the efficiency and/or costs of that reaction. For example, O2 may reduce the efficiency of an anaerobic fermentation process. Processing of unwanted or unnecessary gases in stages of a fermentation process before or after fermentation can increase the burden on such stages (e.g. where the gas stream is compressed before entering a bioreactor, unnecessary energy may be used to compress gases that are not needed in the fermentation). Accordingly, it may be desirable to treat substrate streams, particularly substrate streams derived from industrial sources, to remove unwanted components and increase the concentration of desirable components.

In certain embodiments a culture of a bacterium of the invention is maintained in an aqueous culture medium. Preferably the aqueous culture medium is a minimal anaerobic microbial growth medium. Suitable media are known in the art and described for example in US patent no.s 5,173,429 and 5,593,886 and WO 02/08438, and as described in the Examples section herein after.

Butanol, or a mixed alcohol stream containing butanol and one or more other alcohols, may be recovered from the fermentation broth by methods known in the art, such as fractional distillation or evaporation, pervaporation, and extractive fermentation, including for example, liquid-liquid extraction. By-products such as acids including butyrate may also be recovered from the fermentation broth using methods known in the art. For example, an adsorption system involving an activated charcoal filter or electrodialysis may be used. Alternatively, continuous gas stripping may also be used.

In certain preferred embodiments of the invention, butanol and by-products are recovered from the fermentation broth by continuously removing a portion of the broth from the bioreactor, separating microbial cells from the broth (conveniently by filtration), and recovering butanol and optionally acid from the broth. Alcohols may conveniently be recovered for example by distillation, and acids may be recovered for example by adsorption on activated charcoal. The separated microbial cells are preferably returned to the fermentation bioreactor. The cell free permeate remaining after the alcohol(s) and acid(s) have been removed is also preferably returned to the fermentation bioreactor. Additional nutrients (such as B vitamins) may be added to the cell free permeate to replenish the nutrient medium before it is returned to the bioreactor.

Also, if the pH of the broth was adjusted as described above to enhance adsorption of acetic acid to the activated charcoal, the pH should be re-adjusted to a similar pH to that of the broth in the fermentation bioreactor, before being returned to the bioreactor.

In one embodiment of the invention, butanol is recovered from the fermentation reaction using extractive fermentation procedures in which butanol is recovered into an oil phase in the reactor. Skilled persons would readily appreciate techniques for achieving this

Examples:

The invention will now be described in more detail with reference to the following non-limiting examples.

Genetic modifications were carried out using a plasmid containing a synthetic operon consisting of a strong, native *C. autoethanogenum* promoter controlling a thiolase, 3-hydroxybutyryl-CoA dehydrogenase, crotonase, butyryl-CoA dehydrogenase, and 2 electron transferring flavoproteins genes from *C. acetobutylicum* (Fig. 1-2). This plasmid was methylated *in vivo* using a novel methyltransferase and then transformed into *C. autoethanogenum* DSM23693. Production of 1-butanol as the main fermentation product was shown on different industrial gas streams (steel mill waste gas, syngas).

Construction of expression plasmid:

Standard Recombinant DNA and molecular cloning techniques were used in this invention and are described by Sambrook et al, 1989 and Ausubel et al, 1987. DNA sequences of butanol biosynthetic genes of *Clostridium acetobutylicum* ATCC824 used were obtained from NCBI (Table 1). The phosphotransacetylase/acetate kinase operon promoter of *C. autoethanogenum* DSM10061 were sequenced and used for expression of target genes (Table 1). RT-PCR experiments showed that this promoter is constitutively expressed at a high level (figure 8).

Table 1: Sources of 1-butanol pathway genes

Gene/Promoter	GenBank Citation	SEQ_ID NO.
Thiolase (*thlA*)	NC_003030 *Clostridium acetobutylicum* ATCC 824,	1

	complete genome; GI:15896127; GeneID:1119056	
3-hydroxybutyryl-CoA dehydrogenase (*hbd*)	NC_003030 *Clostridium acetobutylicum* ATCC 824, complete genome; GI:15895965; GeneID:1118891	2
Crotonase (*crt*)	NC_003030 *Clostridium acetobutylicum* ATCC 824, complete genome; GI:15895969; GeneID:1118895	3
butyryl-CoA dehydrogenase (*bcd*)	NC_003030 *Clostridium acetobutylicum* ATCC 824, complete genome; GI:15895968; GeneID:1118894	4
Electron Transfer Flavoprotein A (*etfA*)	NC_003030 *Clostridium acetobutylicum* ATCC 824, complete genome; GI:15895966; GeneID:1118892	5
Electron Transfer Flavoprotein B (*etfB*)	NC_003030 *Clostridium acetobutylicum* ATCC 824, complete genome; GI:15895967; GeneID:1118893	6
phosphotransacetylase/acetate kinase promoter ($P_{pta\text{-}ack}$)	*Clostridium autoethanogenum* DSM10061	7

Genomic DNA from *Clostridium acetobutylicum* ATCC824 and *Clostridum autoethanogenum* DSM10061 was isolated using a modified method by Bertram and Dürre (1989). A 100-ml overnight culture was harvested (6,000 x g, 15 min, 4 °C), washed with potassium phosphate buffer (10 mM, pH 7.5) and suspended in 1.9 ml STE buffer (50 mM Tris-HCl, 1 mM EDTA, 200 mM sucrose; pH 8.0). 300 μl lysozyme (~100,000 U) were added and the mixture was incubated at 37 °C for 30 min, followed by addition of 280 μl of a 10 % (w/v) SDS solution and another incubation for 10 min. RNA was digested at room temperature by addition of 240 μl of an EDTA solution (0.5 M, pH 8), 20 μl Tris-HCl (1 M, pH 7.5), and 10 μl RNase A (Fermentas). Then, 100 μl Proteinase K (0.5 U) were added and proteolysis took place for 1-3 h at 37 °C. Finally, 600 μl of sodium perchlorate (5 M) were added, followed by a phenol-chloroform extraction and an isopropanol precipitation. DNA quantity and quality was inspected spectrophotometrically.

Butanol biosynthesis genes and the phosphotransacetylase/acetate kinase promoter were amplified by PCR with oligonucleotides in table 2 using iProof High Fidelity DNA Polymerase (Bio-Rad Labratories) and the following program: initial denaturation at 98 °C for 30 seconds, followed by 32 cycles of denaturation (98 °C for 10 seconds), annealing (50-62 °C for 30-120 seconds) and elongation (72 °C for 45 seconds), before a final extension step (72 °C for 10 minutes).

Table 2: Oligonucleotides for cloning

Target	Oligonucleotide Name	DNA Sequence (5` to 3`)	SEQ_ID NO.
Ppta-ack	Ppta-ack-NotI-F	GAGCGGCCGCAATATGATATTTATGTCC	8
Ppta-ack	Ppta-ack-NdeI-R	TTCCATATGTTTCATGTTCATTTCCTCC	9
ThlA	ThlA-Cac-NdeI-F	GTTCATATGAAAGAAGTTGTAATAGC	10
ThlA	ThlA-Cac-EcoRI-R	CAAGAATTCCTAGCACTTTTCTAGC	11
crt-bcd-etfB-etfA-	Crt-Cac-KpnI-F	AAGGTACCTTAGGAGGATTAGTCATGG	12

hbd operon			
crt-bcd-etfB-etfA-hbd operon	Crt-hbd-Cac-BamHI-R	GAGGATCCGGATTCTTGTAAACTTATTTTG	13

The amplified 498 bp promoter region of the phosphotransacetylase/acetate kinase operon ($P_{pta-ack}$) was cloned into the *E. coli-Clostridium* shuttle vector pMTL 85141 (Seq. ID 14; FJ797651.1; Nigel Minton, University of Nottingham; Heap et al., 2009) using *Not*I and *Nde*I restriction sites and strain DH5α-$T1^R$ (Invitrogen). The created plasmid pMTL85145 and the 1,194 bp PCR product of the thiolase gene were both cut with *Nde*I and *EcoR*I. A ligation was transformed into *E. coli* XL1-Blue MRF' Kan (Stratagene) resulting in plasmid pMTL85145-thlA. Subsequently, the amplified 4,764 bp PCR fragment of the *crt-bcd-etfB-etfA-hbd* operon from *C. acetobutylicum* ATCC 824 was cloned into this vector using KpnI and BamHI and *E. coli* ABLE K (Stratagene), creating plasmid pMTL85145-thlA-crt-hbd. Finally, the antibiotic resistance cassette was changed from chloramphenicol to clarithromycin. Therefore, an *ermB* cassette was released from vector pMTL82254 (Seq. ID 15; FJ797646.1; Nigel Minton, University of Nottingham; Heap et al., 2009) using restriction enzymes *Pme*I and *Fse*I and exchanged with the *catP* cassette of plasmid pMTL85145-thlA-crt-hbd. The insert of the resulting expression plasmid pMTL85245-thlA-crt-hbd (SEQ_ID No. 31 was completely sequenced using oligonucleotides given in table 3 and results confirmed that the butanol biosynthesis genes were free of mutations (Figure 3).

Table 3: Oligonucleotides for sequencing

Oligonucleotide Name	DNA Sequence (5` to 3`)	SEQ_ID NO.
seq-ThlA-hbd-3562-4162	CAGAGGATGTTAATGAAGTC	16
seq-ThlA-hbd-4163-4763	GCATCAGGATTAAATGACTG	17
seq-ThlA-hbd-4764-5364	ATAGCGAAGTACTTG	18
seq-ThlA-hbd-5365-5965	GATGCAATGACAGCTTTC	19
seq-ThlA-hbd-5966-6566	GGAACAAAAGGTATATCAGC	20
seq-ThlA-hbd-7168-7768	CGGAGCATTTGATAAAGAA	21
seq-ThlA-hbd-7769-8369	GCTGATTGTACATCACTTGA	22
seq-ThlA-hbd-8370-8870	CCAGAATTAATAGCTCAAGT	23

Methylation of DNA:

A hybrid methyltransferase gene fused to an inducible *lac* promoter was designed (Seq. ID 28), by alignment of methyltransferase genes from *C. autoethanogenum* (SEQ_ID No. 24), *C. ljungdahlii* (SEQ_ID No. 25), and *C. ragsdalei* (SEQ_ID No. 26) (figure 4a, 4b and 4c). Expression of the methyltransferase gene resulted in production of a methyltransferase enzyme according to SEQ_ID No. 28. Methyltransferase amino acid sequence alignment data is shown in figure 4d.

The hybrid methyltransferase gene (SEQ_ID No. 27) was chemically synthesized and cloned into vector pGS20 (Seq. ID 29; ATG:biosynthetics GmbH, Merzhausen, Germany) using *EcoRI* (Fig. 5). The resulting methylation plasmid pGS20-methyltransferase was double transformed with the expression plasmid pMTL85245-thlA-crt-hbd into the restriction negative *E. coli* XL1-Blue MRF' Kan (Stratagene). *In vivo* methylation was induced by addition of 1 mM IPTG, and methylated plasmids were isolated using the PureLink™ HiPure Plasmid Maxiprep Kit (Invitrogen). The resulting methylated plasmid composition was used for transformation of *C. autoethanogenum* DSM23693.

Transformation:

During the complete transformation experiment, *C. autoethanogenum* DSM23693 and *C. ljundahlii* (DSM13528) were grown in PETC media (Tab. 4) with 10 g/l fructose and 30 psi steel mill waste gas (collected from New Zealand Steel site in Glenbrook, NZ; composition: 44% CO, 32% N_2, 22% CO_2, 2% H_2) as carbon source at 37 °C using standard anaerobic techniques described by Hungate (1969) and Wolfe (1971).

Table 4: PETC media (ATCC media 1754; http://www.atcc.org/Attachments/2940.pdf)

Media component	**Concentration per 1.0L of media**
NH_4Cl	1 g
KCl	0.1 g
$MgSO_4.7H_2O$	0.2 g
NaCl	0.8 g
KH_2PO_4	0.1 g
$CaCl_2$	0.02 g
Trace metal solution	10 ml
Wolfe's vitamin solution	10 ml
Yeast Extract	1 g
Resazurin (2 g/L stock)	0.5 ml
$NaHCO_3$	2 g
Reducing agent	0.006-0.008 % (v/v)
Distilled water	Up to 1 L, pH 5.5 (adjusted with HCl)

Wolfe's vitamin solution	**per L of Stock**
Biotin	2 mg
Folic acid	2 mg

Pyridoxine hydrochloride	10 mg
Thiamine.HCl	5 mg
Riboflavin	5 mg
Nicotinic acid	5 mg
Calcium D-(+)-pantothenate	5 mg
Vitamin B_{12}	0.1 mg
p-Aminobenzoic acid	5 mg
Thioctic acid	5 mg
Distilled water	To 1 L

Trace metal solution	**per L of stock**
Nitrilotriacetic Acid	2 g
$MnSO_4.H_2O$	1 g
$Fe (SO_4)_2(NH_4)_2.6H_2O$	0.8 g
$CoCl_2.6H_2O$	0.2 g
$ZnSO_4.7H_2O$	0.2 mg
$CuCl_2.2H_2O$	0.02 g
$NaMoO_4.2H_2O$	0.02 g
Na_2SeO_3	0.02 g
$NiCl_2.6H_2O$	0.02 g
$Na_2WO_4.2H_2O$	0.02 g
Distilled water	To 1 L

Reducing agent stock	**per 100 mL of stock**
NaOH	0.9 g
Cystein.HCl	4 g
Na_2S	4 g
Distilled water	To 100 mL

To make competent cells, a 50 ml culture of *C. autoethanogenum* DSM23693 and a 50ml culture of *C. ljundahlii* DSM13528 were subcultured to fresh media for 3 consecutive days. These cells were used to inoculate 50 ml PETC media containing 40 mM DL-threonine at an OD_{600nm} of 0.05. When the culture reached an OD_{600nm} of 0.4, the cells were transferred into an anaerobic chamber and harvested at 4,700 x g and 4 °C. The culture was twice washed with ice-cold electroporation buffer (270 mM sucrose, 1 mM MgCl2, 7 mM sodium phosphate, pH 7.4) and finally suspended in a volume of 600 µl fresh electroporation buffer. This mixture was transferred into a pre-cooled electroporation cuvette with a 0.4 cm electrode gap containing 1 µg of the methylated plasmid mix (and in the case of *C. ljundahlii* 1µl Type 1 restriction inhibitor (Epicentre Biotechnologies)) and immediately pulsed using the Gene pulser Xcell electroporation system (Bio-Rad) with the following settings: 2.5 kV, 600 Ω, and 25 µF. Time constants of 3.7-4.0 ms were achieved. The culture was transferred into 5 ml fresh media. Regeneration of the cells was monitored at a wavelength of 600 nm using a Spectronic Helios Epsilon Spectrophotometer (Thermo) equipped with a tube holder. After an initial drop in biomass, the cells start growing again. Once the biomass has doubled from that point, the cells were harvested, suspended in 200 µl fresh media and plated on selective PETC plates (containing 1.2 % Bacto™ Agar (BD)) with 4 µg/µl Clarithromycin. After 4-5 days of inoculation with 30 psi steel mill gas at 37 °C, 15-80 colonies per plate were clearly visible.

The colonies were used to inoculate 2 ml PETC media containing 4 µg/µl Clarithromycin. When growth occurred, the culture was upscaled into 5 ml and later 50 ml PETC media containing 4 µg/µl Clarithromycin and 30 psi steel mill gas as sole carbon source.

Conformation of the successful transformation:

C. autoethanogenum: To verify the DNA transfer, a plasmid mini prep was performed from 10 ml culture volume using the QIAprep Spin Miniprep Kit (Qiagen). Due to Clostridial exonuclease activity (Burchhardt and Dürre, 1990), the isolated plasmid DNA from 4 analyzed clones were partly degraded and only resulted in a smear on an agarose gel, while a plasmid isolation from the original *C. autoethanogenum* DSM23693 strain didn't result in a signal at all (Fig. 6). However, the quality of the isolated plasmid DNA was sufficient to run a control PCR using 4 sets of primers, covering all relevant different regions of the plasmid (Table 5). The PCR was performed with illustra PuReTaq Ready-To-Go™ PCR Beads (GE Healthcare) using a standard conditions (95 °C for 5 min; 32 cycles of 95 °C for 30 s, 50 °C for 30 s, and 72 °C for 1 min; 72 °C for 10 min). PCR of all 4 analyzed transformants resulted in the same signals as with the original methylated plasmid mix as template (Fig. 6). As a further control, 1 µl of each of the partly degraded isolated plasmids were re-transformed in *E. coli* XL1-Blue MRF' Kan (Stratagene), from where the plasmids could be isolated cleanly and verified by restriction digests.

To confirm the identity of the 4 clones, genomic DNA was isolated (see above) from 40 ml of each culture and a PCR was performed against the 16s rRNA gene (Tab. 5; Weisberg et al., 1991) using illustra PuReTaq Ready-To-Go™ PCR Beads (GE Healthcare) and standard conditions (95 °C for 5 min; 32 cycles of 95 °C for 30 s, 50 °C for 30 s, and 72 °C for 1 min; 72 °C for 10 min). The respective PCR products were purified and sequenced. Sequences of all clones showed at least 99.9% identity against the 16S rRNA gene of *C. autoethanogenum* (Seq. ID 30; Y18178, GI:7271109).

A respective strain was deposited at DSMZ (Deutsche Sammlung für Mikroorganismen und Zellkulturen GmbH, Braunschweig, Germany) under the accession number DSM24138 on 26 October 2010.

C. ljungdahlii: Clostridium ljungdahlii transformants were confirmed using the same method and primer sets. Sequencing of the 16S rRNA gene resulted in a 100 % match with the 16S gene of *Clostridium ljungdahlii* (Seq. ID 119; CP001666, GI:300433347).

Table 5: Oligonucleotides for PCR confirmation of plasmid and species

Target region	Oligonucleotide Name	DNA Sequence (5` to 3`)	Seq ID No.
16s rRNA gene	fD1	CCGAATTCGTCGACAACAGAGTTTGATCCTGGCTCAG	135
16s rRNA gene	rP2	CCCGGGATCCAAGCTTACGGCTACCTTGTTACGACTT	32
Antibiotic resistance cassette (*ermB*)	ermB-F	TTTGTAATTAAGAAGGAG	33
Antibiotic resistance cassette (*ermB*)	ermB-R	GTAGAATCCTTCTTCAAC	34
Insert 1 (*thlA*)	ThlA-Cac-NdeI-F	GTTCATATGAAAGAAGTTGTAATAGC	10
Insert 1 (*thlA*)	ThlA-Cac-EcoRI-R	CAAGAATTCCTAGCACTTTTCTAGC	11
Insert 2 (*crt-bcd-etfAB-hbd*)	Crt-conserved-F	GCTGGAGCAGATAT	35
Insert 2 (*crt-bcd-etfAB-hbd*)	Crt-conserved-R	GCTGTCATTCCTTC	36
Replication origin (ColE1)	ColE1-F	CGTCAGACCCCGTAGAAA	37
Replication origin (ColE1)	ColE1-R	CTCTCCTGTTCCGACCCT	38

1-butanol production:

To demonstrate 1-butanol production from CO as sole energy and carbon source, PETC media without yeast extract and fructose were prepared and inoculated with the novel *C. autoethanogenum* and *C. ljungdahlii* strains harbouring butanol plasmid pMTL85245-thlA-crt-hbd. Bottles were pressurized with 30 psi of a CO containing gas stream from two industrial sources, steel mill waste gas (collected from New Zealand Steel site in Glenbrook, NZ; composition: 44%

CO, 32% N_2, 22% CO_2, 2% H_2) and syngas (Range Fuels Inc., Broomfield, CO; composition: 29 % CO, 45 % H_2, 13 % CH_4, 12 % CO_2, 1 % N_2). 1-Butanol production could be demonstrated on with both strains and both gas mixes over several subculturing periods. Co-production of butyrate was observed as well. Neither 1-butanol nor butyrate were detected in samples of unmodified strains of *C. autoethanogenum* DSM23693 and *C. ljungdahlii* DSM13528 under the same conditions.

Analysis of metabolites were performed by HPLC using an Agilent 1100 Series HPLC system equipped with a RID operated at 35 °C (Refractive Index Detector) and an Alltech IOA-2000 Organic acid column (150 x 6.5 mm, particle size 5 µm) kept at 60 °C. Slightly acidified water was used (0.005 M H_2SO_4) as mobile phase with a flow rate of 0.7 ml/min. To remove proteins and other cell residues, 400 µl samples were mixed with 100 µl of a 2 % (w/v) 5-Sulfosalicylic acid and centrifuged at 14,000 x g for 3 min to separate precipitated residues. 10 µl of the supernatant were then injected into the HPLC for analyses.

In serum bottle experiments the highest 1-butanol production was observed in two static cultures of *C. autoethanogenum* harboring butanol plasmid pMTL85245-thlA-crt-hbd. In these cultures, 1-butanol was the main fermentation end product observed with 1.54 g/l (25.66 mM) (Table 6, Fig. 7). The production of the other metabolites was reduced compared to the original strain *C. autoethanogenum* DSM23693, which only produced ethanol, acetate, and 2,3-butandiol. Although the carbon flux was shifted towards 1-butanol production, the amount of total carbon incorporated into metabolic end products remain almost the same (Table 6). The slight increase of 20 % is likely to be the result of an extra reducing equivalents offload by producing 1-butanol and butyrate compared to ethanol and respectively acetate. The production of 2,3-butandiol which usually acts as electron sink, was completely diminished.

Table 6: Metabolite production and carbon balance of *C. autoethanogenum* harboring butanol plasmid pMTL85245-thlA-crt-hbd compared to original *C. autoethanogenum* DSM23693

				Original *C. autoethanogenum* DSM23693			***C. autoethanogenum* DSM23693 + pMTL85245-thlA-crt-bcd**		
Product	**M [g/mol]**	**P [g/cm^3]**	**Carbon atoms**	**Product [g/l]**	**Product [mmol/l]**	**Carbon [mmol/l]**	**Product [g/l]**	**Product [mmol/l]**	**Carbon [mmol/l]**
Ethanol	46.08	0.789	2	1.02	28.06	56.11	0.37	10.18	20.35
Acetate	60.05	1.049	2	1.87	29.69	59.37	0.30	4.76	9.52
2,3-butandiol	90.12	0.987	4	0.18	2.02	8.09	0	0	0

1-butanol	74.12	0.810	4	0	0	0	1.54	25.66	102.63
Butyrate	88.11	0.960	4	0	0	0	0.31	3.67	14.67
Total						**123.58**			**147.17**

1-butanol production was also observed in cultures of *C. ljungdahlii* DSM13528 harbouring the butanol plasmid pMTL85245-thlA-crt-hbd in significant amounts of up to 0.36 g/L (6mM), although lower compared to *C. autoethanogenum* DSM23693 carrying the same plasmid. This can be explained as *C. autoethanogenum* DSM23693 is a strain with improved alcohol production and correspondingly, the unmodified strain of *C. autoethanogenum* DSM23693 produces more ethanol and less acetate than the unmodified strain of *C. ljungdahlii* DSM13528 (both strains produce neither butanol nor butyrate).

C. ljungdahlii harbouring the butanol plasmid pMTL85245-thlA-crt-hbd had a lower 1-butanol:butryrate ratio than *C. autoethanogenum*. The ratio of 1-butanol to butyrate, however, can be altered by process conditions. This allows production of 1-butanol as the main fermentation product, but also production of butyrate as the main fermentation product in both strains *C. autoethanogenum* and *C. ljungdahlii*. In serum bottle experiments, molar ratios of 1-butanol:butyrate between 50:1 to 1:30 were observed with *C. autoethanogenum* and between 20:1 and 1:30 with *C. ljungdahlii*. Cultures which were incubated under shaking produced generally higher butyrate and lower 1-butanol levels compared to static cultures. The concentration of CO (and H_2) in the headspace was found to have an effect on the 1-butanol:butyrate ratio as well. In cultures with less CO in the headspace, butyrate production was more favoured and could be produced as the main fermentation product. Correspondingly, higher 1-butanol titers were observed on the CO-richer steel mill gas (44 % CO) than on the CO-leaner syngas (29 % CO) in performed serum bottle experiments. A maximum of 1.08 g/l (12.8 mM) butyrate was observed with *Clostridium autoethanogenum* harbouring plasmid pMTL85245-thlA-crt-hbd and a level of 1.03 g7L (12.5 mM) with *C. ljungdahlii* carrying the same plasmid. This effect can be explained by the extra carbon going into the system and also the additional reducing power generated from CO oxidation by the carbon monoxide dehydrogenase (CODH).

Conversion of butyryl-CoA to butyrate and butanol:

The expression plasmid only contains the genes necessary for production of butyryl-CoA from acetyl-CoA. Butyryl-CoA can then be converted directly to butanol by action of a butyraldehyde dehydrogenase and butanol dehydrogenase (Fig. 1). A second possibility is that butyryl-CoA is converted to butyrate via a phosphotransbutyrylase and butyrate kinase (Fig. 1), in which case

ATP is gained via substrate level phosphorylation (SLP). Since operation of the Wood-Ljungdahl pathway requires ATP, acetogenic cells rely on ATP from SLP, which is also reflected in the fact that every acetogenic bacteria known produces acetate (Drake et al., 2006). However, the recombinant cell can now also generate ATP via SLP also by producing butyrate. Butyrate can then be further reduced to butyraldehyde via a aldehyde:ferredoxinoxidoreductase (AOR) (Fig. 1). This reaction could be driven by reduced ferredoxin, provided by oxidation of CO via the carbon monoxide dehydrogenase ($CO + Fd_{red} -> CO_2 + Fd_{ox}$), the initial step in the Wood-Ljungdahl pathway. Butyraldehyde can then be converted to butanol via a butanol dehydrogenase (Fig. 1). Conversion of externally added butyrate to butanol by a culture of *C. autoethanogenum* has been demonstrated (WO2009/113878).

Respective genes/enzymes with butyraldehyde dehydrogenase, butanol dehydrogenase, phophotransbutyrylase, butyrate kinase, and aldehyde:ferredoxin oxidoreductase activity have been identified by the inventors in *C. autoethanogenum*, *C. ljungdahlii*, and *C. ragsdalei* (Tab. 7-10). Potential genes and enzymes were predicted by comparison with characterized genes and enzymes using BLAST (Altschul et al, 1990), COG (Tatusov et al, 2003), and TIGRFAM (Haft et al, 2002) databases. Motif scans were performed against PROSITE (Hulo et al., 2008) Pfam (Finn et al., 2010) databases. Genomes of *C. autoethanogenum*, *C. ljungdahlii*, and *C. ragsdalei* contain several genes encoding enzymes with alcohol and aldehyde dehydrogenase activity. As indicated in tables 7 to 10, some of these were found to have high homology of over 70 % to characterized butyraldehyde and butanol dehydrogenases from *C. acetobutylicum*, *C. beijerinckii*, or *C. saccharobutylicum*, while others have at least in some 40 % identity to these enzymes. All three genomes encode exactly one enzyme with Phosphate acetyl/butyryl transferase activity and one with Acetate/butyrate kinase activity. *C. autoethanogenum*, *C. ljungdahlii*, and *C. ragsdalei* each possess 2 aldehyde:ferredoxin oxidoreductase genes.

Table 7: Genes of *C. autoethanogenum* potentially conferring butyraldehyde and butanol dehydrogenase activity

Sequence	Description	Identity (protein) to characterized enzymes
Seq. ID 39-40	Bifunctional butanol/ butyraldehyde dehydrogenase	• bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. beijerinckii* NCIMB 8052 (Identities = 644/861 (75%), Positives = 748/861 (87%), e-value = 0.0) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (Identities = 594/858 (70%), Positives = 730/858 (86%), e-value = 0.0)
Seq. ID 41-42	Butyraldehyde dehydrogenase	• bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. beijerinckii* NCIMB 8052 (Identities = 367/504 (73%), Positives = 437/504 (87%), e-value = 0.0) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (354/504 (71%), Positives = 440/504 (88%), e-value = 0.0)
Seq. ID 43-44	Butyraldehyde dehydrogenase	• bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (Identities = 173/352 (50%), Positives = 236/352 (68%), e-value = 1e-91)

		• bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. beijerinckii* NCIMB 8052 (Identities = 160/374 (43%), Positives = 234/374 (63%), e-value = 5e-87) • bifunctional aldehyde/alcohol dehydrogenase AdhE1 from *C. acetobutylicum* ATCC824 (Identities = 158/366 (44%), Positives = 235/366 (65%), e-value = 5e-82) • butyraldehyde dehydrogenase Ald from *C. beijerinckii* NCIMB8052 (Identities = 110/354 (32%), Positives = 184/354 (52%), e-value = 9e-44) • butyraldehyde dehydrogenase from *C. saccharoperbutylacetonicum* (111/354 (32%), Positives = 182/354 (52%), e-value = 2e-44)
Seq. ID 45-46	Butyraldehyde dehydrogenase	• bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. beijerinckii* NCIMB 8052 (Identities = 188/477 (40%), Positives = 270/477 (57%), e-value = 9e-84) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (Identities = 164/428 (39%), Positives = 256/428 (60%), e-value = 1e-79)
Seq. ID 119-120	Butanol dehydrogenase	• NADPH-dependet butanol dehydrogenase from *C. saccharobutylicum* (Identities = 285/388 (74%), Positives = 334/388 (87%), e-value = 7e-177) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (Identities = 163/396 (42%), Positives = 237/396 (60%), e-value = 4e-80)
Seq. ID 121-122	Butanol dehydrogenase	• NADPH-dependet butanol dehydrogenase from *C. saccharobutylicum* (Identities = 271/388 (70%), Positives = 328/388 (85%), e-value = 3e-168) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (Identities = 169/403 (42%), Positives = 240/403 (60%), e-value = 3e-83)
Seq. ID 51-52	Butanol dehydrogenase	• bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. beijerinckii* NCIMB 8052 (246/315 (79%), Positives = 287/315 (92%), e-value = 1e-153) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (208/312 (67%), Positives = 260/312 (84%), e-value = 4e-128)
Seq. ID 53-54	Butanol dehydrogenase	• NADPH-dependet butanol dehydrogenase from *C. saccharobutylicum* (Identities = 264/388 (69%), Positives = 326/388 (85%), e-value = 5e-163) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. beijerinckii* NCIMB8052 (Identities = 169/410 (42%), Positives = 246/410 (60%), e-value = 5e-82) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (Identities = 162/402 (41%), Positives = 240/402 (60%), e-value = 2e-78)
Seq. ID 55-56	Butanol dehydrogenase	• NADH-dependent butanol dehydrogenase BdhA from *C. acetobutylicum* ATCC824 (Identities = 161/388 (42%), Positives = 243/388 (63%), e-value = 7e-92) • NADH-dependent butanol dehydrogenase BdhB from *C. acetobutylicum* ATCC824 (Identities = 155/389 (40%), Positives = 242/389 (63%), e-value = 4e-85)
Seq. ID 57-58	Butanol dehydrogenase	• NADPH-dependet butanol dehydrogenase AdhE2 from *C. saccharobutylicum* (Identities = 156/385 (41%), Positives = 236/385 (62%), e-value = 1e-72) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (Identities = 154/412 (38%), Positives = 233/412 (57%), e-value = 8e-70)
Seq. ID 59-60	Phosphate acetyl/butyryl transferase	• phosphate butyryltransferase from *C. acetobutylicum* ATCC 824 (Identities = 85/338 (26%), Positives = 146/338 (44%), e-value = 2e-12)
Seq ID 61-62	Acetate/butyrate kinase	• butyrate kinase from C. acetobutylicum ATCC 824 (Identities = 49/175 (28%), Positives = 78/175 (45%), e-value 5e-08)
Seq ID 63-64	Aldehyde:ferredoxin oxidoreductase	• aldehyde:ferredoxin oxidoreductase from *C. acetobutylicum* ATCC 824 (Identities = 183/618 (30%), Positives = 311/618 (51%), e-value = 6e-72)
Seq ID 65-66	Aldehyde:ferredoxin oxidoreductase	• aldehyde:ferredoxin oxidoreductase from *C. acetobutylicum* ATCC 824 (Identities = 191/633 (31%), Positives = 308/633 (49%), e-value = 2e-70)

Table 8: Genes of *C. ljungdahlii* potentially conferring butyraldehyde and butanol dehydrogenase activity

Sequence	Description	Identity to characterized enzymes
Seq. ID 67-68	Bifunctional butanol/ butyraldehyde dehydrogenase	• bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. beijerinckii* NCIMB 8052 (Identities = 644/862 (75%), Positives = 751/862 (88%), e-value = 0.0) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (Identities = 592/858 (69%), Positives = 729/858 (85%), e-value = 0.0)
Seq. ID 69-70	Bifunctional butanol/	• bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. beijerinckii* NCIMB

	butyraldehyde dehydrogenase	8052 (Identities = 636/860 (74%), Positives = 752/860 (88%), e-value = 0.0) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (Identities = 585/858 (69%), Positives = 733/858 (86%), e-value = 0.0)
Seq. ID 71-72	Butyraldehyde dehydrogenase	• bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (Identities = 209/429 (49%), Positives = 286/429 (67%), e-value = 4e-111) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. beijerinckii* NCIMB 8052 (Identities = 196/467 (42%), Positives = 286/467 (62%), e-value = 1e-102) • bifunctional aldehyde/alcohol dehydrogenase AdhE1 from *C. acetobutylicum* ATCC824 (Identities = 193/443 (44%), Positives = 283/443 (64%), e-value = 7e-100) • butyraldehyde dehydrogenase Ald from *C. beijerinckii* NCIMB8052 (Identities = 125/409 (31%), Positives = 206/409 (51%), e-value = 3e-49) • butyraldehyde dehydrogenase from *C. saccharoperbutylacetonicum* (124/409 (31%), Positives = 204/409 (50%), e-value = 2e-48)
Seq. ID 73-74	Butyraldehyde dehydrogenase	• bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. beijerinckii* NCIMB 8052 (Identities = 188/477 (40%), Positives = 270/477 (57%), e-value = 9e-84) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (Identities = 164/428 (39%), Positives = 256/428 (60%), e-value = 1e-79)
Seq. ID 75-76	Butanol dehydrogenase	• NADPH-dependet butanol dehydrogenase from *C. saccharobutylicum* (Identities = 285/388 (74%), Positives = 335/388 (87%), e-value = 9e-177) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (Identities = 164/396 (42%), Positives = 238/396 (61%), e-value = 1e-80)
Seq. ID 77-78	Butanol dehydrogenase	• NADPH-dependet butanol dehydrogenase from *C. saccharobutylicum* (Identities = 281/388 (73%), Positives = 327/388 (85%), e-value = 2e-173) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (Identities = 169/403 (42%), Positives = 240/403 (60%), e-value = 3e-83)
Seq. ID 79-80	Butanol dehydrogenase	• NADPH-dependet butanol dehydrogenase from *C. saccharobutylicum* (Identities = 264/388 (69%), Positives = 326/388 (85%), e-value = 5e-163) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. beijerinckii* NCIMB8052 (Identities = 169/410 (42%), Positives = 246/410 (60%), e-value = 4e-82) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (Identities = 162/402 (41%), Positives = 240/402 (60%), e-value = 2e-78)
Seq. ID 81-82	Butanol dehydrogenase	• NADH-dependent butanol dehydrogenase BdhA from *C. acetobutylicum* ATCC824 (Identities = 161/388 (42%), Positives = 243/388 (63%), e-value = 7e-92) • NADH-dependent butanol dehydrogenase BdhB from *C. acetobutylicum* ATCC824 (Identities = 155/389 (40%), Positives = 242/389 (63%), e-value = 4e-85)
Seq. ID 83-84	Butanol dehydrogenase	• NADPH-dependet butanol dehydrogenase from *C. saccharobutylicum* (Identities = 150/389 (39%), Positives = 233/389 (60%), e-value = 7e-73) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (Identities = 154/412 (38%), Positives = 233/412 (57%), e-value = 8e-70)
Seq. ID 85-86	Phosphate acetyl/butyryl transferase	• phosphate butyryltransferase from *C. acetobutylicum* ATCC 824 (91/340 (27%), Positives = 156/340 (46%), e-value = 1e-16)
Seq ID 87-88	Acetate/butyrate kinase	• butyrate kinase from C. acetobutylicum ATCC 824 (49/162 (31%), Positives = 77/162 (48%), e-value 5e-08)
Seq ID 89-90	Aldehyde:ferredoxin oxidoreductase	• aldehyde:ferredoxin oxidoreductase from *C. acetobutylicum* ATCC 824 (188/631 (30%), Positives = 318/631 (51%), e-value = 3e-11)
Seq ID 91-92	Aldehyde:ferredoxin oxidoreductase	• aldehyde:ferredoxin oxidoreductase from *C. acetobutylicum* ATCC 824 (Identities = 191/633 (31%), Positives = 308/633 (49%), e-value = 2e-70)

Table 10: Genes of *C. ragsdalei* potentially conferring butyraldehyde and butanol dehydrogenase activity

Sequence	Description	Identity to characterized enzymes
Seq. ID 93-94	Bifunctional butanol/ butyraldehyde dehydrogenase	• bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. beijerinckii* NCIMB 8052 (Identities = 645/861 (75%), Positives = 751/861 (88%), e-value = 0.0) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum*

		ATCC824 (Identities = 591/858 (69%), Positives = 731/858 (86%), e-value = 0.0)
Seq. ID 95-96	Bifunctional butanol/ butyraldehyde dehydrogenase	• bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. beijerinckii* NCIMB 8052 (Identities = 639/860 (75%), Positives = 752/860 (88%), e-value = 0.0) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (Identities = 591/858 (69%), Positives = 735/858 (86%), e-value = 0.0)
Seq. ID 97-98	Butyraldehyde dehydrogenase	• bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (Identities = 214/457 (47%), Positives = 294/457 (65%), e-value = 5e-111) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. beijerinckii* NCIMB 8052 (Identities = 200/457 (44%), Positives = 283/457 (62%), e-value = 1e-103) • bifunctional aldehyde/alcohol dehydrogenase AdhE1 from *C. acetobutylicum* ATCC824 (Identities = 198/457 (44%), Positives = 289/457 (64%), e-value = 4e-101) • butyraldehyde dehydrogenase Ald from *C. beijerinckii* NCIMB8052 (Identities = 125/409 (31%), Positives = 206/409 (51%), e-value = 3e-49) • butyraldehyde dehydrogenase from *C. saccharoperbutylacetonicum* (Identities = 123/409 (31%), Positives = 205/409 (51%), e-value = 1e-48)
Seq. ID 99-100	Butyraldehyde dehydrogenase	• bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. beijerinckii* NCIMB 8052 (Identities = 188/477 (40%), Positives = 270/477 (57%), e-value = 9e-84) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (Identities = 164/428 (39%), Positives = 256/428 (60%), e-value = 1e-79)
Seq. ID 101-102	Butanol dehydrogenase	• NADPH-dependet butanol dehydrogenase from *C. saccharobutylicum* (Identities = 285/388 (74%), Positives = 335/388 (87%), e-value = 9e-177) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (Identities = 164/396 (42%), Positives = 238/396 (61%), e-value = 1e-80)
Seq. ID 103-104	Butanol dehydrogenase	• NADPH-dependet butanol dehydrogenase from *C. saccharobutylicum* (Identities = 281/388 (73%), Positives = 327/388 (85%), e-value = 2e-173) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (Identities = 169/403 (42%), Positives = 240/403 (60%), e-value = 3e-83)
Seq. ID 105-106	Butanol dehydrogenase	• NADPH-dependet butanol dehydrogenase from *C. saccharobutylicum* (Identities = 264/388 (69%), Positives = 326/388 (85%), e-value = 5e-163) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. beijerinckii* NCIMB8052 (Identities = 169/410 (42%), Positives = 246/410 (60%), e-value = 4e-82) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (Identities = 162/402 (41%), Positives = 240/402 (60%), e-value = 2e-78)
Seq. ID 107-108	Butanol dehydrogenase	• NADH-dependent butanol dehydrogenase BdhA from *C. acetobutylicum* ATCC824 (Identities = 162/388 (42%), Positives = 243/388 (63%), e-value = 3e-92) • NADH-dependent butanol dehydrogenase BdhB from *C. acetobutylicum* ATCC824 (Identities = 155/389 (40%), Positives = 242/389 (63%), e-value = 6e-85)
Seq. ID 109-110	Butanol dehydrogenase	• NADPH-dependet butanol dehydrogenase from *C. saccharobutylicum* (Identities = 147/389 (38%), Positives = 227/389 (59%), e-value = 3e-71) • bifunctional aldehyde/alcohol dehydrogenase AdhE2 from *C. acetobutylicum* ATCC824 (Identities = 155/412 (38%), Positives = 233/412 (57%), e-value = 2e-70)
Seq. ID 111-112	Phosphate acetyl/butyryl transferase	• phosphate butyryltransferase from *C. acetobutylicum* ATCC 824 87/325 (27%), Positives = 148/325 (46%), e-value = 2e-16)
Seq ID 113-114	Acetate/butyrate kinase	• butyrate kinase from *C. acetobutylicum* ATCC 824 (Identities = 49/162 (31%), Positives = 77/162 (48%), e-value 4e-11)
Seq ID 115-116	Aldehyde:ferredoxin oxidoreductase	• aldehyde:ferredoxin oxidoreductase from *C. acetobutylicum* ATCC 824 (Identities = 187/633 (30%), Positives = 319/633 (51%), e-value = 3e-74)
Seq ID 117-118	Aldehyde:ferredoxin oxidoreductase	• aldehyde:ferredoxin oxidoreductase from *C. acetobutylicum* ATCC 824 (Identities = 187/633 (30%), Positives = 302/633 (48%), e-value = 1e-69)

Gene expression studies

Gene expression studies were performed to confirm successful expression of introduced Thiolase, 3-hydroxybutyryl-CoA dehydrogenase, Crotonase, Butyryl-CoA dehydrogenase, Electron Transfer Flavoprotein A and Electron Transfer Flavoprotein B genes in *C. autoethanogenum* harboring butanol plasmid pMTL85245-thlA-crt-hbd. In addition, a selection of putative butaraldehyde, butanol dehydrogenase, phosphate acetyl/butyryl transferase acetate/butyrate kinase, aldehyde;ferredoxin oxidoreductase genes identified in the genome of C. autoethanogenum (Table 7) were also found to be expressed under standard fermentation conditions (Figure 60).

A sample was harvested by centrifugation (6,000 x g, 5 min, 4 °C). RNA was isolated by suspending the cell pellet in 100 µL of lysozyme solution (50,000 U lysozyme, 0.5 µL 10% SDS, 10 mM Tris-HCl, 0.1 mM EDTA; pH 8). After 5 min, 350 µL of lysis buffer (containing 10 µL of 2-mercaptoethanol) was added. The cell suspension was mechanistically disrupted by passing five times through an 18-21 gauge needle. RNA was then isolated using PureLink™ RNA Mini Kit (Invitrogen) and eluted in 100 µL of RNase-free water. The RNA was checked via PCR and gel electrophoresis and quantified spectrophotometrically, and treated with DNase I (Roche) if necessary. Quality and integrity of RNA was checked using a BioAnalyzer (Agilent Technologies). The reverse transcription step was carried out using SuperScript III Reverse Transcriptase Kit (Invitrogen). RT-PCR reactions were performed in MyiQ Single Colour Real-Time PCR Detection System (Bio-Rad Labratories) in a reaction volume of 15 µL with 25 ng of cDNA template, 67 nM of each primer (Tab. 11), and 1x iQ SYBR Green Supermix (Bio-Rad Labratories, Hercules, CA 94547, USA). Guanylate kinase and formate tetrahydrofolate ligase were used as housekeeping gene and non-template controls were included. The reaction conditions were 95 °C for 3 min, followed by 40 cycles of 95 °C for 15 s, 55 °C for 15 s and 72 °C for 30 s. A melting-curve analysis was performed immediately after completion of the RT PCR (38 cycles of 58 °C to 95 °C at 1 °C/s), for detection of primer dimerisation or other artifacts of amplification.

mRNA for all heterologous genes could successfully be detected showing that the genes are expressed. The signal for all genes was on a similar level.

Tab. 11: Oligonucleotides for qRT-PCR

Target	Oligonucleotide Name	DNA Sequence (5` to 3`)	SEQ_ID NO.
Guanylate kinase	GnK-F	TCAGGACCTTCTGGAACTGG	131
	GnK-R	ACCTCCCCTTTTCTTGGAGA	132
Formate tetrahydrofolate ligase	FoT4L-F	CAGGTTTCGGTGCTGACCTA	133
	FoT4L-R	AACTCCGCCGTTGTATTTCA	134
Thiolase	thlA-RT-F	TTGATGAAATGATCACTGACGGATT	123
	thlA-RT-R	GAAATGTTCCATCTCTCAGCTATGT	124
3-hydroxybutyryl-CoA	hdb-RT-F	CATCACTTTCAATAACAGAAGTGGC	125

dehydrogenase	hbd-RT-R	TACCTCTACAAGCTTCATAACAGGA	126
Butyryl-CoA dehydrogenase	bcd-RT-F	AAAATGGGTCAGTATGGTATGATGG	127
	bcd-RT-R	TGTAGTACCGCAAACCTTTGATAAT	128
Electron Transfer Flavoprotein A	etfA-RT-F	CAAGTTTACTTGGTGGAACAATAGC	129
	etfA-RT-R	GAGTTGGTCTTACAGTTTTACCAGT	130
Bifunctional butanol/ butyraldehyde dehydrogenase (Seq. ID 39)	adhE-RT-F	CGGCTGCTCAAAAGAAATTTTCTAGC	137
	adhE-RT-R	CCAGAACTCCGCAGGTCTTTTCACCC	138
Butyraldehyde dehydrogenase (Seq. ID 41)	Bld1-RT-F	GGCAGTAGAAGAAAGCGGAATGG	139
	Bld1-RT-R	AAAGCCTGCATCTCTCTCTAAAACTCC	140
Butyraldehyde dehydrogenase (Seq. ID 45)	Bld2-RT-F	TAATGATTTGCTCTCCATCCAAGAATCC	141
	Bld2-RT-R	TCCGATTTCTTCCGCCATACG	142
Butanol Dehydrogenase (Seq. ID 53)	BDH1-RT-F	AGCTGTAGTAGTTGTTGGAGGAGGATCC	143
	BDH1-RT-R	CACAGACGGATCTGGTTCAACACC	144
Butanol Dehydrogenase (Seq. ID 57)	BDH2-RT-F	GAATCTATTCAACTTTTAGAGCAAGTCACTGG	145
	BDH2-RT-R	CAACGGAACTTATTCCAGCTTTGC	146
Phosphate acetyl/butyryl transferase (Seq. ID 59)	Pta-RT-F	GATGCTTTTTATGAATTGAGAAAGAAGAAGG	147
	Pta-RT-R	TGAAACCAATCCATCTGCATCTCC	148
Acetate/butyrate kinase (Seq. ID 61)	Ack-RT-F	TGCAAGATGAAAGTGTTGTAGCAAAGG	149
	Ack-RT-R	ACTTTGTGGTCTTCCATTGGTTGC	150
Aldehyde:ferredoxin oxidoreductase (Seq. ID 63)	AOR1-RT-F	CTTCAACAGGAAACAGATTCGAGAGC	151
	AOR1-RT-R	CCAACACCACCACGTCCTGC	152
Aldehyde:ferredoxin oxidoreductase (Seq. ID 65)	AOR2-RT-F	GGTTGGGATATGATAATAGTAGAGGATAAGGC	153
	AOR2-RT-R	GTAACTTTTCCCCAAAGCTGTGACG	154

The invention has been described herein, with reference to certain preferred embodiments, in order to enable the reader to practice the invention without undue experimentation. However, a person having ordinary skill in the art will readily recognise that many of the components and parameters may be varied or modified to a certain extent or substituted for known equivalents without departing from the scope of the invention. It should be appreciated that such modifications and equivalents are herein incorporated as if individually set forth. Titles, headings, or the like are provided to enhance the reader's comprehension of this document, and should not be read as limiting the scope of the present invention.

The entire disclosures of all applications, patents and publications, cited above and below, if any, are hereby incorporated by reference. However, the reference to any applications, patents and publications in this specification is not, and should not be taken as, an acknowledgment or any form of suggestion that they constitute valid prior art or form part of the common general knowledge in any country in the world.

Throughout this specification and any claims which follow, unless the context requires otherwise, the words "comprise", "comprising" and the like, are to be construed in an inclusive sense as opposed to an exclusive sense, that is to say, in the sense of "including, but not limited to".

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CLAIMS:

1. An acetogenic recombinant microorganism which comprises at least one exogenous nucleic acid encoding (a) an electron transport flavoprotein and (b) at least one enzyme selected from the group consisting of Thiolase, 3-hydroxybutyryl-CoA dehydrogenase, Crotonase/crotonyl-CoA hydratase, Butyryl-CoA dehydrogenase, Phosphotransbutyrylase, butyrate kinase and ferredoxin dependent aldehyde oxidoreductase; and which does not include an exogenous nucleic acid encoding a bifunctional butyraldehyde/butanol dehydrogenase; and produces 1-butanol as the main fermentation product during fermentation of a gaseous substrate comprising carbon monoxide wherein the recombinant microorganism is selected from the group consisting of: *Clostridium autoethanogenum, Clostridium ljungdahlii, Clostridium ragsdalei, Clostridium carboxidivorans, Clostridium drakei, Clostridium scatalogenes, Clostridium aceticum, Clostridium formicoaceticum, Clostridium coskatii.*
2. The acetogenic recombinant microorganism of claim **1**, wherein the microorganism is capable of producing 1-butanol as the major product by fermentation from a gaseous substrate comprising CO at a concentration of greater than lmM or 0.075 grams per liter of fermentation broth.
3. The acetogenic recombinant microorganism of claim **1 or 2**, wherein the microorganism comprises one exogenous nucleic acid encoding: Thiolase, 3-hydroxybutyryl-CoA dehydrogenase, Crotonase, and Butyryl-CoA dehydrogenase.
4. The acetogenic recombinant microorganism of claim **1 or 2**, wherein the at least one electron transport flavoprotein is selected from the group consisting of Electron Transfer Flavoprotein A, and Electron Transfer Flavoprotein B, and both Electron Transfer Flavoproteins A and B.
5. The acetogenic recombinant microorganism of claim **3**, wherein the acetogenic recombinant microorganism further comprises at least one exogenous nucleic acid encoding at least one enzyme selected from the group consisting of phosphotransbutyrylase, butyrate kinase, and ferredoxin dependent aldehyde oxidoreductase.

6. The acetogenic recombinant microorganism of any one of claims **1 to 5**, wherein the microorganism is *Clostridium autoethanogenum* DSM23693.

7. A recombinant microorganism having the defining characteristics of the_microorganism deposited at the DSMZ under the accession number DSM24138.

8. A method for the production of 1-butanol by microbial fermentation of a gaseous substrate comprising CO using the recombinant microorganism of any one of claims 1 to 7.

9. The method of Claim **8** where the gaseous substrate is a steel mill waste gas stream or a syngas stream.

10. The method of claim **8 or 9** where at least one of 1-butanol and a precursor of 1-butanol is produced in a yield from 0.075 grams per litre of fermentation broth (g/l) to 20g/l.

11. The method of any one of claims **8** to **10** where the gaseous substrate comprises at least 20% to 100% CO by volume.

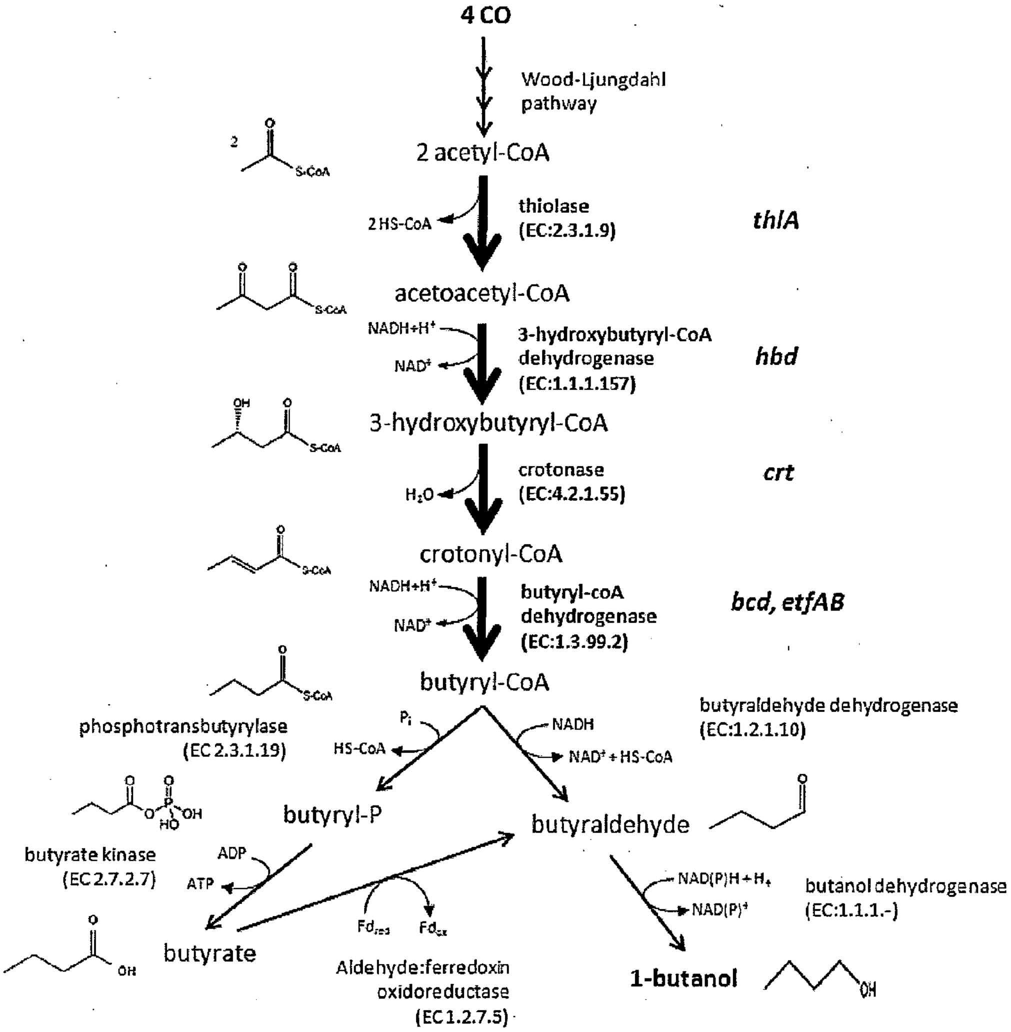
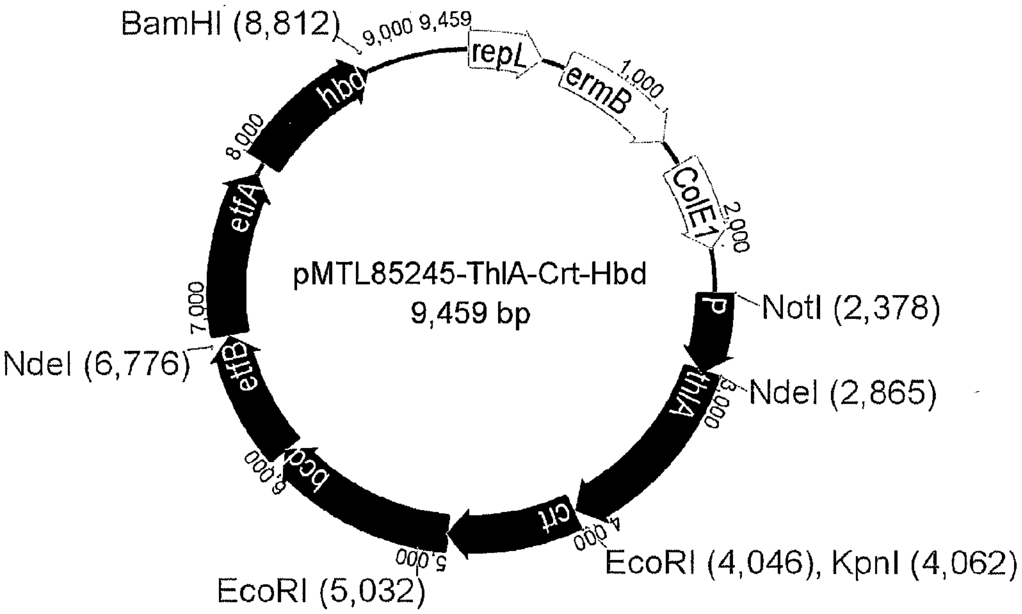

4 CO
Wood-Ljungdahl pathway
2 acetyl-CoA
thiolase (EC:2.3.1.9)
2 HS-CoA
thlA
acetoacetyl-CoA
NADH+H+
NAD+
3-hydroxybutyryl-CoA dehydrogenase (EC:1.1.1.157)
hbd
3-hydroxybutyryl-CoA
crotonase (EC:4.2.1.55)
H2O
crt
crotonyl-CoA
butyryl-coA dehydrogenase (EC:1.3.99.2)
bcd, etfAB
butyryl-CoA
phosphotransbutyrylase (EC 2.3.1.19)
Pi
HS-CoA
NADH
NAD+ + HS-CoA
butyraldehyde dehydrogenase (EC:1.2.1.10)
butyryl-P
butyraldehyde
butyrate kinase (EC 2.7.2.7)
ADP
ATP
Fdred
Fdox
NAD(P)H+H+
NAD(P)+
butanol dehydrogenase (EC:1.1.1.-)
butyrate
Aldehyde:ferredoxin oxidoreductase (EC 1.2.7.5)
1-butanol
S-CoA
OH

Figure 1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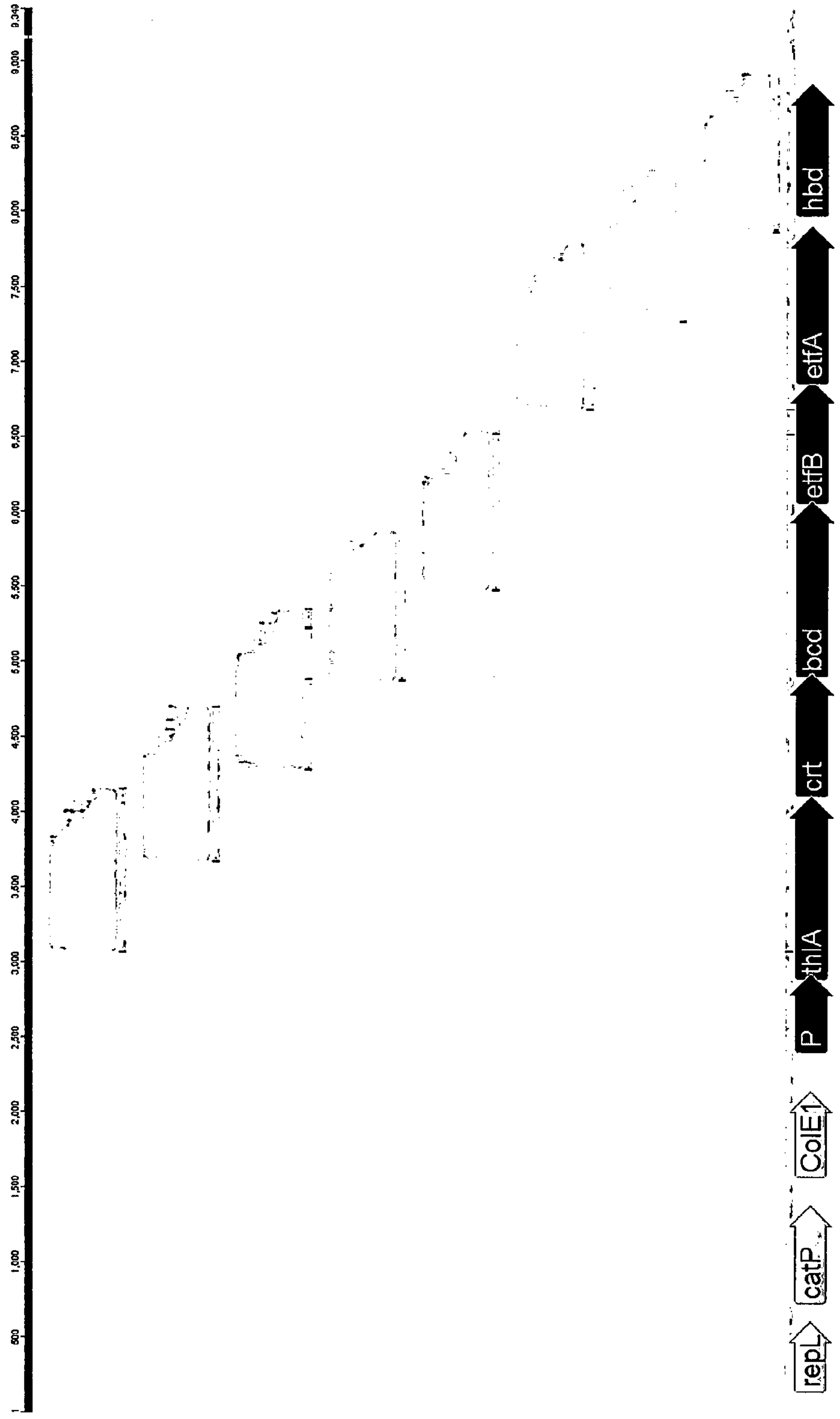
9,459
repL
ermB
1,000
ColE1
2,000
NotI (2,378)
P
NdeI (2,865)
thlA
3,000
crt
4,000
EcoRI (4,046), KpnI (4,062)
5,000
EcoRI (5,032)
bcd
6,000
etfB
NdeI (6,776)
7,000
etfA
8,000
hbd
pMTL85245-ThlA-Crt-Hbd
9,459 bp

Figure 2

Figure 3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7,000
7,500
8,000
8,500
9,000
9,349
repL
catP
ColE1
P
thlA
crt
bcd
etfB
etfA
hbd

Figure 4a

```
     1                 10                            20                         30
CAU
CLJ
CRA  A T G T T T C C C T G T A A T G C A T A T A T T C A G C A C
DMT  A T G T T T C C G T G C A A T G C C T A T A T C G A A T A T
                       40                            50                         60
CAU
CLJ                          A T G A A C A G T T T T A T T G A A
CRA  G G A G A T A G G A A T A T G A A T A A T T T T A T T G A A
DMT  G G T G A T A A A A A T A T G A A C A G C T T T A T C G A A
                       70                            80                         90
CAU
CLJ  G A T G T T G A A C A A A T T T A C A A T T T T A T T A A A
CRA  G A T A T T G A A G A A A T T T A T A A T T T T A T T A A A
DMT  G A T G T G G A A C A G A T C T A C A A C T T C A T T A A A
                      100                           110                        120
CAU                                                  A T G C A T
CLJ  A A A A A T A T A G A T G T A G A A G A G A A G A T G C A T
CRA  A A A A A T A C A G A T G T A G A A G A G A A T A T T C A T
DMT  A A G A A C A T T G A T G T G G A A G A A A A G A T G C A T
                      130                           140                        150
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CLJ  T T T A T A G A A A C T T A T A A G C A A A A A T C T A A T
CRA  T T T A T A G A A A C T T A T A G G C A A A G A C T T A A T
DMT  T T C A T T G A A A C C T A T A A A C A G A A A A G C A A C
                      160                           170                        180
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CLJ  A T G A A G A A A G A A A T T A G C T T T T C A G A A G A A
CRA  A T G A A G A A A G A A A T T A G C T T T T C A G A A G A A
DMT  A T G A A G A A A G A G A T T A G C T T T A G C G A A G A A
                      190                           200                        210
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CLJ  T A C T A T A A A C A G A A A A T T A T G A A T G G A A A A
CRA  T A C T A T A A A C A G A A A A T T A T G A A T G G A A A A
DMT  T A C T A T A A A C A G A A G A T T A T G A A C G G C A A A
                      220                           230                        240
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CLJ  A A T G G A G T A G T G T A T A C T C C T C C G G A A A T G
CRA  A A C G G A G T A G T G T A T A C T C C T C C G G A A A T G
DMT  A A T G G C G T T G T G T A C A C C C C G C C G G A A A T G
                      250                           260                        270
CAU  G C A G C A T T T A T G G T T A A A A A C T T G A T A A A T
CLJ  G C A G C A T T T A T G G T T A A A A A C T T G A T A A A T
CRA  G C A G C A T T T A T G G T T A A A A A C T T G A T A A A T
DMT  G C G G C C T T T A T G G T T A A A A A T C T G A T C A A C
                      280                           290                        300
CAU  G T C A A T G A T G T A A T T G G A A A T C C A T T T A T A
CLJ  G T C A A T G A T G T A A T T G G A A A T C C A T T T A T A
CRA  G T C A A T G A T G T A A T T G A A A A T C C A T T T A T A
DMT  G T T A A C G A T G T T A T T G G C A A T C C G T T T A T T
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Figure 4a (cont.)

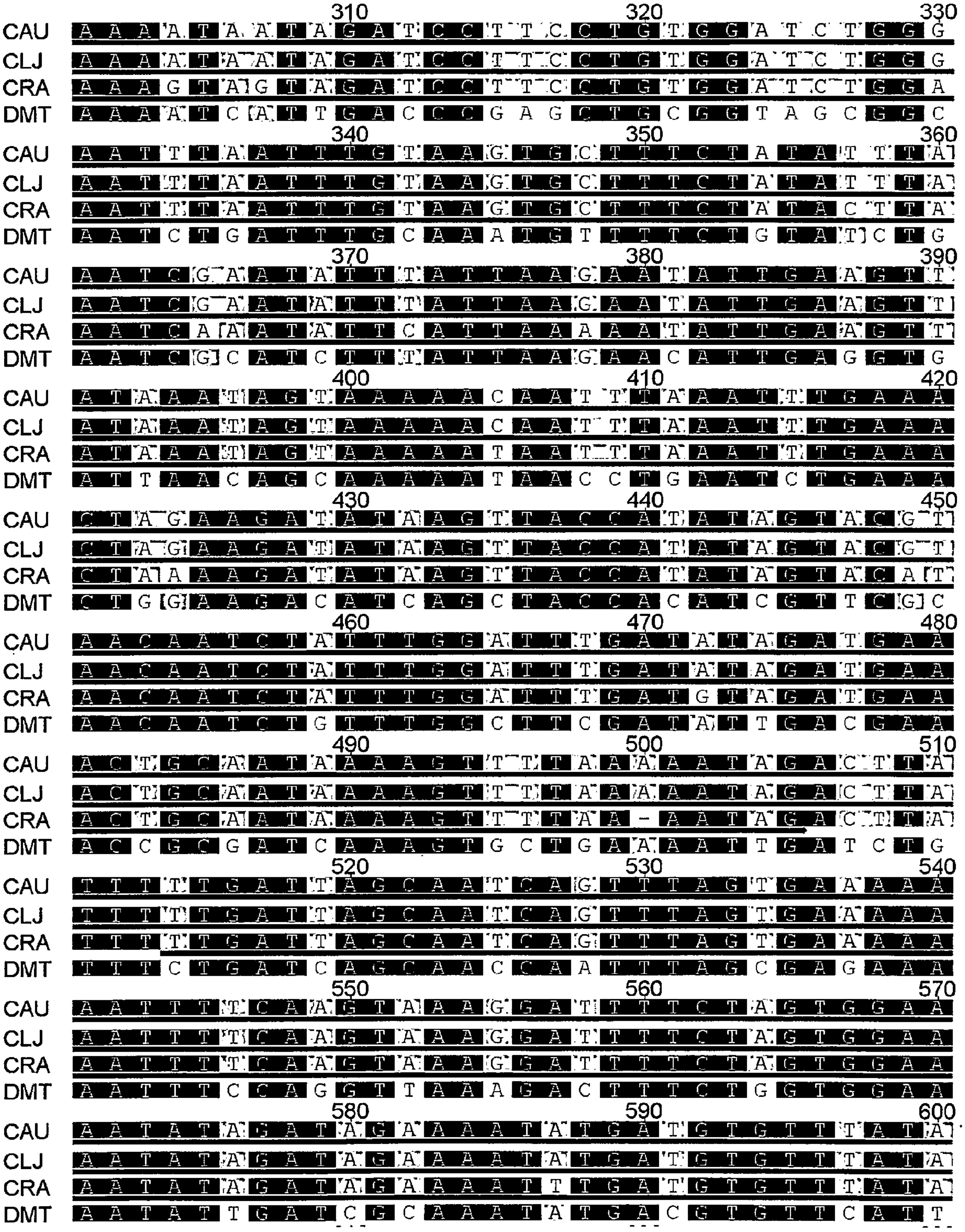

Figure 4a (cont.)

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CRA  G G A A A T C C C C C A T A T A T A G G A C A T A A A T C T
DMT  G G T A A T C C G C C G T A T A T C G G T C A C A A A A G C
                              640                                     650                                     660
CAU  G T A G A T T C T A G T T A T T C A T A T G T T T T A A G A
CLJ  G T A G A T T C T A G T T A T T C A T A T G T T T T A A G A
CRA  G T A G A T T C C A G T T A T T C A T A T A T T T T A A G G
DMT  G T G G A C A G C A G C T A C A G C T A C G T G C T G C G C
                              670                                     680                                     690
CAU  A A A A T A T A T G G A A G T A T A T A T A G A G A C A A A
CLJ  A A A A T A T A T G G A A G T A T A T A T A G A G A C A A A
CRA  A A A A T A T A T G G A A G T A T A T A T A G A G A T A A A
DMT  A A A A T C T A C G G C A G C A T C T A C C G C G A C A A A
                              700                                     710                                     720
CAU  G G A G A C A T A T C C T A C T G T T T T T T T C A A A A A
CLJ  G G A G A C A T A T C C T A C T G T T T T T T T C A A A A A
CRA  G G A G A C A T A T C T T A C T G T T T T T T T C A A A A A
DMT  G G C G A T A T C A G C T A T T G T T T C T T T C A G A A G
                              730                                     740                                     750
CAU  T C A T T A A A G T G T T T A A A G G A G G G A G G A A A A
CLJ  T C A T T A A A G T G T T T A A A G G A G G G A G G A A A A
CRA  T C A T T A A A G T G C T T A A A A G A G G G A G G A A A A
DMT  A G C C T G A A A T G T C T G A A G G A A G G T G G C A A A
                              760                                     770                                     780
CAU  C T G G T T T T T G T T A C T T C T A G G T A T T T T T G T
CLJ  C T G G T T T T T G T T A C T T C T A G G T A T T T T T G T
CRA  T T A C T T T T T G T T A C C T C C A G A T A T T T T T G C
DMT  C T G G T G T T T G T G A C C A G C C G C T A C T T C T G C
                              790                                     800                                     810
CAU  G A A T C T T G C A G C G G A A A A G A A C T T A G A A A G
CLJ  G A A T C T T G C A G C G G A A A A G A A C T T A G A A A G
CRA  G A A T C T T G C A G C G G A A A A G A A C T T A G A A A G
DMT  G A G A G C T G C A G C G G T A A A G A A C T G C G T A A A
                              820                                     830                                     840
CAU  T T T T T A A T T G A A A A T A C C T C T A T T T A T A A A
CLJ  T T T T T A A T T G A A A A T A C C T C T A T T T A T A A A
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                              850                                     860                                     870
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Figure 4a (cont.)

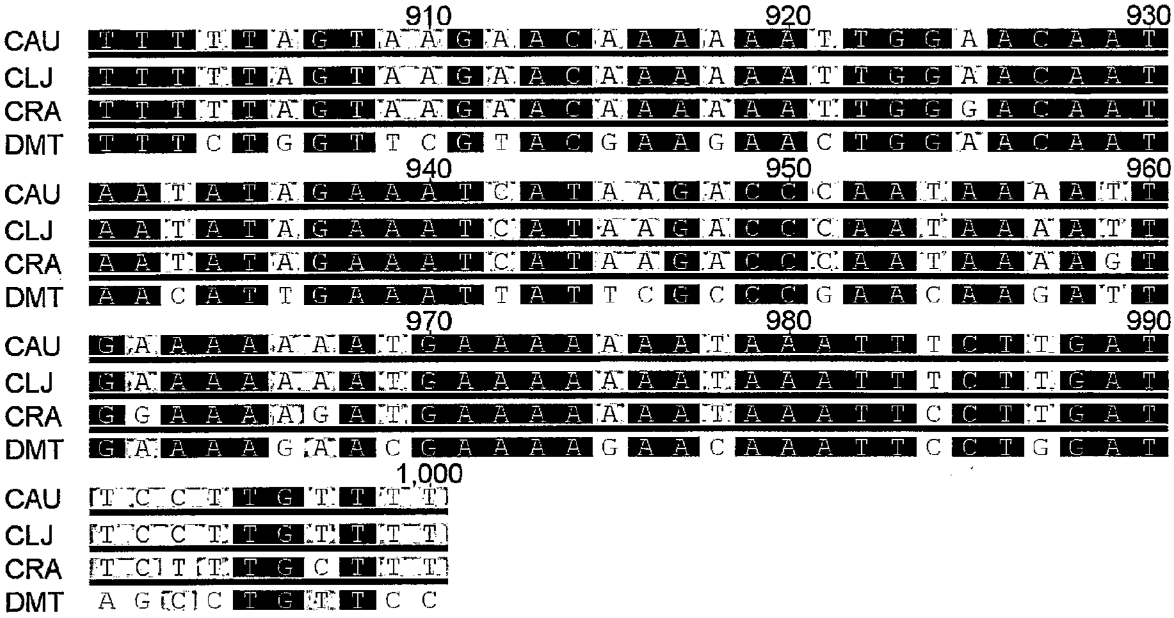
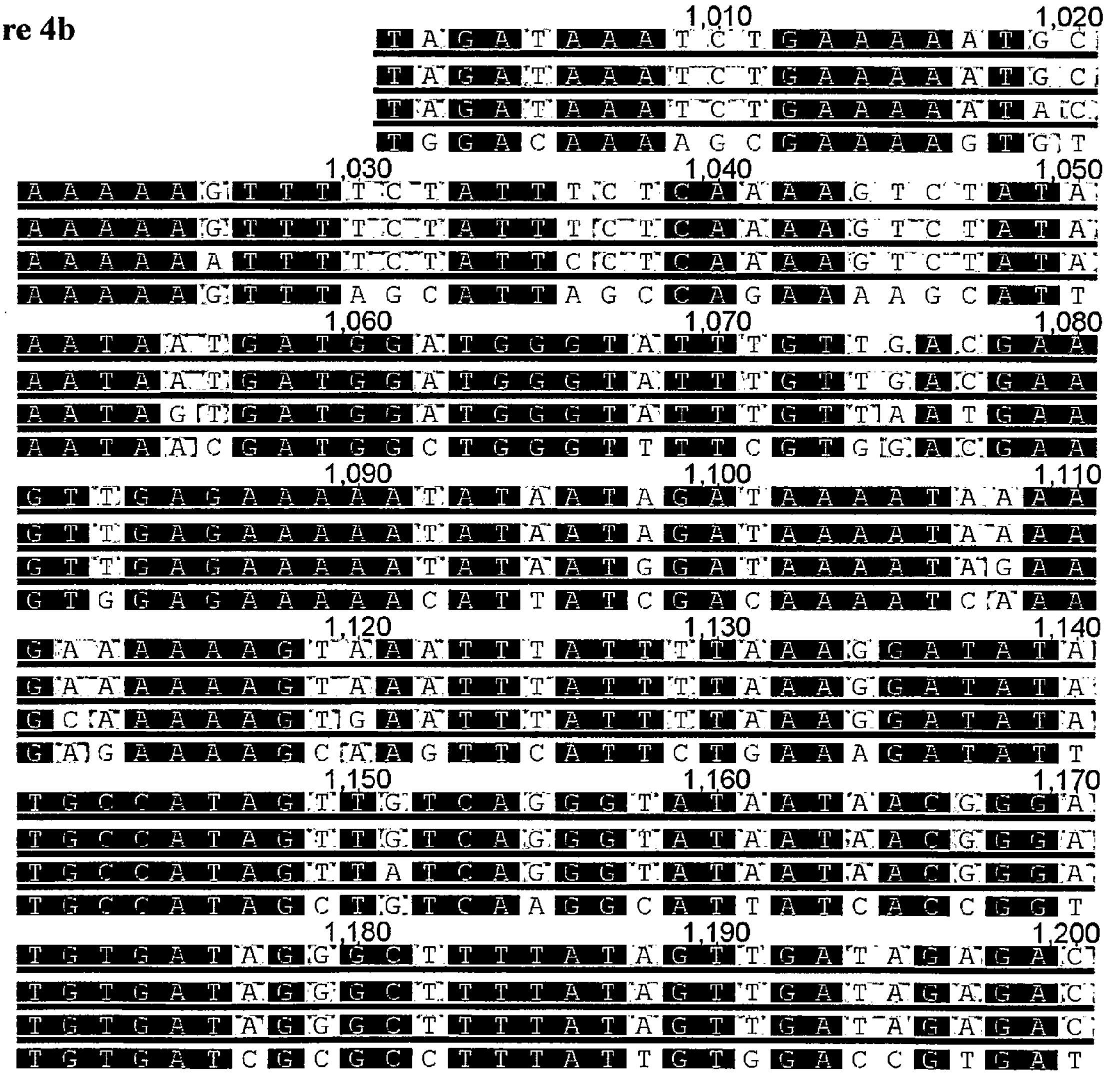


Figure 4b



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                            TGGACAAAAGCGAAAAGTGT
              1,030               1,040          1,050
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CLJ  AAAAAGTTTTCTATTTCTCAAAAGTCTATA
CRA  AAAAAATTTTCTATTCCTCAAAAGTCTATA
DMT  AAAAAGTTTAGCATTAGCCAGAAAAGCATT
              1,060               1,070          1,080
CAU  AATAATGATGGATGGGTATTTGTTGACGAA
CLJ  AATAATGATGGATGGGTATTTGTTGACGAA
CRA  AATAGTGATGGATGGGTATTTGTTAATGAA
DMT  AATAACGATGGCTGGGTTTTCGTGGACGAA
              1,090               1,100          1,110
CAU  GTTGAGAAAAATATAATAGATAAAATAAAA
CLJ  GTTGAGAAAAATATAATAGATAAAATAAAA
CRA  GTTGAGAAAAATATAATGGATAAAATAGAA
DMT  GTGGAGAAAAACATTATCGACAAAATCAAA
              1,120               1,130          1,140
CAU  GAAAAAAGTAAATTTATTTTAAAGGATATA
CLJ  GAAAAAAGTAAATTTATTTTAAAGGATATA
CRA  GCAAAAAGTGAATTTATTTTAAAGGATATA
DMT  GAGAAAAGCAAGTTCATTCTGAAAGATATT
              1,150               1,160          1,170
CAU  TGCCATAGTTGTCAGGGTATAATAACGGGA
CLJ  TGCCATAGTTGTCAGGGTATAATAACGGGA
CRA  TGCCATAGTTATCAGGGTATAATAACGGGA
DMT  TGCCATAGCTGTCAAGGCATTATCACCGGT
              1,180               1,190          1,200
CAU  TGTGATAGGGCTTTTATAGTTGATAGAGAC
CLJ  TGTGATAGGGCTTTTATAGTTGATAGAGAC
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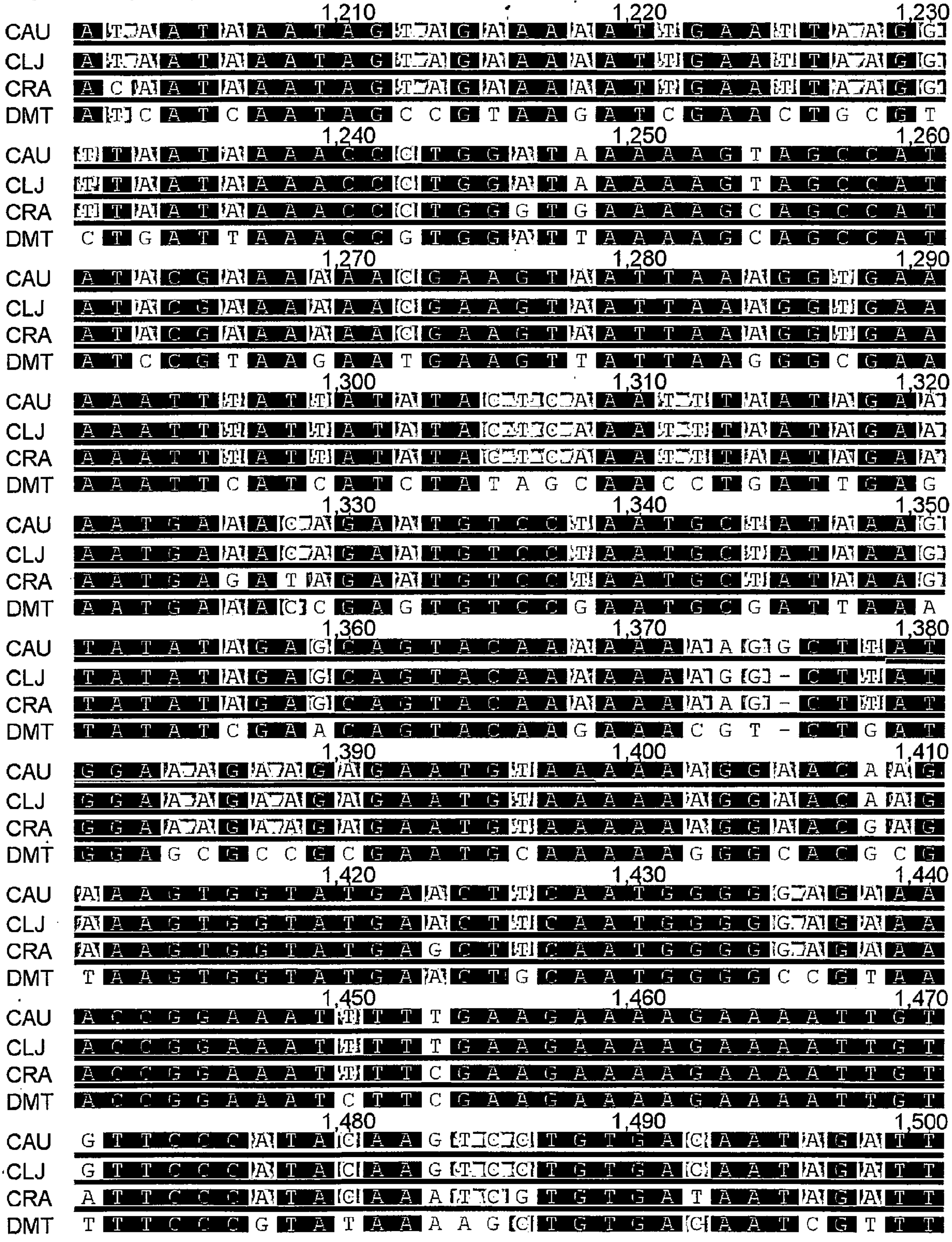
Figure 4b (cont.)



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DMT  ATCATCAATAGCCGTAAGATCGAACTGCGT
                          1,240          1,250          1,260
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CLJ  TTAATAAAACCCTGGATAAAAAGTAGCCAT
CRA  TTAATAAAACCCTGGGTGAAAAGCAGCCAT
DMT  CTGATTAAACCGTGGATTAAAAGCAGCCAT
                          1,270          1,280          1,290
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CLJ  ATACGAAAAAACGAAGTAATTAAAGGTGAA
CRA  ATACGAAAAAACGAAGTAATTAAAGGTGAA
DMT  ATCCGTAAGAATGAAGTTATTAAGGGCGAA
                          1,300          1,310          1,320
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CLJ  AAATTTATTATATACTCAAATTTAATAGAA
CRA  AAATTTATTATATACTCAAATTTAATAGAA
DMT  AAATTCATCATCTATAGCAACCTGATTGAG
                          1,330          1,340          1,350
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CLJ  AATGAAACAGAATGTCCTAATGCTATAAAG
CRA  AATGAGATAGAATGTCCTAATGCTATAAAG
DMT  AATGAAACCGAGTGTCCGAATGCGATTAAA
                          1,360          1,370          1,380
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CLJ  TATATAGAGCAGTACAAAAAAAGG-CTTAT
CRA  TATATAGAGCAGTACAAAAAAAAG-CTTAT
DMT  TATATCGAACAGTACAAGAAACGT-CTGAT
                          1,390          1,400          1,410
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CLJ  GGAAAGAAGAGAATGTAAAAAAGGAACAAG
CRA  GGAAAGAAGAGAATGTAAAAAAGGAACGAG
DMT  GGAGCGCCGCGAATGCAAAAAGGGCACGCG
                          1,420          1,430          1,440
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DMT  TAAGTGGTATGAACTGCAATGGGGCCGTAA
                          1,450          1,460          1,470
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CLJ  ACCGGAAATTTTTGAAGAAAAGAAAATTGT
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                          1,480          1,490          1,500
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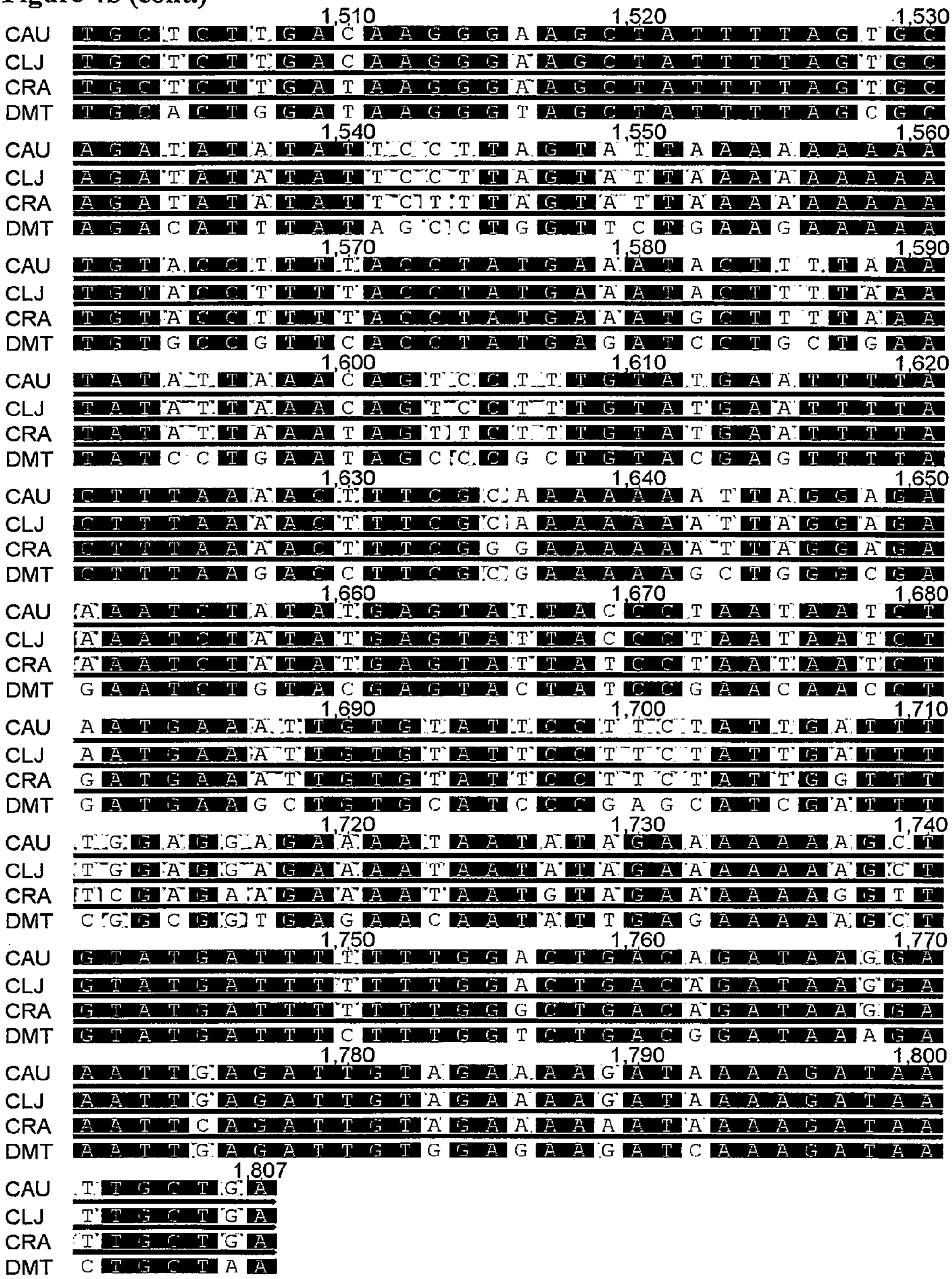
Figure 4b (cont.)



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CRA  T G C T C T T G A T A A G G G A A G C T A T T T T A G T G C
DMT  T G C A C T G G A T A A G G G T A G C T A T T T T A G C G C
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CLJ  A G A T A T A T A T T C C T T A G T A T T A A A A A A A A A
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DMT  A G A C A T T T A T A G C C T G G T T C T G A A G A A A A A
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CRA  C T T T A A A A C T T T C G G G A A A A A A T T A G G A G A
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CRA  A A A T C T A T A T G A G T A T T A T C C T A A T A A T C T
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CLJ  A A T G A A A T T G T G T A T T C C T T C T A T T G A T T T
CRA  G A T G A A A T T G T G T A T T C C T T C T A T T G G T T T
DMT  G A T G A A G C T G T G C A T C C C G A G C A T C G A T T T
                             1,720                          1,730                         1,740
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CRA  T C G A G A A G A A A A T A A T G T A G A A A A A A G G T T
DMT  C G G C G G T G A G A A C A A T A T T G A G A A A A A G C T
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CLJ  G T A T G A T T T T T T T G G A C T G A C A G A T A A G G A
CRA  G T A T G A T T T T T T T G G G C T G A C A G A T A A G G A
DMT  G T A T G A T T T C T T T G G T C T G A C G G A T A A A G A
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CLJ  A A T T G A G A T T G T A G A A A A G A T A A A A G A T A A
CRA  A A T T C A G A T T G T A G A A A A A A T A A A A G A T A A
DMT  A A T T G A G A T T G T G G A G A A G A T C A A A G A T A A
                   1,807
CAU  T T G C T G A
CLJ  T T G C T G A
CRA  T T G C T G A
DMT  C T G C T A A
```

