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(54) **CARBOHYDRATE-ENRICHED RECOMBINANT MICROORGANISMS**

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(57) **ABSTRACT**

The present disclosure relates to recombinant microorganisms engineered for enhanced production of a desired carbohydrate, as well as related biomass, and compositions which are useful, inter alia, as animal feed ingredients. The present disclosure also provides related methods.

Specification includes a Sequence Listing.

CARBOHYDRATE-ENRICHED RECOMBINANT MICROORGANISMS

STATEMENT REGARDING SEQUENCE LISTING

[0001] The "Sequence Listing" submitted electronically concurrently herewith pursuant 37 C.F.R. § 1.821 in computer readable form (CRF) via EFS-Web as file name 200206_416D1_SEQUENCE LISTING.txt is incorporated herein by reference. The electronic copy of the Sequence Listing was created on May 10, 2019, and the size is 277 KB.

TECHNICAL FIELD

[0002] The present disclosure relates to novel recombinant C_1 metabolizing microorganisms comprising an engineered metabolic pathway for the enhanced production of carbohydrates, and related compositions and methods.

BACKGROUND

[0003] Advances in the efficiency in animal feed utilization have been achieved over the past several decades through the use of feed additives. These added substances augment the nutrient-content, energy-content, and/or disease fighting properties of animal feed compositions. A growing challenge for commercial animal producers is the rising cost of grain. The rising costs are due in part to competing demands for grains for biofuel and human food use. With the rising cost of grain and protein components, coupled with limited land available for feed production, alternative low cost animal feed products with beneficial nutritive and disease fighting properties would be highly desirable.

SUMMARY

[0004] In one embodiment, the present disclosure provides a recombinant C_1 metabolizing microorganism comprising an exogenous nucleic acid selected from the group consisting of an exogenous nucleic acid that encodes a carbohydrate biosynthesis enzyme and an exogenous nucleic acid that encodes an expression control sequence that is operably linked to a nucleic acid encoding a native carbohydrate biosynthesis enzyme, wherein the recombinant C_1 metabolizing microorganism is capable of converting a natural gas-derived carbon feedstock into a desired carbohydrate. Typically, the natural gas-derived carbon feedstock is natural gas or methane.

[0005] In another embodiment, the present disclosure provides a biomass derived from the recombinant C_1 metabolizing microorganism of the present disclosure.

[0006] In a further embodiment, the present disclosure provides a carbohydrate composition comprising carbohydrates extracted from the biomass of the present disclosure, wherein the composition exhibits a $\delta^{13}C$ that is less than −30‰.

[0007] In a still further embodiment, the present disclosure provides an animal feed comprising the biomass of the present disclosure.

[0008] In another embodiment, the present disclosure provides a culture or fermentation medium comprising the biomass or composition of the present disclosure.

[0009] The present disclosure additionally provides related methods.

DETAILED DESCRIPTION

[0010] The instant disclosure provides novel recombinant C_1 metabolizing microorganisms that have the ability to utilize relatively low-cost carbon feedstock as an energy source, as well as related biomass, compositions, and methods. The recombinant microorganisms of the present disclosure are engineered for the enhanced production of certain carbohydrates that are commercially desirable. These recombinant microorganisms, as well as the biomass and carbohydrate compositions that are derived from them, are useful as a source of nutrition for animals (such as, for example, livestock, fish, poultry, and the like), as well as cultured or fermented microorganisms.

[0011] In one embodiment, the present disclosure provides a recombinant C_1 metabolizing microorganism, wherein the recombinant C_1 metabolizing microorganism comprises an exogenous nucleic acid selected from the group consisting of an exogenous nucleic acid that encodes a carbohydrate biosynthesis enzyme and an exogenous nucleic acid that encodes an expression control sequence that is operably linked to a nucleic acid encoding a native carbohydrate biosynthesis enzyme, wherein the recombinant C_1 metabolizing microorganism is capable of converting a natural gas carbon feedstock into the carbohydrate. When these recombinant microorganisms are cultured in the presence of a natural gas-derived C_1 substrate, they typically exhibit a $\delta^{13}C$ of less than −30‰, and often less than −40‰, as described in more detail herein. Typically, the recombinant microorganism is a non-photosynthetic C_1 metabolizing microorganism.

[0012] In these embodiments, the recombinant microorganisms of the present disclosure are engineered to convert a natural gas-derived feedstock, which is a relatively low cost and abundant resource (for example, natural gas, or a C_1 substrate such as methane from natural gas) as compared to more costly carbohydrates, to higher valued carbohydrates. As used herein, the term "natural gas-derived feedstock" refers to natural gas, or any of the components isolated from natural gas (including C_1 substrates) or converted from natural gas (i.e., syngas).

[0013] The term "natural gas" refers herein to naturally occurring gas mixtures that may be obtained by conventional processes (e.g., drilling and water flooding of porous reservoirs) or non-conventional processes (e.g., hydraulic fracturing, horizontal drilling or directional drilling of formations having low gas permeability). The gas mixtures are made up of methane and other compounds, including other C_1 compounds, as well as other light alkane gases (such as, for example, ethane, propane, butane, pentane, and the like), carbon dioxide, nitrogen, hydrogen sulfide, or the like, and combinations thereof. Unconventional natural gas may be obtained from sources such as, for example, tight gas sands formed in sandstone or carbonate, coal bed methane formed in coal deposits and adsorbed in coal particles, shale gas formed in fine-grained shale rock and adsorbed in clay particles or held within small pores or microfractures, methane hydrates that are a crystalline combination of natural gas and water formed at low temperature and high pressure in places such as under oceans and permafrost.

[0014] As used herein, "C_1 substrate" or "C_1 compound" refers to any carbon containing molecule or composition that lacks a carbon-carbon bond. Exemplary C_1 substrates include syngas, methane, methanol, formaldehyde, formic acid or a salt thereof, carbon monoxide, carbon dioxide,

methylated amines (e.g., methylamine, dimethylamine, trimethylamine, etc.), methylated thiols, methyl halogens (e.g., bromomethane, chloromethane, iodomethane, dichloromethane, etc.), cyanide, or any combination thereof.

[0015] In certain embodiments of the present disclosure, a natural gas-derived feedstock may be natural gas, a C_1 substrate from natural gas, or syngas. Typically, a C_1 substrate is methane. Exemplary recombinant C_1 metabolizing microorganisms that have utilized a natural gas-derived carbon substrate as a feedstock exhibit a distinctive isotopic carbon signature, which is described in more detail herein. This distinctive isoptopic carbon signature is also exhibited by the compositions and products of such recombinant microorganisms (e.g., biomass, carbohydrate compositions, and the like).

[0016] In another embodiment, the present disclosure provides a recombinant C_1 metabolizing microorganism comprising an exogenous nucleic acid encoding a carbohydrate biosynthesis enzyme, wherein the C_1 metabolizing microorganism is capable of converting methane into a carbohydrate. Exemplary carbohydrates are glucans. In some embodiments, a carbohydrate is a β-(1,3)-glucan, and may be branched or unbranched or a mixture thereof. Usually, a C_1 metabolizing microorganism is a non-photosynthetic C_1 metabolizing microorganism.

[0017] As used herein, "C_1 metabolizing microorganism" or "C_1 metabolizing non-photosynthetic microorganism" refers to any microorganism having the ability to use a C_1 substrate as a source of energy or as its primary source of energy and biomass, and may or may not use other carbon substrates (such as sugars and complex carbohydrates) for energy and biomass. For example, a C_1 metabolizing microorganism may oxidize a C_1 substrate, such as methane or methanol. C_1 metabolizing microorganisms include bacteria (such as methanotrophs and methylotrophs) and yeast. In certain embodiments, a C_1 metabolizing microorganism does not include a photosynthetic microorganism, such as algae. In some embodiments, the C_1 metabolizing microorganism will be an "obligate C_1 metabolizing microorganism," meaning its sole source of energy are C_1 substrates. In further embodiments, a C_1 metabolizing microorganism (e.g., methanotroph) will be cultured in the presence of a C_1 substrate feedstock (i.e., using the C_1 substrate as a source of energy).

[0018] Recombinant C_1 metabolizing microorganisms of the present disclosure are engineered for enhanced production of a desired carbohydrate and in one embodiment, comprise an exogenous nucleic acid encoding a carbohydrate biosynthesis (CB) enzyme. The terms "carbohydrate biosynthesis enzyme" and "CB enzyme" are used interchangeably herein to refer to an enzyme that is involved in the production of a carbohydrate by the recombinant host C_1 metabolizing microorganism.

[0019] Exogenous nucleic acids encoding CB enzymes that are employed in the practice of the present disclosure are typically codon optimized for optimal expression from the recombinant host C_1 metabolizing microorganism and encode an enzyme that is either native to a species heterologous to the host C_1 microorganism or is a mutant (i.e., variant) of an enzyme that exists in nature.

[0020] As used herein, the term "carbohydrate" refers to a monosaccharide, a disaccharide, or a polysaccharide. Suitable exogenous nucleic acids employed in the practice of the present disclosure include those which encode enzymes that are involved in the production of a monosaccharide such as, for example, glucose, fructose, ribose, glyceraldehyde, galactose and the like; a disaccharide, such as, for example lactose, sucrose, maltose, cellulobiose, and the like, and mixtures thereof or a polysaccharide, including, for example, an unbranched or branched glucan, and the like, and mixtures thereof. Exemplary glucans include α-glucans, such as for example, dextran, glycogen, pullulan, starch, and the like, as well as β-glucans, such as, for example, β-1,4-glucan (i.e., cellulose), β-1,3-glucan, β-(1,3)(1,4)-glucan, β-(1,3)(1,6)-glucan, and the like, and mixtures thereof.

[0021] In a specific embodiments, the CB enzyme is an enzyme involved in the production of an unbranched or a branched glucan, or mixture thereof β-glucans are known to have beneficial therapeutic properties, including as a powerful immune stimulant and a powerful antagonist to both benign and malignant tumors. β-glucans are also known to lower cholesterol and triglyceride levels. See D. Akramiené et al., *Medicina* (*kaunas*), 2007; 43(8):597. The β-glucans are a heterogeneous group of glucose polymers made up of β-D-glucopyranosyl units having β-(1,3) and/or β-(1,4), and/or β-(1,6) linkages. They have been isolated from a number of sources, including plants (oat, barley, bran, seaweed, corn, soy, and the like), bacteria (e.g., *Pneumocystis carinii, Cryptococcus neoformans, Aspergillus fumigatus, Histoplasma capsulatum, Candida albicans*, and the like), and fungi (i.e., *Saccharomyces cerevisiae* and mushrooms, such as, for example shiitake (*Lentinus edodes*), maitake (*Grifola frondosa*), schizophylan (*Schizophillum commune*), and SSG (*Sclerotinia sclerotiorum*). β-glucan extracts from *Lentinus edodes* and *Schizophillum commune* have been used for the treatment of cancer in Japan since 1980. Id.

[0022] Exogenous nucleic acids that are suitable for use in the practice of the present disclosure include those which encode enzymes involved in gluconeogenesis, glycogenesis, α- or β-glucan biosynthesis, and other metabolic pathways known to produce a carbohydrate.

[0023] Suitable exogenous nucleic acids include those which encode a gluconeogenesis enzyme selected from the group consisting of a pyruvate carboxylase, a phosphoenolpyruvate carboxykinase, an enolase, a phosphoglycerate mutase, a phosphoglycerate kinase, a glyceraldehyde-3-phosphate dehydrogenase, a Type A aldolase, a fructose 1,6-bisphosphatase, a phosphofructokinase, a phosphoglucose isomerase, a hexokinase, a glucose-6-phosphate, and the like.

[0024] Other suitable exogenous nucleic acids include those which encode a glycogenesis enzyme selected from the group consisting of a glucose-1-phosphate adenyltransferase, a glycogen synthase, and the like.

[0025] The above enzymes can be found in a number of heterologous species, including microorganisms, such as, for example, bacteria and yeast, including, for example, *E. coli, C. glutamicum, Saccharomyces cerevisiae*, and the like, as well as higher order fungi, such as mushrooms, and the like, as well as algae, and plants.

[0026] Suitable exogenous nucleic acids include those which encode a glucan biosynthesis enzyme, such as, for example, a glucan synthase. An exemplary glucan synthase is β-1,3-glucan synthase. The exogenous nucleic acid may encode a glucan biosynthesis enzyme (e.g., a glucan synthase (such as, for example a β-1,3-glucan synthase)) from a plant (oat, barley, bran, seaweed, corn, soy, and the like),

a bacteria (e.g., *Pneumocystis carinii, Cryptococcus neoformans, Aspergillus fumigatus, Histoplasma capsulatum, Candida albicans*, and the like), or a fungi (i.e., *Saccharomyces cerevisiae* and mushrooms, such as, for example shiitake (*Lentinus edodes*), maitake (*Grifola frondosa*), schizophylan (*Schizophillum commune*), and SSG (*Sclerotinia sclerotiorum*). The amino acid and nucleic acid sequences of a number of β-(1,3)-glucan synthases are known. See, e.g., U.S. Pat. No. 5,194,600, WO99/49047, and EP 0 724 644 B1, all of which are incorporated herein by reference. In certain specific embodiments, the exogenous nucleic acid encodes a carbohydrate biosynthesis enzyme having the amino acid sequence of any of SEQ NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, or 38, shown in Table A, hereinbelow. As described above, the exogenous nucleic acid is typically codon optimized for optimal expression from the recombinant C_1 microorganism. Exemplary nucleic acid sequences encoding these CB enzymes are also provided in Table A. These nucleic acid sequences have been codon optimized for expression in *Methylococcus capsulatus* Bath.

TABLE A

Exemplary Carbohydrate Biosynthesis Enzymes

Source/Enzyme Name	Amino Acid Sequence (SEQ ID NO.)	Nucleic Acid Sequence (SEQ ID NO.)
Saccharomyces cerevisiae: mature KRE1 protein	2	1
Saccharomyces cerevisiae: mature KRE2 protein	4	3
Saccharomyces cerevisiae s288c: FKS1	6	5
Saccharomyces cerevisiae: FKS2	8	7
Candida albicans: FKS1	10	9
Zea mays (corn): portion of 1,3-β-D-glucan synthase	12	11
Zea mays (corn): portion of 1,3-β-D-glucan synthase	14	13
Oryza sativa (rice): portion of 1,3-beta-D-glucan synthase	16	15
Oryza sativa (rice): portion of 1,3-beta-D-glucan synthase	18	17
Gycine max (soy): portion of 1,3-beta-D-glucan synthase.	20	19
Veronia mespilifolia: 1,3-beta-D-glucan synthase	22	21
Triticum aestivum (wheat): 1,3-beta-D-glucan synthase	24	23
Horderum vulgars (barley): 1,3-beta-D-glucan synthase	26	25
E. coli: Glucose-1-phosphate adenyltransfersase (Acc. No. YP 49003.1)	28	27
Cornebacterium. Glutamicum (ATCC 13032): Glucose-1-phosphate adenylyltransferase	30	29
Escherichia coli str. K-12 substr. W3110: Glycogen Synthase	32	31
Cornebacterium glutamicum (ATCC 13032): Glycosyltransferase	34	33
E. coli: 1,4-alpha-glucan branching enzyme (Acc. No. YP 492001.1)	36	35
Corynebacterium glutamicum (ATCC 13032): Glycogen branching enzyme	38	37

[0027] Suitable exogenous nucleic acids employed in the practice of the present disclosure include those which encode a variant CB enzyme sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to a reference or parental wild-type polypeptide sequence, such as, for example a reference sequence corresponding to any one of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, or 38, provided that the variant retains the carbohydrate biosynthesis enzyme activity of interest. In certain embodiments, the CB enzyme variant polypeptides will include at least one amino acid substitution (e.g., 1, 2, 3, 5, 6, 7, 8, 9 or 10 or more or up to 20, 25, or 30 substitutions) at a pre-determined position relative to a reference or parental wild-type CB enzyme, provided that a variant retains the CB enzyme activity of interest. The CB enzyme variant polypeptides may further comprise one or more conservative substitutions. A "conservative substitution" is recognized in the art as a substitution of one amino acid for another amino acid that has similar properties. Exemplary conservative substitutions are well known in the art (see, e.g., WO 97/09433, p. 10; Lehninger, Biochemistry, 2nd Edition; Worth Publishers, Inc. NY:NY (1975), pp. 71-'7'7; Lewin, Genes IV, Oxford University Press, NY and Cell Press, Cambridge, Mass. (1990), p. 8, which are incorporated herein by reference). Methods for generating suitable exogenous nucleic acids encoding such variant enzymes are described in more detail herein.

[0028] The "percent identity" between two or more nucleic acid or amino acid sequences is a function of the number of identical positions shared by the sequences (i.e., % identity=number of identical positions/total number of positions×100), taking into account the number of gaps, and the length of each gap that needs to be introduced to optimize alignment of two or more sequences. The comparison of sequences and determination of percent identity between two or more sequences can be accomplished using a mathematical algorithm, such as BLAST and Gapped BLAST programs at their default parameters (e.g., Altschul et al., *J. Mol. Biol.* 215:403, 1990; see also BLASTN at the world wide web at ncbi.nlm.nih.gov/BLAST, which are incorporated herein by reference).

[0029] As indicated above, the exogenous nucleic acids encoding CB enzymes employed in the practice of the present disclosure may be codon optimized for expression in the C_1 metabolizing microorganism. Expression of recombinant proteins may be difficult outside their original host. For example, variation in codon usage bias has been observed across different species of bacteria (Sharp et al., *Nucl. Acids. Res.* 33:1141, 2005, which is incorporated herein by reference). Overexpression of recombinant proteins even within their native host may also be difficult. In certain embodiments, the nucleic acid to be introduced into a host as described herein may be subjected to codon optimization prior to introduction into the host to ensure protein expression is effective or enhanced. Codon optimization refers to alteration of codons in genes or coding regions of nucleic acids before transformation to reflect the typical codon usage of the host without altering the polypeptide encoded by the non-natural DNA molecule. Codon optimization methods for optimum gene expression in heterologous hosts have been previously described (see, e.g., Welch et al., *PLoS One* 4:e7002, 2009; Gustafsson et al., *Trends Biotechnol.* 22:346, 2004; Wu et al., *Nucl. Acids Res.*

35:D76, 2007; Villalobos et al., *BMC Bioinformatics* 7:285, 2006; U.S. Patent Publication Nos. 2011/0111413 and 2008/0292918; disclosure of which methods are incorporated herein by reference, in their entirety). Exogenous nucleic acids encoding CB enzymes that are suitable for use in the practice of the present disclosure include those having a nucleic acid sequence that is at least about 85% identical to a nucleic acid reference sequence selected from the group consisting of SEQ ID NO.:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, and 37. In some embodiments, the exogenous nucleic acid encoding the CB enzyme has a nucleic acid sequence that is at least about 85%, at least about 86%, at least about 87%, at least about 88%, at least about 89%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98% and at least about 99% sequence identity to a nucleic acid reference sequence selected from the group consisting of SEQ ID NO.:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, and 37. Illustrative exogenous nucleic acids that encode a CB enzyme which are suitable for use in the practice of the invention include sequences which have been codon optimized for optimal expression in *Methylococcus capsulatus* Bath, such as, for example, any one of SEQ ID NO.:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, and 37.

[0030] Similarly, exogenous nucleic acid molecules of this disclosure encoding polypeptide variants may be designed using the phylogenetic-based methods described in the references noted above (U.S. Pat. No. 8,005,620; Gustafsson et al.; Welch et al.; Villalobos et al.; Minshull et al., all of which are incorporated herein by reference.).

[0031] An exogenous nucleic acid encoding a carbohydrate biosynthesis enzyme includes polynucleotides that encode a polypeptide, a polypeptide fragment, a peptide, or a fusion polypeptide that has or retains the corresponding carbohydrate biosynthesis enzyme activity. Methods to determine whether a polypeptide has a particular activity by measuring the ability of the polypeptide to convert a substrate into a product are known in the art.

[0032] In some embodiments, the exogenous nucleic acid encodes an expression control sequence that is operably linked to a nucleic acid encoding a native carbohydrate biosynthesis enzyme. Typically, the expression control sequence is one that results in the overexpression of a native carbohydrate biosynthesis enzyme. As used herein, "overexpressed" and "overexpression" when referring to a gene or a protein means an increase in expression or activity of the gene or protein. Increased expression or activity includes expression or activity of a gene or protein being increased above the level of a wildtype (native or non-genetically engineered) control or reference microorganism. A gene or protein is overexpressed if the expression or activity is in a microorganism where it is not normally expressed or active. A gene or protein is overexpressed if the expression or activity is extended or present longer in the recombinant microorganism than in a wild-type control or reference microorganism.

[0033] In addition to the exogenous nucleic acids described hereinabove, recombinant C_1 metabolizing microorganisms of the present disclosure may comprise further genetic modifications which enhance the production of the desired carbohydrate. For example, when the exogenous nucleic acid encodes a carbohydrate biosynthesis enzyme, the recombinant C_1 metabolizing microorganism may further comprise an exogenous expression control sequence that is operatively linked to the exogenous nucleic acid encoding the carbohydrate biosynthesis enzyme to enhance production of the desired carbohydrate. Expression control sequences suitable for use in the practice of the present disclosure are described in more detail herein.

[0034] Alternatively, or in addition, the recombinant C_1 metabolizing microorganism of the present disclosure may further comprise an exogenous expression control sequence operatively linked to an endogenous nucleic acid encoding an endogenous enzyme that utilizes one or more of the same substrates utilized by carbohydrate biosynthesis enzymes, or utilizes the desired carbohydrate as a substrate (i.e., a "competing" endogenous enzyme). This may be done to downregulate the competing endogenous enzyme.

[0035] In some embodiments, it may be desirable to reduce or inhibit a competing endogenous enzyme activity by mutating the competing endogenous enzyme to delete or attenuate its activity. "Inhibit" or "inhibited," as used herein, refers to an alteration, reduction, down regulation, abrogation or deletion, directly or indirectly, in the expression of a target gene or in the activity of a target molecule relative to a control, endogenous or reference molecule, wherein the alteration, reduction, down regulation or abrogation is statistically, biologically, industrially, or clinically significant.

[0036] Various methods for downregulating, inactivating, knocking-out, or deleting endogenous gene function in C_1 metabolizing microorganisms are known in the art. For example, targeted gene disruption is an effective method for gene down-regulation where an exogenous polynucleotide is inserted into a structural gene to disrupt transcription. Genetic cassettes comprising the exogenous insertion DNA (e.g., a genetic marker) flanked by sequence having a high degree of homology to a portion of the target host gene to be disrupted are introduced into the host C_1 metabolizing microorganism. Exogenous DNA disrupts the target host gene via native DNA replication mechanisms. Allelic exchange to construct deletion/insertional mutants in C_1 metabolizing microorganisms, including methanotrophic bacteria, have been described in, for example, Toyama and Lidstrom, *Microbiol.* 144:183, 1998; Stoylar et al., *Microbiol.* 145:1235, 1999; Ali et al., *Microbiol.* 152:2931, 2006; Van Dien et al., *Microbiol.* 149:601, 2003; Martin and Murrell, *FEMS Microbiol. Lett.* 127:243, 2006, all of which are incorporated herein by reference.

[0037] For example, in some embodiments of the present disclosure, a recombinant C_1 metabolizing microorganisms may further comprise a deletion of endogenous glycogen synthase activity and/or endogenous phosphoglucomutase activity. Enzymes involved in other pathways, such as an amino acid synthesis pathway, may also be targeted for down regulation to focus metabolic activities of the host microorganism on carbohydrate biosynthesis.

[0038] The recombinant C_1 metabolizing microorganism may thus be engineered to have the ability to produce the desired carbohydrate at enhanced levels. In some of these embodiments, a recombinant C_1 metabolizing microorganism produces the desired carbohydrate at a level that is at least about 10% greater than that produced by the native C_1 metabolizing microorganism and up to about 2-fold, to about 3-, 4-, 5-, 10-, 20-, 30-, 40-, 50-, 60-, 70-, 80-, 90-, 100-, and up to about 500- or about 1000-fold the level produced by a native C_1 metabolizing microorganism, when cultured in

the presence of a natural gas-derived feedstock (e.g., natural gas, methane, and the like) under at least one set of culture conditions. In other embodiments, a recombinant C_1 metabolizing microorganism produces the desired carbohydrate at a level that is from at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, or is at least about 95% greater than that produced by a native C_1 metabolizing microorganism, and up to about 2-fold, to about 3-, 4-, 5-, 10-, 20-, 30-, 40-, 50-, 60-, 70-, 80-, 90-, 100-, to about 500- or about 1000-fold the level produced by the native C_1 metabolizing microorganism, when cultured in the presence of a natural gas-derived feedstock under at least one set of culture conditions. Typically, the enhanced level of production of a desired carbohydrate by a recombinant C_1 metabolizing microorganism of the present invention is at least about 2-fold, 3-, 4-, 5-, 10-, 20-, 30-, 40-, 50-, 60-, 70-, 80-, 90-, or 100-fold that of the native C_1 metabolizing microorganism, when cultured in the presence of a natural gas-derived feedstock under at least one set of culture conditions.

[0039] Recombinant methods for expression of exogenous nucleic acids in microbial organisms are well known in the art. Such methods can be found described in, for example, Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Third Ed., Cold Spring Harbor Laboratory, New York (2001); and Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley and Sons, Baltimore, Md. (1999), all of which are incorporated herein by reference. Genetic modifications to nucleic acid molecules encoding enzymes, or functional fragments thereof, can confer a biochemical or metabolic capability to a recombinant cell that is altered from its naturally occurring state.

[0040] As used herein, the terms "endogenous" and "native" when referring to a nucleic acid, polypeptide, such as an enzyme, compound or activity refers to a nucleic acid, polypeptide, compound or activity that is normally present in a host cell. The term "homologous" or "homolog" refers to a molecule or activity from an exogenous (non-native) source that is the same or similar molecule or activity as that found in or derived from a host cell, species or strain.

[0041] As used herein, the term "exogenous" when referring to a nucleic acid molecule, construct or sequence refers to a nucleic acid molecule or portion of a nucleic acid molecule sequence that is not native to a cell in which it is expressed, a nucleic acid molecule or portion of a nucleic acid molecule native to a host cell that has been altered or mutated, or a nucleic acid molecule with an altered expression as compared to the native expression levels under similar conditions. For example, an exogenous control sequence (e.g., promoter, enhancer) may be used to regulate expression of a gene or a nucleic acid molecule in a way that is different than the gene or a nucleic acid molecule that is normally expressed in nature or culture. In certain embodiments, an exogenous nucleic acid molecule may be homologous to a native host cell gene, but may have an altered expression level or have a different sequence or both. In other embodiments, exogenous nucleic acid molecules may not be endogenous to a host cell or host genome, but instead may have been added to a host cell by conjugation, transformation, transfection, electroporation, or the like, wherein the added molecule may integrate into the host genome or can exist as extra-chromosomal genetic material (e.g., plasmid or other self-replicating vector).

[0042] In certain embodiments, more than one exogenous nucleic acid molecule can be introduced into a host cell as separate nucleic acid molecules, as a polycistronic nucleic acid molecule, as a single nucleic acid molecule encoding a fusion protein, or any combination thereof, and still be considered as more than one exogenous nucleic acid. For example, a C_1 metabolizing microorganism can be modified to express two or more exogenous nucleic acid molecules, which may be the same or different, that encode one or more carbohydrate biosynthesis enzyme as disclosed herein. In certain embodiments, multiple copies of a carbohydrate biosynthesis enzyme-encoding polynucleotide molecule are introduced into a host cell, which may be two, three, four, five, six, seven, eight, nine, ten or more copies of the same carbohydrate biosynthesis enzyme or different carbohydrate biosynthesis enzyme encoding polynucleotides.

Host Cells and Transformation Methods

[0043] In carrying out the practice of the present invention, the exogenous nucleic acids described hereinabove are transformed into a host cell that is a C_1 metabolizing microorganism. The C_1 metabolizing microorganism employed may be natural, strain adapted (e.g., performing fermentation to select for strains with improved growth rates and increased total biomass yield compared to the parent strain), or recombinantly modified to produce or overexpress the carbohydrate biosynthesis enzyme of interest and/or to have increased growth rates. Typically, the C_1 metabolizing microorganism is a non-photosynthetic C_1 microorganism (e.g., is not an algae or a plant).

[0044] In certain embodiments, the present disclosure employs C_1 metabolizing microorganisms that are prokaryotes or bacteria, such as *Methylomonas, Methylobacter, Methylococcus, Methylosinus, Methylocystis, Methylomicrobium, Methanomonas, Methylophilus, Methylobacillus, Methylobacterium, Hyphomicrobium, Xanthobacter, Bacillus, Paracoccus, Nocardia, Arthrobacter, Rhodopseudomonas*, or *Pseudomonas.*

[0045] In further embodiments, the C_1 metabolizing bacteria employed is a methanotroph or a methylotroph. Exemplary methanotrophs include *Methylomonas, Methylobacter, Methylococcus, Methylosinus, Methylocystis, Methylomicrobium, Methanomonas, Methylocella*, or a combination thereof. Exemplary methylotrophs include *Methylobacterium extorquens, Methylobacterium radiotolerans, Methylobacterium populi, Methylobacterium chloromethanicum, Methylobacterium nodulans*, or a combination thereof. As used herein, the term "methylotrophic bacteria" refers to any bacteria capable of oxidizing any compound in any form (e.g., solid, liquid, gas) that contains at least one carbon and that do not contain carbon-carbon bonds. In certain embodiments, a methylotrophic bacterium may be a methanotroph. For example, "methanotrophic bacteria" refers to any methylotrophic bacteria that have the ability to oxidize methane as a source of carbon and energy, which may be the primary source of carbon and energy. Exemplary methanotrophic bacteria include *Methylomonas, Methylobacter, Methylococcus, Methylosinus, Methylocystis, Methylomicrobium*, or *Methanomonas.*

[0046] Methanotrophic bacteria are classified into three groups based on their carbon assimilation pathways and

internal membrane structure: type I (gamma proteobacteria), type II (alpha proteobacteria, and type X (gamma proteobacteria). Type I methanotrophs use the ribulose monophosphate (RuMP) pathway for carbon assimilation whereas type II methanotrophs use the serine pathway. Type X methanotrophs use the RuMP pathway but also express low levels of enzymes of the serine pathway. Methanotrophic bacteria employed in the practice of the present invention include obligate methanotrophs, which can only utilize C_1 substrates for carbon and energy sources, and facultative methanotrophs, which naturally have the ability to utilize some multi-carbon substrates as a carbon and energy source.