Figure 4c


1
100
200
300
400
500
600
700
800
900
1,000
1,100
1,200
1,300
1,400
1,500
1,600
1,700
1,800
1,900
2,016
Identity
C. autoethanogenum
C. ljungdahlii
C. ragsdalei
orf1
orf2
CLJU_c33980
orf1
orf2

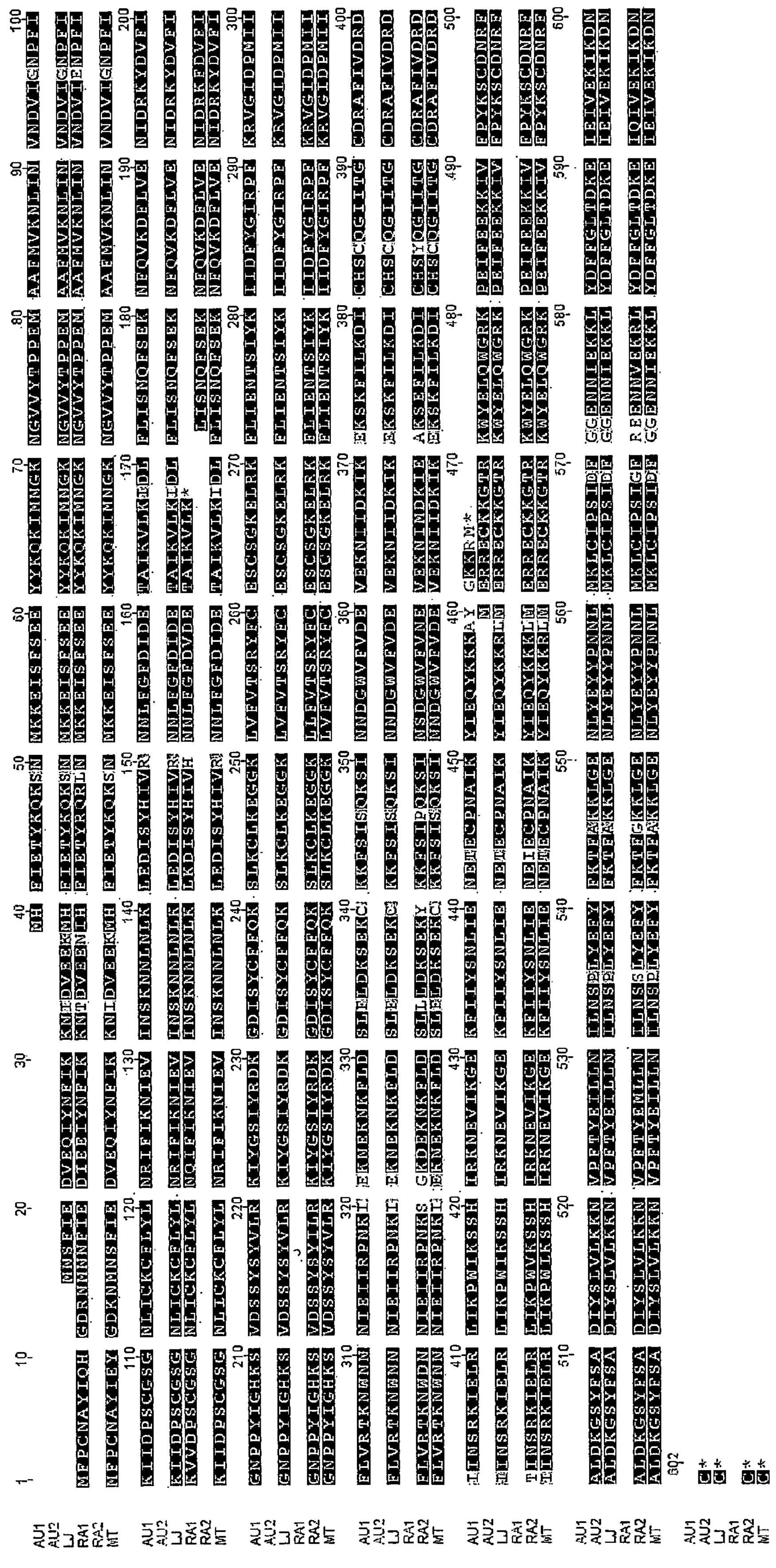

Figure 4d

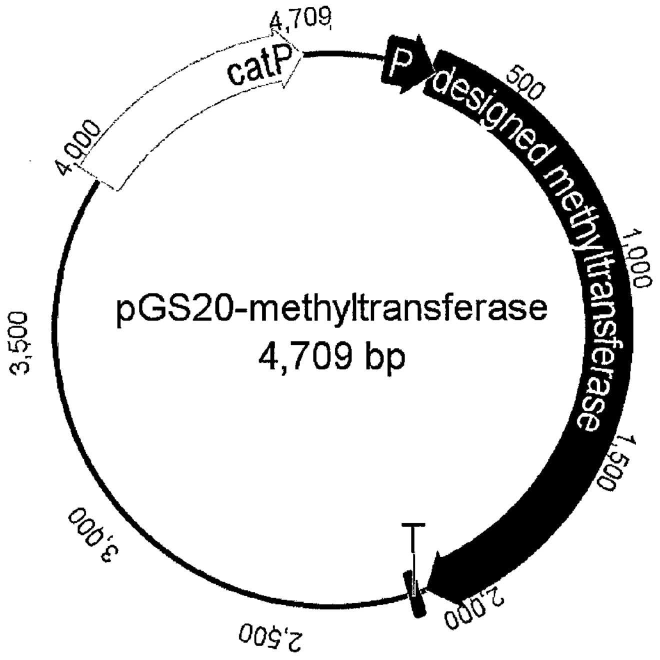
4,709
catP
P
designed methyltransferase
500
1,000
1,500
2,000
2,500
3,000
3,500
4,000
T
pGS20-methyltransferase
4,709 bp

Figure 5

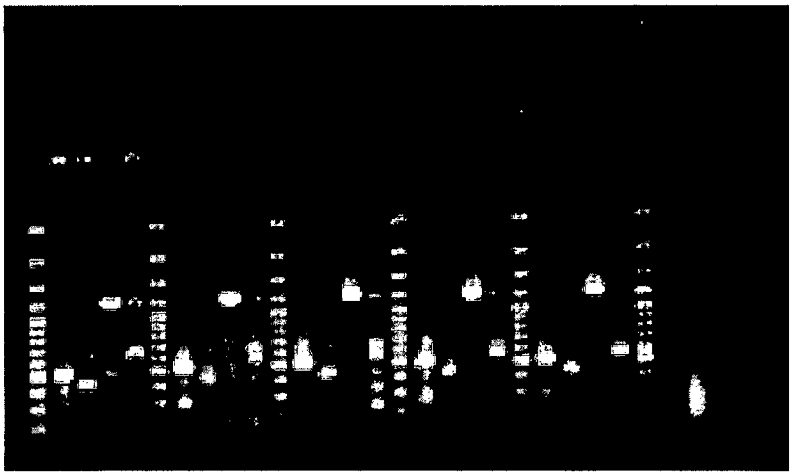

Figure 6

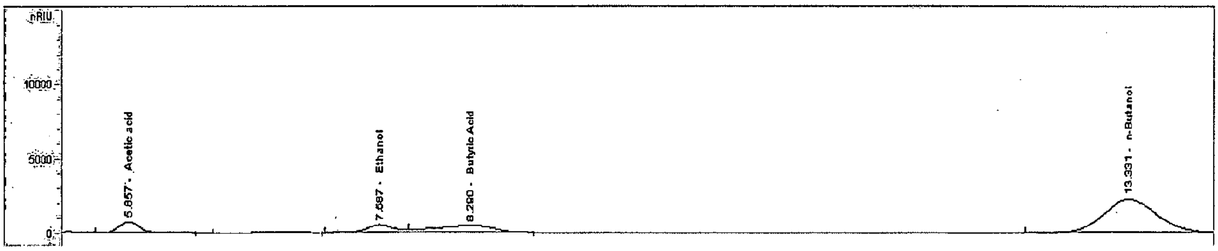

Figure 7

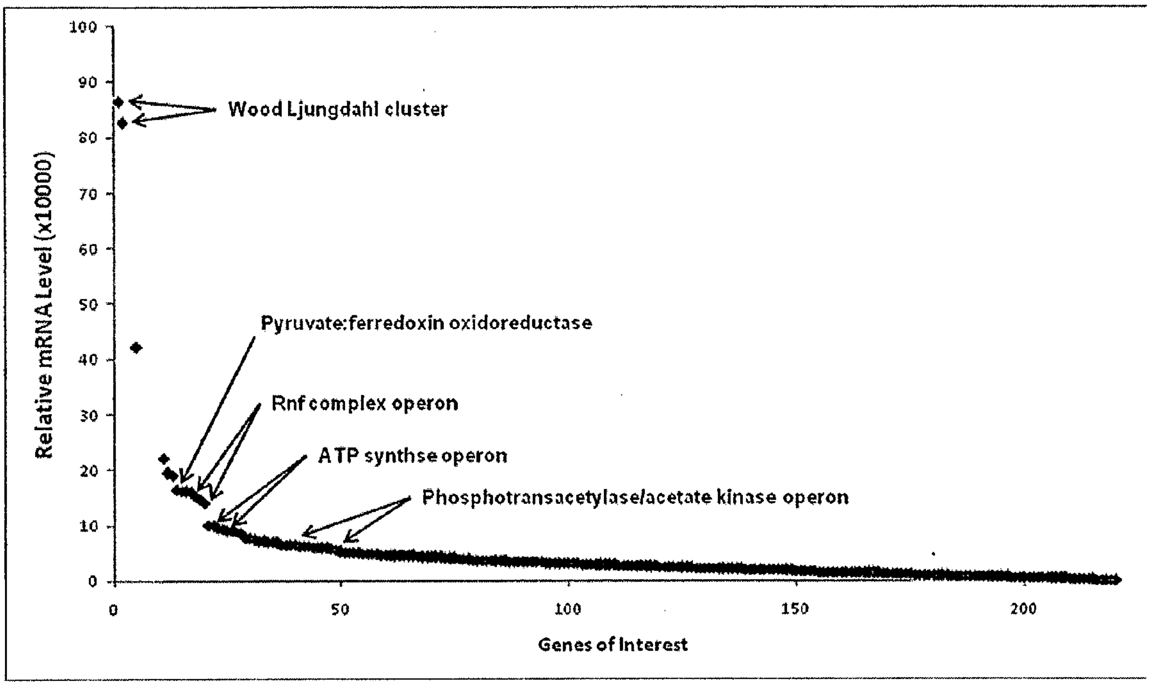
Relative mRNA Level (x10000)
100
90
80
70
60
50
40
30
20
10
0
Wood Ljungdahl cluster
Pyruvate:ferredoxin oxidoreductase
Rnf complex operon
ATP synthse operon
Phosphotransacetylase/acetate kinase operon
0
50
100
150
200
Genes of Interest

Figure 8

Seq. ID 1: *Clostridium acetobutylicum* ATCC824 thiolase gene (*thlA*):

ATGAAAGAAGTTGTAATAGCTAGTGCAGTAAGAACAGCGATTGGATCTTATGGAAAGTCTCTTAAGGATGTACCAGCAGTAG
ATTTAGGAGCTACAGCTATAAAGGAAGCAGTTAAAAAAGCAGGAATAAAACCAGAGGATGTTAATGAAGTCATTTTAGGAA
ATGTTCTTCAAGCAGGTTTAGGACAGAATCCAGCAAGACAGGCATCTTTTAAAGCAGGATTACCAGTTGAAATTCCAGCTATG
ACTATTAATAAGGTTTGTGGTTCAGGACTTAGAACAGTTAGCTTAGCAGCACAAATTATAAAAGCAGGAGATGCTGACGTAA
TAATAGCAGGTGGTATGGAAAATATGTCTAGAGCTCCTTACTTAGCGAATAACGCTAGATGGGGATATAGAATGGGAAACGC
TAAATTTGTTGATGAAATGATCACTGACGGATTGTGGGATGCATTTAATGATTACCACATGGGAATAACAGCAGAAAACATA
GCTGAGAGATGGAACATTTCAAGAGAAGAACAAGATGAGTTTGCTCTTGCATCACAAAAAAAAGCTGAAGAAGCTATAAAAT
CAGGTCAATTTAAAGATGAAATAGTTCCTGTAGTAATTAAAGGCAGAAAGGGAGAAACTGTAGTTGATACAGATGAGCACCC
TAGATTTGGATCAACTATAGAAGGACTTGCAAAATTAAAACCTGCCTTCAAAAAAGATGGAACAGTTACAGCTGGTAATGCAT
CAGGATTAAATGACTGTGCAGCAGTACTTGTAATCATGAGTGCAGAAAAAGCTAAAGAGCTTGGAGTAAAACCACTTGCTAA
GATAGTTTCTTATGGTTCAGCAGGAGTTGACCCAGCAATAATGGGATATGGACCTTTCTATGCAACAAAAGCAGCTATTGAAA
AAGCAGGTTGGACAGTTGATGAATTAGATTTAATAGAATCAAATGAAGCTTTTGCAGCTCAAAGTTTAGCAGTAGCAAAAGA
TTTAAAATTTGATATGAATAAAGTAAATGTAAATGGAGGAGCTATTGCCCTTGGTCATCCAATTGGAGCATCAGGTGCAAGA
ATACTCGTTACTCTTGTACACGCAATGCAAAAAAGAGATGCAAAAAAAGGCTTAGCAACTTTATGTATAGGTGGCGGACAAG
GAACAGCAATATTGCTAGAAAAGTGCTAG

Seq. ID 2: *Clostridium acetobutylicum* ATCC824 3-hydroxybutyryl-CoA dehydrogenase gene (*hbd*):
ATGAAAAAGGTATGTGTTATAGGTGCAGGTACTATGGGTTCAGGAATTGCTCAGGCATTTGCAGCTAAAGGATTTGAAGTAG
TATTAAGAGATATTAAAGATGAATTTGTTGATAGAGGATTAGATTTTATCAATAAAAATCTTTCTAAATTAGTTAAAAAAGGA
AAGATAGAAGAAGCTACTAAAGTTGAAATCTTAACTAGAATTTCCGGAACAGTTGACCTTAATATGGCAGCTGATTGCGATTT
AGTTATAGAAGCAGCTGTTGAAAGAATGGATATTAAAAAGCAGATTTTTGCTGACTTAGACAATATATGCAAGCCAGAAACA
ATTCTTGCATCAAATACATCATCACTTTCAATAACAGAAGTGGCATCAGCAACTAAAAGACCTGATAAGGTTATAGGTATGCA
TTTCTTTAATCCAGCTCCTGTTATGAAGCTTGTAGAGGTAATAAGAGGAATAGCTACATCACAAGAAACTTTTGATGCAGTTA
AAGAGACATCTATAGCAATAGGAAAAGATCCTGTAGAAGTAGCAGAAGCACCAGGATTTGTTGTAAATAGAATATTAATACC
AATGATTAATGAAGCAGTTGGTATATTAGCAGAAGGAATAGCTTCAGTAGAAGACATAGATAAAGCTATGAAACTTGGAGCT
AATCACCCAATGGGACCATTAGAATTAGGTGATTTTATAGGTCTTGATATATGTCTTGCTATAATGGATGTTTTATACTCAGAA
ACTGGAGATTCTAAGTATAGACCACATACATTACTTAAGAAGTATGTAAGAGCAGGATGGCTTGGAAGAAAATCAGGAAAA
GGTTTCTACGATTATTCAAAATAA

Seq. ID 3 *Clostridium acetobutylicum* ATCC824 crotonase (*crt*):
ATGGAACTAAACAATGTCATCCTTGAAAAGGAAGGTAAAGTTGCTGTAGTTACCATTAACAGACCTAAAGCATTAAATGCGTT
AAATAGTGATACACTAAAAGAAATGGATTATGTTATAGGTGAAATTGAAAATGATAGCGAAGTACTTGCAGTAATTTTAACTG
GAGCAGGAGAAAAATCATTTGTAGCAGGAGCAGATATTTCTGAGATGAAGGAAATGAATACCATTGAAGGTAGAAAATTCG
GGATACTTGGAAATAAAGTGTTTAGAAGATTAGAACTTCTTGAAAAGCCTGTAATAGCAGCTGTTAATGGTTTTGCTTTAGGA
GGCGGATGCGAAATAGCTATGTCTTGTGATATAAGAATAGCTTCAAGCAACGCAAGATTTGGTCAACCAGAAGTAGGTCTCG
GAATAACACCTGGTTTTGGTGGTACACAAAGACTTTCAAGATTAGTTGGAATGGGCATGGCAAAGCAGCTTATATTTACTGCA
CAAAATATAAAGGCAGATGAAGCATTAAGAATCGGACTTGTAAATAAGGTAGTAGAACCTAGTGAATTAATGAATACAGCAA
AAGAAATTGCAAACAAAATTGTGAGCAATGCTCCAGTAGCTGTTAAGTTAAGCAAACAGGCTATTAATAGAGGAATGCAGTG
TGATATTGATACTGCTTTAGCATTTGAATCAGAAGCATTTGGAGAATGCTTTTCAACAGAGGATCAAAAGGATGCAATGACAG
CTTTCATAGAGAAAAGAAAAATTGAAGGCTTCAAAAATAGATAG

Figure 9

Seq. ID 4: *Clostridium acetobutylicum* ATCC824 butyryl-CoA dehydrogenase (*bcd*):
ATGGATTTTAATTTAACAAGAGAACAAGAATTAGTAAGACAGATGGTTAGAGAATTTGCTGAAAATGAAGTTAAACCTATAG
CAGCAGAAATTGATGAAACAGAAAGATTTCCAATGGAAAATGTAAAGAAAATGGGTCAGTATGGTATGATGGGAATTCCATT
TTCAAAAGAGTATGGTGGCGCAGGTGGAGATGTATTATCTTATATAATCGCCGTTGAGGAATTATCAAAGGTTTGCGGTACT
ACAGGAGTTATTCTTTCAGCACATACATCACTTTGTGCTTCATTAATAAATGAACATGGTACAGAAGAACAAAAACAAAAATA
TTTAGTACCTTTAGCTAAAGGTGAAAAAATAGGTGCTTATGGATTGACTGAGCCAAATGCAGGAACAGATTCTGGAGCACAA
CAAACAGTAGCTGTACTTGAAGGAGATCATTATGTAATTAATGGTTCAAAAATATTCATAACTAATGGAGGAGTTGCAGATAC
TTTTGTTATATTTGCAATGACTGACAGAACTAAAGGAACAAAAGGTATATCAGCATTTATAATAGAAAAAGGCTTCAAAGGTT
TCTCTATTGGTAAAGTTGAACAAAAGCTTGGAATAAGAGCTTCATCAACAACTGAACTTGTATTTGAAGATATGATAGTACCA
GTAGAAAACATGATTGGTAAAGAAGGAAAAGGCTTCCCTATAGCAATGAAAACTCTTGATGGAGGAAGAATTGGTATAGCA
GCTCAAGCTTTAGGTATAGCTGAAGGTGCTTTCAACGAAGCAAGAGCTTACATGAAGGAGAGAAAACAATTTGGAAGAAGC
CTTGACAAATTCCAAGGTCTTGCATGGATGATGGCAGATATGGATGTAGCTATAGAATCAGCTAGATATTTAGTATATAAAGC
AGCATATCTTAAACAAGCAGGACTTCCATACACAGTTGATGCTGCAAGAGCTAAGCTTCATGCTGCAAATGTAGCAATGGAT
GTAACAACTAAGGCAGTACAATTATTTGGTGGATACGGATATACAAAAGATTATCCAGTTGAAAGAATGATGAGAGATGCTA
AGATAACTGAAATATATGAAGGAACTTCAGAAGTTCAGAAATTAGTTATTTCAGGAAAAATTTTTAGATAA

Seq. ID 5: *Clostridium acetobutylicum* ATCC824 electron transfer flavoprotein (*etfA*):
ATGAATAAAGCAGATTACAAGGGCGTATGGGTGTTTGCTGAACAAAGAGACGGAGAATTACAAAAGGTATCATTGGAATTA
TTAGGTAAAGGTAAGGAAATGGCTGAGAAATTAGGCGTTGAATTAACAGCTGTTTTACTTGGACATAATACTGAAAAAATGT
CAAAGGATTTATTATCTCATGGAGCAGATAAGGTTTTAGCAGCAGATAATGAACTTTTAGCACATTTTTCAACAGATGGATAT
GCTAAAGTTATATGTGATTTAGTTAATGAAAGAAAGCCAGAAATATTATTCATAGGAGCTACTTTCATAGGAAGAGATTTAGG
ACCAAGAATAGCAGCAAGACTTTCTACTGGTTTAACTGCTGATTGTACATCACTTGACATAGATGTAGAAAATAGAGATTTAT
TGGCTACAAGACCAGCGTTTGGTGGAAATTTGATAGCTACAATAGTTTGTTCAGACCACAGACCACAAATGGCTACAGTAAG
ACCTGGTGTGTTTGAAAAATTACCTGTTAATGATGCAAATGTTTCTGATGATAAAATAGAAAAAGTTGCAATTAAATTAACAG
CATCAGACATAAGAACAAAAGTTTCAAAAGTTGTTAAGCTTGCTAAAGATATTGCAGATATCGGAGAAGCTAAGGTATTAGTT
GCTGGTGGTAGAGGAGTTGGAAGCAAAGAAAACTTTGAAAAACTTGAAGAGTTAGCAAGTTTACTTGGTGGAACAATAGCC
GCTTCAAGAGCAGCAATAGAAAAAGAATGGGTTGATAAGGACCTTCAAGTAGGTCAAACTGGTAAAACTGTAAGACCAACTC
TTTATATTGCATGTGGTATATCAGGAGCTATCCAGCATTTAGCAGGTATGCAAGATTCAGATTACATAATTGCTATAAATAAA
GATGTAGAAGCCCCAATAATGAAGGTAGCAGATTTGGCTATAGTTGGTGATGTAAATAAAGTTGTACCAGAATTAATAGCTC
AAGTTAAAGCTGCTAATAATTAA

Seq. ID 6: *Clostridium acetobutylicum* ATCC824 electron transfer flavoprotein (*etfB*):
ATGAATATAGTTGTTTGTTTAAAACAAGTTCCAGATACAGCGGAAGTTAGAATAGATCCAGTTAAGGGAACACTTATAAGAG
AAGGAGTTCCATCAATAATAAATCCAGATGATAAAAACGCACTTGAGGAAGCTTTAGTATTAAAAGATAATTATGGTGCACAT
GTAACAGTTATAAGTATGGGACCTCCACAAGCTAAAAATGCTTTAGTAGAAGCTTTGGCTATGGGTGCTGATGAAGCTGTACT
TTTAACAGATAGAGCATTTGGAGGAGCAGATACACTTGCGACTTCACATACAATTGCAGCAGGAATTAAGAAGCTAAAATAT
GATATAGTTTTTGCTGGAAGGCAGGCTATAGATGGAGATACAGCTCAGGTTGGACCAGAAATAGCTGAGCATCTTGGAATAC
CTCAAGTAACTTATGTTGAGAAAGTTGAAGTTGATGGAGATACTTTAAAGATTAGAAAAGCTTGGGAAGATGGATATGAAGT
TGTTGAAGTTAAGACACCAGTTCTTTTAACAGCAATTAAAGAATTAAATGTTCCAAGATATATGAGTGTAGAAAAAATATTCG
GAGCATTTGATAAAGAAGTAAAAATGTGGACTGCCGATGATATAGATGTAGATAAGGCTAATTTAGGTCTTAAAGGTTCACC
AACTAAAGTTAAGAAGTCATCAACTAAAGAAGTTAAAGGACAGGGAGAAGTTATTGATAAGCCTGTTAAGGAAGCAGCTGC
ATATGTTGTCTCAAAATTAAAAGAAGAACACTATATTTAA

Figure 10

Seq. ID 7: *Clostridium autoethanogenum* DSM10061 phosphotransacetylase/acetate kinase promoter region ($P_{pta\text{-}ack}$):
GAGCGGCCGCAATATGATATTTATGTCCATTGTGAAAGGGATTATATTCAACTATTATTCCAGTTACGTTCATAGAAATTTTCC
TTTCTAAAATATTTTATTCCATGTCAAGAACTCTGTTTATTTCATTAAAGAACTATAAGTACAAAGTATAAGGCATTTGAAAAA
ATAGGCTAGTATATTGATTGATTATTTATTTTAAAATGCCTAAGTGAAATATATACATATTATAACAATAAAATAAGTATTAGT
GTAGGATTTTTAAATAGAGTATCTATTTTCAGATTAAATTTTTGATTATTTGATTTACATTATATAATATTGAGTAAAGTATTGA
CTAGCAAAATTTTTTGATACTTTAATTTGTGAAATTTCTTATCAAAAGTTATATTTTTGAATAATTTTTATTGAAAAATACAACTA
AAAAGGATTATAGTATAAGTGTGTGTAATTTTGTGTTAAATTTAAAGGGAGGAAATGAACATGAAACATATGGAA

Seq. ID 47: Wood-Ljungdahl cluster promoter:
AAGCGGCCGCAAAATAGTTGATAATAATGCAGAGTTATAAACAAAGGTGAAAAGCATTACTTGTATTCTTTTTTATATATTATT
ATAAATTAAAATGAAGCTGTATTAGAAAAAATACACACCTGTAATATAAAATTTTAAATTAATTTTTAATTTTTTCAAAATGTAT
TTTACATGTTTAGAATTTTGATGTATATTAAAATAGTAGAATACATAAGATACTTAATTTAATTAAAGATAGTTAAGTACTTTTC
AATGTGCTTTTTTAGATGTTTAATACAAATCTTTAATTGTAAAAGAAATGCTGTACTATTTACTGTACTAGTGACGGGATTAAA
CTGTATTAATTATAAATAAAAAATAAGTACAGTTGTTTAAAATTATATTTTGTATTAAATCTAATAGTACGATGTAAGTTATTTT
ATACTATTGCTAGTTTAATAAAAAGATTTAATTATATGCTTGAAAAGGAGAGGAATCCATATGCGTA

Seq. ID 48: pyruvate:ferredoxin oxidoreductase promoter:
ATACCATAAATTACTTGAAAAATAGTTGATAATAATGTAGAGTTATAAACAAAGGTGAAAAGCATTACTTGTATTCTTTTTTAT
ATATTATTATAAATTAAAATGAAGCTGTATTAGAAAAAATACACACCTGTAATATAAAATTTTAAATTAATTTTTAATTTTTTCA
AAATGTATTTTACATGTTTAGAATTTTGATGTATATTAAAATAGTAGAATACATAAGATACTTAATTTAATTAAAGATAGTTAA
GTACTTTTCAATGTGCTTTTTTAGATGTTTAATACAAATCTTTAATTGTAAAAGAAATGCTGTACTATTTACTGTACTAGTGACG
GGATTAAACTGTATTAATTATAAATAAAAAATAAGTACAGTTGTTTAAAATTATATTTTGTATTAAATCTAATAGTACGATGTA
AGTTATTTTATACTATTGCTAGTTTAATAAAAAGATTTAATTATATACTTGAAAAGGAGAGGAATTTTTATGCGTAAA

Seq. ID 49: Rnf operon promoter:
TAGAAAAACATGTATACAAAATTAAAAAACTATTATAACACATAGTATCAATATTGAAGGTAATACTGTTCAATATCGATACA
GATAAAAAAAATATATAATACAGAAGAAAAAATTATAAATTTGTGGTATAATATAAAGTATAGTAATTTAAGTTTAAACCTCG
TGAAAACGCTAACAAATAATAGGAGGTGTATTAT

Seq. ID 50: ATP synthase operon promoter:
ATCTGTATATTTTTTCCCATTTTAATTATTTGTACTATAATATTACACTGAGTGTATTGTATATTTAAAAAATATTTGGTACAATT
AGTTAGTTAAATAAATTCTAAATTGTAAATTATCAGAATCCTTATTAAGGAAATACATAGATTTAAGGAGAAATCATAAAAAG
GTGTAATATAAACTGGCTAAAATTGAGCAAAAATTGAGCAATTAAGACTTTTTGATTGTATCTTTTTATATATTTAAGGTATAT
AATCTTATTTATATTGGGGGAACTTGATGAATAAACATATTCTAGAC

Figure 11

Seq. ID 14: *E. coli-Clostridium* shuttle vector pMTL 85141:
CCTGCAGGATAAAAAAATTGTAGATAAATTTTATAAAATAGTTTTATCTACAATTTTTTTATCAGGAAACAGCTATGACCGCGG
CCGCTGTATCCATATGACCATGATTACGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGTCGACGTCACGCGTCCATGGAG
ATCTCGAGGCCTGCAGACATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCA
ACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGT
TGCGCAGCCTGAATGGCGAATGGCGCTAGCATAAAAATAAGAAGCCTGCATTTGCAGGCTTCTTATTTTTATGGCGCGCCGC
ATTCACTTCTTTTCTATATAAATATGAGCGAAGCGAATAAGCGTCGGAAAAGCAGCAAAAAGTTTCCTTTTTGCTGTTGGAGC
ATGGGGGTTCAGGGGGTGCAGTATCTGACGTCAATGCCGAGCGAAAGCGAGCCGAAGGGTAGCATTTACGTTAGATAACCC
CCTGATATGCTCCGACGCTTTATATAGAAAAGAAGATTCAACTAGGTAAAATCTTAATATAGGTTGAGATGATAAGGTTTATA
AGGAATTTGTTTGTTCTAATTTTTCACTCATTTTGTTCTAATTTCTTTTAACAAATGTTCTTTTTTTTTTAGAACAGTTATGATATA
GTTAGAATAGTTTAAAATAAGGAGTGAGAAAAAGATGAAAGAAAGATATGGAACAGTCTATAAAGGCTCTCAGAGGCTCAT
AGACGAAGAAAGTGGAGAAGTCATAGAGGTAGACAAGTTATACCGTAAACAAACGTCTGGTAACTTCGTAAAGGCATATAT
AGTGCAATTAATAAGTATGTTAGATATGATTGGCGGAAAAAAACTTAAAATCGTTAACTATATCCTAGATAATGTCCACTTAA
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CAAAAACAAAAATACCTCTTACTCGAATTTGGGAACTTTGAGCAAGAGGCAAATGAAATAGATTGACCTCCCAATAACACCAC
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AACAGAAAAGAGTATTTTGACCACTACTTTGCAAGTGTACCTTGTACCTACAGCATGACCGTTAAAGTGGATATCACACAAAT
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CTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTG
GCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGC
TGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGA
GAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGA
GGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGA
TGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGC
TCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAG
CCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAGGGCCC

Figure 12

Seq. ID 15: *E. coli-Clostridium* shuttle vector pMTL 82254:
CCTGCAGGATAAAAAAATTGTAGATAAATTTTATAAAATAGTTTTATCTACAATTTTTTTATCAGGAAACAGCTATGACCGCGGCCGCTGTATCCATATGGTATT
TGAAAAAATTGATAAAAATAGTTGGAACAGAAAAGAGTATTTTGACCACTACTTTGCAAGTGTACCTTGTACCTACAGCATGACCGTTAAAGTGGATATCACAC
AAATAAAGGAAAAGGGAATGAAACTATATCCTGCAATGCTTTATTATATTGCAATGATTGTAAACCGCCATTCAGAGTTTAGGACGGCAATCAATCAAGATGG
TGAATTGGGGATATATGATGAGATGATACCAAGCTATACAATATTTCACAATGATACTGAAACATTTTCCAGCCTTTGGACTGAGTGTAAGTCTGACTTTAAAT
CATTTTTAGCAGATTATGAAAGTGATACGCAACGGTATGGAAACAATCATAGAATGGAAGGAAAGCCAAATGCTCCGGAAAACATTTTTAATGTATCTATGAT
ACCGTGGTCAACCTTCGATGGCTTTAATCTGAATTTGCAGAAAGGATATGATTATTTGATTCCTATTTTTACTATGGGGAAATATTATAAAGAAGATAACAAAAT
TATACTTCCTTTGGCAATTCAAGTTCATCACGCAGTATGTGACGGATTTCACATTTGCCGTTTTGTAAACGAATTGCAGGAATTGATAAATAGTTAAACGCGTCC
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TATTTACAAATTCGGCCGGCCGAAGCAAACTTAAGAGTGTGTTGATAGTGCAGTATCTTAAAATTTTGTATAATAGGAATTGAAGTTAAATTAGATGCTAAAAA
TTTGTAATTAAGAAGGAGTGATTACATGAACAAAAATATAAAATATTCTCAAAACTTTTTAACGAGTGAAAAAGTACTCAACCAAATAATAAAACAATTGAATT
TAAAAGAAACCGATACCGTTTACGAAATTGGAACAGGTAAAGGGCATTTAACGACGAAACTGGCTAAAATAAGTAAACAGGTAACGTCTATTGAATTAGACA
GTCATCTATTCAACTTATCGTCAGAAAAATTAAAACTGAATACTCGTGTCACTTTAATTCACCAAGATATTCTACAGTTTCAATTCCCTAACAAACAGAGGTATAA
AATTGTTGGGAGTATTCCTTACCATTTAAGCACACAAATTATTAAAAAAGTGGTTTTTGAAAGCCATGCGTCTGACATCTATCTGATTGTTGAAGAAGGATTCTA
CAAGCGTACCTTGGATATTCACCGAACACTAGGGTTGCTCTTGCACACTCAAGTCTCGATTCAGCAATTGCTTAAGCTGCCAGCGGAATGCTTTCATCCTAAACC
AAAAGTAAACAGTGTCTTAATAAAACTTACCCGCCATACCACAGATGTTCCAGATAAATATTGGAAGCTATATACGTACTTTGTTTCAAAATGGGTCAATCGAG
AATATCGTCAACTGTTTACTAAAAATCAGTTTCATCAAGCAATGAAACACGCCAAAGTAAACAATTTAAGTACCGTTACTTATGAGCAAGTATTGTCTATTTTTA
ATAGTTATCTATTATTTAACGGGAGGAAATAATTCTATGAGTCGCTTTTGTAAATTTGGAAAGTTACACGTTACTAAAGGGAATGTGTTTAAACTCCTTTTTGAT
AATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTA
ATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGC
GCAGATACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGT
GGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCA
CACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGG
TATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGA
CTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGC
TCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACCGAGCGCAGCG
AGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAGGGCCCCCTGCTTCGGGGTCATTATAGCGATTTTTTCGGTATATCCATCCTTTTTCGCACGATA
TACAGGATTTTGCCAAAGGGTTCGTGTAGACTTTCCTTGGTGTATCCAACGGCGTCAGCCGGGCAGGATAGGTGAAGTAGGCCCACCCGCGAGCGGGTGTTC
CTTCTTCACTGTCCCTTATTCGCACCTGGCGGTGCTCAACGGGAATCCTGCTCTGCGAGGCTGGCCGGCTACCGCCGGCGTAACAGATGAGGGCAAGCGGATG
GCTGATGAAACCAAGCCAACCAGGAAGGGCAGCCCACCTATCAAGGTGTACTGCCTTCCAGACGAACGAAGAGCGATTGAGGAAAAGGCGGCGGCGGCCGG
CATGAGCCTGTCGGCCTACCTGCTGGCCGTCGGCCAGGGCTACAAAATCACGGGCGTCGTGGACTATGAGCACGTCCGCGAGCTGGCCCGCATCAATGGCGA
CCTGGGCCGCCTGGGCGGCCTGCTGAAACTCTGGCTCACCGACGACCCGCGCACGGCGCGGTTCGGTGATGCCACGATCCTCGCCCTGCTGGCGAAGATCGA
AGAGAAGCAGGACGAGCTTGGCAAGGTCATGATGGGCGTGGTCCGCCCGAGGGCAGAGCCATGACTTTTTTAGCCGCTAAAACGGCCGGGGGGTGCGCGTG
ATTGCCAAGCACGTCCCCATGCGCTCCATCAAGAAGAGCGACTTCGCGGAGCTGGTGAAGTACATCACCGACGAGCAAGGCAAGACCGATCGGGCCC

Figure 13

Seq. ID 24: Methyltransferase gene cluster of *C. ljungdahlii*:
ATGAACAGTTTTATTGAAGATGTTGAACAAATTTACAATTTTATTAAAAAAAATATAGATGTAGAAGAGAAGATGCATTTTAT
AGAAACTTATAAGCAAAAATCTAATATGAAGAAAGAAATTAGCTTTTCAGAAGAATACTATAAACAGAAAATTATGAATGGA
AAAAATGGAGTAGTGTATACTCCTCCGGAAATGGCAGCATTTATGGTTAAAAACTTGATAAATGTCAATGATGTAATTGGAA
ATCCATTTATAAAAATAATAGATCCTTCCTGTGGATCTGGGAATTTAATTTGTAAGTGCTTTCTATATTTAAATCGAATATTTAT
TAAGAATATTGAAGTTATAAATAGTAAAAACAATTTAAATTTGAAACTAGAAGATATAAGTTACCATATAGTACGTAACAATC
TATTTGGATTTGATATAGATGAAACTGCAATAAAAGTTTTAAAAATAGACTTATTTTTGATTAGCAATCAGTTTAGTGAAAAAA
ATTTTCAAGTAAAGGATTTTCTAGTGGAAAATATAGATAGAAAATATGATGTGTTTATAGGAAATCCTCCGTATATAGGACAT
AAATCTGTAGATTCTAGTTATTCATATGTTTTAAGAAAAATATATGGAAGTATATATAGAGACAAAGGAGACATATCCTACTG
TTTTTTTCAAAAATCATTAAAGTGTTTAAAGGAGGGAGGAAAACTGGTTTTTGTTACTTCTAGGTATTTTTGTGAATCTTGCAG
CGGAAAAGAACTTAGAAAGTTTTTAATTGAAAATACCTCTATTTATAAAATTATAGATTTTTATGGTATAAGACCTTTTAAAAG
AGTAGGTATAGACCCAATGATAATATTTTTAGTAAGAACAAAAAATTGGAACAATAATATAGAAATCATAAGACCCAATAAA
ATTGAAAAAAATGAAAAAAATAAATTTCTTGATTCCTTGTTTTTAGATAAATCTGAAAAATGCAAAAAGTTTTCTATTTCTCAA
AAGTCTATAAATAATGATGGATGGGTATTTGTTGACGAAGTTGAGAAAAATATAATAGATAAAATAAAAGAAAAAAGTAAAT
TTATTTTAAAGGATATATGCCATAGTTGTCAGGGTATAATAACGGGATGTGATAGGGCTTTTATAGTTGATAGAGACATAATA
AATAGTAGAAAAATTGAATTAAGGTTAATAAAACCCTGGATAAAAAGTAGCCATATACGAAAAAACGAAGTAATTAAAGGTG
AAAAATTTATTATATACTCAAATTTAATAGAAAATGAAACAGAATGTCCTAATGCTATAAAGTATATAGAGCAGTACAAAAAA
AGGCTTATGGAAAGAAGAGAATGTAAAAAAGGAACAAGAAAGTGGTATGAACTTCAATGGGGGAGAAAACCGGAAATTTTT
GAAGAAAAGAAAATTGTGTTCCCATACAAGTCCTGTGACAATAGATTTGCTCTTGACAAGGGAAGCTATTTTAGTGCAGATAT
ATATTCCTTAGTATTAAAAAAAAATGTACCTTTTACCTATGAAATACTTTTAAATATATTAAACAGTCCTTTGTATGAATTTTACT
TTAAAACTTTCGCAAAAAAATTAGGAGAAAATCTATATGAGTATTACCCTAATAATCTAATGAAATTGTGTATTCCTTCTATTG
ATTTTGGAGGAGAAAATAATATAGAAAAAAAGCTGTATGATTTTTTTGGACTGACAGATAAGGAAATTGAGATTGTAGAAAA
GATAAAAGATAATTGCTGA

Seq. ID 25: Methyltransferase gene cluster of *C. autoethanogenum*:
ATGCATTTTATAGAAACTTATAAGCAAAAATCTAATATGAAGAAAGAAATTAGCTTTTCAGAAGAATACTATAAACAGAAAAT
TATGAATGGAAAAAATGGAGTAGTGTATACTCCTCCGGAAATGGCAGCATTTATGGTTAAAAACTTGATAAATGTCAATGAT
GTAATTGGAAATCCATTTATAAAAATAATAGATCCTTCCTGTGGATCTGGGAATTTAATTTGTAAGTGCTTTCTATATTTAAATC
GAATATTTATTAAGAATATTGAAGTTATAAATAGTAAAAACAATTTAAATTTGAAACTAGAAGATATAAGTTACCATATAGTAC
GTAACAATCTATTTGGATTTGATATAGATGAAACTGCAATAAAAGTTTTAAAAATAGACTTATTTTTGATTAGCAATCAGTTTA
GTGAAAAAAATTTTCAAGTAAAGGATTTTCTAGTGGAAAATATAGATAGAAAATATGATGTGTTTATAGGAAATCCTCCGTAT
ATAGGACATAAATCTGTAGATTCTAGTTATTCATATGTTTTAAGAAAAATATATGGAAGTATATATAGAGACAAAGGAGACAT
ATCCTACTGTTTTTTTCAAAAATCATTAAAGTGTTTAAAGGAGGGAGGAAAACTGGTTTTTGTTACTTCTAGGTATTTTTGTGA
ATCTTGCAGCGGAAAAGAACTTAGAAAGTTTTTAATTGAAAATACCTCTATTTATAAAATTATAGATTTTTATGGTATAAGACC
TTTTAAAAGAGTAGGTATAGACCCAATGATAATATTTTTAGTAAGAACAAAAAATTGGAACAATAATATAGAAATCATAAGAC
CCAATAAAATTGAAAAAAATGAAAAAAATAAATTTCTTGATTCCTTGTTTTTAGATAAATCTGAAAAATGCAAAAAGTTTTCTA
TTTCTCAAAAGTCTATAAATAATGATGGATGGGTATTTGTTGACGAAGTTGAGAAAAATATAATAGATAAAATAAAAGAAAA
AAGTAAATTTATTTTAAAGGATATATGCCATAGTTGTCAGGGTATAATAACGGGATGTGATAGGGCTTTTATAGTTGATAGAG
ACATAATAAATAGTAGAAAAATTGAATTAAGGTTAATAAAACCCTGGATAAAAAGTAGCCATATACGAAAAAACGAAGTAAT
TAAAGGTGAAAAATTTATTATATACTCAAATTTAATAGAAAATGAAACAGAATGTCCTAATGCTATAAAGTATATAGAGCAGT
ACAAAAAAAGGCTTATGGAAAGAAGAGAATGTAAAAAAGGAACAAGAAAGTGGTATGAACTTCAATGGGGGAGAAAACC
GGAAATTTTTGAAGAAAAGAAAATTGTGTTCCCATACAAGTCCTGTGACAATAGATTTGCTCTTGACAAGGGAAGCTATTTTA
GTGCAGATATATATTCCTTAGTATTAAAAAAAAATGTACCTTTTACCTATGAAATACTTTTAAATATATTAAACAGTCCTTTGTA
TGAATTTTACTTTAAAACTTTCGCAAAAAAATTAGGAGAAAATCTATATGAGTATTACCCTAATAATCTAATGAAATTGTGTAT
TCCTTCTATTGATTTTGGAGGAGAAAATAATATAGAAAAAAAGCTGTATGATTTTTTTGGACTGACAGATAAGGAAATTGAGA
TTGTAGAAAAGATAAAAGATAATTGCTGA

Figure 14

Seq. ID 26: Methyltransferase gene cluster of *C. ragsdalei*:
ATGTTTCCCTGTAATGCATATATTCAGCACGGAGATAGGAATATGAATAATTTTATTGAAGATATTGAAGAAATTTATAATTTT
ATTAAAAAAAATACAGATGTAGAAGAGAATATTCATTTTATAGAAACTTATAGGCAAAGACTTAATATGAAGAAAGAAATTA
GCTTTTCAGAAGAATACTATAAACAGAAAATTATGAATGGAAAAAACGGAGTAGTGTATACTCCTCCGGAAATGGCAGCATT
TATGGTTAAAAACTTGATAAATGTCAATGATGTAATTGAAAATCCATTTATAAAAGTAGTAGATCCTTCCTGTGGATCTGGAA
ATTTAATTTGTAAGTGCTTTCTATACTTAAATCAAATATTCATTAAAAATATTGAAGTTATAAATAGTAAAAATAATTTAAATTT
GAAACTAAAAGATATAAGTTACCATATAGTACATAACAATCTATTTGGATTTGATGTAGATGAAACTGCAATAAAAGTTTTAA
AATAGACTTATTTTTGATTAGCAATCAGTTTAGTGAAAAAAATTTTCAAGTAAAGGATTTTCTAGTGGAAAATATAGATAGAA
AATTTGATGTGTTTATAGGAAATCCCCCATATATAGGACATAAATCTGTAGATTCCAGTTATTCATATATTTTAAGGAAAATAT
ATGGAAGTATATATAGAGATAAAGGAGACATATCTTACTGTTTTTTTCAAAAATCATTAAAGTGCTTAAAAGAGGGAGGAAA
ATTACTTTTTGTTACCTCCAGATATTTTTGCGAATCTTGCAGCGGAAAAGAACTTAGAAAGTTTTTAATTGAAAATACCTCTATT
TATAAAATTATAGATTTTTATGGTATAAGACCTTTTAAAAGAGTAGGTATAGATCCAATGATAATATTTTTAGTAAGAACAAAA
AATTGGGACAATAATATAGAAATCATAAGACCCAATAAAAGTGGAAAAGATGAAAAAAATAAATTCCTTGATTCTTTGCTTTT
AGATAAATCTGAAAAATACAAAAAATTTTCTATTCCTCAAAAGTCTATAAATAGTGATGGATGGGTATTTGTTAATGAAGTTG
AGAAAAATATAATGGATAAAATAGAAGCAAAAAGTGAATTTATTTTAAAGGATATATGCCATAGTTATCAGGGTATAATAAC
GGGATGTGATAGGGCTTTTATAGTTGATAGAGACACAATAAATAGTAGAAAAATTGAATTAAGGTTAATAAAACCCTGGGTG
AAAAGCAGCCATATACGAAAAAACGAAGTAATTAAAGGTGAAAAATTTATTATATACTCAAATTTAATAGAAAATGAGATAG
AATGTCCTAATGCTATAAAGTATATAGAGCAGTACAAAAAAAAGCTTATGGAAAGAAGAGAATGTAAAAAAGGAACGAGAA
AGTGGTATGAGCTTCAATGGGGGAGAAAACCGGAAATTTTCGAAGAAAAGAAAATTGTATTCCCATACAAATCGTGTGATAA
TAGATTTGCTCTTGATAAGGGAAGCTATTTTAGTGCAGATATATATTCTTTAGTATTAAAAAAAAATGTACCTTTTACCTATGA
AATGCTTTTAAATATATTAAATAGTTCTTTGTATGAATTTTACTTTAAAACTTTCGGGAAAAAATTAGGAGAAAATCTATATGA
GTATTATCCTAATAATCTGATGAAATTGTGTATTCCTTCTATTGGTTTTCGAGAAGAAAATAATGTAGAAAAAAGGTTGTATGA
TTTTTTTGGGCTGACAGATAAGGAAATTCAGATTGTAGAAAAAATAAAAGATAATTGCTGA

Figure 15

Seq. ID 27: Nucleotide sequence of novel methyltransferase gene fused with an inducible *lac* Promoter:
GCGGCCGCGCAACGCAATTAATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTT
GTGTGGAATTGTGAGCGGATAACAATTTCACACAGGAAACACATATGTTTCCGTGCAATGCCTATATCGAATATGGTGATAAA
AATATGAACAGCTTTATCGAAGATGTGGAACAGATCTACAACTTCATTAAAAAGAACATTGATGTGGAAGAAAAGATGCATT
TCATTGAAACCTATAAACAGAAAAGCAACATGAAGAAAGAGATTAGCTTTAGCGAAGAATACTATAAACAGAAGATTATGAA
CGGCAAAAATGGCGTTGTGTACACCCCGCCGGAAATGGCGGCCTTTATGGTTAAAAATCTGATCAACGTTAACGATGTTATTG
GCAATCCGTTTATTAAAATCATTGACCCGAGCTGCGGTAGCGGCAATCTGATTTGCAAATGTTTTCTGTATCTGAATCGCATCT
TTATTAAGAACATTGAGGTGATTAACAGCAAAAATAACCTGAATCTGAAACTGGAAGACATCAGCTACCACATCGTTCGCAAC
AATCTGTTTGGCTTCGATATTGACGAAACCGCGATCAAAGTGCTGAAAATTGATCTGTTTCTGATCAGCAACCAATTTAGCGA
GAAAAATTTCCAGGTTAAAGACTTTCTGGTGGAAAATATTGATCGCAAATATGACGTGTTCATTGGTAATCCGCCGTATATCG
GTCACAAAAGCGTGGACAGCAGCTACAGCTACGTGCTGCGCAAAATCTACGGCAGCATCTACCGCGACAAAGGCGATATCA
GCTATTGTTTCTTTCAGAAGAGCCTGAAATGTCTGAAGGAAGGTGGCAAACTGGTGTTTGTGACCAGCCGCTACTTCTGCGA
GAGCTGCAGCGGTAAAGAACTGCGTAAATTCCTGATCGAAAACACGAGCATTTACAAGATCATTGATTTTTACGGCATCCGCC
CGTTCAAACGCGTGGGTATCGATCCGATGATTATTTTTCTGGTTCGTACGAAGAACTGGAACAATAACATTGAAATTATTCGC
CCGAACAAGATTGAAAAGAACGAAAAGAACAAATTCCTGGATAGCCTGTTCCTGGACAAAAGCGAAAAGTGTAAAAAGTTT
AGCATTAGCCAGAAAAGCATTAATAACGATGGCTGGGTTTTCGTGGACGAAGTGGAGAAAAACATTATCGACAAAATCAAA
GAGAAAAGCAAGTTCATTCTGAAAGATATTTGCCATAGCTGTCAAGGCATTATCACCGGTTGTGATCGCGCCTTTATTGTGGA
CCGTGATATCATCAATAGCCGTAAGATCGAACTGCGTCTGATTAAACCGTGGATTAAAAGCAGCCATATCCGTAAGAATGAA
GTTATTAAGGGCGAAAAATTCATCATCTATAGCAACCTGATTGAGAATGAAACCGAGTGTCCGAATGCGATTAAATATATCGA
ACAGTACAAGAAACGTCTGATGGAGCGCCGCGAATGCAAAAAGGGCACGCGTAAGTGGTATGAACTGCAATGGGGCCGTA
AACCGGAAATCTTCGAAGAAAAGAAAATTGTTTTCCCGTATAAAAGCTGTGACAATCGTTTTGCACTGGATAAGGGTAGCTAT
TTTAGCGCAGACATTTATAGCCTGGTTCTGAAGAAAAATGTGCCGTTCACCTATGAGATCCTGCTGAATATCCTGAATAGCCC
GCTGTACGAGTTTTACTTTAAGACCTTCGCGAAAAAGCTGGGCGAGAATCTGTACGAGTACTATCCGAACAACCTGATGAAG
CTGTGCATCCCGAGCATCGATTTCGGCGGTGAGAACAATATTGAGAAAAAGCTGTATGATTTCTTTGGTCTGACGGATAAAG
AAATTGAGATTGTGGAGAAGATCAAAGATAACTGCTAAGAATTC

Figure 16

Seq. ID 28: Protein sequence of novel methyltransferase:
MFPCNAYIEYGDKNMNSFIEDVEQIYNFIKKNIDVEEKMHFIETYKQKSNMKKEISFSEEYYKQKIMNGKNGVVYTPPEMAAFMVK
NLINVNDVIGNPFIKIIDPSCGSGNLICKCFLYLNRIFIKNIEVINSKNNLNLKLEDISYHIVRNNLFGFDIDETAIKVLKIDLFLISNQFSEK
NFQVKDFLVENIDRKYDVFIGNPPYIGHKSVDSSYSYVLRKIYGSIYRDKGDISYCFFQKSLKCLKEGGKLVFVTSRYFCESCSGKELRKF
LIENTSIYKIIDFYGIRPFKRVGIDPMIIFLVRTKNWNNNIEIIRPNKIEKNEKNKFLDSLFLDKSEKCKKFSISQKSINNDGWVFVDEVEK
NIIDKIKEKSKFILKDICHSCQGIITGCDRAFIVDRDIINSRKIELRLIKPWIKSSHIRKNEVIKGEKFIIYSNLIENETECPNAIKYIEQYKKRL
MERRECKKGTRKWYELQWGRKPEIFEEKKIVFPYKSCDNRFALDKGSYFSADIYSLVLKKNVPFTYEILLNILNSPLYEFYFKTFAKKLG
ENLYEYYPNNLMKLCIPSIDFGGENNIEKKLYDFFGLTDKEIEIVEKIKDNC*

Figure 17

Seq. ID 29: Plasmid pGS20:
TTTGCCACCTGACGTCTAAGAAAAGGAATATTCAGCAATTTGCCCGTGCCGAAGAAAGGCCCACCCGTGAAGGTGAGCCAGT
GAGTTGATTGCTACGTAATTAGTTAGTTAGCCCTTAGTGACTCGTAATACGACTCACTATAGGGCTCGAGTCTAGAGAATTCG
ATATCACCCGGGAACTAGTCTGCAGCCCTTTAGTGAGGGTTAATTGGAGTCACTAAGGGTTAGTTAGTTAGATTAGCAGAAA
GTCAAAAGCCTCCGACCGGAGGCTTTTGACTAAAACTTCCCTTGGGGTTATCATTGGGGCTCACTCAAAGGCGGTAATCAGAT
AAAAAAAATCCTTAGCTTTCGCTAAGGATGATTTCTGCTAGAGATGGAATAGACTGGATGGAGGCGGATAAAGTTGCAGGAC
CACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATT
GCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGA
AATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAGACCAAGTTTACTCATATATACTTTAGAT
TGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGA
GTTTTCGTTCCACTGAGCGTCAGACCCCTTAATAAGATGATCTTCTTGAGATCGTTTTGGTCTGCGCGTAATCTCTTGCTCTGA
AAACGAAAAAACCGCCTTGCAGGGCGGTTTTTCGAAGGTTCTCTGAGCTACCAACTCTTTGAACCGAGGTAACTGGCTTGGA
GGAGCGCAGTCACCAAAACTTGTCCTTTCAGTTTAGCCTTAACCGGCGCATGACTTCAAGACTAACTCCTCTAAATCAATTACC
AGTGGCTGCTGCCAGTGGTGCTTTTGCATGTCTTTCCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCG
GACTGAACGGGGGGTTCGTGCATACAGTCCAGCTTGGAGCGAACTGCCTACCCGGAACTGAGTGTCAGGCGTGGAATGAGA
CAAACGCGGCCATAACAGCGGAATGACACCGGTAAACCGAAAGGCAGGAACAGGAGAGCGCACGAGGGAGCCGCCAGGG
GAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCACTGATTTGAGCGTCAGATTTCGTGATGCTTGTCAGGGGGG
CGGAGCCTATGGAAAAACGGCTTTGCCGCGGCCCTCTCACTTCCCTGTTAAGTATCTTCCTGGCATCTTCCAGGAAATCTCCGC
CCCGTTCGTAAGCCATTTCCGCTCGCCGCAGTCGAACGACCGAGCGTAGCGAGTCAGTGAGCGAGGAAGCGGAATATATCCT
GTATCACATATTCTGCTGACGCACCGGTGCAGCCTTTTTTCTCCTGCCACATGAAGCACTTCACTGACACCCTCATCAGTGCCA
ACATAGTAAGCCAGTATACACTCCGCTAGCGCTGAGGTCTGCCTCGTGAAGAAGGTGTTGCTGACTCATACCAGGCCTGAAT
CGCCCCATCATCCAGCCAGAAAGTGAGGGAGCCACGGTTGATGAGAGCTTTGTTGTAGGTGGACCAGTTGGTGATTTTGAAC
TTTTGCTTTGCCACGGAACGGTCTGCGTTGTCGGGAAGATGCGTGATCTGATCCTTCAACTCAGCAAAAGTTCGATTTATTCA
ACAAAGCCACGTTGTGTCTCAAAATCTCTGATGTTACATTGCACAAGATAAAAATATATCATCATGAACAATAAAACTGTCTGC
TTACATAAACAGTAATACAAGGGGTGTTTACTAGAGGTTGATCGGGCACGTAAGAGGTTCCAACTTTCACCATAATGAAATA
AGATCACTACCGGGCGTATTTTTTGAGTTATCGAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAAATCACGGGAT
ATACCACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCATTTCAGTCAGTTGCTCAATGTACCTATAACCAGA
CCGTTCAGCTGGATATTACGGCCTTTTTAAAGACCGTAAAGAAAAATAAGCACAAGTTTTATCCGGCCTTTATTCACATTCTTG
CCCGCCTGATGAACGCTCACCCGGAGTTTCGTATGGCCATGAAAGACGGTGAGCTGGTGATCTGGGATAGTGTTCACCCTTG
TTACACCGTTTTCCATGAGCAAACTGAAACGTTTTCGTCCCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTCCACAT
ATATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTTCCCTAAAGGGTTTATTGAGAATATGTTTTTGTCTCAGC
CAATCCCTGGGTGAGTTTCACCAGTTTTGATTTAAACGTGGCCAATATGGACAACTTCTTCGCCCCCGTTTTCACGATGGGCAA
ATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATCCAGGTTCATCATGCCGTTTGTGATGGCTTCCATGTCGGCC
GCATGCTTAATGAATTACAACAGTACTGTGATGAGTGGCAGGGCGGGGCGTAATAATACTAGCTCCGGCAAAAAAACGGGC
AAGGTGTCACCACCCTGCCCTTTTTCTTTAAAACCGAAAAGATTACTTCGCG

Figure 18

Seq. ID 30: 16s rRNA gene of *C. autoethanogenum* (Y18178, GI:7271109):
GGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGCGATGAAGCTCCTTCGGGAGTGGATTAGCGGCGGA
CGGGTGAGTAACACGTGGGTAACCTACCTCAAAGAGGGGGATAGCCTCCCGAAAGGGAGATTAATACCGCATAATAATCAG
TTTTCACATGGAGACTGATTTAAAGGAGTAATCCGCTTTGAGATGGACCCGCGGCGCATTAGCTAGTTGGTAGGGTAACGGC
CTACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACATTGGAACTGAGAGACGGTCCAGACTCCTACGGG
AGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATTGT
AAAGCTCTGTCTTTGGGGACGATAATGACGGTACCCAAGGAGGAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATA
CGTAGGTGGCGAGCGTTGTCCGGAATTACTGGGCGTAAAGAGTGCGTAGGCGGATATTTAAGTGAGATGTGAAATACCCGG
GCTTAACCCGGGCACTGCATTTCAAACTGGATATCTAGAGTGCGGGAGAGGAGAATGGAATTCCTAGTGTAGCGGTGAAAT
GCGTAGAGATTAGGAAGAACACCAGTGGCGAAGGCGATTCTCTGGACCGTAACTGACGCTGAGGCACGAAAGCGTGGGTA
GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTACTAGGTGTAGGAGGTATCGACCCCTTCTGTGCCG
CAGTAAACACAATAAGTACTCCGCCTGGGAAGTACGATCGCAAGATTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAG
CAGCGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCTGGACTTGACATACCCTGAATATCTTAGAGATAAGA
GAAGCCCTTCGGGGCAGGGATACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTAGGTTAAGTCCTGCAAC
GAGCGCAACCCCTGTTGTTAGTTGCTAACATTTAGTTGAGCACTCTAGCAAGACTGCCGCGGTTAACGCGGAGGAAGGTGGG
GATGACGTCAAATCATCATGCCCCTTATGTCCAGGGCAACACACGTGCTACAATGGGCAGTACAGAGAGAAGCAAGACCGCA
AGGTGGAGCAAACCTCAAAAACTGCCCCCAGTTCGGATTGCAGGCTGAAACTCGCCTACATGAAGTTGGAGTTGCTAGTAAT
CGCGAATCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGAGAGCTGGCAACACCCGA
AGTCCGTAGTCTAACTTAGGAGGACGCGGCCGAAGGTGGGGTTAGTAATTGGGGTGAAGTCGTAACAAGGTAGCCGT

Figure 19

Seq. ID 31: Butanol expression plasmid pMTL85245-thlA-crt-hbd:
ATAAAAAAATTGTAGATAAATTTTATAAAATAGTTTTATCTACAATTTTTTTATCAGGAAACAGCTATGACCGCGGCCGC
AATATGATATTTATGTCCATTGTGAAAGGGATTATATTCAACTATTATTCCAGTTACGTTCATAGAAATTTTCCTTTCTA
AAATATTTTATTCCATGTCAAGAACTCTGTTTATTTCATTAAAGAACTATAAGTACAAAGTATAAGGCATTTGAAAAAAT
AGGCTAGTATATTGATTGATTATTTATTTTAAAATGCCTAAGTGAAATATATACATATTATAACAATAAAATAAGTATTA
GTGTAGGATTTTTAAATAGAGTATCTATTTTCAGATTAAATTTTTGATTATTTGATTTACATTATATAATATTGAGTAAA
GTATTGACTAGCAAAATTTTTTGATACTTTAATTTGTGAAATTTCTTATCAAAAGTTATATTTTTGAATAATTTTTATTG
AAAAATACAACTAAAAAGGATTATAGTATAAGTGTGTGTAATTTTGTGTTAAATTTAAAGGGAGGAAATGAACATGAAAC
ATATGAAAGAAGTTGTAATAGCTAGTGCAGTAAGAACAGCGATTGGATCTTATGGAAAGTCTCTTAAGGATGTACCAGCA
GTAGATTTAGGAGCTACAGCTATAAAGGAAGCAGTTAAAAAAGCAGGAATAAAACCAGAGGATGTTAATGAAGTCATTTT
AGGAAATGTTCTTCAAGCAGGTTTAGGACAGAATCCAGCAAGACAGGCATCTTTTAAAGCAGGATTACCAGTTGAAATTC
CAGCTATGACTATTAATAAGGTTTGTGGTTCAGGACTTAGAACAGTTAGCTTAGCAGCACAAATTATAAAAGCAGGAGAT
GCTGACGTAATAATAGCAGGTGGTATGGAAAATATGTCTAGAGCTCCTTACTTAGCGAATAACGCTAGATGGGGATATAG
AATGGGAAACGCTAAATTTGTTGATGAAATGATCACTGACGGATTGTGGGATGCATTTAATGATTACCACATGGGAATAA
CAGCAGAAAACATAGCTGAGAGATGGAACATTTCAAGAGAAGAACAAGATGAGTTTGCTCTTGCATCACAAAAAAAAGCT
GAAGAAGCTATAAAATCAGGTCAATTTAAAGATGAAATAGTTCCTGTAGTAATTAAAGGCAGAAAGGGAGAAACTGTAGT
TGATACAGATGAGCACCCTAGATTTGGATCAACTATAGAAGGACTTGCAAAATTAAAACCTGCCTTCAAAAAAGATGGAA
CAGTTACAGCTGGTAATGCATCAGGATTAAATGACTGTGCAGCAGTACTTGTAATCATGAGTGCAGAAAAAGCTAAAGAG
CTTGGAGTAAAACCACTTGCTAAGATAGTTTCTTATGGTTCAGCAGGAGTTGACCCAGCAATAATGGGATATGGACCTTT
CTATGCAACAAAAGCAGCTATTGAAAAAGCAGGTTGGACAGTTGATGAATTAGATTTAATAGAATCAAATGAAGCTTTTG
CAGCTCAAAGTTTAGCAGTAGCAAAAGATTTAAAATTTGATATGAATAAAGTAAATGTAAATGGAGGAGCTATTGCCCTT
GGTCATCCAATTGGAGCATCAGGTGCAAGAATACTCGTTACTCTTGTACACGCAATGCAAAAAAGAGATGCAAAAAAAGG
CTTAGCAACTTTATGTATAGGTGGCGGACAAGGAACAGCAATATTGCTAGAAAAGTGCTAGGAATTCGAGCTCGGTACCT
TAGGAGGATTAGTCATGGAACTAAACAATGTCATCCTTGAAAAGGAAGGTAAAGTTGCTGTAGTTACCATTAACAGACCT
AAAGCATTAAATGCGTTAAATAGTGATACACTAAAAGAAATGGATTATGTTATAGGTGAAATTGAAAATGATAGCGAAGT
ACTTGCAGTAATTTTAACTGGAGCAGGAGAAAAATCATTTGTAGCAGGAGCAGATATTTCTGAGATGAAGGAAATGAATA
CCATTGAAGGTAGAAAATTCGGGATACTTGGAAATAAAGTGTTTAGAAGATTAGAACTTCTTGAAAAGCCTGTAATAGCA
GCTGTTAATGGTTTTGCTTTAGGAGGCGGATGCGAAATAGCTATGTCTTGTGATATAAGAATAGCTTCAAGCAACGCAAG
ATTTGGTCAACCAGAAGTAGGTCTCGGAATAACACCTGGTTTTGGTGGTACACAAAGACTTTCAAGATTAGTTGGAATGG
GCATGGCAAAGCAGCTTATATTTACTGCACAAAATATAAAGGCAGATGAAGCATTAAGAATCGGACTTGTAAATAAGGTA
GTAGAACCTAGTGAATTAATGAATACAGCAAAAGAAATTGCAAACAAAATTGTGAGCAATGCTCCAGTAGCTGTTAAGTT
AAGCAAACAGGCTATTAATAGAGGAATGCAGTGTGATATTGATACTGCTTTAGCATTTGAATCAGAAGCATTTGGAGAAT
GCTTTTCAACAGAGGATCAAAAGGATGCAATGACAGCTTTCATAGAGAAAAGAAAAATTGAAGGCTTCAAAAATAGATAG
GAGGTAAGTTTATATGGATTTTAATTTAACAAGAGAACAAGAATTAGTAAGACAGATGGTTAGAGAATTTGCTGAAAATG
AAGTTAAACCTATAGCAGCAGAAATTGATGAAACAGAAAGATTTCCAATGGAAAATGTAAAGAAAATGGGTCAGTATGGT
ATGATGGGAATTCCATTTTCAAAAGAGTATGGTGGCGCAGGTGGAGATGTATTATCTTATATAATCGCCGTTGAGGAATT
ATCAAAGGTTTGCGGTACTACAGGAGTTATTCTTTCAGCACATACATCACTTTGTGCTTCATTAATAAATGAACATGGTA
CAGAAGAACAAAAACAAAAATATTTAGTACCTTTAGCTAAAGGTGAAAAAATAGGTGCTTATGGATTGACTGAGCCAAAT
GCAGGAACAGATTCTGGAGCACAACAAACAGTAGCTGTACTTGAAGGAGATCATTATGTAATTAATGGTTCAAAAATATT
CATAACTAATGGAGGAGTTGCAGATACTTTTGTTATATTTGCAATGACTGACAGAACTAAAGGAACAAAAGGTATATCAG
CATTTATAATAGAAAAAGGCTTCAAAGGTTTCTCTATTGGTAAAGTTGAACAAAAGCTTGGAATAAGAGCTTCATCAACA
ACTGAACTTGTATTTGAAGATATGATAGTACCAGTAGAAAACATGATTGGTAAAGAAGGAAAAGGCTTCCCTATAGCAAT
GAAAACTCTTGATGGAGGAAGAATTGGTATAGCAGCTCAAGCTTTAGGTATAGCTGAAGGTGCTTTCAACGAAGCAAGAG
CTTACATGAAGGAGAGAAAACAATTTGGAAGAAGCCTTGACAAATTCCAAGGTCTTGCATGGATGATGGCAGATATGGAT
GTAGCTATAGAATCAGCTAGATATTTAGTATATAAAGCAGCATATCTTAAACAAGCAGGACTTCCATACACAGTTGATGC
TGCAAGAGCTAAGCTTCATGCTGCAAATGTAGCAATGGATGTAACAACTAAGGCAGTACAATTATTTGGTGGATACGGAT
ATACAAAAGATTATCCAGTTGAAAGAATGATGAGAGATGCTAAGATAACTGAAATATATGAAGGAACTTCAGAAGTTCAG
AAATTAGTTATTTCAGGAAAAATTTTTAGATAATTTAAGGAGGTTAAGAGGATGAATATAGTTGTTTGTTTAAAACAAGT
TCCAGATACAGCGGAAGTTAGAATAGATCCAGTTAAGGGAACACTTATAAGAGAAGGAGTTCCATCAATAATAAATCCAG
ATGATAAAAACGCACTTGAGGAAGCTTTAGTATTAAAAGATAATTATGGTGCACATGTAACAGTTATAAGTATGGGACCT
CCACAAGCTAAAAATGCTTTAGTAGAAGCTTTGGCTATGGGTGCTGATGAAGCTGTACTTTTAACAGATAGAGCATTTGG
AGGAGCAGATACACTTGCGACTTCACATACAATTGCAGCAGGAATTAAGAAGCTAAAATATGATATAGTTTTTGCTGGAA
GGCAGGCTATAGATGGAGATACAGCTCAGGTTGGACCAGAAATAGCTGAGCATCTTGGAATACCTCAAGTAACTTATGTT
GAGAAAGTTGAAGTTGATGGAGATACTTTAAAGATTAGAAAAGCTTGGGAAGATGGATATGAAGTTGTTGAAGTTAAGAC
ACCAGTTCTTTTAACAGCAATTAAAGAATTAAATGTTCCAAGATATATGAGTGTAGAAAAAATATTCGGAGCATTTGATA
AAGAAGTAAAAATGTGGACTGCCGATGATATAGATGTAGATAAGGCTAATTTAGGTCTTAAAGGTTCACCAACTAAAGTT
AAGAAGTCATCAACTAAAGAAGTTAAAGGACAGGGAGAAGTTATTGATAAGCCTGTTAAGGAAGCAGCTGCATATGTTGT
CTCAAAATTAAAAGAAGAACACTATATTTAAGTTAGGAGGGATTTTTCAATGAATAAAGCAGATTACAAGGGCGTATGGG
TGTTTGCTGAACAAAGAGACGGAGAATTACAAAAGGTATCATTGGAATTATTAGGTAAAGGTAAGGAAATGGCTGAGAAA
TTAGGCGTTGAATTAACAGCTGTTTTACTTGGACATAATACTGAAAAAATGTCAAAGGATTTATTATCTCATGGAGCAGA
TAAGGTTTTAGCAGCAGATAATGAACTTTTAGCACATTTTTCAACAGATGGATATGCTAAAGTTATATGTGATTTAGTTA

Figure 20 (Sequence continued in figure 21)