[0047] Exemplary facultative methanotrophs employed in the practice of the present invention include some species of *Methylocella, Methylocystis*, and *Methylocapsa* (e.g., *Methylocella silvestris, Methylocella palustris, Methylocella tundrae, Methylocystis daltona* strain SB2, *Methylocystis bryophila*, and *Methylocapsa aurea* KYG), *Methylobacterium organophilum* (ATCC 27,886), *Methylibium petroleiphilum*, or high growth variants thereof. Exemplary obligate methanotrophic bacteria useful in the practice of the present invention include *Methylococcus capsulatus* Bath (NCIMB 11132), *Methylomonas* sp. 16a (ATCC PTA 2402), *Methylosinus trichosporium* OB3b (NRRL B-11,196), *Methylosinus sporium* (NRRL B-11,197), *Methylocystis parvus* (NRRL B-11,198), *Methylomonas methanica* (NRRL B-11,199), *Methylomonas albus* (NRRL B-11,200), *Methylobacter capsulatus* Y (NRRL B-11,201), *Methylomonas flagellata* sp. AJ-3670 (FERM P-2400), *Methylacidiphilum infernorum, Methylacidiphilum fumariolicum, Methylomicrobium alcaliphilum, Methyloacida kamchatkensis*, or high growth variants thereof.

[0048] Suitable C_1 metabolizing microorganisms useful in the practice of the present invention include syngas metabolizing bacteria such as, for example, *Clostridium, Moorella, Pyrococcus, Eubacterium, Desulfobacterium, Carboxydothermus, Acetogenium, Acetobacterium, Acetoanaerobium, Butyribaceterium, Peptostreptococcus*, and the like. Exemplary syngas metabolizing bacteria include *Clostridium autoethanogenum, Clostridium ljungdahli, Clostridium ragsdalei, Clostridium carboxydivorans, Butyribacterium methylotrophicum, Clostridium woodii, Clostridium neopropanologen*, and the like.

[0049] Other suitable C_1 metabolizing microorganisms useful in the practice of the present invention include eukaryotes such as, for example, yeast, including *Candida, Yarrowia, Hansenula, Pichia, Torulopsis, Rhodotorula*, and the like.

[0050] Each of the microorganisms of this disclosure may be grown as an isolated culture, with a heterologous organism that may aid with growth, or one or more of these bacteria may be combined to generate a mixed culture. The term "heterologous" when referring to an organism refers to a species that is different from the host cell. In still further embodiments, C_1 metabolizing non-photosynthetic microorganisms of this disclosure are obligate C_1 metabolizing non-photosynthetic microorganisms, such as an obligate methanotroph or methylotroph.

[0051] Any one of the aforementioned C_1 metabolizing microorganisms can be used as a parent or reference host cell to make a recombinant C_1 metabolizing microorganisms of this disclosure. As used herein, "recombinant" refers to a non-naturally-occurring organism, microorganism, cell, nucleic acid molecule, or vector that has at least one genetic alteration or has been modified by the introduction of a exogenous nucleic acid molecule, or refers to a cell that has been altered such that the expression of an endogenous nucleic acid molecule or gene can be controlled. Recombinant also refers to a cell that is derived from a cell or is progeny of a cell having one or more such modifications. Genetic alterations include, for example, modifications introducing expressible nucleic acid molecules encoding proteins or enzymes, or other nucleic acid molecule additions, deletions, substitutions or other functional alteration of a cell's genetic material. For example, recombinant cells may express genes or other nucleic acid molecules that are not found in identical form within the native cell (i.e., unmodified or wild type cell), or may provide an altered expression pattern of endogenous genes, such genes that may otherwise be over-expressed, under-expressed, minimally expressed, or not expressed at all.

[0052] Any of the recombinant C_1 metabolizing microorganisms or methanotrophic bacteria described herein may be transformed to comprise at least one exogenous nucleic acid to provide the host with a new or enhanced activity (e.g., enzymatic activity) or may be genetically modified to remove or substantially reduce an endogenous gene function using any of a variety of methods known in the art.

[0053] Transformation refers to the introduction of a nucleic acid molecule (e.g., exogenous nucleic acid molecule) into a host cell. The transformed host cell may carry the exogenous nucleic acid molecule extra-chromosomally or integrated in the chromosome. Integration into a host cell genome and self-replicating vectors generally result in genetically stable inheritance of the transformed nucleic acid molecule. Host cells containing the transformed nucleic acid molecules are referred to as "non-naturally occurring" or "genetically engineered" or "recombinant" or "transformed" or "transgenic" cells (e.g., bacteria).

[0054] Expression systems and expression vectors useful for the expression of exogenous nucleic acids in C_1 metabolizing microorganisms (e.g., methanotrophic bacteria) are known.

[0055] Electroporation of C_1 metabolizing bacteria is described herein and has been previously described in, for example, Toyama et al., *FEMS Microbiol. Lett.* 166:1, 1998; Kim and Wood, *Appl. Microbiol. Biotechnol.* 48:105, 1997; Yoshida et al., *Biotechnol. Lett.* 23:787, 2001, and U.S. Patent Appl. Pub. No. 2008/0026005.

[0056] Bacterial conjugation, which refers to a particular type of transformation involving direct contact of donor and recipient cells, is more frequently used for the transfer of nucleic acid molecules into C_1 metabolizing bacteria. Bacterial conjugation involves mixing "donor" and "recipient" cells together in close contact with each other. Conjugation occurs by formation of cytoplasmic connections between donor and recipient bacteria, with unidirectional transfer of newly synthesized donor nucleic acid molecules into the recipient cells. A recipient in a conjugation reaction is any cell that can accept nucleic acids through horizontal transfer from a donor bacterium. A donor in a conjugation reaction is a bacterium that contains a conjugative plasmid, conjugative transposon, or mobilized plasmid. The physical transfer of the donor plasmid can occur through a self-transmissible plasmid or with the assistance of a "helper" plasmid. Conjugations involving C_1 metabolizing bacteria is described herein and have been previously described in Stolyar et al., *Mikrobiologiya* 64:686, 1995; Motoyama et

al., *Appl. Micro. Biotech.* 42:67, 1994; Lloyd et al., *Arch. Microbiol.* 171:364, 1999; PCT Publication No. WO 02/18617; and Ali et al., *Microbiol.* 152:2931, 2006.

[0057] Expression control sequences suitable for use in the practice of the present invention include, for example, promoters, terminators, enhancers, repressors, inducers, and the like. Promoters suitable for use in the practice of the present invention may be constitutive, leaky, or inducible, and native or non-native to the host cell employed. Exemplary promoters include a pyruvate decarboxylase (PDC) a promoter, a deoxy-xylulose phosphate synthase promoter, a methanol dehydrogenase promoter (MDH) (such as, for example, the promoter in the upstream intergenic region of the mxaF gene from *Methylococcus capsulatus* Bath (Acc. No. MCA0779) or the MDH promoter from *M. extorquens* (See Springer et al., *FEMS Microbiol. Lett.* 160:119 (1998)), a hexulose 6-phosphate synthase promoter, a ribosomal protein S16 promoter, a serine hydroxymethyl transferase promoter, a serine-glyoxylate aminotransferase promoter, a phosphoenolpyruvate carboxylase promoter, a T5 promoter, Trc promoter, a promoter for PHA synthesis (Foellner et al., *Appl. Microbiol. Biotechnol.* 40:284, 1993), a pyruvate decarboxylase promoter (Tokuhiro et al., *Appl. Biochem. Biotechnol.* 131:795, 2006), the lac operon Plac promoter (Toyama et al., *Microbiol.* 143:595, 1997), a hybrid promoter such as Ptrc (Brosius et al., *Gene* 27:161, 1984), promoters identified from native plasmid in methylotrophs (EP 296484), methanotrophs, and the like.

[0058] Additionally, suitable homologous or heterologous promoters for high expression of exogenous nucleic acid molecules may be utilized. For example, U.S. Pat. No. 7,098,005 describes the use of promoters for high expression in the presence of methane or methanol of a heterologous coding nucleic acid in C_1 metabolizing bacteria.

[0059] In certain embodiments, regulated expression of exogenous nucleic acids encoding a carbohydrate biosynthesis enzyme may be desirable to optimize growth rate of the non-naturally occurring C_1 metabolizing microorganism and may improve bacterial growth in a variety of carbon source conditions. This may be achieved through the use of an inducible promoter system.

[0060] In certain embodiments, a nucleic acid encoding CB enzyme is operatively linked to an inducible promoter. Inducible promoter systems employed in the practice of the present invention include those known in the art and include tetracycline inducible promoter system; IPTG/lac operon inducible promoter system, heat shock inducible promoter system; metal-responsive promoter systems; nitrate inducible promoter system; light inducible promoter system; ecdysone inducible promoter system, the inducible/regulatable system described for use in methylotrophic and methanotrophic bacteria (see, e.g., U.S. Patent Appl. No. US 2010/0221813, which is incorporated herein by reference), and the like. For example, in one embodiment, the non-naturally occurring C_1 metabolizing microorganism (e.g., methanotroph, methylotroph) comprises: (1) an exogenous nucleic acid encoding CB enzyme, operatively linked to a promoter flanked by lacO operator sequences, and (2) an exogenous nucleic acid encoding a lad repressor protein operatively linked to a constitutive promoter (e.g., hexulose-6-phosphate synthase promoter). Induction is initiated when Lad repressor protein binds to lacO operator sequences flanking the LDH or other promoter, preventing transcription. IPTG binds lad repressor and releases it from lacO sequences, allowing transcription. By using an inducible promoter system, lactate synthesis may be controlled by the addition of an inducer.

[0061] The expression systems and expression vectors employed in the practice of the present invention optionally contain genetic elements, such as, for example, one or more ribosome binding sites for translation initiation and a transcription termination site, polyadenylation signals, restriction enzyme sites, multiple cloning sites, other coding segments, and the like. In certain embodiments, promoters and/or codon optimization (described in more detail hereinabove) are used for high constitutive expression of exogenous polynucleotides encoding one or more carbohydrate biosynthesis enzymes in host methanotrophic bacteria. Regulated expression of an exogenous nucleic acid in a host methanotrophic bacterium may also be utilized. For example, an inducible/regulatable system of recombinant protein expression in methylotrophic and methanotrophic bacteria as described in, for example, U.S. Patent Appl. No. US 2010/0221813 may be used.

Methods of Producing a Desired Carbohydrate

[0062] The present disclosure provides a method of producing a carbohydrate by culturing a recombinant C_1 metabolizing microorganism of the present disclosure in the presence of methane (from any source), or a natural gas-derived carbon feedstock under conditions sufficient to produce the carbohydrate. In a specific embodiment, the present disclosure provides a method of producing a carbohydrate by culturing a recombinant C_1 metabolizing microorganism in the presence of a natural gas-derived carbon feedstock under conditions sufficient to produce the carbohydrate, wherein the C_1 metabolizing microorganism comprises an exogenous nucleic acid encoding a carbohydrate biosynthesis enzyme. Typically, the natural gas-derived carbon feedstock is natural gas, methane, or syngas. Conditions for culturing exemplary C_1 metabolizing microorganisms are illustrated in Example 1.

[0063] In a further embodiment, the present disclosure provides a method of producing a carbohydrate, said method comprising culturing a recombinant C_1 metabolizing microorganism in the presence of methane under conditions sufficient to produce the carbohydrate, wherein the C_1 metabolizing microorganism comprises an exogenous nucleic acid encoding a carbohydrate biosynthesis enzyme. In this embodiment, methane from any source is suitable for use in the practice of the present invention, including natural gas, bio-methane, and the like. As used herein, the term "bio-methane" refers to methane generated by fermentation of organic matter such as, for example, manure, waste water sludge, municipal solid waste, and the like, under anaerobic conditions.

[0064] A variety of culture methodologies may be used for the microorganisms described herein. For example, C_1 metabolizing microorganisms (such as methanotroph or methylotroph bacteria) may be grown by batch culture or continuous culture methodologies. In certain embodiments, the cultures are grown in a controlled culture unit, such as a fermentor, bioreactor, hollow fiber cell, or the like. Generally cells in log phase are often responsible for the bulk production of a product or intermediate of interest in some systems, whereas stationary or post-exponential phase production can be obtained in other systems.

[0065] A classical batch culturing method is a closed system in which the media composition is set when the culture is started and is not altered during the culture process. That is, media is inoculated at the beginning of the culturing process with one or more microorganisms of choice and then are allowed to grow without adding anything to the system. As used herein, a "batch" culture is in reference to not changing the amount of a particular carbon source initially added, whereas control of factors such as pH and oxygen concentration can be monitored and altered during the culture. In batch systems, metabolite and biomass compositions of the system change constantly up to the time the culture is terminated. Within batch cultures, cells (e.g., bacteria such as methylotrophs) will generally move from a static lag phase to a high growth logarithmic phase to a stationary phase where growth rate is reduced or stopped (and will eventually lead to cell death if conditions do not change).

[0066] A fed-batch system is a variation on the standard batch system in which a carbon substrate of interest is added in increments as the culture progresses. Fed-batch systems are useful when cell metabolism is likely to be inhibited by catabolite repression and when it is desirable to have limited amounts of substrate in the media. Since it is difficult to measure actual substrate concentration in fed-batch systems, an estimate is made based on changes of measureable factors such as pH, dissolved oxygen, and the partial pressure of waste gases. Batch and fed-batch culturing methods are common and known in the art (see, e.g., Thomas D. Brock, Biotechnology: A Textbook of Industrial Microbiology, 2nd Ed. (1989) Sinauer Associates, Inc., Sunderland, Mass.; Deshpande, *Appl. Biochem. Biotechnol.* 36:227, 1992).

[0067] Continuous cultures are "open" systems in the sense that defined culture media is continuously added to a bioreactor while an equal amount of used ("conditioned") media is removed simultaneously for processing. Continuous cultures generally maintain the cells at a constant high, liquid phase density where cells are primarily in logarithmic growth phase. Alternatively, continuous culture may be practiced with immobilized cells (e.g., biofilm) where carbon and nutrients are continuously added and valuable products, by-products, and waste products are continuously removed from the cell mass. Cell immobilization may be achieved with a wide range of solid supports composed of natural materials, synthetic materials, or a combination thereof.

[0068] Continuous or semi-continuous culture allows for the modulation of one or more factors that affect cell growth or end product concentration. For example, one method may maintain a limited nutrient at a fixed rate (e.g., carbon source, nitrogen) and allow all other parameters to change over time. In other embodiments, several factors affecting growth may be continuously altered while cell concentration, as measured by media turbidity, is kept constant. The goal of a continuous culture system is to maintain steady state growth conditions while balancing cell loss due to media being drawn off against the cell growth rate. Methods of modulating nutrients and growth factors for continuous culture processes and techniques for maximizing the rate of product formation are well known in the art (see Brock, 1992).

[0069] Liquid phase bioreactors (e.g., stirred tank, packed bed, one liquid phase, two liquid phase, hollow fiber membrane) are well known in the art and may be used for growth of non-naturally occurring microorganisms and biocatalysis.

[0070] By using gas phase bioreactors, substrates for bioproduction are absorbed from a gas by non-naturally occurring microorganisms, cell lysates or cell-free fractions thereof, rather than from a liquid. Use of gas phase bioreactors with microorganisms is known in the art (e.g., U.S. Pat. Nos. 2,793,096; 4,999,302; 5,585,266; 5,079,168; and 6,143,556; U.S. Statutory Invention Registration H1430; U.S. Patent Application Publication No. 2003/0032170; *Emerging Technologies in Hazardous Waste Management III,* 1993, eds. Tedder and Pohland, pp 411-428). Exemplary gas phase bioreactors include single pass system, closed loop pumping system, and fluidized bed reactor. By utilizing gas phase bioreactors, methane or other gaseous substrates are readily available for bioconversion by polypeptides with, for example, monooxygenase activity. In certain embodiments, methods for converting a gas into a carbohydrate are performed in gas phase bioreactors. In further embodiments, methods for converting a gas into a carbohydrate are performed in fluidized bed reactors. In a fluidized bed reactor, a fluid (i.e., gas or liquid) is passed upward through particle bed carriers, usually sand, granular-activated carbon, or diatomaceous earth, on which microorganisms can attach and grow. The fluid velocity is such that particle bed carriers and attached microorganisms are suspended (i.e., bed fluidization). The microorganisms attached to the particle bed carriers freely circulate in the fluid, allowing for effective mass transfer of substrates in the fluid to the microorganisms and increased microbial growth. Exemplary fluidized bed reactors include plug-flow reactors and completely mixed reactors. Uses of fluidized bed reactors with microbial biofilms are known in the art (e.g., Pfluger et al., *Bioresource Technol.* 102:9919, 2011; Fennell et al., *Biotechnol, Bioengin.* 40:1218, 1992; Ruggeri et al., *Water Sci. Technol.* 29:347, 1994; U.S. Pat. Nos. 4,032,407; 4,009,098; 4,009,105; and 3,846,289).

[0071] Recombinant C_1 metabolizing microorganisms described in the present disclosure may be grown as an isolated pure culture, with a heterologous non-C_1 metabolizing microorganism(s) that may aid with growth, or with one or more different strains or species of C_1 metabolizing microorganisms may be combined to generate a mixed culture.

[0072] In certain embodiments, carbohydrates of the present disclosure are produced during a specific phase of cell growth (e.g., lag phase, log phase, stationary phase, or death phase). It may be desirable for carbon from feedstock to be converted to the carbohydrate rather than to growth and maintenance of C_1 metabolizing microorganism. In some embodiments, non-naturally occurring C_1 metabolizing microorganism (e.g., methanotrophs, methylotrophs) as provided herein are cultured to a low to medium cell density (OD_{600}) and then production of carbohydrate is initiated. In some embodiments, a carbohydrate is produced while methanotrophic bacteria are no longer dividing or dividing very slowly. In some embodiments, the carbohydrate is produced only during stationary phase. In some embodiments, the carbohydrate is produced during log phase and stationary phase.

[0073] The fermenter composition comprising the carbohydrate produced by a recombinant C_1 metabolizing microorganism (e.g., methanotrophs, methylotrophs) provided herein may further comprise other organic compounds asso-

ciated with biological fermentation processes. For example, biological by-products of fermentation may include one or more of alcohols, epoxides, aldehydes, ketones, esters, or a combination thereof. In certain embodiments, the fermenter composition may contain one or more of the following alcohols: methanol, ethanol, butanol, or propanol. Other compounds, such as H_2O, CO, CO_2, CO N_2, H_2, O_2, and unutilized carbon feedstocks, such as methane, ethane, propane, and butane, may also be present in the fermenter off-gas.

[0074] In certain embodiments, the recombinant C_1 metabolizing microorganisms (e.g., methanotrophs, methylotrophs) provided herein produce a carbohydrate of the present invention at about 0.001 g/L of culture to about 500 g/L of culture. In some embodiments, the amount of carbohydrate produced is about 1 g/L of culture to about 100 g/L of culture. In some embodiments, the amount of carbohydrate produced is about 0.001 g/L, 0.01 g/L, 0.025 g/L, 0.05 g/L, 0.1 g/L, 0.15 g/L, 0.2 g/L, 0.25 g/L, 0.3 g/L, 0.4 g/L, 0.5 g/L, 0.6 g/L, 0.7 g/L, 0.8 g/L, 0.9 g/L, 1 g/L, 2.5 g/L, 5 g/L, 7.5 g/L, 10 g/L, 12.5 g/L, 15 g/L, 20 g/L, 25 g/L, 30 g/L, 35 g/L, 40 g/L, 45 g/L, 50 g/L, 60 g/L, 70 g/L, 80 g/L, 90 g/L, 100 g/L, 125 g/L, 150 g/L, 175 g/L, 200 g/L, 225 g/L, 250 g/L, 275 g/L, 300 g/L, 325 g/L, 350 g/L, 375 g/L, 400 g/L, 425 g/L, 450 g/L, 475 g/L, or 500 g/L.

Products

[0075] The present disclosure provides other useful products in addition to the recombinant C_1 metabolizing cells described herein. In one embodiment, the present disclosure provides a biomass comprising a recombinant C_1 metabolizing microorganism as described herein. In a specific embodiment, the present disclosure provides a biomass comprising a recombinant C_1 metabolizing microorganism, wherein the recombinant C_1 metabolizing microorganism comprises an exogenous nucleic acid encoding a carbohydrate biosynthesis enzyme and wherein the recombinant C_1 metabolizing microorganism is capable of converting a natural gas-derived feedstock into a desired carbohydrate. In a specific embodiment, the exogenous nucleic acid encodes a β-glucan biosynthesis enzyme, for example, a β-(1,3)-glucan synthase. In some embodiments, the biomass comprises a recombinant C_1 metabolizing microorganism and a desired carbohydrate, wherein the desired carbohydrate is a β-glucan and the recombinant C_1 metabolizing microorganism comprises an exogenous nucleic acid encoding a β-glucan biosynthesis enzyme, and wherein the C_1 metabolizing microorganism is capable of converting a natural gas-derived feedstock into a β-glucan. Exemplary β-glucans include a β-(1,3)-glucan, a β-(1,3)(1,6)-glucan, a β-(1,3)(1.4)-glucan, and a β-(1,4)-glucan. In certain embodiments, the desired carbohydrate is selected from a β-(1,3)-glucan, a β-(1,3)(1,6)-glucan, or a β-(1,3)(1.4)-glucan. In other embodiments, the desired carbohydrate is a β-(1,3)-glucan.

[0076] In a further embodiment, the present disclosure provides a biomass comprising a recombinant C_1 metabolizing microorganism, wherein the recombinant C_1 metabolizing microorganism comprises an exogenous nucleic acid encoding a carbohydrate biosynthesis enzyme and wherein the recombinant C_1 metabolizing microorganism is capable of converting methane into a desired carbohydrate. In a specific embodiment, the exogenous nucleic acid encodes a β-glucan biosynthesis enzyme, for example, a β-(1,3)-glucan synthase, and the C_1 metabolizing microorganism is capable of converting methane into a β-glucan. Typically the β-glucan is selected from the group consisting of a β-glucan, such as, for example, a β-(1,3)-glucan, a β-(1,3)(1,6)-glucan, a β-(1,3)(1,4)-glucan, and a β-(1,4)-glucan. In certain embodiments, the desired carbohydrate is selected from the group consisting of a β-(1,3)-glucan, a β-(1,3)(1,6)-glucan, a β-(1,3)(1,4)-glucan. In other embodiments, the desired carbohydrate is a β-(1,3)-glucan.

[0077] As used herein, "biomass" refers to organic material having a biological origin, which may include one or more of whole cells, lysed cells, extracellular material, or the like. For example, the material harvested from a cultured microorganism (e.g., bacterial or yeast culture) is considered the biomass, which can include cells, cell membranes, cell cytoplasm, inclusion bodies, products secreted or excreted into the culture medium, or any combination thereof. In certain embodiments, biomass comprises the C_1 metabolizing microorganisms of this disclosure together with the media of the culture in which the C_1 metabolizing microorganisms of this disclosure were grown. In other embodiments, biomass comprises a C_1 metabolizing microorganisms (whole or lysed or both) of this disclosure recovered from a culture grown on a C_1 substrate (e.g., natural gas, methane, and the like). In still other embodiments, biomass comprises the spent media supernatant from a culture of C_1 metabolizing microorganism cultured on a C_1 substrate. Such a culture may be considered a renewable resource. Biomass of the present invention is enriched with respect to levels of the desired carbohydrate.

[0078] Recombinant C_1 metabolizing microorganism of the present disclosure that are provided with a natural gas-derived substrate for cell growth are distinctive with respect to their carbon fingerprint as represented by their $\delta^{13}C$ values (as are the products derived from such recombinant C_1 metabolizing microorganisms). By way of background, stable isotopic measurements and mass balance approaches are widely used to evaluate global sources and sinks of methane (see Whiticar and Faber, *Org. Geochem.* 10:759, 1986; Whiticar, *Org. Geochem.* 16: 531, 1990). To use $\delta^{13}C$ values of residual methane to determine the amount oxidized, it is necessary to know the degree of isotopic fractionation caused by microbial oxidation of methane. For example, aerobic methanotrophs can metabolize methane through a specific enzyme, methane monooxygenase (MMO). Methanotrophs convert methane to methanol and subsequently formaldehyde. Formaldehyde can be further oxidized to CO_2 to provide energy to the cell in the form of reducing equivalents (NADH), or incorporated into biomass through either the RuMP or Serine cycles (Hanson and Hanson, *Microbiol. Rev.* 60:439, 1996), which are directly analogous to carbon assimilation pathways in photosynthetic organisms. More specifically, a Type I methanotroph uses the RuMP pathway for biomass synthesis and generates biomass entirely from CH_4, whereas a Type II methanotroph uses the serine pathway that assimilates 50-70% of the cell carbon from CH_4 and 30-50% from CO_2 (Hanson and Hanson, 1996). Methods for measuring carbon isotope compositions are provided in, for example, Templeton et al. (*Geochim. Cosmochim. Acta* 70:1739, 2006), which methods are hereby incorporated by reference in their entirety. Examples 2 describes the characterization of stable carbon isotope distribution in the cells of different C_1 metabolizing microorganisms. The highly negative $\delta^{13}C$ values for the cells was similarly reflected in the $\delta^{13}C$ of

compounds extracted from these cells, i.e., lipid fractions. The $\delta^{13}C$ of the invention products described herein (i.e., a recombinant C_1 metabolizing microorganism of the present disclosure as described herein), related biomass and carbohydrate compositions derived therefrom) can vary depending on the source and purity of the C_1 substrate used as demonstrated in Example 2.

[0079] In certain embodiments, a recombinant C_1 metabolizing microorganism of the present disclosure, and related biomass and carbohydrate compositions derived therefrom, exhibit a $\delta^{13}C$ of less than −30‰, less than −31‰, less than −32‰, less than −33‰, less than −34‰, less than −35‰, less than −36‰, less than −37‰, less than −38‰, less than −39‰, less than −40‰, less than −41‰, less than −42‰, less than −43‰, less than −44‰, less than −45‰, less than −46‰, less than −47‰, less than −48‰, less than −49‰, less than −50‰, less than −51‰, less than −52‰, less than −53‰, less than −54‰, less than −55‰, less than −56‰, less than −57‰, less than −58‰, less than −59‰, less than −60‰, less than −61‰, less than −62‰, less than −63‰, less than −64‰, less than −65‰, less than −66‰, less than −67‰, less than −68‰, less than −69‰, or less than −70‰.

[0080] In certain embodiments, a recombinant C_1 metabolizing microorganism of the present disclosure, and related biomass and carbohydrate compositions derived therefrom, exhibit a $\delta^{13}C$ of about −35‰ to about −50‰, −45‰ to about −35‰, or about −50‰ to about −40‰, or about −45‰ to about −65‰, or about −60‰ to about −70‰, or about −30‰ to about −70‰.

[0081] In further embodiments, a C_1 metabolizing non-photosynthetic microorganism biomass has a $\delta^{13}C$ of less than about −30‰, or ranges from about −40‰ to about −60‰. In certain embodiments, the biomass comprises a recombinant C_1 metabolizing non-photosynthetic microorganism together with the spent media, or the biomass comprises a spent media supernatant composition from a culture of a recombinant C_1 metabolizing non-photosynthetic microorganism, wherein the $\delta^{13}C$ of the biomass is less than about −30‰. In certain other embodiments, the carbohydrate composition is extracted or concentrated from a biomass, which can comprise recombinant C_1 metabolizing non-photosynthetic microorganisms together with the spent media from a culture, or a spent media supernatant composition from a culture of a recombinant C_1 metabolizing non-photosynthetic microorganism.

[0082] In certain embodiments, a carbohydrate composition derived from a C_1 metabolizing microorganism (which may optionally be an extract or isolate from the C_1 metabolizing microorganism biomass) comprises hydrogen, oxygen, and carbon atoms of at least about 50% to about 80% of the weight of the composition, and wherein the $\delta^{13}C$ of the composition is less than about −35‰ or less than about −36‰ or less than about −37‰ or less than about −38‰ or less than about −39‰ or less than about −40‰. In certain embodiments, a carbohydrate composition derived therefrom comprises molecules having hydrogen, oxygen, and carbon atoms, wherein the hydrogen, oxygen, and carbon atoms are at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, or at least 80%, or at least 90%, or at least 95% of the weight of the composition and wherein the $\delta^{13}C$ of the composition ranges from about −30‰ to about −70‰, or wherein the $\delta^{13}C$ in the biomass decreases as cell density increases by about −5‰ to about −20‰, or wherein the $\delta^{13}C$ of the biomass is higher than that of CO_2 produced at the same time by an average of 5‰ to 15‰ when cultured in the presence or absence of copper.

[0083] Typically, a carbohydrate composition comprises a polysaccharide, and in some instances, it comprises a monosaccharide. In other embodiments the carbohydrate composition comprises a disaccharide. In some embodiments, the carbohydrate comprises a β-glucan. Typically, the β-glucan is a β-(1,3)-glucan. In other embodiments, the β-glucan is a β-(1,3)(1,6)-glucan, or a β-(1,3)(1,4)-glucan, or a β-(1,6)-glucan. Carbohydrate compositions derived from recombinant C_1 metabolizing microorganisms cultivated in the presence of a natural gas-derived substrate exhibit the $\delta^{13}C$ values described hereinabove.

[0084] Characterization of $\delta^{13}C$ of some C_1 metabolizing microorganisms cultivated in the presence of a natural gas-derived feedstock is illustrated in the examples, hereinbelow.