ATGAAAGAAAGCCAGAAATATTATTCATAGGAGCTACTTTCATAGGAAGAGATTTAGGACCAAGAATAGCAGCAAGACTT
TCTACTGGTTTAACTGCTGATTGTACATCACTTGACATAGATGTAGAAAATAGAGATTTATTGGCTACAAGACCAGCGTT
TGGTGGAAATTTGATAGCTACAATAGTTTGTTCAGACCACAGACCACAAATGGCTACAGTAAGACCTGGTGTGTTTGAAA
AATTACCTGTTAATGATGCAAATGTTTCTGATGATAAAATAGAAAAAGTTGCAATTAAATTAACAGCATCAGACATAAGA
ACAAAAGTTTCAAAAGTTGTTAAGCTTGCTAAAGATATTGCAGATATCGGAGAAGCTAAGGTATTAGTTGCTGGTGGTAG
AGGAGTTGGAAGCAAAGAAAACTTTGAAAAACTTGAAGAGTTAGCAAGTTTACTTGGTGGAACAATAGCCGCTTCAAGAG
CAGCAATAGAAAAAGAATGGGTTGATAAGGACCTTCAAGTAGGTCAAACTGGTAAAACTGTAAGACCAACTCTTTATATT
GCATGTGGTATATCAGGAGCTATCCAGCATTTAGCAGGTATGCAAGATTCAGATTACATAATTGCTATAAATAAAGATGT
AGAAGCCCCAATAATGAAGGTAGCAGATTTGGCTATAGTTGGTGATGTAAATAAAGTTGTACCAGAATTAATAGCTCAAG
TTAAAGCTGCTAATAATTAAGATAAATAAAAAGAATTATTTAAAGCTTATTATGCCAAAATACTTATATAGTATTTTGGT
GTAAATGCATTGATAGTTTCTTTAAATTTAGGGAGGTCTGTTTAATGAAAAAGGTATGTGTTATAGGTGCAGGTACTATG
GGTTCAGGAATTGCTCAGGCATTTGCAGCTAAAGGATTTGAAGTAGTATTAAGAGATATTAAAGATGAATTTGTTGATAG
AGGATTAGATTTTATCAATAAAAATCTTTCTAAATTAGTTAAAAAAGGAAAGATAGAAGAAGCTACTAAAGTTGAAATCT
TAACTAGAATTTCCGGAACAGTTGACCTTAATATGGCAGCTGATTGCGATTTAGTTATAGAAGCAGCTGTTGAAAGAATG
GATATTAAAAAGCAGATTTTTGCTGACTTAGACAATATATGCAAGCCAGAAACAATTCTTGCATCAAATACATCATCACT
TTCAATAACAGAAGTGGCATCAGCAACTAAAAGACCTGATAAGGTTATAGGTATGCATTTCTTTAATCCAGCTCCTGTTA
TGAAGCTTGTAGAGGTAATAAGAGGAATAGCTACATCACAAGAAACTTTTGATGCAGTTAAAGAGACATCTATAGCAATA
GGAAAAGATCCTGTAGAAGTAGCAGAAGCACCAGGATTTGTTGTAAATAGAATATTAATACCAATGATTAATGAAGCAGT
TGGTATATTAGCAGAAGGAATAGCTTCAGTAGAAGACATAGATAAAGCTATGAAACTTGGAGCTAATCACCCAATGGGAC
CATTAGAATTAGGTGATTTTATAGGTCTTGATATATGTCTTGCTATAATGGATGTTTTATACTCAGAAACTGGAGATTCT
AAGTATAGACCACATACATTACTTAAGAAGTATGTAAGAGCAGGATGGCTTGGAAGAAAATCAGGAAAAGGTTTCTACGA
TTATTCAAAATAAGTTTACAAGAATCCGGATCCTCTAGAGTCGACGTCACGCGTCCATGGAGATCTCGAGGCCTGCAGAC
ATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCA
GCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAA
TGGCGAATGGCGCTAGCATAAAAATAAGAAGCCTGCATTTGCAGGCTTCTTATTTTTATGGCGCGCCGCATTCACTTCTT
TTCTATATAAATATGAGCGAAGCGAATAAGCGTCGGAAAAGCAGCAAAAAGTTTCCTTTTTGCTGTTGGAGCATGGGGGT
TCAGGGGGTGCAGTATCTGACGTCAATGCCGAGCGAAAGCGAGCCGAAGGGTAGCATTTACGTTAGATAACCCCCTGATA
TGCTCCGACGCTTTATATAGAAAAGAAGATTCAACTAGGTAAAATCTTAATATAGGTTGAGATGATAAGGTTTATAAGGA
ATTTGTTTGTTCTAATTTTTCACTCATTTTGTTCTAATTTCTTTTAACAAATGTTCTTTTTTTTTTAGAACAGTTATGAT
ATAGTTAGAATAGTTTAAAATAAGGAGTGAGAAAAAGATGAAAGAAAGATATGGAACAGTCTATAAAGGCTCTCAGAGGC
TCATAGACGAAGAAAGTGGAGAAGTCATAGAGGTAGACAAGTTATACCGTAAACAAACGTCTGGTAACTTCGTAAAGGCA
TATATAGTGCAATTAATAAGTATGTTAGATATGATTGGCGGAAAAAAACTTAAAATCGTTAACTATATCCTAGATAATGT
CCACTTAAGTAACAATACAATGATAGCTACAACAAGAGAAATAGCAAAAGCTACAGGAACAAGTCTACAAACAGTAATAA
CAACACTTAAAATCTTAGAAGAAGGAAATATTATAAAAAGAAAAACTGGAGTATTAATGTTAAACCCTGAACTACTAATG
AGAGGCGACGACCAAAAACAAAAATACCTCTTACTCGAATTTGGGAACTTTGAGCAAGAGGCAAATGAAATAGATTGACC
TCCCAATAACACCACGTAGTTATTGGGAGGTCAATCTATGAAATGCGATTAAGGGCCGGCCGAAGCAAACTTAAGAGTGT
GTTGATAGTGCAGTATCTTAAAATTTTGTATAATAGGAATTGAAGTTAAATTAGATGCTAAAAATTTGTAATTAAGAAGG
AGTGATTACATGAACAAAAATATAAAATATTCTCAAAACTTTTTAACGAGTGAAAAAGTACTCAACCAAATAATAAAACA
ATTGAATTTAAAAGAAACCGATACCGTTTACGAAATTGGAACAGGTAAAGGGCATTTAACGACGAAACTGGCTAAAATAA
GTAAACAGGTAACGTCTATTGAATTAGACAGTCATCTATTCAACTTATCGTCAGAAAAATTAAAACTGAATACTCGTGTC
ACTTTAATTCACCAAGATATTCTACAGTTTCAATTCCCTAACAAACAGAGGTATAAAATTGTTGGGAGTATTCCTTACCA
TTTAAGCACACAAATTATTAAAAAAGTGGTTTTTGAAAGCCATGCGTCTGACATCTATCTGATTGTTGAAGAAGGATTCT
ACAAGCGTACCTTGGATATTCACCGAACACTAGGGTTGCTCTTGCACACTCAAGTCTCGATTCAGCAATTGCTTAAGCTG
CCAGCGGAATGCTTTCATCCTAAACCAAAAGTAAACAGTGTCTTAATAAAACTTACCCGCCATACCACAGATGTTCCAGA
TAAATATTGGAAGCTATATACGTACTTTGTTTCAAAATGGGTCAATCGAGAATATCGTCAACTGTTTACTAAAAATCAGT
TTCATCAAGCAATGAAACACGCCAAAGTAAACAATTTAAGTACCGTTACTTATGAGCAAGTATTGTCTATTTTTAATAGT
TATCTATTATTTAACGGGAGGAAATAATTCTATGAGTCGCTTTTGTAAATTTGGAAAGTTACACGTTACTAAAGGGAATG
TGTTTAAACTCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTA
GAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACC
AGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAA
ATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTA
ATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAA
GGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACC
TACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGA
ACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACT
TGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCC
TGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCTTT
GAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAAT
ACGCAGGGCCCCCTGCAGG

Figure 21

Seq. ID 39: Nucleotide acid bifunctional butanol/ butyraldehyde dehydrogenase of *C. autoethanogenum*:
ATGAGAAATTTGTTTATATTTAACAGCATAAAAAATAAGAAAGAGGTGTCATTAATGAAGGTAACTAAGGTAACTAACGTTG
AAGAATTAATGAAAAAGTTAGATGAAGTAACGGCTGCTCAAAAGAAATTTTCTAGCTATACTCAAGAACAAGTGGATGAAAT
TTTCAGGCAGGCAGCTATGGCAGCCAATAGTGCTAGAATAGACTTAGCTAAAATGGCAGTGGAAGAAAGCGGAATGGGAAT
TGTAGAAGACAAGGTCATTAAAAATCATTTTGTTGCAGAATATATATATAACAAATATAAGGGTGAAAAGACCTGCGGAGTT
CTGGAACAAGATGAAGGCTTTGGTATGGTTAGAATTGCAGAACCTGTAGGAGTTATTGCAGCAGTAGTTCCAACAACTAATC
CAACATCTACAGCAATATTTAAATCACTAATAGCTTTAAAAACTAGAAATGGTATAGTTTTTTCACCACATCCAAGGGCAAAAA
AATCAACTATTGCAGCAGCTAAGATAGTACTTGATGCAGCAGTTAAAGCTGGTGCCCCTGAAGGAATTATAGGCTGGATAGA
TGAACCTTCTATTGAACTTTCACAGGTGGTAATGAAAGAAGCAGATCTAATTCTTGCAACTGGTGGACCAGGTATGGTTAAGG
CTGCCTATTCTTCAGGAAAGCCTGCTATAGGAGTTGGTCCAGGTAATACACCTGCTGTAATTGATGAAAGTGCCGACATTAAA
ATGGCAGTAAATTCAATACTACTTTCAAAAACTTTTGATAATGGTATGATTTGTGCTTCAGAGCAGTCAGTAATAGTTGCAAGC
TCAATATACGATGAAGTCAAGAAAGAGTTTGCAGATAGAGGAGCATATATATTAAGTAAGGATGAAACAGATAAGGTTGGA
AAAACAATCATGATTAATGGAGCTTTAAATGCTGGAATTGTAGGGCAAAGTGCCTTTAAAATAGCTCAGATGGCGGGAGTCA
GTGTACCGGAAGATGCTAAAATACTTATAGGAGAAGTTAAATCGGTAGAACCTGAAGAAGAGCCCTTTGCTCATGAAAAGCT
GTCTCCAGTTCTAGCCATGTACAAAGCAAAAGATTTTGATGAAGCACTTCTAAAGGCTGGAAGATTAGTTGAACGAGGTGGA
ATAGGGCATACATCTGTATTGTATGTAAATTCGATGACGGAAAAAGTAAAAGTAGAAAAGTTCAGAGAAACTATGAAGACCG
GTAGAACATTGATAAATATGCCTTCAGCGCAAGGCGCTATAGGAGATATATATAACTTTAAACTAGCTCCTTCTTTGACATTAG
GCTGTGGTTCCTGGGGAGGAAACTCTGTATCAGAAAATGTTGGACCTAAACATTTGTTAAACATAAAGAGTGTTGCTGAGAG
GAGAGAAAATATGCTTTGGTTTAGAGTACCTGAAAAGGTTTATTTCAAATATGGCAGCCTTGGAGTTGCACTAAAAGAACTG
AGAATTATGGAGAAGAAAAAGGCGTTTATAGTAACGGATAAAGTTCTTTATCAATTAGGTTATGTAGATAAAATTACAAAGA
ACCTCGATGAATTAAGAGTTTCATATAAAATATTTACAGATGTAGAACCAGATCCAACCCTTGCTACAGCTAAAAAAGGTGCA
GCAGAACTGCTTTCCTATGAACCAGATACAATTATAGCAGTTGGTGGTGGTTCGGCAATGGATGCTGCCAAGATCATGTGGG
TAATGTATGAGCATCCAGAAGTAAGATTTGAAGATTTGGCCATGAGATTTATGGATATAAGAAAGAGAGTATATGTTTTTCCT
AAGATGGGAGAAAAGGCAATGATGATTTCAGTAGCAACATCCGCAGGAACAGGGTCAGAAGTTACTCCATTTGCAGTAATTA
CGGACGAAAGAACAGGAGCTAAATATCCTCTGGCTGATTATGAATTAACTCCAAACATGGCTATAGTTGATGCAGAACTTAT
GATGGGAATGCCAAAGGGGCTAACAGCAGCTTCAGGTATAGATGCGTTGACTCATGCACTGGAGGCCTATGTGTCAATAATG
GCTTCAGAATATACCAACGGATTGGCTCTTGAAGCAACAAGATTAGTATTCAAATATTTGCCAATAGCTTATACAGAAGGTAC
AATTAATGTAAAGGCAAGAGAAAAAATGGCTCATGCTTCATGTATTGCAGGTATGGCCTTTGCCAATGCATTTTTAGGGGTAT
GCCACTCTATGGCACATAAATTGGGAGCACAGCACCACATACCACATGGAATTGCCAATGCACTTATGATAGATGAAGTTATA
AAATTCAATGCTGTAGAGGCTCCAAGGAAACAAGCGGCATTTCCACAATATAAATATCCAAATGTTAAAAGAAGATATGCTA
GAATAGCTGATTACCTAAATTTAGGTGGAAGTACAGATGATGAAAAAGTACAATTGCTAATAAATGCTATAGATGACTTAAA
AACTAAGTTAAATATTCCAAAGACTATTAAAGAAGCAGGAGTTTCAGAAGATAAATTCTATGCTACTTTAGATACAATGTCAG
AACTGGCTTTTGATGATCAATGTACAGGAGCTAATCCACGATATCCACTAATAGGAGAAATAAAACAAATGTATATAAATGCA
TTTGATACACCAAAGGCAACTGTGGAGAAGAAAACAAGAAAGAAAAAGTAA

Figure 22

Seq 40: AA sequence bifunctional butanol/butyraldehyde dehydrogenase of *C. autoethanogenum*:
MRNLFIFNSIKNKKEVSLMKVTKVTNVEELMKKLDEVTAAQKKFSSYTQEQVDEIFRQAAMAANSARIDLAKMAVEES
GMGIVEDKVIKNHFVAEYIYNKYKGEKTCGVLEQDEGFGMVRIAEPVGVIAAVVPTTNPTSTAIFKSLIALKTRNGIVFSP
HPRAKKSTIAAAKIVLDAAVKAGAPEGIIGWIDEPSIELSQVVMKEADLILATGGPGMVKAAYSSGKPAIGVGPGNTPA
VIDESADIKMAVNSILLSKTFDNGMICASEQSVIVASSIYDEVKKEFADRGAYILSKDETDKVGKTIMINGALNAGIVGQS
AFKIAQMAGVSVPEDAKILIGEVKSVEPEEEPFAHEKLSPVLAMYKAKDFDEALLKAGRLVERGGIGHTSVLYVNSMTE
KVKVEKFRETMKTGRTLINMPSAQGAIGDIYNFKLAPSLTLGCGSWGGNSVSENVGPKHLLNIKSVAERRENMLWFR
VPEKVYFKYGSLGVALKELRIMEKKKAFIVTDKVLYQLGYVDKITKNLDELRVSYKIFTDVEPDPTLATAKKGAAELLSYEP
DTIIAVGGGSAMDAAKIMWVMYEHPEVRFEDLAMRFMDIRKRVYVFPKMGEKAMMISVATSAGTGSEVTPFAVIT
DERTGAKYPLADYELTPNMAIVDAELMMGMPKGLTAASGIDALTHALEAYVSIMASEYTNGLALEATRLVFKYLPIAYT
EGTINVKAREKMAHASCIAGMAFANAFLGVCHSMAHKLGAQHHIPHGIANALMIDEVIKFNAVEAPRKQAAFPQYK
YPNVKRRYARIADYLNLGGSTDDEKVQLLINAIDDLKTKLNIPKTIKEAGVSEDKFYATLDTMSELAFDDQCTGANPRYP
LIGEIKQMYINAFDTPKATVEKKTRKKK*

FIGURE 23

Seq. ID 41: Nucleotide acid sequence of butyraldehyde dehydrogenase of *C. autoethanogenum*:
ATGAAAGTTACAAACGTAGAAGAACTAATGAAAAGACTAGAAGAAATAAAGGATGCTCAAAAGAAATTTGCTACATATACTC
AAGAACAAGTGGATGAAATTTTTAGACAAGCAGCTATGGCAGCTAATAGTGCTAGAATAGAACTAGCTAAAATGGCAGTAG
AAGAAAGCGGAATGGGAATTGTAGAAGACAAGGTTATTAAAAATCACTTTGCTTCAGAATATATATATAACAAATATAAGGA
TGAAAAAACCTGTGGAGTTTTAGAGAGAGATGCAGGCTTTGGTATAGTTAGAATTGCGGAACCTGTAGGAGTTATTGCAGCA
GTAGTTCCAACAACTAATCCAACATCTACAGCAATATTTAAATCACTAATAGCTTTAAAAACTAGAAATGGTATAATTTTTTCAC
CCCATCCAAGGGCAAAGAAATCAACTATTGCAGCAGCTAAAATAGTACTTGACGCTGCAGTTAAAGCTGGTGCTCCTGAAGG
AATTATAGGATGGATAGATGAACCTTCCATTGAACTTTCACAGGTGGTAATGGGAGAAGCAAATTTAATTCTTGCAACTGGTG
GTCCGGGTATGGTTAAGGCTGCCTATTCTTCAGGCAAACCTGCTGTGGGAGTTGGTCCAGGTAACACACCTGCTGTAATTGAT
GAAAGTGCCGACATTAAAATGGCAGTAAATTCAATATTACTATCAAAAACTTTTGATAATGGTATGATTTGTGCCTCAGAGCA
GTCAGTAATAGTTTTAGACTCAATATATGAGGAAGTTAAAAAAGAATTTGCTTATAGGGGTGCTTATATATTAAGTAAGGATG
AAACAGATAAGGTTGGAAAAATAATTTTAAAAAATGGAGCCTTAAATGCAGGTATTGTAGGACAACCTGCTTTTAAAATAGC
ACAGCTGGCAGGAGTGGATGTACCAGAAAAAGCTAAAGTACTTATAGGAGAGGTAGAATCGGTAGAACTTGAAGAACCATT
TTCTCATGAAAAGTTATCTCCAGTTTTAGCTATGTACAGGGCAAGAAATTTTGAGGATGCCATTGCAAAAACTGATAAACTGG
TTAGGGCAGGTGGATTTGGACATACATCTTCATTGTATATAAATCCAATGACAGAAAAAGCAAAAGTAGAAAAATTTAGTACT
ATGATGAAAACATCAAGAACTATAATTAACACACCTTCATCCCAAGGTGGTATAGGTGATATATATAACTTTAAACTAGCTCCT
TCTTTGACATTAGGCTGCGGTTCCTGGGGGGGAAATTCTGTATCCGAAAATGTTGGGCCTAAACATTTATTAAACATAAAAAG
TGTTGCTGAGAGGAGAGAAAATATGCTTTGGTTTAGAGTACCTGAAAAGGTTTATTTCAAATATGGTAGTCTTGGAGTTGCAT
TAAAAGAGTTAAAAGTTATGAATAAGAAGAAAGTATTTATAGTAACAGATAAAGTTCTTTATCAATTAGGTTATGTGGACAAA
GTTACAAAAGTTCTTGAGGAACTAAAAATTTCCTATAAGGTATTTACAGATGTAGAACCAGATCCAACCCTTGCTACAGCTAA
AAAAGGTGCAGCAGAACTGCTTTCCTATGAACCGGATACAATTATATCAGTTGGTGGTGGTTCAGCAATGGATGCAGCTAAG
ATCATGTGGGTAATGTATGAGCATCCAGAAGTAAAATTTGAAGATTTAGCTATGAGATTTATGGATATAAGAAAGAGAGTAT
ATGTTTTCCCTAAGATGGGAGAAAAGGCAATGATGATTTCAGTAGCAACATCCGCAGGAACAGGGTCGGAAGTTACTCCATT
TGCAGTAATCACTGATGAAAAAACAGGAGCTAAATATCCATTAGCTGATTATGAACTAACTCCAGACATGGCTATAGTTGATG
CAGAACTTATGATGGGAATGCCAAGAGGACTTACAGCAGCTTCGGGTATAGATGCATTAACCCATGCACTGGAGGCGTATGT
GTCAATAATGGCTACAGAATTTACCAATGGATTAGCCCTTGAAGCAGTAAAGTTGATATTTGAATATTTACCAAAAGCTTATA
CAGAAGGTACAACTAATGTAAAGGCAAGAGAAAAGATGGCTCATGCTTCATGTATTGCAGGTATGGCCTTTGCAAATGCATT
TTTAGGGGTATGCCACTCTATGGCACATAAATTGGGAGCACAGCATCACATACCACATGGAATTGCCAATGCACTTATGATAG
ATGAAGTTATAAAATTCAATGCTGTAGATGATCCAATAAAACAAGCTGCATTTCCCCAATACGAGTATCCAAATGCTAGGTAT
AGATATGCTCAGATAGCTGATTGTCTGAACTTGGGAGGAAATACAGAAGAGGAAAAGGTACAACTATTAATAAATGCTATAG
ATGATTTAAAAGCTAAGTTAAATATTCCAGAAACTATAAAAGAAGCAGGAGTTTCAGAAGATAAATTCTATGCTACTTTAGAT
AAAATGTCAGAATTAGCTTTTGATGATCAGTGTACAGGAGCTAATCCAAGATATCCACTGATAAGTGAAATAAAACAAATGTA
TATAAATGTTTTTGATAAAACCGAACCAATTGTAGAAGATGAAGAAAAGTAA

Seq. ID 42: Amino acid sequence of butyraldehyde dehydrogenase of *C. autoethanogenum*:
MKVTNVEELMKRLEEIKDAQKKFATYTQEQVDEIFRQAAMAANSARIELAKMAVEESGMGIVEDKVIKNHFASEYIYNKYKDEKTC
GVLERDAGFGIVRIAEPVGVIAAVVPTTNPTSTAIFKSLIALKTRNGIIFSPHPRAKKSTIAAAKIVLDAAVKAGAPEGIIGWIDEPSIELS
QVVMGEANLILATGGPGMVKAAYSSGKPAVGVGPGNTPAVIDESADIKMAVNSILLSKTFDNGMICASEQSVIVLDSIYEEVKKEF
AYRGAYILSKDETDKVGKIILKNGALNAGIVGQPAFKIAQLAGVDVPEKAKVLIGEVESVELEEPFSHEKLSPVLAMYRARNFEDAIAK
TDKLVRAGGFGHTSSLYINPMTEKAKVEKFSTMMKTSRTIINTPSSQGGIGDIYNFKLAPSLTLGCGSWGGNSVSENVGPKHLLNIK
SVAERRENMLWFRVPEKVYFKYGSLGVALKELKVMNKKKVFIVTDKVLYQLGYVDKVTKVLEELKNFL*

FIGURE 24

Seq. ID 43: Nucleotide acid sequence of butyraldehyde dehydrogenase of *C. autoethanogenum*:
TTGGAAAATTTTGATAAAGACTTACGTTCTATACAAGAAGCAAGAGATCTTGCACGTTTAGGAAAAATTGCAGCAGACCAAAT
TGCTGATTATACTGAAGAACAAATTGATAAAATCCTATGTAATATGGTTAGGGTAGCAGAAGAAAATGCAGTTTGCCTTGGTA
AAATGGCTGCAGAAGAAACTGGTTTTGGAAAAGCTGAAGATAAGGCTTATAAGAACCATATGGCTGCTACTACAGTATATAA
TTACATCAAGGATATGAAGACTATTGGTGTTATAAAAGAAGATAAAAGTGAAGGTGTAATTGAATTTGCAGAACCAGTTGGT
TTATTAATGGGTATTGTACCATCTACAAATCCAACATCTACTGTTATTTATAAATCAATCATTGCAATTAAATCAAGAAATGCAA
TTGTATTCTCACCACACCCAGCTGCATTAAAATGTTCAACAAAAGCAATAGAACTTATGCGTGATGCAGCAGTAGCAGCAGGA
GCTCCTGCAAATGTAATTGGTGGTATTGTTACACCATCTATACAAGCTACAAATGAACTTATGAAAGCTAAAGAAGTTGCTAT
GATAATTGCAACTGGAGGCCCTGGAATGGTAAAGGCTGCATATAGTTCAGGAACACCTGCAATAGGCGTTGGTGCTGGTAAC
TCTCCATCCTATATTGAAAGAACTGCTGATGTTCATCAATCAGTTAAAGATATAATAGCTAGTAAGAGTTTTGACTATGGTACT
ATTTGTGCATCCGAGCAGTCTGTAATTGCAGAAGAATGCAACCATGATGAAATAGTAGCTGAATTTAAGAAACAAGGCGGAT
ATTTCATGACAGCTGAAGAAACTGCAAAAGTTTGCAGCGTACTTTTTAAACCTGGTACACACAGCATGAGCGCTAAGTTTGTA
GGAAGAGCTCCTCAGGTTATAGCAGAAGCTGCAGGTTTCACAGTTCCAGAAGGAACAAAAGTATTAATAGGAGAACAAGGC
GGAGTTGGTAATGGTTACCCTCTATCTTATGAGAAACTTACAACAGTACTTGCTTTCTATACAGTTAAAGATTGGCATGAAGC
ATGTGAGCTTAGTATAAGATTACTTCAAAATGGTCTTGGACATACAATGAACATTCATACAAATGATAGAGACTTAGTAATGA
AGTTTGCTAAAAAACCAGCATCCCGTATCTTAGTTAATACTGGTGGAAGCCAGGGAGGTACTGGTGCAAGCACAGGATTAGC
ACCTGCATTTACATTAGGTTGTGGTACATGGGGAGGAAGCTCTGTTTCTGAAAATGTTACTCCATTACATTTAATCAATATAAA
GAGAGTAGCATATGGTCTTAAAGATTGTACTACATTAGCTGCAGACGATACAACTTTCAATCATCCTGAACTTTGCGGAAGCA
AAAATGACTTAGGATTCTGTGCTACAAGCCCTGCAGAATTTGCAGCAAAGAGCAATTGTGATAGCACTGCTGCAGATACTACT
GATAATGATAAACTTGCTAGACTCGTAAGTGAATTAGTAGCTGCAATGAAGGGAGCTAACTAA

Seq. ID 44: Amino acid sequence of butyraldehyde dehydrogenase of *C. autoethanogenum*:
MENFDKDLRSIQEARDLARLGKIAADQIADYTEEQIDKILCNMVRVAEENAVCLGKMAAEETGFGKAEDKAYKNHMAATTVYNYI
KDMKTIGVIKEDKSEGVIEFAEPVGLLMGIVPSTNPTSTVIYKSIIAIKSRNAIVFSPHPAALKCSTKAIELMRDAAVAAGAPANVIGGI
VTPSIQATNELMKAKEVAMIIATGGPGMVKAAYSSGTPAIGVGAGNSPSYIERTADVHQSVKDIIASKSFDYGTICASEQSVIAEECN
HDEIVAEFKKQGGYFMTAEETAKVCSVLFKPGTHSMSAKFVGRAPQVIAEAAGFTVPEGTKVLIGEQGGVGNGYPLSYEKLTTVLA
FYTVKDWHEACELSIRLLQNGLGHTMNIHTNDRDLVMKFAKKPASRILVNTGGSQGGTGASTGLAPAFTLGCGTWGGSSVSENV
TPLHLINIKRVAYGLKDCTTLAADDTTFNHPELCGSKNDLGFCATSPAEFAAKSNCDSTAADTTDNDKLARLVSELVAAMKGAN

FIGURE 25

Seq. ID 45: Nucleotide acid sequence of butyraldehyde dehydrogenase of *C. autoethanogenum*:
GTGGAAAATGCTGCACGAGCACAAAAAATGTTAGCAACCTTTCCACAAGAAAAGCTAGATGAGATTGTTGAACGTATGGCGG
AAGAAATCGGAAAACATACCCGAGAGCTTGCTGTAATGTCACAGGATGAAACTGGTTATGGAAAATGGCAGGATAAATGCA
TCAAAAACCGATTTGCCTGTGAGTATTTGCCAGCTAAGCTTAGAGGAATGCGATGTGTAGGTATTATTAATGAAAATGGTCAG
GATAAGACCATGGATGTAGGTGTACCTATGGGTGTAATTATTGCATTATGTCCTGCAACTAGTCCGGTTTCTACTACCATATAT
AAGGCATTGATTGCAATTAAGTCTGGTAATGCAATTATCTTTTCTCCACATCCTAGAGCAAAGGAGACAATTTGTAAGGCGCT
TGACATCATGATTCGTGCAGCTGAAGGATATGGGCTTCCAGAAGGAGCTCTTGCATACTTACATACTGTGACGCCTAGTGGA
ACAATCGAATTGATGAACCATATTGCGACTTCTTTGATTATGAATACAGGTGTTCCCGGGATGCTTAAAGCAGCATATAATTCT
GGGAAACCTGTTATATATGGAGGAACTGGTAATGGACCAGCATTTATTGAACGTACAGCTGACATCAAACAGGCGGTAAAA
GATATTATTGCTAGTAAGACCTTTGATAACGGAATAGTACCATCAGCTGAACAATCTATTGTTGTAGATAGCTGTGTTGCATCT
GATGTTAAACGTGAGTTGCAAAATAATGGTGCATATTTCATGACAGAGGAGGAAGCACAAAAACTAGGTTCTCTCTTTTTCCG
TTCTGATGGCAGTATGGATTCAGAAATGGTTGGCAAATCCGCACAAAGATTGGCTAAAAAAGCAGGTTTCAGCATTCCTGAA
AGTAGCACAGTGCTAATTTCAGAGCAGAAATATGTTTCTCAAGATAATCCTTATTCCAAGGAGAAACTTTGTCCGGTACTAGC
TTACTACATTGAAGATGATTGGATGCATGCATGTGAAAAGTGTATTGAACTGCTGTTAAGTGAGAGACATGGTCACACTCTTG
TTATACATTCAAAAGACGAAGATGTAATTCGCCAGTTTGCATTAAAAAAACCTGTAGGTAGGATACTTGTTAATACGCCTGCT
TCCTTTGGTAGTATGGGTGCTACAAGTAATTTATTTCCTGCTTTAACTTTAGGTAGTGGATCGGCAGGTAAAGGTATTACCTCC
GATAATGTTTCACCAATGAATCTTATTTACGTCCGCAAAGTCGGATATGGCGTACGGAATGTAGAAGAGATTGTCAATACTAA
TGGATTGTTTACAGAAGAAAAAAGTGATTTGAATGGAATGACAAAAAAGTCAGACTATAATCCAGAGGATATACAAATGTTA
CAGCATATTTTAAAAAAAGCTATGGAAAAAATTAAATAG

FIGURE 26

Seq. ID 46: Amino acid sequence of butyraldehyde dehydrogenase of *C. autoethanogenum*:
MENAARAQKMLATFPQEKLDEIVERMAEEIGKHTRELAVMSQDETGYGKWQDKCIKNRFACEYLPAKLRGMRCVGIINENGQD
KTMDVGVPMGVIIALCPATSPVSTTIYKALIAIKSGNAIIFSPHPRAKETICKALDIMIRAAEGYGLPEGALAYLHTVTPSGTIELMNHI
ATSLIMNTGVPGMLKAAYNSGKPVIYGGTGNGPAFIERTADIKQAVKDIIASKTFDNGIVPSAEQSIVVDSCVASDVKRELQNNGAY
FMTEEEAQKLGSLFFRSDGSMDSEMVGKSAQRLAKKAGFSIPESSTVLISEQKYVSQDNPYSKEKLCPVLAYYIEDDWMHACEKCIE
LLLSERHGHTLVIHSKDEDVIRQFALKKPVGRILVNTPASFGSMGATSNLFPALTLGSGSAGKGITSDNVSPMNLIYVRKVGYGVRN
VEEIVNTNGLFTEEKSDLNGMTKKSDYNPEDIQMLQHILKKAMEKIK*

Seq. ID 119: Nucleotide acid sequence of butanol dehydrogenase of *C. autoethanogenum*:
ATGGCAAGATTTACTTTACCAAGAGACATTTATTTTGGAGAAAATTCATTAGAAACCTTGAAAGACCTAGATGGAAAAAAAGC
TGTTATTGTCGTAGGTGGTGGATCCATGAAACGATTTGGATTCCTTGATAAGGTAGTAAACTACTTAAAAGAAGCAGGTATTG
AATCAAAATTAATAGAAGGAGTTGAACCAGATCCATCTGTAGAAACTGTTATGAATGGCGCTAAACTAATGAGAGAATATGA
ACCAGATTTAATAGTATCAATAGGTGGAGGTTCACCAATTGACGCAGCAAAAGCTATGTGGATATTCTATGAATACCCTGAGT
TTACTTTTAAAGAGGCTGTGGTTCCTTTTGGTCTTCCTAAATTAAGACAAAAAGCAACATTTATAGCTATACCTTCTACAAGTG
GTACTGCAACAGAAGTAACGGCATTTTCTGTAATAACAGACTATAAAGCTAAAATTAAATATCCTTTAGCTGACTTCAATTTAA
CACCAGATATAGCTATAATTGATCCAGCATTAGCTCAAACAATGCCACCTAAATTAACTGCACATACTGGAATGGATGCACTT
ACCCATGCTATTGAAGCATATGTTGCAGGACTTCATTCAGTTTTCTCAGATCCTCTTGCTATTCAAGCTATAGTTATGGTAAATC
AGTATTTAATTAAATCTTACAATGAAGATAAAGAAGCTAGAAACCAAATGCATTTAGCTCAATGTTTAGCTGGAATGGCATTT
TCAAATGCACTTCTTGGAATAACTCACAGTTTAGCACATAAAACAGGTGCAGTATTCCATATTCCTCATGGATGTGCCAATGCA
ATATATCTTCCCTATGTTATAGATTTCAATAAAAAAGCTTGTACACCAAGATATGCTGATATAGCTAGGAGTCTTAAACTTCCA
GGAAATACTGATGATGAATTAGTAGATTCATTAACTAACATGATTAAAGATATGAACAAGAGTATGGATATTCCTTTGACATT
AAAAGATTACGGAGTAGATGAAAAAGAATTTAAAGATAATGAAGATTTTATAGCTCATAATGCCGTATTAGATGCCTGCACT
GGATCAAATCCTAGAAGTATAAATGATGCTGAAATGAAAAAATTGTTAGAATACATCTATTATGGTAAAAAGGTTGATTTTTA
A

FIGURE 27

Seq. ID 120: Amino acid sequence of butanol dehydrogenase of *C. autoethanogenum*:
MARFTLPRDIYFGENSLETLKDLDGKKAVIVVGGGSMKRFGFLDKVVNYLKEAGIESKLIEGVEPDPSVETVMNGAKLMREYEPDLI
VSIGGGSPIDAAKAMWIFYEYPEFTFKEAVVPFGLPKLRQKATFIAIPSTSGTATEVTAFSVITDYKAKIKYPLADFNLTPDIAIIDPALA
QTMPPKLTAHTGMDALTHAIEAYVAGLHSVFSDPLAIQAIVMVNQYLIKSYNEDKEARNQMHLAQCLAGMAFSNALLGITHSLAH
KTGAVFHIPHGCANAIYLPYVIDFNKKACTPRYADIARSLKLPGNTDDELVDSLTNMIKDMNKSMDIPLTLKDYGVDEKEFKDNEDF
IAHNAVLDACTGSNPRSINDAEMKKLLEYIYYGKKVDF*

Seq. ID 121: Nucleotide acid sequence of butanol dehydrogenase of *C. autoethanogenum*:
ATGGGAAGATTTACTTTGCCTAGGGATATTTACTTTGGTGAAAATGCCTTAGAAAATTTAAAAAATTTAGATGGAAATAAAGC
AGTAGTTGTTGTAGGTGGGGGATCTATGAAGAGATTTGGATTCTTAGCCAAAGTTGAAAAATACTTAAAAGAAACTGGTATG
GAAGTTAAATTAATAGAAGGTGTTGAGCCTGATCCGTCTGTTGATACTGTTATGAATGGCGCTAAAATAATGAGAGACTTTAA
CCCAGATTGGATAGTATCAATAGGTGGAGGATCTCCCATAGATGCTGCTAAAGCAATGTGGATATTTTATGAATACCCCGACT
TTACATTTGAAAAAGCGGTAGTCCCTTTTGGAATTCCTAAATTAAGGCAGAAGGCACAATTTGTTGCTATACCTTCTACAAGTG
GAACAGCAACTGAAGTAACATCATTTTCTGTAATAACAGACTATAAAGCTAAAATAAAATATCCTCTTGCAGATTTTAACCTTA
CCCCTGATATAGCTATAATAGATCCGTCTCTTGCAGAAACAATGCCCAAAAAGCTTACAGCACACACTGGAATGGATGCACTT
ACTCACGCAATAGAAGCATATGTAGCAAGTTTACATTCAGATTTCTCAGATCCACTTGCTATGCATGCTATAACCATGATTCAT
AAATATTTATTGAAATCCTATGAAGAAGATAAAGAAGCTAGAGGACATATGCATATAGCCCAATGTCTAGCTGGGATGGCAT
TTTCAAATGCTCTCCTTGGAATAACTCATAGTATAGCACATAAAACTGGTGCAGTATTTCACATACCTCATGGGTGTGCTAATG
CCATATACTTACCTTATGTTATAGATTTTAACAAGAAAGCTTGTTCAGAAAGATATGCTAAAATAGCCAAAAAGCTGCATCTAT
CAGGAAATAGTGAAGATGAGCTAATAGATTCATTAACTGAAATGATTCGTACTATGAACAAAAAGATGGATATTCCTCTCACC
ATAAAAGATTATGGTATAAGCGAAAACGATTTTAATGAAAACCTAGATTTTATAGCTCACAATGCCATGATGGATGCCTGCAC
TGGATCCAATCCTAGAGCAATAACTGAGGAAGAAATGAAAAAGCTCTTGCAGTATATGTATAATGGGCAAAAGGTTAATTTC
TAG

FIGURE 28

Seq. ID 122: Amino acid sequence of butanol dehydrogenase of *C. autoethanogenum*:
MGRFTLPRDIYFGENALENLKNLDGNKAVVVVGGGSMKRFGFLAKVEKYLKETGMEVKLIEGVEPDPSVDTVMNGA
KIMRDFNPDWIVSIGGGSPIDAAKAMWIFYEYPDFTFEKAVVPFGIPKLRQKAQFVAIPSTSGTATEVTSFSVITDYKAKI
KYPLADFNLTPDIAIIDPSLAETMPKKLTAHTGMDALTHAIEAYVASLHSDFSDPLAMHAITMIHKYLLKSYEEDKEARG
HMHIAQCLAGMAFSNALLGITHSIAHKTGAVFHIPHGCANAIYLPYVIDFNKKACSERYAKIAKKLHLSGNSEDELIDSLT
EMIRTMNKKMDIPLTIKDYGISENDFNENLDFIAHNAMMDACTGSNPRAITEEEMKKLLQYMYNGQKVNF*

Seq. ID 51: Nucleotide acid sequence of butanol dehydrogenase of *C. autoethanogenum*:
ATGAAAGTTACAAACGTAGAAGAACTAATGAAAAGACTAGAAGAAATAAAGGATGCTCAAAAGAAATTTGCTAC
ATATACTCAAGAACAAGTGGATGAAATTTTTAGACAAGCAGCTATGGCAGCTAATAGTGCTAGAATAGAACTAGC
TAAAATGGCAGTAGAAGAAAGCGGAATGGGAATTGTAGAAGACAAGGTTATTAAAAATCACTTTGCTTCAGAAT
ATATATATAACAAATATAAGGATGAAAAAACCTGTGGAGTTTTAGAGAGAGATGCAGGCTTTGGTATAGTTAGA
ATTGCGGAACCTGTAGGAGTTATTGCAGCAGTAGTTCCAACAACTAATCCAACATCTACAGCAATATTTAAATCAC
TAATAGCTTTAAAAACTAGAAATGGTATAATTTTTTCACCCCATCCAAGGGCAAAGAAATCAACTATTGCAGCAGC
TAAAATAGTACTTGACGCTGCAGTTAAAGCTGGTGCTCCTGAAGGAATTATAGGATGGATAGATGAACCTTCCAT
TGAACTTTCACAGGTGGTAATGGGAGAAGCAAATTTAATTCTTGCAACTGGTGGTCCGGGTATGGTTAAGGCTGC
CTATTCTTCAGGCAAACCTGCTGTGGGAGTTGGTCCAGGTAACACACCTGCTGTAATTGATGAAAGTGCCGACAT
TAAAATGGCAGTAAATTCAATATTACTATCAAAAACTTTTGATAATGGTATGATTTGTGCCTCAGAGCAGTCAGTA
ATAGTTTTAGACTCAATATATGAGGAAGTTAAAAAAGAATTTGCTTATAGGGGTGCTTATATATTAAGTAAGGAT
GAAACAGATAAGGTTGGAAAAATAATTTTAAAAAATGGAGCCTTAAATGCAGGTATTGTAGGACAACCTGCTTTT
AAAATAGCACAGCTGGCAGGAGTGGATGTACCAGAAAAAGCTAAAGTACTTATAGGAGAGGTAGAATCGGTAG
AACTTGAAGAACCATTTTCTCATGAAAAGTTATCTCCAGTTTTAGCTATGTACAGGGCAAGAAATTTTGAGGATGC
CATTGCAAAAACTGATAAACTGGTTAGGGCAGGTGGATTTGGACATACATCTTCATTGTATATAAATCCAATGAC
AGAAAAAGCAAAAGTAGAAAAATTTAGTACTATGATGAAAACATCAAGAACTATAATTAACACACCTTCATCCCA
AGGTGGTATAGGTGATATATATAACTTTAAACTAGCTCCTTCTTTGACATTAGGCTGCGGTTCCTGGGGGGGAAA
TTCTGTATCCGAAAATGTTGGGCCTAAACATTTATTAAACATAAAAAGTGTTGCTGAGAGGAGAGAAAATATGCT
TTGGTTTAGAGTACCTGAAAAGGTTTATTTCAAATATGGTAGTCTTGGAGTTGCATTAAAAGAGTTAAAAGTTATG
AATAAGAAGAAAGTATTTATAGTAACAGATAAAGTTCTTTATCAATTAGGTTATGTGGACAAAGTTACAAAAGTT
CTTGAGGAACTAAAAATTTCCTATAAGGTATTTACAGATGTAGAACCAGATCCAACCCTTGCTACAGCTAAAAAA
GGTGCAGCAGAACTGCTTTCCTATGAACCGGATACAATTATATCAGTTGGTGGTGGTTCAGCAATGGATGCAGCT
AAGATCATGTGGGTAATGTATGAGCATCCAGAAGTAAAATTTGAAGATTTAGCTATGAGATTTATGGATATAAGA
AAGAGAGTATATGTTTTCCCTAAGATGGGAGAAAAGGCAATGATGATTTCAGTAGCAACATCCGCAGGAACAGG
GTCGGAAGTTACTCCATTTGCAGTAATCACTGATGAAAAAACAGGAGCTAAATATCCATTAGCTGATTATGAACT
AACTCCAGACATGGCTATAGTTGATGCAGAACTTATGATGGGAATGCCAAGAGGACTTACAGCAGCTTCGGGTA
TAGATGCATTAACCCATGCACTGGAGGCGTATGTGTCAATAATGGCTACAGAATTTACCAATGGATTAGCCCTTG
AAGCAGTAAAGTTGATATTTGAATATTTACCAAAAGCTTATACAGAAGGTACAACTAATGTAAAGGCAAGAGAAA
AGATGGCTCATGCTTCATGTATTGCAGGTATGGCCTTTGCAAATGCATTTTTAGGGGTATGCCACTCTATGGCACA
TAAATTGGGAGCACAGCATCACATACCACATGGAATTGCCAATGCACTTATGATAGATGAAGTTATAAAATTCAA
TGCTGTAGATGATCCAATAAAACAAGCTGCATTTCCCCAATACGAGTATCCAAATGCTAGGTATAGATATGCTCA
GATAGCTGATTGTCTGAACTTGGGAGGAAATACAGAAGAGGAAAAGGTACAACTATTAATAAATGCTATAGATG
ATTTAAAAGCTAAGTTAAATATTCCAGAAACTATAAAAGAAGCAGGAGTTTCAGAAGATAAATTCTATGCTACTTT
AGATAAAATGTCAGAATTAGCTTTTGATGATCAGTGTACAGGAGCTAATCCAAGATATCCACTGATAAGTGAAAT
AAAACAAATGTATATAAATGTTTTTGATAAAACCGAACCAATTGTAGAAGATGAAGAAAAGTAA

FIGURE 29

Seq. ID 52: Amino acid sequence of butanol dehydrogenase of *C. autoethanogenum*:
MDAAKIMWVMYEHPEVKFEDLAMRFMDIRKRVYVFPKMGEKAMMISVATSAGTGSEVTPFAVITDEKTGAKYPLADYELTPDM
AIVDAELMMGMPRGLTAASGIDALTHALEAYVSIMATEFTNGLALEAVKLIFEYLPKAYTEGTTNVKAREKMAHASCIAGMAFAN
AFLGVCHSMAHKLGAQHHIPHGIANALMIDEVIKFNAVDDPIKQAAFPQYEYPNARYRYAQIADCLNLGGNTEEEKVQLLINAIDD
LKAKLNIPETIKEAGVSEDKFYATLDKMSELAFDDQCTGANPRYPLISEIKQMYINVFDKTEPIVEDEEK*

Seq. ID 53: Nucleotide acid sequence of butanol dehydrogenase of *C. autoethanogenum*:
ATGGAAATAAAATTAGGGGGAATAATAATGGAGAGATTTACGTTGCCAAGAGACATTTACTTTGGAGAAGATGCTTTGGGTG
CTTTGAAAACGTTAAAAGGTAAGAAAGCTGTAGTAGTTGTTGGAGGAGGATCCATGAAGAGATTCGGTTTCCTTGACAAGGT
AGAAGAATACTTAAAAGAAGCAAACATAGAAGTTAAACTAATAGAAGGTGTTGAACCAGATCCGTCTGTGGAAACCGTTATG
AAAGGTGCCAAAATAATGACAGAATTTGGGCCAGATTGGATAGTTGCTATTGGAGGAGGTTCACCAATAGATGCTGCAAAG
GCTATGTGGCTATTTTATGAATATCCAGATTTTACTTTTAAACAAGCAATTGTTCCGTTTGGATTACCAGAATTAAGACAAAAA
GCTAAATTTGTAGCTATAGCTTCTACTAGTGGAACAGCTACTGAAGTTACTTCATTTTCAGTAATAACTGATTATAAAGCTAAA
ATAAAGTATCCTTTAGCTGACTTCAATTTGACACCGGATATAGCTATAGTTGATCCAGCATTAGCCCAGACAATGCCACCTAAA
TTAACTGCACATACTGGTATGGATGCATTAACTCATGCACTAGAAGCTTATGTAGCATCAGCTAGATCAGATATTTCAGATCCA
CTTGCAATACATTCCATAATTATGACAAGGGATAACTTACTTAAATCCTATAAGGGTGATAAAGATGCTAGAAATAAGATGCA
TATATCACAATGTTTAGCAGGTATGGCATTTTCTAATGCACTTCTTGGTATAACTCATAGTTTAGCACATAAAACAGGAGCTGT
ATGGCACATACCACATGGATGCGCTAATGCAATATATCTTCCATATGTTTTAGATTTTAATAAAAAAGCTTGCTCAGATAGATA
TGCTAATATAGCTAAAATATTAGGACTTAAAGGAACTACTGAAGATGAATTGGTAGATTCTCTAGTTAAAATGGTACAAGATA
TGGATAAGGAATTGAATATACCTTTGACCTTAAAAGATTATGGTATAAGCAAAGATGATTTCAATTCAAATGTTGATTTTATAG
CAAAGAATGCGCTCTTAGATGCATGTACAGGAGCTAATCCAAGGCCTATAGATTTTGATCAAATGAAAAAGATACTTCAATGT
ATATATGATGGAAAAAAGGTAACTTTTTAA

FIGURE 30

Seq. ID 54: Amino acid sequence of butanol dehydrogenase of *C. autoethanogenum*:
MEIKLGGIIMERFTLPRDIYFGEDALGALKTLKGKKAVVVVGGGSMKRFGFLDKVEEYLKEANIEVKLIEGVEPDPSVETVMKGAKI
MTEFGPDWIVAIGGGSPIDAAKAMWLFYEYPDFTFKQAIVPFGLPELRQKAKFVAIASTSGTATEVTSFSVITDYKAKIKYPLADFNL
TPDIAIVDPALAQTMPPKLTAHTGMDALTHALEAYVASARSDISDPLAIHSIIMTRDNLLKSYKGDKDARNKMHISQCLAGMAFSN
ALLGITHSLAHKTGAVWHIPHGCANAIYLPYVLDFNKKACSDRYANIAKILGLKGTTEDELVDSLVKMVQDMDKELNIPLTLKDYGIS
KDDFNSNVDFIAKNALLDACTGANPRPIDFDQMKKILQCIYDGKKVTF*

Seq. ID 55: Nucleotide acid sequence of butanol dehydrogenase of *C. autoethanogenum*:
GTGAGGGATGTTATTATGGAAAACTTTATTTTTAAAAATGCTACAGAAATTATTTTTGGTAAGGATACCGAAAATCTTGTAGG
AAGTAAAGTAAAGGAGTATTCAAAGTCAGATAAAATACTCTTTTGCTATGGGGGAGGAAGCATAAAAAGATCTGGTCTATAT
GATAGAGTTATAAAGTCCTTAAAAGAAAATGGAATTGAATTTATAGAACTTCCAGGAATTAAACCTAATCCAAGATTAGGACC
TGTTAAAGAAGGTATAAGACTATGTAGAGAAAATAATATAAAATTTGTACTATCTGTAGGAGGAGGAAGTTCAGCAGATACG
GCTAAAGCTATTGCTGTAGGAGTACCTTATAAAGGAGACGTATGGGATTTTTATACGGGCAAAGCTGAAGTGAAAGAGGCTC
TTCCTGTAGGAGTTGTAATAACATTACCTGCTACAGGTACAGAATCTAGTAATAGTTCTGTTATTATGAATGAAGATGGTTGG
TTTAAAAAAGGATTAAATACAGTACTTATAAGACCTGCTTTTTCAATTATGAATCCTGAACTTACTTTTACACTACCAGAGTATC
AAACTGCTTGTGGTGCTTGTGACATTATGGCACATATAATGGAAAGATATTTTACAAATGTGAAACATGTAGATATAACTGAT
AGGCTTTGCGAAGCTGCACTTAGAAATGTTATAAATAATGCCCCAATAGTTTTAAAAGATCCCAAAAACTATGATGCTAGGGC
AGAAATTATGTGGACCGGTACTATAGCTCATAATGATGTGCTTAGTGCGGGTAGAATAGGTGATTGGGCTTCTCACAAAATT
GAACATGAATTGAGTGGGGAAACAGACATTGCCCATGGAGCAGGACTTGCAATTGTATTTCCTGCATGGATGAAATATGTAT
ATAAACACGATATCAATAGATTTGTACAATTTGCAGTAAGGGTATGGGATGTAGATTTATCTTATAGTTCCTGCGAAGATATT
GTACTTGAAGGCATAAGGAGAATGACAGCATTTTTCAAGAGCATGGGGTTACCTGTAACTTTAAAAGAAGGAAGTATAGGA
GAAGATAAAATTGAAGAAATGGCTAATAAGTGCACGGATAATGGAACTAAAACTGTAGGACAATTTGTAAAATTAAATAAAG
ATGATATTGTAAAAATATTAAATTTAGCTAAATAA

FIGURE 31

Seq. ID 56: Amino acid sequence of butanol dehydrogenase of *C. autoethanogenum*:
VRDVIMENFIFKNATEIIFGKDTENLVGSKVKEYSKSDKILFCYGGGSIKRSGLYDRVIKSLKENGIEFIELPGIKPNPRLGPVKEGIRLCR
ENNIKFVLSVGGGSSADTAKAIAVGVPYKGDVWDFYTGKAEVKEALPVGVVITLPATGTESSNSSVIMNEDGWFKKGLNTVLIRPA
FSIMNPELTFTLPEYQTACGACDIMAHIMERYFTNVKHVDITDRLCEAALRNVINNAPIVLKDPKNYDARAEIMWTGTIAHNDVLS
AGRIGDWASHKIEHELSGETDIAHGAGLAIVFPAWMKYVYKHDINRFVQFAVRVWDVDLSYSSCEDIVLEGIRRMTAFFKSMGLP
VTLKEGSIGEDKIEEMANKCTDNGTKTVGQFVKLNKDDIVKILNLAK*

Seq. ID 57: Nucleotide acid sequence of butanol dehydrogenase of *C. autoethanogenum*:
ATGGAAGACAAGTTTGAAAATTTTAATTTGAAATCCAAGATTTATTTTAATAGGGAATCTATTCAACTTTTAGAGCAAGTCACT
GGTTCTCGAGCATTTATTGTTGCAGATGCTATTATGGGAAAACTTGGATATCTTCAAAAAGTAATAGATTACCTAAGCAAAGC
TGGAATAAGTTCCGTTGTTTTTACGGGGGTACACCCTGATCCAGACGTCAATGTAATTGCAGATGCAATGAAATTGTACAAAA
AAAGCGACGCAGATGTTCTCGTAGCACTAGGTGGAGGATCCAGTATTGATACCGCTAAGGGAATAATGTATTTTGCATGTAA
TTTAGGAAAAGCAATGGGCCAAGAAATGAAAAAACCTCTATTTATTGCAATTCCATCAACAAGTGGTACAGGCTCTGAAGTA
ACAAACTTTACTGTTATTACTTCTCAGAAAGAAAAGGTATGCATTATAGATGATTTTATTGCACCAGATGTTGCAATACTTGAC
TCAAGTTGTATTGATGGTCTGCCTCAGCGTATTGTAGCAGATACTGGTATAGATGTTCTAGTTCATTCTATTGAAGCCTATGTT
TCCAAAAAAGCAACTGACTTTACAGACGCTCTTGCTGAAAAAGCAGTTAAATTAATTTTTGAGAATCTTCCAAAAATTTATAAC
GATAGTAAGGATTCCGAAGCTCGAGATCATGTTCAAAACGCTTCCTGTATAGCAGGAATAGCATTTACAAATGCTGGTCTTGG
AATTAATCACAGCTTGGCTCATGCTATGGGTGGATCTTTCCACATTCCTCACGGCCGATCCAATGCACTTCTACTTAATGCAGT
AATGGAATACAACGCTAGCTTGGTTGGAAATGCAAGCGAACATGCTATGGAAAAATACGCAAAACTAGCATCAATTCTACAC
CTTCCAGCTCGAACAACTCGCGAAGGCGCTGTAAGTTTTATTGAAGCTGTAGATAAATTAATAAAATCCCTAGGTGTTGAAGA
TAATATTCGATCTCTTGGGATTAAAGAAGATGAGTTTCAAAGTGCTCTAAATCATATGGCAGAAACAGCAATGCAAGATAGAT
GCACTCCAACTAATCCTAGAAAACCTTCTAAAGAAGAACTTATACATATTTATCAAAAATGTTATTAA

FIGURE 32

Seq. ID 58: Amino acid sequence of butanol dehydrogenase of *C. autoethanogenum*:
MEDKFENFNLKSKIYFNRESIQLLEQVTGSRAFIVADAIMGKLGYLQKVIDYLSKAGISSVVFTGVHPDPDVNVIADAMKLYKKSDAD
VLVALGGGSSIDTAKGIMYFACNLGKAMGQEMKKPLFIAIPSTSGTGSEVTNFTVITSQKEKVCIIDDFIAPDVAILDSSCIDGLPQRIV
ADTGIDVLVHSIEAYVSKKATDFTDALAEKAVKLIFENLPKIYNDSKDSEARDHVQNASCIAGIAFTNAGLGINHSLAHAMGGSFHIP
HGRSNALLLNAVMEYNASLVGNASEHAMEKYAKLASILHLPARTTREGAVSFIEAVDKLIKSLGVEDNIRSLGIKEDEFQSALNHMA
ETAMQDRCTPTNPRKPSKEELIHIYQKCY*

Seq. ID 59: Nucleotide of phosphate acetyl/butyryl transferase from *C. autoethanogenum*:
ATGGAAAAAATTTGGAGTAAGGCAAAGGAAGACAAAAAAAAGATTGTCTTAGCTGAAGGAGAAGAAGAAAGAACTCTTCAA
GCTTGTGAAAAAATAATTAAAGAGGGTATTGCAAATTTAATCCTTGTAGGGAATGAAAAGGTAATAAAAGAAAAAGCGTCAA
AATTAGGTGTAAGTTTAAATGGAGCAGAAATAGTAGATCCAGAGATTTCAGATAAACTAAAGGCATATGCAGATGCTTTTTAT
GAATTGAGAAAGAAGAAGGGAATAACGCCAGAAAAAGCGGATAAAATAGTAAGAGATCCAATATACTTTGCTACAATGATG
GTTAAACTTGGAGATGCAGATGGATTGGTTTCAGGTGCGGTTCATACTACAGGCGATCTTTTGAGACCAGGACTTCAAATAGT
AAAGACAGCTCCAGGTACATCAGTAGTTTCCAGTACATTTATAATGGAAGTACCAAATTGTGAGTATGGTGACAATGGTGTAC
TTCTATTTGCTGATTGTGCTGTAAATCCATGCCCAGATAGTGATCAATTGGCTTCAATTGCAATAAGTACAGCAGAAACTGCAA
AGAACTTATGTGGAATGGATCCAAAAGTAGCAATGCTTTCATTTTCTACTAAGGGAAGTGCAAAACACGAATTAGTAGACAA
AGTTAGAAATGCTGTAGAGATTGCAAAAAAAGCTAAACCAGATTTAAGTTTAGACGGAGAATTACAATTAGATGCCTCTATC
GTAGAAAAGGTTGCAAGTTTAAAGGCTCCTGGAAGTGAAGTAGCAGGAAAAGCAAATGTACTTGTATTTCCAGATCTCCAAG
CAGGAAATATAGGCTATAAACTCGTTCAAAGATTTGCAAAAGCAGATGCTATAGGACCTGTATGCCAAGGATTTGCAAAACC
TATAAATGATTTGTCAAGAGGATGTAATTCTGATGATATAGTAAATGTAGTAGCTGTAACAGCAGTTCAAGCACAAGCTCAAA
AGTAA

Seq. ID 60: Amino acid sequence of phosphate acetyl/butyryl transferase from *C. autoethanogenum*:
MEKIWSKAKEDKKKIVLAEGEEERTLQACEKIIKEGIANLILVGNEKVIKEKASKLGVSLNGAEIVDPEISDKLKAYADAFYELRKKKGIT
PEKADKIVRDPIYFATMMVKLGDADGLVSGAVHTTGDLLRPGLQIVKTAPGTSVVSSTFIMEVPNCEYGDNGVLLFADCAVNPCP
DSDQLASIAISTAETAKNLCGMDPKVAMLSFSTKGSAKHELVDKVRNAVEIAKKAKPDLSLDGELQLDASIVEKVASLKAPGSEVAG
KANVLVFPDLQAGNIGYKLVQRFAKADAIGPVCQGFAKPINDLSRGCNSDDIVNVVAVTAVQAQAQK*

FIGURE 33

Seq. ID 61: Nucleotide sequence of acetate/butyrate kinase from *C. autoethanogenum*:
ATGAAAATATTAGTAGTAAACTGTGGAAGTTCATCTTTAAAATATCAACTTATTGATATGCAAGATGAAAGTGTTGTAGCAAA
GGGTCTTGTAGAAAGAATAGGAATGGACGGTTCAATTTTAACACACAAAGTTAATGGAGAAAAGTTTGTTACAGAGCAACCA
ATGGAAGACCACAAAGTTGCTATACAATTAGTATTAAATGCTCTTGTAGATAAAAAACATGGTGTAATAAAAGACATGTCAGA
AATATCCGCTGTAGGACATAGAGTTTTGCACGGTGGAAAGAAATATGCAGCATCCATTCTTATTGACGAAAATGTAATGAAA
GCAATAGAAGAATGTATCCCACTAGGACCACTACATAATCCAGCTAATATAATGGGAATAGATGCTTGTAAAAAATTAATGCC
AAATACTCCAATGGTAGCAGTATTTGATACAGCATTTCATCAGACAATGCCAGATTATGCTTATACTTATGCAATACCTTATGA
TATATCTGAAAAGTATGATATCAGAAAATATGGTTTTCATGGAACTTCTCATAGATTCGTTTCAATTGAAGCAGCTAAATTATT
AAAGAAAGATCCAAAAGATCTTAAGTTAATAACTTGTCATTTAGGAAATGGAGCTAGCATATGTGCAGTAAACCAAGGAAAA
GCAGTAGATACAACTATGGGACTTACTCCTCTTGCAGGACTTGTAATGGGAACTAGATGCGGTGATATAGATCCAGCTATAGT
ACCATTTGTAATGAAAAGAACAGGCATGTCTGTAGATGAAGTGGATACCTTAATGAATAAAAAGTCAGGAATACTTGGAGTA
TCAGGAGTAAGCAGTGATTTTAGAGATGTAGAAGAAGCTGCAAATTCAGGAAATGATAGAGCAAAACTTGCATTAAATATGT
ATTATCACAAAGTTAAATCTTTCATAGGAGCTTATGTTGCAGTTTTAAATGGAGCAGATGCTATAATATTTACGGCAGGACTTG
GAGAAAATTCAGCAACTAGCAGATCTGCTATATGTAATGGATTAAGCTATTTTGGAATTAAAATAGATGAAGAAAAGAATAA
GAAAAGGGGAGAGGCACTAGAAATAAGCACACCTGATTCAAAGATAAAAGTATTAGTAATTCCTACAAATGAAGAACTTATG
ATAGCTAGGGATACAAAAGAAATAGTTGAAAATAAATAA

Seq. ID 62: Amino acid sequence of acetate/butyrate kinase from *C. autoethanogenum*:
MKILVVNCGSSSLKYQLIDMQDESVVAKGLVERIGMDGSILTHKVNGEKFVTEQPMEDHKVAIQLVLNALVDKKHGVIKDMSEISA
VGHRVLHGGKKYAASILIDENVMKAIEECIPLGPLHNPANIMGIDACKKLMPNTPMVAVFDTAFHQTMPDYAYTYAIPYDISEKYDI
RKYGFHGTSHRFVSIEAAKLLKKDPKDLKLITCHLGNGASICAVNQGKAVDTTMGLTPLAGLVMGTRCGDIDPAIVPFVMKRTGMS
VDEVDTLMNKKSGILGVSGVSSDFRDVEEAANSGNDRAKLALNMYYHKVKSFIGAYVAVLNGADAIIFTAGLGENSATSRSAICNG
LSYFGIKIDEEKNKKRGEALEISTPDSKIKVLVIPTNEELMIARDTKEIVENK*

FIGURE 34

Seq. ID 63: Nucleotide sequence of aldehyde:ferredoxin oxidoreductase from *C. autoethanogenum*:
GTGGAAGAATTGAAAATTGACAAAGCTAAAAAATTTATAGGTGCAAGAGGGTTAGGCGTAAAAACCTTATTTGACGAAGTA
GATCCAAAGGTAGATCCATTATCACCTGATAACAAATTTATTATAGCAGCGGGACCACTTACAGGTGCACCTGTTCCAACAAG
CGGAAGATTCATGGTAGTTACTAAATCACCTTTAACAGGAACTATTGCTATTGCAAATTCAGGTGGAAAATGGGGAGCAGAA
TTCAAAGCAGCTGGATACGATATGATAATCGTTGAAGGTAAATCTGATAAAGAAGTTTATGTAAATATAGTAGATGATAAAG
TAGAATTTAGGGATGCTTCTCATGTTTGGGGAAAACTAACAGAAGAAACTACAAAAATGCTTCAACAGGAAACAGATTCGAG
AGCTAAGGTTTTATGCATAGGACCAGCTGGGGAAAAGTTATCACTTATGGCAGCAGTTATGAATGATGTTGATAGAACAGCA
GGACGTGGTGGTGTTGGAGCTGTTATGGGTTCAAAGAACTTAAAAGCTATTGTAGTTAAAGGAAGCGGAAAAGTAAAATTA
TTTGATGAACAAAAAGTGAAGGAAGTAGCACTTGAGAAAACAAATATTTTAAGAAAAGATCCAGTAGCTGGTGGAGGACTTC
CAACATACGGAACAGCTGTACTTGTTAATATTATAAATGAAAATGGTGTACATCCAGTAAAGAATTTTCAAAAATCTTATACA
GATCAAGCAGATAAGATCAGTGGAGAAACTTTAACTAAAGATTGCTTAGTTAGAAAAAATCCTTGCTATAGGTGTCCAATTGC
CTGTGGAAGATGGGTAAAACTTGATGATGGAACTGAATGTGGAGGACCAGAATATGAAACATTATGGTCATTTGGATCTGAT
TGTGATGTATACGATATAAATGCTGTAAATACAGCAAATATGTTGTGTAATGAATATGGACTAGATACCATTACAGCAGGATG
TACTATTGCAGCAGCTATGGAACTTTATCAAAGAGGTTATATTAAGGATGAAGAAATAGCAGCAGATGGATTGTCACTTAATT
GGGGAGATGCTAAGTCCATGGTTGAATGGGTAAAGAAAATGGGACTTAGAGAAGGATTTGGAGACAAGATGGCAGATGGT
TCATACAGACTTTGTGACTCATACGGTGTACCTGAGTATTCAATGACTGTAAAAAAACAGGAACTTCCAGCATATGACCCAAG
AGGAATACAGGGACATGGCATTACTTATGCTGTTAACAATAGGGGAGGATGTCACATTAAGGGATATATGGTAAGTCCTGAA
ATACTTGGCTATCCAGAAAAACTTGATAGACTTGCAGTGGAAGGAAAAGCAGGATATGCTAGAGTATTCCATGATTTAACAG
CTGTTATAGATTCACTTGGATTATGTATTTTTACAACATTTGGTCTTGGTGCACAGGATTATGTTGATATGTATAATGCAGTAG
TTGGTGGAGAATTACATGATGTAAATTCTTTAATGTTAGCTGGAGATAGAATATGGACTTTAGAAAAAATATTTAACTTAAAA
GCAGGCATAGATAGTTCACAGGATACTCTTCCAAAGAGATTGCTTGAAGAACAAATTCCAGAAGGACCATCAAAAGGAGAA
GTTCATAAGTTAGATGTACTACTACCTGAATATTATTCAGTACGTGGATGGGATAAAAATGGTATTCCTACAGAGGAAACGTT
AAAGAAATTAGGATTAGATGAATACGTAGGTAAGCTTTAG

Seq. ID 64: Amino acid sequence of aldehyde:ferredoxin oxidoreductase from *C. autoethanogenum*:
MEELKIDKAKKFIGARGLGVKTLFDEVDPKVDPLSPDNKFIIAAGPLTGAPVPTSGRFMVVTKSPLTGTIAIANSGGKWGAEFKAAG
YDMIIVEGKSDKEVYVNIVDDKVEFRDASHVWGKLTEETTKMLQQETDSRAKVLCIGPAGEKLSLMAAVMNDVDRTAGRGGVGA
VMGSKNLKAIVVKGSGKVKLFDEQKVKEVALEKTNILRKDPVAGGGLPTYGTAVLVNIINENGVHPVKNFQKSYTDQADKISGETLT
KDCLVRKNPCYRCPIACGRWVKLDDGTECGGPEYETLWSFGSDCDVYDINAVNTANMLCNEYGLDTITAGCTIAAAMELYQRGYI
KDEEIAADGLSLNWGDAKSMVEWVKKMGLREGFGDKMADGSYRLCDSYGVPEYSMTVKKQELPAYDPRGIQGHGITYAVNNR
GGCHIKGYMVSPEILGYPEKLDRLAVEGKAGYARVFHDLTAVIDSLGLCIFTTFGLGAQDYVDMYNAVVGGELHDVNSLMLAGDRI
WTLEKIFNLKAGIDSSQDTLPKRLLEEQIPEGPSKGEVHKLDVLLPEYYSVRGWDKNGIPTEETLKKLGLDEYVGKL*

FIGURE 35

Seq. ID 65: Nucleotide sequence of aldehyde:ferredoxin oxidoreductase from *C. autoethanogenum*:
ATGTATGGTTATGATGGTAAAGTATTAAGAATTAATTTAAAAGAAAGAACTTGCAAATCAGAAAATTTAGATTTA
GATAAAGCTAAAAAGTTTATAGGTTGTAGGGGACTAGGTGTTAAAACTTTATTTGATGAAATAGATCCTAAAATA
GATGCATTATCACCAGAAAATAAATTTATAATTGTAACAGGTCCTTTAACTGGAGCTCCGGTTCCAACTAGTGGAA
GGTTTATGGTAGTTACTAAAGCACCGCTTACAGGAACTATAGGAATTTCAAATTCGGGTGGAAAATGGGGAGTA
GACTTAAAAAAAGCTGGTTGGGATATGATAATAGTAGAGGATAAGGCTGATTCACCAGTTTACATTGAAATAGTA
GATGATAAGGTAGAAATTAAAGACGCGTCACAGCTTTGGGGAAAAGTTACATCAGAAACTACAAAAGAGTTAGA
AAAGATAACTGAGAATAAATCAAAGGTATTATGTATAGGACCTGCTGGTGAACGATTGTCTCTTATGGCAGCAGT
TATGAATGATGTAGATAGAACTGCAGCAAGAGGCGGCGTTGGTGCAGTTATGGGATCTAAAAACTTAAAAGCTA
TTACAGTTAAAGGAACTGGAAAAATAGCTTTAGCTGATAAAGAAAAAGTAAAAAAAGTGTCCGTAGAAAAAATT
ACAACATTAAAAAATGATCCAGTAGCTGGTCAGGGAATGCCAACTTATGGTACAGCTATACTGGTTAATATAATA
AATGAAAATGGAGTTCATCCTGTAAAGAATTTTCAAGAGTCTTATACGAATCAAGCAGATAAAATAAGTGGAGAG
ACTCTTACTGCTAACCAACTAGTAAGGAAAAATCCTTGTTACAGCTGTCCTATAGGTTGTGGAAGATGGGTTAGA
CTAAAAGATGGCACAGAGTGCGGAGGACCAGAATATGAAACACTGTGGTGTTTTGGATCTGACTGTGGTTCATA
TGATTTAGATGCTATAAATGAAGCTAATATGTTATGTAATGAATATGGTATTGATACTATTACTTGTGGTGCAACA
ATTGCTGCAGCTATGGAACTTTATCAAAGAGGATATATAAAAGACGAAGAAATAGCTGGAGATAACCTATCTCTC
AAGTGGGGTGATACGGAATCTATGATTGGCTGGATAAAGAGAATGGTATATAGTGAAGGCTTTGGAGCAAAGA
TGACAAATGGTTCATATAGGCTTTGTGAAGGTTATGGAGCACCGGAGTATTCTATGACAGTTAAAAAGCAGGAA
ATTCCAGCATATGATCCAAGGGGAATACAGGGACACGGTATTACCTATGCAGTTAATAATAGAGGAGGCTGTCA
TATTAAGGGATACATGATTAACCCTGAAATATTAGGTTATCCTGAAAAACTTGATAGATTTGCATTAGATGGTAAA
GCAGCTTATGCCAAATTATTTCATGATTTAACTGCTGTAATTGATTCTTTAGGATTGTGCATATTCACTACATTTGG
GCTTGGAATACAGGATTATGTAGATATGTATAATGCAGTAGTAGGAGAATCTACTTATGATGCAGATTCACTATT
AGAGGCAGGAGATAGAATCTGGACTCTTGAGAAATTATTTAATCTTGCAGCTGGAATAGACAGCAGCCAGGATA
CTCTACCAAAGAGATTGTTAGAAGAACCTATTCCAGATGGCCCATCAAAGGGAGAAGTTCATAGGCTAGATGTTC
TTCTGCCAGAATATTACTCAGTACGAGGATGGAGTAAAGAGGGTATACCTACAGAAGAAACATTAAAGAAATTA
GGATTAGATGAATATATAGGTAAGTTCTAG

Seq. ID 66: Amino acid sequence of aldehyde:ferredoxin oxidoreductase from *C. autoethanogenum*:
MYGYDGKVLRINLKERTCKSENLDLDKAKKFIGCRGLGVKTLFDEIDPKIDALSPENKFIIVTGPLTGAPVPTSGRFMVVT
KAPLTGTIGISNSGGKWGVDLKKAGWDMIIVEDKADSPVYIEIVDDKVEIKDASQLWGKVTSETTKELEKITENKSKVLC
IGPAGERLSLMAAVMNDVDRTAARGGVGAVMGSKNLKAITVKGTGKIALADKEKVKKVSVEKITTLKNDPVAGQGM
PTYGTAILVNIINENGVHPVKNFQESYTNQADKISGETLTANQLVRKNPCYSCPIGCGRWVRLKDGTECGGPEYETLW
CFGSDCGSYDLDAINEANMLCNEYGIDTITCGATIAAAMELYQRGYIKDEEIAGDNLSLKWGDTESMIGWIKRMVYSE
GFGAKMTNGSYRLCEGYGAPEYSMTVKKQEIPAYDPRGIQGHGITYAVNNRGGCHIKGYMINPEILGYPEKLDRFALD
GKAAYAKLFHDLTAVIDSLGLCIFTTFGLGIQDYVDMYNAVVGESTYDADSLLEAGDRIWTLEKLFNLAAGIDSSQDTLP
KRLLEEPIPDGPSKGEVHRLDVLLPEYYSVRGWSKEGIPTEETLKKLGLDEYIGKF*

FIGURE 36

Seq. ID 67: Nucleotide acid sequence of bifunctional butanol/ butyraldehyde dehydrogenase of *C. ljungdahlii*:
ATGAAGGTAACTAAGGTAACTAACGTTGAAGAATTAATGAAAAAGTTAGATGAAGTAACGGCTGCTCAAAAGAAATTTTCTA
GCTATACTCAAGAACAAGTGGATGAAATTTTCAGGCAGGCAGCTATGGCAGCCAATAGTGCTAGAATAGACTTAGCTAAAAT
GGCAGTGGAAGAAAGCGGAATGGGAATTGTAGAAGACAAGGTCATTAAAAATCATTTTGTTGCAGAGTATATATATAACAA
ATATAAGGGTGAAAAAACCTGTGGAGTTCTGGAACAAGATGAAGGCTTTGGTATGGTTAGAATTGCAGAACCTGTAGGAGT
TATTGCAGCAGTAGTCCCAACAACTAATCCAACATCTACAGCAATATTTAAATCACTAATAGCTTTAAAAACTAGAAATGGTAT
AGTTTTTTCGCCACATCCAAGGGCAAAAAAATCAACTATTGCAGCAGCTAAGATAGTACTTGATGCTGCAGTTAAAGCTGGTG
CTCCTGAAGGAATTATAGGATGGATAGATGAACCTTCTATTGAACTTTCACAGGTGGTAATGAAAGAAGCAGATCTAATTCTT
GCAACTGGTGGACCAGGTATGGTTAAGGCTGCCTATTCTTCAGGAAAGCCTGCTATAGGAGTTGGTCCAGGTAACACGCCTG
CTGTAATTGATGAAAGTGCTGACATTAAAATGGCAGTAAATTCAATACTATTATCAAAAACTTTTGATAATGGTATGATTTGTG
CTTCAGAGCAGTCAGTAGTAGTTGCAAGCTCAATATACGATGAAGTCAAGAAAGAGTTTGCAGATAGAGGAGCATATATATT
AAGTAAGGATGAAACAGAGAAGGTTGGAAAAACAATTATAATTAATGGAGCCTTAAATGCTGGCATTGTAGGGCAAAGTGC
TTTTAAAATAGCACAGATGGCAGGAGTGAGTGTACCAGAAGATGCTAAAGTACTTATAGGAGAAGTTAAATCAGTAGAACCG
GAAGAAGAGCCCTTTGCGCATGAAAAGCTATCTCCAGTTTTAGCTATGTACAAAGCAAAAGATTTTGACGAAGCACTCCTAAA
GGCTGGAAGATTAGTTGAACGAGGTGGAATTGGGCATACATCTGTATTATATGTAAATGCAATGACGGAAAAAGTAAAGGT
AGAAAAGTTCAGAGAAACTATGAAGACTGGTAGAACATTGATAAATATGCCTTCAGCACAAGGTGCTATAGGAGATATATAT
AACTTTAAGCTAGCTCCTTCTTTGACACTAGGTTGTGGTTCCTGGGGAGGAAACTCTGTATCAGAAAATGTTGGTCCTAAACA
TTTATTAAACATAAAGAGTGTTGCTGAGAGGAGAGAAAATATGCTTTGGTTTAGAGTACCTGAAAAGGTTTATTTCAAATATG
GTAGTCTTGGAGTTGCACTAAAAGAACTGAGAATTATGGAGAAGAAAAAGGCATTTATAGTAACGGATAAAGTTCTTTATCA
ATTAGGTTATGTAGATAAAATTACAAAAAATCTGGATGAATTAAGAGTTTCATATAAAATATTTACAGATGTAGAACCAGATC
CAACCCTTGCTACAGCTAAAAAAGGTGCAGCAGAACTGTTAGCTTATGAACCAGATACAATTATAGCAGTCGGTGGTGGTTC
AGCAATGGATGCAGCCAAGATCATGTGGGTAATGTATGAGCATCCAGAAGTAAGATTTGAAGATTTAGCTATGAGATTTATG
GATATAAGAAAGAGAGTGTATGTTTTCCCTAAAATGGGAGAAAAGGCAATGATGATTTCAGTAGCAACATCCGCAGGAACA
GGGTCGGAAGTTACGCCATTTGCAGTAATTACGGATGAAAGAACAGGAGCTAAATATCCTCTGGCTGATTATGAATTGACTC
CAAACATGGCTATAGTTGATGCAGAACTTATGATGGGAATGCCAAAGGGACTAACAGCAGCTTCAGGTATAGATGCATTAAC
CCATGCGCTGGAGGCCTATGTATCAATAATGGCTTCAGAATATACCAATGGATTGGCTCTTGAAGCAACAAGATTAGTATTTA
AATATTTGCCAATAGCTTATACAGAAGGTACAACTAATGTAAAGGCAAGAGAAAAAATGGCTCATGCTTCATGTATTGCAGGT
ATGGCCTTTGCCAATGCATTTTTAGGGGTATGCCACTCCATGGCACATAAATTGGGAGCACAGCACCACATACCACATGGAAT
TGCCAATGCACTTATGATAGATGAAGTTATAAAGTTCAATGCTGTAGAGGCTCCAAGGAAACAAGCGGCATTTCCACAATATA
AATATCCAAATGTTAAAAGAAGATATGCTAGAATAGCTGATTACTTAAATTTAGGTGGAAGTACAGATGATGAAAAAGTACA
ATTTTTAATAAATGCTATAGATGACTTGAAAACCAAGTTAAATATTCCAAAGACTATTAAAGAAGCGGGAGTTTCAGAAGATA
AATTCTATGCTACTTTAGATACAATGTCAGAACTGGCTTTTGATGATCAATGTACAGGAGCTAATCCAAGATATCCATTAATAG
GAGAAATAAAACAAATGTATATAAATGCATTTGATACACCAAAGGCAACTGTGGAGAAGAAAACAAGAAAGAAAAAATAA

FIGURE 37

Seq. ID 68: Amino acid sequence of bifunctional butanol/ butyraldehyde dehydrogenase of *C. ljungdahlii*:
MKVTKVTNVEELMKKLDEVTAAQKKFSSYTQEQVDEIFRQAAMAANSARIDLAKMAVEESGMGIVEDKVIKNHFVAEYIYNKYKG
EKTCGVLEQDEGFGMVRIAEPVGVIAAVVPTTNPTSTAIFKSLIALKTRNGIVFSPHPRAKKSTIAAAKIVLDAAVKAGAPEGIIGWID
EPSIELSQVVMKEADLILATGGPGMVKAAYSSGKPAIGVGPGNTPAVIDESADIKMAVNSILLSKTFDNGMICASEQSVVVASSIYD
EVKKEFADRGAYILSKDETEKVGKTIIINGALNAGIVGQSAFKIAQMAGVSVPEDAKVLIGEVKSVEPEEEPFAHEKLSPVLAMYKAK
DFDEALLKAGRLVERGGIGHTSVLYVNAMTEKVKVEKFRETMKTGRTLINMPSAQGAIGDIYNFKLAPSLTLGCGSWGGNSVSEN
VGPKHLLNIKSVAERRENMLWFRVPEKVYFKYGSLGVALKELRIMEKKKAFIVTDKVLYQLGYVDKITKNLDELRVSYKIFTDVEPDPT
LATAKKGAAELLAYEPDTIIAVGGGSAMDAAKIMWVMYEHPEVRFEDLAMRFMDIRKRVYVFPKMGEKAMMISVATSAGTGSE
VTPFAVITDERTGAKYPLADYELTPNMAIVDAELMMGMPKGLTAASGIDALTHALEAYVSIMASEYTNGLALEATRLVFKYLPIAYT
EGTTNVKAREKMAHASCIAGMAFANAFLGVCHSMAHKLGAQHHIPHGIANALMIDEVIKFNAVEAPRKQAAFPQYKYPNVKRRY
ARIADYLNLGGSTDDEKVQFLINAIDDLKTKLNIPKTIKEAGVSEDKFYATLDTMSELAFDDQCTGANPRYPLIGEIKQMYINAFDTPK
ATVEKKTRKKK*