[0085] The present disclosure further provides an animal feed comprising the recombinant C_1 metabolizing microorganism, related biomass, and/or carbohydrate composition of the present disclosure. As contemplated in the practice of the present invention, the animal feed may be a livestock feed (such as, for example, pig feed, cattle feed, sheep feed, and the like), a poultry feed (such as, for example, chicken feed, turkey feed, and the like), or a fish feed (such as, for example, salmon feed, shell fish feed, and the like). The animal feed may further comprise an additive, such as, for example, a plant-derived material (including, for example, those derived from grains such as, for example, corn, barley, oats, rice, rye, wheat, sorghum, Brewer's spent grain, and the like; and those derived from legumes, such as, for example, alfalfa, clover, peas, beans, lentils, soybeans, and the like), an animal-derived material (such as, for example, fish meal), and/or a microorganism-derived material (including, for example, biomass from a heterologous microorganism that may be, for example, a bacteria, a yeast, or an algae). In some embodiments, the plant-derived material additive is soy meal or pea protein,

[0086] In a further embodiment, the present disclosure provides a culture or fermentation medium comprising the recombinant C_1 metabolizing microorganism, related biomass, and/or carbohydrate composition of the present disclosure. Typically, the culture or fermentation medium further comprises an amino acid and/or water. In an additional embodiment, the present disclosure provides a cell culture composition comprising a culture or fermentation medium as described herein, and a second microorganism. Typically, a second microorganism is a bacteria, a yeast, or an algae.

[0087] Embodiments of the present invention include the following:

[0088] 1. A biomass derived from a culture of a recombinant C_1 metabolizing microorganism, wherein the recombinant microorganism comprises an exogenous nucleic acid encoding a carbohydrate biosynthesis enzyme, wherein the recombinant C_1 metabolizing is capable of converting a natural gas-derived carbon feedstock into a desired carbohydrate.

[0089] 2. A biomass derived from a culture of a recombinant C_1 metabolizing microorganism, wherein the recombinant C_1 metabolizing microorganism comprises an exogenous nucleic acid encoding a carbohydrate biosynthesis enzyme, wherein the recombinant C_1 metabolizing microorganism is capable of converting methane into a desired carbohydrate.

[0090] 3. The biomass of any of embodiments 1-2, wherein the recombinant C_1 metabolizing microorganism is a non-photosynthetic C_1 metabolizing microorganism.

[0091] 4. The biomass of any of embodiments 1-3, wherein the carbohydrate is selected from the group consisting of a polysaccharide, a disaccharide, and a monosaccharide.

[0092] 5. The biomass of embodiment 4, wherein the carbohydrate is a monosaccharide.

[0093] 6. The biomass of embodiment 4, wherein the carbohydrate is a disaccharide.

[0094] 7. The biomass of embodiment 4, wherein the carbohydrate is a polysaccharide.

[0095] 8. The biomass of embodiment 7, wherein the polysaccharide is a β-glucan.

[0096] 9. The biomass of embodiment 8, wherein the β-glucan is β-(1,3)-glucan.

[0097] 10. The biomass of embodiment 8, wherein the β-glucan is β-(1,3)(1,6)-glucan.

[0098] 11. The biomass of embodiment 8, wherein the β-glucan is β-(1,3)(1,4)-glucan.

[0099] 12. The biomass of embodiment 8, wherein the β-glucan is β-(1,4)-glucan.

[0100] 13. The biomass of embodiment 8, wherein the β-glucan is β-(1,6)-glucan.

[0101] 14. The biomass of any of embodiments 1-13, wherein the sequence of the exogenous nucleic acid is codon optimized for optimal expression from the recombinant C_1 metabolizing microorganism.

[0102] 15. The biomass of any of embodiments 1-14, wherein the exogenous nucleic acid encodes a gluconeogenesis enzyme.

[0103] 16. The biomass of embodiment 15, wherein the gluconeogenesis enzyme is selected from the group consisting of a pyruvate carboxylase, a phosphoenolpyruvate carboxykinase, an enolase, a phosphoglycerate mutase, a phosphoglycerate kinase, a glyceraldehyde-3-phosphate dehydrogenase, a Type A aldolase, a fructose 1,6-bisphosphatase, a phosphofructokinase, a phosphoglucose isomerase, a hexokinase, and a glucose-6-phosphate.

[0104] 17. The biomass of any of embodiments 1-14, wherein the exogenous nucleic acid encodes a glycogenesis enzyme.

[0105] 18. The biomass of embodiment 17, wherein the glycogenesis enzyme is selected from the group consisting of a glucose-1-phosphate adenyltransferase, a glycogen synthase, and a 1,4-alpha-glucan-branching protein.

[0106] 19. The biomass of any of embodiments 8-14, wherein the exogenous nucleic acid is a β-glucan synthase.

[0107] 20. The biomass of any of embodiments 1-19, wherein the exogenous nucleic acid encodes a carbohydrate biosynthesis enzyme that is endogenous to a bacteria.

[0108] 21. The biomass of any of embodiments 1-19, wherein the exogenous nucleic acid encodes a carbohydrate biosynthesis enzyme that is endogenous to an organism selected from the group consisting of a yeast, a fungi, and a plant.

[0109] 22. The biomass of any of embodiments 1-19, wherein the exogenous nucleic acid encodes a carbohydrate biosynthesis enzyme that is endogenous to a microorganism selected from the group consisting of *E. coli* and *C. glutamicum.*

[0110] 23. The biomass of any of embodiments 1-14, wherein the exogenous nucleic acid encodes a carbohydrate biosynthesis enzyme selected from the group consisting of any of SEQ ID NOs:2, 4, 6, 8 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, and 38.

[0111] 24. The biomass of any of embodiments 1-23, wherein the exogenous nucleic acid encoding carbohydrate biosynthesis pathway enzyme is operatively linked to an expression control sequence.

[0112] 25. The biomass of embodiment 24, wherein the expression control sequence is an exogenous expression control sequence.

[0113] 26. The biomass of any of embodiments 1-25, wherein the C_1 metabolizing microorganism further comprises a deletion of an endogenous enzyme activity. 27. The biomass according to any of embodiments 1-26, wherein the C_1 metabolizing microorganism is a methanotroph.

[0114] 28. The biomass according to embodiment 27, wherein the methanotroph is *Methylomonas, Methylobacter, Methylococcus, Methylosinus, Methylocystis, Methylomicrobium, Methanomonas, Methylocella*, or *Methylocapsa.*

[0115] 29. The biomass of embodiment 27, wherein the methanotroph is selected from the group consisting of *Methylococcus capsulatus* Bath strain, *Methylomonas methanica* 16a (ATCC PTA 2402), *Methylosinus trichosporium* OB3b (NRRL B-11,196), *Methylosinus sporium* (NRRL B-11,197), *Methylocystis parvus* (NRRL B-11,198), *Methylomonas methanica* (NRRL B-11,199), *Methylomonas albus* (NRRL B-11,200), *Methylobacter capsulatus* (NRRL B-11,201), *Methylobacterium organophilum* (ATCC 27,886), *Methylomonas* sp AJ-3670 (FERM P-2400), *Methylocella silvestris, Methylocella palustris* (ATCC 700799), *Methylocella tundrae, Methylocystis* daltona strain SB2, *Methylocystis bryophila, Methylocapsa aurea* KYG, *Methylacidiphilum infernorum, Methylibium petroleiphilum*, and *Methylomicrobium alcahphilum.*

[0116] 30. The biomass according to any one of embodiments 1 and 3-29, wherein the natural gas-derived carbon feedstock is selected from the group consisting of natural gas, syngas, methane, methanol, formaldehyde, formic acid, carbon monoxide, carbon dioxide, cyanide, a methylamine, a methylthiol, a methylhalogen, and any combination or two or more thereof.

[0117] 31. The biomass of embodiment 30, wherein the natural gas-derived carbon feedstock is natural gas.

[0118] 32. The biomass of any of embodiments 1, and 3-30, wherein the natural gas-derived carbon feedstock is methane.

[0119] 33. The biomass of embodiment 30, wherein the natural gas-derived carbon feedstock is syngas.

[0120] 34. The biomass of embodiment 30, wherein the C_1 metabolizing microorganism is a syngas metabolizing bacteria.

[0121] 35. The biomass according to embodiment 34, wherein the syngas metabolizing bacteria is selected from the group consisting of *Clostridiumautoethanogenum, Clostridium ljungdahli, Clostridium ragsdalei, Clostridium carboxydivorans, Butyridbacterium methylotrophicum, Clostridium woodii*, and *Clostridium neopropanologen.*

[0122] 36. The biomass according to any one of embodiments 1 and 3-35, wherein the $\delta^{13}C$ of the biomass is less than −40‰.

[0123] 37. The biomass of embodiment 2, wherein the methane is bio-methane.

[0124] 38. A composition comprising a carbohydrate composition, wherein the carbohydrate composition exhibits a $\delta^{13}C$ of less than −40‰.

[0125] 39. The composition of embodiment 38, wherein the carbohydrate comprises a β-glucan.

[0126] 40. The composition of embodiment 39, wherein the β-glucan is β-(1,3)-glucan.

[0127] 41. An animal feed comprising the biomass of any of embodiments 1-37 or the composition of any of embodiments 38-40.

[0128] 42. The animal feed of embodiment 41, further comprising a plant-derived material.

[0129] 43. The animal feed of embodiment 41, wherein the plant-derived material is selected from the group consisting of soybean meal and pea protein.

[0130] 44. A culture or fermentation medium comprising the biomass of any of embodiments 1-37 or the composition of any of embodiments 38-40.

[0131] 45. A recombinant C_1 metabolizing microorganism, wherein the recombinant microorganism comprises an exogenous nucleic acid encoding a carbohydrate biosynthesis enzyme, wherein the recombinant C_1 metabolizing microorganism is capable of converting a natural gas-derived carbon feedstock into a desired carbohydrate.

[0132] 46. A recombinant C_1 metabolizing microorganism, wherein the recombinant C_1 metabolizing microorganism comprises an exogenous nucleic acid encoding a carbohydrate biosynthesis enzyme, wherein the recombinant C_1 metabolizing microorganism is capable of converting methane into a desired carbohydrate.

[0133] 47. The recombinant C_1 metabolizing microorganism of any of embodiments 45-46, wherein the recombinant C_1 metabolizing microorganism is a non-photosynthetic C_1 metabolizing microorganism.

[0134] 48. The recombinant C_1 metabolizing microorganism of any of embodiments 45-47, wherein the carbohydrate is selected from the group consisting of a polysaccharide, a disaccharide, and a monosaccharide.

[0135] 49. The recombinant C_1 metabolizing microorganism of embodiment 48, wherein the carbohydrate is a monosaccharide.

[0136] 50. The recombinant C_1 metabolizing microorganism of embodiment 48, wherein the carbohydrate is a disaccharide.

[0137] 51. The recombinant C_1 metabolizing microorganism of embodiment 48, wherein the carbohydrate is a polysaccharide.

[0138] 52. The recombinant C_1 metabolizing microorganism of embodiment 51, wherein the polysaccharide is a β-glucan.

[0139] 53. The recombinant C_1 metabolizing microorganism of embodiment 52, wherein the β-glucan is β-(1,3)-glucan.

[0140] 54. The recombinant C_1 metabolizing microorganism of embodiment 52, wherein the β-glucan is β-(1,3)(1,6)-glucan.

[0141] 55. The recombinant C_1 metabolizing microorganism of embodiment 52, wherein the β-glucan is β-(1,3)(1,4)-glucan.

[0142] 56. The recombinant C_1 metabolizing microorganism of embodiment 52, wherein the β-glucan is β-(1,4)-glucan.

[0143] 57. The recombinant C_1 metabolizing microorganism of embodiment 52, wherein the β-glucan is β-(1,6)-glucan.

[0144] 58. The recombinant C_1 metabolizing microorganism of any of embodiments 45-57, wherein the sequence of the exogenous nucleic acid is codon optimized for optimal expression from the recombinant C_1 metabolizing microorganism.

[0145] 59. The recombinant C_1 metabolizing microorganism of any of embodiments 45-58, wherein the exogenous nucleic acid encodes a gluconeogenesis enzyme.

[0146] 60. The recombinant C_1 metabolizing microorganism of embodiment 59, wherein the gluconeogenesis enzyme is selected from the group consisting of a pyruvate carboxylase, a phosphoenolpyruvate carboxykinase, an enolase, a phosphoglycerate mutase, a phosphoglycerate kinase, a glyceraldehyde-3-phosphate dehydrogenase, a Type A aldolase, a fructose 1,6-bisphosphatase, a phosphofructokinase, a phosphoglucose isomerase, a hexokinase, and a glucose-6-phosphate.

[0147] 61. The recombinant C_1 metabolizing microorganism of any of embodiments 45-58, wherein the exogenous nucleic acid encodes a glycogenesis enzyme.

[0148] 62. The recombinant C_1 metabolizing microorganism of embodiment 61, wherein the glycogenesis enzyme is selected from the group consisting of a glucose-1-phosphate adenyltransferase, a glycogen synthase, and a 1,4-alpha-glucan-branching protein.

[0149] 63. The recombinant C_1 metabolizing microorganism of any of embodiments 52-57, wherein the exogenous nucleic acid is a β-glucan synthase.

[0150] 64. The recombinant C_1 metabolizing microorganism of any of embodiments 45-63, wherein the exogenous nucleic acid encodes a carbohydrate biosynthesis enzyme that is endogenous to a bacteria.

[0151] 65. The recombinant C_1 metabolizing microorganism of any of embodiments 45-63, wherein the exogenous nucleic acid encodes a carbohydrate biosynthesis enzyme that is endogenous to an organism selected from the group consisting of a yeast, a fungi, and a plant.

[0152] 66. The recombinant C_1 metabolizing microorganism of any of embodiments 45-63, wherein the exogenous nucleic acid encodes a carbohydrate biosynthesis enzyme that is endogenous to a microorganism selected from the group consisting of *E. coli*, and *C. glutamicum*.

[0153] 67. The recombinant C_1 metabolizing microorganism of any of embodiments 45-57, wherein the exogenous nucleic acid encodes a carbohydrate biosynthesis enzyme selected from the group consisting of any of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, and 38.

[0154] 68. The recombinant C_1 metabolizing microorganism of any of embodiments 45-67, wherein the exogenous nucleic acid encoding carbohydrate biosynthesis pathway enzyme is operatively linked to an expression control sequence.

[0155] 69. The recombinant C_1 metabolizing microorganism of embodiment 68, wherein the expression control sequence is an exogenous expression control sequence.

[0156] 70. The recombinant C_1 metabolizing microorganism of any of embodiments 45-69, wherein the C_1 metabolizing microorganism further comprises a deletion of an endogenous enzyme activity.

[0157] 71. The recombinant C_1 metabolizing microorganism according to any of embodiments 45-70, wherein the C_1 metabolizing microorganism is a methanotroph.

[0158] 72. The recombinant C_1 metabolizing microorganism according to embodiment 71, wherein the methanotroph is *Methylomonas, Methylobacter, Methylococcus, Methylosinus, Methylocystis, Methylomicrobium, Methanomonas, Methylocella*, or *Methylocapsa.*

[0159] 73. The recombinant C_1 metabolizing microorganism of embodiment 71, wherein the methanotroph is selected from the group consisting of *Methylococcus capsulatus* Bath strain, *Methylomonas methanica* 16a (ATCC PTA 2402), *Methylosinus trichosporium* OB3b (NRRL B-11,196), *Methylosinus sporium* (NRRL B-11,197), *Methylocystis parvus* (NRRL B-11,198), *Methylomonas methanica* (NRRL B-11,199), *Methylomonas albus* (NRRL B-11, 200), *Methylobacter capsulatus* (NRRL B-11,201), *Methylobacterium organophilum* (ATCC 27,886), *Methylomonas* sp AJ-3670 (FERM P-2400), *Methylocella silvestris, Methylocella palustris* (ATCC 700799), *Methylocella tundrae, Methylocystis daltona* strain SB2, *Methylocystis bryophila, Methylocapsa aurea* KYG, *Methylacidiphilum infernorum, Methylibium petroleiphilum*, and *Methylomicrobium alcahphilum.*

[0160] 74. The recombinant C_1 metabolizing microorganism according to any one of embodiments 45 and 47-73 wherein the natural gas-derived carbon feedstock is selected from the group consisting of natural gas, syngas, methane, methanol, formaldehyde, formic acid, carbon monoxide, carbon dioxide, cyanide, a methylamine, a methylthiol, a methylhalogen, and any combination or two or more thereof.

[0161] 75. The recombinant C_1 metabolizing microorganism of embodiment 74, wherein the natural gas-derived carbon feedstock is natural gas.

[0162] 76. The recombinant C_1 metabolizing microorganism of embodiment 74, wherein the natural gas-derived carbon feedstock is methane.

[0163] 77. The recombinant C_1 metabolizing microorganism of embodiment 74, wherein the natural gas-derived carbon feedstock is syngas.

[0164] 78. The recombinant C_1 metabolizing microorganism of embodiment 77, wherein the C_1 metabolizing microorganism is a syngas metabolizing bacteria.

[0165] 79. The biomass according to embodiment 78, wherein the syngas metabolizing bacteria is selected from the group consisting of *Clostridiumautoethanogenum, Clostridium ljungdahli, Clostridium ragsdalei, Clostridium carboxydivorans, Butyridbacterium methylotrophicum, Clostridium woodii*, and *Clostridium neopropanologen.*

[0166] 80. The recombinant C_1 metabolizing microorganism according to any one of embodiments 45 and 47-79, wherein the $\delta^{13}C$ of the biomass is less than −40‰.

[0167] 81. The recombinant C_1 metabolizing microorganism of embodiment 46, wherein the methane is bio-methane.

[0168] 82. A method of producing a carbohydrate, said method comprising culturing the recombinant C_1 metabolizing microorganism of any of embodiments 45 and 47-68 in the presence of a natural gas-derived carbon feedstock under conditions sufficient to produce the carbohydrate.

[0169] 83. A method of producing a carbohydrate, said method comprising culturing the recombinant C_1 metabolizing microorganism of embodiment 46 in the presence of a methane under conditions sufficient to produce the carbohydrate.

[0170] 84. The method of embodiment 83, wherein the carbohydrate is a β-glucan.

[0171] 85. A carbohydrate produced by the method of embodiment 82, wherein the carbohydrate exhibits a $\delta^{13}C$ in the range of from about −40‰ to about −60‰.

[0172] The foregoing and other aspects of the invention may be better understood in connection with the following, non-limiting examples.

EXAMPLES

Example 1

Culture and Bioreactor Conditions for C_1 Metabolizing Microorganisms

[0173] Exemplary C_1 metabolizing microorganisms of the instant disclosure (methanotrophs, methylotrophs, clostridia) were cultured in tubes, in vials, in bottles, on plates, or in a bioreactor (fermentation). Growth conditions, media, and carbon source for various microorganisms are described in this example.

Methylosinus trichosporium Strain OB3b (NCIMB 11131); *Methylomonas* sp. Strain 16a (ATCC PTA-2402); or *Methylomonas methanica*

[0174] For serum bottles, the bacteria were cultured at 30° C. in Higgins minimal nitrate salts medium (NSM; Cornish et al., *J. Gen. Microbiol.* 130:2565, 1984; Park et al., *Biotechnol. Bioeng.* 38:423, 1991) or MM-W1 medium. The headspace composition was adjusted to a 1:1 volume of methane:air. The bottles were shaken at a rate of 200-250 rpm. Alternatively, the culture was maintained on NSM-media plates containing 1.5% w/v agar grown in a gas-tight chamber containing a 1:1 (v/v) methane:air gas mixture, or in the presence of methanol vapor (via 0.5 mL methanol in the lid of parafilm-sealed plates) or on NSM-media plates supplemented with 0.5% methanol. Plates were incubated inverted in a humidified chamber at 30° C.

[0175] The composition of the NSM medium used was as follows: 1.0 g $MgSO_4*7H_2O$, 0.20 g $CaCl_2*6H_2O$, 2.0 ml chelated iron solution (0.1 g ferric (III) ammonium citrate or 0.5 g ferric (III) chloride; 0.2 g EDTA, sodium salt; 0.3 ml HCl, concentrated; 100.0 ml distilled deionized H_2O), 1.0 g KNO_3, 0.5 ml trace element solution (500.0 mg EDTA, 200.0 mg $FeSO_4$. $7H_2O$, 10.0 mg $ZnSO_4*7H_2O$, 3.0 mg $MnCl_2*4H_2O$, 30.0 mg H_3BO_3, 20.0 mg $CoCl_2*6H_2O$, 1.0 mg $CaCl_2*2H_2O$, 2.0 mg $NiCl_2*6H_2O$, 3.0 mg $Na_2MoO_4*2H_2O$, 1.0 L distilled water), 0.272 g KH_2PO_4, 0.717 g $Na_2HPO_4*12H_2O$, optionally 12.5 g purified agar (e.g., Oxoid L28 or Bacto™ agar; used when making plates), 1.0 L distilled deionized water, pH adjusted to 6.8 and autoclaved at 121° C. for 15 minutes.

[0176] For fermentation, a 2-liter bioreactor containing 1 L of sterilized defined media MM-W1 was inoculated with cells from serum bottle batch cultures (10-20% v/v) grown in MM-W1 supplied with a 1:1 (v/v) mixture of methane and air. The composition of medium MM-W1 used was as follows: 0.8 mM $MgSO_4*7H_2O$, 10 mM $NaNO_3$, 0.14 mM $CaCl_2$, 1.2 mM$NaHCO_3$, 2.35 mM KH_2PO_4, 3.4 mM K_2HPO_4, 20.7 μM$Na_2MoO_4*2H_2O$, 1 μM $CuSO_4*5H_2O$, 10 μM Fe^{III}-Na-EDTA, and 1 mL per liter of trace metals solution (containing, per liter 500 mg $FeSO_4*7H_2O$, 400 mg $ZnSO_4*7H_2O$, 20 mg $MnCl_2*7H_2O$, 50 mg $CoCl_2*6H_2O$, 10 mg $NiCl_2*6H_2O$, 15 mg H_3BO_3, 250 mg EDTA). Phosphate, bicarbonate, and Fe^{III}-Na-EDTA were added after the

media was autoclaved and cooled. Bicarbonate was added up to 0.1% (w/v) in certain fermentations. The reactor contents were stirred with an overhead impeller at a constant 750 rpm. The culture was fed with a constant methane sparging at about 60 mL/min to about 120 mL/min, while concentrated oxygen (at least 85%) was supplied at a variable rate of about 10-100 mL/min to maintain a dissolved oxygen level of about 40% to about 80% (relative to air saturation of the media).

[0177] Temperature in the bioreactor was maintained at 30° C. and pH was maintained at 7.1±0.1 using automated addition of 0.5M NaOH and 0.5M HCl, along with other additions, to the culture about every 4 hours to about 24 hours (corresponding to an OD_{600} increase of approximately 5 OD units). The other additions alternated between a metal addition (10 μM CuSO4, 5 μM FeSO4, 5 μM Fe^{III}-Na-EDTA final concentrations) and a nutrient addition (5.75 mM KxHyPO4, 10 mM NaNO3). Under these conditions, essentially linear growth was observed, with an effective biomass generation rate of about 2.7 to about 3.3 grams dry cell weight per liter per day to an OD_{600} of greater than 20. Culture biomass was harvested by centrifugation, washed once in MM-W 1 media, and recovered biomass was either frozen at −80° C. or used immediately for fractionation of cellular components (e.g., lipid extraction).

[0178] A semi-continuous fermentation approach can also be applied to maintain biomass productivity and reduce time associated with fermentation shut-down and start-up (i.e., turn-around time or lead time).

[0179] Harvesting of the bacterial biomass was performed at approximately 12-24 hour intervals, as the culture density approached (but before entering) stationary phase. Approximately half of the bioreactor volume was removed by transferring to a separate container via centrifugal pump. An equal volume of sterilized or recycled media was then returned to the bioreactor such that the optical density of the reactor was approximately half of its initial value. The bioreactor fermentation was continued according to the above protocol so that multiple cycles of growth and biomass recovery could be carried out during a single fermentation run.

Methylococcus capsulatus Bath (NCIMB 11132)

[0180] The bacteria were cultured at 42° C. in serum bottles containing Higgins minimal nitrate salts medium (NSM) or MM-W1 medium. The headspace composition was adjusted to a 1:1 volume of methane:air. The bottles were shaken at a rate of 200-250 rpm. Alternatively, the culture was maintained on NSM-media plates solidified with 1.5% w/v agar grown in a gas-tight chamber containing a 1:1 (v/v) methane:air gas mixture. Plates were incubated inverted in the chamber at 42° C.

[0181] For fermentation, a 3-liter bioreactor containing 1.25 L sterilized media MMF1.1 was inoculated with cells from serum bottle batch cultures (10-20% v/v) grown in the same media supplied with a 1:1 (v/v) mixture of methane and air. The composition of medium MMF1.1 was as follows: 0.8 mM $MgSO_4*7H_2O$, 40 mM $NaNO_3$, 0.14 mM $CaCl_2$, 6 mM $NaHCO_3$, 4.7 mM KH_2PO_4, 6.8 mM K_2HPO_4, 20.7 μM $Na2MoO_4*2H_2O$, 6 μM $CuSO_4*5H_2O$, 10 μM Fe^{III}-Na-EDTA, and 1 mL per liter of trace metals solution (containing, per liter 500 mg $FeSO_4*7H_2O$, 400 mg $ZnSO_4*7H_2O$, 20 mg $MnCl_2*7H_2O$, 50 mg $CoCl_2*6H_2O$, 10 mg $NiCl_2*6H_2O$, 15 mg H_3BO_3, 250 mg EDTA). Phosphate, bicarbonate, and Fe^{III}-Na-EDTA were added after media was autoclaved and cooled. The reactor contents were stirred with an overhead impeller at a constant 750 rpm. The culture was fed with a constant methane sparging at about 60 to about 200 mL/min, while concentrated oxygen (>85%) was supplied at a variable rate of 15-90 mL/min and the dissolved oxygen level was maintained below 10% (relative to air saturation of the media).

[0182] Temperature in the bioreactor was maintained at 44° C. and pH was maintained at 7.0±0.1 using automated addition of 0.5M NaOH and 0.5M HCl, along with additions of copper and iron (5 μM CuSO4, 5 μM $FeSO_4$, 10 μM Fe^{III}-Na-EDTA final concentration) to the culture every 3-6 hours (corresponding to an OD_{600} increase of approximately 3-5 OD units after reaching OD 5). Under these conditions, essentially linear growth was observed, with effective biomass generation rate of more than 5 grams dry cell weight per liter per day to an OD_{600} of greater than 10. Culture biomass was harvested by centrifugation, the cells washed once in MM-W1 media and cell pellets were either frozen at −80° C. or used immediately for fractionation of cellular components.

[0183] Nutrient depletion was recognized as an issue that could limit the growth yield during fermentation. To avoid limitation of nutrients, mainly nitrogen and phosphate, nutrient feeds composed of 2-fold concentrated MMF1.1 were initiated after culture OD_{600} exceeded 5. The nutrient feed was initiated at dilution rates corresponding to approximately half of the cultures' growth rate to avoid wash-out and to maintain an increase in OD while expanding the culture volume. The bioreactor fermentation was continued according to the above protocol so that multiple cycles of growth and biomass recovery could be carried out during a single fermentation run.

Methylobacterium extorquens or *Methylosinus trichosporium* Strain OB3b (NCIMB 11131)

[0184] The bacteria is cultured at 30° C. in tubes containing Higgins minimal nitrate salts medium (NSM) supplemented with 0.5% methanol. The tubes are shaken at a rate of 200-250 rpm. Alternatively, the cultures are maintained on NSM-media plates containing 1.5% w/v agar grown in the presence of methanol vapor (via 0.5 mL methanol in the lid of parafilm-sealed plates) or supplemented with 0.5% methanol. Plates are incubated inverted in a humidified chamber under normal atmosphere at 30° C.

[0185] For fermentation, a 2-liter bioreactor containing 1 L defined media MM-W1 is inoculated with cells from culture tube batch culture (10-20% v/v). The composition of medium MM-W1 was as described above. The reactor contents are stirred with an overhead impeller at a constant 800 rpm. The culture is fed with an initial bolus of methanol to a final concentration of 0.5% and variable methanol feed, while pure oxygen was supplied at a variable rate of 30-100 mL/min to maintain a dissolved oxygen level of 60-90% (relative to air saturation of the media).

[0186] Temperature in the bioreactor was maintained at 30° C. and pH was maintained at 7.1±0.1 using automated addition of 0.5M NaOH and 1M HCl, along with the metal and nutrient additions as described above. Under these conditions, essentially linear growth is observed, with effective biomass generation rate 2.7 to 3.3 grams dry cell weight per liter per day to an OD_{600} of greater than 20. Culture biomass was harvested by centrifugation, the cells washed

once in MM-W 1 media and cell pellets were either frozen at −80° C. or used immediately for fractionation of cellular components.

[0187] A semi-continuous fermentation approach can also be applied to maintain biomass productivity and reduce time associated with fermentation shut-down and start-up (i.e., turn-around time or lead time).

[0188] Harvesting of the accumulated bacterial biomass was performed at approximately 12-24 hour intervals, as the culture density approached (but before entering) stationary phase. Approximately half of the bioreactor volume was removed by transferring to a separate container via centrifugal pump. An equal volume of fresh or recycled media was then returned to the bioreactor such that the optical density of the reactor was approximately half of its initial value. The bioreactor fermentation was continued according to the above protocol so that multiple cycles of growth and biomass recovery was carried out during a single fermentation run.

Clostridium autoethanogenum and *Clostridium ljungdahlii*

[0189] The *Clostridium* bacteria are cultivated anaerobically in 100 mL modified PETC medium (ATCC medium 1754) at 37° C. in plastic-coated 500 ml-Schott Duran® GL45 bottles with butyl rubber stoppers and 200 kPa steel mill waste gas. Growth is monitored by measuring the optical density at 600 nm (OD_{600}).