FIGURE 38

Seq. ID 69: Nucleotide acid sequence of bifunctional butanol/ butyraldehyde dehydrogenase of *C. ljungdahlii*:
ATGAAAGTTACAAACGTAGAAGAACTAATGAAAAGACTAGAAGAAATAAAGGATGCTCAAAAGAAATTTGCTACATATACTC
AAGAACAAGTGGATGAAATTTTTAGACAAGCAGCTATGGCAGCTAATAGTGCTAGAATAGAACTAGCTAAAATGGCAGTAG
AAGAAAGCGGAATGGGAATTGTAGAAGACAAGGTCATTAAAAATCACTTTGCCTCAGAATATATATATAACAAATATAAGGA
TGAAAAAACCTGTGGAGTTTTAGAGAGAGATGCAGGATTTGGTATAGTTAGAATTGCGGAACCTGTAGGAGTTATCGCAGCA
GTAGTTCCAACAACTAATCCAACATCTACAGCAATATTTAAATCACTAATAGCTTTAAAAACTAGAAATGGTATAATTTTTTCAC
CCCATCCAAGGGCAAAGAAATCAACTATTGCAGCAGCTAAAATAGTACTTGACGCTGCAGTTAAAGCTGGTGCTCCTGAAGG
AATTATAGGATGGATAGATGAACCTTCCATTGAACTTTCACAGGTGGTAATGGGAGAAGCAAATTTAATTCTTGCAACTGGTG
GCCCGGGTATGGTTAAGGCTGCCTATTCTTCAGGCAAACCTGCTGTGGGAGTTGGTCCAGGTAACACACCTGCTGTAATTGAT
GAAAGTGCCGACATTAAAATGGCAGTAAATTCAATATTACTATCAAAGACTTTTGATAATGGTATGATTTGTGCCTCAGAGCA
GTCAGTAATAGTTTTAGACTCAATATATGAGGAAGTTAAAAAAGAATTTGCTTATAGGGGTGCTTATATATTAAGTAAGGATG
AAACAGATAAGGTTGGAAAAATAATTTTAAAAAATGGAGCCTTAAATGCAGGTATTGTAGGACAACCTGCTTTTAAAATAGC
ACAGCTGGCAGGAGTGGATGTACCAGAAAAAGCTAAAGTACTTATAGGAGAGGTAGAATCGGTAGAACTTGAAGAACCATT
TTCTCATGAAAAGTTATCTCCAGTTTTAGCTATGTACAGGGCAAGAAATTTTGAGGATGCCATTGCAAAAACTGATAAACTGG
TTAGGTCAGGTGGATTTGGACATACATCTTCATTATATGTAAATCCAATGACAGAGAAAGCAAAAGTAGAAAAATTTAGTACT
ATGATGAAAACATCAAGAACTATAATTAACACACCTTCATCCCAAGGTGGTATAGGTGATATATATAACTTTAAACTAGCTCCT
TCTTTGACATTAGGCTGCGGTTCCTGGGGAGGAAATTCTGTATCCGAAAATGTTGGGCCTAAACATTTATTAAACATAAAAAG
TGTTGCTGAGAGGAGAGAAAATATGCTTTGGTTTAGAGTACCTGAAAAGGTTTATTTCAAATATGGTAGTCTTGGAGTTGCAT
TAAAAGAATTAAAAGTTATGAATAAGAAGAAAGTATTTATAGTAACAGATAAAGTTCTTTATCAATTAGGTTATGTGGACAAA
GTTACAAAAGTTCTTGAGGAACTAAAAATTTCCTATAAGGTATTTACAGATGTAGAACCAGATCCAACCCTTGCTACAGCTAA
AAAAGGTGCAGCAGAACTGCTTTCCTATGAACCGGATACAATTATATCAGTTGGTGGTGGCTCAGCAATGGATGCAGCTAAG
ATCATGTGGGTAATGTATGAGCATCCAGAAGTAAAATTTGAAGATTTAGCTATGAGATTTATGGATATAAGAAAGAGAGTAT
ATGTTTTCCCTAAGATGGGAGAAAAGGCAATGATGATTTCAGTAGCAACATCCGCAGGAACAGGGTCGGAAGTTACTCCATT
TGCAGTAATCACTGATGAAAAAACAGGAGCTAAATATCCATTAGCTGATTATGAACTAACTCCAGACATGGCTATAGTTGATG
CAGAACTTATGATGGGAATGCCAAGAGGACTTACAGCAGCTTCGGGTATAGATGCATTAACCCATGCACTGGAGGCATATGT
GTCAATAATGGCTACAGAATTTACCAATGGATTAGCCCTTGAAGCAGTAAAGTTGATATTTGAATATTTACCAAAAGCTTATA
CAGAAGGTACAACTAATGTAAAGGCAAGAGAAAAGATGGTTCATGCTTCATGTATTGCAGGTATGGCCTTTGCAAATGCATT
TTTAGGGGTATGCCACTCTATGGCACATAAATTGGGAGCACAGCATCACATACCACATGGAATTGCCAATGCACTTATGATAG
ATGAAGTTATAAAATTCAATGCTGTAGATGATCCAATAAAACAAGCTGCATTTCCCCAATACGAGTATCCAAATGCTAGGTAT
AGATATGCTCAGATAGCTGATTGTCTGAACTTGGGAGGAAATACAGAAGAGGAAAAGGTACAACTATTAATAAATGCTATAG
ATGATTTAAAAGCTAAGTTAAATATTCCAGAAACTATAAAAGAAGCAGGAGTTTCAGAAGATAAATTCTATGCTACTTTAGAT
AAAATGTCAGAATTAGCTTTTGATGATCAGTGTACAGGAGCTAATCCAAGATATCCACTGATAAGTGAAATAAAACAAATGTA
TATAAATGTTTTTGATAAAACCGAACCAATTGTAGAAGATGAAGAAAAGTAA

FIGURE 39

Seq. ID 70: Amino acid sequence of bifunctional butanol/ butyraldehyde dehydrogenase of *C. ljungdahlii*:
MKVTNVEELMKRLEEIKDAQKKFATYTQEQVDEIFRQAAMAANSARIELAKMAVEESGMGIVEDKVIKNHFASEYIYN
KYKDEKTCGVLERDAGFGIVRIAEPVGVIAAVVPTTNPTSTAIFKSLIALKTRNGIIFSPHPRAKKSTIAAAKIVLDAAVKAG
APEGIIGWIDEPSIELSQVVMGEANLILATGGPGMVKAAYSSGKPAVGVGPGNTPAVIDESADIKMAVNSILLSKTFDN
GMICASEQSVIVLDSIYEEVKKEFAYRGAYILSKDETDKVGKIILKNGALNAGIVGQPAFKIAQLAGVDVPEKAKVLIGEV
ESVELEEPFSHEKLSPVLAMYRARNFEDAIAKTDKLVRSGGFGHTSSLYVNPMTEKAKVEKFSTMMKTSRTIINTPSSQ
GGIGDIYNFKLAPSLTLGCGSWGGNSVSENVGPKHLLNIKSVAERRENMLWFRVPEKVYFKYGSLGVALKELKVMNKK
KVFIVTDKVLYQLGYVDKVTKVLEELKISYKVFTDVEPDPTLATAKKGAAELLSYEPDTIISVGGGSAMDAAKIMWVMY
EHPEVKFEDLAMRFMDIRKRVYVFPKMGEKAMMISVATSAGTGSEVTPFAVITDEKTGAKYPLADYELTPDMAIVDA
ELMMGMPRGLTAASGIDALTHALEAYVSIMATEFTNGLALEAVKLIFEYLPKAYTEGTTNVKAREKMVHASCIAGMAF
ANAFLGVCHSMAHKLGAQHHIPHGIANALMIDEVIKFNAVDDPIKQAAFPQYEYPNARYRYAQIADCLNLGGNTEEE
KVQLLINAIDDLKAKLNIPETIKEAGVSEDKFYATLDKMSELAFDDQCTGANPRYPLISEIKQMYINVFDKTEPIVEDEEK*

Seq. ID 71: Nucleotide acid sequence of butyraldehyde dehydrogenase of *C. ljungdahlii*:
TTGGAAAATTTTGATAAAGACTTACGTTCTATACAAGAAGCAAGAGATCTTGCACGTTTAGGAAAAATTGCAGCA
GACCAAATTGCTGATTATACTGAAGAACAAATTGATAAAATCCTATGTAATATGGTTAGGGTAGCAGAAGAAAAT
GCAGTTTGCCTTGGTAAAATGGCTGCAGAAGAAACTGGTTTTGGAAAAGCTGAAGATAAGGCTTATAAGAACCA
TATGGCTGCTACTACAGTATATAATTACATCAAGGATATGAAGACTATTGGTGTTATAAAAGAAGATAAAAGTGA
AGGTGTAATTGAATTTGCAGAACCAGTTGGTTTATTAATGGGTATTGTACCATCTACAAATCCAACATCTACTGTT
ATTTATAAATCAATCATTGCAATTAAATCAAGAAATGCAATTGTATTCTCACCACACCCAGCTGCATTAAAATGTTC
AACAAAAGCAATAGAACTTATGCGTGATGCAGCAGTAGCAGCAGGAGCTCCTGCAAATGTAATTGGTGGTATTG
TTACACCATCTATACAAGCTACAAATGAACTTATGAAAGCTAAAGAAGTTGCTATGATAATTGCAACTGGAGGCC
CTGGAATGGTAAAGGCTGCATATAGTTCAGGAACACCTGCAATAGGCGTTGGTGCTGGTAACTCTCCATCCTATA
TTGAAAGAACTGCTGATGTTCATCAATCAGTTAAAGATATAATAGCTAGTAAGAGTTTTGACTATGGTACTATTTG
TGCATCCGAGCAGTCTGTAATTGCAGAAGAATGCAACCATGATGAAATAGTAGCTGAATTTAAGAAACAAGGCG
GATATTTCATGACAGCTGAAGAAACTGCAAAAGTTTGCAGCGTACTTTTTAAACCTGGTACACACAGCATGAGCG
CTAAGTTTGTAGGAAGAGCTCCTCAGGTTATAGCAGAAGCTGCAGGTTTCACAGTTCCAGAAGGAACAAAAGTA
TTAATAGGAGAACAAGGCGGAGTTGGTAATGGTTACCCTCTATCTTATGAGAAACTTACAACAGTACTTGCTTTCT
ATACAGTTAAAGATTGGCATGAAGCATGTGAGCTTAGTATAAGATTACTTCAAAATGGTCTTGGACATACAATGA
ACATTCATACAAATGATAGAGACTTAGTAATGAAGTTTGCTAAAAAACCAGCATCCCGTATCTTAGTTAATACTGG
TGGAAGCCAGGGAGGTACTGGTGCAAGCACAGGATTAGCACCTGCATTTACATTAGGTTGTGGTACATGGGGAG
GAAGCTCTGTTTCTGAAAATGTTACTCCATTACATTTAATCAATATAAAGAGAGTAGCATATGGTCTTAAAGATTG
TACTACATTAGCTGCAGACGATACAACTTTCAATCATCCTGAACTTTGCGGAAGCAAAAATGACTTAGGATTCTGT
GCTACAAGCCCTGCAGAATTTGCAGCAAAGAGCAATTGTGATAGCACTGCTGCAGATACTACTGATAATGATAAA
CTTGCTAGACTCGTAAGTGAATTAGTAGCTGCAATGAAGGGAGCTAACTAA

FIGURE 40

Seq. ID 72: Amino acid sequence of butyraldehyde dehydrogenase of *C. ljungdahlii*:
MENFDKDLRSIQEARDLARLGKIAADQIADYTEEQIDKILCNMVRVAEENAVCLGKMAAEETGFGKAEDKAYKNHMA
ATTVYNYIKDMKTIGVIKEDKSEGVIEFAEPVGLLMGIVPSTNPTSTVIYKSIIAIKSRNAIVFSPHPAALKCSTKAIELMRD
AAVAAGAPANVIGGIVTPSIQATNELMKAKEVAMIIATGGPGMVKAAYSSGTPAIGVGAGNSPSYIERTADVHQSVK
DIIASKSFDYGTICASEQSVIAEECNHDEIVAEFKKQGGYFMTAEETAKVCSVLFKPGTHSMSAKFVGRAPQVIAEAAGF
TVPEGTKVLIGEQGGVGNGYPLSYEKLTTVLAFYTVKDWHEACELSIRLLQNGLGHTMNIHTNDRDLVMKFAKKPASR
ILVNTGGSQGGTGASTGLAPAFTLGCGTWGGSSVSENVTPLHLINIKRVAYGLKDCTTLAADDTTFNHPELCGSKNDL
GFCATSPAEFAAKSNCDSTAADTTDNDKLARLVSELVAAMKGAN

Seq. ID 73: Nucleotide acid sequence of butyraldehyde dehydrogenase of *C. ljungdahlii*:
ATGAATATTATTGATAATGATTTGCTCTCCATCCAAGAATCCCGAATCCTTGTGGAAAATGCTGCACGAGCACAAA
AAATGTTAGCAACCTTTCCACAAGAAAAGCTAGATGAGATTGTTGAACGTATGGCGGAAGAAATCGGAAAACAT
ACCCGAGAGCTTGCTGTAATGTCACAGGATGAAACTGGTTATGGAAAATGGCAGGATAAATGCATCAAAAACCG
ATTTGCCTGTGAGTATTTGCCAGCTAAGCTTAGAGGAATGCGATGTGTAGGTATTATTAATGAAAATGGTCAGGA
TAAGACCATGGATGTAGGTGTACCTATGGGTGTAATTATTGCATTATGTCCTGCAACTAGTCCGGTTTCTACTACC
ATATATAAGGCATTGATTGCAATTAAGTCTGGTAATGCAATTATCTTTTCTCCACATCCTAGAGCAAAGGAGACAA
TTTGTAAGGCGCTTGACATCATGATTCGTGCAGCTGAAGGATATGGGCTTCCAGAAGGAGCTCTTGCATACTTAC
ATACTGTGACGCCTAGTGGAACAATCGAATTGATGAACCATATTGCGACTTCTTTGATTATGAATACAGGTGTTCC
CGGGATGCTTAAAGCAGCATATAATTCTGGGAAACCTGTTATATATGGAGGAACTGGTAATGGACCAGCATTTAT
TGAACGTACAGCTGACATCAAACAGGCGGTAAAAGATATTATTGCTAGTAAGACCTTTGATAACGGAATAGTACC
ATCAGCTGAACAATCTATTGTTGTAGATAGCTGTGTTGCATCTGATGTTAAACGTGAGTTGCAAAATAATGGTGC
ATATTTCATGACAGAGGAGGAAGCACAAAAACTAGGTTCTCTCTTTTTCCGTTCTGATGGCAGTATGGATTCAGA
AATGGTTGGCAAATCCGCACAAAGATTGGCTAAAAAAGCAGGTTTCAGCATTCCTGAAAGTAGCACAGTGCTAAT
TTCAGAGCAGAAATATGTTTCTCAAGATAATCCTTATTCCAAGGAGAAACTTTGTCCGGTACTAGCTTACTACATT
GAAGATGATTGGATGCATGCATGTGAAAAGTGTATTGAACTGCTGTTAAGTGAGAGACATGGTCACACTCTTGTT
ATACATTCAAAAGACGAAGATGTAATTCGCCAGTTTGCATTAAAAAAACCTGTAGGTAGGATACTTGTTAATACG
CCTGCTTCCTTTGGTAGTATGGGTGCTACAAGTAATTTATTTCCTGCTTTAACTTTAGGTAGTGGATCGGCAGGTA
AAGGTATTACCTCCGATAATGTTTCACCAATGAATCTTATTTACGTCCGCAAAGTCGGATATGGCGTACGGAATGT
AGAAGAGATTGTCAATACTAATGGATTGTTTACAGAAGAAAAAAGTGATTTGAATGGAATGACAAAAAAGTCAG
ACTATAATCCAGAGGATATACAAATGTTACAGCATATTTTAAAAAAAGCTATGGAAAAAATTAAATAG

Seq. ID 74: Amino acid sequence of butyraldehyde dehydrogenase of *C. ljungdahlii*:
MNIIDNDLLSIQESRILVENAARAQKMLATFPQEKLDEIVERMAEEIGKHTRELAVMSQDETGYGKWQDKCIKNRFAC
EYLPAKLRGMRCVGIINENGQDKTMDVGVPMGVIIALCPATSPVSTTIYKALIAIKSGNAIIFSPHPRAKETICKALDIMIR
AAEGYGLPEGALAYLHTVTPSGTIELMNHIATSLIMNTGVPGMLKAAYNSGKPVIYGGTGNGPAFIERTADIKQAVKDI
IASKTFDNGIVPSAEQSIVVDSCVASDVKRELQNNGAYFMTEEEAQKLGSLFFRSDGSMDSEMVGKSAQRLAKKAGFS
IPESSTVLISEQKYVSQDNPYSKEKLCPVLAYYIEDDWMHACEKCIELLLSERHGHTLVIHSKDEDVIRQFALKKPVGRILV
NTPASFGSMGATSNLFPALTLGSGSAGKGITSDNVSPMNLIYVRKVGYGVRNVEEIVNTNGLFTEEKSDLNGMTKKSD
YNPEDIQMLQHILKKAMEKIK*

FIGURE 41

Seq. ID 75: Nucleotide acid sequence of butanol dehydrogenase of *C. ljungdahlii*:
ATGGCAAGATTTACTTTACCAAGAGACATTTATTTTGGAGAAAATTCATTAGAAACCTTGAAAGACCTAGATGGA
AAAAAAGCTGTTATTGTCGTAGGTGGTGGATCCATGAAACGATTTGGATTCCTTGATAAGGTAGTAAACTACTTA
AAAGAAGCAGGTATTGAATCAAAATTAATAGAAGGAGTTGAACCAGATCCATCTGTAGAAACTGTTATGAATGG
CGCTAAACTAATGAGAGAATATGAACCAGATTTAATAGTATCAATAGGTGGAGGTTCACCAATTGACGCAGCAAA
AGCTATGTGGATATTCTATGAATACCCTGAGTTTACTTTTAAAGAGGCTGTGGTTCCTTTTGGTCTTCCTAAATTAA
GACAAAAAGCAACATTTATAGCTATACCTTCTACAAGTGGTACTGCAACAGAAGTAACGGCATTTTCTGTAATAAC
AGACTATAAAGCTAAAATTAAATATCCTTTAGCTGACTTCAATTTAACACCAGATATAGCTATAATTGATCCAGCAT
TAGCTCAAACAATGCCACCTAAATTAACTGCACATACTGGAATGGATGCACTTACCCATGCTATTGAAGCATATGT
TGCAGGACTTCATTCAGTTTTCTCAGATCCTCTTGCTATTCAAGCTATAGTTATGGTAAATCAGTATTTAATTAAAT
CTTACAATGAAGATAAAGAAGCTAGAAACCAAATGCATTTAGCTCAATGTTTAGCTGGAATGGCATTTTCAAATG
CACTTCTTGGAATAACTCACAGTTTAGCACATAAAACAGGTGCAGTATTCCATATCCCTCATGGATGTGCCAATGC
AATATATCTTCCTTATGTTATAGATTTCAATAAAAAAGCTTGTGCACCAAGATATGCTGAAATAGCTAGGAGTCTT
AAACTTCCAGGAAATACTGATGATGAATTAGTAGATTCATTAACCAACATGATTAAAGATATGAATAAGAGTATG
GATATTCCTTTAACATTAAAAGATTACGGAGTAGATGAAAAAGAATTTAAAGATAGTGAAGATTTTATAGCTCAC
AATGCCGTATTAGATGCCTGCACTGGATCAAATCCTAGAAGTATAAATGATACTGAAATGAAAAAGTTATTAGAA
TACATCTATTATGGTAAAAAGGTTGATTTTTAA

Seq. ID 76: Amino acid sequence of butanol dehydrogenase of *C. ljungdahlii*:
MARFTLPRDIYFGENSLETLKDLDGKKAVIVVGGGSMKRFGFLDKVVNYLKEAGIESKLIEGVEPDPSVETVMNGAKL
MREYEPDLIVSIGGGSPIDAAKAMWIFYEYPEFTFKEAVVPFGLPKLRQKATFIAIPSTSGTATEVTAFSVITDYKAKIKYP
LADFNLTPDIAIIDPALAQTMPPKLTAHTGMDALTHAIEAYVAGLHSVFSDPLAIQAIVMVNQYLIKSYNEDKEARNQ
MHLAQCLAGMAFSNALLGITHSLAHKTGAVFHIPHGCANAIYLPYVIDFNKKACAPRYAEIARSLKLPGNTDDELVDSL
TNMIKDMNKSMDIPLTLKDYGVDEKEFKDSEDFIAHNAVLDACTGSNPRSINDTEMKKLLEYIYYGKKVDF*

Seq. ID 77: Nucleotide acid sequence of butanol dehydrogenase of *C. ljungdahlii*:
ATGGGAAGATTTACTTTGCCTAGGGATATTTACTTTGGTGAAAATGCCTTAGAAAATTTAAAAAATTTAGATGGA
AATAAAGCAGTAGTTGTTGTAGGTGGGGGATCTATGAAGAGATTTGGATTCTTAGCCAAAGTTGAAAAATACTTA
AAAGAAACTGGTATGGAAGTTAAATTAATAGAAGGTGTTGAGCCTGATCCGTCTGTTGATACTGTTATGAATGGC
GCTAAAATAATGAGAGACTTTAACCCAGATTGGATAGTATCAATAGGTGGAGGATCTCCCATAGATGCTGCTAAA
GCAATGTGGATATTTTATGAATACCCCGACTTTACATTTGAAAAAGCGGTAGTCCCTTTTGGAATTCCTAAATTAA
GGCAGAAGGCACAATTTGTTGCTATACCTTCTACAAGTGGAACAGCAACTGAAGTAACATCATTTTCTGTAATAAC
AGACTATAAAGCTAAAATAAAATATCCTCTTGCAGATTTTAACCTTACCCCTGATATAGCTATAATAGATCCGTCTC
TTGCAGAAACAATGCCCAAAAAGCTTACAGCACACACTGGAATGGATGCACTTACTCACGCAATAGAAGCATATG
TAGCAAGTTTACATTCAGATTTCTCAGATCCACTTGCTATGCATGCTATAACCATGATTCATAAATATTTATTGAAA
TCCTATGAAGAAGATAAAGAAGCTAGAGGACATATGCATATAGCCCAATGTCTAGCTGGGATGGCATTTTCAAAT
GCTCTCCTTGGAATAACTCATAGTATAGCACATAAAACTGGTGCAGTATTTCACATACCTCATGGGTGTGCTAATG
CCATATACTTACCTTATGTTATAGATTTTAACAAGAAAGCTTGTTCAGAAAGATATGCTAAAATAGCCAAAAAGCT
GCATCTATCAGGAAATAGTGAAGATGAGCTAATAGATTCATTAACTGAAATGATTCGTACTATGAACAAAAAGAT
GGATATTCCTCTCACCATAAAAGATTATGGTATAAGCGAAAACGATTTTAATGAAAACCTAGATTTTATAGCTCAC
AATGCCATGATGGATGCCTGCACTGGATCCAATCCTAGAGCAATAACTGAGGAAGAAATGAAAAAGCTCTTGCA
GTATATGTATAATGGGCAAAAGGTTAATTTCTAG

FIGURE 42

Seq. ID 78: Amino acid sequence of butanol dehydrogenase of *C. ljungdahlii*:
MGRFTLPRDIYFGENALENLKNLDGNKAVVVVGGGSMKRFGFLAKVEKYLKETGMEVKLIEGVEPDPSVDTVMNGA
KIMRDFNPDWIVSIGGGSPIDAAKAMWIFYEYPDFTFEKAVVPFGIPKLRQKAQFVAIPSTSGTATEVTSFSVITDYKAKI
KYPLADFNLTPDIAIIDPSLAETMPKKLTAHTGMDALTHAIEAYVASLHSDFSDPLAMHAITMIHKYLLKSYEEDKEARG
HMHIAQCLAGMAFSNALLGITHSIAHKTGAVFHIPHGCANAIYLPYVIDFNKKACSERYAKIAKKLHLSGNSEDELIDSLT
EMIRTMNKKMDIPLTIKDYGISENDFNENLDFIAHNAMMDACTGSNPRAITEEEMKKLLQYMYNGQKVNF*

Seq. ID 79: Nucleotide acid sequence of butanol dehydrogenase of *C. ljungdahlii*:
ATGGAGAGATTTACGTTGCCAAGAGACATTTACTTTGGAGAAGATGCTTTGGGTGCTTTGAAAACGTTAAAAGGT
AAGAAAGCTGTAGTAGTTGTTGGAGGAGGATCCATGAAGAGATTCGGTTTCCTTGACAAGGTAGAAGAATACTT
AAAAGAAGCAAACATAGAAGTTAAACTAATAGAAGGTGTTGAACCAGATCCGTCTGTGGAAACCGTTATGAAAG
GTGCCAAAATAATGACAGAATTTGGGCCAGATTGGATAGTTGCTATTGGAGGAGGTTCACCAATAGATGCTGCA
AAGGCTATGTGGCTATTTTATGAATATCCAGATTTTACTTTTAAACAAGCAATTGTTCCGTTTGGATTACCAGAATT
AAGACAAAAAGCTAAATTTGTAGCTATAGCTTCTACTAGTGGAACAGCTACTGAAGTTACTTCATTTTCAGTAATA
ACTGATTATAAAGCTAAAATAAAGTATCCTTTAGCTGACTTCAATTTGACACCGGATATAGCTATAGTTGATCCAG
CATTAGCCCAGACAATGCCACCTAAATTAACTGCACATACTGGTATGGATGCATTAACTCATGCACTAGAAGCTTA
TGTAGCATCAGCTAGATCAGATATTTCAGATCCACTTGCAATACATTCCATAATTATGACAAGGGATAACTTACTT
AAATCCTATAAGGGTGATAAAGATGCTAGAAATAAGATGCATATATCACAATGTTTAGCAGGTATGGCATTTTCT
AATGCACTTCTTGGTATAACTCATAGTTTAGCACATAAAACAGGAGCTGTATGGCACATACCACATGGATGCGCT
AATGCAATATATCTTCCATATGTTTTAGATTTTAATAAAAAAGCTTGCTCAGATAGATATGCTAATATAGCTAAAAT
ATTAGGACTTAAAGGAACTACTGAAGATGAATTGGTAGATTCTCTAGTTAAAATGGTACAAGATATGGATAAGG
AATTGAATATACCTTTGACCTTAAAAGATTATGGTATAAGCAAAGATGATTTCAATTCAAATGTTGATTTTATAGC
AAAGAATGCGCTCTTAGATGCATGTACAGGAGCTAATCCAAGGCCTATAGATTTTGATCAAATGAAAAAGATACT
TCAATGTATATATGATGGAAAAAAGGTAACTTTTTAA

Seq. ID 80: Amino acid sequence of butanol dehydrogenase of *C. ljungdahlii*:
MERFTLPRDIYFGEDALGALKTLKGKKAVVVVGGGSMKRFGFLDKVEEYLKEANIEVKLIEGVEPDPSVETVMKGAKIM
TEFGPDWIVAIGGGSPIDAAKAMWLFYEYPDFTFKQAIVPFGLPELRQKAKFVAIASTSGTATEVTSFSVITDYKAKIKYP
LADFNLTPDIAIVDPALAQTMPPKLTAHTGMDALTHALEAYVASARSDISDPLAIHSIIMTRDNLLKSYKGDKDARNKM
HISQCLAGMAFSNALLGITHSLAHKTGAVWHIPHGCANAIYLPYVLDFNKKACSDRYANIAKILGLKGTTEDELVDSLVK
MVQDMDKELNIPLTLKDYGISKDDFNSNVDFIAKNALLDACTGANPRPIDFDQMKKILQCIYDGKKVTF*

FIGURE 43

Seq. ID 81: Nucleotide acid sequence of butanol dehydrogenase of *C. ljungdahlii*:
ATGGAAAACTTTATTTTTAAAAATGCTACAGAAATTATTTTTGGTAAGGATACCGAAAATCTTGTAGGAAGTAAA
GTAAAGGAGTATTCAAAGTCAGATAAAATACTCTTTTGCTATGGGGGAGGAAGCATAAAAAGATCTGGTCTATAT
GATAGAGTTATAAAGTCCTTAAAAGAAAATGGAATTGAATTTATAGAACTTCCAGGAATTAAACCTAATCCAAGA
TTAGGACCTGTTAAAGAAGGTATAAGACTATGTAGAGAAAATAATATAAAATTTGTACTATCTGTAGGAGGAGG
AAGTTCAGCAGATACGGCTAAAGCTATTGCTGTAGGAGTACCTTATAAAGGAGACGTATGGGATTTTTATACGGG
CAAAGCTGAAGTGAAAGAGGCTCTTCCTGTAGGAGTTGTAATAACATTACCTGCTACAGGTACAGAATCTAGTAA
TAGTTCTGTTATTATGAATGAAGATGGTTGGTTTAAAAAAGGATTAAATACAGTACTTATAAGACCTGCTTTTTCA
ATTATGAATCCTGAACTTACTTTTACACTACCAGAGTATCAAACTGCTTGTGGTGCTTGTGACATTATGGCACATAT
AATGGAAAGATATTTTACAAATGTGAAACATGTAGATATAACTGATAGGCTTTGCGAAGCTGCACTTAGAAATGT
TATAAATAATGCCCCAATAGTTTTAAAAGATCCCAAAAACTATGATGCTAGGGCAGAAATTATGTGGACCGGTAC
TATAGCTCATAATGATGTGCTTAGTGCGGGTAGAATAGGTGATTGGGCTTCTCACAAAATTGAACATGAATTGAG
TGGGGAAACAGACATTGCCCATGGAGCAGGACTTGCAATTGTATTTCCTGCATGGATGAAATATGTATATAAACA
CGATATCAATAGATTTGTACAATTTGCAGTAAGGGTATGGGATGTAGATTTATCTTATAGTTCCTGCGAAGATATT
GTACTTGAAGGCATAAGGAGAATGACAGCATTTTTCAAGAGCATGGGGTTACCTGTAACTTTAAAAGAAGGAAG
TATAGGAGAAGATAAAATTGAAGAAATGGCTAATAAGTGCACGGATAATGGAACTAAAACTGTAGGACAATTTG
TAAAATTAAATAAAGATGATATTGTAAAAATATTAAATTTAGCTAAATAA

Seq. ID 82: Amino acid sequence of butanol dehydrogenase of *C. ljungdahlii*:
MENFIFKNATEIIFGKDTENLVGSKVKEYSKSDKILFCYGGGSIKRSGLYDRVIKSLKENGIEFIELPGIKPNPRLGPVKEGIR
LCRENNIKFVLSVGGGSSADTAKAIAVGVPYKGDVWDFYTGKAEVKEALPVGVVITLPATGTESSNSSVIMNEDGWFK
KGLNTVLIRPAFSIMNPELTFTLPEYQTACGACDIMAHIMERYFTNVKHVDITDRLCEAALRNVINNAPIVLKDPKNYDA
RAEIMWTGTIAHNDVLSAGRIGDWASHKIEHELSGETDIAHGAGLAIVFPAWMKYVYKHDINRFVQFAVRVWDVDL
SYSSCEDIVLEGIRRMTAFFKSMGLPVTLKEGSIGEDKIEEMANKCTDNGTKTVGQFVKLNKDDIVKILNLAK*

Seq. ID 83: Nucleotide acid sequence of butanol dehydrogenase of *C. ljungdahlii*:
ATGGAAGACAAGTTTGAAAATTTTAATTTGAAATCCAAGATTTATTTTAATAGGGAATCTATTCAACTTTTAGAGC
AAGTCACTGGTTCTCGAGCATTTATTGTTGCAGATGCTATTATGGGAAAACTTGGATATCTTCAAAAAGTAATAGA
TTACCTAAGCAAAGCTGGAATAAGTTCCGTTGTTTTTACGGGGGTACACCCTGATCCAGACGTCAATGTAATTGCA
GATGCAATGAAATTGTACAAAAAAAGCGACGCAGATGTTCTCGTAGCACTAGGTGGAGGATCCAGTATTGATAC
CGCTAAGGGAATAATGTATTTTGCATGTAATTTAGGAAAAGCAATGGGCCAAGAAATGAAAAAACCTCTATTTAT
TGCAATTCCATCAACAAGTGGTACAGGCTCTGAAGTAACAAACTTTACTGTTATTACTTCTCAGAAAGAAAAGGTA
TGCATTATAGATGATTTTATTGCACCAGATGTTGCAATACTTGACTCAAGTTGTATTGATGGTCTGCCTCAGCGTA
TTGTAGCAGATACTGGTATAGATGTTCTAGTTCATTCTATTGAAGCCTATGTTTCCAAAAAAGCAACTGACTTTAC
AGACGCTCTTGCTGAAAAAGCAGTTAAATTAATTTTTGAGAATCTTCCAAAAATTTATAACGATAGTAAGGATTCC
GAAGCTCGAGATCATGTTCAAAACGCTTCCTGTATAGCAGGAATAGCATTTACAAATGCTGGTCTTGGAATTAAT
CACAGCTTGGCTCATGCTATGGGTGGATCTTTCCACATTCCTCACGGCCGATCCAATGCACTTCTACTTAATGCAG
TAATGGAATACAACGCTAGCTTGGTTGGAAATGCAAGCGAACATGCTATGGAAAAATACGCAAAACTAGCATCA
ATTCTACACCTTCCAGCTCGAACAACTCGCGAAGGCGCTGTAAGTTTTATTGAAGCTGTAGATAAATTAATAAAAT
CCCTAGGTGTTGAAGATAATATTCGATCTCTTGGGATTAAAGAAGATGAGTTTCAAAGTGCTCTAAATCATATGG
CAGAAACAGCAATGCAAGATAGATGCACTCCAACTAATCCTAGAAAACCTTCTAAAGAAGAACTTATACATATTT
ATCAAAAATGTTATTAA

FIGURE 44

Seq. ID 84: Amino acid sequence of butanol dehydrogenase of *C. ljungdahlii*:
MEDKFENFNLKSKIYFNRESIQLLEQVTGSRAFIVADAIMGKLGYLQKVIDYLSKAGISSVVFTGVHPDPDVNVIADAMK
LYKKSDADVLVALGGGSSIDTAKGIMYFACNLGKAMGQEMKKPLFIAIPSTSGTGSEVTNFTVITSQKEKVCIIDDFIAPD
VAILDSSCIDGLPQRIVADTGIDVLVHSIEAYVSKKATDFTDALAEKAVKLIFENLPKIYNDSKDSEARDHVQNASCIAGIA
FTNAGLGINHSLAHAMGGSFHIPHGRSNALLLNAVMEYNASLVGNASEHAMEKYAKLASILHLPARTTREGAVSFIEA
VDKLIKSLGVEDNIRSLGIKEDEFQSALNHMAETAMQDRCTPTNPRKPSKEELIHIYQKCY*

Seq. ID 85: Nucleotide sequence of phosphate acetyl/butyryl transferase from *C. ljungdahlii*:
ATGAAATTGATGGAAAAAATTTGGAGTAAGGCAAAGGAAGACAAAAAAAAGATTGTCTTAGCTGAAGGAGAAG
AAGAAAGAACTCTTCAAGCTTGTGAAAAAATAATTAAAGAGGGTATTGCAAATTTAATCCTTGTAGGGAATGAAA
AGGTAATAAAAGAAAAAGCGTCAAAATTAGGTGTAAGTTTAAATGGAGCAGAAATAGTAGATCCAGAGACTTCA
GATAAACTAAAGGCATATGCAGATGCTTTTTATGAATTGAGAAAGAAGAAGGGAATAACGCCAGAAAAAGCGG
ATAAAATAGTAAGAGATCCAATATACTTTGCTACAATGATGGTTAAACTTGGAGATGCAGATGGATTGGTTTCAG
GTGCGGTTCATACTACAGGTGATCTTTTGAGACCAGGACTTCAAATAGTAAAGACAGCTCCAGGTACATCAGTAG
TTTCCAGTACATTTATAATGGAAGTACCAAATTGTGAGTATGGTGACAATGGTGTACTTCTATTTGCTGATTGTGC
TGTAAATCCATGCCCAGATAGTGATCAATTGGCTTCAATTGCAATAAGTACAGCAGAAACTGCAAAGAACTTATG
TGGAATGGATCCAAAAGTAGCAATGCTTTCATTTTCTACTAAGGGAAGTGCAAAACACGAATTAGTAGACAAAGT
TAGAAATGCTGTAGAGATTGCAAAAAAAGCTAAACCAGATTTAAGTTTAGACGGAGAATTACAATTAGATGCCTC
TATCGTAGAAAAGGTTGCAAGTTTAAAGGCTCCTGGAAGTGAAGTAGCAGGAAAAGCAAATGTACTTGTATTTCC
AGATCTCCAAGCAGGAAATATAGGCTATAAACTCGTTCAAAGATTTGCAAAAGCAGATGCTATAGGACCTGTATG
CCAAGGATTTGCAAAACCTATAAATGATTTGTCAAGAGGATGTAATTCTGATGATATAGTAAATGTAGTAGCTGT
AACAGCAGTTCAAGCACAAGCTCAAAAGTAA

Seq. ID 86: Amino acid sequence of phosphate acetyl/butyryl transferase from *C. ljungdahlii*:
MKLMEKIWSKAKEDKKKIVLAEGEEERTLQACEKIIKEGIANLILVGNEKVIKEKASKLGVSLNGAEIVDPETSDKLKAYA
DAFYELRKKKGITPEKADKIVRDPIYFATMMVKLGDADGLVSGAVHTTGDLLRPGLQIVKTAPGTSVVSSTFIMEVPNC
EYGDNGVLLFADCAVNPCPDSDQLASIAISTAETAKNLCGMDPKVAMLSFSTKGSAKHELVDKVRNAVEIAKKAKPDL
SLDGELQLDASIVEKVASLKAPGSEVAGKANVLVFPDLQAGNIGYKLVQRFAKADAIGPVCQGFAKPINDLSRGCNSD
DIVNVVAVTAVQAQAQK*

Seq. ID 87: Nucleotide sequence of acetate/butyrate kinase from *C. ljungdahlii*:
ATGAAAATATTAGTAGTAAACTGTGGAAGTTCATCTTTAAAATATCAACTTATTGATATGCAAGATGAAAGTGTTG
TAGCAAAGGGTCTTGTAGAAAGAATAGGAATGGACGGTTCAATTTTAACACACAAAGTTAATGGAGAAAAGTTT
GTTACAGAGCAAACAATGGAAGACCACAAAGTTGCTATACAATTAGTATTAAATGCTCTTGTAGATAAAAAACAT
GGTGTAATAAAAGACATGTCAGAAATATCCGCTGTAGGACATAGAGTCTTGCACGGTGGAAAGAAATATGCAGC
ATCCATTCTTATTGACGAAAATGTAATGAAAGCAATAGAAGAATGTATCCCACTAGGACCACTACATAATCCAGCT
AATATAATGGGAATAGATGCTTGTAAAAAATTAATGCCAAATACTCCAATGGTAGCAGTATTTGATACAGCATTTC
ATCAGACAATGCCAGATTATGCTTATACTTATGCAATACCTTATGATATATCTGAAAAGTATGATATCAGAAAATA
TGGTTTTCATGGAACTTCTCATAGATTCGTTTCAATTGAAGCAGCTAAATTATTAAAGAAAGATCCAAAAGATCTT
AAGTTAATAACTTGTCATTTAGGAAATGGAGCTAGCATATGTGCAGTAAACCAAGGAAAAGCAGTAGATACAAC
GATGGGACTTACTCCTCTTGCAGGACTTGTAATGGGAACTAGATGCGGTGATATAGATCCAGCTATAGTACCATT
TGTAATGAAAAGAACAGGCATGTCTGTAGATGAAGTGGATACCTTAATGAATAAAAAGTCAGGAATACTTGGAG
TATCAGGAGTAAGCAGTGATTTTAGAGATGTAGAAGAAGCTGCAAATTCAGGAAATGATAGAGCAAAACTTGCA
TTAAATATGTATTATCACAAAGTTAAATCTTTCATAGGAGCTTATGTTGCAGTTTTAAATGGAGCAGATGCTATAA
TATTTACAGCAGGACTTGGAGAAAATTCAGCAACTAGCAGATCTGCTATATGTAATGGATTAAGCTATTTTGGAA
TTAAAATAGATGAAGAAAAGAATAAGAAAAGGGGAGAGGCACTAGAAATAAGCACACCTGATTCAAAGATAAA
AGTATTAGTAATTCCTACAAATGAAGAACTTATGATAGCTAGGGATACAAAAGAAATAGTTGAAAATAAATAA

FIGURE 45

Seq. ID 88: Amino acid sequence of acetate/butyrate kinase from *C. ljungdahlii*:
MKILVVNCGSSSLKYQLIDMQDESVVAKGLVERIGMDGSILTHKVNGEKFVTEQTMEDHKVAIQLVLNALVDKKHGVI
KDMSEISAVGHRVLHGGKKYAASILIDENVMKAIEECIPLGPLHNPANIMGIDACKKLMPNTPMVAVFDTAFHQTMP
DYAYTYAIPYDISEKYDIRKYGFHGTSHRFVSIEAAKLLKKDPKDLKLITCHLGNGASICAVNQGKAVDTTMGLTPLAGLV
MGTRCGDIDPAIVPFVMKRTGMSVDEVDTLMNKKSGILGVSGVSSDFRDVEEAANSGNDRAKLALNMYYHKVKSFI
GAYVAVLNGADAIIFTAGLGENSATSRSAICNGLSYFGIKIDEEKNKKRGEALEISTPDSKIKVLVIPTNEELMIARDTKEIV
ENK*

Seq. ID 89: Nucleotide sequence of aldehyde:ferredoxin oxidoreductase from *C. ljungdahlii*:
ATGTACGGATATAAGGGTAAGGTATTAAGAATTAATCTAAGTAGTAAAACTTATATAGTGGAAGAATTGAAAATT
GACAAAGCTAAAAAATTTATAGGTGCAAGAGGGTTAGGCGTAAAAACCTTATTTGACGAAGTAGATCCAAAGGT
AGATCCATTATCACCTGATAACAAATTTATTATAGCAGCGGGACCACTTACAGGTGCACCTGTTCCAACAAGCGG
AAGATTCATGGTAGTTACTAAATCACCTTTAACAGGAACTATTGCTATTGCAAATTCAGGTGGAAAATGGGGAGC
AGAATTCAAAGCAGCTGGATACGATATGATAATCGTTGAAGGTAAATCTGATAAAGAAGTTTATGTAAATATAGT
AGATGATAAAGTAGAATTTAGGGATGCTTCTCATGTTTGGGGAAAACTAACAGAAGAAACTACAAAAATGCTTCA
ACAGGAAACAGATTCGAGAGCTAAGGTTTTATGCATAGGACCAGCTGGGGAAAAGTTATCACTTATGGCAGCAG
TTATGAATGATGTTGATAGAACAGCAGGACGTGGTGGTGTTGGAGCTGTTATGGGTTCAAAGAACTTAAAAGCT
ATTGTAGTTAAAGGAAGCGGAAAAGTAAAATTATTTGATGAACAAAAAGTGAAGGAAGTAGCACTTGAGAAAAC
AAATATTTTAAGAAAAGATCCAGTAGCTGGTGGAGGACTTCCAACATACGGAACAGCTGTACTTGTTAATATTAT
AAATGAAAATGGTGTACATCCAGTAAAGAATTTTCAAAAATCTTATACAGATCAAGCAGATAAGATCAGTGGAGA
AACTTTAACTAAAGATTGCTTAGTTAGAAAAAATCCTTGCTATAGGTGTCCAATTGCCTGTGGAAGATGGGTAAA
ACTTGATGATGGAACTGAATGTGGAGGACCAGAATATGAAACATTATGGTCATTTGGATCTGATTGTGATGTATA
CGATATAAATGCTGTAAATACAGCAAATATGTTGTGTAATGAATATGGATTAGATACCATTACAGCAGGATGTAC
TATTGCAGCAGCTATGGAACTTTATCAAAGAGGTTATATTAAGGATGAAGAAATAGCAGCAGATGGATTGTCACT
TAATTGGGGAGATGCTAAGTCCATGGTTGAATGGGTAAAGAAAATGGGACTTAGAGAAGGATTTGGAGACAAG
ATGGCAGATGGTTCATACAGACTTTGTGACTCATACGGTGTACCTGAGTATTCAATGACTGTAAAAAAACAGGAA
CTTCCAGCATATGACCCAAGAGGAATACAGGGACATGGTATTACTTATGCTGTTAACAATAGGGGAGGATGTCAC
ATTAAGGGATATATGGTAAGTCCTGAAATACTTGGCTATCCAGAAAAACTTGATAGACTTGCAGTGGAAGGAAA
AGCAGGATATGCTAGAGTATTCCATGATTTAACAGCTGTTATAGATTCACTTGGATTATGTATTTTTACAACATTTG
GTCTTGGTGCACAGGATTATGTTGATATGTATAATGCAGTAGTTGGTGGAGAATTACATGATGTAAATTCTTTAAT
GTTAGCTGGAGATAGAATATGGACTTTAGAAAAAATATTTAACTTAAAGGCAGGCATAGATAGTTCACAGGATAC
TCTTCCAAAGAGATTGCTTGAAGAACAAATTCCAGAAGGACCATCAAAAGGAGAAGTTCATAAGTTAGATGTACT
ACTACCTGAATATTATTCAGTACGTGGATGGGATAAAAATGGTATTCCTACAGAGGAAACGTTAAAGAAATTAGG
ATTAGATGAATACGTAGGTAAGCTTTAG

Seq. ID 90: Amino acid sequence of aldehyde:ferredoxin oxidoreductase from *C. ljungdahlii*:
MYGYKGKVLRINLSSKTYIVEELKIDKAKKFIGARGLGVKTLFDEVDPKVDPLSPDNKFIIAAGPLTGAPVPTSGRFMVVT
KSPLTGTIAIANSGGKWGAEFKAAGYDMIIVEGKSDKEVYVNIVDDKVEFRDASHVWGKLTEETTKMLQQETDSRAK
VLCIGPAGEKLSLMAAVMNDVDRTAGRGGVGAVMGSKNLKAIVVKGSGKVKLFDEQKVKEVALEKTNILRKDPVAG
GGLPTYGTAVLVNIINENGVHPVKNFQKSYTDQADKISGETLTKDCLVRKNPCYRCPIACGRWVKLDDGTECGGPEYE
TLWSFGSDCDVYDINAVNTANMLCNEYGLDTITAGCTIAAAMELYQRGYIKDEEIAADGLSLNWGDAKSMVEWVKK
MGLREGFGDKMADGSYRLCDSYGVPEYSMTVKKQELPAYDPRGIQGHGITYAVNNRGGCHIKGYMVSPEILGYPEKL
DRLAVEGKAGYARVFHDLTAVIDSLGLCIFTTFGLGAQDYVDMYNAVVGGELHDVNSLMLAGDRIWTLEKIFNLKAGI
DSSQDTLPKRLLEEQIPEGPSKGEVHKLDVLLPEYYSVRGWDKNGIPTEETLKKLGLDEYVGKL*

FIGURE 46

Seq. ID 91: Nucleotide sequence of aldehyde:ferredoxin oxidoreductase from *C. ljungdahlii*:
ATGTATGGTTATGATGGTAAAGTATTAAGAATTAATTTAAAAGAAAGAACTTGCAAATCAGAAAATTTAGATTTA
GATAAAGCTAAAAAGTTTATAGGTTGTAGGGGACTAGGTGTTAAAACTTTATTTGATGAAATAGATCCTAAAATA
GATGCATTATCACCAGAAAATAAATTTATAATTGTAACAGGTCCTTTAACTGGAGCTCCGGTTCCAACTAGTGGAA
GGTTTATGGTAGTTACTAAAGCACCGCTTACAGGAACTATAGGAATTTCAAATTCGGGTGGAAAATGGGGAGTA
GACTTAAAAAAAGCTGGTTGGGATATGATAATAGTAGAGGATAAGGCTGATTCACCAGTTTACATTGAAATAGTA
GATGATAAGGTAGAAATTAAAGACGCGTCACAGCTTTGGGGAAAAGTTACATCAGAAACTACAAAAGAGTTAGA
AAAGATAACTGAGAATAAATCAAAGGTATTATGTATAGGACCTGCTGGTGAACGATTGTCTCTTATGGCAGCAGT
TATGAATGATGTAGATAGAACTGCAGCAAGAGGCGGCGTTGGTGCAGTTATGGGATCTAAAAACTTAAAAGCTA
TTACAGTTAAAGGAACTGGAAAAATAGCTTTAGCTGATAAAGAAAAAGTAAAAAAAGTGTCCGTAGAAAAAATT
ACAACATTAAAAAATGATCCAGTAGCTGGTCAGGGAATGCCAACTTATGGTACAGCTATACTGGTTAATATAATA
AATGAAAATGGAGTTCATCCTGTAAAGAATTTTCAAGAGTCTTATACGAATCAAGCAGATAAAATAAGTGGAGAG
ACTCTTACTGCTAACCAACTAGTAAGGAAAAATCCTTGTTACAGCTGTCCTATAGGTTGTGGAAGATGGGTTAGA
CTAAAAGATGGCACAGAGTGCGGAGGACCAGAATATGAAACACTGTGGTGTTTTGGATCTGACTGTGGTTCATA
TGATTTAGATGCTATAAATGAAGCTAATATGTTATGTAATGAATATGGTATTGATACTATTACTTGTGGTGCAACA
ATTGCTGCAGCTATGGAACTTTATCAAAGAGGATATATAAAAGACGAAGAAATAGCTGGAGATAACCTATCTCTC
AAGTGGGGTGATACGGAATCTATGATTGGCTGGATAAAGAGAATGGTATATAGTGAAGGCTTTGGAGCAAAGA
TGACAAATGGTTCATATAGGCTTTGTGAAGGTTATGGAGCACCGGAGTATTCTATGACAGTTAAAAAGCAGGAA
ATTCCAGCATATGATCCAAGGGGAATACAGGGACACGGTATTACCTATGCAGTTAATAATAGAGGAGGCTGTCA
TATTAAGGGATATATGATTAACCCTGAAATATTAGGTTATCCTGAAAAACTTGATAGATTTGCATTAGATGGTAAA
GCAGCTTATGCCAAATTATTTCATGATTTAACTGCTGTAATTGATTCTTTAGGATTGTGCATATTCACTACATTTGG
GCTTGGAATACAGGATTATGTAGATATGTATAATGCAGTAGTAGGAGAATCTACTTATGATGCAGATTCACTATT
AGAGGCAGGAGATAGAATCTGGACTCTTGAGAAATTATTTAATCTTGCAGCTGGAATAGACAGCAGCCAGGATA
CTCTACCAAAGAGATTGTTAGAAGAACCTATTCCAGATGGCCCATCAAAGGGAGAAGTTCATAGGCTAGATGTTC
TTCTGCCAGAATATTACTCAGTACGAGGATGGAGTAAAGAGGGTATACCTACAGAAGAAACATTAAAGAAATTA
GGATTAGATGAATATATAGGTAAGTTCTAG

Seq. ID 92: Amino acid sequence of aldehyde:ferredoxin oxidoreductase from *C. ljungdahlii*:
MYGYDGKVLRINLKERTCKSENLDLDKAKKFIGCRGLGVKTLFDEIDPKIDALSPENKFIIVTGPLTGAPVPTSGRFMVVT
KAPLTGTIGISNSGGKWGVDLKKAGWDMIIVEDKADSPVYIEIVDDKVEIKDASQLWGKVTSETTKELEKITENKSKVLC
IGPAGERLSLMAAVMNDVDRTAARGGVGAVMGSKNLKAITVKGTGKIALADKEKVKKVSVEKITTLKNDPVAGQGM
PTYGTAILVNIINENGVHPVKNFQESYTNQADKISGETLTANQLVRKNPCYSCPIGCGRWVRLKDGTECGGPEYETLW
CFGSDCGSYDLDAINEANMLCNEYGIDTITCGATIAAAMELYQRGYIKDEEIAGDNLSLKWGDTESMIGWIKRMVYSE
GFGAKMTNGSYRLCEGYGAPEYSMTVKKQEIPAYDPRGIQGHGITYAVNNRGGCHIKGYMINPEILGYPEKLDRFALD
GKAAYAKLFHDLTAVIDSLGLCIFTTFGLGIQDYVDMYNAVVGESTYDADSLLEAGDRIWTLEKLFNLAAGIDSSQDTLP
KRLLEEPIPDGPSKGEVHRLDVLLPEYYSVRGWSKEGIPTEETLKKLGLDEYIGKF*

FIGURE 47

Seq. ID 93: Nucleotide Acid sequence of bifunctional butanol/ butyraldehyde dehydrogenase from *C. ragsdalei*:
ATGCCAAGAAATCTGTTTATATTTAACAGCATGAAAAATAAGAAAGAGGTGTCATTAATGAAGGTAACTAAGGTAACTAACG
TTGAAGAATTAATGAAAAAGTTAGATGAAGTAACGGCTGCTCAAAAAAAATTCTCTAGTTATAGTCAGGAACAAGTGGATGA
GATCTTTAGGCAGGCAGCTATGGCAGCCAATAGTGCTAGAATAGATCTAGCTAAAATGGCAGTGGAAGAAAGCGGAATGGG
AATTGTAGAAGACAAGGTTATTAAAAATCATTTTGTTTCAGAATATATATATAACAAATATAAGGATGAAAAGACCTGTGGAG
TTTTAGAAGAAGACCAAGGTTTTGGTATGGTTAGAATTGCGGAACCTGTAGGGGTTATAGCAGCAGTAGTTCCAACAACTAA
TCCAACATCCACAGCAATCTTTAAATCTTTAATAGCTTTGAAAACTAGAAATGGTATAGTTTTTTCACCACATCCAAGAGCAAA
AAAATCAACTATTGCAGCAGCTAAGATAGTACTTGATGCAGCAGTTAAAGCTGGTGCTCCTGAAGGAATTATAGGATGGATA
GATGAACCTTCCATTGAACTCTCACAGGTGGTAATGAAAGAAGCAGATTTAATTCTTGCAACTGGTGGCCCGGGTATGGTTAA
GGCTGCCTATTCTTCAGGAAAGCCTGCTATAGGAGTTGGCCCAGGTAACACACCTGCTGTAATTGATGAAAGTGCTGATATTA
AAATGGCAGTAAATTCAATACTCCTTTCAAAAACTTTTGATAATGGTATGATTTGTGCTTCAGAGCAGTCAGTAGTAGTTGTAA
GCTCAATATACGATGAAGTCAAGAAAGAATTTGCAGATAGAGGAGCGTATATATTAAGTAAGGATGAAACAGATAAGGTTG
GAAAAACAATTATGATTAATGGCGCTCTAAATGCTGGCATTGTAGGGCAAAGTGCTTTTAAAATAGCACAGATGGCAGGAGT
GAGTGTACCAGAGGATGCTAAAGTACTTATAGGAGAAGTTAAATCAGTAGAACCTGAAGAAGAGCCCTTTGCTCATGAAAAG
CTGTCTCCAGTTTTAGCTATGTACAAAGCAAAAGATTTTGATGAAGCACTTCTAAAGGCTGGAAGATTAGTTGAACGAGGTG
GAATTGGGCATACATCTGTATTATATGTAAATTCAATGACGGAAAAAGTAAAAGTAGAAAAGTTCAGAGAAACTATGAAGAC
TGGTAGAACATTGATAAATATGCCTTCAGCACAAGGTGCTATAGGAGATATATATAACTTTAAACTAGCTCCTTCTTTGACGCT
AGGATGTGGTTCCTGGGGAGGAAACTCTGTATCAGAAAATGTTGGACCTAAACATTTATTAAACATAAAAAGTGTTGCTGAG
AGGAGAGAAAATATGCTTTGGTTTAGAGTACCTGAAAAAGTTTATTTCAAATATGGTAGTCTTGGAGTTGCATTAAAGGAATT
GAGAACTTTGGAGAAGAAAAAGGCATTTATAGTAACGGATAAGGTTCTTTATCAATTAGGTTATGTAGATAAAATTACAAAA
AATCTCGATGAATTAAGAGTTTCATATAAAATATTTACAGATGTAGAACCAGATCCAACCCTTGCTACAGCTAAAAAAGGTGC
ATCAGAACTGCTTTCCTATGAACCAGATACAATTATAGCAGTTGGTGGTGGTTCGGCAATGGATGCAGCCAAGATCATGTGG
GTAATGTATGAGCATCCAGAAGTAAGATTTGAAGATTTGGCTATGAGATTTATGGATATAAGAAAGAGAGTATATGTTTTTCC
TAAGATGGGTGAAAAAGCAATGATGATTTCAGTAGCAACATCCGCAGGAACAGGATCTGAAGTTACTCCATTTGCAGTAATT
ACGGATGAAAGAACAGGAGCTAAATATCCACTGGCTGATTATGAATTGACTCCAAACATGGCTATAATTGATGCAGAACTTAT
GATGGGAATGCCAAAAGGGCTTACAGCAGCTTCGGGTATAGATGCATTAACCCATGCACTGGAGGCGTATGTATCAATAATG
GCTTCAGAATATACCAATGGATTGGCTCTTGAAGCAACAAGATTAGTATTTAAATATTTGCCAATAGCTTATACAGAAGGTAC
AACTAATGTAAAGGCAAGAGAAAAAATGGCTCATGCTTCAACTATAGCAGGTATGGCTTTTGCCAATGCATTCTTAGGGGTAT
GTCACTCTATGGCACATAAATTGGGAGCACAGCACCATATACCACATGGAATTGCCAATGCGCTTATGATAGATGAAGTTATA
AAATTCAATGCTGTAGAGGCTCCAAGGAAACAAGCGGCATTTCCACAATATAAGTACCCAAATGTTAAAAGAAGATATGCTA
GAATAGCTGATTACTTAAATTTAGGAGGAAGCACAGATGATGAAAAAGTACAATTGCTAATAAATGCTATAGATGACTTAAA
AACTAAGTTAAATATTCCAAAGACTATTAAAGAGGCAGGAGTTTCAGAAGATAAATTCTATGCTACTTTAGACACAATGTCAG
AACTGGCTTTTGATGATCAATGTACAGGAGCTAATCCAAGATATCCACTAATAGGAGAAATAAAACAAATGTATATAAATGCA
TTTGATACACCAAAGGCAACTGTGGAGAAGAAAACAAAAAGAAAAATAAACATATAA

FIGURE 48

Seq. ID 94: Amino Acid sequence of bifunctional butanol/ butyraldehyde dehydrogenase from *C. ragsdalei*:
MPRNLFIFNSMKNKKEVSLMKVTKVTNVEELMKKLDEVTAAQKKFSSYSQEQVDEIFRQAAMAANSARIDLAKMAVEESGMGIV
EDKVIKNHFVSEYIYNKYKDEKTCGVLEEDQGFGMVRIAEPVGVIAAVVPTTNPTSTAIFKSLIALKTRNGIVFSPHPRAKKSTIAAAKI
VLDAAVKAGAPEGIIGWIDEPSIELSQVVMKEADLILATGGPGMVKAAYSSGKPAIGVGPGNTPAVIDESADIKMAVNSILLSKTFD
NGMICASEQSVVVVSSIYDEVKKEFADRGAYILSKDETDKVGKTIMINGALNAGIVGQSAFKIAQMAGVSVPEDAKVLIGEVKSVEP
EEEPFAHEKLSPVLAMYKAKDFDEALLKAGRLVERGGIGHTSVLYVNSMTEKVKVEKFRETMKTGRTLINMPSAQGAIGDIYNFKLA
PSLTLGCGSWGGNSVSENVGPKHLLNIKSVAERRENMLWFRVPEKVYFKYGSLGVALKELRTLEKKKAFIVTDKVLYQLGYVDKITK
NLDELRVSYKIFTDVEPDPTLATAKKGASELLSYEPDTIIAVGGGSAMDAAKIMWVMYEHPEVRFEDLAMRFMDIRKRVYVFPKM
GEKAMMISVATSAGTGSEVTPFAVITDERTGAKYPLADYELTPNMAIIDAELMMGMPKGLTAASGIDALTHALEAYVSIMASEYTN
GLALEATRLVFKYLPIAYTEGTTNVKAREKMAHASTIAGMAFANAFLGVCHSMAHKLGAQHHIPHGIANALMIDEVIKFNAVEAPR
KQAAFPQYKYPNVKRRYARIADYLNLGGSTDDEKVQLLINAIDDLKTKLNIPKTIKEAGVSEDKFYATLDTMSELAFDDQCTGANPR
YPLIGEIKQMYINAFDTPKATVEKKTKRKINI*

FIGURE 49

Seq. ID 95: Nucleotide Acid sequence of bifunctional butanol/ butyraldehyde dehydrogenase from *C. ragsdalei*:

ATGAAAGTTACAAACGTGGAAGAATTAATGAAAAGACTAGAAGAGATAAAGGATGCTCAAAAGAAATTTGCTAC
ATATACTCAAGAACAAGTGGATGAAATTTTTAGACAAGCAGCTATGGCAGCCAATAGTGCTAGAATAGAACTAGC
TAAAATGGCAGTGGAAGAAAGCGGAATGGGAATTGTAGAAGACAAGGTTATTAAAAATCACTTTGCCTCAGAAT
ATATATATAACAAATATAAGGATGAAAAGACCTGTGGAGTTTTAGAAAGAGATGCAGGCTTTGGTATAGTTAGA
ATTGCGGAACCTGTAGGGGTTATTGCAGCAGTAGTTCCAACAACTAATCCAACATCTACAGCAATCTTTAAATCAC
TAATAGCTTTAAAAACTAGAAATGGTATAATTTTTTCACCGCATCCAAGGGCAAAGAAATCAACTATTGCAGCAGC
TAAAATAGTACTTGATGCTGCAGTTAAAGCTGGTGCTCCCGAAGGAATTATAGGATGGATAGATGAACCTTCCAT
TGAACTTTCACAGGTGGTAATGGGAGAAGCAAATTTAATTCTTGCAACTGGTGGCCCGGGTATGGTTAAGGCTGC
CTATTCTTCAGGAAAACCTGCTGTAGGAGTTGGCCCAGGTAATACACCTGCTATAATTGATGAAAGTGCCGATAT
TAAAATGGCAGTAAATTCAATATTACTCTCAAAAACTTTTGATAATGGTATGATTTGTGCCTCAGAGCAGTCAGTA
ATAGTTTTAGACTCAATATATGAGGAAGTTAAAAAAGAATTTGCTTATAGGGGAGCTTATATATTGAGTGAGGAT
GAAACAGATAAGGTTGGAAAAATAATTTTAAAAAATGGAGCCTTAAATGCTGGTATTGTAGGACAAAGTGCTTTT
AAAATAGCACAGCTGGCAGGAGTGAACGTACCAGAAAAAGCTAAAGTACTTATAGGAGAGGTAGAATCAGTAG
AACTTGAAGAACCATTTTCTCATGAAAAGTTATCTCCAGTTTTAGCTATGTACAGGGCAAGAGATTTTGAGGATGC
CATTGCAAAAACTGATAAACTGGTTAGGGCAGGTGGATTTGGACATACATCTTCATTATATGTAAATCCAATGAC
AGAAAAAGCAAAAGTAGAAAAATTTAGTACTATGATGAAAACATCAAGAACTATAATTAACACACCTTCATCTCA
AGGTGGTATAGGTGACATATATAACTTTAAGCTAGCTCCTTCGCTGACGCTAGGCTGCGGATCTTGGGGAGGAA
ACTCTGTATCCGAAAATGTTGGGCCTAAACATTTATTAAACATAAAAAGTGTTGCTGAGAGGAGAGAAAATATGC
TTTGGTTTAGAGTGCCTGAAAAGGTTTATTTCAAATACGGTAGTCTTGGAGTTGCATTAAAAGAATTAAAAGTTAT
GAATAAGAAGAAAGTATTTATAGTAACAGATAAAGTCCTTTATCAATTAGGTTATGTGGACAAAGTTACAAAAGT
TCTTGAGGAACTAAAAATTTCCTATAAAGTATTTACAGATGTAGAACCAGATCCAACCCTTGCTACAGCTAAAAAA
GGTGCAGCAGAATTGCTGTCATATGAACCGGATACAATTATATCAGTTGGTGGTGGTTCAGCAATGGATGCAGCC
AAGATTATGTGGGTAATGTATGAGCATCCAGAAGTAAAATTTGAAGATTTAGCTATGAGATTTATGGATATAAGA
AAGAGAGTATATGTTTTCCCTAAGATGGGAGAAAAAGCAATGATGATTTCAGTAGCAACATCCGCAGGTACAGG
ATCAGAAGTTACTCCATTTGCAGTAATTACAGATGAAAAAACAGGAGCTAAATATCCATTAGCTGATTATGAGTT
AACTCCAAACATGGCTATAGTTGATGCAGAACTTATGATGGGAATGCCAAGAGGACTTACGGCAGCGTCAGGTA
TAGATGCATTAACTCATGCACTGGAAGCTTATGTATCAATAATGGCTACAGAATTTACCAATGGATTAGCCCTTGA
AGCAGTAAAGTTGATATTTGAATATTTACCAAAAGCTTATACAGAAGGTACAACTAATGTAAAGGCAAGAGAAAA
AATGGCTCATGCTTCATGTATTGCTGGTATGGCTTTTGCAAATGCATTCTTAGGGGTATGCCACTCTATGGCACAT
AAATTAGGAGCACAGCACCACATACCACATGGAATTGCTAATGCACTTATGATAGATGAAGTTATAAAATTCAAT
GCTGTAGATGATCCAATAAAACAAGCTGCATTTCCTCAATACGAGTATCCAAATGCCAAGTATAGATATGCTCAG
ATAGCTGATTGTCTCAACTTAGGAGGAAATACAGAAGATGAAAAGGTGCAATTATTAATAAATGCTATAGATGAT
CTAAAAGCTAAGTTAAATATTCCAGAAACGATTAAAGAAGCAGGAGTTTCAGAAGAAAAATTCTATACTACTTTA
GATAAAATGTCAGAATTAGCTTTTGATGATCAATGTACAGGAGCTAACCCAAGGTATCCACTAATAAGTGAAATA
AAACAAATGTATATAAATGTTTTTGATAAAACTGAACCAATTGTAGAAGATGAAGAAAAGTAA

FIGURE 50

Seq. ID 96: Amino Acid sequence of bifunctional butanol/ butyraldehyde dehydrogenase from *C. ragsdalei*:
MKVTNVEELMKRLEEIKDAQKKFATYTQEQVDEIFRQAAMAANSARIELAKMAVEESGMGIVEDKVIKNHFASEYIYN
KYKDEKTCGVLERDAGFGIVRIAEPVGVIAAVVPTTNPTSTAIFKSLIALKTRNGIIFSPHPRAKKSTIAAAKIVLDAAVKAG
APEGIIGWIDEPSIELSQVVMGEANLILATGGPGMVKAAYSSGKPAVGVGPGNTPAIIDESADIKMAVNSILLSKTFDN
GMICASEQSVIVLDSIYEEVKKEFAYRGAYILSEDETDKVGKIILKNGALNAGIVGQSAFKIAQLAGVNVPEKAKVLIGEVE
SVELEEPFSHEKLSPVLAMYRARDFEDAIAKTDKLVRAGGFGHTSSLYVNPMTEKAKVEKFSTMMKTSRTIINTPSSQG
GIGDIYNFKLAPSLTLGCGSWGGNSVSENVGPKHLLNIKSVAERRENMLWFRVPEKVYFKYGSLGVALKELKVMNKKK
VFIVTDKVLYQLGYVDKVTKVLEELKISYKVFTDVEPDPTLATAKKGAAELLSYEPDTIISVGGGSAMDAAKIMWVMYE
HPEVKFEDLAMRFMDIRKRVYVFPKMGEKAMMISVATSAGTGSEVTPFAVITDEKTGAKYPLADYELTPNMAIVDAE
LMMGMPRGLTAASGIDALTHALEAYVSIMATEFTNGLALEAVKLIFEYLPKAYTEGTTNVKAREKMAHASCIAGMAFA
NAFLGVCHSMAHKLGAQHHIPHGIANALMIDEVIKFNAVDDPIKQAAFPQYEYPNAKYRYAQIADCLNLGGNTEDEK
VQLLINAIDDLKAKLNIPETIKEAGVSEEKFYTTLDKMSELAFDDQCTGANPRYPLISEIKQMYINVFDKTEPIVEDEEK*

Seq. ID 97: Nucleotide Acid sequence of butyraldehyde dehydrogenase from *C. ragsdalei*:
ATGGAGGGAACACAATTGGAAAATTTTGATAAAGACTTACGCTCTATACAAGAAGCAAGAGATCTTGCACGTTTA
GGAAAAATTGCAGCATGTGAAATTGCTGATTATACTGAAGAACAAATTGATAAAATCCTATGTAATATGGTTAGG
GTAGCAGAGGAAAATGCAGTTTGCCTTGGTAAAATGGCTGCAGAAGAAACTGGTTTTGGAAAAGCTGAAGATAA
GGCTTATAAGAACCATATGGCTGCTACTACAGTATATAATTATATCAAGGATATGAAGACTATTGGTGTTATAAAA
GAAGATAAAAGTCAAGGTGTAATTGAATTTGCTGAACCAGTTGGTTTATTAATGGGTATTGTACCATCTACAAATC
CAACATCTACTGTTATCTATAAATCAATCATTGCAATTAAATCAAGAAATGCAATTGTATTCTCACCACACCCAGCT
GCATTAAAATGTTCAACAAAAGCAATAGAACTTATGCGTGATGCAGCAGTAGCAGCAGGAGCTCCTGCAAATGT
AATTGGCGGTATTGTTACACCATCTATACAAGCTACAAATGAACTTATGAAAGCTAAAGAAGTTGCTATGATAATT
GCCACTGGAGGCCCTGGAATGGTAAAGGCTGCTTATAGTTCAGGAACACCTGCAATAGGCGTTGGTGCTGGTAA
CTCTCCATCTTATATAGAAAGAACTGCTGATGTTCATCAATCAGTTAAAGATATAATTGCTAGTAAGAGTTTTGAC
TATGGTACTATTTGTGCATCTGAGCAATCAATAATTGTTGAAGAATGCAACCATGATGAAGTAATAGCTGAGTTG
AAGAAACAAGGCGGATATTTCATGACAGCTGAAGAAACTGCAAAAGTTTGCAGTATACTTTTTAAGCCTGGTACA
CACAGTATGAGTGCTAAGTTTGTAGGAAGAGCTCCTCAGGTTATAGCAGCAGCTGCAGGTTTCTCAGTTCCAGAA
GGAACAAAAGTTTTAGTAGGAGAACAAGGCGGAGTTGGTAATGGTTACCCTCTATCTTATGAGAAACTTACAACA
GTACTTGCTTTCTATACAGTTAAAGATTGGCATGAAGCATGTGATCTTAGTATAAGATTACTTCAAAATGGTCTTG
GACATACTATGAACATTCATACAAATGACAGAGACTTAGTAATGAAGTTTGCTAAAAAACCAGCATCCCGTATATT
AGTTAATACTGGTGGAAGCCAAGGAGGTACTGGTGCAAGCACAGGATTAGCACCTGCATTTACATTAGGTTGTG
GTACATGGGGAGGAAGCTCTGTTTCCGAAAATGTTACTCCATTACATTTAATCAATATAAAGAGAGTTGCATATG
GTCTTAAAGATTGTTCTACATTAGCTGCAGATGATACAACTTTCAATCATCCTGAACTTTGTGGAAGCAAAAATGA
CTTAGGATGCTGTGCTACAAGCCCTGCAGAATTTGCAGCAAATAGCAATTGTGCTAGCACTGCTGCGGATACTAC
TGATAATGATAAACTTGCTAGACTCGTAAGTGAATTAGTAGCTGCAATGAAGGGAGCTAACTAA

FIGURE 51

Seq. ID 98: Amino Acid sequence of butyraldehyde dehydrogenase from *C. ragsdalei*:
MEGTQLENFDKDLRSIQEARDLARLGKIAACEIADYTEEQIDKILCNMVRVAEENAVCLGKMAAEETGFGKAEDKAYK
NHMAATTVYNYIKDMKTIGVIKEDKSQGVIEFAEPVGLLMGIVPSTNPTSTVIYKSIIAIKSRNAIVFSPHPAALKCSTKAI
ELMRDAAVAAGAPANVIGGIVTPSIQATNELMKAKEVAMIIATGGPGMVKAAYSSGTPAIGVGAGNSPSYIERTADV
HQSVKDIIASKSFDYGTICASEQSIIVEECNHDEVIAELKKQGGYFMTAEETAKVCSILFKPGTHSMSAKFVGRAPQVIAA
AAGFSVPEGTKVLVGEQGGVGNGYPLSYEKLTTVLAFYTVKDWHEACDLSIRLLQNGLGHTMNIHTNDRDLVMKFAK
KPASRILVNTGGSQGGTGASTGLAPAFTLGCGTWGGSSVSENVTPLHLINIKRVAYGLKDCSTLAADDTTFNHPELCGS
KNDLGCCATSPAEFAANSNCASTAADTTDNDKLARLVSELVAAMKGAN*

Seq. ID 99: Nucleotide Acid sequence of butyraldehyde dehydrogenase from *C. ragsdalei*:
GTGGAAAATGCTGCACGAGCACAAAAAATGTTAGCAACTTTTCCGCAAGAAAAGTTAGATGAGATTGTTGAACG
TATGGCTGAAGAAATCGGAAAACATACCCGAGAGCTTGCTGTAATGTCACAGGATGAAACTGGTTATGGAAAAT
GGCAGGATAAATGCATCAAAAACCGATTTGCCTGTGAATATTTGCCAGCTAAGCTTAGAGGAATGCGATGTGTA
GGTATTATTAACGAAAATGGTCAGGATAAGACCATGGATGTAGGTGTACCTATGGGTGTAATTATTGCATTATGT
CCTGCAACTAGTCCGGTTTCTACTACCATATATAAGGCATTAATTGCAATTAAGTCTGGTAATGCAATTATCTTTTC
TCCACATCCTAGAGCAAAGGAGACAATTTGTAAGGCGCTTGACATCATGATTCGTGCAGCTGAAGGATATGGGCT
GCCAGAAGGAGCTCTTGCATACTTACATACTGTGACGCCTAGTGGAACAATCGAATTGATGAACCATGAGGCGA
CTTCTTTGATTATGAATACAGGCGTTCCCGGGATGCTTAAAGCGTCATATAGATCTGGAAAACCTGTGATCTATGG
AGGAACTGGTAATGGACCAGCATTTATTGAACGTACAGCTGACATCAAGCAGGCGGTAAGAGATATTATTGCTA
GTAAGACCTTTGATAACGGAATAGTACCATCATCTGAACAATCTATTGTTGTAGATAGCTGTGTTGCATCTGATGT
TAAACGTGAGTTGCAAAATAGTGGTGCATATTTCATGACAGAGGAGGAAGCACAAAAACTGGGTTCTCTCTTTTT
CCGTTCTGATGGTAGTATGGATTCAGAAATGGTTGGCAAATCCGCACAGAGATTGGCTAAGAAAGCAGGTTTCA
GTATTCCTGAAAGTAGCACAGTGCTAATTTCAGAGCAGAAATATGTTTCCCAAGATAATCCTTATTCCAAGGAGA
AACTTTGTCCGGTACTAGCTTACTACATTGAAGATGATTGGATGCATGCATGTGAAAAGTGTATTGAGCTGCTATT
AAGTGAGAGACATGGTCACACTCTTGTTATACATTCAAAAGACGAAGATGTAATTCGCCAGTTTGCATTAAAAAA
ACCTGTAGGCAGGATACTTGTTAATACGCCTGCTTCCTTTGGTAGTATGGGTGCTACAAGTAATTTATTTCCTGCTT
TAACTTTAGGTAGTGGATCGGCAGGTAAAGGTATTACCTCCGATAATGTTTCACCAATGAATCTTATTTACGTCCG
TAAAGTCGGATATGGCGTACGGAATGTAGAAGAGATTATTAATACTAATGGATTGTTTACAGAAGAAAAAAGTG
ATTTGAGTGGTATGACAAAGCAGTCAGACTATAATCCAGAGGATATACAAATGTTGCAGCATATTTTGAAAAAAG
CTATGGAAAAAATTAAATAG

Seq. ID 100: Amino Acid sequence of butyraldehyde dehydrogenase from *C. ragsdalei*:
VENAARAQKMLATFPQEKLDEIVERMAEEIGKHTRELAVMSQDETGYGKWQDKCIKNRFACEYLPAKLRGMRCVGII
NENGQDKTMDVGVPMGVIIALCPATSPVSTTIYKALIAIKSGNAIIFSPHPRAKETICKALDIMIRAAEGYGLPEGALAYL
HTVTPSGTIELMNHEATSLIMNTGVPGMLKASYRSGKPVIYGGTGNGPAFIERTADIKQAVRDIIASKTFDNGIVPSSEQ
SIVVDSCVASDVKRELQNSGAYFMTEEEAQKLGSLFFRSDGSMDSEMVGKSAQRLAKKAGFSIPESSTVLISEQKYVSQ
DNPYSKEKLCPVLAYYIEDDWMHACEKCIELLLSERHGHTLVIHSKDEDVIRQFALKKPVGRILVNTPASFGSMGATSNL
FPALTLGSGSAGKGITSDNVSPMNLIYVRKVGYGVRNVEEIINTNGLFTEEKSDLSGMTKQSDYNPEDIQMLQHILKKA
MEKIK*

FIGURE 52

Seq. ID 101: Nucleotide Acid sequence of butanol dehydrogenase from *C. ragsdalei*:
ATGGCAAGATTTACTTTACCAAGAGACATTTATTTTGGAGAAAATTCATTAGAGACCTTGAAAAACCTAGATGGA
AAAAAAGCTGTCATTGTCGTAGGTGGAGGATCCATGAAAAGATTTGGATTCCTTGATAAGGTAGTAGACTACTTA
AAAGAAGCAGGTATTGAATCAAAATTAATAGAAGGCGTTGAGCCAGATCCATCCGTAGAAACTGTTATGAATGG
TGCTAAACTAATGAGGGAATATGGGCCAGATTTAATAATATCAATAGGTGGAGGTTCACCAATTGATGCAGCAA
AAGCTATGTGGATATTCTATGAATACCCTGAGTTTACTTTTAAAGAAGCTGTAGTTCCTTTTGGTCTTCCTAAATTA
AGACAAAAAGCAACATTTATAGCTATCCCTTCTACAAGTGGTACTGCAACGGAAGTAACTGCATTTTCTGTAATAA
CAGACTATAAAGCTAAAATTAAATATCCTTTGGCTGACTTCAATTTAACACCAGATATAGCTATAATTGATCCAGT
ATTAGCTCAAACAATGCCGCCTAAATTAACTGCACATACTGGAATGGATGCACTTACTCACGCTATTGAAGCATAT
GTTGCAGGACTTCATTCAGTTTTCTCGGACCCACTTGCTATTCAAGCTATAGTCATGGTAAATCAATATTTAATTAA
ATCTTACAATGAAGATAAAGAAGCTAGGGATCAAATGCATTTAGCTCAATGTTTAGCTGGAATGGCATTTTCAAA
TGCACTTCTTGGAATAACTCACAGTTTAGCACATAAAACAGGTGCAGTATTCCATATCCCTCATGGATGTGCTAAT
GCAATATATCTTCCTTATGTTATAGATTTCAATAAAAAAGCTTGTGCACCAAGATATGCTGATATAGCTAGGAGTC
TTAAACTTCCAGGAAATACTGATGATGAATTAGTAGATTCATTAACTAATATGATTAAAGATATGAACAAGAGTAT
GGATATTCCTTTGACATTAAAAGATTATGGAGTAGATGAAAAAGAATTTAAAGATAGTGAAGATTTTATAGCTCA
TAATGCCGTATTAGATGCCTGTACTGGATCAAATCCTAGAAGCATAAATGATGCTGAAATGAAAAAGTTGTTAGA
ATACATCTATTATGGTAAAAAGGTTGATTTTTAA

Seq. ID 102: Amino Acid sequence of butanol dehydrogenase from *C. ragsdalei*:
MARFTLPRDIYFGENSLETLKNLDGKKAVIVVGGGSMKRFGFLDKVVDYLKEAGIESKLIEGVEPDPSVETVMNGAKL
MREYGPDLIISIGGGSPIDAAKAMWIFYEYPEFTFKEAVVPFGLPKLRQKATFIAIPSTSGTATEVTAFSVITDYKAKIKYPL
ADFNLTPDIAIIDPVLAQTMPPKLTAHTGMDALTHAIEAYVAGLHSVFSDPLAIQAIVMVNQYLIKSYNEDKEARDQM
HLAQCLAGMAFSNALLGITHSLAHKTGAVFHIPHGCANAIYLPYVIDFNKKACAPRYADIARSLKLPGNTDDELVDSLT
NMIKDMNKSMDIPLTLKDYGVDEKEFKDSEDFIAHNAVLDACTGSNPRSINDAEMKKLLEYIYYGKKVDF*

Seq. ID 103: Nucleotide Acid sequence of butanol dehydrogenase from *C. ragsdalei*:
ATGGGAAGATTTACTTTGCCTAGGGATATTTACTTTGGTGAAAATGCCTTAGAAAATTTAAAAAATTTAGATGGA
AATAAAGCAGTAGTTGTTGTAGGTGGAGGATCTATGAAGAGATTTGGGTTCTTAGCCAAAGTTGAAGAATACTTA
AAAGAAGCAGGTATGGAAGTTAAATTAATAGAAGGTGTTGAGCCTGATCCATCTGTTGATACTGTTATGAATGGT
GCTAAAATAATGAGAGACTTTAATCCAGACTGGATAGTATCAATAGGTGGAGGATCTCCCATCGATGCTGCCAAA
GCAATGTGGATATTTTATGAATACCCTGACTTTACATTTGAAAAAGCGGTAGTCCCTTTTGGGATTCCTAAATTAA
GGCAAAAGGCACAATTTGTTGCTATACCTTCTACAAGTGGAACAGCAACTGAAGTAACATCATTTTCTGTAATAAC
AGACTATAAAGCTAAAATAAAATATCCTCTTGCAGATTTTAACCTTACCCCTGATATAGCTATAATAGATCCGTCTC
TTGCAGAAACAATGCCTAAAAAGCTTACAGCACACACTGGAATGGATGCACTTACTCACGCAATAGAAGCATATG
TGGCAAGTTTACATTCAGATTTCTCAGATCCACTTGCTATGCATGCTATAACCATGATTCATAAATATTTATTGAAA
TCCTATGAAGAAGATAAAGAAGCTAGGGGCCATATGCACATAGCCCAATGTCTAGCTGGAATGGCATTTTCAAAT
GCACTCCTTGGAATAACTCATAGTATAGCACATAAAACTGGCGCAGTATTCCACATACCTCATGGGTGTGCTAATG
CCATATACTTACCTTATGTTATAGATTTTAACAAGAAAGCTTGTTCAGAAAGATATGCTAAAATAGCTAAAAAGCT
TCATCTATCAGGGAATAGTGAAGATGAATTAATAGATTCATTAACAGAAATGATTTGTACTATGAATAAAAAGAT
GGATATTCCTCTTACTATAAAAGATTATGGTATAAGCGAAAACGATTTTAATGAAAACCTAGATTTTATAGCTCAC
AATGCTATGATGGATGCTTGCACTGGATCTAATCCTAGAGCAATAACTGAGGAAGAAATGAAAAAGCTCTTGCA
GTATATGTATAATGGGCAAAAGGTTAATTTCTAG

FIGURE 53

Seq. ID 104: Amino Acid sequence of butanol dehydrogenase from *C. ragsdalei*:
MGRFTLPRDIYFGENALENLKNLDGNKAVVVVGGGSMKRFGFLAKVEEYLKEAGMEVKLIEGVEPDPSVDTVMNGA
KIMRDFNPDWIVSIGGGSPIDAAKAMWIFYEYPDFTFEKAVVPFGIPKLRQKAQFVAIPSTSGTATEVTSFSVITDYKAKI
KYPLADFNLTPDIAIIDPSLAETMPKKLTAHTGMDALTHAIEAYVASLHSDFSDPLAMHAITMIHKYLLKSYEEDKEARG
HMHIAQCLAGMAFSNALLGITHSIAHKTGAVFHIPHGCANAIYLPYVIDFNKKACSERYAKIAKKLHLSGNSEDELIDSLT
EMICTMNKKMDIPLTIKDYGISENDFNENLDFIAHNAMMDACTGSNPRAITEEEMKKLLQYMYNGQKVNF*

Seq. ID 105: Nucleotide Acid sequence of butanol dehydrogenase from *C. ragsdalei*:
ATGATTTTAAAAACTAAACTTTTTGGGCAAACTTATGAATTTAAAAATATGAAGGAAGTATTGGCAAAAGCTAAT
GAAGAAAAATCGGGAGATGCTTTAGCTGGAATCATAGCAAAAAGTACAGCGGAGAGAGTTGCAGCAAAGGTTG
TTTTGTCTGAAATAACTCTTGAGGAATTAAGGAATAATCCTGTAGTTCCTTATGAGGAGGATGAAGTAACAAGAG
TAATACAAGATATGATTGATAAAGAAGCCTATAATAAAATCAAAGCTATGACAGTTGGCGAATTTAGAGAATTTA
TATTAAAATCAGAAGAAGCCGATATAAAAGAAATAAGAGATGGATTAACTTCTGAGATGATAGCAGGTGTAACT
AAGCTTATGAGTAATATGGACTTAGTATATGCTTCTAAAAAAATAAGAAATATTGCTACTTGCAATACTACTATTG
GTGAAAAGGGAACAGTCTCTTCAAGACTTCAGCCTAATCATGCAGCAGATAGTATAGATGGAATTATGGCTTCTG
TAATGGAAGGGATAAGCTATGGTATAGGTGATGCTGTAATAGGTTTAAACCCTGTAGTAGATACCATAGATAATA
TATCAGAGATTTTGAAAAATTTTAAGCAGTTCATGATAAAATGGGATATACCTACACAAAATTGTGTACTTGCTCA
TATAACAACGCAAATGGAGGCTTTAAAGAAAGGAGTTCCTATGGATCTGATGTTCCAGAGTATAGCTGGTTCACA
AAAATCCAATAAAGGCTTTGGAATAAGTGTGAAGCTTATGGATGAAGCTTATGAACTTATGAAGGAAAAAAAGA
GCTCCAAAGGTCCTAATTTTATGTATTTTGAAACAGGCCAGGGTTCTGAGCTTTCTTCAGAAGGCCATAATGGAGC
AGATCAGCTTACAATGGAAGCAAGATGTTATGGTCTTGCAAAAAAATATAATCCATTCCTTGTAAACTCTGTGGTG
GGATTCATAGGACCAGAATATCTATATGATGGAAAACAAATTATAAGAGCAGGCTTAGAAGATCATTTTATGGGT
AAGTTAACAGGACTTCCTATGGGTGTTGATGTATGTTATACAAACCATATGAAAGCAGATCAAAATGATTTGGAA
AATTTAGCATTACTCCTTGCAGCAGCTGACTGTACTTATTTTATGGGTATACCTGGAGGAGATGACGTAATGCTTA
TGTATCAAACTACCAGCTATCATGATGTAGCTTCTATCAGGGACATTATGCGTAAAAATCCTATAAAAGAATTTGA
AGAAAGAATGGAAGCTCTAGGAATAATGAAAAATGGAAGGCTCACAGAAATAGCTGGTGATCCATCTATATTTA
TGATTTAG

Seq. ID 106: Amino Acid sequence of butanol dehydrogenase from *C. ragsdalei*:
MILKTKLFGQTYEFKNMKEVLAKANEEKSGDALAGIIAKSTAERVAAKVVLSEITLEELRNNPVVPYEEDEVTRVIQDMI
DKEAYNKIKAMTVGEFREFILKSEEADIKEIRDGLTSEMIAGVTKLMSNMDLVYASKKIRNIATCNTTIGEKGTVSSRLQP
NHAADSIDGIMASVMEGISYGIGDAVIGLNPVVDTIDNISEILKNFKQFMIKWDIPTQNCVLAHITTQMEALKKGVPM
DLMFQSIAGSQKSNKGFGISVKLMDEAYELMKEKKSSKGPNFMYFETGQGSELSSEGHNGADQLTMEARCYGLAKKY
NPFLVNSVVGFIGPEYLYDGKQIIRAGLEDHFMGKLTGLPMGVDVCYTNHMKADQNDLENLALLLAAADCTYFMGIP
GGDDVMLMYQTTSYHDVASIRDIMRKNPIKEFEERMEALGIMKNGRLTEIAGDPSIFMI*

FIGURE 54

Seq. ID 107: Nucleotide Acid sequence of butanol dehydrogenase from *C. ragsdalei*:
ATGGAAAACTTTATTTTTAAAAATGCTACAGAAATTATTTTTGGTAAGGATACCGAAGATCTTGTAGGAAGTAAA
GTAAAGGAGTATTCAAAGTCAGATAAAATACTCTTTTGCTATGGGGGAGGAAGTATAAAGAGATCGGGCCTCTA
TGATAGAGTTATAAAGTCCTTAAAAGAAAATGGAATTGAATTTATAGAACTTCCAGGAATTAAACCTAATCCAAG
ATTAGGACCTGTTAAAGAAGGTATAAGACTATGTAGAGAAAATAATATAAAATTTGTACTATCTGTAGGAGGAG
GAAGTTCAGCAGATACAGCTAAAGCTATTGCTGTAGGAGTACCTTATAAAGGAGATGTATGGGATTTTTATACGG
GCAAAGCTGAAGTAAAAGAGGCTCTTCCTGTAGGAGTTGTAATAACATTACCTGCTACAGGTACAGAATCTAGTA
ATAGTTCTGTTATTATGAATGAAGATGGTTGGTTTAAAAAAGGATTAAATACGGTACTTATAAGACCTGCTTTTTC
AATTATGAATCCTGAACTTACTTTTACACTACCAGAATATCAAACTGCTTGTGGTGCTTGTGACATTATGGCACATA
TAATGGAAAGATATTTTACAAATGTGAAACATGTAGATTTAACTGATAGGCTTTGCGAAGCTGCACTTAGAAATG
TTATAAATAATGCCCCAATAGTTTTAAAAGATCCTAAAAATTATGATGCTAGGGCAGAAATTATGTGGACTGGTA
CTATAGCTCATAATGATGTGCTTAGTACAGGTAGAATAGGTGATTGGGCTTCTCACAAAATTGAACATGAATTAA
GTGGGGAAACAGATATTGCCCATGGAGCAGGACTTGCAATTGTATTTCCTGCATGGATGAAATATGTATATAAAC
ATGATATCAATAGATTTGTACAATTTGCAGTAAGGGTATGGGATGTAGATTTATCTTATAGTTCCTGTGAAGATAT
TGTACTTGAAGGCATAAGGAGAATGACAGCATTTTTCAAGAGCATGGGGTTACCTATAACTTTAAAAGAAGGAA
GTATAGGAGAAGATAAAATTGAAGAAATGGCTAATAAGTGCACGGATAATGGAACCAAAACTGTAGGACAATTT
GTAAAACTAAATAAAGATGATATTGTAAAAATATTAAATTTAGCTAGATAA

Seq. ID 108: Amino Acid sequence of butanol dehydrogenase from *C. ragsdalei*:
MENFIFKNATEIIFGKDTEDLVGSKVKEYSKSDKILFCYGGGSIKRSGLYDRVIKSLKENGIEFIELPGIKPNPRLGPVKEGIR
LCRENNIKFVLSVGGGSSADTAKAIAVGVPYKGDVWDFYTGKAEVKEALPVGVVITLPATGTESSNSSVIMNEDGWFK
KGLNTVLIRPAFSIMNPELTFTLPEYQTACGACDIMAHIMERYFTNVKHVDLTDRLCEAALRNVINNAPIVLKDPKNYD
ARAEIMWTGTIAHNDVLSTGRIGDWASHKIEHELSGETDIAHGAGLAIVFPAWMKYVYKHDINRFVQFAVRVWDVD
LSYSSCEDIVLEGIRRMTAFFKSMGLPITLKEGSIGEDKIEEMANKCTDNGTKTVGQFVKLNKDDIVKILNLAR*

Seq. ID 109: Nucleotide Acid sequence of butanol dehydrogenase from *C. ragsdalei*:
ATGGAAGACAAGTTTGAAAATTTTAATTTGAAATCCAAGATTTATTTTAATAGGGAATCCATACAACTTTTAGAGC
AGGTTACTGGCTCTCGAGCATTTATTGTTGCAGATGCCATTATGGGAAAACTTGGATATCTTCAAAAAGTAATAG
ATTCCCTAAGTAAAGCCGGAATAAGTTCCGTTGTTTTTACGGGAGTACACCCTGATCCAGATGTCAATGTAATTGC
AGATGCAATGAAATTGTACAACAAAAGCGATGCAGATGTTCTCGTTGCACTAGGTGGAGGCTCCAGCATTGATAC
CGCCAAAGGAATAATGTATTTTGCATGTAATTTAGGAAAAGCAATGGGCCAGGAAATGAAAAAGCCCCTGTTTAT
TGCAATTCCATCAACAAGTGGAACAGGCTCTGAAGTAACAAACTTTACTGTTATTACTTCTCAGAAAGAAAAGGT
ATGCATTGTAGATGATTTTATTGCACCAGACGTTGCAATACTTGACTCTAGTTGTATTGATGGTCTGCCTCAACGT
ATTGTAGCAGATACTGGTATAGATGTTCTAGTTCATTCTATTGAAGCCTATGTTTCCAAAAAAGCAACTGACTTTA
CAGACGCTCTTGCTGAAAAAGCAGTTAAATTGATTTTTGAGAATCTTCCAAAAATTTATAACGATAGTAAAGATTC
TGAAGCTCGAGATCATGTTCAAAACGCTTCTTGTATAGCAGGAATAGCATTTACAAATGCTGGTCTTGGAATTAAT
CACAGCTTGGCTCATGCTATGGGTGGATCTTTTCACATTCCTCACGGCCGATCCAATGCACTTTTACTTAATGCAGT
AATGGAATACAATGCTAGCTTAGTGGGAAATGCAAACGATCATGCTATGGAAAAATACGCAAAACTAGCATCAG
TTCTACACCTTCCAGCTCGAACAACTCGTGAAGGCGCTGTAAGTTTTATCGAAGCTGTAAATAAATTAATAAAATC
CCTAGGTGTTGAAGATAATATTCGAGCTCTTGGAATTAAAGAAGACGATTTTCAAGGTGCTCTAAATCATATGGC
AGAAACAGCAATGCAAGATAGATGCACTCCAACTAATCCTAGAAAACCTTCTAAAGAAGAACTGATACATATTTA
TCAAAAATGCTATTAA

FIGURE 55

Seq. ID 110: Amino Acid sequence of butanol dehydrogenase from *C. ragsdalei*:
MEDKFENFNLKSKIYFNRESIQLLEQVTGSRAFIVADAIMGKLGYLQKVIDSLSKAGISSVVFTGVHPDPDVNVIADAMK
LYNKSDADVLVALGGGSSIDTAKGIMYFACNLGKAMGQEMKKPLFIAIPSTSGTGSEVTNFTVITSQKEKVCIVDDFIAP
DVAILDSSCIDGLPQRIVADTGIDVLVHSIEAYVSKKATDFTDALAEKAVKLIFENLPKIYNDSKDSEARDHVQNASCIAGI
AFTNAGLGINHSLAHAMGGSFHIPHGRSNALLLNAVMEYNASLVGNANDHAMEKYAKLASVLHLPARTTREGAVSFI
EAVNKLIKSLGVEDNIRALGIKEDDFQGALNHMAETAMQDRCTPTNPRKPSKEELIHIYQKCY*

Seq. ID 111: Nucleotide sequence of phosphate acetyl/butyryl transferase from *C. ragsdalei*:
ATGGAAAAAATTTGGAATAAGGCAAAGGAAGACAAAAAAAAGATTGTCTTAGCTGAAGGAGAAGAAGAAAGAA
CTCTTCAAGCTTGTGAAAAAATAATTAAAGAAGGTATTGCAAATTTAATCCTTGTAGGGAATGAAAAGGTAATAG
AGGAGAAGGCATCAAAATTAGGCGTAAGTTTAAATGGAGCAGAAATAGTAGATCCAGAAACCTCGGATAAACTA
AAAAAATATGCAGATGCTTTTTATGAATTGAGAAAGAAGAAGGGAATAACACCAGAAAAAGCGGATAAAATAGT
AAGAGATCCAATATATTTTGCTACGATGATGGTTAAGCTTGGAGATGCAGATGGATTGGTTTCAGGTGCAGTGCA
TACTACAGGTGATCTTTTGAGACCAGGACTTCAAATAGTAAAGACAGCTCCAGGTACATCAGTAGTTTCCAGCAC
ATTTATAATGGAAGTACCAAATTGTGAATATGGTGACAATGGTGTACTTCTATTTGCTGATTGTGCTGTAAATCCA
TGCCCAGATAGTGATCAATTGGCTTCAATTGCAATAAGTACAGCAGAAACTGCAAAGAACTTATGTGGAATGGAT
CCAAAAGTAGCAATGCTTTCATTTTCTACTAAGGGAAGTGCAAAACACGAATTAGTAGATAAAGTTAGAAATGCT
GTAGAAATTGCCAAAAAAGCTAAACCAGATTTAAGTTTGGACGGAGAATTACAATTAGATGCCTCTATCGTAGAA
AAGGTTGCAAGTTTAAAGGCTCCTGAAAGTGAAGTAGCAGGAAAAGCAAATGTACTTGTATTTCCAGATCTCCAA
GCAGGAAATATAGGTTATAAACTTGTTCAAAGATTTGCAAAAGCTGATGCTATAGGACCTGTATGCCAGGGATTT
GCAAAACCTATAAATGATTTGTCAAGAGGATGTAACTCCGATGATATAGTAAATGTAGTAGCTGTAACAGCAGTT
CAGGCACAAGCTCAAAAGTAA

Seq. ID 112: Amino acid sequence of phosphate acetyl/butyryl transferase from *C. ragsdalei*:
MEKIWNKAKEDKKKIVLAEGEEERTLQACEKIIKEGIANLILVGNEKVIEEKASKLGVSLNGAEIVDPETSDKLKKYADAFY
ELRKKKGITPEKADKIVRDPIYFATMMVKLGDADGLVSGAVHTTGDLLRPGLQIVKTAPGTSVVSSTFIMEVPNCEYGD
NGVLLFADCAVNPCPDSDQLASIAISTAETAKNLCGMDPKVAMLSFSTKGSAKHELVDKVRNAVEIAKKAKPDLSLDG
ELQLDASIVEKVASLKAPESEVAGKANVLVFPDLQAGNIGYKLVQRFAKADAIGPVCQGFAKPINDLSRGCNSDDIVNV
VAVTAVQAQAQK*

Seq. ID 113: Nucleotide sequence of acetate/butyrate kinase from *C. ragsdalei*:
ATGAAAATATTAGTAGTAAACTGTGGAAGTTCATCTTTAAAATATCAACTTATTGATATGAAAGATGAAAGCGTT
GTGGCAAAAGGACTTGTAGAAAGAATAGGAGCAGAAGGTTCAGTTTTAACACATAAAGTTAACGGAGAAAAGTT
TGTTACAGAGCAGCCAATGGAAGATCATAAAGTTGCTATACAATTAGTATTAAATGCTCTTGTAGATAAAAAACA
TGGTGTAATAAAAGATATGTCAGAAATATCTGCTGTAGGGCATAGAGTTTTGCATGGTGGAAAAAAATATGCGG
CATCCATTCTTATTGATGACAATGTAATGAAAGCAATAGAAGAATGTATTCCATTAGGACCATTACATAATCCAGC
TAATATAATGGGAATAGATGCTTGTAAAAAACTAATGCCAAATACTCCAATGGTAGCAGTATTTGATACAGCATTT
CATCAGACAATGCCAGATTATGCTTATACTTATGCAATACCTTATGATATATCTGAAAAGTATGATATCAGAAAAT
ATGGTTTTCATGGAACTTCTCATAGATTCGTTTCAATTGAAGCAGCCAAGTTGTTAAAGAAAGATCCAAAAGATCT
TAAGCTAATAACTTGTCATTTAGGAAATGGAGCTAGTATATGTGCAGTAAACCAGGGAAAAGCAGTAGATACAA
CTATGGGACTTACTCCCCTTGCAGGACTTGTAATGGGAACTAGATGTGGTGATATAGATCCAGCTATAATACCATT
TGTAATGAAAAGAACAGGTATGTCTGTAGATGAAATGGATACTTTAATGAACAAAAAGTCAGGAATACTTGGAG
TATCAGGAGTAAGCAGCGATTTTAGAGATGTAGAAGAAGCTGCAAATTCAGGAAATGATAGAGCAAAACTTGCA
TTAAATATGTATTATCACAAAGTTAAATCTTTCATAGGAGCTTATGTTGCAGTTTTAAATGGAGCAGATGCTATAA
TATTTACAGCAGGACTTGGAGAAAATTCAGCTACTAGCAGATCTGCTATATGTAAGGGATTAAGCTATTTTGGAA
TTAAAATAGATGAAGAAAAGAATAAGAAAAGGGGAGAAGCACTAGAAATAAGCACACCTGATTCAAAGATAAA
AGTATTAGTAATTCCTACAAATGAAGAACTTATGATAGCTAGGGATACAAAAGAAATAGTTGAAAATAAATAA

FIGURE 56

Seq. ID 114: Amino acid sequence of acetate/butyrate kinase from *C. ragsdalei*:
MKILVVNCGSSSLKYQLIDMKDESVVAKGLVERIGAEGSVLTHKVNGEKFVTEQPMEDHKVAIQLVLNALVDKKHGVI
KDMSEISAVGHRVLHGGKKYAASILIDDNVMKAIEECIPLGPLHNPANIMGIDACKKLMPNTPMVAVFDTAFHQTMP
DYAYTYAIPYDISEKYDIRKYGFHGTSHRFVSIEAAKLLKKDPKDLKLITCHLGNGASICAVNQGKAVDTTMGLTPLAGLV
MGTRCGDIDPAIIPFVMKRTGMSVDEMDTLMNKKSGILGVSGVSSDFRDVEEAANSGNDRAKLALNMYYHKVKSFI
GAYVAVLNGADAIIFTAGLGENSATSRSAICKGLSYFGIKIDEEKNKKRGEALEISTPDSKIKVLVIPTNEELMIARDTKEIV
ENK*

Seq. ID 115: Nucleotide sequence of aldehyde:ferredoxin oxidoreductase from *C. ragsdalei*:
ATGTACGGATATAATGGTAAGGTATTAAGAATTAATCTAAGTAGTAAAACTTATATAGTGGAAGAATTGAAAATT
GACAAAGCTAAAAAATTTATAGGTGCAAGAGGTTTAGGCGTAAAAACCTTATTTGACGAAGTAGATCCAAAGGT
AGATCCATTATCACCTGATAACAAATTTATTATAGCAGCGGGACCACTTACAGGTGCGCCTGTTCCAACAAGCGG
AAGATTCATGGTAGTTACTAAATCACCTTTAACAGGAACTATTGCTATTGCAAATTCAGGTGGAAAATGGGGAGC
AGAATTCAAAGCAGCTGGATACGATATGATAATCGTTGAAGGTAAATCTGATAAAGAAGTTTATGTAAATATAGT
AGATGATAAAGTAGAATTTAGGGATGCTTCTCATGTTTGGGGAAAACTAACAGAAGAAACTACAAAAATGCTTCA
ACAGGAAACAGATTCGAGAGCTAAGGTTTTATGCATAGGACCAGCTGGGGAAAAATTATCACTTATGGCAGCAG
TTATGAATGATGTTGATAGAACAGCAGGACGTGGTGGTGTTGGAGCTGTTATGGGCTCAAAGAACTTAAAAGCT
ATTGTAGTTAAAGGAAGCGGAAAAGTAAAATTATTTGATGAGCAAAAAGTGAAAGAAGTAGCACTTGAGAAAAC
AAATATTTTAAGAAAAGATCCAGTAGCTGGTGGAGGACTTCCAACATACGGAACAGCTGTACTTGTTAATATTAT
AAATGAAAATGGCGTACATCCAGTAAAAAATTTCCAAAAATCTTATACAGATCAGGCAGATAAGATCAGTGGAG
AAACTTTAACTAAAGATTGCTTAGTTAGAAAAAATCCTTGCTATAGGTGTCCAATTGCCTGTGGAAGATGGGTAA
AACTTGATGATGGAACTGAATGTGGAGGACCAGAATATGAAACATTATGGTCATTTGGATCTGATTGTGATGTAT
ACGATATAAATGCTGTAAATACAGCAAATATGTTGTGTAATGAATATGGATTAGATACCATTACAGCAGGATGTA
CTATTGCAGCAGCTATGGAACTTTATCAAAGAGGTTATATTAAGGATGAAGAAATAGCAGCAGATGGATTGTCAC
TTAATTGGGGAGATGCTAAGTCCATGGTTGAATGGGTAAAGAAAATGGGACTTAGAGAAGGATTTGGAGACAA
GATGGCAGATGGTTCATACAGACTTTGTGACTCATACGGTGTACCTGAGTATTCAATGACTGTAAAAAAACAAGA
AATCCCAGCATATGACCCAAGAGGAATACAGGGACATGGTATAACTTATGCTGTTAACAATAGGGGAGGGTGTC
ATATTAAGGGATATATGGTAAGCCCTGAAATACTTGGTTATCCAGAAAAACTTGATAGACTTGCAGTGGAAGGAA
AAGCAGGATATGCTAGAGTATTCCATGATTTAACAGCTGTTATAGATTCACTTGGATTATGTATTTTTACAACATTT
GGTCTTGGTGCACAGGATTATGTTGATTTGTATAATGCAGTAGTTGGTGGAGAATTACATGATGTAGACTCTTTA
ATGTTAGCTGGAGATAGAATATGGACTTTAGAAAAAATATTTAACTTAAAGGCAGGCATAGATAGTTCACAGGAT
ACTCTTCCAAAGAGATTGCTTGAGGAACCAGTTCCAGAAGGACCATCAAAAGGAGAGATTCATAGATTAGATGTA
CTTCTTCCTGAATATTATTCAGTACGTGGATGGGATAAAAATGGTATACCTACAGAGGAAACGTTAAAGAAATTA
GGATTAGATGAATATGTAGGTAAGTTTTAA

Seq. ID 116: Amino acid sequence of aldehyde:ferredoxin oxidoreductase from *C. ragsdalei*:
MYGYNGKVLRINLSSKTYIVEELKIDKAKKFIGARGLGVKTLFDEVDPKVDPLSPDNKFIIAAGPLTGAPVPTSGRFMVVT
KSPLTGTIAIANSGGKWGAEFKAAGYDMIIVEGKSDKEVYVNIVDDKVEFRDASHVWGKLTEETTKMLQQETDSRAK
VLCIGPAGEKLSLMAAVMNDVDRTAGRGGVGAVMGSKNLKAIVVKGSGKVKLFDEQKVKEVALEKTNILRKDPVAG
GGLPTYGTAVLVNIINENGVHPVKNFQKSYTDQADKISGETLTKDCLVRKNPCYRCPIACGRWVKLDDGTECGGPEYE
TLWSFGSDCDVYDINAVNTANMLCNEYGLDTITAGCTIAAAMELYQRGYIKDEEIAADGLSLNWGDAKSMVEWVKK
MGLREGFGDKMADGSYRLCDSYGVPEYSMTVKKQEIPAYDPRGIQGHGITYAVNNRGGCHIKGYMVSPEILGYPEKL
DRLAVEGKAGYARVFHDLTAVIDSLGLCIFTTFGLGAQDYVDLYNAVVGGELHDVDSLMLAGDRIWTLEKIFNLKAGID
SSQDTLPKRLLEEPVPEGPSKGEIHRLDVLLPEYYSVRGWDKNGIPTEETLKKLGLDEYVGKF*

FIGURE 57

Seq. ID 117: Nucleotide sequence of aldehyde:ferredoxin oxidoreductase from *C. ragsdalei*:
ATGTATGGTTATAATGGTAAAGTATTAAGAATTAATTTAAAAGAAAGAACTTGCAAATCAGAAAATTTAGATTTAGATAAAGC
TAAAAAGTTTATAGGCTGTAGGGGACTAGGTGTTAAAACTTTATTTGATGAAATAGATCCTAAAATAGATGCATTATCACCAG
AAAATAAATTTATAATTGTAACAGGTCCGTTAACTGGAGCTCCAGTTCCAACTAGTGGAAGGTTTATGGTAGTTACTAAAGCA
CCGCTTACAGGAACTATAGGAATTTCAAATTCGGGTGGAAAATGGGGAGTAGACTTGAAAAAAGCTGGCTGGGATATGATA
ATAGTAGAGGATAAGGCTGATTCACCAGTTTACATTGAAATAGTAGATGATAAAGTAGAAATTAAAGATGCGTCACAGCTTT
GGGGAAAAGTTACATCAGAAACTACAAAAGAGTTAGAAAAGATAACTGAGAATAGATCAAAGGTATTATGTATAGGACCTG
CTGGTGAAAGATTGTCCCTTATGGCAGCAGTTATGAATGATGTAGATAGAACTGCAGCAAGAGGCGGCGTTGGTGCAGTTAT
GGGATCTAAAAACTTAAAAGCTATTACAGTTAAAGGAACTGGAAAAATAGCTTTAGCTGATAAAGAAAAAGTAAAAAAAGTG
TCCGTAGAAAAAATTACAACATTAAAAAATGATCCAGTAGCTGGTCAGGGAATGCCAACTTATGGTACAGCTATACTGGTTAA
TATAATAAATGAAAATGGAGTTCATCCTGTAAATAATTTTCAAGAATCTTATACGGATCAAGCAGATAAAATAAGTGGAGAGA
CTCTTACTGCTAACCAACTAGTAAGGAAAAATCCTTGTTACAGCTGTCCTATAGGTTGTGGAAGATGGGTTAGACTAAAAGAT
GGTACAGAGTGCGGAGGACCGGAGTATGAAACACTGTGGTGTTTTGGCTCTGACTGTGGTTCATATGATTTAGATGCTATAA
ATGAAGCTAATATGTTATGTAATGAATATGGTATTGATACTATTACCTGTGGTGCAACAATTGCTGCAGCTATGGAACTTTATC
AAAGAGGATATGTAAAAGATGAAGAAATAGCCGGAGATAACCTATCTCTCAAGTGGGGAGATACGGAGTCTATGATTGGCT
GGATAAAGAAAATGGTATATAGTGAAGGCTTTGGAGCAAAGATGACAAATGGTTCATATAGGCTTTGTGAAGGTTATGGAG
TACCTGAGTATTCTATGACAGTTAAAAAGCAAGAAATTCCAGCATATGATCCAAGGGGAATACAGGGACATGGTATTACCTAT
GCAGTTAATAATAGAGGAGGATGTCATATTAAGGGATATATGATTAATCCTGAAATATTAGGTTATCCGGAAAAACTTGATA
GATTTGCATTAGATGGTAAAGCAGCCTATGCCAAAATGATGCATGATTTAACTGCTGTAATTGATTCTTTAGGATTGTGCATAT
TCACTACATTTGGGCTTGGAATACAGGATTATGTAGATATGTATAATGCAGTAGTAGGAGAATCTACTTGTGATTCAGATTCA
CTATTAGAGGCAGGAGATAGAGTATGGACTCTTGAAAAATTATTTAATCTTGCAGCTGGAATAGACAGCAGCCAGGATACTC
TACCAAAGAGATTGTTAGAAGAACCTATTCCAGATGGTCCATCAAAGGGACACGTTCATAGGCTAGATGTTCTTCTGCCAGAA
TATTACTCAGTACGAGGATGGAGTAAAGAGGGTATACCTACAGAAGAAACATTAAAGAAATTAGGATTAGATGAATATATAG
GTAAGTTCTAG

Seq. ID 118: Amino acid sequence of aldehyde:ferredoxin oxidoreductase from *C. ragsdalei*:
MYGYNGKVLRINLKERTCKSENLDLDKAKKFIGCRGLGVKTLFDEIDPKIDALSPENKFIIVTGPLTGAPVPTSGRFMVVTKAPLTGTI
GISNSGGKWGVDLKKAGWDMIIVEDKADSPVYIEIVDDKVEIKDASQLWGKVTSETTKELEKITENRSKVLCIGPAGERLSLMAAV
MNDVDRTAARGGVGAVMGSKNLKAITVKGTGKIALADKEKVKKVSVEKITTLKNDPVAGQGMPTYGTAILVNIINENGVHPVNN
FQESYTDQADKISGETLTANQLVRKNPCYSCPIGCGRWVRLKDGTECGGPEYETLWCFGSDCGSYDLDAINEANMLCNEYGIDTIT
CGATIAAAMELYQRGYVKDEEIAGDNLSLKWGDTESMIGWIKKMVYSEGFGAKMTNGSYRLCEGYGVPEYSMTVKKQEIPAYDP
RGIQGHGITYAVNNRGGCHIKGYMINPEILGYPEKLDRFALDGKAAYAKMMHDLTAVIDSLGLCIFTTFGLGIQDYVDMYNAVVGE
STCDSDSLLEAGDRVWTLEKLFNLAAGIDSSQDTLPKRLLEEPIPDGPSKGHVHRLDVLLPEYYSVRGWSKEGIPTEETLKKLGLDEYI
GKF*

FIGURE 58

Seq. ID 136: 16S rRNA gene of *Clostridium ljungdahlii* (CP001666.1, GI:300433347)
TTAAATTAAGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGCGATGAAGCTCCTTC
GGGAGTGGATTAGCGGCGGACGGGTGAGTAACACGTGGGTAACCTACCTCAAAGAGGGGGATAGCCTCCCGAAAGGGAGA
TTAATACCGCATAATAATCAGTTTTCACATGGAGACTGATTTAAAGGAGTAATCCGCTTTGAGATGGACCCGCGGCGCATTAG
CTAGTTGGTAGGGTAACGGCCTACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACATTGGAACTGAGAG
ACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCAACGCCGCGTGAGT
GAAGAAGGTTTTCGGATTGTAAAGCTCTGTCTTTGGGGACGATAATGACGGTACCCAAGGAGGAAGCCACGGCTAACTACGT
GCCAGCAGCCGCGGTAATACGTAGGTGGCGAGCGTTGTCCGGAATTACTGGGCGTAAAGAGTGCGTAGGCGGATATTTAAG
TGAGATGTGAAATACCCGGGCTTAACCCGGGCACTGCATTTCAAACTGGATATCTAGAGTGCGGGAGAGGAGAATGGAATT
CCTAGTGTAGCGGTGAAATGCGTAGAGATTAGGAAGAACACCAGTGGCGAAGGCGATTCTCTGGACCGTAACTGACGCTGA
GGCACGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTACTAGGTGTAGGAGGT
ATCGACCCCTTCTGTGCCGCAGTAAACACAATAAGTACTCCGCCTGGGAAGTACGATCGCAAGATTAAAACTCAAAGGAATT
GACGGGGGCCCGCACAAGCAGCGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCTGGACTTGACATACCCT
GAATATCTTAGAGATAAGAGAAGCCCTTCGGGGCAGGGATACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATG
TTAGGTTAAGTCCTGCAACGAGCGCAACCCCTGTTGTTAGTTGCTAACATTTAGTTGAGCACTCTAGCAAGACTGCCGCGGTT
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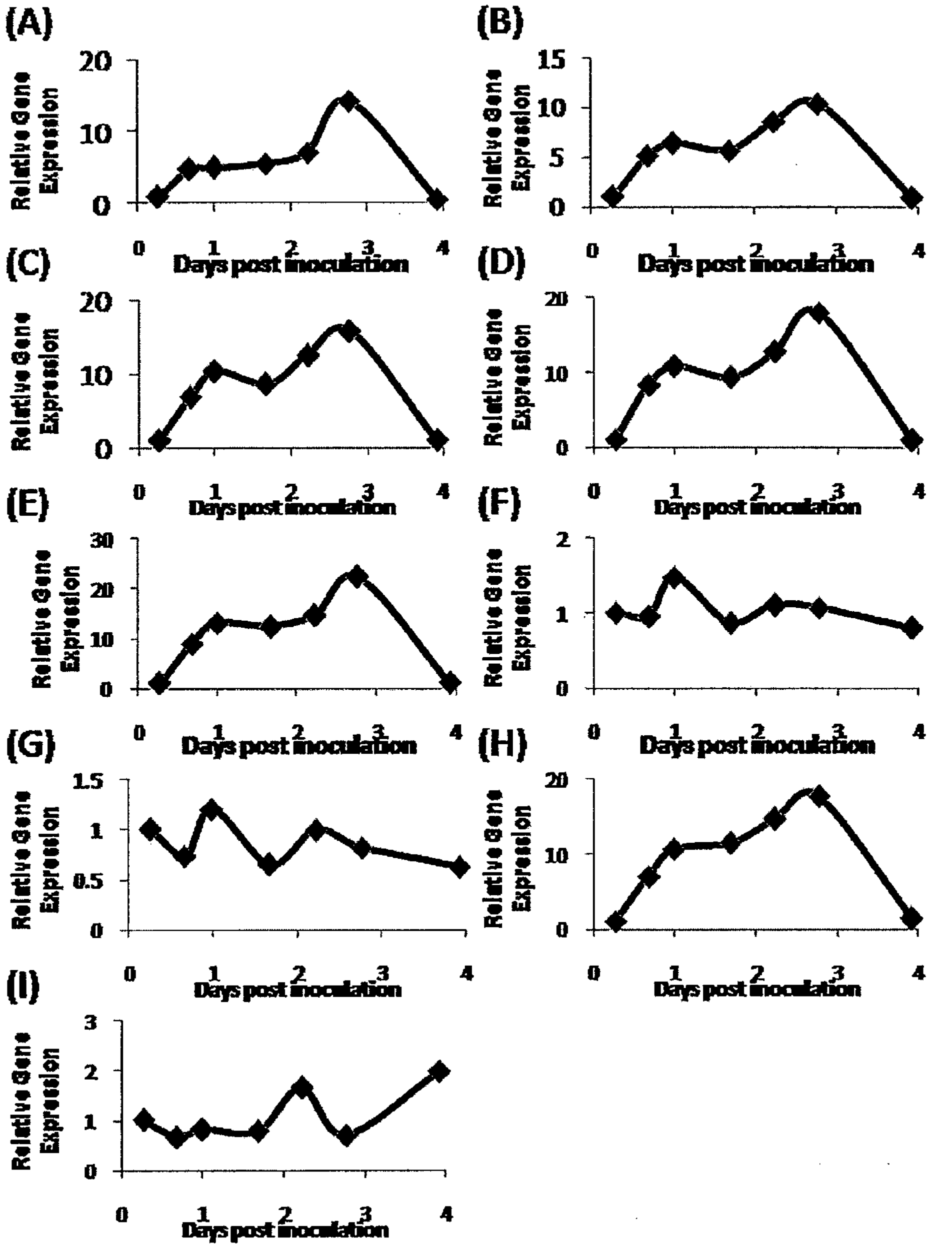
FIGURE 59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0 1 2 3 4
Days post inoculation
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Days post inoculation
(C)
20
10
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Relative Gene Expression
0 1 2 3 4
Days post inoculation
(D)
20
10
0
Relative Gene Expression
0 1 2 3 4
Days post inoculation
(E)
30
20
10
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Days post inoculation
(F)
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1
0
Relative Gene Expression
0 1 2 3 4
Days post inoculation
(G)
1.5
1
0.5
0
Relative Gene Expression
0 1 2 3 4
Days post inoculation
(H)
20
10
0
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Days post inoculation
(I)
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2
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0 1 2 3 4
Days post inoculation

FIGURE 60

SEQUENCE LISTING

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KOEPKE, Michael
LIEW, FungMin

<120> RECOMBINANT MICROORGANISM AND METHODS OF PRODUCTION THEREOF

<130> 508747PCTPR

<150> US 61/405,871
<151> 2010-10-22

<150> US 13/049,263
<151> 2011-03-16

<160> 154

<170> PatentIn version 3.5

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Ile Asp Val Glu Glu Lys Met His Phe Ile Glu Thr Tyr Lys Gln Lys
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Ser Asn Met Lys Lys Glu Ile Ser Phe Ser Glu Glu Tyr Tyr Lys Gln
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Lys Ile Met Asn Gly Lys Asn Gly Val Val Tyr Thr Pro Pro Glu Met
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SequenceListing

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Ser Tyr His Ile Val Arg Asn Asn Leu Phe Gly Phe Asp Ile Asp Glu
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Thr Ala Ile Lys Val Leu Lys Ile Asp Leu Phe Leu Ile Ser Asn Gln
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Phe Ser Glu Lys Asn Phe Gln Val Lys Asp Phe Leu Val Glu Asn Ile
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gctgtcattc cttc                                                    14


<210>  37
<211>  18
<212>  DNA
<213>  synthetic primer

<400>  37
cgtcagaccc cgtagaaa                                                18


<210>  38
<211>  18
<212>  DNA
<213>  synthetic primer

<400>  38
ctctcctgtt ccgaccct                                                18


<210>  39
<211>  2688
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<212> DNA
<213> C. autoethanogenum

<400> 39
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gtaactaagg taactaacgt tgaagaatta atgaaaaagt tagatgaagt aacggctgct 120
caaaagaaat tttctagcta tactcaagaa caagtggatg aaattttcag gcaggcagct 180
atggcagcca atagtgctag aatagactta gctaaaatgg cagtggaaga aagcggaatg 240
ggaattgtag aagacaaggt cattaaaaat cattttgttg cagaatatat atataacaaa 300
tataagggtg aaaagacctg cggagttctg gaacaagatg aaggctttgg tatggttaga 360
attgcagaac ctgtaggagt tattgcagca gtagttccaa caactaatcc aacatctaca 420
gcaatattta aatcactaat agctttaaaa actagaaatg gtatagtttt ttcaccacat 480
ccaagggcaa aaaaatcaac tattgcagca gctaagatag tacttgatgc agcagttaaa 540
gctggtgccc ctgaaggaat tataggctgg atagatgaac cttctattga actttcacag 600
gtggtaatga aagaagcaga tctaattctt gcaactggtg gaccaggtat ggttaaggct 660
gcctattctt caggaaagcc tgctatagga gttggtccag gtaatacacc tgctgtaatt 720
gatgaaagtg ccgacattaa aatggcagta aattcaatac tactttcaaa aacttttgat 780
aatggtatga tttgtgcttc agagcagtca gtaatagttg caagctcaat atacgatgaa 840
gtcaagaaag agtttgcaga tagaggagca tatatattaa gtaaggatga aacagataag 900
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gaagttaaat cggtagaacc tgaagaagag ccctttgctc atgaaaagct gtctccagtt 1080
ctagccatgt acaaagcaaa agattttgat gaagcacttc taaaggctgg aagattagtt 1140
gaacgaggtg gaatagggca tacatctgta ttgtatgtaa attcgatgac ggaaaaagta 1200
aaagtagaaa agttcagaga aactatgaag accggtagaa cattgataaa tatgccttca 1260
gcgcaaggcg ctataggaga tatatataac tttaaactag ctccttcttt gacattaggc 1320
tgtggttcct ggggaggaaa ctctgtatca gaaaatgttg gacctaaaca tttgttaaac 1380
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tatttcaaat atggcagcct tggagttgca ctaaaagaac tgagaattat ggagaagaaa 1500
aaggcgttta tagtaacgga taaagttctt tatcaattag gttatgtaga taaaattaca 1560
aagaacctcg atgaattaag agtttcatat aaaatattta cagatgtaga accagatcca 1620
acccttgcta cagctaaaaa aggtgcagca gaactgcttt cctatgaacc agatacaatt 1680
atagcagttg gtggtggttc ggcaatggat gctgccaaga tcatgtgggt aatgtatgag 1740
catccagaag taagatttga agatttggcc atgagattta tggatataag aaagagagta 1800
tatgtttttc ctaagatggg agaaaaggca atgatgattt cagtagcaac atccgcagga 1860
acagggtcag aagttactcc atttgcagta attacggacg aaagaacagg agctaaatat 1920

cctctggctg attatgaatt aactccaaac atggctatag ttgatgcaga acttatgatg 1980

ggaatgccaa aggggctaac agcagcttca ggtatagatg cgttgactca tgcactggag 2040

gcctatgtgt caataatggc ttcagaatat accaacggat tggctcttga agcaacaaga 2100

ttagtattca aatatttgcc aatagcttat acagaaggta caattaatgt aaaggcaaga 2160

gaaaaaatgg ctcatgcttc atgtattgca ggtatggcct ttgccaatgc atttttaggg 2220

gtatgccact ctatggcaca taaattggga gcacagcacc acataccaca tggaattgcc 2280

aatgcactta tgatagatga agttataaaa ttcaatgctg tagaggctcc aaggaaacaa 2340

gcggcatttc cacaatataa atatccaaat gttaaaagaa gatatgctag aatagctgat 2400

tacctaaatt taggtggaag tacagatgat gaaaaagtac aattgctaat aaatgctata 2460

gatgacttaa aaactaagtt aaatattcca aagactatta aagaagcagg agtttcagaa 2520

gataaattct atgctacttt agatacaatg tcagaactgg cttttgatga tcaatgtaca 2580

ggagctaatc cacgatatcc actaatagga gaaataaaac aaatgtatat aaatgcattt 2640

gatacaccaa aggcaactgt ggagaagaaa acaagaaaga aaaagtaa 2688

<210> 40
<211> 895
<212> PRT
<213> C. autoethanogenum

<400> 40

Met Arg Asn Leu Phe Ile Phe Asn Ser Ile Lys Asn Lys Lys Glu Val
1 5 10 15

Ser Leu Met Lys Val Thr Lys Val Thr Asn Val Glu Glu Leu Met Lys
20 25 30

Lys Leu Asp Glu Val Thr Ala Ala Gln Lys Lys Phe Ser Ser Tyr Thr
35 40 45

Gln Glu Gln Val Asp Glu Ile Phe Arg Gln Ala Ala Met Ala Ala Asn
50 55 60

Ser Ala Arg Ile Asp Leu Ala Lys Met Ala Val Glu Glu Ser Gly Met
65 70 75 80

Gly Ile Val Glu Asp Lys Val Ile Lys Asn His Phe Val Ala Glu Tyr
85 90 95

Ile Tyr Asn Lys Tyr Lys Gly Glu Lys Thr Cys Gly Val Leu Glu Gln
100 105 110

Asp Glu Gly Phe Gly Met Val Arg Ile Ala Glu Pro Val Gly Val Ile
115 120 125

Ala Ala Val Val Pro Thr Thr Asn Pro Thr Ser Thr Ala Ile Phe Lys
130 135 140

```
Ser Leu Ile Ala Leu Lys Thr Arg Asn Gly Ile Val Phe Ser Pro His
145                 150                 155                 160

Pro Arg Ala Lys Lys Ser Thr Ile Ala Ala Ala Lys Ile Val Leu Asp
                165                 170                 175

Ala Ala Val Lys Ala Gly Ala Pro Glu Gly Ile Ile Gly Trp Ile Asp
            180                 185                 190

Glu Pro Ser Ile Glu Leu Ser Gln Val Val Met Lys Glu Ala Asp Leu
        195                 200                 205

Ile Leu Ala Thr Gly Gly Pro Gly Met Val Lys Ala Ala Tyr Ser Ser
    210                 215                 220

Gly Lys Pro Ala Ile Gly Val Gly Pro Gly Asn Thr Pro Ala Val Ile
225                 230                 235                 240

Asp Glu Ser Ala Asp Ile Lys Met Ala Val Asn Ser Ile Leu Leu Ser
                245                 250                 255

Lys Thr Phe Asp Asn Gly Met Ile Cys Ala Ser Glu Gln Ser Val Ile
            260                 265                 270

Val Ala Ser Ser Ile Tyr Asp Glu Val Lys Lys Glu Phe Ala Asp Arg
        275                 280                 285

Gly Ala Tyr Ile Leu Ser Lys Asp Glu Thr Asp Lys Val Gly Lys Thr
    290                 295                 300

Ile Met Ile Asn Gly Ala Leu Asn Ala Gly Ile Val Gly Gln Ser Ala
305                 310                 315                 320

Phe Lys Ile Ala Gln Met Ala Gly Val Ser Val Pro Glu Asp Ala Lys
                325                 330                 335

Ile Leu Ile Gly Glu Val Lys Ser Val Glu Pro Glu Glu Glu Pro Phe
            340                 345                 350

Ala His Glu Lys Leu Ser Pro Val Leu Ala Met Tyr Lys Ala Lys Asp
        355                 360                 365

Phe Asp Glu Ala Leu Leu Lys Ala Gly Arg Leu Val Glu Arg Gly Gly
    370                 375                 380

Ile Gly His Thr Ser Val Leu Tyr Val Asn Ser Met Thr Glu Lys Val
385                 390                 395                 400

Lys Val Glu Lys Phe Arg Glu Thr Met Lys Thr Gly Arg Thr Leu Ile
                405                 410                 415
```

Asn Met Pro Ser Ala Gln Gly Ala Ile Gly Asp Ile Tyr Asn Phe Lys
            420   425   430

Leu Ala Pro Ser Leu Thr Leu Gly Cys Gly Ser Trp Gly Gly Asn Ser
        435   440   445

Val Ser Glu Asn Val Gly Pro Lys His Leu Leu Asn Ile Lys Ser Val
    450   455   460

Ala Glu Arg Arg Glu Asn Met Leu Trp Phe Arg Val Pro Glu Lys Val
465   470   475   480

Tyr Phe Lys Tyr Gly Ser Leu Gly Val Ala Leu Lys Glu Leu Arg Ile
                485   490   495

Met Glu Lys Lys Lys Ala Phe Ile Val Thr Asp Lys Val Leu Tyr Gln
            500   505   510

Leu Gly Tyr Val Asp Lys Ile Thr Lys Asn Leu Asp Glu Leu Arg Val
        515   520   525

Ser Tyr Lys Ile Phe Thr Asp Val Glu Pro Asp Pro Thr Leu Ala Thr
    530   535   540

Ala Lys Lys Gly Ala Ala Glu Leu Leu Ser Tyr Glu Pro Asp Thr Ile
545   550   555   560

Ile Ala Val Gly Gly Gly Ser Ala Met Asp Ala Ala Lys Ile Met Trp
                565   570   575

Val Met Tyr Glu His Pro Glu Val Arg Phe Glu Asp Leu Ala Met Arg
            580   585   590

Phe Met Asp Ile Arg Lys Arg Val Tyr Val Phe Pro Lys Met Gly Glu
        595   600   605

Lys Ala Met Met Ile Ser Val Ala Thr Ser Ala Gly Thr Gly Ser Glu
    610   615   620

Val Thr Pro Phe Ala Val Ile Thr Asp Glu Arg Thr Gly Ala Lys Tyr
625   630   635   640

Pro Leu Ala Asp Tyr Glu Leu Thr Pro Asn Met Ala Ile Val Asp Ala
                645   650   655

Glu Leu Met Met Gly Met Pro Lys Gly Leu Thr Ala Ala Ser Gly Ile
            660   665   670

Asp Ala Leu Thr His Ala Leu Glu Ala Tyr Val Ser Ile Met Ala Ser
        675   680   685

Glu Tyr Thr Asn Gly Leu Ala Leu Glu Ala Thr Arg Leu Val Phe Lys
690 695 700

Tyr Leu Pro Ile Ala Tyr Thr Glu Gly Thr Ile Asn Val Lys Ala Arg
705 710 715 720

Glu Lys Met Ala His Ala Ser Cys Ile Ala Gly Met Ala Phe Ala Asn
725 730 735

Ala Phe Leu Gly Val Cys His Ser Met Ala His Lys Leu Gly Ala Gln
740 745 750

His His Ile Pro His Gly Ile Ala Asn Ala Leu Met Ile Asp Glu Val
755 760 765

Ile Lys Phe Asn Ala Val Glu Ala Pro Arg Lys Gln Ala Ala Phe Pro
770 775 780

Gln Tyr Lys Tyr Pro Asn Val Lys Arg Arg Tyr Ala Arg Ile Ala Asp
785 790 795 800

Tyr Leu Asn Leu Gly Gly Ser Thr Asp Asp Glu Lys Val Gln Leu Leu
805 810 815

Ile Asn Ala Ile Asp Asp Leu Lys Thr Lys Leu Asn Ile Pro Lys Thr
820 825 830

Ile Lys Glu Ala Gly Val Ser Glu Asp Lys Phe Tyr Ala Thr Leu Asp
835 840 845

Thr Met Ser Glu Leu Ala Phe Asp Asp Gln Cys Thr Gly Ala Asn Pro
850 855 860

Arg Tyr Pro Leu Ile Gly Glu Ile Lys Gln Met Tyr Ile Asn Ala Phe
865 870 875 880

Asp Thr Pro Lys Ala Thr Val Glu Lys Lys Thr Arg Lys Lys Lys
885 890 895

<210> 41
<211> 2613
<212> DNA
<213> c. autoethanogenum

<400> 41
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aagaaatttg ctacatatac tcaagaacaa gtggatgaaa tttttagaca agcagctatg 120

gcagctaata gtgctagaat agaactagct aaaatggcag tagaagaaag cggaatggga 180

attgtagaag acaaggttat taaaaatcac tttgcttcag aatatatata taacaaatat 240 aaggatgaaa aaacctgtgg agttttagag agagatgcag gctttggtat agttagaatt 300

gcggaacctg taggagttat tgcagcagta gttccaacaa ctaatccaac atctacagca 360

atatttaaat cactaatagc tttaaaaact agaaatggta taattttttc accccatcca 420

agggcaaaga aatcaactat tgcagcagct aaaatagtac ttgacgctgc agttaaagct 480

ggtgctcctg aaggaattat aggatggata gatgaacctt ccattgaact ttcacaggtg 540

gtaatgggag aagcaaattt aattcttgca actggtggtc cgggtatggt taaggctgcc 600

tattcttcag gcaaacctgc tgtgggagtt ggtccaggta acacacctgc tgtaattgat 660

gaaagtgccg acattaaaat ggcagtaaat tcaatattac tatcaaaaac ttttgataat 720

ggtatgattt gtgcctcaga gcagtcagta atagttttag actcaatata tgaggaagtt 780

aaaaaagaat ttgcttatag gggtgcttat atattaagta aggatgaaac agataaggtt 840

ggaaaaataa ttttaaaaaa tggagcctta aatgcaggta ttgtaggaca acctgctttt 900

aaaatagcac agctggcagg agtggatgta ccagaaaaag ctaaagtact tataggagag 960

gtagaatcgg tagaacttga agaaccattt tctcatgaaa agttatctcc agttttagct 1020

atgtacaggg caagaaattt tgaggatgcc attgcaaaaa ctgataaact ggttagggca 1080

ggtggatttg gacatacatc ttcattgtat ataaatccaa tgacagaaaa agcaaaagta 1140

gaaaaattta gtactatgat gaaaacatca agaactataa ttaacacacc ttcatcccaa 1200

ggtggtatag gtgatatata taactttaaa ctagctcctt ctttgacatt aggctgcggt 1260

tcctgggggg gaaattctgt atccgaaaat gttgggccta aacatttatt aaacataaaa 1320

agtgttgctg agaggagaga aaatatgctt tggtttagag tacctgaaaa ggtttatttc 1380

aaatatggta gtcttggagt tgcattaaaa gagttaaaag ttatgaataa gaagaaagta 1440

tttatagtaa cagataaagt tctttatcaa ttaggttatg tggacaaagt tacaaaagtt 1500

cttgaggaac taaaaatttc ctataaggta tttacagatg tagaaccaga tccaaccctt 1560

gctacagcta aaaaaggtgc agcagaactg ctttcctatg aaccggatac aattatatca 1620

gttggtggtg gttcagcaat ggatgcagct aagatcatgt gggtaatgta tgagcatcca 1680

gaagtaaaat ttgaagattt agctatgaga tttatggata taagaaagag agtatatgtt 1740

ttccctaaga tgggagaaaa ggcaatgatg atttcagtag caacatccgc aggaacaggg 1800

tcggaagtta ctccatttgc agtaatcact gatgaaaaaa caggagctaa atatccatta 1860

gctgattatg aactaactcc agacatggct atagttgatg cagaacttat gatgggaatg 1920

ccaagaggac ttacagcagc ttcgggtata gatgcattaa cccatgcact ggaggcgtat 1980

gtgtcaataa tggctacaga atttaccaat ggattagccc ttgaagcagt aaagttgata 2040

tttgaatatt taccaaaagc ttatacagaa ggtacaacta atgtaaaggc aagagaaaag 2100

atggctcatg cttcatgtat tgcaggtatg gcctttgcaa atgcattttt aggggtatgc 2160

cactctatgg cacataaatt gggagcacag catcacatac cacatggaat tgccaatgca 2220

cttatgatag atgaagttat aaaattcaat gctgtagatg atccaataaa acaagctgca 2280 tttccccaat acgagtatcc aaatgctagg tatagatatg ctcagatagc tgattgtctg 2340

aacttgggag gaaatacaga agaggaaaag gtacaactat taataaatgc tatagatgat 2400

ttaaaagcta agttaaatat tccagaaact ataaaagaag caggagtttc agaagataaa 2460

ttctatgcta ctttagataa aatgtcagaa ttagcttttg atgatcagtg tacaggagct 2520

aatccaagat atccactgat aagtgaaata aaacaaatgt atataaatgt ttttgataaa 2580

accgaaccaa ttgtagaaga tgaagaaaag taa 2613

<210> 42
<211> 508
<212> PRT
<213> C. autoethanogenum

<400> 42

Met Lys Val Thr Asn Val Glu Glu Leu Met Lys Arg Leu Glu Glu Ile
1 5 10 15

Lys Asp Ala Gln Lys Lys Phe Ala Thr Tyr Thr Gln Glu Gln Val Asp
20 25 30

Glu Ile Phe Arg Gln Ala Ala Met Ala Ala Asn Ser Ala Arg Ile Glu
35 40 45

Leu Ala Lys Met Ala Val Glu Glu Ser Gly Met Gly Ile Val Glu Asp
50 55 60

Lys Val Ile Lys Asn His Phe Ala Ser Glu Tyr Ile Tyr Asn Lys Tyr
65 70 75 80

Lys Asp Glu Lys Thr Cys Gly Val Leu Glu Arg Asp Ala Gly Phe Gly
85 90 95

Ile Val Arg Ile Ala Glu Pro Val Gly Val Ile Ala Ala Val Val Pro
100 105 110

Thr Thr Asn Pro Thr Ser Thr Ala Ile Phe Lys Ser Leu Ile Ala Leu
115 120 125

Lys Thr Arg Asn Gly Ile Ile Phe Ser Pro His Pro Arg Ala Lys Lys
130 135 140

Ser Thr Ile Ala Ala Ala Lys Ile Val Leu Asp Ala Ala Val Lys Ala
145 150 155 160

Gly Ala Pro Glu Gly Ile Ile Gly Trp Ile Asp Glu Pro Ser Ile Glu
165 170 175

Leu Ser Gln Val Val Met Gly Glu Ala Asn Leu Ile Leu Ala Thr Gly
180 185 190

```
Gly Pro Gly Met Val Lys Ala Ala Tyr Ser Ser Gly Lys Pro Ala Val
        195                 200                 205

Gly Val Gly Pro Gly Asn Thr Pro Ala Val Ile Asp Glu Ser Ala Asp
    210                 215                 220

Ile Lys Met Ala Val Asn Ser Ile Leu Leu Ser Lys Thr Phe Asp Asn
225                 230                 235                 240

Gly Met Ile Cys Ala Ser Glu Gln Ser Val Ile Val Leu Asp Ser Ile
                245                 250                 255

Tyr Glu Glu Val Lys Lys Glu Phe Ala Tyr Arg Gly Ala Tyr Ile Leu
            260                 265                 270

Ser Lys Asp Glu Thr Asp Lys Val Gly Lys Ile Ile Leu Lys Asn Gly
        275                 280                 285

Ala Leu Asn Ala Gly Ile Val Gly Gln Pro Ala Phe Lys Ile Ala Gln
    290                 295                 300

Leu Ala Gly Val Asp Val Pro Glu Lys Ala Lys Val Leu Ile Gly Glu
305                 310                 315                 320

Val Glu Ser Val Glu Leu Glu Glu Pro Phe Ser His Glu Lys Leu Ser
                325                 330                 335

Pro Val Leu Ala Met Tyr Arg Ala Arg Asn Phe Glu Asp Ala Ile Ala
            340                 345                 350

Lys Thr Asp Lys Leu Val Arg Ala Gly Gly Phe Gly His Thr Ser Ser
        355                 360                 365

Leu Tyr Ile Asn Pro Met Thr Glu Lys Ala Lys Val Glu Lys Phe Ser
    370                 375                 380

Thr Met Met Lys Thr Ser Arg Thr Ile Ile Asn Thr Pro Ser Ser Gln
385                 390                 395                 400

Gly Gly Ile Gly Asp Ile Tyr Asn Phe Lys Leu Ala Pro Ser Leu Thr
                405                 410                 415

Leu Gly Cys Gly Ser Trp Gly Gly Asn Ser Val Ser Glu Asn Val Gly
            420                 425                 430

Pro Lys His Leu Leu Asn Ile Lys Ser Val Ala Glu Arg Arg Glu Asn
        435                 440                 445

Met Leu Trp Phe Arg Val Pro Glu Lys Val Tyr Phe Lys Tyr Gly Ser
    450                 455                 460
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Leu Gly Val Ala Leu Lys Glu Leu Lys Val Met Asn Lys Lys Lys Val
465 470 475 480

Phe Ile Val Thr Asp Lys Val Leu Tyr Gln Leu Gly Tyr Val Asp Lys
485 490 495

Val Thr Lys Val Leu Glu Glu Leu Lys Asn Phe Leu
500 505

<210> 43
<211> 1554
<212> DNA
<213> c. autoethanogenum

<400> 43
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ggaaaaattg cagcagacca aattgctgat tatactgaag aacaaattga taaaatccta 120

tgtaatatgg ttagggtagc agaagaaaat gcagtttgcc ttggtaaaat ggctgcagaa 180

gaaactggtt ttggaaaagc tgaagataag gcttataaga accatatggc tgctactaca 240

gtatataatt acatcaagga tatgaagact attggtgtta taaaagaaga taaaagtgaa 300

ggtgtaattg aatttgcaga accagttggt ttattaatgg gtattgtacc atctacaaat 360

ccaacatcta ctgttattta taaatcaatc attgcaatta aatcaagaaa tgcaattgta 420

ttctcaccac acccagctgc attaaaatgt tcaacaaaag caatagaact tatgcgtgat 480

gcagcagtag cagcaggagc tcctgcaaat gtaattggtg gtattgttac accatctata 540

caagctacaa atgaacttat gaaagctaaa gaagttgcta tgataattgc aactggaggc 600

cctggaatgg taaaggctgc atatagttca ggaacacctg caataggcgt tggtgctggt 660

aactctccat cctatattga aagaactgct gatgttcatc aatcagttaa agatataata 720

gctagtaaga gttttgacta tggtactatt tgtgcatccg agcagtctgt aattgcagaa 780

gaatgcaacc atgatgaaat agtagctgaa tttaagaaac aaggcggata tttcatgaca 840

gctgaagaaa ctgcaaaagt ttgcagcgta ctttttaaac ctggtacaca cagcatgagc 900

gctaagtttg taggaagagc tcctcaggtt atagcagaag ctgcaggttt cacagttcca 960

gaaggaacaa aagtattaat aggagaacaa ggcggagttg gtaatggtta ccctctatct 1020

tatgagaaac ttacaacagt acttgctttc tatacagtta aagattggca tgaagcatgt 1080

gagcttagta taagattact tcaaaatggt cttggacata caatgaacat tcatacaaat 1140

gatagagact tagtaatgaa gtttgctaaa aaaccagcat cccgtatctt agttaatact 1200

ggtggaagcc agggaggtac tggtgcaagc acaggattag cacctgcatt tacattaggt 1260

tgtggtacat ggggaggaag ctctgtttct gaaaatgtta ctccattaca tttaatcaat 1320

ataaagagag tagcatatgg tcttaaagat tgtactacat tagctgcaga cgatacaact 1380

ttcaatcatc ctgaactttg cggaagcaaa aatgacttag gattctgtgc tacaagccct 1440

gcagaatttg cagcaaagag caattgtgat agcactgctg cagatactac tgataatgat 1500

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aaacttgcta gactcgtaag tgaattagta gctgcaatga agggagctaa ctaa           1554


<210>  44
<211>  517
<212>  PRT
<213>  c. autoethanogenum

<400>  44

Met Glu Asn Phe Asp Lys Asp Leu Arg Ser Ile Gln Glu Ala Arg Asp
1               5                   10                  15


Leu Ala Arg Leu Gly Lys Ile Ala Ala Asp Gln Ile Ala Asp Tyr Thr
            20                  25                  30


Glu Glu Gln Ile Asp Lys Ile Leu Cys Asn Met Val Arg Val Ala Glu
        35                  40                  45


Glu Asn Ala Val Cys Leu Gly Lys Met Ala Ala Glu Glu Thr Gly Phe
    50                  55                  60


Gly Lys Ala Glu Asp Lys Ala Tyr Lys Asn His Met Ala Ala Thr Thr
65                  70                  75                  80


Val Tyr Asn Tyr Ile Lys Asp Met Lys Thr Ile Gly Val Ile Lys Glu
                85                  90                  95


Asp Lys Ser Glu Gly Val Ile Glu Phe Ala Glu Pro Val Gly Leu Leu
            100                 105                 110


Met Gly Ile Val Pro Ser Thr Asn Pro Thr Ser Thr Val Ile Tyr Lys
        115                 120                 125


Ser Ile Ile Ala Ile Lys Ser Arg Asn Ala Ile Val Phe Ser Pro His
    130                 135                 140


Pro Ala Ala Leu Lys Cys Ser Thr Lys Ala Ile Glu Leu Met Arg Asp
145                 150                 155                 160


Ala Ala Val Ala Ala Gly Ala Pro Ala Asn Val Ile Gly Gly Ile Val
                165                 170                 175


Thr Pro Ser Ile Gln Ala Thr Asn Glu Leu Met Lys Ala Lys Glu Val
            180                 185                 190


Ala Met Ile Ile Ala Thr Gly Gly Pro Gly Met Val Lys Ala Ala Tyr
        195                 200                 205


Ser Ser Gly Thr Pro Ala Ile Gly Val Gly Ala Gly Asn Ser Pro Ser
    210                 215                 220


Tyr Ile Glu Arg Thr Ala Asp Val His Gln Ser Val Lys Asp Ile Ile
225                 230                 235                 240
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```
Ala Ser Lys Ser Phe Asp Tyr Gly Thr Ile Cys Ala Ser Glu Gln Ser
                245                 250                 255

Val Ile Ala Glu Glu Cys Asn His Asp Glu Ile Val Ala Glu Phe Lys
            260                 265                 270

Lys Gln Gly Gly Tyr Phe Met Thr Ala Glu Glu Thr Ala Lys Val Cys
        275                 280                 285

Ser Val Leu Phe Lys Pro Gly Thr His Ser Met Ser Ala Lys Phe Val
    290                 295                 300

Gly Arg Ala Pro Gln Val Ile Ala Glu Ala Ala Gly Phe Thr Val Pro
305                 310                 315                 320

Glu Gly Thr Lys Val Leu Ile Gly Glu Gln Gly Gly Val Gly Asn Gly
                325                 330                 335

Tyr Pro Leu Ser Tyr Glu Lys Leu Thr Thr Val Leu Ala Phe Tyr Thr
            340                 345                 350

Val Lys Asp Trp His Glu Ala Cys Glu Leu Ser Ile Arg Leu Leu Gln
        355                 360                 365

Asn Gly Leu Gly His Thr Met Asn Ile His Thr Asn Asp Arg Asp Leu
    370                 375                 380

Val Met Lys Phe Ala Lys Lys Pro Ala Ser Arg Ile Leu Val Asn Thr
385                 390                 395                 400

Gly Gly Ser Gln Gly Gly Thr Gly Ala Ser Thr Gly Leu Ala Pro Ala
                405                 410                 415

Phe Thr Leu Gly Cys Gly Thr Trp Gly Gly Ser Ser Val Ser Glu Asn
            420                 425                 430

Val Thr Pro Leu His Leu Ile Asn Ile Lys Arg Val Ala Tyr Gly Leu
        435                 440                 445

Lys Asp Cys Thr Thr Leu Ala Ala Asp Asp Thr Thr Phe Asn His Pro
    450                 455                 460

Glu Leu Cys Gly Ser Lys Asn Asp Leu Gly Phe Cys Ala Thr Ser Pro
465                 470                 475                 480

Ala Glu Phe Ala Ala Lys Ser Asn Cys Asp Ser Thr Ala Ala Asp Thr
                485                 490                 495

Thr Asp Asn Asp Lys Leu Ala Arg Leu Val Ser Glu Leu Val Ala Ala
            500                 505                 510
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Met Lys Gly Ala Asn
515

<210> 45
<211> 1446
<212> DNA
<213> c. autoethanogenum

<400> 45
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gagattgttg aacgtatggc ggaagaaatc ggaaaacata cccgagagct tgctgtaatg 120

tcacaggatg aaactggtta tggaaaatgg caggataaat gcatcaaaaa ccgatttgcc 180

tgtgagtatt tgccagctaa gcttagagga atgcgatgtg taggtattat taatgaaaat 240

ggtcaggata agaccatgga tgtaggtgta cctatgggtg taattattgc attatgtcct 300

gcaactagtc cggtttctac taccatatat aaggcattga ttgcaattaa gtctggtaat 360

gcaattatct tttctccaca tcctagagca aaggagacaa tttgtaaggc gcttgacatc 420

atgattcgtg cagctgaagg atatgggctt ccagaaggag ctcttgcata cttacatact 480

gtgacgccta gtggaacaat cgaattgatg aaccatattg cgacttcttt gattatgaat 540

acaggtgttc ccgggatgct taaagcagca tataattctg ggaaacctgt tatatatgga 600

ggaactggta atggaccagc atttattgaa cgtacagctg acatcaaaca ggcggtaaaa 660

gatattattg ctagtaagac ctttgataac ggaatagtac catcagctga acaatctatt 720

gttgtagata gctgtgttgc atctgatgtt aaacgtgagt tgcaaaataa tggtgcatat 780

ttcatgacag aggaggaagc acaaaaacta ggttctctct ttttccgttc tgatggcagt 840

atggattcag aaatggttgg caaatccgca caaagattgg ctaaaaaagc aggtttcagc 900

attcctgaaa gtagcacagt gctaatttca gagcagaaat atgtttctca agataatcct 960

tattccaagg agaaactttg tccggtacta gcttactaca ttgaagatga ttggatgcat 1020

gcatgtgaaa agtgtattga actgctgtta agtgagagac atggtcacac tcttgttata 1080

cattcaaaag acgaagatgt aattcgccag tttgcattaa aaaaacctgt aggtaggata 1140

cttgttaata cgcctgcttc ctttggtagt atgggtgcta caagtaattt atttcctgct 1200

ttaactttag gtagtggatc ggcaggtaaa ggtattacct ccgataatgt ttcaccaatg 1260

aatcttattt acgtccgcaa agtcggatat ggcgtacgga atgtagaaga gattgtcaat 1320

actaatggat tgtttacaga agaaaaaagt gatttgaatg gaatgacaaa aaagtcagac 1380

tataatccag aggatataca aatgttacag catattttaa aaaaagctat ggaaaaaatt 1440

aaatag 1446

<210> 46
<211> 481
<212> PRT
<213> c. autoethanogenum

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<400>  46

Met Glu Asn Ala Ala Arg Ala Gln Lys Met Leu Ala Thr Phe Pro Gln
1               5                   10                  15

Glu Lys Leu Asp Glu Ile Val Glu Arg Met Ala Glu Glu Ile Gly Lys
            20                  25                  30

His Thr Arg Glu Leu Ala Val Met Ser Gln Asp Glu Thr Gly Tyr Gly
        35                  40                  45

Lys Trp Gln Asp Lys Cys Ile Lys Asn Arg Phe Ala Cys Glu Tyr Leu
    50                  55                  60

Pro Ala Lys Leu Arg Gly Met Arg Cys Val Gly Ile Ile Asn Glu Asn
65                  70                  75                  80

Gly Gln Asp Lys Thr Met Asp Val Gly Val Pro Met Gly Val Ile Ile
                85                  90                  95

Ala Leu Cys Pro Ala Thr Ser Pro Val Ser Thr Thr Ile Tyr Lys Ala
            100                 105                 110

Leu Ile Ala Ile Lys Ser Gly Asn Ala Ile Ile Phe Ser Pro His Pro
        115                 120                 125

Arg Ala Lys Glu Thr Ile Cys Lys Ala Leu Asp Ile Met Ile Arg Ala
    130                 135                 140

Ala Glu Gly Tyr Gly Leu Pro Glu Gly Ala Leu Ala Tyr Leu His Thr
145                 150                 155                 160

Val Thr Pro Ser Gly Thr Ile Glu Leu Met Asn His Ile Ala Thr Ser
                165                 170                 175

Leu Ile Met Asn Thr Gly Val Pro Gly Met Leu Lys Ala Ala Tyr Asn
            180                 185                 190

Ser Gly Lys Pro Val Ile Tyr Gly Gly Thr Gly Asn Gly Pro Ala Phe
        195                 200                 205

Ile Glu Arg Thr Ala Asp Ile Lys Gln Ala Val Lys Asp Ile Ile Ala
    210                 215                 220

Ser Lys Thr Phe Asp Asn Gly Ile Val Pro Ser Ala Glu Gln Ser Ile
225                 230                 235                 240

Val Val Asp Ser Cys Val Ala Ser Asp Val Lys Arg Glu Leu Gln Asn
                245                 250                 255

Asn Gly Ala Tyr Phe Met Thr Glu Glu Glu Ala Gln Lys Leu Gly Ser
            260                 265                 270
```

Leu Phe Phe Arg Ser Asp Gly Ser Met Asp Ser Glu Met Val Gly Lys
275 280 285

Ser Ala Gln Arg Leu Ala Lys Lys Ala Gly Phe Ser Ile Pro Glu Ser
290 295 300

Ser Thr Val Leu Ile Ser Glu Gln Lys Tyr Val Ser Gln Asp Asn Pro
305 310 315 320

Tyr Ser Lys Glu Lys Leu Cys Pro Val Leu Ala Tyr Tyr Ile Glu Asp
325 330 335

Asp Trp Met His Ala Cys Glu Lys Cys Ile Glu Leu Leu Leu Ser Glu
340 345 350

Arg His Gly His Thr Leu Val Ile His Ser Lys Asp Glu Asp Val Ile
355 360 365

Arg Gln Phe Ala Leu Lys Lys Pro Val Gly Arg Ile Leu Val Asn Thr
370 375 380

Pro Ala Ser Phe Gly Ser Met Gly Ala Thr Ser Asn Leu Phe Pro Ala
385 390 395 400

Leu Thr Leu Gly Ser Gly Ser Ala Gly Lys Gly Ile Thr Ser Asp Asn
405 410 415

Val Ser Pro Met Asn Leu Ile Tyr Val Arg Lys Val Gly Tyr Gly Val
420 425 430

Arg Asn Val Glu Glu Ile Val Asn Thr Asn Gly Leu Phe Thr Glu Glu
435 440 445

Lys Ser Asp Leu Asn Gly Met Thr Lys Lys Ser Asp Tyr Asn Pro Glu
450 455 460

Asp Ile Gln Met Leu Gln His Ile Leu Lys Lys Ala Met Glu Lys Ile
465 470 475 480

Lys

<210> 47
<211> 490
<212> DNA
<213> C. autoethanogenum

<400> 47
aagcggccgc aaaatagttg ataataatgc agagttataa acaaaggtga aaagcattac 60

ttgtattctt ttttatatat tattataaat taaaatgaag ctgtattaga aaaaatacac 120 acctgtaata taaaatttta aattaatttt taattttttc aaaatgtatt ttacatgttt 180

agaattttga tgtatattaa aatagtagaa tacataagat acttaattta attaaagata 240

gttaagtact tttcaatgtg cttttttaga tgtttaatac aaatctttaa ttgtaaaaga 300

aatgctgtac tatttactgt actagtgacg ggattaaact gtattaatta taaataaaaa 360

ataagtacag ttgtttaaaa ttatattttg tattaaatct aatagtacga tgtaagttat 420

tttatactat tgctagttta ataaaaagat ttaattatat gcttgaaaag gagaggaatc 480

catatgcgta 490

<210> 48
<211> 500
<212> DNA
<213> c. autoethanogenum

<400> 48
ataccataaa ttacttgaaa aatagttgat aataatgtag agttataaac aaaggtgaaa 60

agcattactt gtattctttt ttatatatta ttataaatta aaatgaagct gtattagaaa 120

aaatacacac ctgtaatata aaattttaaa ttaattttta atttttcaa aatgtatttt 180

acatgtttag aattttgatg tatattaaaa tagtagaata cataagatac ttaatttaat 240

taaagatagt taagtacttt tcaatgtgct tttttagatg tttaatacaa atctttaatt 300

gtaaaagaaa tgctgtacta tttactgtac tagtgacggg attaaactgt attaattata 360

aataaaaaat aagtacagtt gtttaaaatt atattttgta ttaaatctaa tagtacgatg 420

taagttattt tatactattg ctagtttaat aaaaagattt aattatatac ttgaaaagga 480

gaggaatttt tatgcgtaaa 500

<210> 49
<211> 200
<212> DNA
<213> c. autoethanogenum

<400> 49
tagaaaaaca tgtatacaaa attaaaaaac tattataaca catagtatca atattgaagg 60

taatactgtt caatatcgat acagataaaa aaaatatata atacagaaga aaaaattata 120

aatttgtggt ataatataaa gtatagtaat ttaagtttaa acctcgtgaa aacgctaaca 180

aataatagga ggtgtattat 200

<210> 50
<211> 300
<212> DNA
<213> c. autoethanogenum

<400> 50
atctgtatat tttttcccat tttaattatt tgtactataa tattacactg agtgtattgt 60

atatttaaaa aatatttggt acaattagtt agttaaataa attctaaatt gtaaattatc 120

agaatcctta ttaaggaaat acatagattt aaggagaaat cataaaaagg tgtaatataa 180

actggctaaa attgagcaaa aattgagcaa ttaagacttt ttgattgtat ctttttatat 240 atttaaggta tataatctta tttatattgg gggaacttga tgaataaaca tattctagac 300