[0190] The modified PETC medium contains (per liter) 1 g NH_4Cl, 0.4 g KCl, 0.2 g $MgSO_4*7\ H_2O$, 0.8 g NaCl, 0.1 g KH_2PO_4, 20 mg $CaCl_2*2\ H_2O$, 10 ml trace elements solution (see below), 10 ml Wolfe's vitamin solution (see below), 2 g $NaHCO_3$, and 1 mg resazurin. After the pH is adjusted to 5.6, the medium is boiled, dispensed anaerobically, and autoclaved at 121° C. for 15 min. Steel mill waste gas (composition: 44% CO, 32% N_2, 22% CO_2, 2% H_2) or equivalent synthetic mixtures are used as a carbon source. The media has a final pH of 5.9 and is reduced with cysteine-HCl and Na_2S at a concentration of 0.008% (w/v).

[0191] The trace elements solution contains 2 g nitrilotriacetic acid (adjusted to pH 6 with KOH before addition of the remaining ingredients), 1 g $MnSO_4$, 0.8 g $Fe(SO_4)_2(NH_4)_2*6\ H_2O$, 0.2 g $CoCl_2*6\ H_2O$, 0.2 mg $ZnSO_4*7\ H_2O$, 20 mg $CuCl_2*2\ H_2O$, 20 mg $NiCl_2*6\ H_2O$, 20 mg $Na_2MoO_4*2\ H_2O$, 20 mg Na_2SeO_4, and 20 mg Na_2WO_4 per liter.

[0192] Wolfe's vitamin solution (Wolin et al., *J. Biol. Chem.* 238:2882, 1963) contains (per liter) 2 mg biotin, 2 mg folic acid, 10 mg pyridoxine hydrochloride, 5 mg thiamine-HCl, 5 mg riboflavin, 5 mg nicotinic acid, 5 mg calcium D-(+)-pantothenate, 0.1 mg vitamin B12, 5 mg p-aminobenzoic acid, and 5 mg thioctic acid.

[0193] a. *Clostridium autoethanogenum* Fermentation

[0194] Fermentation of *Clostridium autoethanogenum* is conducted using methods similar to those described in, for example, U.S. Patent Appl. No. 2011/0300593. Briefly, a 2-liter bioreactor containing 1.3 L Solution A (3.083 g NH_4Ac; 0.61 g $MgCl_2*6H_2O$; 0.294 g $CaCl_2*2H_2O$; 0.15 g KCl; 0.12 g NaCl (optional); up to 1 L with distilled water) is sparged with N_2 gas. An 85% solution of H_3PO_4 (2.025 mL, 30 mM) is added and the pH adjusted to 5.3 using concentrated, aqueous NH_4OH. Then 13.5 mL Solution B (20.0 mg Biotin; 20.0 mg Folic acid; 10.0 mg pyridoxine HCl; 50.0 mg thiamine*HCl; 50.0 mg Riboflavin; 50.0 mg nicotinic acid; 50.0 mg calcium D-(*)-pantothenate; 50.0 mg vitamin B12; 50.0 mg p-aminobenzoic acid; 50.0 mg thioctic acid; up to 1 L with distilled water) is added and the solution sparged with N_2 gas. Chromium (II) chloride is added until the oxidation-reduction potential (ORP) of the solution decreases to approximately −200 mV, wherein resazurin (1.35 mL of a 2 g/L solution) is added. Sodium polysulfide (5.4 mL of a 3M solution, see below) is added and the solution sparged with N_2 and then CO containing gas (1% H_2; 13% N_2; 71% CO; 15% CO_2). A metal sulfide solution (150 mL, see below) is added and the solution sparged a further 30 minutes, before inoculation with an actively growing *C. autoethanogenum* culture at a level of approximately 5% (v/v).

[0195] The sodium polysulfide solution is prepared in a 500 ml flask that is charged with Na_2S (93.7 g, 0.39 mol) and 200 ml H_2O. The solution is stirred until the salt dissolves and sulfur (25 g, 0.1 mol) is added under constant N_2 flow. After stirring at room temperature for 2 hours, the sodium polysulfide solution (about 4 M with respect to Na and about 5 M with respect to sulfur), now a clear reddish brown liquid, is transferred into N_2 purged serum bottles, and wrapped in aluminum foil.

[0196] The chromium (II) solution is prepared in a 1 L three necked flask that is fitted with a gas tight inlet and outlet to allow working under inert gas and subsequent transfer of the desired product into a suitable storage flask. The flask is charged with $CrCl_3*6\ H_2O$ (40 g, 0.15 mol), zinc granules [20 mesh] (18.3 g, 0.28 mol), mercury (13.55 g, 1 mL, 0.0676 mol) and 500 mL distilled water. Following flushing with N_2 for one hour, the mixture is warmed to about 80° C. to initiate the reaction. Following two hours of stirring under a constant N_2 flow, the mixture is cooled to room temperature and continuously stirred for another 48 hours by which time the reaction mixture turns into a deep blue solution. The solution is transferred into N_2 purged serum bottles and stored at 4° C. for future use.

[0197] The metal sulfide solution is prepared by adding about 950 mL Solution A into a 1 L fermenter and sparging with N_2 gas. An 85% solution of H_3PO_4 (1.5 mL, 30 mM) is added and the pH adjusted to 5.3 using concentrated aqueous NH_4OH. Solution B (10 mL) is added and the solution sparged with N_2. Chromium (II) chloride is added until the oxidation-reduction potential (ORP) of the solution decreases to approximately −200 mV, wherein resazurin (1 mL of a 2 g/L solution) is added. Solution C (1/10; 10 ml $FeCl_3$; 5 ml $CoCl_2$; 5 ml $NiCl_2$; 1 ml H_3BO_3; 1 ml Na_2MoO_4; 1 ml $MnCl_2$; 1 ml Na_2WO_4; 1 ml $ZnCl_2$; 1 ml Na_2SeO_3; into 1 L media) is added, then sodium polysulfide (2 mL of a 3M solution) is added, and then the solution is sparged with N_2 gas.

[0198] Fermentation of a substrate comprising CO by *C. autoethanogenum* under batch conditions in the presence of polysulfide results in a substantially increased rate of accumulation and a final biomass accumulation of approximately 4 g/L over a 2-3 day period. For example, following a short lag phase of approximately 1 day, the biomass can increase from about 0.5 g/L up to at least 3.5 g/L over approximately 36 hours of fermentation. Furthermore, acetate is not produced during the growth phase in the presence of polysulfide (as is typically found in batch fermentations) and in certain circumstances some of the acetate is consumed, such that there is a net decrease in the amount of acetate in the fermenter. Culture biomass was harvested by centrifugation,

the cells washed once in media and cell pellets were either frozen at −80° C. or used immediately for fractionation of cellular components.

[0199] A semi-continuous fermentation approach can also be applied to maintain biomass productivity and reduce time associated with fermentation shut-down and start-up (i.e., turn-around time or lead time).

[0200] Harvesting of the accumulated bacterial biomass was performed at approximately 12-24 hour intervals, as the culture density approached (but before entering) stationary phase. Approximately half of the bioreactor volume was removed by transferring to a separate container via centrifugal pump. An equal volume of fresh or recycled media was then returned to the bioreactor such that the optical density of the reactor was approximately half of its initial value. The bioreactor fermentation was continued according to the above protocol so that multiple cycles of growth and biomass recovery was carried out during a single fermentation run.

[0201] b. *Clostridium ljungdahlii* Fermentation

[0202] Fermentation of *Clostridium ljungdahlii* is performed using similar methods to those described in, for example, U.S. Pat. Nos. 5,173,429 and 5,593,886. Briefly, batch fermentations are conducted using a biologically pure culture of *C. ljungdahlii*. Preparation of the medium ((1) 80.0 mL of a salt comprising KH_2PO_4 3.00 g/L, K_2HPO_4 3.00 g/L, $(NH_4)_2SO_4$ 6.00 g/L, NaCl 6.00 g/L, $MgSO_4*2H_2O$ 1.25 g/L; (2) 1.0 g of yeast extract; (3) 1.0 g of trypticase; (4) 3.0 ml of PFN (Pfenning) trace metal solution comprising $FeCl_2*4H_2O$ 1500 mg, $ZnSO_4*7H_2O$ 100 mg, $MnCl_2*4H_2O$ 30 mg, H_3BO_3 300 mg, $CoCl_2*6H_2O$ 200 mg, $CuCl_2*H_2O$ 10 mg, $NiCl_2*6H_2O$ 20 mg, $NaMoO_4*2H_2O$ 30 mg, $Na_z SeO_3$ 10 mg, and distilled water up to 1 L; (5) 10.0 ml of B vitamins comprising Pyridoxal HCl 10 mg, Riboflavin 50 mg, Thiamine HCl 50 mg, Nictotinic acid 50 mg, Ca-D-Pantotheinate 50 mg, Lipoic acid 60 mg, p-aminobenzoic acid 50 mg, Folic acid 20 mg, Biotin 20 mg, cyanocobalamin 50 mg, and distilled water up to 1 L; (6) 0.5 g of cysteine HCl; (7) 0.06 g $CaCl_2*2H_2O$; (8) 2.0 g $NaHCO_3$; (9) 1.0 mL resazurin (0.01%); and (10) 920.0 mL distilled water) is carried out anaerobically in an atmosphere of 80% nitrogen and 20% CO_2. The pH of the medium is controlled during fermentation and maintained at 5.0 with HCl. If required, adjustments to the pH are made with sterile 10% NaOH or 1.0% acetic acid solution. The medium is transferred to 157.5 mL serum bottles and sealed with butyl rubber stoppers and aluminum seals. The bottles are then autoclaved at 121° C. for 20 minutes.

[0203] Approximately 48 hours before commencing the experiment, a seed culture is prepared from a stock culture of the *C. ljungdahlii* in a bottle similar to those as described above. The seed culture is grown in a shaker incubator at 37° C. and shaken at 100 rpm. Reducing solutions (2.0 ml Na_2S, 2.5% solution and 2.0 ml cysteine-HCl, 3.5% solution) are added to the culture, which is placed in the shaker incubator for approximately 15 minutes to allow for complete oxygen removal and temperature acclimation. Unlike the procedure used for isolating a biologically pure culture of the organism, addition of methane inhibitors is not required in batch fermentations.

[0204] Fermentation with *C. ljungdahlii* is performed in a New Brunswick Scientific Bioflow IIc 2.5-liter fermenter containing nutrient media at 37° C., and a constant fluid level of 1.5 liters is maintained while the fluid is agitated at variable rates of up to 1,000 revolutions per minute with gas introduced at a rate of approximately 500 cubic centimeters per minute. Optimal gas retention times are in the range of three minutes. The gas feed is varied with its uptake by the bacteria, which is in turn a function of the cell density.

[0205] Harvesting of the accumulated bacterial biomass was performed at approximately 12-24 hour intervals, as the culture density approached (but before entering) stationary phase. Approximately half of the bioreactor volume was removed by transferring to a separate container via centrifugal pump. An equal volume of fresh or recycled media was then returned to the bioreactor such that the optical density of the reactor was approximately half of its initial value. The bioreactor fermentation was continued according to the above protocol so that multiple cycles of growth and biomass recovery was carried out during a single fermentation run.

Example 2

Stable Carbon Isotope Distribution in Lipids from C_1 Metabolizing Microorganisms

[0206] Dry samples of *M. trichosporium* biomass and lipid fractions were analyzed for carbon and nitrogen content (% dry weight), and carbon (^{13}C) and nitrogen (^{15}N) stable isotope ratios via elemental analyzer/continuous flow isotope ratio mass spectrometry using a CHNOS Elemental Analyzer (vario ISOTOPE cube, Elementar, Hanau, Germany) coupled with an IsoPrime100 IRMS (Isoprime, Cheadle, UK). Samples of methanotrophic biomass cultured in fermenters or serum bottles were centrifuged, resuspended in deionized water and volumes corresponding to 0.2-2 mg carbon (about 0.5-5 mg dry cell weight) were transferred to 5×9 mm tin capsules (Costech Analytical Technologies, Inc., Valencia, Calif.) and dried at 80° C. for 24 hours. Similarly, previously extracted lipid fractions were suspended in chloroform and volumes containing 0.1-1.5 mg carbon were transferred to tin capsules and evaporated to dryness at 80° C. for 24 hours. Standards containing 0.1 mg carbon provided reliable $\delta^{13}C$ values.

[0207] The isotope ratio is expressed in "delta" notation (‰), wherein the isotopic composition of a material relative to that of a standard on a per million deviation basis is given by $\delta^{13}C$ (or $\delta^{15}N$)$=(R_{Sample}/R_{Standard\text{-}1})\times 1{,}000$, wherein R is the molecular ratio of heavy to light isotope forms. The standard for carbon is the Vienna Pee Dee Belemnite (V-PDB) and for nitrogen is air. The NIST (National Institute of Standards and Technology) proposed SRM (Standard Reference Material) No. 1547, peach leaves, was used as a calibration standard. All isotope analyses were conducted at the Center for Stable Isotope Biogeochemistry at the University of California, Berkeley. Long-term external precision for C and N isotope analyses is 0.10‰ and 0.15‰, respectively.

[0208] *M. trichosporium* strain OB3b was grown on methane in three different fermentation batches, *M capsulatus* Bath was grown on methane in two different fermentation batches, and *Methylomonas* sp. 16a was grown on methane in a single fermentation batch. The biomass from each of these cultures was analyzed for stable carbon isotope distribution ($\delta^{13}C$ values; see Table 3).

TABLE 3

Stable Carbon Isotope Distribution in Different Methanotrophs

Methanotroph	Batch No.	EFT (h)†	OD_{600}	DCW*	$\delta^{13}C$ Cells
Mt OB3b	68A	48	1.80	1.00	−57.9
		64	1.97	1.10	−57.8
		71	2.10	1.17	−58.0
		88	3.10	1.73	−58.1
		97	4.30	2.40	−57.8
		113	6.00	3.35	−57.0
		127	8.40	4.69	−56.3
Mt OB3b	68B	32	2.90	1.62	−58.3
		41	4.60	2.57	−58.4
		47	5.89	3.29	−58.0
		56	7.90	4.41	−57.5
Mt OB3b	68C	72	5.32	2.97	−57.9
		79.5	5.90	3.29	−58.0
		88	5.60	3.12	−57.8
		94	5.62	3.14	−57.7
Mc Bath	62B	10	2.47	0.88	−59.9
		17.5	5.80	2.06	−61.0
		20	7.32	2.60	−61.1
		23	9.34	3.32	−60.8
		26	10.30	3.66	−60.1
Mc Bath	62A	10	2.95	1.05	−55.9
		13.5	3.59	1.27	−56.8
		17.5	5.40	1.92	−55.2
		23	6.08	2.16	−57.2
		26	6.26	2.22	−57.6
Mms 16a	66B	16	2.13	0.89	−65.5
		18	2.59	1.09	−65.1
		20.3	3.62	1.52	−65.5
		27	5.50	2.31	−66.2
		40.5	9.80	4.12	−66.3

*DCW, Dry Cell Weight is reported in g/L calculated from the measured optical densities (OD_{600}) using specific correlation factors relating OD of 1.0 to 0.558 g/L for Mt OB3b, OD of 1.0 to 0.355 g/L for Me Bath, and OD of 1.0 to 0.42 g/L for Mms 16a. For Mt OB3b, the initial concentration of bicarbonate used per fermentation was 1.2 mM or 0.01% (Batch No. 68C) and 0.1% or 12 mM (Batch Nos. 68A and 68B).
†EFT = effective fermentation time in hours

[0209] In addition, stable carbon isotope analysis was performed for biomass and corresponding lipid fractions (see Table 4) from strains *Methylosinus trichosporium* OB3b (Mt OB3b), *Methylococcus capsulatus* Bath (Mc Bath), and *Methylomonas* sp. 16a (Mms 16a) grown on methane in bioreactors as described in Example 1.