<210> 51
<211> 2613
<212> DNA
<213> c. autoethanogenum

<400> 51
atgaaagtta caaacgtaga agaactaatg aaaagactag aagaaataaa ggatgctcaa 60

aagaaatttg ctacatatac tcaagaacaa gtggatgaaa tttttagaca agcagctatg 120

gcagctaata gtgctagaat agaactagct aaaatggcag tagaagaaag cggaatggga 180

attgtagaag acaaggttat taaaaatcac tttgcttcag aatatatata taacaaatat 240

aaggatgaaa aaacctgtgg agttttagag agagatgcag gctttggtat agttagaatt 300

gcggaacctg taggagttat tgcagcagta gttccaacaa ctaatccaac atctacagca 360

atatttaaat cactaatagc tttaaaaact agaaatggta taattttttc accccatcca 420

agggcaaaga aatcaactat tgcagcagct aaaatagtac ttgacgctgc agttaaagct 480

ggtgctcctg aaggaattat aggatggata gatgaacctt ccattgaact ttcacaggtg 540

gtaatgggag aagcaaattt aattcttgca actggtggtc cgggtatggt taaggctgcc 600

tattcttcag gcaaacctgc tgtgggagtt ggtccaggta acacacctgc tgtaattgat 660

gaaagtgccg acattaaaat ggcagtaaat tcaatattac tatcaaaaac ttttgataat 720

ggtatgattt gtgcctcaga gcagtcagta atagttttag actcaatata tgaggaagtt 780

aaaaaagaat ttgcttatag gggtgcttat atattaagta aggatgaaac agataaggtt 840

ggaaaaataa ttttaaaaaa tggagcctta aatgcaggta ttgtaggaca acctgctttt 900

aaaatagcac agctggcagg agtggatgta ccagaaaaag ctaaagtact tataggagag 960

gtagaatcgg tagaacttga agaaccattt tctcatgaaa agttatctcc agttttagct 1020

atgtacaggg caagaaattt tgaggatgcc attgcaaaaa ctgataaact ggttagggca 1080

ggtggatttg gacatacatc ttcattgtat ataaatccaa tgacagaaaa agcaaaagta 1140

gaaaaattta gtactatgat gaaaacatca agaactataa ttaacacacc ttcatcccaa 1200

ggtggtatag gtgatatata taactttaaa ctagctcctt ctttgacatt aggctgcggt 1260

tcctgggggg gaaattctgt atccgaaaat gttgggccta aacatttatt aaacataaaa 1320

agtgttgctg agaggagaga aaatatgctt tggtttagag tacctgaaaa ggtttatttc 1380

aaatatggta gtcttggagt tgcattaaaa gagttaaaag ttatgaataa gaagaaagta 1440

tttatagtaa cagataaagt tctttatcaa ttaggttatg tggacaaagt tacaaaagtt 1500

cttgaggaac taaaaatttc ctataaggta tttacagatg tagaaccaga tccaaccctt 1560

gctacagcta aaaaaggtgc agcagaactg ctttcctatg aaccggatac aattatatca 1620

gttggtggtg gttcagcaat ggatgcagct aagatcatgt gggtaatgta tgagcatcca 1680

gaagtaaaat ttgaagattt agctatgaga tttatggata taagaaagag agtatatgtt 1740 ttccctaaga tgggagaaaa ggcaatgatg atttcagtag caacatccgc aggaacaggg 1800

tcggaagtta ctccatttgc agtaatcact gatgaaaaaa caggagctaa atatccatta 1860

gctgattatg aactaactcc agacatggct atagttgatg cagaacttat gatgggaatg 1920

ccaagaggac ttacagcagc ttcgggtata gatgcattaa cccatgcact ggaggcgtat 1980

gtgtcaataa tggctacaga atttaccaat ggattagccc ttgaagcagt aaagttgata 2040

tttgaatatt taccaaaagc ttatacagaa ggtacaacta atgtaaaggc aagagaaaag 2100

atggctcatg cttcatgtat tgcaggtatg gcctttgcaa atgcattttt aggggtatgc 2160

cactctatgg cacataaatt gggagcacag catcacatac cacatggaat tgccaatgca 2220

cttatgatag atgaagttat aaaattcaat gctgtagatg atccaataaa acaagctgca 2280

tttccccaat acgagtatcc aaatgctagg tatagatatg ctcagatagc tgattgtctg 2340

aacttgggag gaaatacaga agaggaaaag gtacaactat taataaatgc tatagatgat 2400

ttaaaagcta agttaaatat tccagaaact ataaaagaag caggagtttc agaagataaa 2460

ttctatgcta ctttagataa aatgtcagaa ttagcttttg atgatcagtg tacaggagct 2520

aatccaagat atccactgat aagtgaaata aaacaaatgt atataaatgt tttgataaa 2580

accgaaccaa ttgtagaaga tgaagaaaag taa 2613

<210> 52
<211> 324
<212> PRT
<213> c. autoethanogenum

<400> 52

Met Asp Ala Ala Lys Ile Met Trp Val Met Tyr Glu His Pro Glu Val
1 5 10 15

Lys Phe Glu Asp Leu Ala Met Arg Phe Met Asp Ile Arg Lys Arg Val
20 25 30

Tyr Val Phe Pro Lys Met Gly Glu Lys Ala Met Met Ile Ser Val Ala
35 40 45

Thr Ser Ala Gly Thr Gly Ser Glu Val Thr Pro Phe Ala Val Ile Thr
50 55 60

Asp Glu Lys Thr Gly Ala Lys Tyr Pro Leu Ala Asp Tyr Glu Leu Thr
65 70 75 80

Pro Asp Met Ala Ile Val Asp Ala Glu Leu Met Met Gly Met Pro Arg
85 90 95

Gly Leu Thr Ala Ala Ser Gly Ile Asp Ala Leu Thr His Ala Leu Glu
100 105 110

Ala Tyr Val Ser Ile Met Ala Thr Glu Phe Thr Asn Gly Leu Ala Leu
115 120 125

```
Glu Ala Val Lys Leu Ile Phe Glu Tyr Leu Pro Lys Ala Tyr Thr Glu
    130                 135                 140

Gly Thr Thr Asn Val Lys Ala Arg Glu Lys Met Ala His Ala Ser Cys
145                 150                 155                 160

Ile Ala Gly Met Ala Phe Ala Asn Ala Phe Leu Gly Val Cys His Ser
                165                 170                 175

Met Ala His Lys Leu Gly Ala Gln His His Ile Pro His Gly Ile Ala
            180                 185                 190

Asn Ala Leu Met Ile Asp Glu Val Ile Lys Phe Asn Ala Val Asp Asp
        195                 200                 205

Pro Ile Lys Gln Ala Ala Phe Pro Gln Tyr Glu Tyr Pro Asn Ala Arg
    210                 215                 220

Tyr Arg Tyr Ala Gln Ile Ala Asp Cys Leu Asn Leu Gly Gly Asn Thr
225                 230                 235                 240

Glu Glu Glu Lys Val Gln Leu Leu Ile Asn Ala Ile Asp Asp Leu Lys
                245                 250                 255

Ala Lys Leu Asn Ile Pro Glu Thr Ile Lys Glu Ala Gly Val Ser Glu
            260                 265                 270

Asp Lys Phe Tyr Ala Thr Leu Asp Lys Met Ser Glu Leu Ala Phe Asp
        275                 280                 285

Asp Gln Cys Thr Gly Ala Asn Pro Arg Tyr Pro Leu Ile Ser Glu Ile
    290                 295                 300

Lys Gln Met Tyr Ile Asn Val Phe Asp Lys Thr Glu Pro Ile Val Glu
305                 310                 315                 320

Asp Glu Glu Lys


<210>  53
<211>  1194
<212>  DNA
<213>  C. autoethanogenum

<400>  53
atggaaataa aattaggggg aataataatg gagagattta cgttgccaag agacatttac      60

tttggagaag atgctttggg tgctttgaaa acgttaaaag gtaagaaagc tgtagtagtt     120

gttggaggag gatccatgaa gagattcggt ttccttgaca aggtagaaga atacttaaaa     180

gaagcaaaca tagaagttaa actaatagaa ggtgttgaac cagatccgtc tgtggaaacc     240
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gttatgaaag gtgccaaaat aatgacagaa tttgggccag attggatagt tgctattgga 300

ggaggttcac caatagatgc tgcaaaggct atgtggctat tttatgaata tccagatttt 360

acttttaaac aagcaattgt tccgtttgga ttaccagaat taagacaaaa agctaaattt 420

gtagctatag cttctactag tggaacagct actgaagtta cttcattttc agtaataact 480

gattataaag ctaaaataaa gtatccttta gctgacttca atttgacacc ggatatagct 540

atagttgatc cagcattagc ccagacaatg ccacctaaat taactgcaca tactggtatg 600

gatgcattaa ctcatgcact agaagcttat gtagcatcag ctagatcaga tatttcagat 660

ccacttgcaa tacattccat aattatgaca agggataact tacttaaatc ctataagggt 720

gataaagatg ctagaaataa gatgcatata tcacaatgtt tagcaggtat ggcattttct 780

aatgcacttc ttggtataac tcatagttta gcacataaaa caggagctgt atggcacata 840

ccacatggat gcgctaatgc aatatatctt ccatatgttt tagattttaa taaaaaagct 900

tgctcagata gatatgctaa tatagctaaa atattaggac ttaaaggaac tactgaagat 960

gaattggtag attctctagt taaaatggta caagatatgg ataaggaatt gaatatacct 1020

ttgaccttaa aagattatgg tataagcaaa gatgatttca attcaaatgt tgattttata 1080

gcaaagaatg cgctcttaga tgcatgtaca ggagctaatc caaggcctat agattttgat 1140

caaatgaaaa agatacttca atgtatatat gatggaaaaa aggtaacttt ttaa 1194

<210> 54
<211> 397
<212> PRT
<213> c. autoethanogenum

<400> 54

Met Glu Ile Lys Leu Gly Gly Ile Ile Met Glu Arg Phe Thr Leu Pro
1 5 10 15

Arg Asp Ile Tyr Phe Gly Glu Asp Ala Leu Gly Ala Leu Lys Thr Leu
20 25 30

Lys Gly Lys Lys Ala Val Val Val Val Gly Gly Gly Ser Met Lys Arg
35 40 45

Phe Gly Phe Leu Asp Lys Val Glu Glu Tyr Leu Lys Glu Ala Asn Ile
50 55 60

Glu Val Lys Leu Ile Glu Gly Val Glu Pro Asp Pro Ser Val Glu Thr
65 70 75 80

Val Met Lys Gly Ala Lys Ile Met Thr Glu Phe Gly Pro Asp Trp Ile
85 90 95

Val Ala Ile Gly Gly Gly Ser Pro Ile Asp Ala Ala Lys Ala Met Trp
100 105 110

```
Leu Phe Tyr Glu Tyr Pro Asp Phe Thr Phe Lys Gln Ala Ile Val Pro
        115                 120                 125

Phe Gly Leu Pro Glu Leu Arg Gln Lys Ala Lys Phe Val Ala Ile Ala
    130                 135                 140

Ser Thr Ser Gly Thr Ala Thr Glu Val Thr Ser Phe Ser Val Ile Thr
145                 150                 155                 160

Asp Tyr Lys Ala Lys Ile Lys Tyr Pro Leu Ala Asp Phe Asn Leu Thr
                165                 170                 175

Pro Asp Ile Ala Ile Val Asp Pro Ala Leu Ala Gln Thr Met Pro Pro
            180                 185                 190

Lys Leu Thr Ala His Thr Gly Met Asp Ala Leu Thr His Ala Leu Glu
        195                 200                 205

Ala Tyr Val Ala Ser Ala Arg Ser Asp Ile Ser Asp Pro Leu Ala Ile
    210                 215                 220

His Ser Ile Ile Met Thr Arg Asp Asn Leu Leu Lys Ser Tyr Lys Gly
225                 230                 235                 240

Asp Lys Asp Ala Arg Asn Lys Met His Ile Ser Gln Cys Leu Ala Gly
                245                 250                 255

Met Ala Phe Ser Asn Ala Leu Leu Gly Ile Thr His Ser Leu Ala His
            260                 265                 270

Lys Thr Gly Ala Val Trp His Ile Pro His Gly Cys Ala Asn Ala Ile
        275                 280                 285

Tyr Leu Pro Tyr Val Leu Asp Phe Asn Lys Lys Ala Cys Ser Asp Arg
    290                 295                 300

Tyr Ala Asn Ile Ala Lys Ile Leu Gly Leu Lys Gly Thr Thr Glu Asp
305                 310                 315                 320

Glu Leu Val Asp Ser Leu Val Lys Met Val Gln Asp Met Asp Lys Glu
                325                 330                 335

Leu Asn Ile Pro Leu Thr Leu Lys Asp Tyr Gly Ile Ser Lys Asp Asp
            340                 345                 350

Phe Asn Ser Asn Val Asp Phe Ile Ala Lys Asn Ala Leu Leu Asp Ala
        355                 360                 365

Cys Thr Gly Ala Asn Pro Arg Pro Ile Asp Phe Asp Gln Met Lys Lys
    370                 375                 380
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Ile Leu Gln Cys Ile Tyr Asp Gly Lys Lys Val Thr Phe
385 390 395

<210> 55
<211> 1191
<212> DNA
<213> C. autoethanogenum

<400> 55
gtgagggatg ttattatgga aaactttatt tttaaaaatg ctacagaaat tatttttggt 60

aaggataccg aaaatcttgt aggaagtaaa gtaaaggagt attcaaagtc agataaaata 120

ctcttttgct atgggggagg aagcataaaa agatctggtc tatatgatag agttataaag 180

tccttaaaag aaaatggaat tgaatttata gaacttccag gaattaaacc taatccaaga 240

ttaggacctg ttaaagaagg tataagacta tgtagagaaa ataatataaa atttgtacta 300

tctgtaggag gaggaagttc agcagatacg gctaaagcta ttgctgtagg agtaccttat 360

aaaggagacg tatgggattt ttatacgggc aaagctgaag tgaaagaggc tcttcctgta 420

ggagttgtaa taacattacc tgctacaggt acagaatcta gtaatagttc tgttattatg 480

aatgaagatg gttggtttaa aaaaggatta aatacagtac ttataagacc tgctttttca 540

attatgaatc ctgaacttac ttttacacta ccagagtatc aaactgcttg tggtgcttgt 600

gacattatgg cacatataat ggaaagatat tttacaaatg tgaaacatgt agatataact 660

gataggcttt gcgaagctgc acttagaaat gttataaata atgccccaat agttttaaaa 720

gatcccaaaa actatgatgc tagggcagaa attatgtgga ccggtactat agctcataat 780

gatgtgctta gtgcgggtag aataggtgat tgggcttctc acaaaattga acatgaattg 840

agtggggaaa cagacattgc ccatggagca ggacttgcaa ttgtatttcc tgcatggatg 900

aaatatgtat ataaacacga tatcaataga tttgtacaat ttgcagtaag ggtatgggat 960

gtagatttat cttatagttc ctgcgaagat attgtacttg aaggcataag gagaatgaca 1020

gcatttttca agagcatggg gttacctgta actttaaaag aaggaagtat aggagaagat 1080

aaaattgaag aaatggctaa taagtgcacg gataatggaa ctaaaactgt aggacaattt 1140

gtaaaattaa ataaagatga tattgtaaaa atattaaatt tagctaaata a 1191

<210> 56
<211> 396
<212> PRT
<213> C. autoethanogenum

<400> 56

Val Arg Asp Val Ile Met Glu Asn Phe Ile Phe Lys Asn Ala Thr Glu
1 5 10 15

Ile Ile Phe Gly Lys Asp Thr Glu Asn Leu Val Gly Ser Lys Val Lys
20 25 30

Glu Tyr Ser Lys Ser Asp Lys Ile Leu Phe Cys Tyr Gly Gly Gly Ser
35 40 45

```
Ile Lys Arg Ser Gly Leu Tyr Asp Arg Val Ile Lys Ser Leu Lys Glu
    50                  55                  60

Asn Gly Ile Glu Phe Ile Glu Leu Pro Gly Ile Lys Pro Asn Pro Arg
65                  70                  75                  80

Leu Gly Pro Val Lys Glu Gly Ile Arg Leu Cys Arg Glu Asn Asn Ile
                85                  90                  95

Lys Phe Val Leu Ser Val Gly Gly Gly Ser Ser Ala Asp Thr Ala Lys
            100                 105                 110

Ala Ile Ala Val Gly Val Pro Tyr Lys Gly Asp Val Trp Asp Phe Tyr
        115                 120                 125

Thr Gly Lys Ala Glu Val Lys Glu Ala Leu Pro Val Gly Val Val Ile
    130                 135                 140

Thr Leu Pro Ala Thr Gly Thr Glu Ser Ser Asn Ser Ser Val Ile Met
145                 150                 155                 160

Asn Glu Asp Gly Trp Phe Lys Lys Gly Leu Asn Thr Val Leu Ile Arg
                165                 170                 175

Pro Ala Phe Ser Ile Met Asn Pro Glu Leu Thr Phe Thr Leu Pro Glu
            180                 185                 190

Tyr Gln Thr Ala Cys Gly Ala Cys Asp Ile Met Ala His Ile Met Glu
        195                 200                 205

Arg Tyr Phe Thr Asn Val Lys His Val Asp Ile Thr Asp Arg Leu Cys
    210                 215                 220

Glu Ala Ala Leu Arg Asn Val Ile Asn Asn Ala Pro Ile Val Leu Lys
225                 230                 235                 240

Asp Pro Lys Asn Tyr Asp Ala Arg Ala Glu Ile Met Trp Thr Gly Thr
                245                 250                 255

Ile Ala His Asn Asp Val Leu Ser Ala Gly Arg Ile Gly Asp Trp Ala
            260                 265                 270

Ser His Lys Ile Glu His Glu Leu Ser Gly Glu Thr Asp Ile Ala His
        275                 280                 285

Gly Ala Gly Leu Ala Ile Val Phe Pro Ala Trp Met Lys Tyr Val Tyr
    290                 295                 300

Lys His Asp Ile Asn Arg Phe Val Gln Phe Ala Val Arg Val Trp Asp
305                 310                 315                 320
```

Val Asp Leu Ser Tyr Ser Ser Cys Glu Asp Ile Val Leu Glu Gly Ile
325 330 335

Arg Arg Met Thr Ala Phe Phe Lys Ser Met Gly Leu Pro Val Thr Leu
340 345 350

Lys Glu Gly Ser Ile Gly Glu Asp Lys Ile Glu Glu Met Ala Asn Lys
355 360 365

Cys Thr Asp Asn Gly Thr Lys Thr Val Gly Gln Phe Val Lys Leu Asn
370 375 380

Lys Asp Asp Ile Val Lys Ile Leu Asn Leu Ala Lys
385 390 395

<210> 57
<211> 1149
<212> DNA
<213> C. autoethanogenum

<400> 57
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attcaacttt tagagcaagt cactggttct cgagcattta ttgttgcaga tgctattatg 120
ggaaaacttg gatatcttca aaaagtaata gattacctaa gcaaagctgg aataagttcc 180
gttgttttta cgggggtaca ccctgatcca gacgtcaatg taattgcaga tgcaatgaaa 240
ttgtacaaaa aaagcgacgc agatgttctc gtagcactag gtggaggatc cagtattgat 300
accgctaagg gaataatgta ttttgcatgt aatttaggaa aagcaatggg ccaagaaatg 360
aaaaaacctc tatttattgc aattccatca acaagtggta caggctctga agtaacaaac 420
tttactgtta ttacttctca gaaagaaaag gtatgcatta tagatgattt tattgcacca 480
gatgttgcaa tacttgactc aagttgtatt gatggtctgc ctcagcgtat tgtagcagat 540
actggtatag atgttctagt tcattctatt gaagcctatg tttccaaaaa agcaactgac 600
tttacagacg ctcttgctga aaaagcagtt aaattaattt ttgagaatct tccaaaaatt 660
tataacgata gtaaggattc cgaagctcga gatcatgttc aaaacgcttc ctgtatagca 720
ggaatagcat ttacaaatgc tggtcttgga attaatcaca gcttggctca tgctatgggt 780
ggatctttcc acattcctca cggccgatcc aatgcacttc tacttaatgc agtaatggaa 840
tacaacgcta gcttggttgg aaatgcaagc gaacatgcta tggaaaaata cgcaaaacta 900
gcatcaattc tacaccttcc agctcgaaca actcgcgaag gcgctgtaag ttttattgaa 960
gctgtagata aattaataaa atccctaggt gttgaagata atattcgatc tcttgggatt 1020
aaagaagatg agtttcaaag tgctctaaat catatggcag aaacagcaat gcaagataga 1080
tgcactccaa ctaatcctag aaaaccttct aaagaagaac ttatacatat ttatcaaaaa 1140
tgttattaa 1149

SequenceListing

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<210>  58
<211>  307
<212>  PRT
<213>  C. autoethanogenum

<400>  58

Met Glu Asp Lys Phe Glu Asn Phe Asn Leu Lys Ser Lys Ile Tyr Phe
1               5                   10                  15

Asn Arg Glu Ser Ile Gln Leu Leu Glu Gln Val Thr Gly Ser Arg Ala
            20                  25                  30

Phe Ile Val Ala Asp Ala Ile Met Gly Lys Leu Gly Tyr Leu Gln Lys
        35                  40                  45

Val Ile Asp Tyr Leu Ser Lys Ala Gly Ile Ser Ser Val Val Phe Thr
    50                  55                  60

Gly Val His Pro Asp Pro Asp Val Asn Val Ile Ala Asp Ala Met Lys
65                  70                  75                  80

Leu Tyr Lys Lys Ser Asp Ala Asp Val Leu Val Ala Leu Gly Gly Gly
                85                  90                  95

Ser Ser Ile Asp Thr Ala Lys Gly Ile Met Tyr Phe Ala Cys Asn Leu
            100                 105                 110

Gly Lys Ala Met Gly Gln Glu Met Lys Lys Pro Leu Phe Ile Ala Ile
        115                 120                 125

Pro Ser Thr Ser Gly Thr Gly Ser Glu Val Thr Asn Phe Thr Val Ile
    130                 135                 140

Thr Ser Gln Lys Glu Lys Val Cys Ile Ile Asp Asp Phe Ile Ala Pro
145                 150                 155                 160

Asp Val Ala Ile Leu Asp Ser Ser Cys Ile Asp Gly Leu Pro Gln Arg
                165                 170                 175

Ile Val Ala Asp Thr Gly Ile Asp Val Leu Val His Ser Ile Glu Ala
            180                 185                 190

Tyr Val Ser Lys Lys Ala Thr Asp Phe Thr Asp Ala Leu Ala Glu Lys
        195                 200                 205

Ala Val Lys Leu Ile Phe Glu Asn Leu Pro Lys Ile Tyr Asn Asp Ser
    210                 215                 220

Lys Asp Ser Glu Ala Arg Asp His Val Gln Asn Ala Ser Cys Ile Ala
225                 230                 235                 240
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Gly Ile Ala Phe Thr Asn Ala Gly Leu Gly Ile Asn His Ser Leu Ala
245 250 255

His Ala Met Gly Gly Ser Phe His Ile Pro His Gly Arg Ser Asn Ala
260 265 270

Leu Leu Leu Asn Ala Val Met Glu Tyr Asn Ala Ser Leu Val Gly Asn
275 280 285

Ala Ser Glu His Ala Met Glu Lys Tyr Ala Lys Leu Ala Ser Ile Leu
290 295 300

His Leu Pro
305

<210> 59
<211> 993
<212> DNA
<213> c. autoethanogenum

<400> 59
atggaaaaaa tttggagtaa ggcaaaggaa gacaaaaaaa agattgtctt agctgaagga 60

gaagaagaaa gaactcttca agcttgtgaa aaaataatta aagagggtat tgcaaattta 120

atccttgtag ggaatgaaaa ggtaataaaa gaaaaagcgt caaaattagg tgtaagttta 180

aatggagcag aaatagtaga tccagagatt tcagataaac taaaggcata tgcagatgct 240

ttttatgaat tgagaaagaa gaagggaata acgccagaaa aagcggataa aatagtaaga 300

gatccaatat actttgctac aatgatggtt aaacttggag atgcagatgg attggtttca 360

ggtgcggttc atactacagg cgatcttttg agaccaggac ttcaaatagt aaagacagct 420

ccaggtacat cagtagtttc cagtacattt ataatggaag taccaaattg tgagtatggt 480

gacaatggtg tacttctatt tgctgattgt gctgtaaatc catgcccaga tagtgatcaa 540

ttggcttcaa ttgcaataag tacagcagaa actgcaaaga acttatgtgg aatggatcca 600

aaagtagcaa tgctttcatt ttctactaag ggaagtgcaa aacacgaatt agtagacaaa 660

gttagaaatg ctgtagagat tgcaaaaaaa gctaaaccag atttaagttt agacggagaa 720

ttacaattag atgcctctat cgtagaaaag gttgcaagtt taaaggctcc tggaagtgaa 780

gtagcaggaa aagcaaatgt acttgtattt ccagatctcc aagcaggaaa tataggctat 840

aaactcgttc aaagatttgc aaaagcagat gctataggac ctgtatgcca aggatttgca 900

aaacctataa atgatttgtc aagaggatgt aattctgatg atatagtaaa tgtagtagct 960

gtaacagcag ttcaagcaca agctcaaaag taa 993

<210> 60
<211> 330
<212> PRT
<213> c. autoethanogenum

<400> 60

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Met Glu Lys Ile Trp Ser Lys Ala Lys Glu Asp Lys Lys Lys Ile Val
1               5                   10                  15

Leu Ala Glu Gly Glu Glu Glu Arg Thr Leu Gln Ala Cys Glu Lys Ile
            20                  25                  30

Ile Lys Glu Gly Ile Ala Asn Leu Ile Leu Val Gly Asn Glu Lys Val
        35                  40                  45

Ile Lys Glu Lys Ala Ser Lys Leu Gly Val Ser Leu Asn Gly Ala Glu
    50                  55                  60

Ile Val Asp Pro Glu Ile Ser Asp Lys Leu Lys Ala Tyr Ala Asp Ala
65                  70                  75                  80

Phe Tyr Glu Leu Arg Lys Lys Lys Gly Ile Thr Pro Glu Lys Ala Asp
                85                  90                  95

Lys Ile Val Arg Asp Pro Ile Tyr Phe Ala Thr Met Met Val Lys Leu
            100                 105                 110

Gly Asp Ala Asp Gly Leu Val Ser Gly Ala Val His Thr Thr Gly Asp
        115                 120                 125

Leu Leu Arg Pro Gly Leu Gln Ile Val Lys Thr Ala Pro Gly Thr Ser
    130                 135                 140

Val Val Ser Ser Thr Phe Ile Met Glu Val Pro Asn Cys Glu Tyr Gly
145                 150                 155                 160

Asp Asn Gly Val Leu Leu Phe Ala Asp Cys Ala Val Asn Pro Cys Pro
                165                 170                 175

Asp Ser Asp Gln Leu Ala Ser Ile Ala Ile Ser Thr Ala Glu Thr Ala
            180                 185                 190

Lys Asn Leu Cys Gly Met Asp Pro Lys Val Ala Met Leu Ser Phe Ser
        195                 200                 205

Thr Lys Gly Ser Ala Lys His Glu Leu Val Asp Lys Val Arg Asn Ala
    210                 215                 220

Val Glu Ile Ala Lys Lys Ala Lys Pro Asp Leu Ser Leu Asp Gly Glu
225                 230                 235                 240

Leu Gln Leu Asp Ala Ser Ile Val Glu Lys Val Ala Ser Leu Lys Ala
                245                 250                 255

Pro Gly Ser Glu Val Ala Gly Lys Ala Asn Val Leu Val Phe Pro Asp
            260                 265                 270
```

Leu Gln Ala Gly Asn Ile Gly Tyr Lys Leu Val Gln Arg Phe Ala Lys
275 280 285

Ala Asp Ala Ile Gly Pro Val Cys Gln Gly Phe Ala Lys Pro Ile Asn
290 295 300

Asp Leu Ser Arg Gly Cys Asn Ser Asp Asp Ile Val Asn Val Val Ala
305 310 315 320

Val Thr Ala Val Gln Ala Gln Ala Gln Lys
325 330

<210> 61
<211> 1197
<212> DNA
<213> c. autoethanogenum

<400> 61
atgaaaatat tagtagtaaa ctgtggaagt tcatctttaa aatatcaact tattgatatg 60

caagatgaaa gtgttgtagc aaagggtctt gtagaaagaa taggaatgga cggttcaatt 120

ttaacacaca aagttaatgg agaaaagttt gttacagagc aaccaatgga agaccacaaa 180

gttgctatac aattagtatt aaatgctctt gtagataaaa aacatggtgt aataaaagac 240

atgtcagaaa tatccgctgt aggacataga gttttgcacg gtggaaagaa atatgcagca 300

tccattctta ttgacgaaaa tgtaatgaaa gcaatagaag aatgtatccc actaggacca 360

ctacataatc cagctaatat aatgggaata gatgcttgta aaaaattaat gccaaatact 420

ccaatggtag cagtatttga tacagcattt catcagacaa tgccagatta tgcttatact 480

tatgcaatac cttatgatat atctgaaaag tatgatatca gaaaatatgg ttttcatgga 540

acttctcata gattcgtttc aattgaagca gctaaattat taaagaaaga tccaaaagat 600

cttaagttaa taacttgtca tttaggaaat ggagctagca tatgtgcagt aaaccaagga 660

aaagcagtag atacaactat gggacttact cctcttgcag gacttgtaat gggaactaga 720

tgcggtgata tagatccagc tatagtacca tttgtaatga aaagaacagg catgtctgta 780

gatgaagtgg ataccttaat gaataaaaag tcaggaatac ttggagtatc aggagtaagc 840

agtgatttta gagatgtaga agaagctgca aattcaggaa atgatagagc aaaacttgca 900

ttaaatatgt attatcacaa agttaaatct ttcataggag cttatgttgc agttttaaat 960

ggagcagatg ctataatatt tacggcagga cttggagaaa attcagcaac tagcagatct 1020

gctatatgta atggattaag ctattttgga attaaaatag atgaagaaaa gaataagaaa 1080

aggggagagg cactagaaat aagcacacct gattcaaaga taaaagtatt agtaattcct 1140

acaaatgaag aacttatgat agctagggat acaaaagaaa tagttgaaaa taaataa 1197

<210> 62
<211> 398
<212> PRT
<213> c. autoethanogenum

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<400>  62

Met Lys Ile Leu Val Val Asn Cys Gly Ser Ser Ser Leu Lys Tyr Gln
1               5                   10                  15

Leu Ile Asp Met Gln Asp Glu Ser Val Val Ala Lys Gly Leu Val Glu
            20                  25                  30

Arg Ile Gly Met Asp Gly Ser Ile Leu Thr His Lys Val Asn Gly Glu
        35                  40                  45

Lys Phe Val Thr Glu Gln Pro Met Glu Asp His Lys Val Ala Ile Gln
    50                  55                  60

Leu Val Leu Asn Ala Leu Val Asp Lys Lys His Gly Val Ile Lys Asp
65                  70                  75                  80

Met Ser Glu Ile Ser Ala Val Gly His Arg Val Leu His Gly Gly Lys
                85                  90                  95

Lys Tyr Ala Ala Ser Ile Leu Ile Asp Glu Asn Val Met Lys Ala Ile
            100                 105                 110

Glu Glu Cys Ile Pro Leu Gly Pro Leu His Asn Pro Ala Asn Ile Met
        115                 120                 125

Gly Ile Asp Ala Cys Lys Lys Leu Met Pro Asn Thr Pro Met Val Ala
    130                 135                 140

Val Phe Asp Thr Ala Phe His Gln Thr Met Pro Asp Tyr Ala Tyr Thr
145                 150                 155                 160

Tyr Ala Ile Pro Tyr Asp Ile Ser Glu Lys Tyr Asp Ile Arg Lys Tyr
                165                 170                 175

Gly Phe His Gly Thr Ser His Arg Phe Val Ser Ile Glu Ala Ala Lys
            180                 185                 190

Leu Leu Lys Lys Asp Pro Lys Asp Leu Lys Leu Ile Thr Cys His Leu
        195                 200                 205

Gly Asn Gly Ala Ser Ile Cys Ala Val Asn Gln Gly Lys Ala Val Asp
    210                 215                 220

Thr Thr Met Gly Leu Thr Pro Leu Ala Gly Leu Val Met Gly Thr Arg
225                 230                 235                 240

Cys Gly Asp Ile Asp Pro Ala Ile Val Pro Phe Val Met Lys Arg Thr
                245                 250                 255

Gly Met Ser Val Asp Glu Val Asp Thr Leu Met Asn Lys Lys Ser Gly
            260                 265                 270
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```
Ile Leu Gly Val Ser Gly Val Ser Ser Asp Phe Arg Asp Val Glu Glu
        275                 280                 285

Ala Ala Asn Ser Gly Asn Asp Arg Ala Lys Leu Ala Leu Asn Met Tyr
    290                 295                 300

Tyr His Lys Val Lys Ser Phe Ile Gly Ala Tyr Val Ala Val Leu Asn
305                 310                 315                 320

Gly Ala Asp Ala Ile Ile Phe Thr Ala Gly Leu Gly Glu Asn Ser Ala
                325                 330                 335

Thr Ser Arg Ser Ala Ile Cys Asn Gly Leu Ser Tyr Phe Gly Ile Lys
            340                 345                 350

Ile Asp Glu Glu Lys Asn Lys Lys Arg Gly Glu Ala Leu Glu Ile Ser
        355                 360                 365

Thr Pro Asp Ser Lys Ile Lys Val Leu Val Ile Pro Thr Asn Glu Glu
    370                 375                 380

Leu Met Ile Ala Arg Asp Thr Lys Glu Ile Val Glu Asn Lys
385                 390                 395

<210>  63
<211>  1767
<212>  DNA
<213>  C. autoethanogenum

<400>  63
gtggaagaat tgaaaattga caaagctaaa aaatttatag gtgcaagagg gttaggcgta      60

aaaaccttat ttgacgaagt agatccaaag gtagatccat tatcacctga taacaaattt     120

attatagcag cgggaccact tacaggtgca cctgttccaa caagcggaag attcatggta     180

gttactaaat cacctttaac aggaactatt gctattgcaa attcaggtgg aaaatgggga     240

gcagaattca aagcagctgg atacgatatg ataatcgttg aaggtaaatc tgataaagaa     300

gtttatgtaa atatagtaga tgataaagta gaatttaggg atgcttctca tgtttgggga     360

aaactaacag aagaaactac aaaaatgctt caacaggaaa cagattcgag agctaaggtt     420

ttatgcatag gaccagctgg ggaaaagtta tcacttatgg cagcagttat gaatgatgtt     480

gatagaacag caggacgtgg tggtgttgga gctgttatgg gttcaaagaa cttaaaagct     540

attgtagtta aaggaagcgg aaaagtaaaa ttatttgatg aacaaaaagt gaaggaagta     600

gcacttgaga aacaaatat tttaagaaaa gatccagtag ctggtggagg acttccaaca     660

tacggaacag ctgtacttgt taatattata aatgaaaatg gtgtacatcc agtaaagaat     720

tttcaaaaat cttatacaga tcaagcagat aagatcagtg gagaaacttt aactaaagat     780

tgcttagtta gaaaaaatcc ttgctatagg tgtccaattg cctgtggaag atgggtaaaa     840
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cttgatgatg gaactgaatg tggaggacca gaatatgaaa cattatggtc atttggatct      900

gattgtgatg tatacgatat aaatgctgta aatacagcaa atatgttgtg taatgaatat      960

ggactagata ccattacagc aggatgtact attgcagcag ctatggaact ttatcaaaga     1020

ggttatatta aggatgaaga aatagcagca gatggattgt cacttaattg gggagatgct     1080

aagtccatgg ttgaatgggt aaagaaaatg ggacttagag aaggatttgg agacaagatg     1140

gcagatggtt catacagact ttgtgactca tacggtgtac ctgagtattc aatgactgta     1200

aaaaaacagg aacttccagc atatgaccca agaggaatac agggacatgg cattacttat     1260

gctgttaaca ataggggagg atgtcacatt aagggatata tggtaagtcc tgaaatactt     1320

ggctatccag aaaaacttga tagacttgca gtggaaggaa aagcaggata tgctagagta     1380

ttccatgatt taacagctgt tatagattca cttggattat gtatttttac aacatttggt     1440

cttggtgcac aggattatgt tgatatgtat aatgcagtag ttggtggaga attacatgat     1500

gtaaattctt taatgttagc tggagataga atatggactt tagaaaaaat atttaactta     1560

aaagcaggca tagatagttc acaggatact cttccaaaga gattgcttga agaacaaatt     1620

ccagaaggac catcaaaagg agaagttcat aagttagatg tactactacc tgaatattat     1680

tcagtacgtg gatgggataa aaatggtatt cctacagagg aaacgttaaa gaaattagga     1740

ttagatgaat acgtaggtaa gctttag                                         1767

<210>  64
<211>  588
<212>  PRT
<213>  c. autoethanogenum

<400>  64

Met Glu Glu Leu Lys Ile Asp Lys Ala Lys Lys Phe Ile Gly Ala Arg
1               5                   10                  15


Gly Leu Gly Val Lys Thr Leu Phe Asp Glu Val Asp Pro Lys Val Asp
            20                  25                  30


Pro Leu Ser Pro Asp Asn Lys Phe Ile Ile Ala Ala Gly Pro Leu Thr
        35                  40                  45


Gly Ala Pro Val Pro Thr Ser Gly Arg Phe Met Val Val Thr Lys Ser
    50                  55                  60


Pro Leu Thr Gly Thr Ile Ala Ile Ala Asn Ser Gly Gly Lys Trp Gly
65                  70                  75                  80


Ala Glu Phe Lys Ala Ala Gly Tyr Asp Met Ile Ile Val Glu Gly Lys
                85                  90                  95


Ser Asp Lys Glu Val Tyr Val Asn Ile Val Asp Asp Lys Val Glu Phe
            100                 105                 110
```

```
Arg Asp Ala Ser His Val Trp Gly Lys Leu Thr Glu Glu Thr Thr Lys
        115                 120                 125

Met Leu Gln Gln Glu Thr Asp Ser Arg Ala Lys Val Leu Cys Ile Gly
    130                 135                 140

Pro Ala Gly Glu Lys Leu Ser Leu Met Ala Ala Val Met Asn Asp Val
145                 150                 155                 160

Asp Arg Thr Ala Gly Arg Gly Gly Val Gly Ala Val Met Gly Ser Lys
                165                 170                 175

Asn Leu Lys Ala Ile Val Val Lys Gly Ser Gly Lys Val Lys Leu Phe
            180                 185                 190

Asp Glu Gln Lys Val Lys Glu Val Ala Leu Glu Lys Thr Asn Ile Leu
        195                 200                 205

Arg Lys Asp Pro Val Ala Gly Gly Gly Leu Pro Thr Tyr Gly Thr Ala
    210                 215                 220

Val Leu Val Asn Ile Ile Asn Glu Asn Gly Val His Pro Val Lys Asn
225                 230                 235                 240

Phe Gln Lys Ser Tyr Thr Asp Gln Ala Asp Lys Ile Ser Gly Glu Thr
                245                 250                 255

Leu Thr Lys Asp Cys Leu Val Arg Lys Asn Pro Cys Tyr Arg Cys Pro
            260                 265                 270

Ile Ala Cys Gly Arg Trp Val Lys Leu Asp Asp Gly Thr Glu Cys Gly
        275                 280                 285

Gly Pro Glu Tyr Glu Thr Leu Trp Ser Phe Gly Ser Asp Cys Asp Val
    290                 295                 300

Tyr Asp Ile Asn Ala Val Asn Thr Ala Asn Met Leu Cys Asn Glu Tyr
305                 310                 315                 320

Gly Leu Asp Thr Ile Thr Ala Gly Cys Thr Ile Ala Ala Ala Met Glu
                325                 330                 335

Leu Tyr Gln Arg Gly Tyr Ile Lys Asp Glu Glu Ile Ala Ala Asp Gly
            340                 345                 350

Leu Ser Leu Asn Trp Gly Asp Ala Lys Ser Met Val Glu Trp Val Lys
        355                 360                 365

Lys Met Gly Leu Arg Glu Gly Phe Gly Asp Lys Met Ala Asp Gly Ser
    370                 375                 380
```

```
Tyr Arg Leu Cys Asp Ser Tyr Gly Val Pro Glu Tyr Ser Met Thr Val
385                 390                 395                 400

Lys Lys Gln Glu Leu Pro Ala Tyr Asp Pro Arg Gly Ile Gln Gly His
                405                 410                 415

Gly Ile Thr Tyr Ala Val Asn Asn Arg Gly Gly Cys His Ile Lys Gly
            420                 425                 430

Tyr Met Val Ser Pro Glu Ile Leu Gly Tyr Pro Glu Lys Leu Asp Arg
        435                 440                 445

Leu Ala Val Glu Gly Lys Ala Gly Tyr Ala Arg Val Phe His Asp Leu
    450                 455                 460

Thr Ala Val Ile Asp Ser Leu Gly Leu Cys Ile Phe Thr Thr Phe Gly
465                 470                 475                 480

Leu Gly Ala Gln Asp Tyr Val Asp Met Tyr Asn Ala Val Val Gly Gly
                485                 490                 495

Glu Leu His Asp Val Asn Ser Leu Met Leu Ala Gly Asp Arg Ile Trp
            500                 505                 510

Thr Leu Glu Lys Ile Phe Asn Leu Lys Ala Gly Ile Asp Ser Ser Gln
        515                 520                 525

Asp Thr Leu Pro Lys Arg Leu Leu Glu Glu Gln Ile Pro Glu Gly Pro
    530                 535                 540

Ser Lys Gly Glu Val His Lys Leu Asp Val Leu Leu Pro Glu Tyr Tyr
545                 550                 555                 560

Ser Val Arg Gly Trp Asp Lys Asn Gly Ile Pro Thr Glu Glu Thr Leu
                565                 570                 575

Lys Lys Leu Gly Leu Asp Glu Tyr Val Gly Lys Leu
            580                 585
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<210> 65
<211> 1824
<212> DNA
<213> C. autoethanogenum

<400> 65

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atgtatggtt atgatggtaa agtattaaga attaatttaa aagaaagaac ttgcaaatca      60

gaaaatttag atttagataa agctaaaaag tttataggtt gtaggggact aggtgttaaa     120

actttatttg atgaaataga tcctaaaata gatgcattat caccagaaaa taaatttata     180

attgtaacag gtcctttaac tggagctccg gttccaacta gtggaaggtt tatggtagtt     240

actaaagcac cgcttacagg aactatagga atttcaaatt cgggtggaaa atggggagta     300
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gacttaaaaa aagctggttg ggatatgata atagtagagg ataaggctga ttcaccagtt 360

tacattgaaa tagtagatga taaggtagaa attaaagacg cgtcacagct ttggggaaaa 420

gttacatcag aaactacaaa agagttagaa aagataactg agaataaatc aaaggtatta 480

tgtataggac ctgctggtga acgattgtct cttatggcag cagttatgaa tgatgtagat 540

agaactgcag caagaggcgg cgttggtgca gttatgggat ctaaaaactt aaaagctatt 600

acagttaaag gaactggaaa aatagcttta gctgataaag aaaaagtaaa aaaagtgtcc 660

gtagaaaaaa ttacaacatt aaaaaatgat ccagtagctg gtcagggaat gccaacttat 720

ggtacagcta tactggttaa tataataaat gaaaatggag ttcatcctgt aaagaatttt 780

caagagtctt atacgaatca agcagataaa ataagtggag agactcttac tgctaaccaa 840

ctagtaagga aaaatccttg ttacagctgt cctataggtt gtggaagatg ggttagacta 900

aaagatggca cagagtgcgg aggaccagaa tatgaaacac tgtggtgttt tggatctgac 960

tgtggttcat atgatttaga tgctataaat gaagctaata tgttatgtaa tgaatatggt 1020

attgatacta ttacttgtgg tgcaacaatt gctgcagcta tggaacttta tcaaagagga 1080

tatataaaag acgaagaaat agctggagat aacctatctc tcaagtgggg tgatacggaa 1140

tctatgattg gctggataaa gagaatggta tatagtgaag gctttggagc aaagatgaca 1200

aatggttcat ataggctttg tgaaggttat ggagcaccgg agtattctat gacagttaaa 1260

aagcaggaaa ttccagcata tgatccaagg ggaatacagg gacacggtat tacctatgca 1320

gttaataata gaggaggctg tcatattaag ggatacatga ttaaccctga aatattaggt 1380

tatcctgaaa aacttgatag atttgcatta gatggtaaag cagcttatgc caaattattt 1440

catgatttaa ctgctgtaat tgattcttta ggattgtgca tattcactac atttgggctt 1500

ggaatacagg attatgtaga tatgtataat gcagtagtag gagaatctac ttatgatgca 1560

gattcactat tagaggcagg agatagaatc tggactcttg agaaattatt taatcttgca 1620

gctggaatag acagcagcca ggatactcta ccaaagagat tgttagaaga acctattcca 1680

gatggcccat caaagggaga agttcatagg ctagatgttc ttctgccaga atattactca 1740

gtacgaggat ggagtaaaga gggtatacct acagaagaaa cattaaagaa attaggatta 1800

gatgaatata taggtaagtt ctag 1824

<210> 66
<211> 607
<212> PRT
<213> c. autoethanogenum

<400> 66

Met Tyr Gly Tyr Asp Gly Lys Val Leu Arg Ile Asn Leu Lys Glu Arg
1 5 10 15

Thr Cys Lys Ser Glu Asn Leu Asp Leu Asp Lys Ala Lys Lys Phe Ile
20 25 30

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Gly Cys Arg Gly Leu Gly Val Lys Thr Leu Phe Asp Glu Ile Asp Pro
        35                  40                  45

Lys Ile Asp Ala Leu Ser Pro Glu Asn Lys Phe Ile Ile Val Thr Gly
    50                  55                  60

Pro Leu Thr Gly Ala Pro Val Pro Thr Ser Gly Arg Phe Met Val Val
65                  70                  75                  80

Thr Lys Ala Pro Leu Thr Gly Thr Ile Gly Ile Ser Asn Ser Gly Gly
                85                  90                  95

Lys Trp Gly Val Asp Leu Lys Lys Ala Gly Trp Asp Met Ile Ile Val
            100                 105                 110

Glu Asp Lys Ala Asp Ser Pro Val Tyr Ile Glu Ile Val Asp Asp Lys
        115                 120                 125

Val Glu Ile Lys Asp Ala Ser Gln Leu Trp Gly Lys Val Thr Ser Glu
    130                 135                 140

Thr Thr Lys Glu Leu Glu Lys Ile Thr Glu Asn Lys Ser Lys Val Leu
145                 150                 155                 160

Cys Ile Gly Pro Ala Gly Glu Arg Leu Ser Leu Met Ala Ala Val Met
                165                 170                 175

Asn Asp Val Asp Arg Thr Ala Ala Arg Gly Gly Val Gly Ala Val Met
            180                 185                 190

Gly Ser Lys Asn Leu Lys Ala Ile Thr Val Lys Gly Thr Gly Lys Ile
        195                 200                 205

Ala Leu Ala Asp Lys Glu Lys Val Lys Lys Val Ser Val Glu Lys Ile
    210                 215                 220

Thr Thr Leu Lys Asn Asp Pro Val Ala Gly Gln Gly Met Pro Thr Tyr
225                 230                 235                 240

Gly Thr Ala Ile Leu Val Asn Ile Ile Asn Glu Asn Gly Val His Pro
                245                 250                 255

Val Lys Asn Phe Gln Glu Ser Tyr Thr Asn Gln Ala Asp Lys Ile Ser
            260                 265                 270

Gly Glu Thr Leu Thr Ala Asn Gln Leu Val Arg Lys Asn Pro Cys Tyr
        275                 280                 285

Ser Cys Pro Ile Gly Cys Gly Arg Trp Val Arg Leu Lys Asp Gly Thr
    290                 295                 300
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Glu Cys Gly Gly Pro Glu Tyr Glu Thr Leu Trp Cys Phe Gly Ser Asp
305                 310                 315                 320

Cys Gly Ser Tyr Asp Leu Asp Ala Ile Asn Glu Ala Asn Met Leu Cys
                325                 330                 335

Asn Glu Tyr Gly Ile Asp Thr Ile Thr Cys Gly Ala Thr Ile Ala Ala
            340                 345                 350

Ala Met Glu Leu Tyr Gln Arg Gly Tyr Ile Lys Asp Glu Glu Ile Ala
        355                 360                 365

Gly Asp Asn Leu Ser Leu Lys Trp Gly Asp Thr Glu Ser Met Ile Gly
    370                 375                 380

Trp Ile Lys Arg Met Val Tyr Ser Glu Gly Phe Gly Ala Lys Met Thr
385                 390                 395                 400

Asn Gly Ser Tyr Arg Leu Cys Glu Gly Tyr Gly Ala Pro Glu Tyr Ser
                405                 410                 415

Met Thr Val Lys Lys Gln Glu Ile Pro Ala Tyr Asp Pro Arg Gly Ile
            420                 425                 430

Gln Gly His Gly Ile Thr Tyr Ala Val Asn Asn Arg Gly Gly Cys His
        435                 440                 445

Ile Lys Gly Tyr Met Ile Asn Pro Glu Ile Leu Gly Tyr Pro Glu Lys
    450                 455                 460

Leu Asp Arg Phe Ala Leu Asp Gly Lys Ala Ala Tyr Ala Lys Leu Phe
465                 470                 475                 480

His Asp Leu Thr Ala Val Ile Asp Ser Leu Gly Leu Cys Ile Phe Thr
                485                 490                 495

Thr Phe Gly Leu Gly Ile Gln Asp Tyr Val Asp Met Tyr Asn Ala Val
            500                 505                 510

Val Gly Glu Ser Thr Tyr Asp Ala Asp Ser Leu Leu Glu Ala Gly Asp
        515                 520                 525

Arg Ile Trp Thr Leu Glu Lys Leu Phe Asn Leu Ala Ala Gly Ile Asp
    530                 535                 540

Ser Ser Gln Asp Thr Leu Pro Lys Arg Leu Leu Glu Glu Pro Ile Pro
545                 550                 555                 560

Asp Gly Pro Ser Lys Gly Glu Val His Arg Leu Asp Val Leu Leu Pro
                565                 570                 575
```

Glu Tyr Tyr Ser Val Arg Gly Trp Ser Lys Glu Gly Ile Pro Thr Glu
580 585 590

Glu Thr Leu Lys Lys Leu Gly Leu Asp Glu Tyr Ile Gly Lys Phe
595 600 605

<210> 67
<211> 2634
<212> DNA
<213> c. ljungdahlii

<400> 67
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gcagctatgg cagccaatag tgctagaata gacttagcta aaatggcagt ggaagaaagc 180

ggaatgggaa ttgtagaaga caaggtcatt aaaaatcatt ttgttgcaga gtatatatat 240

aacaaatata agggtgaaaa aacctgtgga gttctggaac aagatgaagg ctttggtatg 300

gttagaattg cagaacctgt aggagttatt gcagcagtag tcccaacaac taatccaaca 360

tctacagcaa tatttaaatc actaatagct ttaaaaacta gaaatggtat agtttttttcg 420

ccacatccaa gggcaaaaaa atcaactatt gcagcagcta agatagtact tgatgctgca 480

gttaaagctg gtgctcctga aggaattata ggatggatag atgaaccttc tattgaactt 540

tcacaggtgg taatgaaaga agcagatcta attcttgcaa ctggtggacc aggtatggtt 600

aaggctgcct attcttcagg aaagcctgct ataggagttg gtccaggtaa cacgcctgct 660

gtaattgatg aaagtgctga cattaaaatg gcagtaaatt caatactatt atcaaaaact 720

tttgataatg gtatgatttg tgcttcagag cagtcagtag tagttgcaag ctcaatatac 780

gatgaagtca agaaagagtt tgcagataga ggagcatata tattaagtaa ggatgaaaca 840

gagaaggttg gaaaaacaat tataattaat ggagccttaa atgctggcat tgtagggcaa 900

agtgctttta aaatagcaca gatggcagga gtgagtgtac cagaagatgc taaagtactt 960

ataggagaag ttaaatcagt agaaccggaa gaagagccct ttgcgcatga aaagctatct 1020

ccagttttag ctatgtacaa agcaaaagat tttgacgaag cactcctaaa ggctggaaga 1080

ttagttgaac gaggtggaat tgggcataca tctgtattat atgtaaatgc aatgacggaa 1140

aaagtaaagg tagaaaagtt cagagaaact atgaagactg gtagaacatt gataaatatg 1200

ccttcagcac aaggtgctat aggagatata tataacttta agctagctcc ttctttgaca 1260

ctaggttgtg gttcctgggg aggaaactct gtatcagaaa atgttggtcc taaacattta 1320

ttaaacataa agagtgttgc tgagaggaga gaaaatatgc tttggtttag agtacctgaa 1380

aaggtttatt tcaaatatgg tagtcttgga gttgcactaa aagaactgag aattatggag 1440

aagaaaaagg catttatagt aacggataaa gttctttatc aattaggtta tgtagataaa 1500

attacaaaaa atctggatga attaagagtt tcatataaaa tatttacaga tgtagaacca 1560

gatccaaccc ttgctacagc taaaaaaggt gcagcagaac tgttagctta tgaaccagat 1620 acaattatag cagtcggtgg tggttcagca atggatgcag ccaagatcat gtgggtaatg 1680

tatgagcatc cagaagtaag atttgaagat ttagctatga gatttatgga tataagaaag 1740

agagtgtatg ttttccctaa aatgggagaa aaggcaatga tgatttcagt agcaacatcc 1800

gcaggaacag ggtcggaagt tacgccattt gcagtaatta cggatgaaag aacaggagct 1860

aaatatcctc tggctgatta tgaattgact ccaaacatgg ctatagttga tgcagaactt 1920

atgatgggaa tgccaaaggg actaacagca gcttcaggta tagatgcatt aacccatgcg 1980

ctggaggcct atgtatcaat aatggcttca gaatatacca atggattggc tcttgaagca 2040

acaagattag tatttaaata tttgccaata gcttatacag aaggtacaac taatgtaaag 2100

gcaagagaaa aaatggctca tgcttcatgt attgcaggta tggcctttgc caatgcattt 2160

ttaggggtat gccactccat ggcacataaa ttgggagcac agcaccacat accacatgga 2220

attgccaatg cacttatgat agatgaagtt ataaagttca atgctgtaga ggctccaagg 2280

aaacaagcgg catttccaca atataaatat ccaaatgtta aaagaagata tgctagaata 2340

gctgattact taaatttagg tggaagtaca gatgatgaaa aagtacaatt tttaataaat 2400

gctatagatg acttgaaaac caagttaaat attccaaaga ctattaaaga agcgggagtt 2460

tcagaagata aattctatgc tactttagat acaatgtcag aactggcttt tgatgatcaa 2520

tgtacaggag ctaatccaag atatccatta ataggagaaa taaaacaaat gtatataaat 2580

gcatttgata caccaaaggc aactgtggag aagaaaacaa gaaagaaaaa ataa 2634

<210> 68
<211> 877
<212> PRT
<213> C. ljungdahlii

<400> 68

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Met Lys Val Thr Lys Val Thr Asn Val Glu Glu Leu Met Lys Lys Leu
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Asp Glu Val Thr Ala Ala Gln Lys Lys Phe Ser Ser Tyr Thr Gln Glu
            20                  25                  30

Gln Val Asp Glu Ile Phe Arg Gln Ala Ala Met Ala Ala Asn Ser Ala
        35                  40                  45

Arg Ile Asp Leu Ala Lys Met Ala Val Glu Glu Ser Gly Met Gly Ile
    50                  55                  60

Val Glu Asp Lys Val Ile Lys Asn His Phe Val Ala Glu Tyr Ile Tyr
65                  70                  75                  80

Asn Lys Tyr Lys Gly Glu Lys Thr Cys Gly Val Leu Glu Gln Asp Glu
                85                  90                  95

Gly Phe Gly Met Val Arg Ile Ala Glu Pro Val Gly Val Ile Ala Ala
            100                 105                 110
```

```
Val Val Pro Thr Thr Asn Pro Thr Ser Thr Ala Ile Phe Lys Ser Leu
        115                 120                 125

Ile Ala Leu Lys Thr Arg Asn Gly Ile Val Phe Ser Pro His Pro Arg
    130                 135                 140

Ala Lys Lys Ser Thr Ile Ala Ala Ala Lys Ile Val Leu Asp Ala Ala
145                 150                 155                 160

Val Lys Ala Gly Ala Pro Glu Gly Ile Ile Gly Trp Ile Asp Glu Pro
                165                 170                 175

Ser Ile Glu Leu Ser Gln Val Val Met Lys Glu Ala Asp Leu Ile Leu
            180                 185                 190

Ala Thr Gly Gly Pro Gly Met Val Lys Ala Ala Tyr Ser Ser Gly Lys
        195                 200                 205

Pro Ala Ile Gly Val Gly Pro Gly Asn Thr Pro Ala Val Ile Asp Glu
    210                 215                 220

Ser Ala Asp Ile Lys Met Ala Val Asn Ser Ile Leu Leu Ser Lys Thr
225                 230                 235                 240

Phe Asp Asn Gly Met Ile Cys Ala Ser Glu Gln Ser Val Val Val Ala
                245                 250                 255

Ser Ser Ile Tyr Asp Glu Val Lys Lys Glu Phe Ala Asp Arg Gly Ala
            260                 265                 270

Tyr Ile Leu Ser Lys Asp Glu Thr Glu Lys Val Gly Lys Thr Ile Ile
        275                 280                 285

Ile Asn Gly Ala Leu Asn Ala Gly Ile Val Gly Gln Ser Ala Phe Lys
    290                 295                 300

Ile Ala Gln Met Ala Gly Val Ser Val Pro Glu Asp Ala Lys Val Leu
305                 310                 315                 320

Ile Gly Glu Val Lys Ser Val Glu Pro Glu Glu Glu Pro Phe Ala His
                325                 330                 335

Glu Lys Leu Ser Pro Val Leu Ala Met Tyr Lys Ala Lys Asp Phe Asp
            340                 345                 350

Glu Ala Leu Leu Lys Ala Gly Arg Leu Val Glu Arg Gly Gly Ile Gly
        355                 360                 365

His Thr Ser Val Leu Tyr Val Asn Ala Met Thr Glu Lys Val Lys Val
    370                 375                 380
```

```
Glu Lys Phe Arg Glu Thr Met Lys Thr Gly Arg Thr Leu Ile Asn Met
385                 390                 395                 400

Pro Ser Ala Gln Gly Ala Ile Gly Asp Ile Tyr Asn Phe Lys Leu Ala
                405                 410                 415

Pro Ser Leu Thr Leu Gly Cys Gly Ser Trp Gly Gly Asn Ser Val Ser
            420                 425                 430

Glu Asn Val Gly Pro Lys His Leu Leu Asn Ile Lys Ser Val Ala Glu
        435                 440                 445

Arg Arg Glu Asn Met Leu Trp Phe Arg Val Pro Glu Lys Val Tyr Phe
    450                 455                 460

Lys Tyr Gly Ser Leu Gly Val Ala Leu Lys Glu Leu Arg Ile Met Glu
465                 470                 475                 480

Lys Lys Lys Ala Phe Ile Val Thr Asp Lys Val Leu Tyr Gln Leu Gly
                485                 490                 495

Tyr Val Asp Lys Ile Thr Lys Asn Leu Asp Glu Leu Arg Val Ser Tyr
            500                 505                 510

Lys Ile Phe Thr Asp Val Glu Pro Asp Pro Thr Leu Ala Thr Ala Lys
        515                 520                 525

Lys Gly Ala Ala Glu Leu Leu Ala Tyr Glu Pro Asp Thr Ile Ile Ala
    530                 535                 540

Val Gly Gly Gly Ser Ala Met Asp Ala Ala Lys Ile Met Trp Val Met
545                 550                 555                 560

Tyr Glu His Pro Glu Val Arg Phe Glu Asp Leu Ala Met Arg Phe Met
                565                 570                 575

Asp Ile Arg Lys Arg Val Tyr Val Phe Pro Lys Met Gly Glu Lys Ala
            580                 585                 590

Met Met Ile Ser Val Ala Thr Ser Ala Gly Thr Gly Ser Glu Val Thr
        595                 600                 605

Pro Phe Ala Val Ile Thr Asp Glu Arg Thr Gly Ala Lys Tyr Pro Leu
    610                 615                 620

Ala Asp Tyr Glu Leu Thr Pro Asn Met Ala Ile Val Asp Ala Glu Leu
625                 630                 635                 640

Met Met Gly Met Pro Lys Gly Leu Thr Ala Ala Ser Gly Ile Asp Ala
                645                 650                 655
```

```
Leu Thr His Ala Leu Glu Ala Tyr Val Ser Ile Met Ala Ser Glu Tyr
            660                 665                 670

Thr Asn Gly Leu Ala Leu Glu Ala Thr Arg Leu Val Phe Lys Tyr Leu
        675                 680                 685

Pro Ile Ala Tyr Thr Glu Gly Thr Thr Asn Val Lys Ala Arg Glu Lys
    690                 695                 700

Met Ala His Ala Ser Cys Ile Ala Gly Met Ala Phe Ala Asn Ala Phe
705                 710                 715                 720

Leu Gly Val Cys His Ser Met Ala His Lys Leu Gly Ala Gln His His
                725                 730                 735

Ile Pro His Gly Ile Ala Asn Ala Leu Met Ile Asp Glu Val Ile Lys
            740                 745                 750

Phe Asn Ala Val Glu Ala Pro Arg Lys Gln Ala Ala Phe Pro Gln Tyr
        755                 760                 765

Lys Tyr Pro Asn Val Lys Arg Arg Tyr Ala Arg Ile Ala Asp Tyr Leu
    770                 775                 780

Asn Leu Gly Gly Ser Thr Asp Asp Glu Lys Val Gln Phe Leu Ile Asn
785                 790                 795                 800

Ala Ile Asp Asp Leu Lys Thr Lys Leu Asn Ile Pro Lys Thr Ile Lys
                805                 810                 815

Glu Ala Gly Val Ser Glu Asp Lys Phe Tyr Ala Thr Leu Asp Thr Met
            820                 825                 830

Ser Glu Leu Ala Phe Asp Asp Gln Cys Thr Gly Ala Asn Pro Arg Tyr
        835                 840                 845

Pro Leu Ile Gly Glu Ile Lys Gln Met Tyr Ile Asn Ala Phe Asp Thr
    850                 855                 860

Pro Lys Ala Thr Val Glu Lys Lys Thr Arg Lys Lys Lys
865                 870                 875
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<210> 69
<211> 2613
<212> DNA
<213> c. ljungdahlii

<400> 69
atgaaagtta caaacgtaga agaactaatg aaaagactag aagaaataaa ggatgctcaa 60

aagaaatttg ctacatatac tcaagaacaa gtggatgaaa tttttagaca agcagctatg 120

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gcagctaata gtgctagaat agaactagct aaaatggcag tagaagaaag cggaatggga      180
attgtagaag acaaggtcat taaaaatcac tttgcctcag aatatatata taacaaatat      240
aaggatgaaa aaacctgtgg agttttagag agagatgcag gatttggtat agttagaatt      300
gcggaacctg taggagttat cgcagcagta gttccaacaa ctaatccaac atctacagca      360
atatttaaat cactaatagc tttaaaaact agaaatggta taattttttc accccatcca      420
agggcaaaga aatcaactat tgcagcagct aaaatagtac ttgacgctgc agttaaagct      480
ggtgctcctg aaggaattat aggatggata gatgaacctt ccattgaact ttcacaggtg      540
gtaatgggag aagcaaattt aattcttgca actggtggcc cgggtatggt taaggctgcc      600
tattcttcag gcaaacctgc tgtgggagtt ggtccaggta acacacctgc tgtaattgat      660
gaaagtgccg acattaaaat ggcagtaaat tcaatattac tatcaaagac ttttgataat      720
ggtatgattt gtgcctcaga gcagtcagta atagttttag actcaatata tgaggaagtt      780
aaaaaagaat ttgcttatag gggtgcttat atattaagta aggatgaaac agataaggtt      840
ggaaaaataa ttttaaaaaa tggagcctta aatgcaggta ttgtaggaca acctgctttt      900
aaaatagcac agctggcagg agtggatgta ccagaaaaag ctaaagtact tataggagag      960
gtagaatcgg tagaacttga agaaccattt tctcatgaaa agttatctcc agttttagct     1020
atgtacaggg caagaaattt tgaggatgcc attgcaaaaa ctgataaact ggttaggtca     1080
ggtggatttg gacatacatc ttcattatat gtaaatccaa tgacagagaa agcaaaagta     1140
gaaaaattta gtactatgat gaaaacatca agaactataa ttaacacacc ttcatcccaa     1200
ggtggtatag gtgatatata taactttaaa ctagctcctt ctttgacatt aggctgcggt     1260
tcctggggag gaaattctgt atccgaaaat gttgggccta aacatttatt aaacataaaa     1320
agtgttgctg agaggagaga aaatatgctt tggtttagag tacctgaaaa ggtttatttc     1380
aaatatggta gtcttggagt tgcattaaaa gaattaaaag ttatgaataa gaagaaagta     1440
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cttgaggaac taaaaatttc ctataaggta tttacagatg tagaaccaga tccaaccctt     1560
gctacagcta aaaaaggtgc agcagaactg ctttcctatg aaccggatac aattatatca     1620
gttggtggtg gctcagcaat ggatgcagct aagatcatgt gggtaatgta tgagcatcca     1680
gaagtaaaat ttgaagattt agctatgaga tttatggata taagaaagag agtatatgtt     1740
ttccctaaga tgggagaaaa ggcaatgatg atttcagtag caacatccgc aggaacaggg     1800
tcggaagtta ctccatttgc agtaatcact gatgaaaaaa caggagctaa atatccatta     1860
gctgattatg aactaactcc agacatggct atagttgatg cagaacttat gatgggaatg     1920
ccaagaggac ttacagcagc ttcgggtata gatgcattaa cccatgcact ggaggcatat     1980
gtgtcaataa tggctacaga atttaccaat ggattagccc ttgaagcagt aaagttgata     2040
tttgaatatt taccaaaagc ttatacagaa ggtacaacta atgtaaaggc aagagaaaag     2100
atggttcatg cttcatgtat tgcaggtatg gcctttgcaa atgcattttt aggggtatgc     2160
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cactctatgg cacataaatt gggagcacag catcacatac cacatggaat tgccaatgca 2220

cttatgatag atgaagttat aaaattcaat gctgtagatg atccaataaa acaagctgca 2280

tttccccaat acgagtatcc aaatgctagg tatagatatg ctcagatagc tgattgtctg 2340

aacttgggag gaaatacaga agaggaaaag gtacaactat taataaatgc tatagatgat 2400

ttaaaagcta agttaaatat tccagaaact ataaaagaag caggagtttc agaagataaa 2460

ttctatgcta ctttagataa aatgtcagaa ttagcttttg atgatcagtg tacaggagct 2520

aatccaagat atccactgat aagtgaaata aaacaaatgt atataaatgt tttgataaa 2580

accgaaccaa ttgtagaaga tgaagaaaag taa 2613

<210> 70
<211> 870
<212> PRT
<213> c. ljungdahlii

<400> 70

Met Lys Val Thr Asn Val Glu Glu Leu Met Lys Arg Leu Glu Glu Ile
1 5 10 15

Lys Asp Ala Gln Lys Lys Phe Ala Thr Tyr Thr Gln Glu Gln Val Asp
20 25 30

Glu Ile Phe Arg Gln Ala Ala Met Ala Ala Asn Ser Ala Arg Ile Glu
35 40 45

Leu Ala Lys Met Ala Val Glu Glu Ser Gly Met Gly Ile Val Glu Asp
50 55 60

Lys Val Ile Lys Asn His Phe Ala Ser Glu Tyr Ile Tyr Asn Lys Tyr
65 70 75 80

Lys Asp Glu Lys Thr Cys Gly Val Leu Glu Arg Asp Ala Gly Phe Gly
85 90 95

Ile Val Arg Ile Ala Glu Pro Val Gly Val Ile Ala Ala Val Val Pro
100 105 110

Thr Thr Asn Pro Thr Ser Thr Ala Ile Phe Lys Ser Leu Ile Ala Leu
115 120 125

Lys Thr Arg Asn Gly Ile Ile Phe Ser Pro His Pro Arg Ala Lys Lys
130 135 140

Ser Thr Ile Ala Ala Ala Lys Ile Val Leu Asp Ala Ala Val Lys Ala
145 150 155 160

Gly Ala Pro Glu Gly Ile Ile Gly Trp Ile Asp Glu Pro Ser Ile Glu
165 170 175

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Leu Ser Gln Val Val Met Gly Glu Ala Asn Leu Ile Leu Ala Thr Gly
            180                 185                 190

Gly Pro Gly Met Val Lys Ala Ala Tyr Ser Ser Gly Lys Pro Ala Val
        195                 200                 205

Gly Val Gly Pro Gly Asn Thr Pro Ala Val Ile Asp Glu Ser Ala Asp
    210                 215                 220

Ile Lys Met Ala Val Asn Ser Ile Leu Leu Ser Lys Thr Phe Asp Asn
225                 230                 235                 240

Gly Met Ile Cys Ala Ser Glu Gln Ser Val Ile Val Leu Asp Ser Ile
                245                 250                 255

Tyr Glu Glu Val Lys Lys Glu Phe Ala Tyr Arg Gly Ala Tyr Ile Leu
            260                 265                 270

Ser Lys Asp Glu Thr Asp Lys Val Gly Lys Ile Ile Leu Lys Asn Gly
        275                 280                 285

Ala Leu Asn Ala Gly Ile Val Gly Gln Pro Ala Phe Lys Ile Ala Gln
    290                 295                 300

Leu Ala Gly Val Asp Val Pro Glu Lys Ala Lys Val Leu Ile Gly Glu
305                 310                 315                 320

Val Glu Ser Val Glu Leu Glu Glu Pro Phe Ser His Glu Lys Leu Ser
                325                 330                 335

Pro Val Leu Ala Met Tyr Arg Ala Arg Asn Phe Glu Asp Ala Ile Ala
            340                 345                 350

Lys Thr Asp Lys Leu Val Arg Ser Gly Gly Phe Gly His Thr Ser Ser
        355                 360                 365

Leu Tyr Val Asn Pro Met Thr Glu Lys Ala Lys Val Glu Lys Phe Ser
    370                 375                 380

Thr Met Met Lys Thr Ser Arg Thr Ile Ile Asn Thr Pro Ser Ser Gln
385                 390                 395                 400

Gly Gly Ile Gly Asp Ile Tyr Asn Phe Lys Leu Ala Pro Ser Leu Thr
                405                 410                 415

Leu Gly Cys Gly Ser Trp Gly Gly Asn Ser Val Ser Glu Asn Val Gly
            420                 425                 430

Pro Lys His Leu Leu Asn Ile Lys Ser Val Ala Glu Arg Arg Glu Asn
        435                 440                 445
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```
Met Leu Trp Phe Arg Val Pro Glu Lys Val Tyr Phe Lys Tyr Gly Ser
    450                 455                 460

Leu Gly Val Ala Leu Lys Glu Leu Lys Val Met Asn Lys Lys Lys Val
465                 470                 475                 480

Phe Ile Val Thr Asp Lys Val Leu Tyr Gln Leu Gly Tyr Val Asp Lys
                485                 490                 495

Val Thr Lys Val Leu Glu Glu Leu Lys Ile Ser Tyr Lys Val Phe Thr
            500                 505                 510

Asp Val Glu Pro Asp Pro Thr Leu Ala Thr Ala Lys Lys Gly Ala Ala
        515                 520                 525

Glu Leu Leu Ser Tyr Glu Pro Asp Thr Ile Ile Ser Val Gly Gly Gly
    530                 535                 540

Ser Ala Met Asp Ala Ala Lys Ile Met Trp Val Met Tyr Glu His Pro
545                 550                 555                 560

Glu Val Lys Phe Glu Asp Leu Ala Met Arg Phe Met Asp Ile Arg Lys
                565                 570                 575

Arg Val Tyr Val Phe Pro Lys Met Gly Glu Lys Ala Met Met Ile Ser
            580                 585                 590

Val Ala Thr Ser Ala Gly Thr Gly Ser Glu Val Thr Pro Phe Ala Val
        595                 600                 605

Ile Thr Asp Glu Lys Thr Gly Ala Lys Tyr Pro Leu Ala Asp Tyr Glu
    610                 615                 620

Leu Thr Pro Asp Met Ala Ile Val Asp Ala Glu Leu Met Met Gly Met
625                 630                 635                 640

Pro Arg Gly Leu Thr Ala Ala Ser Gly Ile Asp Ala Leu Thr His Ala
                645                 650                 655

Leu Glu Ala Tyr Val Ser Ile Met Ala Thr Glu Phe Thr Asn Gly Leu
            660                 665                 670

Ala Leu Glu Ala Val Lys Leu Ile Phe Glu Tyr Leu Pro Lys Ala Tyr
        675                 680                 685

Thr Glu Gly Thr Thr Asn Val Lys Ala Arg Glu Lys Met Val His Ala
    690                 695                 700

Ser Cys Ile Ala Gly Met Ala Phe Ala Asn Ala Phe Leu Gly Val Cys
705                 710                 715                 720
```

His Ser Met Ala His Lys Leu Gly Ala Gln His His Ile Pro His Gly
725 730 735

Ile Ala Asn Ala Leu Met Ile Asp Glu Val Ile Lys Phe Asn Ala Val
740 745 750

Asp Asp Pro Ile Lys Gln Ala Ala Phe Pro Gln Tyr Glu Tyr Pro Asn
755 760 765

Ala Arg Tyr Arg Tyr Ala Gln Ile Ala Asp Cys Leu Asn Leu Gly Gly
770 775 780

Asn Thr Glu Glu Glu Lys Val Gln Leu Leu Ile Asn Ala Ile Asp Asp
785 790 795 800

Leu Lys Ala Lys Leu Asn Ile Pro Glu Thr Ile Lys Glu Ala Gly Val
805 810 815

Ser Glu Asp Lys Phe Tyr Ala Thr Leu Asp Lys Met Ser Glu Leu Ala
820 825 830

Phe Asp Asp Gln Cys Thr Gly Ala Asn Pro Arg Tyr Pro Leu Ile Ser
835 840 845

Glu Ile Lys Gln Met Tyr Ile Asn Val Phe Asp Lys Thr Glu Pro Ile
850 855 860

Val Glu Asp Glu Glu Lys
865 870

<210> 71
<211> 1554
<212> DNA
<213> C. ljundahlii

<400> 71
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ggaaaaattg cagcagacca aattgctgat tatactgaag aacaaattga taaaatccta 120

tgtaatatgg ttagggtagc agaagaaaat gcagtttgcc ttggtaaaat ggctgcagaa 180

gaaactggtt ttggaaaagc tgaagataag gcttataaga accatatggc tgctactaca 240

gtatataatt acatcaagga tatgaagact attggtgtta taaaagaaga taaaagtgaa 300

ggtgtaattg aatttgcaga accagttggt ttattaatgg gtattgtacc atctacaaat 360

ccaacatcta ctgttattta taaatcaatc attgcaatta aatcaagaaa tgcaattgta 420

ttctcaccac acccagctgc attaaaatgt tcaacaaaag caatagaact tatgcgtgat 480

gcagcagtag cagcaggagc tcctgcaaat gtaattggtg gtattgttac accatctata 540

caagctacaa atgaacttat gaaagctaaa gaagttgcta tgataattgc aactggaggc 600

cctggaatgg taaaggctgc atatagttca ggaacacctg caataggcgt tggtgctggt 660 aactctccat cctatattga aagaactgct gatgttcatc aatcagttaa agatataata 720

gctagtaaga gttttgacta tggtactatt tgtgcatccg agcagtctgt aattgcagaa 780

gaatgcaacc atgatgaaat agtagctgaa tttaagaaac aaggcggata tttcatgaca 840

gctgaagaaa ctgcaaaagt ttgcagcgta ctttttaaac ctggtacaca cagcatgagc 900

gctaagtttg taggaagagc tcctcaggtt atagcagaag ctgcaggttt cacagttcca 960

gaaggaacaa aagtattaat aggagaacaa ggcggagttg gtaatggtta ccctctatct 1020

tatgagaaac ttacaacagt acttgctttc tatacagtta aagattggca tgaagcatgt 1080

gagcttagta taagattact tcaaaatggt cttggacata caatgaacat tcatacaaat 1140

gatagagact tagtaatgaa gtttgctaaa aaaccagcat cccgtatctt agttaatact 1200

ggtggaagcc agggaggtac tggtgcaagc acaggattag cacctgcatt tacattaggt 1260

tgtggtacat ggggaggaag ctctgtttct gaaaatgtta ctccattaca tttaatcaat 1320

ataaagagag tagcatatgg tcttaaagat tgtactacat tagctgcaga cgatacaact 1380

ttcaatcatc ctgaactttg cggaagcaaa aatgacttag gattctgtgc tacaagccct 1440

gcagaatttg cagcaaagag caattgtgat agcactgctg cagatactac tgataatgat 1500

aaacttgcta gactcgtaag tgaattagta gctgcaatga agggagctaa ctaa 1554

<210> 72
<211> 517
<212> PRT
<213> c. ljungdahlii

<400> 72

Met Glu Asn Phe Asp Lys Asp Leu Arg Ser Ile Gln Glu Ala Arg Asp
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Leu Ala Arg Leu Gly Lys Ile Ala Ala Asp Gln Ile Ala Asp Tyr Thr
20 25 30

Glu Glu Gln Ile Asp Lys Ile Leu Cys Asn Met Val Arg Val Ala Glu
35 40 45

Glu Asn Ala Val Cys Leu Gly Lys Met Ala Ala Glu Glu Thr Gly Phe
50 55 60

Gly Lys Ala Glu Asp Lys Ala Tyr Lys Asn His Met Ala Ala Thr Thr
65 70 75 80

Val Tyr Asn Tyr Ile Lys Asp Met Lys Thr Ile Gly Val Ile Lys Glu
85 90 95

Asp Lys Ser Glu Gly Val Ile Glu Phe Ala Glu Pro Val Gly Leu Leu
100 105 110

Met Gly Ile Val Pro Ser Thr Asn Pro Thr Ser Thr Val Ile Tyr Lys
115 120 125

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Ser Ile Ile Ala Ile Lys Ser Arg Asn Ala Ile Val Phe Ser Pro His
    130                 135                 140

Pro Ala Ala Leu Lys Cys Ser Thr Lys Ala Ile Glu Leu Met Arg Asp
145                 150                 155                 160

Ala Ala Val Ala Ala Gly Ala Pro Ala Asn Val Ile Gly Gly Ile Val
                165                 170                 175

Thr Pro Ser Ile Gln Ala Thr Asn Glu Leu Met Lys Ala Lys Glu Val
            180                 185                 190

Ala Met Ile Ile Ala Thr Gly Gly Pro Gly Met Val Lys Ala Ala Tyr
        195                 200                 205

Ser Ser Gly Thr Pro Ala Ile Gly Val Gly Ala Gly Asn Ser Pro Ser
    210                 215                 220

Tyr Ile Glu Arg Thr Ala Asp Val His Gln Ser Val Lys Asp Ile Ile
225                 230                 235                 240

Ala Ser Lys Ser Phe Asp Tyr Gly Thr Ile Cys Ala Ser Glu Gln Ser
                245                 250                 255

Val Ile Ala Glu Glu Cys Asn His Asp Glu Ile Val Ala Glu Phe Lys
            260                 265                 270

Lys Gln Gly Gly Tyr Phe Met Thr Ala Glu Glu Thr Ala Lys Val Cys
        275                 280                 285

Ser Val Leu Phe Lys Pro Gly Thr His Ser Met Ser Ala Lys Phe Val
    290                 295                 300

Gly Arg Ala Pro Gln Val Ile Ala Glu Ala Ala Gly Phe Thr Val Pro
305                 310                 315                 320

Glu Gly Thr Lys Val Leu Ile Gly Glu Gln Gly Gly Val Gly Asn Gly
                325                 330                 335

Tyr Pro Leu Ser Tyr Glu Lys Leu Thr Thr Val Leu Ala Phe Tyr Thr
            340                 345                 350

Val Lys Asp Trp His Glu Ala Cys Glu Leu Ser Ile Arg Leu Leu Gln
        355                 360                 365

Asn Gly Leu Gly His Thr Met Asn Ile His Thr Asn Asp Arg Asp Leu
    370                 375                 380

Val Met Lys Phe Ala Lys Lys Pro Ala Ser Arg Ile Leu Val Asn Thr
385                 390                 395                 400
```

Gly Gly Ser Gln Gly Gly Thr Gly Ala Ser Thr Gly Leu Ala Pro Ala
405 410 415

Phe Thr Leu Gly Cys Gly Thr Trp Gly Gly Ser Ser Val Ser Glu Asn
420 425 430

Val Thr Pro Leu His Leu Ile Asn Ile Lys Arg Val Ala Tyr Gly Leu
435 440 445

Lys Asp Cys Thr Thr Leu Ala Ala Asp Asp Thr Thr Phe Asn His Pro
450 455 460

Glu Leu Cys Gly Ser Lys Asn Asp Leu Gly Phe Cys Ala Thr Ser Pro
465 470 475 480

Ala Glu Phe Ala Ala Lys Ser Asn Cys Asp Ser Thr Ala Ala Asp Thr
485 490 495

Thr Asp Asn Asp Lys Leu Ala Arg Leu Val Ser Glu Leu Val Ala Ala
500 505 510

Met Lys Gly Ala Asn
515

<210> 73
<211> 1497
<212> DNA
<213> c. ljungdahlii

<400> 73
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gctgcacgag cacaaaaaat gttagcaacc tttccacaag aaaagctaga tgagattgtt 120

gaacgtatgg cggaagaaat cggaaaacat acccgagagc ttgctgtaat gtcacaggat 180

gaaactggtt atggaaaatg gcaggataaa tgcatcaaaa accgatttgc ctgtgagtat 240

ttgccagcta agcttagagg aatgcgatgt gtaggtatta ttaatgaaaa tggtcaggat 300

aagaccatgg atgtaggtgt acctatgggt gtaattattg cattatgtcc tgcaactagt 360

ccggtttcta ctaccatata taaggcattg attgcaatta agtctggtaa tgcaattatc 420

ttttctccac atcctagagc aaaggagaca atttgtaagg cgcttgacat catgattcgt 480

gcagctgaag gatatgggct tccagaagga gctcttgcat acttacatac tgtgacgcct 540

agtggaacaa tcgaattgat gaaccatatt gcgacttctt tgattatgaa tacaggtgtt 600

cccgggatgc ttaaagcagc atataattct gggaaacctg ttatatatgg aggaactggt 660

aatggaccag catttattga acgtacagct gacatcaaac aggcggtaaa agatattatt 720

gctagtaaga cctttgataa cggaatagta ccatcagctg aacaatctat tgttgtagat 780

agctgtgttg catctgatgt taaacgtgag ttgcaaaata atggtgcata tttcatgaca 840

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gaggaggaag cacaaaaact aggttctctc tttttccgtt ctgatggcag tatggattca      900

gaaatggttg gcaaatccgc acaaagattg gctaaaaaag caggtttcag cattcctgaa      960

agtagcacag tgctaatttc agagcagaaa tatgtttctc aagataatcc ttattccaag     1020

gagaaacttt gtccggtact agcttactac attgaagatg attggatgca tgcatgtgaa     1080

aagtgtattg aactgctgtt aagtgagaga catggtcaca ctcttgttat acattcaaaa     1140

gacgaagatg taattcgcca gtttgcatta aaaaaacctg taggtaggat acttgttaat     1200

acgcctgctt cctttggtag tatgggtgct acaagtaatt tatttcctgc tttaacttta     1260

ggtagtggat cggcaggtaa aggtattacc tccgataatg tttcaccaat gaatcttatt     1320

tacgtccgca aagtcggata tggcgtacgg aatgtagaag agattgtcaa tactaatgga     1380

ttgtttacag aagaaaaaag tgatttgaat ggaatgacaa aaaagtcaga ctataatcca     1440

gaggatatac aaatgttaca gcatatttta aaaaaagcta tggaaaaaat taaatag        1497
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<210>  74
<211>  498
<212>  PRT
<213>  C. ljungdahlii

<400>  74

Met Asn Ile Ile Asp Asn Asp Leu Leu Ser Ile Gln Glu Ser Arg Ile
1               5                   10                  15

Leu Val Glu Asn Ala Ala Arg Ala Gln Lys Met Leu Ala Thr Phe Pro
            20                  25                  30

Gln Glu Lys Leu Asp Glu Ile Val Glu Arg Met Ala Glu Glu Ile Gly
        35                  40                  45

Lys His Thr Arg Glu Leu Ala Val Met Ser Gln Asp Glu Thr Gly Tyr
    50                  55                  60

Gly Lys Trp Gln Asp Lys Cys Ile Lys Asn Arg Phe Ala Cys Glu Tyr
65                  70                  75                  80

Leu Pro Ala Lys Leu Arg Gly Met Arg Cys Val Gly Ile Ile Asn Glu
                85                  90                  95

Asn Gly Gln Asp Lys Thr Met Asp Val Gly Val Pro Met Gly Val Ile
            100                 105                 110

Ile Ala Leu Cys Pro Ala Thr Ser Pro Val Ser Thr Thr Ile Tyr Lys
        115                 120                 125

Ala Leu Ile Ala Ile Lys Ser Gly Asn Ala Ile Ile Phe Ser Pro His
    130                 135                 140

Pro Arg Ala Lys Glu Thr Ile Cys Lys Ala Leu Asp Ile Met Ile Arg
145                 150                 155                 160
```

```
Ala Ala Glu Gly Tyr Gly Leu Pro Glu Gly Ala Leu Ala Tyr Leu His
                165                 170                 175

Thr Val Thr Pro Ser Gly Thr Ile Glu Leu Met Asn His Ile Ala Thr
            180                 185                 190

Ser Leu Ile Met Asn Thr Gly Val Pro Gly Met Leu Lys Ala Ala Tyr
        195                 200                 205

Asn Ser Gly Lys Pro Val Ile Tyr Gly Gly Thr Gly Asn Gly Pro Ala
    210                 215                 220

Phe Ile Glu Arg Thr Ala Asp Ile Lys Gln Ala Val Lys Asp Ile Ile
225                 230                 235                 240

Ala Ser Lys Thr Phe Asp Asn Gly Ile Val Pro Ser Ala Glu Gln Ser
                245                 250                 255

Ile Val Val Asp Ser Cys Val Ala Ser Asp Val Lys Arg Glu Leu Gln
            260                 265                 270

Asn Asn Gly Ala Tyr Phe Met Thr Glu Glu Glu Ala Gln Lys Leu Gly
        275                 280                 285

Ser Leu Phe Phe Arg Ser Asp Gly Ser Met Asp Ser Glu Met Val Gly
    290                 295                 300

Lys Ser Ala Gln Arg Leu Ala Lys Lys Ala Gly Phe Ser Ile Pro Glu
305                 310                 315                 320

Ser Ser Thr Val Leu Ile Ser Glu Gln Lys Tyr Val Ser Gln Asp Asn
                325                 330                 335

Pro Tyr Ser Lys Glu Lys Leu Cys Pro Val Leu Ala Tyr Tyr Ile Glu
            340                 345                 350

Asp Asp Trp Met His Ala Cys Glu Lys Cys Ile Glu Leu Leu Leu Ser
        355                 360                 365

Glu Arg His Gly His Thr Leu Val Ile His Ser Lys Asp Glu Asp Val
    370                 375                 380

Ile Arg Gln Phe Ala Leu Lys Lys Pro Val Gly Arg Ile Leu Val Asn
385                 390                 395                 400

Thr Pro Ala Ser Phe Gly Ser Met Gly Ala Thr Ser Asn Leu Phe Pro
                405                 410                 415

Ala Leu Thr Leu Gly Ser Gly Ser Ala Gly Lys Gly Ile Thr Ser Asp
            420                 425                 430
```

Asn Val Ser Pro Met Asn Leu Ile Tyr Val Arg Lys Val Gly Tyr Gly
435 440 445

Val Arg Asn Val Glu Glu Ile Val Asn Thr Asn Gly Leu Phe Thr Glu
450 455 460

Glu Lys Ser Asp Leu Asn Gly Met Thr Lys Lys Ser Asp Tyr Asn Pro
465 470 475 480

Glu Asp Ile Gln Met Leu Gln His Ile Leu Lys Lys Ala Met Glu Lys
485 490 495

Ile Lys

<210> 75
<211> 1167
<212> DNA
<213> c. ljungdahlii

<400> 75
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aaagacctag atggaaaaaa agctgttatt gtcgtaggtg gtggatccat gaaacgattt 120
ggattccttg ataaggtagt aaactactta aaagaagcag gtattgaatc aaaattaata 180
gaaggagttg aaccagatcc atctgtagaa actgttatga atggcgctaa actaatgaga 240
gaatatgaac cagatttaat agtatcaata ggtggaggtt caccaattga cgcagcaaaa 300
gctatgtgga tattctatga ataccctgag tttactttta aagaggctgt ggttcctttt 360
ggtcttccta aattaagaca aaaagcaaca tttatagcta taccttctac aagtggtact 420
gcaacagaag taacggcatt ttctgtaata acagactata aagctaaaat taaatatcct 480
ttagctgact tcaatttaac accagatata gctataattg atccagcatt agctcaaaca 540
atgccaccta aattaactgc acatactgga atggatgcac ttacccatgc tattgaagca 600
tatgttgcag gacttcattc agttttctca gatcctcttg ctattcaagc tatagttatg 660
gtaaatcagt atttaattaa atcttacaat gaagataaag aagctagaaa ccaaatgcat 720
ttagctcaat gtttagctgg aatggcattt tcaaatgcac ttcttggaat aactcacagt 780
ttagcacata aaacaggtgc agtattccat atccctcatg gatgtgccaa tgcaatatat 840
cttccttatg ttatagattt caataaaaaa gcttgtgcac caagatatgc tgaaatagct 900
aggagtctta aacttccagg aaatactgat gatgaattag tagattcatt aaccaacatg 960
attaaagata tgaataagag tatggatatt cctttaacat taaaagatta cggagtagat 1020
gaaaaagaat ttaaagatag tgaagatttt atagctcaca atgccgtatt agatgcctgc 1080
actggatcaa atcctagaag tataaatgat actgaaatga aaaagttatt agaatacatc 1140
tattatggta aaaaggttga tttttaa 1167

SequenceListing

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<210>  76
<211>  388
<212>  PRT
<213>  c. ljundahlii

<400>  76

Met Ala Arg Phe Thr Leu Pro Arg Asp Ile Tyr Phe Gly Glu Asn Ser
1               5                   10                  15

Leu Glu Thr Leu Lys Asp Leu Asp Gly Lys Lys Ala Val Ile Val Val
            20                  25                  30

Gly Gly Gly Ser Met Lys Arg Phe Gly Phe Leu Asp Lys Val Val Asn
        35                  40                  45

Tyr Leu Lys Glu Ala Gly Ile Glu Ser Lys Leu Ile Glu Gly Val Glu
    50                  55                  60

Pro Asp Pro Ser Val Glu Thr Val Met Asn Gly Ala Lys Leu Met Arg
65                  70                  75                  80

Glu Tyr Glu Pro Asp Leu Ile Val Ser Ile Gly Gly Gly Ser Pro Ile
                85                  90                  95

Asp Ala Ala Lys Ala Met Trp Ile Phe Tyr Glu Tyr Pro Glu Phe Thr
            100                 105                 110

Phe Lys Glu Ala Val Val Pro Phe Gly Leu Pro Lys Leu Arg Gln Lys
        115                 120                 125

Ala Thr Phe Ile Ala Ile Pro Ser Thr Ser Gly Thr Ala Thr Glu Val
    130                 135                 140

Thr Ala Phe Ser Val Ile Thr Asp Tyr Lys Ala Lys Ile Lys Tyr Pro
145                 150                 155                 160

Leu Ala Asp Phe Asn Leu Thr Pro Asp Ile Ala Ile Ile Asp Pro Ala
                165                 170                 175

Leu Ala Gln Thr Met Pro Pro Lys Leu Thr Ala His Thr Gly Met Asp
            180                 185                 190

Ala Leu Thr His Ala Ile Glu Ala Tyr Val Ala Gly Leu His Ser Val
        195                 200                 205

Phe Ser Asp Pro Leu Ala Ile Gln Ala Ile Val Met Val Asn Gln Tyr
    210                 215                 220

Leu Ile Lys Ser Tyr Asn Glu Asp Lys Glu Ala Arg Asn Gln Met His
225                 230                 235                 240
```

```
Leu Ala Gln Cys Leu Ala Gly Met Ala Phe Ser Asn Ala Leu Leu Gly
                245                 250                 255

Ile Thr His Ser Leu Ala His Lys Thr Gly Ala Val Phe His Ile Pro
            260                 265                 270

His Gly Cys Ala Asn Ala Ile Tyr Leu Pro Tyr Val Ile Asp Phe Asn
        275                 280                 285

Lys Lys Ala Cys Ala Pro Arg Tyr Ala Glu Ile Ala Arg Ser Leu Lys
    290                 295                 300

Leu Pro Gly Asn Thr Asp Asp Glu Leu Val Asp Ser Leu Thr Asn Met
305                 310                 315                 320

Ile Lys Asp Met Asn Lys Ser Met Asp Ile Pro Leu Thr Leu Lys Asp
                325                 330                 335

Tyr Gly Val Asp Glu Lys Glu Phe Lys Asp Ser Glu Asp Phe Ile Ala
            340                 345                 350

His Asn Ala Val Leu Asp Ala Cys Thr Gly Ser Asn Pro Arg Ser Ile
        355                 360                 365

Asn Asp Thr Glu Met Lys Lys Leu Leu Glu Tyr Ile Tyr Tyr Gly Lys
    370                 375                 380

Lys Val Asp Phe
385
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<210>  77
<211>  1167
<212>  DNA
<213>  c. ljundahlii

<400>  77
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aaaaatttag atggaaataa agcagtagtt gttgtaggtg gggatctat gaagagattt      120

ggattcttag ccaaagttga aaaatactta aaagaaactg gtatggaagt taaattaata      180

gaaggtgttg agcctgatcc gtctgttgat actgttatga atggcgctaa aataatgaga      240

gactttaacc cagattggat agtatcaata ggtggaggat ctcccataga tgctgctaaa      300

gcaatgtgga tattttatga ataccccgac tttacatttg aaaaagcggt agtccctttt      360

ggaattccta aattaaggca gaaggcacaa tttgttgcta taccttctac aagtggaaca      420

gcaactgaag taacatcatt ttctgtaata acagactata aagctaaaat aaaatatcct      480

cttgcagatt ttaaccttac ccctgatata gctataatag atccgtctct tgcagaaaca      540

atgcccaaaa agcttacagc acacactgga atggatgcac ttactcacgc aatagaagca      600

tatgtagcaa gtttacattc agatttctca gatccacttg ctatgcatgc tataaccatg      660
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attcataaat atttattgaa atcctatgaa gaagataaag aagctagagg acatatgcat      720
atagcccaat gtctagctgg gatggcattt tcaaatgctc tccttggaat aactcatagt      780
atagcacata aaactggtgc agtatttcac atacctcatg ggtgtgctaa tgccatatac      840
ttaccttatg ttatagattt taacaagaaa gcttgttcag aaagatatgc taaaatagcc      900
aaaaagctgc atctatcagg aaatagtgaa gatgagctaa tagattcatt aactgaaatg      960
attcgtacta tgaacaaaaa gatggatatt cctctcacca taaaagatta tggtataagc     1020
gaaaacgatt ttaatgaaaa cctagatttt atagctcaca atgccatgat ggatgcctgc     1080
actggatcca atcctagagc aataactgag gaagaaatga aaaagctctt gcagtatatg     1140
tataatgggc aaaaggttaa tttctag                                         1167
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<210>  78
<211>  388
<212>  PRT
<213>  c. ljundahlii

<400>  78
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Met Gly Arg Phe Thr Leu Pro Arg Asp Ile Tyr Phe Gly Glu Asn Ala
1               5                   10                  15

Leu Glu Asn Leu Lys Asn Leu Asp Gly Asn Lys Ala Val Val Val Val
            20                  25                  30

Gly Gly Gly Ser Met Lys Arg Phe Gly Phe Leu Ala Lys Val Glu Lys
        35                  40                  45

Tyr Leu Lys Glu Thr Gly Met Glu Val Lys Leu Ile Glu Gly Val Glu
    50                  55                  60

Pro Asp Pro Ser Val Asp Thr Val Met Asn Gly Ala Lys Ile Met Arg
65                  70                  75                  80

Asp Phe Asn Pro Asp Trp Ile Val Ser Ile Gly Gly Gly Ser Pro Ile
                85                  90                  95

Asp Ala Ala Lys Ala Met Trp Ile Phe Tyr Glu Tyr Pro Asp Phe Thr
            100                 105                 110

Phe Glu Lys Ala Val Val Pro Phe Gly Ile Pro Lys Leu Arg Gln Lys
        115                 120                 125

Ala Gln Phe Val Ala Ile Pro Ser Thr Ser Gly Thr Ala Thr Glu Val
    130                 135                 140

Thr Ser Phe Ser Val Ile Thr Asp Tyr Lys Ala Lys Ile Lys Tyr Pro
145                 150                 155                 160

Leu Ala Asp Phe Asn Leu Thr Pro Asp Ile Ala Ile Ile Asp Pro Ser
                165                 170                 175
```

```
Leu Ala Glu Thr Met Pro Lys Lys Leu Thr Ala His Thr Gly Met Asp
            180                 185                 190

Ala Leu Thr His Ala Ile Glu Ala Tyr Val Ala Ser Leu His Ser Asp
        195                 200                 205

Phe Ser Asp Pro Leu Ala Met His Ala Ile Thr Met Ile His Lys Tyr
    210                 215                 220

Leu Leu Lys Ser Tyr Glu Glu Asp Lys Glu Ala Arg Gly His Met His
225                 230                 235                 240

Ile Ala Gln Cys Leu Ala Gly Met Ala Phe Ser Asn Ala Leu Leu Gly
                245                 250                 255

Ile Thr His Ser Ile Ala His Lys Thr Gly Ala Val Phe His Ile Pro
            260                 265                 270

His Gly Cys Ala Asn Ala Ile Tyr Leu Pro Tyr Val Ile Asp Phe Asn
        275                 280                 285

Lys Lys Ala Cys Ser Glu Arg Tyr Ala Lys Ile Ala Lys Lys Leu His
    290                 295                 300

Leu Ser Gly Asn Ser Glu Asp Glu Leu Ile Asp Ser Leu Thr Glu Met
305                 310                 315                 320

Ile Arg Thr Met Asn Lys Lys Met Asp Ile Pro Leu Thr Ile Lys Asp
                325                 330                 335

Tyr Gly Ile Ser Glu Asn Asp Phe Asn Glu Asn Leu Asp Phe Ile Ala
            340                 345                 350

His Asn Ala Met Met Asp Ala Cys Thr Gly Ser Asn Pro Arg Ala Ile
        355                 360                 365

Thr Glu Glu Glu Met Lys Lys Leu Leu Gln Tyr Met Tyr Asn Gly Gln
    370                 375                 380

Lys Val Asn Phe
385

<210>  79
<211>  1167
<212>  DNA
<213>  C. ljundahlii

<400>  79
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aaaacgttaa aaggtaagaa agctgtagta gttgttggag gaggatccat gaagagattc       120
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ggtttccttg acaaggtaga agaatactta aaagaagcaa acatagaagt taaactaata      180

gaaggtgttg aaccagatcc gtctgtggaa accgttatga aaggtgccaa aataatgaca      240

gaatttgggc cagattggat agttgctatt ggaggaggtt caccaataga tgctgcaaag      300

gctatgtggc tattttatga atatccagat tttacttta aacaagcaat tgttccgttt      360

ggattaccag aattaagaca aaaagctaaa tttgtagcta tagcttctac tagtggaaca      420

gctactgaag ttacttcatt ttcagtaata actgattata aagctaaaat aaagtatcct      480

ttagctgact tcaatttgac accggatata gctatagttg atccagcatt agcccagaca      540

atgccaccta aattaactgc acatactggt atggatgcat taactcatgc actagaagct      600

tatgtagcat cagctagatc agatatttca gatccacttg caatacattc cataattatg      660

acaagggata acttacttaa atcctataag ggtgataaag atgctagaaa taagatgcat      720

atatcacaat gtttagcagg tatggcattt tctaatgcac ttcttggtat aactcatagt      780

ttagcacata aaacaggagc tgtatggcac ataccacatg gatgcgctaa tgcaatatat      840

cttccatatg ttttagattt taataaaaaa gcttgctcag atagatatgc taatatagct      900

aaaatattag gacttaaagg aactactgaa gatgaattgg tagattctct agttaaaatg      960

gtacaagata tggataagga attgaatata cctttgacct taaaagatta tggtataagc     1020

aaagatgatt tcaattcaaa tgttgatttt atagcaaaga atgcgctctt agatgcatgt     1080

acaggagcta atccaaggcc tatagatttt gatcaaatga aaaagatact tcaatgtata     1140

tatgatggaa aaaaggtaac tttttaa                                         1167

<210>  80
<211>  388
<212>  PRT
<213>  c. ljungdahlii

<400>  80

Met Glu Arg Phe Thr Leu Pro Arg Asp Ile Tyr Phe Gly Glu Asp Ala
1               5                   10                  15


Leu Gly Ala Leu Lys Thr Leu Lys Gly Lys Lys Ala Val Val Val Val
            20                  25                  30


Gly Gly Gly Ser Met Lys Arg Phe Gly Phe Leu Asp Lys Val Glu Glu
        35                  40                  45


Tyr Leu Lys Glu Ala Asn Ile Glu Val Lys Leu Ile Glu Gly Val Glu
    50                  55                  60


Pro Asp Pro Ser Val Glu Thr Val Met Lys Gly Ala Lys Ile Met Thr
65                  70                  75                  80


Glu Phe Gly Pro Asp Trp Ile Val Ala Ile Gly Gly Gly Ser Pro Ile
                85                  90                  95
```

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Asp Ala Ala Lys Ala Met Trp Leu Phe Tyr Glu Tyr Pro Asp Phe Thr
            100                 105                 110

Phe Lys Gln Ala Ile Val Pro Phe Gly Leu Pro Glu Leu Arg Gln Lys
        115                 120                 125

Ala Lys Phe Val Ala Ile Ala Ser Thr Ser Gly Thr Ala Thr Glu Val
    130                 135                 140

Thr Ser Phe Ser Val Ile Thr Asp Tyr Lys Ala Lys Ile Lys Tyr Pro
145                 150                 155                 160

Leu Ala Asp Phe Asn Leu Thr Pro Asp Ile Ala Ile Val Asp Pro Ala
                165                 170                 175

Leu Ala Gln Thr Met Pro Pro Lys Leu Thr Ala His Thr Gly Met Asp
            180                 185                 190

Ala Leu Thr His Ala Leu Glu Ala Tyr Val Ala Ser Ala Arg Ser Asp
        195                 200                 205

Ile Ser Asp Pro Leu Ala Ile His Ser Ile Ile Met Thr Arg Asp Asn
    210                 215                 220

Leu Leu Lys Ser Tyr Lys Gly Asp Lys Asp Ala Arg Asn Lys Met His
225                 230                 235                 240

Ile Ser Gln Cys Leu Ala Gly Met Ala Phe Ser Asn Ala Leu Leu Gly
                245                 250                 255

Ile Thr His Ser Leu Ala His Lys Thr Gly Ala Val Trp His Ile Pro
            260                 265                 270

His Gly Cys Ala Asn Ala Ile Tyr Leu Pro Tyr Val Leu Asp Phe Asn
        275                 280                 285

Lys Lys Ala Cys Ser Asp Arg Tyr Ala Asn Ile Ala Lys Ile Leu Gly
    290                 295                 300

Leu Lys Gly Thr Thr Glu Asp Glu Leu Val Asp Ser Leu Val Lys Met
305                 310                 315                 320

Val Gln Asp Met Asp Lys Glu Leu Asn Ile Pro Leu Thr Leu Lys Asp
                325                 330                 335

Tyr Gly Ile Ser Lys Asp Asp Phe Asn Ser Asn Val Asp Phe Ile Ala
            340                 345                 350

Lys Asn Ala Leu Leu Asp Ala Cys Thr Gly Ala Asn Pro Arg Pro Ile
        355                 360                 365
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Asp Phe Asp Gln Met Lys Lys Ile Leu Gln Cys Ile Tyr Asp Gly Lys
370 375 380

Lys Val Thr Phe
385

<210> 81
<211> 1176
<212> DNA
<213> c. ljundahlii

<400> 81
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ggaggaagca taaaaagatc tggtctatat gatagagtta taaagtcctt aaaagaaaat 180

ggaattgaat ttatagaact tccaggaatt aaacctaatc caagattagg acctgttaaa 240

gaaggtataa gactatgtag agaaaataat ataaaatttg tactatctgt aggaggagga 300

agttcagcag atacggctaa agctattgct gtaggagtac cttataaagg agacgtatgg 360

gatttttata cgggcaaagc tgaagtgaaa gaggctcttc ctgtaggagt tgtaataaca 420

ttacctgcta caggtacaga atctagtaat agttctgtta ttatgaatga agatggttgg 480

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ataatggaaa gatattttac aaatgtgaaa catgtagata taactgatag gctttgcgaa 660

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gatgctaggg cagaaattat gtggaccggt actatagctc ataatgatgt gcttagtgcg 780

ggtagaatag gtgattgggc ttctcacaaa attgaacatg aattgagtgg ggaaacagac 840

attgcccatg gagcaggact tgcaattgta tttcctgcat ggatgaaata tgtatataaa 900

cacgatatca atagatttgt acaatttgca gtaagggtat gggatgtaga tttatcttat 960

agttcctgcg aagatattgt acttgaaggc ataaggagaa tgacagcatt tttcaagagc 1020

atggggttac ctgtaacttt aaaagaagga agtataggag aagataaaat tgaagaaatg 1080

gctaataagt gcacggataa tggaactaaa actgtaggac aatttgtaaa attaaataaa 1140

gatgatattg taaaaatatt aaatttagct aaataa 1176

<210> 82
<211> 391
<212> PRT
<213> c. ljundahlii

<400> 82

Met Glu Asn Phe Ile Phe Lys Asn Ala Thr Glu Ile Ile Phe Gly Lys
1 5 10 15

Asp Thr Glu Asn Leu Val Gly Ser Lys Val Lys Glu Tyr Ser Lys Ser
20 25 30

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Asp Lys Ile Leu Phe Cys Tyr Gly Gly Gly Ser Ile Lys Arg Ser Gly
        35                  40                  45

Leu Tyr Asp Arg Val Ile Lys Ser Leu Lys Glu Asn Gly Ile Glu Phe
    50                  55                  60

Ile Glu Leu Pro Gly Ile Lys Pro Asn Pro Arg Leu Gly Pro Val Lys
65                  70                  75                  80

Glu Gly Ile Arg Leu Cys Arg Glu Asn Asn Ile Lys Phe Val Leu Ser
                85                  90                  95

Val Gly Gly Gly Ser Ser Ala Asp Thr Ala Lys Ala Ile Ala Val Gly
            100                 105                 110

Val Pro Tyr Lys Gly Asp Val Trp Asp Phe Tyr Thr Gly Lys Ala Glu
        115                 120                 125

Val Lys Glu Ala Leu Pro Val Gly Val Val Ile Thr Leu Pro Ala Thr
    130                 135                 140

Gly Thr Glu Ser Ser Asn Ser Ser Val Ile Met Asn Glu Asp Gly Trp
145                 150                 155                 160

Phe Lys Lys Gly Leu Asn Thr Val Leu Ile Arg Pro Ala Phe Ser Ile
                165                 170                 175

Met Asn Pro Glu Leu Thr Phe Thr Leu Pro Glu Tyr Gln Thr Ala Cys
            180                 185                 190

Gly Ala Cys Asp Ile Met Ala His Ile Met Glu Arg Tyr Phe Thr Asn
        195                 200                 205

Val Lys His Val Asp Ile Thr Asp Arg Leu Cys Glu Ala Ala Leu Arg
    210                 215                 220

Asn Val Ile Asn Asn Ala Pro Ile Val Leu Lys Asp Pro Lys Asn Tyr
225                 230                 235                 240

Asp Ala Arg Ala Glu Ile Met Trp Thr Gly Thr Ile Ala His Asn Asp
                245                 250                 255

Val Leu Ser Ala Gly Arg Ile Gly Asp Trp Ala Ser His Lys Ile Glu
            260                 265                 270

His Glu Leu Ser Gly Glu Thr Asp Ile Ala His Gly Ala Gly Leu Ala
        275                 280                 285

Ile Val Phe Pro Ala Trp Met Lys Tyr Val Tyr Lys His Asp Ile Asn
    290                 295                 300
```

Arg Phe Val Gln Phe Ala Val Arg Val Trp Asp Val Asp Leu Ser Tyr
305 310 315 320

Ser Ser Cys Glu Asp Ile Val Leu Glu Gly Ile Arg Arg Met Thr Ala
325 330 335

Phe Phe Lys Ser Met Gly Leu Pro Val Thr Leu Lys Glu Gly Ser Ile
340 345 350

Gly Glu Asp Lys Ile Glu Glu Met Ala Asn Lys Cys Thr Asp Asn Gly
355 360 365

Thr Lys Thr Val Gly Gln Phe Val Lys Leu Asn Lys Asp Asp Ile Val
370 375 380

Lys Ile Leu Asn Leu Ala Lys
385 390

<210> 83
<211> 1149
<212> DNA
<213> c. ljungdahlii

<400> 83
atggaagaca agtttgaaaa ttttaatttg aaatccaaga tttattttaa tagggaatct 60

attcaacttt tagagcaagt cactggttct cgagcattta ttgttgcaga tgctattatg 120

ggaaaacttg gatatcttca aaaagtaata gattacctaa gcaaagctgg aataagttcc 180

gttgttttta cgggggtaca ccctgatcca gacgtcaatg taattgcaga tgcaatgaaa 240

ttgtacaaaa aaagcgacgc agatgttctc gtagcactag gtggaggatc cagtattgat 300

accgctaagg gaataatgta ttttgcatgt aatttaggaa aagcaatggg ccaagaaatg 360

aaaaaacctc tatttattgc aattccatca acaagtggta caggctctga agtaacaaac 420

tttactgtta ttacttctca gaaagaaaag gtatgcatta tagatgattt tattgcacca 480

gatgttgcaa tacttgactc aagttgtatt gatggtctgc ctcagcgtat tgtagcagat 540

actggtatag atgttctagt tcattctatt gaagcctatg tttccaaaaa agcaactgac 600

tttacagacg ctcttgctga aaaagcagtt aaattaattt ttgagaatct tccaaaaatt 660

tataacgata gtaaggattc cgaagctcga gatcatgttc aaaacgcttc ctgtatagca 720

ggaatagcat ttacaaatgc tggtcttgga attaatcaca gcttggctca tgctatgggt 780

ggatctttcc acattcctca cggccgatcc aatgcacttc tacttaatgc agtaatggaa 840

tacaacgcta gcttggttgg aaatgcaagc gaacatgcta tggaaaaata cgcaaaacta 900

gcatcaattc tacaccttcc agctcgaaca actcgcgaag gcgctgtaag ttttattgaa 960

gctgtagata aattaataaa atccctaggt gttgaagata atattcgatc tcttgggatt 1020

aaagaagatg agtttcaaag tgctctaaat catatggcag aaacagcaat gcaagataga 1080

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tgcactccaa ctaatcctag aaaaccttct aaagaagaac ttatacatat ttatcaaaaa      1140

tgttattaa                                                              1149


<210>  84
<211>  382
<212>  PRT
<213>  c. lungdahlii

<400>  84

Met Glu Asp Lys Phe Glu Asn Phe Asn Leu Lys Ser Lys Ile Tyr Phe
1               5                   10                  15


Asn Arg Glu Ser Ile Gln Leu Leu Glu Gln Val Thr Gly Ser Arg Ala
            20                  25                  30


Phe Ile Val Ala Asp Ala Ile Met Gly Lys Leu Gly Tyr Leu Gln Lys
        35                  40                  45


Val Ile Asp Tyr Leu Ser Lys Ala Gly Ile Ser Ser Val Val Phe Thr
    50                  55                  60


Gly Val His Pro Asp Pro Asp Val Asn Val Ile Ala Asp Ala Met Lys
65                  70                  75                  80


Leu Tyr Lys Lys Ser Asp Ala Asp Val Leu Val Ala Leu Gly Gly Gly
                85                  90                  95


Ser Ser Ile Asp Thr Ala Lys Gly Ile Met Tyr Phe Ala Cys Asn Leu
            100                 105                 110


Gly Lys Ala Met Gly Gln Glu Met Lys Lys Pro Leu Phe Ile Ala Ile
        115                 120                 125


Pro Ser Thr Ser Gly Thr Gly Ser Glu Val Thr Asn Phe Thr Val Ile
    130                 135                 140


Thr Ser Gln Lys Glu Lys Val Cys Ile Ile Asp Asp Phe Ile Ala Pro
145                 150                 155                 160


Asp Val Ala Ile Leu Asp Ser Ser Cys Ile Asp Gly Leu Pro Gln Arg
                165                 170                 175


Ile Val Ala Asp Thr Gly Ile Asp Val Leu Val His Ser Ile Glu Ala
            180                 185                 190


Tyr Val Ser Lys Lys Ala Thr Asp Phe Thr Asp Ala Leu Ala Glu Lys
        195                 200                 205


Ala Val Lys Leu Ile Phe Glu Asn Leu Pro Lys Ile Tyr Asn Asp Ser
    210                 215                 220
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Lys Asp Ser Glu Ala Arg Asp His Val Gln Asn Ala Ser Cys Ile Ala
225 230 235 240

Gly Ile Ala Phe Thr Asn Ala Gly Leu Gly Ile Asn His Ser Leu Ala
245 250 255

His Ala Met Gly Gly Ser Phe His Ile Pro His Gly Arg Ser Asn Ala
260 265 270

Leu Leu Leu Asn Ala Val Met Glu Tyr Asn Ala Ser Leu Val Gly Asn
275 280 285

Ala Ser Glu His Ala Met Glu Lys Tyr Ala Lys Leu Ala Ser Ile Leu
290 295 300

His Leu Pro Ala Arg Thr Thr Arg Glu Gly Ala Val Ser Phe Ile Glu
305 310 315 320

Ala Val Asp Lys Leu Ile Lys Ser Leu Gly Val Glu Asp Asn Ile Arg
325 330 335

Ser Leu Gly Ile Lys Glu Asp Glu Phe Gln Ser Ala Leu Asn His Met
340 345 350

Ala Glu Thr Ala Met Gln Asp Arg Cys Thr Pro Thr Asn Pro Arg Lys
355 360 365

Pro Ser Lys Glu Glu Leu Ile His Ile Tyr Gln Lys Cys Tyr
370 375 380

<210> 85
<211> 1002
<212> DNA
<213> c. ljungdahlii

<400> 85
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gctgaaggag aagaagaaag aactcttcaa gcttgtgaaa aaataattaa agagggtatt 120

gcaaatttaa tccttgtagg gaatgaaaag gtaataaaag aaaaagcgtc aaaattaggt 180

gtaagtttaa atggagcaga aatagtagat ccagagactt cagataaact aaaggcatat 240

gcagatgctt tttatgaatt gagaaagaag aagggaataa cgccagaaaa agcggataaa 300

atagtaagag atccaatata ctttgctaca atgatggtta aacttggaga tgcagatgga 360

ttggtttcag gtgcggttca tactacaggt gatcttttga gaccaggact tcaaatagta 420

aagacagctc caggtacatc agtagtttcc agtacattta taatggaagt accaaattgt 480

gagtatggtg acaatggtgt acttctattt gctgattgtg ctgtaaatcc atgcccagat 540

agtgatcaat tggcttcaat tgcaataagt acagcagaaa ctgcaaagaa cttatgtgga 600

atggatccaa aagtagcaat gctttcattt tctactaagg gaagtgcaaa acacgaatta 660

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gtagacaaag ttagaaatgc tgtagagatt gcaaaaaaag ctaaaccaga tttaagttta      720

gacggagaat tacaattaga tgcctctatc gtagaaaagg ttgcaagttt aaaggctcct      780

ggaagtgaag tagcaggaaa agcaaatgta cttgtatttc cagatctcca agcaggaaat      840

ataggctata aactcgttca aagatttgca aaagcagatg ctataggacc tgtatgccaa      900

ggatttgcaa aacctataaa tgatttgtca agaggatgta attctgatga tatagtaaat      960

gtagtagctg taacagcagt tcaagcacaa gctcaaaagt aa                        1002
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<210>  86
<211>  333
<212>  PRT
<213>  C. ljungdahlii

<400>  86

Met Lys Leu Met Glu Lys Ile Trp Ser Lys Ala Lys Glu Asp Lys Lys
1               5                   10                  15

Lys Ile Val Leu Ala Glu Gly Glu Glu Glu Arg Thr Leu Gln Ala Cys
            20                  25                  30

Glu Lys Ile Ile Lys Glu Gly Ile Ala Asn Leu Ile Leu Val Gly Asn
        35                  40                  45

Glu Lys Val Ile Lys Glu Lys Ala Ser Lys Leu Gly Val Ser Leu Asn
    50                  55                  60

Gly Ala Glu Ile Val Asp Pro Glu Thr Ser Asp Lys Leu Lys Ala Tyr
65                  70                  75                  80

Ala Asp Ala Phe Tyr Glu Leu Arg Lys Lys Lys Gly Ile Thr Pro Glu
                85                  90                  95

Lys Ala Asp Lys Ile Val Arg Asp Pro Ile Tyr Phe Ala Thr Met Met
            100                 105                 110

Val Lys Leu Gly Asp Ala Asp Gly Leu Val Ser Gly Ala Val His Thr
        115                 120                 125

Thr Gly Asp Leu Leu Arg Pro Gly Leu Gln Ile Val Lys Thr Ala Pro
    130                 135                 140

Gly Thr Ser Val Val Ser Ser Thr Phe Ile Met Glu Val Pro Asn Cys
145                 150                 155                 160

Glu Tyr Gly Asp Asn Gly Val Leu Leu Phe Ala Asp Cys Ala Val Asn
                165                 170                 175

Pro Cys Pro Asp Ser Asp Gln Leu Ala Ser Ile Ala Ile Ser Thr Ala
            180                 185                 190
```

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Glu Thr Ala Lys Asn Leu Cys Gly Met Asp Pro Lys Val Ala Met Leu
        195                 200                 205

Ser Phe Ser Thr Lys Gly Ser Ala Lys His Glu Leu Val Asp Lys Val
    210                 215                 220

Arg Asn Ala Val Glu Ile Ala Lys Lys Ala Lys Pro Asp Leu Ser Leu
225                 230                 235                 240

Asp Gly Glu Leu Gln Leu Asp Ala Ser Ile Val Glu Lys Val Ala Ser
                245                 250                 255

Leu Lys Ala Pro Gly Ser Glu Val Ala Gly Lys Ala Asn Val Leu Val
            260                 265                 270

Phe Pro Asp Leu Gln Ala Gly Asn Ile Gly Tyr Lys Leu Val Gln Arg
        275                 280                 285

Phe Ala Lys Ala Asp Ala Ile Gly Pro Val Cys Gln Gly Phe Ala Lys
    290                 295                 300

Pro Ile Asn Asp Leu Ser Arg Gly Cys Asn Ser Asp Asp Ile Val Asn
305                 310                 315                 320

Val Val Ala Val Thr Ala Val Gln Ala Gln Ala Gln Lys
                325                 330


<210>  87
<211>  1197
<212>  DNA
<213>  C. ljungdahlii

<400>  87
atgaaaatat tagtagtaaa ctgtggaagt tcatctttaa aatatcaact tattgatatg      60

caagatgaaa gtgttgtagc aaagggtctt gtagaaagaa taggaatgga cggttcaatt     120

ttaacacaca aagttaatgg agaaaagttt gttacagagc aaacaatgga agaccacaaa     180

gttgctatac aattagtatt aaatgctctt gtagataaaa aacatggtgt aataaaagac     240

atgtcagaaa tatccgctgt aggacataga gtcttgcacg gtggaaagaa atatgcagca     300

tccattctta ttgacgaaaa tgtaatgaaa gcaatagaag aatgtatccc actaggacca     360

ctacataatc cagctaatat aatgggaata gatgcttgta aaaaattaat gccaaatact     420

ccaatggtag cagtatttga tacagcattt catcagacaa tgccagatta tgcttatact     480

tatgcaatac cttatgatat atctgaaaag tatgatatca gaaaatatgg ttttcatgga     540

acttctcata gattcgtttc aattgaagca gctaaattat taaagaaaga tccaaaagat     600

cttaagttaa taacttgtca tttaggaaat ggagctagca tatgtgcagt aaaccaagga     660

aaagcagtag atacaacgat gggacttact cctcttgcag gacttgtaat gggaactaga     720

tgcggtgata tagatccagc tatagtacca tttgtaatga aaagaacagg catgtctgta     780
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gatgaagtgg ataccttaat gaataaaaag tcaggaatac ttggagtatc aggagtaagc 840

agtgatttta gagatgtaga agaagctgca aattcaggaa atgatagagc aaaacttgca 900

ttaaatatgt attatcacaa agttaaatct ttcataggag cttatgttgc agttttaaat 960

ggagcagatg ctataatatt tacagcagga cttggagaaa attcagcaac tagcagatct 1020

gctatatgta atggattaag ctattttgga attaaaatag atgaagaaaa gaataagaaa 1080

aggggagagg cactagaaat aagcacacct gattcaaaga taaaagtatt agtaattcct 1140

acaaatgaag aacttatgat agctagggat acaaaagaaa tagttgaaaa taaataa 1197

<210> 88
<211> 398
<212> PRT
<213> c. ljungdahlii

<400> 88

Met Lys Ile Leu Val Val Asn Cys Gly Ser Ser Ser Leu Lys Tyr Gln
1 5 10 15

Leu Ile Asp Met Gln Asp Glu Ser Val Val Ala Lys Gly Leu Val Glu
20 25 30

Arg Ile Gly Met Asp Gly Ser Ile Leu Thr His Lys Val Asn Gly Glu
35 40 45

Lys Phe Val Thr Glu Gln Thr Met Glu Asp His Lys Val Ala Ile Gln
50 55 60

Leu Val Leu Asn Ala Leu Val Asp Lys Lys His Gly Val Ile Lys Asp
65 70 75 80

Met Ser Glu Ile Ser Ala Val Gly His Arg Val Leu His Gly Gly Lys
85 90 95

Lys Tyr Ala Ala Ser Ile Leu Ile Asp Glu Asn Val Met Lys Ala Ile
100 105 110

Glu Glu Cys Ile Pro Leu Gly Pro Leu His Asn Pro Ala Asn Ile Met
115 120 125

Gly Ile Asp Ala Cys Lys Lys Leu Met Pro Asn Thr Pro Met Val Ala
130 135 140

Val Phe Asp Thr Ala Phe His Gln Thr Met Pro Asp Tyr Ala Tyr Thr
145 150 155 160

Tyr Ala Ile Pro Tyr Asp Ile Ser Glu Lys Tyr Asp Ile Arg Lys Tyr
165 170 175

Gly Phe His Gly Thr Ser His Arg Phe Val Ser Ile Glu Ala Ala Lys
180 185 190

```
Leu Leu Lys Lys Asp Pro Lys Asp Leu Lys Leu Ile Thr Cys His Leu
        195                 200                 205

Gly Asn Gly Ala Ser Ile Cys Ala Val Asn Gln Gly Lys Ala Val Asp
    210                 215                 220

Thr Thr Met Gly Leu Thr Pro Leu Ala Gly Leu Val Met Gly Thr Arg
225                 230                 235                 240

Cys Gly Asp Ile Asp Pro Ala Ile Val Pro Phe Val Met Lys Arg Thr
                245                 250                 255

Gly Met Ser Val Asp Glu Val Asp Thr Leu Met Asn Lys Lys Ser Gly
            260                 265                 270

Ile Leu Gly Val Ser Gly Val Ser Ser Asp Phe Arg Asp Val Glu Glu
        275                 280                 285

Ala Ala Asn Ser Gly Asn Asp Arg Ala Lys Leu Ala Leu Asn Met Tyr
    290                 295                 300

Tyr His Lys Val Lys Ser Phe Ile Gly Ala Tyr Val Ala Val Leu Asn
305                 310                 315                 320

Gly Ala Asp Ala Ile Ile Phe Thr Ala Gly Leu Gly Glu Asn Ser Ala
                325                 330                 335

Thr Ser Arg Ser Ala Ile Cys Asn Gly Leu Ser Tyr Phe Gly Ile Lys
            340                 345                 350

Ile Asp Glu Glu Lys Asn Lys Lys Arg Gly Glu Ala Leu Glu Ile Ser
        355                 360                 365

Thr Pro Asp Ser Lys Ile Lys Val Leu Val Ile Pro Thr Asn Glu Glu
    370                 375                 380

Leu Met Ile Ala Arg Asp Thr Lys Glu Ile Val Glu Asn Lys
385                 390                 395
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<210> 89
<211> 1824
<212> DNA
<213> c. ljungdahlii

<400> 89

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atgtacggat ataagggtaa ggtattaaga attaatctaa gtagtaaaac ttatatagtg      60

gaagaattga aaattgacaa agctaaaaaa tttataggtg caagagggtt aggcgtaaaa     120

accttatttg acgaagtaga tccaaaggta gatccattat cacctgataa caaatttatt     180

atagcagcgg gaccacttac aggtgcacct gttccaacaa gcggaagatt catggtagtt     240
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actaaatcac ctttaacagg aactattgct attgcaaatt caggtggaaa atggggagca 300

gaattcaaag cagctggata cgatatgata atcgttgaag gtaaatctga taaagaagtt 360

tatgtaaata tagtagatga taaagtagaa tttagggatg cttctcatgt ttggggaaaa 420

ctaacagaag aaactacaaa aatgcttcaa caggaaacag attcgagagc taaggtttta 480

tgcataggac cagctgggga aaagttatca cttatggcag cagttatgaa tgatgttgat 540

agaacagcag gacgtggtgg tgttggagct gttatgggtt caaagaactt aaaagctatt 600

gtagttaaag gaagcggaaa agtaaaatta tttgatgaac aaaaagtgaa ggaagtagca 660

cttgagaaaa caaatatttt aagaaaagat ccagtagctg gtggaggact tccaacatac 720

ggaacagctg tacttgttaa tattataaat gaaaatggtg tacatccagt aaagaatttt 780

caaaaatctt atacagatca agcagataag atcagtggag aaactttaac taaagattgc 840

ttagttagaa aaaatccttg ctataggtgt ccaattgcct gtggaagatg ggtaaaactt 900

gatgatggaa ctgaatgtgg aggaccagaa tatgaaacat tatggtcatt tggatctgat 960

tgtgatgtat acgatataaa tgctgtaaat acagcaaata tgttgtgtaa tgaatatgga 1020

ttagatacca ttacagcagg atgtactatt gcagcagcta tggaacttta tcaaagaggt 1080

tatattaagg atgaagaaat agcagcagat ggattgtcac ttaattgggg agatgctaag 1140

tccatggttg aatgggtaaa gaaaatggga cttagagaag gatttggaga caagatggca 1200

gatggttcat acagactttg tgactcatac ggtgtacctg agtattcaat gactgtaaaa 1260

aaacaggaac ttccagcata tgacccaaga ggaatacagg gacatggtat tacttatgct 1320

gttaacaata ggggaggatg tcacattaag ggatatatgg taagtcctga aatacttggc 1380

tatccagaaa aacttgatag acttgcagtg gaaggaaaag caggatatgc tagagtattc 1440

catgatttaa cagctgttat agattcactt ggattatgta tttttacaac atttggtctt 1500

ggtgcacagg attatgttga tatgtataat gcagtagttg gtggagaatt acatgatgta 1560

aattctttaa tgttagctgg agatagaata tggactttag aaaaaatatt taacttaaag 1620

gcaggcatag atagttcaca ggatactctt ccaaagagat tgcttgaaga acaaattcca 1680

gaaggaccat caaaaggaga agttcataag ttagatgtac tactacctga atattattca 1740

gtacgtggat gggataaaaa tggtattcct acagaggaaa cgttaaagaa attaggatta 1800

gatgaatacg taggtaagct ttag 1824

<210> 90
<211> 607
<212> PRT
<213> C. ljungdahlii

<400> 90

Met Tyr Gly Tyr Lys Gly Lys Val Leu Arg Ile Asn Leu Ser Ser Lys
1 5 10 15

Thr Tyr Ile Val Glu Glu Leu Lys Ile Asp Lys Ala Lys Lys Phe Ile
20 25 30

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Gly Ala Arg Gly Leu Gly Val Lys Thr Leu Phe Asp Glu Val Asp Pro
        35                  40                  45

Lys Val Asp Pro Leu Ser Pro Asp Asn Lys Phe Ile Ile Ala Ala Gly
    50                  55                  60

Pro Leu Thr Gly Ala Pro Val Pro Thr Ser Gly Arg Phe Met Val Val
65                  70                  75                  80

Thr Lys Ser Pro Leu Thr Gly Thr Ile Ala Ile Ala Asn Ser Gly Gly
                85                  90                  95

Lys Trp Gly Ala Glu Phe Lys Ala Ala Gly Tyr Asp Met Ile Ile Val
            100                 105                 110

Glu Gly Lys Ser Asp Lys Glu Val Tyr Val Asn Ile Val Asp Asp Lys
        115                 120                 125

Val Glu Phe Arg Asp Ala Ser His Val Trp Gly Lys Leu Thr Glu Glu
    130                 135                 140

Thr Thr Lys Met Leu Gln Gln Glu Thr Asp Ser Arg Ala Lys Val Leu
145                 150                 155                 160

Cys Ile Gly Pro Ala Gly Glu Lys Leu Ser Leu Met Ala Ala Val Met
                165                 170                 175

Asn Asp Val Asp Arg Thr Ala Gly Arg Gly Gly Val Gly Ala Val Met
            180                 185                 190

Gly Ser Lys Asn Leu Lys Ala Ile Val Val Lys Gly Ser Gly Lys Val
        195                 200                 205

Lys Leu Phe Asp Glu Gln Lys Val Lys Glu Val Ala Leu Glu Lys Thr
    210                 215                 220

Asn Ile Leu Arg Lys Asp Pro Val Ala Gly Gly Gly Leu Pro Thr Tyr
225                 230                 235                 240

Gly Thr Ala Val Leu Val Asn Ile Ile Asn Glu Asn Gly Val His Pro
                245                 250                 255

Val Lys Asn Phe Gln Lys Ser Tyr Thr Asp Gln Ala Asp Lys Ile Ser
            260                 265                 270

Gly Glu Thr Leu Thr Lys Asp Cys Leu Val Arg Lys Asn Pro Cys Tyr
        275                 280                 285

Arg Cys Pro Ile Ala Cys Gly Arg Trp Val Lys Leu Asp Asp Gly Thr
    290                 295                 300
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Glu Cys Gly Gly Pro Glu Tyr Glu Thr Leu Trp Ser Phe Gly Ser Asp
305 310 315 320

Cys Asp Val Tyr Asp Ile Asn Ala Val Asn Thr Ala Asn Met Leu Cys
325 330 335

Asn Glu Tyr Gly Leu Asp Thr Ile Thr Ala Gly Cys Thr Ile Ala Ala
340 345 350

Ala Met Glu Leu Tyr Gln Arg Gly Tyr Ile Lys Asp Glu Glu Ile Ala
355 360 365

Ala Asp Gly Leu Ser Leu Asn Trp Gly Asp Ala Lys Ser Met Val Glu
370 375 380

Trp Val Lys Lys Met Gly Leu Arg Glu Gly Phe Gly Asp Lys Met Ala
385 390 395 400

Asp Gly Ser Tyr Arg Leu Cys Asp Ser Tyr Gly Val Pro Glu Tyr Ser
405 410 415

Met Thr Val Lys Lys Gln Glu Leu Pro Ala Tyr Asp Pro Arg Gly Ile
420 425 430

Gln Gly His Gly Ile Thr Tyr Ala Val Asn Asn Arg Gly Gly Cys His
435 440 445

Ile Lys Gly Tyr Met Val Ser Pro Glu Ile Leu Gly Tyr Pro Glu Lys
450 455 460

Leu Asp Arg Leu Ala Val Glu Gly Lys Ala Gly Tyr Ala Arg Val Phe
465 470 475 480

His Asp Leu Thr Ala Val Ile Asp Ser Leu Gly Leu Cys Ile Phe Thr
485 490 495

Thr Phe Gly Leu Gly Ala Gln Asp Tyr Val Asp Met Tyr Asn Ala Val
500 505 510

Val Gly Gly Glu Leu His Asp Val Asn Ser Leu Met Leu Ala Gly Asp
515 520 525

Arg Ile Trp Thr Leu Glu Lys Ile Phe Asn Leu Lys Ala Gly Ile Asp
530 535 540

Ser Ser Gln Asp Thr Leu Pro Lys Arg Leu Leu Glu Glu Gln Ile Pro
545 550 555 560

Glu Gly Pro Ser Lys Gly Glu Val His Lys Leu Asp Val Leu Leu Pro
565 570 575

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Glu Tyr Tyr Ser Val Arg Gly Trp Asp Lys Asn Gly Ile Pro Thr Glu
            580                 585                 590

Glu Thr Leu Lys Lys Leu Gly Leu Asp Glu Tyr Val Gly Lys Leu
        595                 600                 605
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<210> 91
<211> 1824
<212> DNA
<213> c. ljungdahlii

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<400>  91
atgtatggtt atgatggtaa agtattaaga attaatttaa aagaaagaac ttgcaaatca      60

gaaaatttag atttagataa agctaaaaag tttataggtt gtaggggact aggtgttaaa     120

actttatttg atgaaataga tcctaaaata gatgcattat caccagaaaa taaatttata     180

attgtaacag gtcctttaac tggagctccg gttccaacta gtggaaggtt tatggtagtt     240

actaaagcac cgcttacagg aactatagga atttcaaatt cgggtggaaa atggggagta     300

gacttaaaaa aagctggttg ggatatgata atagtagagg ataaggctga ttcaccagtt     360

tacattgaaa tagtagatga taaggtagaa attaaagacg cgtcacagct ttggggaaaa     420

gttacatcag aaactacaaa agagttagaa aagataactg agaataaatc aaaggtatta     480

tgtataggac ctgctggtga acgattgtct cttatggcag cagttatgaa tgatgtagat     540

agaactgcag caagaggcgg cgttggtgca gttatgggat ctaaaaactt aaaagctatt     600

acagttaaag gaactggaaa aatagcttta gctgataaag aaaaagtaaa aaaagtgtcc     660

gtagaaaaaa ttacaacatt aaaaaatgat ccagtagctg gtcagggaat gccaacttat     720

ggtacagcta tactggttaa tataataaat gaaaatggag ttcatcctgt aaagaatttt     780

caagagtctt atacgaatca agcagataaa ataagtggag agactcttac tgctaaccaa     840

ctagtaagga aaaatccttg ttacagctgt cctataggtt gtggaagatg ggttagacta     900

aaagatggca cagagtgcgg aggaccagaa tatgaaacac tgtggtgttt tggatctgac     960

tgtggttcat atgatttaga tgctataaat gaagctaata tgttatgtaa tgaatatggt    1020

attgatacta ttacttgtgg tgcaacaatt gctgcagcta tggaacttta tcaaagagga    1080

tatataaaag acgaagaaat agctggagat aacctatctc tcaagtgggg tgatacggaa    1140

tctatgattg gctggataaa gagaatggta tatagtgaag gctttggagc aaagatgaca    1200

aatggttcat ataggctttg tgaaggttat ggagcaccgg agtattctat gacagttaaa    1260

aagcaggaaa ttccagcata tgatccaagg ggaatacagg gacacggtat tacctatgca    1320

gttaataata gaggaggctg tcatattaag ggatatatga ttaaccctga aatattaggt    1380

tatcctgaaa aacttgatag atttgcatta gatggtaaag cagcttatgc caaattattt    1440

catgatttaa ctgctgtaat tgattcttta ggattgtgca tattcactac atttgggctt    1500

ggaatacagg attatgtaga tatgtataat gcagtagtag gagaatctac ttatgatgca    1560
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gattcactat tagaggcagg agatagaatc tggactcttg agaaattatt taatcttgca      1620

gctggaatag acagcagcca ggatactcta ccaaagagat tgttagaaga acctattcca      1680

gatggcccat caaagggaga agttcatagg ctagatgttc ttctgccaga atattactca      1740

gtacgaggat ggagtaaaga gggtatacct acagaagaaa cattaaagaa attaggatta      1800

gatgaatata taggtaagtt ctag                                             1824


<210>  92
<211>  607
<212>  PRT
<213>  c. lungdahlii

<400>  92

Met Tyr Gly Tyr Asp Gly Lys Val Leu Arg Ile Asn Leu Lys Glu Arg
1               5                   10                  15


Thr Cys Lys Ser Glu Asn Leu Asp Leu Asp Lys Ala Lys Lys Phe Ile
                20                  25                  30


Gly Cys Arg Gly Leu Gly Val Lys Thr Leu Phe Asp Glu Ile Asp Pro
        35                  40                  45


Lys Ile Asp Ala Leu Ser Pro Glu Asn Lys Phe Ile Ile Val Thr Gly
    50                  55                  60


Pro Leu Thr Gly Ala Pro Val Pro Thr Ser Gly Arg Phe Met Val Val
65                  70                  75                  80


Thr Lys Ala Pro Leu Thr Gly Thr Ile Gly Ile Ser Asn Ser Gly Gly
                85                  90                  95


Lys Trp Gly Val Asp Leu Lys Lys Ala Gly Trp Asp Met Ile Ile Val
            100                 105                 110


Glu Asp Lys Ala Asp Ser Pro Val Tyr Ile Glu Ile Val Asp Asp Lys
        115                 120                 125


Val Glu Ile Lys Asp Ala Ser Gln Leu Trp Gly Lys Val Thr Ser Glu
    130                 135                 140


Thr Thr Lys Glu Leu Glu Lys Ile Thr Glu Asn Lys Ser Lys Val Leu
145                 150                 155                 160


Cys Ile Gly Pro Ala Gly Glu Arg Leu Ser Leu Met Ala Ala Val Met
                165                 170                 175


Asn Asp Val Asp Arg Thr Ala Ala Arg Gly Gly Val Gly Ala Val Met
            180                 185                 190


Gly Ser Lys Asn Leu Lys Ala Ile Thr Val Lys Gly Thr Gly Lys Ile
        195                 200                 205
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Ala Leu Ala Asp Lys Glu Lys Val Lys Lys Val Ser Val Glu Lys Ile
    210                 215                 220

Thr Thr Leu Lys Asn Asp Pro Val Ala Gly Gln Gly Met Pro Thr Tyr
225                 230                 235                 240

Gly Thr Ala Ile Leu Val Asn Ile Ile Asn Glu Asn Gly Val His Pro
                245                 250                 255

Val Lys Asn Phe Gln Glu Ser Tyr Thr Asn Gln Ala Asp Lys Ile Ser
            260                 265                 270

Gly Glu Thr Leu Thr Ala Asn Gln Leu Val Arg Lys Asn Pro Cys Tyr
        275                 280                 285

Ser Cys Pro Ile Gly Cys Gly Arg Trp Val Arg Leu Lys Asp Gly Thr
    290                 295                 300

Glu Cys Gly Gly Pro Glu Tyr Glu Thr Leu Trp Cys Phe Gly Ser Asp
305                 310                 315                 320

Cys Gly Ser Tyr Asp Leu Asp Ala Ile Asn Glu Ala Asn Met Leu Cys
                325                 330                 335

Asn Glu Tyr Gly Ile Asp Thr Ile Thr Cys Gly Ala Thr Ile Ala Ala
            340                 345                 350

Ala Met Glu Leu Tyr Gln Arg Gly Tyr Ile Lys Asp Glu Glu Ile Ala
        355                 360                 365

Gly Asp Asn Leu Ser Leu Lys Trp Gly Asp Thr Glu Ser Met Ile Gly
    370                 375                 380

Trp Ile Lys Arg Met Val Tyr Ser Glu Gly Phe Gly Ala Lys Met Thr
385                 390                 395                 400

Asn Gly Ser Tyr Arg Leu Cys Glu Gly Tyr Gly Ala Pro Glu Tyr Ser
                405                 410                 415

Met Thr Val Lys Lys Gln Glu Ile Pro Ala Tyr Asp Pro Arg Gly Ile
            420                 425                 430

Gln Gly His Gly Ile Thr Tyr Ala Val Asn Asn Arg Gly Gly Cys His
        435                 440                 445

Ile Lys Gly Tyr Met Ile Asn Pro Glu Ile Leu Gly Tyr Pro Glu Lys
    450                 455                 460

Leu Asp Arg Phe Ala Leu Asp Gly Lys Ala Ala Tyr Ala Lys Leu Phe
465                 470                 475                 480
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His Asp Leu Thr Ala Val Ile Asp Ser Leu Gly Leu Cys Ile Phe Thr
485 490 495

Thr Phe Gly Leu Gly Ile Gln Asp Tyr Val Asp Met Tyr Asn Ala Val
500 505 510

Val Gly Glu Ser Thr Tyr Asp Ala Asp Ser Leu Leu Glu Ala Gly Asp
515 520 525

Arg Ile Trp Thr Leu Glu Lys Leu Phe Asn Leu Ala Ala Gly Ile Asp
530 535 540

Ser Ser Gln Asp Thr Leu Pro Lys Arg Leu Leu Glu Glu Pro Ile Pro
545 550 555 560

Asp Gly Pro Ser Lys Gly Glu Val His Arg Leu Asp Val Leu Leu Pro
565 570 575

Glu Tyr Tyr Ser Val Arg Gly Trp Ser Lys Glu Gly Ile Pro Thr Glu
580 585 590

Glu Thr Leu Lys Lys Leu Gly Leu Asp Glu Tyr Ile Gly Lys Phe
595 600 605

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<211> 2697
<212> DNA
<213> C. ragsdalei

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aaggtaacta aggtaactaa cgttgaagaa ttaatgaaaa agttagatga agtaacggct 120

gctcaaaaaa aattctctag ttatagtcag gaacaagtgg atgagatctt taggcaggca 180

gctatggcag ccaatagtgc tagaatagat ctagctaaaa tggcagtgga agaaagcgga 240

atgggaattg tagaagacaa ggttattaaa aatcattttg tttcagaata tatatataac 300

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agaattgcgg aacctgtagg ggttatagca gcagtagttc caacaactaa tccaacatcc 420

acagcaatct ttaaatcttt aatagctttg aaaactagaa atggtatagt tttttcacca 480

catccaagag caaaaaaatc aactattgca gcagctaaga tagtacttga tgcagcagtt 540

aaagctggtg ctcctgaagg aattatagga tggatagatg aaccttccat tgaactctca 600

caggtggtaa tgaaagaagc agatttaatt cttgcaactg gtggcccggg tatggttaag 660

gctgcctatt cttcaggaaa gcctgctata ggagttggcc caggtaacac acctgctgta 720

attgatgaaa gtgctgatat taaaatggca gtaaattcaa tactcctttc aaaaactttt 780

gataatggta tgatttgtgc ttcagagcag tcagtagtag ttgtaagctc aatatacgat 840

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aaggttggaa aaacaattat gattaatggc gctctaaatg ctggcattgt agggcaaagt      960

gcttttaaaa tagcacagat ggcaggagtg agtgtaccag aggatgctaa agtacttata     1020

ggagaagtta aatcagtaga acctgaagaa gagccctttg ctcatgaaaa gctgtctcca     1080

gttttagcta tgtacaaagc aaaagatttt gatgaagcac ttctaaaggc tggaagatta     1140

gttgaacgag gtggaattgg gcatacatct gtattatatg taaattcaat gacggaaaaa     1200

gtaaaagtag aaaagttcag agaaactatg aagactggta gaacattgat aaatatgcct     1260

tcagcacaag gtgctatagg agatatatat aactttaaac tagctccttc tttgacgcta     1320

ggatgtggtt cctggggagg aaactctgta tcagaaaatg ttggacctaa acatttatta     1380

aacataaaaa gtgttgctga gaggagagaa aatatgcttt ggtttagagt acctgaaaaa     1440

gtttatttca aatatggtag tcttggagtt gcattaaagg aattgagaac tttggagaag     1500

aaaaaggcat ttatagtaac ggataaggtt ctttatcaat taggttatgt agataaaatt     1560

acaaaaaatc tcgatgaatt aagagtttca tataaaatat ttacagatgt agaaccagat     1620

ccaacccttg ctacagctaa aaaaggtgca tcagaactgc tttcctatga accagataca     1680

attatagcag ttggtggtgg ttcggcaatg gatgcagcca agatcatgtg ggtaatgtat     1740

gagcatccag aagtaagatt tgaagatttg gctatgagat ttatggatat aagaaagaga     1800

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atgggaatgc caaaagggct tacagcagct tcgggtatag atgcattaac ccatgcactg     2040

gaggcgtatg tatcaataat ggcttcagaa tataccaatg gattggctct tgaagcaaca     2100

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agagaaaaaa tggctcatgc ttcaactata gcaggtatgg cttttgccaa tgcattctta     2220

ggggtatgtc actctatggc acataaattg ggagcacagc accatatacc acatggaatt     2280

gccaatgcgc ttatgataga tgaagttata aaattcaatg ctgtagaggc tccaaggaaa     2340

caagcggcat ttccacaata taagtaccca aatgttaaaa gaagatatgc tagaatagct     2400

gattacttaa atttaggagg aagcacagat gatgaaaaag tacaattgct aataaatgct     2460

atagatgact taaaaactaa gttaaatatt ccaaagacta ttaaagaggc aggagtttca     2520

gaagataaat tctatgctac tttagacaca atgtcagaac tggcttttga tgatcaatgt     2580

acaggagcta atccaagata tccactaata ggagaaataa aacaaatgta tataaatgca     2640

tttgatacac caaaggcaac tgtggagaag aaaacaaaaa gaaaaataaa catataa        2697
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<211>  898
<212>  PRT
<213>  C. ragsdalei
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<400> 94

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Val Ser Leu Met Lys Val Thr Lys Val Thr Asn Val Glu Glu Leu Met
            20                  25                  30

Lys Lys Leu Asp Glu Val Thr Ala Ala Gln Lys Lys Phe Ser Ser Tyr
        35                  40                  45

Ser Gln Glu Gln Val Asp Glu Ile Phe Arg Gln Ala Ala Met Ala Ala
    50                  55                  60

Asn Ser Ala Arg Ile Asp Leu Ala Lys Met Ala Val Glu Glu Ser Gly
65                  70                  75                  80

Met Gly Ile Val Glu Asp Lys Val Ile Lys Asn His Phe Val Ser Glu
                85                  90                  95

Tyr Ile Tyr Asn Lys Tyr Lys Asp Glu Lys Thr Cys Gly Val Leu Glu
            100                 105                 110

Glu Asp Gln Gly Phe Gly Met Val Arg Ile Ala Glu Pro Val Gly Val
        115                 120                 125

Ile Ala Ala Val Val Pro Thr Thr Asn Pro Thr Ser Thr Ala Ile Phe
    130                 135                 140

Lys Ser Leu Ile Ala Leu Lys Thr Arg Asn Gly Ile Val Phe Ser Pro
145                 150                 155                 160

His Pro Arg Ala Lys Lys Ser Thr Ile Ala Ala Ala Lys Ile Val Leu
                165                 170                 175

Asp Ala Ala Val Lys Ala Gly Ala Pro Glu Gly Ile Ile Gly Trp Ile
            180                 185                 190

Asp Glu Pro Ser Ile Glu Leu Ser Gln Val Val Met Lys Glu Ala Asp
        195                 200                 205

Leu Ile Leu Ala Thr Gly Gly Pro Gly Met Val Lys Ala Ala Tyr Ser
    210                 215                 220

Ser Gly Lys Pro Ala Ile Gly Val Gly Pro Gly Asn Thr Pro Ala Val
225                 230                 235                 240

Ile Asp Glu Ser Ala Asp Ile Lys Met Ala Val Asn Ser Ile Leu Leu
                245                 250                 255

Ser Lys Thr Phe Asp Asn Gly Met Ile Cys Ala Ser Glu Gln Ser Val
            260                 265                 270
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Val Val Val Ser Ser Ile Tyr Asp Glu Val Lys Lys Glu Phe Ala Asp
        275                 280                 285

Arg Gly Ala Tyr Ile Leu Ser Lys Asp Glu Thr Asp Lys Val Gly Lys
    290                 295                 300

Thr Ile Met Ile Asn Gly Ala Leu Asn Ala Gly Ile Val Gly Gln Ser
305                 310                 315                 320

Ala Phe Lys Ile Ala Gln Met Ala Gly Val Ser Val Pro Glu Asp Ala
                325                 330                 335

Lys Val Leu Ile Gly Glu Val Lys Ser Val Glu Pro Glu Glu Glu Pro
            340                 345                 350

Phe Ala His Glu Lys Leu Ser Pro Val Leu Ala Met Tyr Lys Ala Lys
        355                 360                 365

Asp Phe Asp Glu Ala Leu Leu Lys Ala Gly Arg Leu Val Glu Arg Gly
    370                 375                 380

Gly Ile Gly His Thr Ser Val Leu Tyr Val Asn Ser Met Thr Glu Lys
385                 390                 395                 400

Val Lys Val Glu Lys Phe Arg Glu Thr Met Lys Thr Gly Arg Thr Leu
                405                 410                 415

Ile Asn Met Pro Ser Ala Gln Gly Ala Ile Gly Asp Ile Tyr Asn Phe
            420                 425                 430

Lys Leu Ala Pro Ser Leu Thr Leu Gly Cys Gly Ser Trp Gly Gly Asn
        435                 440                 445

Ser Val Ser Glu Asn Val Gly Pro Lys His Leu Leu Asn Ile Lys Ser
    450                 455                 460

Val Ala Glu Arg Arg Glu Asn Met Leu Trp Phe Arg Val Pro Glu Lys
465                 470                 475                 480

Val Tyr Phe Lys Tyr Gly Ser Leu Gly Val Ala Leu Lys Glu Leu Arg
                485                 490                 495

Thr Leu Glu Lys Lys Lys Ala Phe Ile Val Thr Asp Lys Val Leu Tyr
            500                 505                 510

Gln Leu Gly Tyr Val Asp Lys Ile Thr Lys Asn Leu Asp Glu Leu Arg
        515                 520                 525

Val Ser Tyr Lys Ile Phe Thr Asp Val Glu Pro Asp Pro Thr Leu Ala
    530                 535                 540
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Thr Ala Lys Lys Gly Ala Ser Glu Leu Leu Ser Tyr Glu Pro Asp Thr
545                 550                 555                 560

Ile Ile Ala Val Gly Gly Gly Ser Ala Met Asp Ala Ala Lys Ile Met
                565                 570                 575

Trp Val Met Tyr Glu His Pro Glu Val Arg Phe Glu Asp Leu Ala Met
            580                 585                 590

Arg Phe Met Asp Ile Arg Lys Arg Val Tyr Val Phe Pro Lys Met Gly
        595                 600                 605

Glu Lys Ala Met Met Ile Ser Val Ala Thr Ser Ala Gly Thr Gly Ser
    610                 615                 620

Glu Val Thr Pro Phe Ala Val Ile Thr Asp Glu Arg Thr Gly Ala Lys
625                 630                 635                 640

Tyr Pro Leu Ala Asp Tyr Glu Leu Thr Pro Asn Met Ala Ile Ile Asp
                645                 650                 655

Ala Glu Leu Met Met Gly Met Pro Lys Gly Leu Thr Ala Ala Ser Gly
            660                 665                 670

Ile Asp Ala Leu Thr His Ala Leu Glu Ala Tyr Val Ser Ile Met Ala
        675                 680                 685

Ser Glu Tyr Thr Asn Gly Leu Ala Leu Glu Ala Thr Arg Leu Val Phe
    690                 695                 700

Lys Tyr Leu Pro Ile Ala Tyr Thr Glu Gly Thr Thr Asn Val Lys Ala
705                 710                 715                 720

Arg Glu Lys Met Ala His Ala Ser Thr Ile Ala Gly Met Ala Phe Ala
                725                 730                 735

Asn Ala Phe Leu Gly Val Cys His Ser Met Ala His Lys Leu Gly Ala
            740                 745                 750

Gln His His Ile Pro His Gly Ile Ala Asn Ala Leu Met Ile Asp Glu
        755                 760                 765

Val Ile Lys Phe Asn Ala Val Glu Ala Pro Arg Lys Gln Ala Ala Phe
    770                 775                 780

Pro Gln Tyr Lys Tyr Pro Asn Val Lys Arg Arg Tyr Ala Arg Ile Ala
785                 790                 795                 800

Asp Tyr Leu Asn Leu Gly Gly Ser Thr Asp Asp Glu Lys Val Gln Leu
                805                 810                 815
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Leu Ile Asn Ala Ile Asp Asp Leu Lys Thr Lys Leu Asn Ile Pro Lys
820 825 830

Thr Ile Lys Glu Ala Gly Val Ser Glu Asp Lys Phe Tyr Ala Thr Leu
835 840 845

Asp Thr Met Ser Glu Leu Ala Phe Asp Asp Gln Cys Thr Gly Ala Asn
850 855 860

Pro Arg Tyr Pro Leu Ile Gly Glu Ile Lys Gln Met Tyr Ile Asn Ala
865 870 875 880

Phe Asp Thr Pro Lys Ala Thr Val Glu Lys Lys Thr Lys Arg Lys Ile
885 890 895

Asn Ile

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<211> 2613
<212> DNA
<213> C. ragsdalei

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gcagccaata gtgctagaat agaactagct aaaatggcag tggaagaaag cggaatggga 180

attgtagaag acaaggttat taaaaatcac tttgcctcag aatatatata taacaaatat 240

aaggatgaaa agacctgtgg agttttagaa agagatgcag gctttggtat agttagaatt 300

gcggaacctg taggggttat tgcagcagta gttccaacaa ctaatccaac atctacagca 360

atctttaaat cactaatagc tttaaaaact agaaatggta taattttttc accgcatcca 420

agggcaaaga aatcaactat tgcagcagct aaaatagtac ttgatgctgc agttaaagct 480

ggtgctcccg aaggaattat aggatggata gatgaacctt ccattgaact ttcacaggtg 540

gtaatgggag aagcaaattt aattcttgca actggtggcc cgggtatggt taaggctgcc 600

tattcttcag gaaaacctgc tgtaggagtt ggcccaggta atacacctgc tataattgat 660

gaaagtgccg atattaaaat ggcagtaaat tcaatattac tctcaaaaac ttttgataat 720

ggtatgattt gtgcctcaga gcagtcagta atagttttag actcaatata tgaggaagtt 780

aaaaaagaat ttgcttatag gggagcttat atattgagtg aggatgaaac agataaggtt 840

ggaaaaataa ttttaaaaaa tggagcctta aatgctggta ttgtaggaca aagtgctttt 900

aaaatagcac agctggcagg agtgaacgta ccagaaaaag ctaaagtact tataggagag 960

gtagaatcag tagaacttga agaaccattt tctcatgaaa agttatctcc agttttagct 1020

atgtacaggg caagagattt tgaggatgcc attgcaaaaa ctgataaact ggttagggca 1080 ggtggatttg gacatacatc ttcattatat gtaaatccaa tgacagaaaa agcaaaagta 1140

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gtatcaataa tggctacaga atttaccaat ggattagccc ttgaagcagt aaagttgata 2040

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aacttaggag gaaatacaga agatgaaaag gtgcaattat taataaatgc tatagatgat 2400

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<212> PRT
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<400> 96

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Lys Asp Ala Gln Lys Lys Phe Ala Thr Tyr Thr Gln Glu Gln Val Asp
20 25 30

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        35                  40                  45

Leu Ala Lys Met Ala Val Glu Glu Ser Gly Met Gly Ile Val Glu Asp
    50                  55                  60

Lys Val Ile Lys Asn His Phe Ala Ser Glu Tyr Ile Tyr Asn Lys Tyr
65                  70                  75                  80

Lys Asp Glu Lys Thr Cys Gly Val Leu Glu Arg Asp Ala Gly Phe Gly
                85                  90                  95

Ile Val Arg Ile Ala Glu Pro Val Gly Val Ile Ala Ala Val Val Pro
            100                 105                 110

Thr Thr Asn Pro Thr Ser Thr Ala Ile Phe Lys Ser Leu Ile Ala Leu
        115                 120                 125

Lys Thr Arg Asn Gly Ile Ile Phe Ser Pro His Pro Arg Ala Lys Lys
    130                 135                 140

Ser Thr Ile Ala Ala Ala Lys Ile Val Leu Asp Ala Ala Val Lys Ala
145                 150                 155                 160

Gly Ala Pro Glu Gly Ile Ile Gly Trp Ile Asp Glu Pro Ser Ile Glu
                165                 170                 175

Leu Ser Gln Val Val Met Gly Glu Ala Asn Leu Ile Leu Ala Thr Gly
            180                 185                 190

Gly Pro Gly Met Val Lys Ala Ala Tyr Ser Ser Gly Lys Pro Ala Val
        195                 200                 205

Gly Val Gly Pro Gly Asn Thr Pro Ala Ile Ile Asp Glu Ser Ala Asp
    210                 215                 220

Ile Lys Met Ala Val Asn Ser Ile Leu Leu Ser Lys Thr Phe Asp Asn
225                 230                 235                 240

Gly Met Ile Cys Ala Ser Glu Gln Ser Val Ile Val Leu Asp Ser Ile
                245                 250                 255

Tyr Glu Glu Val Lys Lys Glu Phe Ala Tyr Arg Gly Ala Tyr Ile Leu
            260                 265                 270

Ser Glu Asp Glu Thr Asp Lys Val Gly Lys Ile Ile Leu Lys Asn Gly
        275                 280                 285

Ala Leu Asn Ala Gly Ile Val Gly Gln Ser Ala Phe Lys Ile Ala Gln
    290                 295                 300
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Leu Ala Gly Val Asn Val Pro Glu Lys Ala Lys Val Leu Ile Gly Glu
305                 310                 315                 320

Val Glu Ser Val Glu Leu Glu Glu Pro Phe Ser His Glu Lys Leu Ser
                325                 330                 335

Pro Val Leu Ala Met Tyr Arg Ala Arg Asp Phe Glu Asp Ala Ile Ala
            340                 345                 350

Lys Thr Asp Lys Leu Val Arg Ala Gly Gly Phe Gly His Thr Ser Ser
        355                 360                 365

Leu Tyr Val Asn Pro Met Thr Glu Lys Ala Lys Val Glu Lys Phe Ser
    370                 375                 380

Thr Met Met Lys Thr Ser Arg Thr Ile Ile Asn Thr Pro Ser Ser Gln
385                 390                 395                 400

Gly Gly Ile Gly Asp Ile Tyr Asn Phe Lys Leu Ala Pro Ser Leu Thr
                405                 410                 415

Leu Gly Cys Gly Ser Trp Gly Gly Asn Ser Val Ser Glu Asn Val Gly
            420                 425                 430

Pro Lys His Leu Leu Asn Ile Lys Ser Val Ala Glu Arg Arg Glu Asn
        435                 440                 445

Met Leu Trp Phe Arg Val Pro Glu Lys Val Tyr Phe Lys Tyr Gly Ser
    450                 455                 460

Leu Gly Val Ala Leu Lys Glu Leu Lys Val Met Asn Lys Lys Lys Val
465                 470                 475                 480

Phe Ile Val Thr Asp Lys Val Leu Tyr Gln Leu Gly Tyr Val Asp Lys
                485                 490                 495

Val Thr Lys Val Leu Glu Glu Leu Lys Ile Ser Tyr Lys Val Phe Thr
            500                 505                 510

Asp Val Glu Pro Asp Pro Thr Leu Ala Thr Ala Lys Lys Gly Ala Ala
        515                 520                 525

Glu Leu Leu Ser Tyr Glu Pro Asp Thr Ile Ile Ser Val Gly Gly Gly
    530                 535                 540

Ser Ala Met Asp Ala Ala Lys Ile Met Trp Val Met Tyr Glu His Pro
545                 550                 555                 560

Glu Val Lys Phe Glu Asp Leu Ala Met Arg Phe Met Asp Ile Arg Lys
                565                 570                 575
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Arg Val Tyr Val Phe Pro Lys Met Gly Glu Lys Ala Met Met Ile Ser
            580                 585                 590

Val Ala Thr Ser Ala Gly Thr Gly Ser Glu Val Thr Pro Phe Ala Val
        595                 600                 605

Ile Thr Asp Glu Lys Thr Gly Ala Lys Tyr Pro Leu Ala Asp Tyr Glu
    610                 615                 620

Leu Thr Pro Asn Met Ala Ile Val Asp Ala Glu Leu Met Met Gly Met
625                 630                 635                 640

Pro Arg Gly Leu Thr Ala Ala Ser Gly Ile Asp Ala Leu Thr His Ala
                645                 650                 655

Leu Glu Ala Tyr Val Ser Ile Met Ala Thr Glu Phe Thr Asn Gly Leu
            660                 665                 670

Ala Leu Glu Ala Val Lys Leu Ile Phe Glu Tyr Leu Pro Lys Ala Tyr
        675                 680                 685

Thr Glu Gly Thr Thr Asn Val Lys Ala Arg Glu Lys Met Ala His Ala
    690                 695                 700

Ser Cys Ile Ala Gly Met Ala Phe Ala Asn Ala Phe Leu Gly Val Cys
705                 710                 715                 720

His Ser Met Ala His Lys Leu Gly Ala Gln His His Ile Pro His Gly
                725                 730                 735

Ile Ala Asn Ala Leu Met Ile Asp Glu Val Ile Lys Phe Asn Ala Val
            740                 745                 750

Asp Asp Pro Ile Lys Gln Ala Ala Phe Pro Gln Tyr Glu Tyr Pro Asn
        755                 760                 765

Ala Lys Tyr Arg Tyr Ala Gln Ile Ala Asp Cys Leu Asn Leu Gly Gly
    770                 775                 780

Asn Thr Glu Asp Glu Lys Val Gln Leu Leu Ile Asn Ala Ile Asp Asp
785                 790                 795                 800

Leu Lys Ala Lys Leu Asn Ile Pro Glu Thr Ile Lys Glu Ala Gly Val
                805                 810                 815

Ser Glu Glu Lys Phe Tyr Thr Thr Leu Asp Lys Met Ser Glu Leu Ala
            820                 825                 830

Phe Asp Asp Gln Cys Thr Gly Ala Asn Pro Arg Tyr Pro Leu Ile Ser
        835                 840                 845
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Glu Ile Lys Gln Met Tyr Ile Asn Val Phe Asp Lys Thr Glu Pro Ile
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Val Glu Asp Glu Glu Lys
865   870

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<211> 1569
<212> DNA
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attgataaaa tcctatgtaa tatggttagg gtagcagagg aaaatgcagt ttgccttggt 180

aaaatggctg cagaagaaac tggttttgga aaagctgaag ataaggctta taagaaccat 240

atggctgcta ctacagtata taattatatc aaggatatga agactattgg tgttataaaa 300

gaagataaaa gtcaaggtgt aattgaattt gctgaaccag ttggtttatt aatgggtatt 360

gtaccatcta caaatccaac atctactgtt atctataaat caatcattgc aattaaatca 420

agaaatgcaa ttgtattctc accacaccca gctgcattaa aatgttcaac aaaagcaata 480

gaacttatgc gtgatgcagc agtagcagca ggagctcctg caaatgtaat tggcggtatt 540

gttacaccat ctatacaagc tacaaatgaa cttatgaaag ctaaagaagt tgctatgata 600

attgccactg gaggccctgg aatggtaaag gctgcttata gttcaggaac acctgcaata 660

ggcgttggtg ctggtaactc tccatcttat atagaaagaa ctgctgatgt tcatcaatca 720

gttaaagata taattgctag taagagtttt gactatggta ctatttgtgc atctgagcaa 780

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acacacagta tgagtgctaa gtttgtagga agagctcctc aggttatagc agcagctgca 960

ggtttctcag ttccagaagg aacaaaagtt ttagtaggag aacaaggcgg agttggtaat 1020

ggttaccctc tatcttatga gaaacttaca acagtacttg ctttctatac agttaaagat 1080

tggcatgaag catgtgatct tagtataaga ttacttcaaa atggtcttgg acatactatg 1140

aacattcata caaatgacag agacttagta atgaagtttg ctaaaaaacc agcatcccgt 1200

atattagtta atactggtgg aagccaagga ggtactggtg caagcacagg attagcacct 1260

gcatttacat taggttgtgg tacatgggga ggaagctctg tttccgaaaa tgttactcca 1320

ttacatttaa tcaatataaa gagagttgca tatggtctta aagattgttc tacattagct 1380

gcagatgata caactttcaa tcatcctgaa ctttgtggaa gcaaaaatga cttaggatgc 1440

tgtgctacaa gccctgcaga atttgcagca aatagcaatt gtgctagcac tgctgcggat 1500

actactgata atgataaact tgctagactc gtaagtgaat tagtagctgc aatgaaggga 1560

gctaactaa 1569

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<210>  98
<211>  522
<212>  PRT
<213>  c. ragsdalei

<400>  98

Met Glu Gly Thr Gln Leu Glu Asn Phe Asp Lys Asp Leu Arg Ser Ile
1               5                   10                  15

Gln Glu Ala Arg Asp Leu Ala Arg Leu Gly Lys Ile Ala Ala Cys Glu
            20                  25                  30

Ile Ala Asp Tyr Thr Glu Glu Gln Ile Asp Lys Ile Leu Cys Asn Met
        35                  40                  45

Val Arg Val Ala Glu Glu Asn Ala Val Cys Leu Gly Lys Met Ala Ala
    50                  55                  60

Glu Glu Thr Gly Phe Gly Lys Ala Glu Asp Lys Ala Tyr Lys Asn His
65                  70                  75                  80

Met Ala Ala Thr Thr Val Tyr Asn Tyr Ile Lys Asp Met Lys Thr Ile
                85                  90                  95

Gly Val Ile Lys Glu Asp Lys Ser Gln Gly Val Ile Glu Phe Ala Glu
            100                 105                 110

Pro Val Gly Leu Leu Met Gly Ile Val Pro Ser Thr Asn Pro Thr Ser
        115                 120                 125

Thr Val Ile Tyr Lys Ser Ile Ile Ala Ile Lys Ser Arg Asn Ala Ile
    130                 135                 140

Val Phe Ser Pro His Pro Ala Ala Leu Lys Cys Ser Thr Lys Ala Ile
145                 150                 155                 160

Glu Leu Met Arg Asp Ala Ala Val Ala Ala Gly Ala Pro Ala Asn Val
                165                 170                 175

Ile Gly Gly Ile Val Thr Pro Ser Ile Gln Ala Thr Asn Glu Leu Met
            180                 185                 190

Lys Ala Lys Glu Val Ala Met Ile Ile Ala Thr Gly Gly Pro Gly Met
        195                 200                 205

Val Lys Ala Ala Tyr Ser Ser Gly Thr Pro Ala Ile Gly Val Gly Ala
    210                 215                 220

Gly Asn Ser Pro Ser Tyr Ile Glu Arg Thr Ala Asp Val His Gln Ser
225                 230                 235                 240
```

```
Val Lys Asp Ile Ile Ala Ser Lys Ser Phe Asp Tyr Gly Thr Ile Cys
                245                 250                 255

Ala Ser Glu Gln Ser Ile Ile Val Glu Glu Cys Asn His Asp Glu Val
            260                 265                 270

Ile Ala Glu Leu Lys Lys Gln Gly Gly Tyr Phe Met Thr Ala Glu Glu
        275                 280                 285

Thr Ala Lys Val Cys Ser Ile Leu Phe Lys Pro Gly Thr His Ser Met
    290                 295                 300

Ser Ala Lys Phe Val Gly Arg Ala Pro Gln Val Ile Ala Ala Ala Ala
305                 310                 315                 320

Gly Phe Ser Val Pro Glu Gly Thr Lys Val Leu Val Gly Glu Gln Gly
                325                 330                 335

Gly Val Gly Asn Gly Tyr Pro Leu Ser Tyr Glu Lys Leu Thr Thr Val
            340                 345                 350

Leu Ala Phe Tyr Thr Val Lys Asp Trp His Glu Ala Cys Asp Leu Ser
        355                 360                 365

Ile Arg Leu Leu Gln Asn Gly Leu Gly His Thr Met Asn Ile His Thr
    370                 375                 380

Asn Asp Arg Asp Leu Val Met Lys Phe Ala Lys Lys Pro Ala Ser Arg
385                 390                 395                 400

Ile Leu Val Asn Thr Gly Gly Ser Gln Gly Gly Thr Gly Ala Ser Thr
                405                 410                 415

Gly Leu Ala Pro Ala Phe Thr Leu Gly Cys Gly Thr Trp Gly Gly Ser
            420                 425                 430

Ser Val Ser Glu Asn Val Thr Pro Leu His Leu Ile Asn Ile Lys Arg
        435                 440                 445

Val Ala Tyr Gly Leu Lys Asp Cys Ser Thr Leu Ala Ala Asp Asp Thr
    450                 455                 460

Thr Phe Asn His Pro Glu Leu Cys Gly Ser Lys Asn Asp Leu Gly Cys
465                 470                 475                 480

Cys Ala Thr Ser Pro Ala Glu Phe Ala Ala Asn Ser Asn Cys Ala Ser
                485                 490                 495

Thr Ala Ala Asp Thr Thr Asp Asn Asp Lys Leu Ala Arg Leu Val Ser
            500                 505                 510
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Glu Leu Val Ala Ala Met Lys Gly Ala Asn
515 520

<210> 99
<211> 1446
<212> DNA
<213> c. ragsdalei

<400> 99
gtggaaaatg ctgcacgagc acaaaaaatg ttagcaactt ttccgcaaga aaagttagat 60

gagattgttg aacgtatggc tgaagaaatc ggaaaacata cccgagagct tgctgtaatg 120

tcacaggatg aaactggtta tggaaaatgg caggataaat gcatcaaaaa ccgatttgcc 180

tgtgaatatt tgccagctaa gcttagagga atgcgatgtg taggtattat taacgaaaat 240

ggtcaggata agaccatgga tgtaggtgta cctatgggtg taattattgc attatgtcct 300

gcaactagtc cggtttctac taccatatat aaggcattaa ttgcaattaa gtctggtaat 360

gcaattatct tttctccaca tcctagagca aaggagacaa tttgtaaggc gcttgacatc 420

atgattcgtg cagctgaagg atatgggctg ccagaaggag ctcttgcata cttacatact 480

gtgacgccta gtggaacaat cgaattgatg aaccatgagg cgacttcttt gattatgaat 540

acaggcgttc ccgggatgct taaagcgtca tatagatctg gaaaacctgt gatctatgga 600

ggaactggta atggaccagc atttattgaa cgtacagctg acatcaagca ggcggtaaga 660

gatattattg ctagtaagac ctttgataac ggaatagtac catcatctga acaatctatt 720

gttgtagata gctgtgttgc atctgatgtt aaacgtgagt tgcaaaatag tggtgcatat 780

ttcatgacag aggaggaagc acaaaaactg ggttctctct ttttccgttc tgatggtagt 840

atggattcag aaatggttgg caaatccgca cagagattgg ctaagaaagc aggtttcagt 900

attcctgaaa gtagcacagt gctaatttca gagcagaaat atgtttccca agataatcct 960

tattccaagg agaaactttg tccggtacta gcttactaca ttgaagatga ttggatgcat 1020

gcatgtgaaa agtgtattga gctgctatta agtgagagac atggtcacac tcttgttata 1080

cattcaaaag acgaagatgt aattcgccag tttgcattaa aaaaacctgt aggcaggata 1140

cttgttaata cgcctgcttc ctttggtagt atgggtgcta caagtaattt atttcctgct 1200

ttaactttag gtagtggatc ggcaggtaaa ggtattacct ccgataatgt ttcaccaatg 1260

aatcttattt acgtccgtaa agtcggatat ggcgtacgga atgtagaaga gattattaat 1320

actaatggat tgtttacaga agaaaaaagt gatttgagtg gtatgacaaa gcagtcagac 1380

tataatccag aggatataca aatgttgcag catattttga aaaaagctat ggaaaaaatt 1440

aaatag 1446

<210> 100
<211> 481
<212> PRT
<213> c. ragsdalei

<400> 100

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Val Glu Asn Ala Ala Arg Ala Gln Lys Met Leu Ala Thr Phe Pro Gln
1               5                   10                  15

Glu Lys Leu Asp Glu Ile Val Glu Arg Met Ala Glu Glu Ile Gly Lys
            20                  25                  30

His Thr Arg Glu Leu Ala Val Met Ser Gln Asp Glu Thr Gly Tyr Gly
        35                  40                  45

Lys Trp Gln Asp Lys Cys Ile Lys Asn Arg Phe Ala Cys Glu Tyr Leu
    50                  55                  60

Pro Ala Lys Leu Arg Gly Met Arg Cys Val Gly Ile Ile Asn Glu Asn
65                  70                  75                  80

Gly Gln Asp Lys Thr Met Asp Val Gly Val Pro Met Gly Val Ile Ile
                85                  90                  95

Ala Leu Cys Pro Ala Thr Ser Pro Val Ser Thr Thr Ile Tyr Lys Ala
            100                 105                 110

Leu Ile Ala Ile Lys Ser Gly Asn Ala Ile Ile Phe Ser Pro His Pro
        115                 120                 125

Arg Ala Lys Glu Thr Ile Cys Lys Ala Leu Asp Ile Met Ile Arg Ala
    130                 135                 140

Ala Glu Gly Tyr Gly Leu Pro Glu Gly Ala Leu Ala Tyr Leu His Thr
145                 150                 155                 160

Val Thr Pro Ser Gly Thr Ile Glu Leu Met Asn His Glu Ala Thr Ser
                165                 170                 175

Leu Ile Met Asn Thr Gly Val Pro Gly Met Leu Lys Ala Ser Tyr Arg
            180                 185                 190

Ser Gly Lys Pro Val Ile Tyr Gly Gly Thr Gly Asn Gly Pro Ala Phe
        195                 200                 205

Ile Glu Arg Thr Ala Asp Ile Lys Gln Ala Val Arg Asp Ile Ile Ala
    210                 215                 220

Ser Lys Thr Phe Asp Asn Gly Ile Val Pro Ser Ser Glu Gln Ser Ile
225                 230                 235                 240

Val Val Asp Ser Cys Val Ala Ser Asp Val Lys Arg Glu Leu Gln Asn
                245                 250                 255

Ser Gly Ala Tyr Phe Met Thr Glu Glu Glu Ala Gln Lys Leu Gly Ser
            260                 265                 270
```

Leu Phe Phe Arg Ser Asp Gly Ser Met Asp Ser Glu Met Val Gly Lys
275 280 285

Ser Ala Gln Arg Leu Ala Lys Lys Ala Gly Phe Ser Ile Pro Glu Ser
290 295 300

Ser Thr Val Leu Ile Ser Glu Gln Lys Tyr Val Ser Gln Asp Asn Pro
305 310 315 320

Tyr Ser Lys Glu Lys Leu Cys Pro Val Leu Ala Tyr Tyr Ile Glu Asp
325 330 335

Asp Trp Met His Ala Cys Glu Lys Cys Ile Glu Leu Leu Leu Ser Glu
340 345 350

Arg His Gly His Thr Leu Val Ile His Ser Lys Asp Glu Asp Val Ile
355 360 365

Arg Gln Phe Ala Leu Lys Lys Pro Val Gly Arg Ile Leu Val Asn Thr
370 375 380

Pro Ala Ser Phe Gly Ser Met Gly Ala Thr Ser Asn Leu Phe Pro Ala
385 390 395 400

Leu Thr Leu Gly Ser Gly Ser Ala Gly Lys Gly Ile Thr Ser Asp Asn
405 410 415

Val Ser Pro Met Asn Leu Ile Tyr Val Arg Lys Val Gly Tyr Gly Val
420 425 430

Arg Asn Val Glu Glu Ile Ile Asn Thr Asn Gly Leu Phe Thr Glu Glu
435 440 445

Lys Ser Asp Leu Ser Gly Met Thr Lys Gln Ser Asp Tyr Asn Pro Glu
450 455 460

Asp Ile Gln Met Leu Gln His Ile Leu Lys Lys Ala Met Glu Lys Ile
465 470 475 480

Lys

<210> 101
<211> 1167
<212> DNA
<213> c. ragsdalei

<400> 101
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aaaaacctag atggaaaaaa agctgtcatt gtcgtaggtg gaggatccat gaaaagattt 120

ggattccttg ataaggtagt agactactta aaagaagcag gtattgaatc aaaattaata 180

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gaaggcgttg agccagatcc atccgtagaa actgttatga atggtgctaa actaatgagg      240

gaatatgggc cagatttaat aatatcaata ggtggaggtt caccaattga tgcagcaaaa      300

gctatgtgga tattctatga ataccctgag tttactttta aagaagctgt agttcctttt      360

ggtcttccta aattaagaca aaaagcaaca tttatagcta tcccttctac aagtggtact      420

gcaacggaag taactgcatt ttctgtaata acagactata aagctaaaat taaatatcct      480

ttggctgact tcaatttaac accagatata gctataattg atccagtatt agctcaaaca      540

atgccgccta aattaactgc acatactgga atggatgcac ttactcacgc tattgaagca      600

tatgttgcag gacttcattc agttttctcg gacccacttg ctattcaagc tatagtcatg      660

gtaaatcaat atttaattaa atcttacaat gaagataaag aagctaggga tcaaatgcat      720

ttagctcaat gtttagctgg aatggcattt tcaaatgcac ttcttggaat aactcacagt      780

ttagcacata aaacaggtgc agtattccat atccctcatg gatgtgctaa tgcaatatat      840

cttccttatg ttatagattt caataaaaaa gcttgtgcac caagatatgc tgatatagct      900

aggagtctta aacttccagg aaatactgat gatgaattag tagattcatt aactaatatg      960

attaaagata tgaacaagag tatggatatt cctttgacat taaaagatta tggagtagat     1020

gaaaaagaat ttaaagatag tgaagatttt atagctcata atgccgtatt agatgcctgt     1080

actggatcaa atcctagaag cataaatgat gctgaaatga aaaagttgtt agaatacatc     1140

tattatggta aaaaggttga tttttaa                                         1167
```

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<210>  102
<211>  388
<212>  PRT
<213>  c. ragsdalei

<400>  102

Met Ala Arg Phe Thr Leu Pro Arg Asp Ile Tyr Phe Gly Glu Asn Ser
1               5                   10                  15


Leu Glu Thr Leu Lys Asn Leu Asp Gly Lys Lys Ala Val Ile Val Val
            20                  25                  30


Gly Gly Gly Ser Met Lys Arg Phe Gly Phe Leu Asp Lys Val Val Asp
        35                  40                  45


Tyr Leu Lys Glu Ala Gly Ile Glu Ser Lys Leu Ile Glu Gly Val Glu
    50                  55                  60


Pro Asp Pro Ser Val Glu Thr Val Met Asn Gly Ala Lys Leu Met Arg
65                  70                  75                  80


Glu Tyr Gly Pro Asp Leu Ile Ile Ser Ile Gly Gly Gly Ser Pro Ile
                85                  90                  95


Asp Ala Ala Lys Ala Met Trp Ile Phe Tyr Glu Tyr Pro Glu Phe Thr
            100                 105                 110
```

```
Phe Lys Glu Ala Val Val Pro Phe Gly Leu Pro Lys Leu Arg Gln Lys
        115                 120                 125

Ala Thr Phe Ile Ala Ile Pro Ser Thr Ser Gly Thr Ala Thr Glu Val
    130                 135                 140

Thr Ala Phe Ser Val Ile Thr Asp Tyr Lys Ala Lys Ile Lys Tyr Pro
145                 150                 155                 160

Leu Ala Asp Phe Asn Leu Thr Pro Asp Ile Ala Ile Ile Asp Pro Val
                165                 170                 175

Leu Ala Gln Thr Met Pro Pro Lys Leu Thr Ala His Thr Gly Met Asp
            180                 185                 190

Ala Leu Thr His Ala Ile Glu Ala Tyr Val Ala Gly Leu His Ser Val
        195                 200                 205

Phe Ser Asp Pro Leu Ala Ile Gln Ala Ile Val Met Val Asn Gln Tyr
    210                 215                 220

Leu Ile Lys Ser Tyr Asn Glu Asp Lys Glu Ala Arg Asp Gln Met His
225                 230                 235                 240

Leu Ala Gln Cys Leu Ala Gly Met Ala Phe Ser Asn Ala Leu Leu Gly
                245                 250                 255

Ile Thr His Ser Leu Ala His Lys Thr Gly Ala Val Phe His Ile Pro
            260                 265                 270

His Gly Cys Ala Asn Ala Ile Tyr Leu Pro Tyr Val Ile Asp Phe Asn
        275                 280                 285

Lys Lys Ala Cys Ala Pro Arg Tyr Ala Asp Ile Ala Arg Ser Leu Lys
    290                 295                 300

Leu Pro Gly Asn Thr Asp Asp Glu Leu Val Asp Ser Leu Thr Asn Met
305                 310                 315                 320

Ile Lys Asp Met Asn Lys Ser Met Asp Ile Pro Leu Thr Leu Lys Asp
                325                 330                 335

Tyr Gly Val Asp Glu Lys Glu Phe Lys Asp Ser Glu Asp Phe Ile Ala
            340                 345                 350

His Asn Ala Val Leu Asp Ala Cys Thr Gly Ser Asn Pro Arg Ser Ile
        355                 360                 365

Asn Asp Ala Glu Met Lys Lys Leu Leu Glu Tyr Ile Tyr Tyr Gly Lys
    370                 375                 380
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Lys Val Asp Phe
385

<210> 103
<211> 1167
<212> DNA
<213> c. ragsdalei

<400> 103
atgggaagat ttactttgcc tagggatatt tactttggtg aaaatgcctt agaaaattta 60

aaaaatttag atggaaataa agcagtagtt gttgtaggtg gaggatctat gaagagattt 120

gggttcttag ccaaagttga agaatactta aaagaagcag gtatggaagt taaattaata 180

gaaggtgttg agcctgatcc atctgttgat actgttatga atggtgctaa aataatgaga 240

gactttaatc cagactggat agtatcaata ggtggaggat ctcccatcga tgctgccaaa 300

gcaatgtgga tattttatga ataccctgac tttacatttg aaaaagcggt agtccctttt 360

gggattccta aattaaggca aaaggcacaa tttgttgcta taccttctac aagtggaaca 420

gcaactgaag taacatcatt ttctgtaata acagactata aagctaaaat aaaatatcct 480

cttgcagatt ttaaccttac ccctgatata gctataatag atccgtctct tgcagaaaca 540

atgcctaaaa agcttacagc acacactgga atggatgcac ttactcacgc aatagaagca 600

tatgtggcaa gtttacattc agatttctca gatccacttg ctatgcatgc tataaccatg 660

attcataaat atttattgaa atcctatgaa gaagataaag aagctagggg ccatatgcac 720

atagcccaat gtctagctgg aatggcattt tcaaatgcac tccttggaat aactcatagt 780

atagcacata aaactggcgc agtattccac atacctcatg ggtgtgctaa tgccatatac 840

ttaccttatg ttatagattt taacaagaaa gcttgttcag aaagatatgc taaaatagct 900

aaaaagcttc atctatcagg gaatagtgaa gatgaattaa tagattcatt aacagaaatg 960

atttgtacta tgaataaaaa gatggatatt cctcttacta taaaagatta tggtataagc 1020

gaaaacgatt ttaatgaaaa cctagatttt atagctcaca atgctatgat ggatgcttgc 1080

actggatcta atcctagagc aataactgag gaagaaatga aaaagctctt gcagtatatg 1140

tataatgggc aaaaggttaa tttctag 1167

<210> 104
<211> 388
<212> PRT
<213> c. ragsdalei

<400> 104

Met Gly Arg Phe Thr Leu Pro Arg Asp Ile Tyr Phe Gly Glu Asn Ala
1 5 10 15

Leu Glu Asn Leu Lys Asn Leu Asp Gly Asn Lys Ala Val Val Val Val
20 25 30

```
Gly Gly Gly Ser Met Lys Arg Phe Gly Phe Leu Ala Lys Val Glu Glu
        35                  40                  45

Tyr Leu Lys Glu Ala Gly Met Glu Val Lys Leu Ile Glu Gly Val Glu
    50                  55                  60

Pro Asp Pro Ser Val Asp Thr Val Met Asn Gly Ala Lys Ile Met Arg
65                  70                  75                  80

Asp Phe Asn Pro Asp Trp Ile Val Ser Ile Gly Gly Gly Ser Pro Ile
                85                  90                  95

Asp Ala Ala Lys Ala Met Trp Ile Phe Tyr Glu Tyr Pro Asp Phe Thr
            100                 105                 110

Phe Glu Lys Ala Val Val Pro Phe Gly Ile Pro Lys Leu Arg Gln Lys
        115                 120                 125

Ala Gln Phe Val Ala Ile Pro Ser Thr Ser Gly Thr Ala Thr Glu Val
    130                 135                 140

Thr Ser Phe Ser Val Ile Thr Asp Tyr Lys Ala Lys Ile Lys Tyr Pro
145                 150                 155                 160

Leu Ala Asp Phe Asn Leu Thr Pro Asp Ile Ala Ile Ile Asp Pro Ser
                165                 170                 175

Leu Ala Glu Thr Met Pro Lys Lys Leu Thr Ala His Thr Gly Met Asp
            180                 185                 190

Ala Leu Thr His Ala Ile Glu Ala Tyr Val Ala Ser Leu His Ser Asp
        195                 200                 205

Phe Ser Asp Pro Leu Ala Met His Ala Ile Thr Met Ile His Lys Tyr
    210                 215                 220

Leu Leu Lys Ser Tyr Glu Glu Asp Lys Glu Ala Arg Gly His Met His
225                 230                 235                 240

Ile Ala Gln Cys Leu Ala Gly Met Ala Phe Ser Asn Ala Leu Leu Gly
                245                 250                 255

Ile Thr His Ser Ile Ala His Lys Thr Gly Ala Val Phe His Ile Pro
            260                 265                 270

His Gly Cys Ala Asn Ala Ile Tyr Leu Pro Tyr Val Ile Asp Phe Asn
        275                 280                 285

Lys Lys Ala Cys Ser Glu Arg Tyr Ala Lys Ile Ala Lys Lys Leu His
    290                 295                 300
```

Leu Ser Gly Asn Ser Glu Asp Glu Leu Ile Asp Ser Leu Thr Glu Met
305 310 315 320

Ile Cys Thr Met Asn Lys Lys Met Asp Ile Pro Leu Thr Ile Lys Asp
325 330 335

Tyr Gly Ile Ser Glu Asn Asp Phe Asn Glu Asn Leu Asp Phe Ile Ala
340 345 350

His Asn Ala Met Met Asp Ala Cys Thr Gly Ser Asn Pro Arg Ala Ile
355 360 365

Thr Glu Glu Glu Met Lys Lys Leu Leu Gln Tyr Met Tyr Asn Gly Gln
370 375 380

Lys Val Asn Phe
385

<210> 105
<211> 1359
<212> DNA
<213> c. ragsdalei

<400> 105
atgattttaa aaactaaact ttttgggcaa acttatgaat ttaaaaatat gaaggaagta 60
ttggcaaaag ctaatgaaga aaaatcggga gatgctttag ctggaatcat agcaaaaagt 120
acagcggaga gagttgcagc aaaggttgtt ttgtctgaaa taactcttga ggaattaagg 180
aataatcctg tagttcctta tgaggaggat gaagtaacaa gagtaataca agatatgatt 240
gataaagaag cctataataa aatcaaagct atgacagttg gcgaatttag agaatttata 300
ttaaaatcag aagaagccga tataaaagaa ataagagatg gattaacttc tgagatgata 360
gcaggtgtaa ctaagcttat gagtaatatg gacttagtat atgcttctaa aaaaataaga 420
aatattgcta cttgcaatac tactattggt gaaaagggaa cagtctcttc aagacttcag 480
cctaatcatg cagcagatag tatagatgga attatggctt ctgtaatgga agggataagc 540
tatggtatag gtgatgctgt aataggttta aaccctgtag tagataccat agataatata 600
tcagagattt tgaaaaattt taagcagttc atgataaaat gggatatacc tacacaaaat 660
tgtgtacttg ctcatataac aacgcaaatg gaggctttaa agaaaggagt tcctatggat 720
ctgatgttcc agagtatagc tggttcacaa aaatccaata aaggctttgg aataagtgtg 780
aagcttatgg atgaagctta tgaacttatg aaggaaaaaa agagctccaa aggtcctaat 840
tttatgtatt ttgaaacagg ccagggttct gagctttctt cagaaggcca taatggagca 900
gatcagctta caatggaagc aagatgttat ggtcttgcaa aaaaatataa tccattcctt 960
gtaaactctg tggtgggatt cataggacca gaatatctat atgatggaaa acaaattata 1020
agagcaggct tagaagatca ttttatgggt aagttaacag gacttcctat gggtgttgat 1080
gtatgttata caaaccatat gaaagcagat caaaatgatt tggaaaattt agcattactc 1140

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cttgcagcag ctgactgtac ttattttatg ggtatacctg gaggagatga cgtaatgctt      1200

atgtatcaaa ctaccagcta tcatgatgta gcttctatca gggacattat gcgtaaaaat      1260

cctataaaag aatttgaaga aagaatggaa gctctaggaa taatgaaaaa tggaaggctc      1320

acagaaatag ctggtgatcc atctatattt atgatttag                             1359
```

```
<210>  106
<211>  452
<212>  PRT
<213>  c. ragsdalei

<400>  106

Met Ile Leu Lys Thr Lys Leu Phe Gly Gln Thr Tyr Glu Phe Lys Asn
1               5                   10                  15

Met Lys Glu Val Leu Ala Lys Ala Asn Glu Glu Lys Ser Gly Asp Ala
            20                  25                  30

Leu Ala Gly Ile Ile Ala Lys Ser Thr Ala Glu Arg Val Ala Ala Lys
        35                  40                  45

Val Val Leu Ser Glu Ile Thr Leu Glu Glu Leu Arg Asn Asn Pro Val
    50                  55                  60

Val Pro Tyr Glu Glu Asp Glu Val Thr Arg Val Ile Gln Asp Met Ile
65                  70                  75                  80

Asp Lys Glu Ala Tyr Asn Lys Ile Lys Ala Met Thr Val Gly Glu Phe
                85                  90                  95

Arg Glu Phe Ile Leu Lys Ser Glu Glu Ala Asp Ile Lys Glu Ile Arg
            100                 105                 110

Asp Gly Leu Thr Ser Glu Met Ile Ala Gly Val Thr Lys Leu Met Ser
        115                 120                 125

Asn Met Asp Leu Val Tyr Ala Ser Lys Lys Ile Arg Asn Ile Ala Thr
    130                 135                 140

Cys Asn Thr Thr Ile Gly Glu Lys Gly Thr Val Ser Ser Arg Leu Gln
145                 150                 155                 160

Pro Asn His Ala Ala Asp Ser Ile Asp Gly Ile Met Ala Ser Val Met
                165                 170                 175

Glu Gly Ile Ser Tyr Gly Ile Gly Asp Ala Val Ile Gly Leu Asn Pro
            180                 185                 190

Val Val Asp Thr Ile Asp Asn Ile Ser Glu Ile Leu Lys Asn Phe Lys
        195                 200                 205
```

```
Gln Phe Met Ile Lys Trp Asp Ile Pro Thr Gln Asn Cys Val Leu Ala
    210                 215                 220

His Ile Thr Thr Gln Met Glu Ala Leu Lys Lys Gly Val Pro Met Asp
225                 230                 235                 240

Leu Met Phe Gln Ser Ile Ala Gly Ser Gln Lys Ser Asn Lys Gly Phe
                245                 250                 255

Gly Ile Ser Val Lys Leu Met Asp Glu Ala Tyr Glu Leu Met Lys Glu
            260                 265                 270

Lys Lys Ser Ser Lys Gly Pro Asn Phe Met Tyr Phe Glu Thr Gly Gln
        275                 280                 285

Gly Ser Glu Leu Ser Ser Glu Gly His Asn Gly Ala Asp Gln Leu Thr
    290                 295                 300

Met Glu Ala Arg Cys Tyr Gly Leu Ala Lys Lys Tyr Asn Pro Phe Leu
305                 310                 315                 320

Val Asn Ser Val Val Gly Phe Ile Gly Pro Glu Tyr Leu Tyr Asp Gly
                325                 330                 335

Lys Gln Ile Ile Arg Ala Gly Leu Glu Asp His Phe Met Gly Lys Leu
            340                 345                 350

Thr Gly Leu Pro Met Gly Val Asp Val Cys Tyr Thr Asn His Met Lys
        355                 360                 365

Ala Asp Gln Asn Asp Leu Glu Asn Leu Ala Leu Leu Leu Ala Ala Ala
    370                 375                 380

Asp Cys Thr Tyr Phe Met Gly Ile Pro Gly Gly Asp Asp Val Met Leu
385                 390                 395                 400

Met Tyr Gln Thr Thr Ser Tyr His Asp Val Ala Ser Ile Arg Asp Ile
                405                 410                 415

Met Arg Lys Asn Pro Ile Lys Glu Phe Glu Glu Arg Met Glu Ala Leu
            420                 425                 430

Gly Ile Met Lys Asn Gly Arg Leu Thr Glu Ile Ala Gly Asp Pro Ser
        435                 440                 445

Ile Phe Met Ile
    450
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<210> 107
<211> 1176
<212> DNA
<213> C. ragsdalei

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<400>  107
atggaaaact ttatttttaa aaatgctaca gaaattattt ttggtaagga taccgaagat      60

cttgtaggaa gtaaagtaaa ggagtattca aagtcagata aaatactctt ttgctatggg     120

ggaggaagta taaagagatc gggcctctat gatagagtta taaagtcctt aaaagaaaat     180

ggaattgaat ttatagaact tccaggaatt aaacctaatc caagattagg acctgttaaa     240

gaaggtataa gactatgtag agaaaataat ataaaatttg tactatctgt aggaggagga     300

agttcagcag atacagctaa agctattgct gtaggagtac cttataaagg agatgtatgg     360

gatttttata cgggcaaagc tgaagtaaaa gaggctcttc ctgtaggagt tgtaataaca     420

ttacctgcta caggtacaga atctagtaat agttctgtta ttatgaatga agatggttgg     480

tttaaaaaag gattaaatac ggtacttata agacctgctt tttcaattat gaatcctgaa     540

cttactttta cactaccaga atatcaaact gcttgtggtg cttgtgacat tatggcacat     600

ataatggaaa gatattttac aaatgtgaaa catgtagatt taactgatag gctttgcgaa     660

gctgcactta gaaatgttat aaataatgcc ccaatagttt taaaagatcc taaaaattat     720

gatgctaggg cagaaattat gtggactggt actatagctc ataatgatgt gcttagtaca     780

ggtagaatag gtgattgggc ttctcacaaa attgaacatg aattaagtgg ggaaacagat     840

attgcccatg gagcaggact tgcaattgta tttcctgcat ggatgaaata tgtatataaa     900

catgatatca atagatttgt acaatttgca gtaagggtat gggatgtaga tttatcttat     960

agttcctgtg aagatattgt acttgaaggc ataaggagaa tgacagcatt tttcaagagc    1020

atggggttac ctataacttt aaaagaagga agtataggag aagataaaat tgaagaaatg    1080

gctaataagt gcacggataa tggaaccaaa actgtaggac aatttgtaaa actaaataaa    1140

gatgatattg taaaaatatt aaatttagct agataa                               1176

<210>  108
<211>  391
<212>  PRT
<213>  c. ragsdalei

<400>  108

Met Glu Asn Phe Ile Phe Lys Asn Ala Thr Glu Ile Ile Phe Gly Lys
1               5                   10                  15


Asp Thr Glu Asp Leu Val Gly Ser Lys Val Lys Glu Tyr Ser Lys Ser
            20                  25                  30


Asp Lys Ile Leu Phe Cys Tyr Gly Gly Gly Ser Ile Lys Arg Ser Gly
        35                  40                  45


Leu Tyr Asp Arg Val Ile Lys Ser Leu Lys Glu Asn Gly Ile Glu Phe
    50                  55                  60


Ile Glu Leu Pro Gly Ile Lys Pro Asn Pro Arg Leu Gly Pro Val Lys
65                  70                  75                  80
```

SequenceListing

```
Glu Gly Ile Arg Leu Cys Arg Glu Asn Asn Ile Lys Phe Val Leu Ser
                85                  90                  95

Val Gly Gly Gly Ser Ser Ala Asp Thr Ala Lys Ala Ile Ala Val Gly
            100                 105                 110

Val Pro Tyr Lys Gly Asp Val Trp Asp Phe Tyr Thr Gly Lys Ala Glu
        115                 120                 125

Val Lys Glu Ala Leu Pro Val Gly Val Val Ile Thr Leu Pro Ala Thr
    130                 135                 140

Gly Thr Glu Ser Ser Asn Ser Ser Val Ile Met Asn Glu Asp Gly Trp
145                 150                 155                 160

Phe Lys Lys Gly Leu Asn Thr Val Leu Ile Arg Pro Ala Phe Ser Ile
                165                 170                 175

Met Asn Pro Glu Leu Thr Phe Thr Leu Pro Glu Tyr Gln Thr Ala Cys
            180                 185                 190

Gly Ala Cys Asp Ile Met Ala His Ile Met Glu Arg Tyr Phe Thr Asn
        195                 200                 205

Val Lys His Val Asp Leu Thr Asp Arg Leu Cys Glu Ala Ala Leu Arg
    210                 215                 220

Asn Val Ile Asn Asn Ala Pro Ile Val Leu Lys Asp Pro Lys Asn Tyr
225                 230                 235                 240

Asp Ala Arg Ala Glu Ile Met Trp Thr Gly Thr Ile Ala His Asn Asp
                245                 250                 255

Val Leu Ser Thr Gly Arg Ile Gly Asp Trp Ala Ser His Lys Ile Glu
            260                 265                 270

His Glu Leu Ser Gly Glu Thr Asp Ile Ala His Gly Ala Gly Leu Ala
        275                 280                 285

Ile Val Phe Pro Ala Trp Met Lys Tyr Val Tyr Lys His Asp Ile Asn
    290                 295                 300

Arg Phe Val Gln Phe Ala Val Arg Val Trp Asp Val Asp Leu Ser Tyr
305                 310                 315                 320

Ser Ser Cys Glu Asp Ile Val Leu Glu Gly Ile Arg Arg Met Thr Ala
                325                 330                 335

Phe Phe Lys Ser Met Gly Leu Pro Ile Thr Leu Lys Glu Gly Ser Ile
            340                 345                 350
```

Gly Glu Asp Lys Ile Glu Glu Met Ala Asn Lys Cys Thr Asp Asn Gly
        355   360   365

Thr Lys Thr Val Gly Gln Phe Val Lys Leu Asn Lys Asp Asp Ile Val
    370   375   380

Lys Ile Leu Asn Leu Ala Arg
385   390

<210> 109
<211> 1149
<212> DNA
<213> c. ragsdalei

<400> 109
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atacaacttt tagagcaggt tactggctct cgagcattta ttgttgcaga tgccattatg 120

ggaaaacttg gatatcttca aaaagtaata gattccctaa gtaaagccgg aataagttcc 180

gttgttttta cgggagtaca ccctgatcca gatgtcaatg taattgcaga tgcaatgaaa 240

ttgtacaaca aaagcgatgc agatgttctc gttgcactag gtggaggctc cagcattgat 300

accgccaaag gaataatgta ttttgcatgt aatttaggaa aagcaatggg ccaggaaatg 360

aaaaagcccc tgtttattgc aattccatca acaagtggaa caggctctga agtaacaaac 420

tttactgtta ttacttctca gaaagaaaag gtatgcattg tagatgattt tattgcacca 480

gacgttgcaa tacttgactc tagttgtatt gatggtctgc ctcaacgtat tgtagcagat 540

actggtatag atgttctagt tcattctatt gaagcctatg tttccaaaaa agcaactgac 600

tttacagacg ctcttgctga aaaagcagtt aaattgattt ttgagaatct tccaaaaatt 660

tataacgata gtaaagattc tgaagctcga gatcatgttc aaaacgcttc ttgtatagca 720

ggaatagcat ttacaaatgc tggtcttgga attaatcaca gcttggctca tgctatgggt 780

ggatcttttc acattcctca cggccgatcc aatgcacttt tacttaatgc agtaatggaa 840

tacaatgcta gcttagtggg aaatgcaaac gatcatgcta tggaaaaata cgcaaaacta 900

gcatcagttc tacaccttcc agctcgaaca actcgtgaag gcgctgtaag ttttatcgaa 960

gctgtaaata aattaataaa atccctaggt gttgaagata atattcgagc tcttggaatt 1020

aaagaagacg attttcaagg tgctctaaat catatggcag aaacagcaat gcaagataga 1080

tgcactccaa ctaatcctag aaaaccttct aaagaagaac tgatacatat ttatcaaaaa 1140

tgctattaa 1149

<210> 110
<211> 382
<212> PRT
<213> c. ragsdalei

<400> 110

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Met Glu Asp Lys Phe Glu Asn Phe Asn Leu Lys Ser Lys Ile Tyr Phe
1               5                   10                  15

Asn Arg Glu Ser Ile Gln Leu Leu Glu Gln Val Thr Gly Ser Arg Ala
            20                  25                  30

Phe Ile Val Ala Asp Ala Ile Met Gly Lys Leu Gly Tyr Leu Gln Lys
        35                  40                  45

Val Ile Asp Ser Leu Ser Lys Ala Gly Ile Ser Ser Val Val Phe Thr
    50                  55                  60

Gly Val His Pro Asp Pro Asp Val Asn Val Ile Ala Asp Ala Met Lys
65                  70                  75                  80

Leu Tyr Asn Lys Ser Asp Ala Asp Val Leu Val Ala Leu Gly Gly Gly
                85                  90                  95

Ser Ser Ile Asp Thr Ala Lys Gly Ile Met Tyr Phe Ala Cys Asn Leu
            100                 105                 110

Gly Lys Ala Met Gly Gln Glu Met Lys Lys Pro Leu Phe Ile Ala Ile
        115                 120                 125

Pro Ser Thr Ser Gly Thr Gly Ser Glu Val Thr Asn Phe Thr Val Ile
    130                 135                 140

Thr Ser Gln Lys Glu Lys Val Cys Ile Val Asp Asp Phe Ile Ala Pro
145                 150                 155                 160

Asp Val Ala Ile Leu Asp Ser Ser Cys Ile Asp Gly Leu Pro Gln Arg
                165                 170                 175

Ile Val Ala Asp Thr Gly Ile Asp Val Leu Val His Ser Ile Glu Ala
            180                 185                 190

Tyr Val Ser Lys Lys Ala Thr Asp Phe Thr Asp Ala Leu Ala Glu Lys
        195                 200                 205

Ala Val Lys Leu Ile Phe Glu Asn Leu Pro Lys Ile Tyr Asn Asp Ser
    210                 215                 220

Lys Asp Ser Glu Ala Arg Asp His Val Gln Asn Ala Ser Cys Ile Ala
225                 230                 235                 240

Gly Ile Ala Phe Thr Asn Ala Gly Leu Gly Ile Asn His Ser Leu Ala
                245                 250                 255

His Ala Met Gly Gly Ser Phe His Ile Pro His Gly Arg Ser Asn Ala
            260                 265                 270
```

```
Leu Leu Leu Asn Ala Val Met Glu Tyr Asn Ala Ser Leu Val Gly Asn
        275                 280                 285

Ala Asn Asp His Ala Met Glu Lys Tyr Ala Lys Leu Ala Ser Val Leu
    290                 295                 300

His Leu Pro Ala Arg Thr Thr Arg Glu Gly Ala Val Ser Phe Ile Glu
305                 310                 315                 320

Ala Val Asn Lys Leu Ile Lys Ser Leu Gly Val Glu Asp Asn Ile Arg
                325                 330                 335

Ala Leu Gly Ile Lys Glu Asp Asp Phe Gln Gly Ala Leu Asn His Met
            340                 345                 350

Ala Glu Thr Ala Met Gln Asp Arg Cys Thr Pro Thr Asn Pro Arg Lys
        355                 360                 365

Pro Ser Lys Glu Glu Leu Ile His Ile Tyr Gln Lys Cys Tyr
    370                 375                 380

<210>  111
<211>  993
<212>  DNA
<213>  C. ragsdalei

<400>  111
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gaagaagaaa gaactcttca agcttgtgaa aaaataatta aagaaggtat tgcaaattta     120

atccttgtag ggaatgaaaa ggtaatagag gagaaggcat caaaattagg cgtaagttta     180

aatggagcag aaatagtaga tccagaaacc tcggataaac taaaaaaata tgcagatgct     240

ttttatgaat tgagaaagaa gaagggaata acaccagaaa aagcggataa aatagtaaga     300

gatccaatat attttgctac gatgatggtt aagcttggag atgcagatgg attggtttca     360

ggtgcagtgc atactacagg tgatcttttg agaccaggac ttcaaatagt aaagacagct     420

ccaggtacat cagtagtttc cagcacattt ataatggaag taccaaattg tgaatatggt     480

gacaatggtg tacttctatt tgctgattgt gctgtaaatc catgcccaga tagtgatcaa     540

ttggcttcaa ttgcaataag tacagcagaa actgcaaaga acttatgtgg aatggatcca     600

aaagtagcaa tgctttcatt ttctactaag ggaagtgcaa aacacgaatt agtagataaa     660

gttagaaatg ctgtagaaat tgccaaaaaa gctaaaccag atttaagttt ggacggagaa     720

ttacaattag atgcctctat cgtagaaaag gttgcaagtt taaaggctcc tgaaagtgaa     780

gtagcaggaa aagcaaatgt acttgtattt ccagatctcc aagcaggaaa tataggttat     840

aaacttgttc aaagatttgc aaaagctgat gctataggac ctgtatgcca gggatttgca     900

aaacctataa atgatttgtc aagaggatgt aactccgatg atatagtaaa tgtagtagct     960

gtaacagcag ttcaggcaca agctcaaaag taa                                  993
```

<210> 112
<211> 330
<212> PRT
<213> c. ragsdalei

<400> 112

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Met Glu Lys Ile Trp Asn Lys Ala Lys Glu Asp Lys Lys Lys Ile Val
1               5                   10                  15

Leu Ala Glu Gly Glu Glu Glu Arg Thr Leu Gln Ala Cys Glu Lys Ile
            20                  25                  30

Ile Lys Glu Gly Ile Ala Asn Leu Ile Leu Val Gly Asn Glu Lys Val
        35                  40                  45

Ile Glu Glu Lys Ala Ser Lys Leu Gly Val Ser Leu Asn Gly Ala Glu
    50                  55                  60

Ile Val Asp Pro Glu Thr Ser Asp Lys Leu Lys Lys Tyr Ala Asp Ala
65                  70                  75                  80

Phe Tyr Glu Leu Arg Lys Lys Lys Gly Ile Thr Pro Glu Lys Ala Asp
                85                  90                  95

Lys Ile Val Arg Asp Pro Ile Tyr Phe Ala Thr Met Met Val Lys Leu
            100                 105                 110

Gly Asp Ala Asp Gly Leu Val Ser Gly Ala Val His Thr Thr Gly Asp
        115                 120                 125

Leu Leu Arg Pro Gly Leu Gln Ile Val Lys Thr Ala Pro Gly Thr Ser
    130                 135                 140

Val Val Ser Ser Thr Phe Ile Met Glu Val Pro Asn Cys Glu Tyr Gly
145                 150                 155                 160

Asp Asn Gly Val Leu Leu Phe Ala Asp Cys Ala Val Asn Pro Cys Pro
                165                 170                 175

Asp Ser Asp Gln Leu Ala Ser Ile Ala Ile Ser Thr Ala Glu Thr Ala
            180                 185                 190

Lys Asn Leu Cys Gly Met Asp Pro Lys Val Ala Met Leu Ser Phe Ser
        195                 200                 205

Thr Lys Gly Ser Ala Lys His Glu Leu Val Asp Lys Val Arg Asn Ala
    210                 215                 220

Val Glu Ile Ala Lys Lys Ala Lys Pro Asp Leu Ser Leu Asp Gly Glu
225                 230                 235                 240
```

```
Leu Gln Leu Asp Ala Ser Ile Val Glu Lys Val Ala Ser Leu Lys Ala
                245                 250                 255

Pro Glu Ser Glu Val Ala Gly Lys Ala Asn Val Leu Val Phe Pro Asp
            260                 265                 270

Leu Gln Ala Gly Asn Ile Gly Tyr Lys Leu Val Gln Arg Phe Ala Lys
        275                 280                 285

Ala Asp Ala Ile Gly Pro Val Cys Gln Gly Phe Ala Lys Pro Ile Asn
    290                 295                 300

Asp Leu Ser Arg Gly Cys Asn Ser Asp Asp Ile Val Asn Val Val Ala
305                 310                 315                 320

Val Thr Ala Val Gln Ala Gln Ala Gln Lys
                325                 330


<210>  113
<211>  1197
<212>  DNA
<213>  C. ragsdalei

<400>  113
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aaagatgaaa gcgttgtggc aaaaggactt gtagaaagaa taggagcaga aggttcagtt     120

ttaacacata aagttaacgg agaaaagttt gttacagagc agccaatgga agatcataaa     180

gttgctatac aattagtatt aaatgctctt gtagataaaa aacatggtgt aataaaagat     240

atgtcagaaa tatctgctgt agggcataga gttttgcatg gtggaaaaaa atatgcggca     300

tccattctta ttgatgacaa tgtaatgaaa gcaatagaag aatgtattcc attaggacca     360

ttacataatc cagctaatat aatgggaata gatgcttgta aaaaactaat gccaaatact     420

ccaatggtag cagtatttga tacagcattt catcagacaa tgccagatta tgcttatact     480

tatgcaatac cttatgatat atctgaaaag tatgatatca gaaaatatgg ttttcatgga     540

acttctcata gattcgtttc aattgaagca gccaagttgt taaagaaaga tccaaaagat     600

cttaagctaa taacttgtca tttaggaaat ggagctagta tatgtgcagt aaaccaggga     660

aaagcagtag atacaactat gggacttact ccccttgcag gacttgtaat gggaactaga     720

tgtggtgata tagatccagc tataatacca tttgtaatga aaagaacagg tatgtctgta     780

gatgaaatgg atactttaat gaacaaaaag tcaggaatac ttggagtatc aggagtaagc     840

agcgatttta gagatgtaga agaagctgca aattcaggaa atgatagagc aaaacttgca     900

ttaaatatgt attatcacaa agttaaatct ttcataggag cttatgttgc agttttaaat     960

ggagcagatg ctataatatt tacagcagga cttggagaaa attcagctac tagcagatct    1020

gctatatgta agggattaag ctattttgga attaaaatag atgaagaaaa gaataagaaa    1080

aggggagaag cactagaaat aagcacacct gattcaaaga taaaagtatt agtaattcct    1140
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acaaatgaag aacttatgat agctagggat acaaaagaaa tagttgaaaa taaataa        1197


<210>  114
<211>  398
<212>  PRT
<213>  c. ragsdalei

<400>  114

Met Lys Ile Leu Val Val Asn Cys Gly Ser Ser Ser Leu Lys Tyr Gln
1               5                   10                  15


Leu Ile Asp Met Lys Asp Glu Ser Val Val Ala Lys Gly Leu Val Glu
            20                  25                  30


Arg Ile Gly Ala Glu Gly Ser Val Leu Thr His Lys Val Asn Gly Glu
        35                  40                  45


Lys Phe Val Thr Glu Gln Pro Met Glu Asp His Lys Val Ala Ile Gln
    50                  55                  60


Leu Val Leu Asn Ala Leu Val Asp Lys Lys His Gly Val Ile Lys Asp
65                  70                  75                  80


Met Ser Glu Ile Ser Ala Val Gly His Arg Val Leu His Gly Gly Lys
                85                  90                  95


Lys Tyr Ala Ala Ser Ile Leu Ile Asp Asp Asn Val Met Lys Ala Ile
            100                 105                 110


Glu Glu Cys Ile Pro Leu Gly Pro Leu His Asn Pro Ala Asn Ile Met
        115                 120                 125


Gly Ile Asp Ala Cys Lys Lys Leu Met Pro Asn Thr Pro Met Val Ala
    130                 135                 140


Val Phe Asp Thr Ala Phe His Gln Thr Met Pro Asp Tyr Ala Tyr Thr
145                 150                 155                 160


Tyr Ala Ile Pro Tyr Asp Ile Ser Glu Lys Tyr Asp Ile Arg Lys Tyr
                165                 170                 175


Gly Phe His Gly Thr Ser His Arg Phe Val Ser Ile Glu Ala Ala Lys
            180                 185                 190


Leu Leu Lys Lys Asp Pro Lys Asp Leu Lys Leu Ile Thr Cys His Leu
        195                 200                 205


Gly Asn Gly Ala Ser Ile Cys Ala Val Asn Gln Gly Lys Ala Val Asp
    210                 215                 220


Thr Thr Met Gly Leu Thr Pro Leu Ala Gly Leu Val Met Gly Thr Arg
225                 230                 235                 240
```

Cys Gly Asp Ile Asp Pro Ala Ile Ile Pro Phe Val Met Lys Arg Thr
245 250 255

Gly Met Ser Val Asp Glu Met Asp Thr Leu Met Asn Lys Lys Ser Gly
260 265 270

Ile Leu Gly Val Ser Gly Val Ser Ser Asp Phe Arg Asp Val Glu Glu
275 280 285

Ala Ala Asn Ser Gly Asn Asp Arg Ala Lys Leu Ala Leu Asn Met Tyr
290 295 300

Tyr His Lys Val Lys Ser Phe Ile Gly Ala Tyr Val Ala Val Leu Asn
305 310 315 320

Gly Ala Asp Ala Ile Ile Phe Thr Ala Gly Leu Gly Glu Asn Ser Ala
325 330 335

Thr Ser Arg Ser Ala Ile Cys Lys Gly Leu Ser Tyr Phe Gly Ile Lys
340 345 350

Ile Asp Glu Glu Lys Asn Lys Lys Arg Gly Glu Ala Leu Glu Ile Ser
355 360 365

Thr Pro Asp Ser Lys Ile Lys Val Leu Val Ile Pro Thr Asn Glu Glu
370 375 380

Leu Met Ile Ala Arg Asp Thr Lys Glu Ile Val Glu Asn Lys
385 390 395

<210> 115
<211> 1824
<212> DNA
<213> c. ragsdalei

<400> 115
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gaagaattga aaattgacaa agctaaaaaa tttataggtg caagaggttt aggcgtaaaa 120

accttatttg acgaagtaga tccaaaggta gatccattat cacctgataa caaatttatt 180

atagcagcgg gaccacttac aggtgcgcct gttccaacaa gcggaagatt catggtagtt 240

actaaatcac ctttaacagg aactattgct attgcaaatt caggtggaaa atggggagca 300

gaattcaaag cagctggata cgatatgata atcgttgaag gtaaatctga taaagaagtt 360

tatgtaaata tagtagatga taaagtagaa tttagggatg cttctcatgt ttggggaaaa 420

ctaacagaag aaactacaaa aatgcttcaa caggaaacag attcgagagc taaggtttta 480

tgcataggac cagctgggga aaaattatca cttatggcag cagttatgaa tgatgttgat 540

agaacagcag gacgtggtgg tgttggagct gttatgggct caaagaactt aaaagctatt 600 gtagttaaag gaagcggaaa agtaaaatta tttgatgagc aaaaagtgaa agaagtagca 660

cttgagaaaa caaatatttt aagaaaagat ccagtagctg gtggaggact tccaacatac 720

ggaacagctg tacttgttaa tattataaat gaaaatggcg tacatccagt aaaaaatttc 780

caaaaatctt atacagatca ggcagataag atcagtggag aaactttaac taaagattgc 840

ttagttagaa aaaatccttg ctataggtgt ccaattgcct gtggaagatg ggtaaaactt 900

gatgatggaa ctgaatgtgg aggaccagaa tatgaaacat tatggtcatt tggatctgat 960

tgtgatgtat acgatataaa tgctgtaaat acagcaaata tgttgtgtaa tgaatatgga 1020

ttagatacca ttacagcagg atgtactatt gcagcagcta tggaacttta tcaaagaggt 1080

tatattaagg atgaagaaat agcagcagat ggattgtcac ttaattgggg agatgctaag 1140

tccatggttg aatgggtaaa gaaaatggga cttagagaag gatttggaga caagatggca 1200

gatggttcat acagactttg tgactcatac ggtgtacctg agtattcaat gactgtaaaa 1260

aaacaagaaa tcccagcata tgacccaaga ggaatacagg gacatggtat aacttatgct 1320

gttaacaata ggggagggtg tcatattaag ggatatatgg taagccctga aatacttggt 1380

tatccagaaa aacttgatag acttgcagtg gaaggaaaag caggatatgc tagagtattc 1440

catgatttaa cagctgttat agattcactt ggattatgta tttttacaac atttggtctt 1500

ggtgcacagg attatgttga tttgtataat gcagtagttg gtggagaatt acatgatgta 1560

gactctttaa tgttagctgg agatagaata tggactttag aaaaaatatt taacttaaag 1620

gcaggcatag atagttcaca ggatactctt ccaaagagat tgcttgagga accagttcca 1680

gaaggaccat caaaaggaga gattcataga ttagatgtac ttcttcctga atattattca 1740

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gatgaatatg taggtaagtt ttaa 1824

<210> 116
<211> 607
<212> PRT
<213> c. ragsdalei

<400> 116

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Met Tyr Gly Tyr Asn Gly Lys Val Leu Arg Ile Asn Leu Ser Ser Lys
1               5                   10                  15

Thr Tyr Ile Val Glu Glu Leu Lys Ile Asp Lys Ala Lys Lys Phe Ile
            20                  25                  30

Gly Ala Arg Gly Leu Gly Val Lys Thr Leu Phe Asp Glu Val Asp Pro
        35                  40                  45

Lys Val Asp Pro Leu Ser Pro Asp Asn Lys Phe Ile Ile Ala Ala Gly
    50                  55                  60

Pro Leu Thr Gly Ala Pro Val Pro Thr Ser Gly Arg Phe Met Val Val
65                  70                  75                  80
```

```
Thr Lys Ser Pro Leu Thr Gly Thr Ile Ala Ile Ala Asn Ser Gly Gly
                85                  90                  95

Lys Trp Gly Ala Glu Phe Lys Ala Ala Gly Tyr Asp Met Ile Ile Val
            100                 105                 110

Glu Gly Lys Ser Asp Lys Glu Val Tyr Val Asn Ile Val Asp Asp Lys
        115                 120                 125

Val Glu Phe Arg Asp Ala Ser His Val Trp Gly Lys Leu Thr Glu Glu
    130                 135                 140

Thr Thr Lys Met Leu Gln Gln Glu Thr Asp Ser Arg Ala Lys Val Leu
145                 150                 155                 160

Cys Ile Gly Pro Ala Gly Glu Lys Leu Ser Leu Met Ala Ala Val Met
                165                 170                 175

Asn Asp Val Asp Arg Thr Ala Gly Arg Gly Gly Val Gly Ala Val Met
            180                 185                 190

Gly Ser Lys Asn Leu Lys Ala Ile Val Val Lys Gly Ser Gly Lys Val
        195                 200                 205

Lys Leu Phe Asp Glu Gln Lys Val Lys Glu Val Ala Leu Glu Lys Thr
    210                 215                 220

Asn Ile Leu Arg Lys Asp Pro Val Ala Gly Gly Gly Leu Pro Thr Tyr
225                 230                 235                 240

Gly Thr Ala Val Leu Val Asn Ile Ile Asn Glu Asn Gly Val His Pro
                245                 250                 255

Val Lys Asn Phe Gln Lys Ser Tyr Thr Asp Gln Ala Asp Lys Ile Ser
            260                 265                 270

Gly Glu Thr Leu Thr Lys Asp Cys Leu Val Arg Lys Asn Pro Cys Tyr
        275                 280                 285

Arg Cys Pro Ile Ala Cys Gly Arg Trp Val Lys Leu Asp Asp Gly Thr
    290                 295                 300

Glu Cys Gly Gly Pro Glu Tyr Glu Thr Leu Trp Ser Phe Gly Ser Asp
305                 310                 315                 320

Cys Asp Val Tyr Asp Ile Asn Ala Val Asn Thr Ala Asn Met Leu Cys
                325                 330                 335

Asn Glu Tyr Gly Leu Asp Thr Ile Thr Ala Gly Cys Thr Ile Ala Ala
            340                 345                 350
```

```
Ala Met Glu Leu Tyr Gln Arg Gly Tyr Ile Lys Asp Glu Glu Ile Ala
        355                 360                 365

Ala Asp Gly Leu Ser Leu Asn Trp Gly Asp Ala Lys Ser Met Val Glu
    370                 375                 380

Trp Val Lys Lys Met Gly Leu Arg Glu Gly Phe Gly Asp Lys Met Ala
385                 390                 395                 400

Asp Gly Ser Tyr Arg Leu Cys Asp Ser Tyr Gly Val Pro Glu Tyr Ser
                405                 410                 415

Met Thr Val Lys Lys Gln Glu Ile Pro Ala Tyr Asp Pro Arg Gly Ile
            420                 425                 430

Gln Gly His Gly Ile Thr Tyr Ala Val Asn Asn Arg Gly Gly Cys His
        435                 440                 445

Ile Lys Gly Tyr Met Val Ser Pro Glu Ile Leu Gly Tyr Pro Glu Lys
    450                 455                 460

Leu Asp Arg Leu Ala Val Glu Gly Lys Ala Gly Tyr Ala Arg Val Phe
465                 470                 475                 480

His Asp Leu Thr Ala Val Ile Asp Ser Leu Gly Leu Cys Ile Phe Thr
                485                 490                 495

Thr Phe Gly Leu Gly Ala Gln Asp Tyr Val Asp Leu Tyr Asn Ala Val
            500                 505                 510

Val Gly Gly Glu Leu His Asp Val Asp Ser Leu Met Leu Ala Gly Asp
        515                 520                 525

Arg Ile Trp Thr Leu Glu Lys Ile Phe Asn Leu Lys Ala Gly Ile Asp
    530                 535                 540

Ser Ser Gln Asp Thr Leu Pro Lys Arg Leu Leu Glu Glu Pro Val Pro
545                 550                 555                 560

Glu Gly Pro Ser Lys Gly Glu Ile His Arg Leu Asp Val Leu Leu Pro
                565                 570                 575

Glu Tyr Tyr Ser Val Arg Gly Trp Asp Lys Asn Gly Ile Pro Thr Glu
            580                 585                 590

Glu Thr Leu Lys Lys Leu Gly Leu Asp Glu Tyr Val Gly Lys Phe
        595                 600                 605

<210>  117
<211>  1824
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<212> DNA
<213> c. ragsdalei

<400> 117
atgtatggtt ataatggtaa agtattaaga attaatttaa aagaaagaac ttgcaaatca 60

gaaaatttag atttagataa agctaaaaag tttataggct gtaggggact aggtgttaaa 120

actttatttg atgaaataga tcctaaaata gatgcattat caccagaaaa taaatttata 180

attgtaacag gtccgttaac tggagctcca gttccaacta gtggaaggtt tatggtagtt 240

actaaagcac cgcttacagg aactatagga atttcaaatt cgggtggaaa atggggagta 300

gacttgaaaa aagctggctg ggatatgata atagtagagg ataaggctga ttcaccagtt 360

tacattgaaa tagtagatga taaagtagaa attaaagatg cgtcacagct ttggggaaaa 420

gttacatcag aaactacaaa agagttagaa aagataactg agaatagatc aaaggtatta 480

tgtataggac ctgctggtga aagattgtcc cttatggcag cagttatgaa tgatgtagat 540

agaactgcag caagaggcgg cgttggtgca gttatgggat ctaaaaactt aaaagctatt 600

acagttaaag gaactggaaa aatagcttta gctgataaag aaaaagtaaa aaaagtgtcc 660

gtagaaaaaa ttacaacatt aaaaaatgat ccagtagctg gtcagggaat gccaacttat 720

ggtacagcta tactggttaa tataataaat gaaaatggag ttcatcctgt aaataatttt 780

caagaatctt atacggatca agcagataaa ataagtggag agactcttac tgctaaccaa 840

ctagtaagga aaaatccttg ttacagctgt cctataggtt gtggaagatg ggttagacta 900

aaagatggta cagagtgcgg aggaccggag tatgaaacac tgtggtgttt tggctctgac 960

tgtggttcat atgatttaga tgctataaat gaagctaata tgttatgtaa tgaatatggt 1020

attgatacta ttacctgtgg tgcaacaatt gctgcagcta tggaacttta tcaaagagga 1080

tatgtaaaag atgaagaaat agccggagat aacctatctc tcaagtgggg agatacggag 1140

tctatgattg gctggataaa gaaaatggta tatagtgaag gctttggagc aaagatgaca 1200

aatggttcat ataggctttg tgaaggttat ggagtacctg agtattctat gacagttaaa 1260

aagcaagaaa ttccagcata tgatccaagg ggaatacagg gacatggtat tacctatgca 1320

gttaataata gaggaggatg tcatattaag ggatatatga ttaatcctga aatattaggt 1380

tatccggaaa aacttgatag atttgcatta gatggtaaag cagcctatgc caaaatgatg 1440

catgatttaa ctgctgtaat tgattcttta ggattgtgca tattcactac atttgggctt 1500

ggaatacagg attatgtaga tatgtataat gcagtagtag gagaatctac ttgtgattca 1560

gattcactat tagaggcagg agatagagta tggactcttg aaaaattatt taatcttgca 1620

gctggaatag acagcagcca ggatactcta ccaaagagat tgttagaaga acctattcca 1680

gatggtccat caaagggaca cgttcatagg ctagatgttc ttctgccaga atattactca 1740

gtacgaggat ggagtaaaga gggtatacct acagaagaaa cattaaagaa attaggatta 1800

gatgaatata taggtaagtt ctag 1824

<210> 118

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<211>  607
<212>  PRT
<213>  c. ragsdalei

<400>  118

Met Tyr Gly Tyr Asn Gly Lys Val Leu Arg Ile Asn Leu Lys Glu Arg
1               5                   10                  15


Thr Cys Lys Ser Glu Asn Leu Asp Leu Asp Lys Ala Lys Lys Phe Ile
            20                  25                  30


Gly Cys Arg Gly Leu Gly Val Lys Thr Leu Phe Asp Glu Ile Asp Pro
        35                  40                  45


Lys Ile Asp Ala Leu Ser Pro Glu Asn Lys Phe Ile Ile Val Thr Gly
    50                  55                  60


Pro Leu Thr Gly Ala Pro Val Pro Thr Ser Gly Arg Phe Met Val Val
65                  70                  75                  80


Thr Lys Ala Pro Leu Thr Gly Thr Ile Gly Ile Ser Asn Ser Gly Gly
                85                  90                  95


Lys Trp Gly Val Asp Leu Lys Lys Ala Gly Trp Asp Met Ile Ile Val
            100                 105                 110


Glu Asp Lys Ala Asp Ser Pro Val Tyr Ile Glu Ile Val Asp Asp Lys
        115                 120                 125


Val Glu Ile Lys Asp Ala Ser Gln Leu Trp Gly Lys Val Thr Ser Glu
    130                 135                 140


Thr Thr Lys Glu Leu Glu Lys Ile Thr Glu Asn Arg Ser Lys Val Leu
145                 150                 155                 160


Cys Ile Gly Pro Ala Gly Glu Arg Leu Ser Leu Met Ala Ala Val Met
                165                 170                 175


Asn Asp Val Asp Arg Thr Ala Ala Arg Gly Gly Val Gly Ala Val Met
            180                 185                 190


Gly Ser Lys Asn Leu Lys Ala Ile Thr Val Lys Gly Thr Gly Lys Ile
        195                 200                 205


Ala Leu Ala Asp Lys Glu Lys Val Lys Lys Val Ser Val Glu Lys Ile
    210                 215                 220


Thr Thr Leu Lys Asn Asp Pro Val Ala Gly Gln Gly Met Pro Thr Tyr
225                 230                 235                 240


Gly Thr Ala Ile Leu Val Asn Ile Ile Asn Glu Asn Gly Val His Pro
                245                 250                 255
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Val Asn Asn Phe Gln Glu Ser Tyr Thr Asp Gln Ala Asp Lys Ile Ser
            260                 265                 270

Gly Glu Thr Leu Thr Ala Asn Gln Leu Val Arg Lys Asn Pro Cys Tyr
        275                 280                 285

Ser Cys Pro Ile Gly Cys Gly Arg Trp Val Arg Leu Lys Asp Gly Thr
    290                 295                 300

Glu Cys Gly Gly Pro Glu Tyr Glu Thr Leu Trp Cys Phe Gly Ser Asp
305                 310                 315                 320

Cys Gly Ser Tyr Asp Leu Asp Ala Ile Asn Glu Ala Asn Met Leu Cys
                325                 330                 335

Asn Glu Tyr Gly Ile Asp Thr Ile Thr Cys Gly Ala Thr Ile Ala Ala
            340                 345                 350

Ala Met Glu Leu Tyr Gln Arg Gly Tyr Val Lys Asp Glu Glu Ile Ala
        355                 360                 365

Gly Asp Asn Leu Ser Leu Lys Trp Gly Asp Thr Glu Ser Met Ile Gly
    370                 375                 380

Trp Ile Lys Lys Met Val Tyr Ser Glu Gly Phe Gly Ala Lys Met Thr
385                 390                 395                 400

Asn Gly Ser Tyr Arg Leu Cys Glu Gly Tyr Gly Val Pro Glu Tyr Ser
                405                 410                 415

Met Thr Val Lys Lys Gln Glu Ile Pro Ala Tyr Asp Pro Arg Gly Ile
            420                 425                 430

Gln Gly His Gly Ile Thr Tyr Ala Val Asn Asn Arg Gly Gly Cys His
        435                 440                 445

Ile Lys Gly Tyr Met Ile Asn Pro Glu Ile Leu Gly Tyr Pro Glu Lys
    450                 455                 460

Leu Asp Arg Phe Ala Leu Asp Gly Lys Ala Ala Tyr Ala Lys Met Met
465                 470                 475                 480

His Asp Leu Thr Ala Val Ile Asp Ser Leu Gly Leu Cys Ile Phe Thr
                485                 490                 495

Thr Phe Gly Leu Gly Ile Gln Asp Tyr Val Asp Met Tyr Asn Ala Val
            500                 505                 510

Val Gly Glu Ser Thr Cys Asp Ser Asp Ser Leu Leu Glu Ala Gly Asp
        515                 520                 525
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Arg Val Trp Thr Leu Glu Lys Leu Phe Asn Leu Ala Ala Gly Ile Asp
    530                 535                 540

Ser Ser Gln Asp Thr Leu Pro Lys Arg Leu Leu Glu Glu Pro Ile Pro
545                 550                 555                 560

Asp Gly Pro Ser Lys Gly His Val His Arg Leu Asp Val Leu Leu Pro
                565                 570                 575

Glu Tyr Tyr Ser Val Arg Gly Trp Ser Lys Glu Gly Ile Pro Thr Glu
            580                 585                 590

Glu Thr Leu Lys Lys Leu Gly Leu Asp Glu Tyr Ile Gly Lys Phe
        595                 600                 605
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<210> 119
<211> 1167
<212> DNA
<213> C. autoethanogenum

<400> 119

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atggcaagat ttactttacc aagagacatt tattttggag aaaattcatt agaaaccttg        60
aaagacctag atggaaaaaa agctgttatt gtcgtaggtg gtggatccat gaaacgattt       120
ggattccttg ataaggtagt aaactactta aaagaagcag gtattgaatc aaaattaata       180
gaaggagttg aaccagatcc atctgtagaa actgttatga atggcgctaa actaatgaga       240
gaatatgaac cagatttaat agtatcaata ggtggaggtt caccaattga cgcagcaaaa       300
gctatgtgga tattctatga ataccctgag tttactttta aagaggctgt ggttcctttt       360
ggtcttccta aattaagaca aaaagcaaca tttatagcta taccttctac aagtggtact       420
gcaacagaag taacggcatt ttctgtaata acagactata aagctaaaat taaatatcct       480
ttagctgact tcaatttaac accagatata gctataattg atccagcatt agctcaaaca       540
atgccaccta aattaactgc acatactgga atggatgcac ttacccatgc tattgaagca       600
tatgttgcag gacttcattc agttttctca gatcctcttg ctattcaagc tatagttatg       660
gtaaatcagt atttaattaa atcttacaat gaagataaag aagctagaaa ccaaatgcat       720
ttagctcaat gtttagctgg aatggcattt tcaaatgcac ttcttggaat aactcacagt       780
ttagcacata aaacaggtgc agtattccat attcctcatg gatgtgccaa tgcaatatat       840
cttccctatg ttatagattt caataaaaaa gcttgtacac caagatatgc tgatatagct       900
aggagtctta aacttccagg aaatactgat gatgaattag tagattcatt aactaacatg       960
attaaagata tgaacaagag tatggatatt cctttgacat taaaagatta cggagtagat      1020
gaaaaagaat ttaaagataa tgaagatttt atagctcata atgccgtatt agatgcctgc      1080
actggatcaa atcctagaag tataaatgat gctgaaatga aaaaattgtt agaatacatc      1140
tattatggta aaaaggttga tttttaa                                          1167
```

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<210>  120
<211>  388
<212>  PRT
<213>  C. autoethanogenum

<400>  120

Met Ala Arg Phe Thr Leu Pro Arg Asp Ile Tyr Phe Gly Glu Asn Ser
1               5                   10                  15

Leu Glu Thr Leu Lys Asp Leu Asp Gly Lys Lys Ala Val Ile Val Val
            20                  25                  30

Gly Gly Gly Ser Met Lys Arg Phe Gly Phe Leu Asp Lys Val Val Asn
        35                  40                  45

Tyr Leu Lys Glu Ala Gly Ile Glu Ser Lys Leu Ile Glu Gly Val Glu
    50                  55                  60

Pro Asp Pro Ser Val Glu Thr Val Met Asn Gly Ala Lys Leu Met Arg
65                  70                  75                  80

Glu Tyr Glu Pro Asp Leu Ile Val Ser Ile Gly Gly Gly Ser Pro Ile
                85                  90                  95

Asp Ala Ala Lys Ala Met Trp Ile Phe Tyr Glu Tyr Pro Glu Phe Thr
            100                 105                 110

Phe Lys Glu Ala Val Val Pro Phe Gly Leu Pro Lys Leu Arg Gln Lys
        115                 120                 125

Ala Thr Phe Ile Ala Ile Pro Ser Thr Ser Gly Thr Ala Thr Glu Val
    130                 135                 140

Thr Ala Phe Ser Val Ile Thr Asp Tyr Lys Ala Lys Ile Lys Tyr Pro
145                 150                 155                 160

Leu Ala Asp Phe Asn Leu Thr Pro Asp Ile Ala Ile Ile Asp Pro Ala
                165                 170                 175

Leu Ala Gln Thr Met Pro Pro Lys Leu Thr Ala His Thr Gly Met Asp
            180                 185                 190

Ala Leu Thr His Ala Ile Glu Ala Tyr Val Ala Gly Leu His Ser Val
        195                 200                 205

Phe Ser Asp Pro Leu Ala Ile Gln Ala Ile Val Met Val Asn Gln Tyr
    210                 215                 220

Leu Ile Lys Ser Tyr Asn Glu Asp Lys Glu Ala Arg Asn Gln Met His
225                 230                 235                 240
```

Leu Ala Gln Cys Leu Ala Gly Met Ala Phe Ser Asn Ala Leu Leu Gly
245 250 255

Ile Thr His Ser Leu Ala His Lys Thr Gly Ala Val Phe His Ile Pro
260 265 270

His Gly Cys Ala Asn Ala Ile Tyr Leu Pro Tyr Val Ile Asp Phe Asn
275 280 285

Lys Lys Ala Cys Thr Pro Arg Tyr Ala Asp Ile Ala Arg Ser Leu Lys
290 295 300

Leu Pro Gly Asn Thr Asp Asp Glu Leu Val Asp Ser Leu Thr Asn Met
305 310 315 320

Ile Lys Asp Met Asn Lys Ser Met Asp Ile Pro Leu Thr Leu Lys Asp
325 330 335

Tyr Gly Val Asp Glu Lys Glu Phe Lys Asp Asn Glu Asp Phe Ile Ala
340 345 350

His Asn Ala Val Leu Asp Ala Cys Thr Gly Ser Asn Pro Arg Ser Ile
355 360 365

Asn Asp Ala Glu Met Lys Lys Leu Leu Glu Tyr Ile Tyr Tyr Gly Lys
370 375 380

Lys Val Asp Phe
385

<210> 121
<211> 1167
<212> DNA
<213> c. autoethanogenum

<400> 121
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aaaaatttag atggaaataa agcagtagtt gttgtaggtg ggggatctat gaagagattt 120

ggattcttag ccaaagttga aaaatactta aaagaaactg gtatggaagt taaattaata 180

gaaggtgttg agcctgatcc gtctgttgat actgttatga atggcgctaa aataatgaga 240

gactttaacc cagattggat agtatcaata ggtggaggat ctcccataga tgctgctaaa 300

gcaatgtgga tattttatga ataccccgac tttacatttg aaaaagcggt agtccctttt 360

ggaattccta aattaaggca gaaggcacaa tttgttgcta taccttctac aagtggaaca 420

gcaactgaag taacatcatt ttctgtaata acagactata aagctaaaat aaaatatcct 480

cttgcagatt ttaaccttac ccctgatata gctataatag atccgtctct tgcagaaaca 540

atgcccaaaa agcttacagc acacactgga atggatgcac ttactcacgc aatagaagca 600

tatgtagcaa gtttacattc agatttctca gatccacttg ctatgcatgc tataaccatg 660

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attcataaat atttattgaa atcctatgaa gaagataaag aagctagagg acatatgcat        720

atagcccaat gtctagctgg gatggcattt tcaaatgctc tccttggaat aactcatagt        780

atagcacata aaactggtgc agtatttcac atacctcatg ggtgtgctaa tgccatatac        840

ttaccttatg ttatagattt taacaagaaa gcttgttcag aaagatatgc taaaatagcc        900

aaaaagctgc atctatcagg aaatagtgaa gatgagctaa tagattcatt aactgaaatg        960

attcgtacta tgaacaaaaa gatggatatt cctctcacca taaaagatta tggtataagc       1020

gaaaacgatt ttaatgaaaa cctagatttt atagctcaca atgccatgat ggatgcctgc       1080

actggatcca atcctagagc aataactgag gaagaaatga aaaagctctt gcagtatatg       1140

tataatgggc aaaaggttaa tttctag                                           1167
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<210>  122
<211>  388
<212>  PRT
<213>  c. autoethanogenum

<400>  122

Met Gly Arg Phe Thr Leu Pro Arg Asp Ile Tyr Phe Gly Glu Asn Ala
1               5                   10                  15

Leu Glu Asn Leu Lys Asn Leu Asp Gly Asn Lys Ala Val Val Val Val
            20                  25                  30

Gly Gly Gly Ser Met Lys Arg Phe Gly Phe Leu Ala Lys Val Glu Lys
        35                  40                  45

Tyr Leu Lys Glu Thr Gly Met Glu Val Lys Leu Ile Glu Gly Val Glu
    50                  55                  60

Pro Asp Pro Ser Val Asp Thr Val Met Asn Gly Ala Lys Ile Met Arg
65                  70                  75                  80

Asp Phe Asn Pro Asp Trp Ile Val Ser Ile Gly Gly Gly Ser Pro Ile
                85                  90                  95

Asp Ala Ala Lys Ala Met Trp Ile Phe Tyr Glu Tyr Pro Asp Phe Thr
            100                 105                 110

Phe Glu Lys Ala Val Val Pro Phe Gly Ile Pro Lys Leu Arg Gln Lys
        115                 120                 125

Ala Gln Phe Val Ala Ile Pro Ser Thr Ser Gly Thr Ala Thr Glu Val
    130                 135                 140

Thr Ser Phe Ser Val Ile Thr Asp Tyr Lys Ala Lys Ile Lys Tyr Pro
145                 150                 155                 160

Leu Ala Asp Phe Asn Leu Thr Pro Asp Ile Ala Ile Ile Asp Pro Ser
                165                 170                 175
```

```
Leu Ala Glu Thr Met Pro Lys Lys Leu Thr Ala His Thr Gly Met Asp
            180                 185                 190

Ala Leu Thr His Ala Ile Glu Ala Tyr Val Ala Ser Leu His Ser Asp
        195                 200                 205

Phe Ser Asp Pro Leu Ala Met His Ala Ile Thr Met Ile His Lys Tyr
    210                 215                 220

Leu Leu Lys Ser Tyr Glu Glu Asp Lys Glu Ala Arg Gly His Met His
225                 230                 235                 240

Ile Ala Gln Cys Leu Ala Gly Met Ala Phe Ser Asn Ala Leu Leu Gly
                245                 250                 255

Ile Thr His Ser Ile Ala His Lys Thr Gly Ala Val Phe His Ile Pro
            260                 265                 270

His Gly Cys Ala Asn Ala Ile Tyr Leu Pro Tyr Val Ile Asp Phe Asn
        275                 280                 285

Lys Lys Ala Cys Ser Glu Arg Tyr Ala Lys Ile Ala Lys Lys Leu His
    290                 295                 300

Leu Ser Gly Asn Ser Glu Asp Glu Leu Ile Asp Ser Leu Thr Glu Met
305                 310                 315                 320

Ile Arg Thr Met Asn Lys Lys Met Asp Ile Pro Leu Thr Ile Lys Asp
                325                 330                 335

Tyr Gly Ile Ser Glu Asn Asp Phe Asn Glu Asn Leu Asp Phe Ile Ala
            340                 345                 350

His Asn Ala Met Met Asp Ala Cys Thr Gly Ser Asn Pro Arg Ala Ile
        355                 360                 365

Thr Glu Glu Glu Met Lys Lys Leu Leu Gln Tyr Met Tyr Asn Gly Gln
    370                 375                 380

Lys Val Asn Phe
385


<210>  123
<211>  25
<212>  DNA
<213>  synthetic primer

<400>  123
ttgatgaaat gatcactgac ggatt                                            25


<210>  124
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<211>  25
<212>  DNA
<213>  synthetic primer

<400>  124
gaaatgttcc atctctcagc tatgt                                             25


<210>  125
<211>  25
<212>  DNA
<213>  synthetic primer

<400>  125
catcactttc aataacagaa gtggc                                             25


<210>  126
<211>  25
<212>  DNA
<213>  synthetic primer

<400>  126
tacctctaca agcttcataa cagga                                             25


<210>  127
<211>  25
<212>  DNA
<213>  synthetic primer

<400>  127
aaaatgggtc agtatggtat gatgg                                             25


<210>  128
<211>  25
<212>  DNA
<213>  synthetic primer

<400>  128
tgtagtaccg caaacctttg ataat                                             25


<210>  129
<211>  25
<212>  DNA
<213>  synthetic primer

<400>  129
caagtttact tggtggaaca atagc                                             25


<210>  130
<211>  25
<212>  DNA
<213>  synthetic primer

<400>  130
gagttggtct tacagtttta ccagt                                             25


<210>  131
<211>  20
<212>  DNA
<213>  synthetic primer

<400>  131
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tcaggacctt ctggaactgg                                              20


<210>  132
<211>  20
<212>  DNA
<213>  synthetic primer

<400>  132
acctcccctt ttcttggaga                                              20


<210>  133
<211>  20
<212>  DNA
<213>  synthetic primer

<400>  133
caggtttcgg tgctgaccta                                              20


<210>  134
<211>  20
<212>  DNA
<213>  synthetic primer

<400>  134
aactccgccg ttgtatttca                                              20


<210>  135
<211>  37
<212>  DNA
<213>  synthetic primer

<400>  135
ccgaattcgt cgacaacaga gtttgatcct ggctcag                           37


<210>  136
<211>  1461
<212>  DNA
<213>  C. ljungdahlii

<400>  136
gcactgcatt tcaaactgga tatctagagt gcgggagagg agaatggaat tcctagtgta      660

gcggtgaaat gcgtagagat taggaagaac accagtggcg aaggcgattc tctggaccgt      720

aactgacgct gaggcacgaa agcgtgggta gcaaacagga ttagataccc tggtagtcca      780

cgccgtaaac gatgagtact aggtgtagga ggtatcgacc ccttctgtgc cgcagtaaac      840

acaataagta ctccgcctgg gaagtacgat cgcaagatta aaactcaaag gaattgacgg      900

gggcccgcac aagcagcgga gcatgtggtt taattcgaag caacgcgaag aaccttacct      960

ggacttgaca taccctgaat atcttagaga taagagaagc ccttcggggc agggatacag     1020

gtggtgcatg gttgtcgtca gctcgtgtcg tgagatgtta ggttaagtcc tgcaacgagc     1080

gcaacccctg ttgttagttg ctaacattta gttgagcact ctagcaagac tgccgcggtt     1140

aacgcggagg aaggtgggga tgacgtcaaa tcatcatgcc ccttatgtcc agggcaacac     1200

acgtgctaca atgggcagta cagagagaag caagaccgca aggtggagca aacctcaaaa     1260

actgccccca gttcggattg caggctgaaa ctcgcctaca tgaagttgga gttgctagta     1320
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atcgcgaatc agaatgtcgc ggtgaatacg ttcccgggcc ttgtacacac cgcccgtcac 1380

accatgagag ctggcaacac ccgaagtccg tagtctaact taggaggacg cggccgaagg 1440

tggggttagt aattggggtg a 1461

<210> 137
<211> 26
<212> DNA
<213> C. autoethanogenum

<400> 137
cggctgctca aaagaaattt tctagc

<210> 138
<211> 26
<212> DNA
<213> C. autoethanogenum

<400> 138
ccagaactcc gcaggtcttt tcaccc

<210> 139
<211> 23
<212> DNA
<213> C. autoethanogenum

<400> 139
ggcagtagaa gaaagcggaa tgg

<210> 140
<211> 27
<212> DNA
<213> C. autoethanogenum

<400> 140
aaagcctgca tctctctcta aaactcc

<210> 141
<211> 28
<212> DNA
<213> C. autoethanogenum

<400> 141
taatgatttg ctctccatcc aagaatcc

<210> 142
<211> 21
<212> DNA
<213> C. autoethanogenum

<400> 142
tccgatttct tccgccatac g

<210> 143
<211> 28
<212> DNA
<213> C. autoethanogenum

<400> 143

agctgtagta gttgttggag gaggatcc

<210> 144
<211> 24
<212> DNA
<213> C. autoethanogenum

<400> 144
cacagacgga tctggttcaa cacc

<210> 145
<211> 32
<212> DNA
<213> C. autoethanogenum

<400> 145
gaatctattc aacttttaga gcaagtcact gg

<210> 146
<211> 24
<212> DNA
<213> C. autoethanogenum

<400> 146
caacggaact tattccagct ttgc

<210> 147
<211> 31
<212> DNA
<213> C. autoethanogenum

<400> 147
gatgcttttt atgaattgag aaagaagaag g

<210> 148
<211> 24
<212> DNA
<213> C. autoethanogenum

<400> 148
tgaaaccaat ccatctgcat ctcc

<210> 149
<211> 27
<212> DNA
<213> C. autoethanogenum

<400> 149
tgcaagatga aagtgttgta gcaaagg

<210> 150
<211> 24
<212> DNA
<213> C. autoethanogenum

<400> 150
actttgtggt cttccattgg ttgc

<210> 151
<211> 26

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<212>  DNA
<213>  C. autoethanogenum

<400>  151
cttcaacagg aaacagattc gagagc


<210>  152
<211>  20
<212>  DNA
<213>  C. autoethanogenum

<400>  152
ccaacaccac cacgtcctgc


<210>  153
<211>  32
<212>  DNA
<213>  C. autoethanogenum

<400>  153
ggttgggata tgataatagt agaggataag gc


<210>  154
<211>  25
<212>  DNA
<213>  C. autoethanogenum

<400>  154
gtaacttttc cccaaagctg tgacg
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