TABLE 4

Stable Carbon Isotope Distribution in Cells and Lipids

Batch No.	Strain	$\delta^{13}C$ Cells	$\delta^{13}C$ Lipids
68C	Mt OB3b	−57.7	−48.6
62A	Mc Bath	−57.6	−52.8
66A	Mms 16a	−64.4	−42.2

[0210] Biomass from strains Mt OB3b, Mc Bath and Mms 16a were harvested at 94 h (3.14 g DCW/L), 26 h (2.2 g DCW/L) and 39 h (1.14 g DCW/L), respectively. The $\delta^{13}C$ values for lipids in Table 4 represent an average of duplicate determinations.

Example 3

Effect of Methane Source and Purity on Stable Carbon Isotope Distribution in Lipids

[0211] To examine methanotroph growth on methane containing natural gas components, a series of 0.5-liter serum bottles containing 100 mL defined media MMS1.0 were inoculated with *Methylosinus trichosporium* OB3b or *Methylococcus capsulatus* Bath from a serum bottle batch culture (5% v/v) grown in the same media supplied with a 1:1 (v/v) mixture of methane and air. The composition of medium MMS1.0 was as follows: 0.8 mM $MgSO_4*7H_2O$, 30 mM $NaNO_3$, 0.14 mM $CaCl_2$, 1.2 mM $NaHCO_3$, 2.35 mM KH_2PO_4, 3.4 mM K_2HPO_4, 20.7 μM $Na_2MoO_4*2H_2O$, 6 μM $CuSO_4*5H_2O$, 10 μM Fe^{III}-Na-EDTA, and 1 mL per liter of a trace metals solution (containing, per L: 500 mg FeSO4*7H2O, 400 mg $ZnSO_4*7H_2O$, 20 mg $MnCl_2*7H2O$, 50 mg $CoCl_2*6H_2O$, 10 mg $NiCl_2*6H_2O$, 15 mg H_3BO_3, 250 mg EDTA). Phosphate, bicarbonate, and Fe^{III}-Na-EDTA were added after media was autoclaved and cooled. The final pH of the media was 7.0±0.1.

[0212] The inoculated bottles were sealed with rubber sleeve stoppers and injected with 60 mL methane gas added via syringe through sterile 0.45 μm filter and sterile 27G needles. Duplicate cultures were each injected with 60 mL volumes of (A) methane of 99% purity (grade 2.0, Praxair through Alliance Gas, San Carlos, Calif.), (B) methane of 70% purity representing a natural gas standard (Sigma-Aldrich; also containing 9% ethane, 6% propane, 3% methylpropane, 3% butane, and other minor hydrocarbon components), (C) methane of 85% purity delivered as a 1:1 mixture of methane sources A and B; and (D) >93% methane (grade 1.3, Specialty Chemical Products, South Houston, Tex.; in-house analysis showed composition >99% methane). The cultures were incubated at 30° C. (*M trichosporium* strain OB3b) or 42° C. (*M capsulatus* Bath) with rotary shaking at 250 rpm and growth was measured at approximately 12 hour intervals by withdrawing 1 mL samples to determine OD_{600}. At these times, the bottles were vented and headspace replaced with 60 mL of the respective methane source (A, B, C, or D) and 60 mL of concentrated oxygen (at least 85% purity). At about 24 hour intervals, 5 mL samples were removed, cells recovered by centrifugation (8,000 rpm, 10 minutes), and then stored at −80° C. before analysis.

[0213] Analysis of carbon and nitrogen content (% dry weight), and carbon (^{13}C) and nitrogen (^{15}N) stable isotope ratios, for methanotrophic biomass derived from *M trichosporium* strain OB3b and *M capsulatus* Bath were carried out. Table 5 shows the results of stable carbon isotope analysis for biomass samples from *M capsulatus* Bath grown on methane having different levels of purity and in various batches of bottle cultures.

TABLE 5

Stable Carbon Isotope Distribution of *M. capsulatus* Bath Grown on Different Methane Sources having Different Purity

Methane*	Batch No.	Time (h)†	OD_{600}	DCW (g/L)	$\delta^{13}C$ Cells
A	62C	22	1.02	0.36	−40.3
		56	2.01	0.71	−41.7
		73	2.31	0.82	−42.5
	62D	22	1.14	0.40	−39.3
		56	2.07	0.73	−41.6
		73	2.39	0.85	−42.0
B	62E	22	0.47	0.17	−44.7
		56	0.49	0.17	−45.4
		73	0.29	0.10	−45.4
	62F	22	0.62	0.22	−42.3
		56	0.63	0.22	−43.6
		73	0.30	0.11	−43.7

TABLE 5-continued

Stable Carbon Isotope Distribution of *M. capsulatus* Bath Grown on Different Methane Sources having Different Purity

Methane*	Batch No.	Time (h)†	OD_{600}	DCW (g/L)	$\delta^{13}C$ Cells
C	62G	22	0.70	0.25	−40.7
		56	1.14	0.40	−44.8
		73	1.36	0.48	−45.8
	62H	22	0.62	0.22	−40.9
		56	1.03	0.37	−44.7
		73	1.23	0.44	−45.9

*Methane purity: A: 99% methane, grade 2.0 (min. 99%); B: 70% methane, natural gas standard (contains 9% ethane, 6% propane, 3% methylpropane, 3% butane); C: 85% methane (1:1 mix of A and B methane)
†Time = bottle culture time in hours

[0214] The average $\delta^{13}C$ for *M. capsulatus* Bath grown on one source of methane (A, 99%) was −41.2±1.2, while the average $\delta^{13}C$ for *M. capsulatus* Bath grown on a different source of methane (B, 70%) was −44.2±1.2. When methane sources A and B were mixed, an intermediate average $\delta^{13}C$ of −43.8±2.4 was observed. These data show that the $\delta^{13}C$ of cell material grown on methane sources A and B are significantly different from each other due to the differences in the $\delta^{13}C$ of the input methane. But, cells grown on a mixture of the two gasses preferentially utilize ^{12}C and, therefore, show a trend to more negative $\delta^{13}C$ values.

[0215] A similar experiment was performed to examine whether two different methanotrophs, *Methylococcus capsulatus* Bath and *Methylosinus trichosporium* OB3b, grown on different methane sources and in various batches of bottle cultures showed a difference in $\delta^{13}C$ distribution (see Table 6).

TABLE 6

Stable Carbon Isotope Distribution of Different Methanotrophs Grown on Different Methane Sources of Different Purity

Strain	Methane*	Batch No.	Time (h)†	OD_{600}	DCW (g/L)	$\delta^{13}C$ Cells
Mc Bath	A	62I	18	0.494	0.18	−54.3
			40	2.33	0.83	−42.1
			48	3.08	1.09	−37.1
Mc Bath	D	62J	18	0.592	0.21	−38.3
			40	1.93	0.69	−37.8
			48	2.5	0.89	−37.8
Mc Bath	D	62K	18	0.564	0.20	−38.6
			40	1.53	0.54	−37.5
			48	2.19	0.78	−37.6
Mt OB3b	A	68D	118	0.422	0.24	−50.2
			137	0.99	0.55	−47.7
			162	1.43	0.80	−45.9
Mt OB3b	A	68E	118	0.474	0.26	−49.9
			137	1.065	0.59	−47.6
			162	1.51	0.84	−45.2
Mt OB3b	D	68F	118	0.534	0.30	−45.6
			137	1.119	0.62	−38.7
			162	1.63	0.91	−36.4
Mt OB3b	D	68G	118	0.544	0.30	−44.8
			137	1.131	0.63	−39.1
			162	1.6	0.89	−34.2

*Methane sources and purity:
A: 99% methane (grade 2.0);
D: >93% methane (grade 1.3)
†Time = bottle culture time in hours

[0216] The average $\delta^{13}C$ for *M capsulatus* grown on a first methane source (A) was −44.5±8.8, while the average $\delta^{13}C$ for *M. trichosporium* was −47.8±2.0 grown on the same methane source. The average $\delta^{13}C$ for *M. capsulatus* grown on the second methane source (B) was −37.9±0.4, while the average $\delta^{13}C$ for *M. trichosporium* was −39.8±4.5. These data show that the $\delta^{13}C$ of cell material grown on a methane source is highly similar to the $\delta^{13}C$ of cell material from a different strain grown on the same source of methane. Thus, the observed $\delta^{13}C$ of cell material appears to be primarily dependent on the composition of the input gas rather than a property of a particular bacterial strain being studied.

[0217] The various embodiments described above can be combined to provide further embodiments. All of the patent and non-patent publications referred to in this specification or listed in the Application Data Sheet, including the disclosure of U.S. provisional application No. 61/928,366, filed Jan. 16, 2014, are incorporated herein by reference in their entirety. Aspects of the embodiments can be modified, if necessary to employ concepts of the various patents, applications and publications to provide further embodiments.

[0218] These and other changes can be made to the embodiments in light of the above-detailed description. In general, in the following embodiments, the terms used should not be construed to limit the embodiments to the specific embodiments disclosed in the specification and the embodiments, but should be construed to include all possible embodiments along with the full scope of equivalents to which such embodiments are entitled. Accordingly, the embodiments are not limited by the disclosure.

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<221> NAME/KEY: CDS
<222> LOCATION: (1)..(852)
<223> OTHER INFORMATION: Saccharomyces cerevisiae mature KRE1 protein
(codon optimized)

<400> SEQUENCE: 1

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gtc atg gcc gct gtt acc acc caa gtc acc gtc gtc acc aat gtt gct       48
Val Met Ala Ala Val Thr Thr Gln Val Thr Val Val Thr Asn Val Ala
1               5                   10                  15

gga gcc ctt gtc acc gaa acc acc atc tgg gac ccc gcg acc gcc gca       96
Gly Ala Leu Val Thr Glu Thr Thr Ile Trp Asp Pro Ala Thr Ala Ala
            20                  25                  30

gcc gca gcg acg acc acc gcc cag acg ggc ttc ttc acc acc gtg ttc      144
Ala Ala Ala Thr Thr Thr Ala Gln Thr Gly Phe Phe Thr Thr Val Phe
        35                  40                  45

acg acc acc aac gac gtg ggt acc act gtc acg ctg acg cag acc gtg      192
Thr Thr Thr Asn Asp Val Gly Thr Thr Val Thr Leu Thr Gln Thr Val
    50                  55                  60

aat cgc gcc acg atg ctg ccc act acc acg acg agc acc agc agc acc      240
Asn Arg Ala Thr Met Leu Pro Thr Thr Thr Thr Ser Thr Ser Ser Thr
65                  70                  75                  80

ggc aag acc acc acg acg gtg ccg act gcg acg tcc tcg ctc agt tcg      288
Gly Lys Thr Thr Thr Thr Val Pro Thr Ala Thr Ser Ser Leu Ser Ser
                85                  90                  95

ggc ctg tcg acc gtc acc acc acg aac gac ctg ggc acg acc gtg acg      336
Gly Leu Ser Thr Val Thr Thr Thr Asn Asp Leu Gly Thr Thr Val Thr
            100                 105                 110

ctc acc cag acc ttc acg cac tcc tcc acg tcc gcg acc tcc tcg gcc      384
Leu Thr Gln Thr Phe Thr His Ser Ser Thr Ser Ala Thr Ser Ser Ala
        115                 120                 125

tcc tcg tcg gtg agc tcg tcc gtc agt agc agt ggc tcc tcc agc agc      432
Ser Ser Ser Val Ser Ser Ser Val Ser Ser Ser Gly Ser Ser Ser Ser
    130                 135                 140

gtc aag acc acg acc tcg acc ggc tcc gcg gtg gcg gaa acc ggg tgg      480
Val Lys Thr Thr Thr Ser Thr Gly Ser Ala Val Ala Glu Thr Gly Trp
145                 150                 155                 160

gac ccg agc acg gat ttt acc gag ccg cca gtg agc gcg gtc acc agc      528
Asp Pro Ser Thr Asp Phe Thr Glu Pro Pro Val Ser Ala Val Thr Ser
                165                 170                 175

ctc tcg atc gac tcg tat ata acg atc acc gag ggc acc acc tcg acc      576
Leu Ser Ile Asp Ser Tyr Ile Thr Ile Thr Glu Gly Thr Thr Ser Thr
            180                 185                 190

tac act acc acc cgg gcg ccg acc tcg atg tgg gtg acc gtc gtc cgc      624
Tyr Thr Thr Thr Arg Ala Pro Thr Ser Met Trp Val Thr Val Val Arg
        195                 200                 205

cag ggg aac acg atc acc gtg caa acc acc ttc gtc cag cgc ttc agc      672
Gln Gly Asn Thr Ile Thr Val Gln Thr Thr Phe Val Gln Arg Phe Ser
    210                 215                 220

tcc caa tac gtg acc gtg gat tcc gtc ggc agc atc ggc atg ggt acg      720
Ser Gln Tyr Val Thr Val Asp Ser Val Gly Ser Ile Gly Met Gly Thr
225                 230                 235                 240
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```
ctg acc ggt acc gtc ggc gtg atc aag tcc gcc atc aag aaa acc gtg      768
Leu Thr Gly Thr Val Gly Val Ile Lys Ser Ala Ile Lys Lys Thr Val
                245                 250                 255

tcc cat aac gag gcc cag cat ctc ggc atg tcg tcg ttc acg tcg att      816
Ser His Asn Glu Ala Gln His Leu Gly Met Ser Ser Phe Thr Ser Ile
            260                 265                 270

ctg ggt ggc ctc ctc acg gtc ttg atc tgg ttc ctg                      852
Leu Gly Gly Leu Leu Thr Val Leu Ile Trp Phe Leu
        275                 280


<210> SEQ ID NO 2
<211> LENGTH: 284
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 2

Val Met Ala Ala Val Thr Thr Gln Val Thr Val Val Thr Asn Val Ala
1               5                   10                  15

Gly Ala Leu Val Thr Glu Thr Thr Ile Trp Asp Pro Ala Thr Ala Ala
            20                  25                  30

Ala Ala Ala Thr Thr Thr Ala Gln Thr Gly Phe Phe Thr Thr Val Phe
        35                  40                  45

Thr Thr Thr Asn Asp Val Gly Thr Thr Val Thr Leu Thr Gln Thr Val
    50                  55                  60

Asn Arg Ala Thr Met Leu Pro Thr Thr Thr Thr Ser Thr Ser Ser Thr
65                  70                  75                  80

Gly Lys Thr Thr Thr Thr Val Pro Thr Ala Thr Ser Ser Leu Ser Ser
                85                  90                  95

Gly Leu Ser Thr Val Thr Thr Thr Asn Asp Leu Gly Thr Thr Val Thr
            100                 105                 110

Leu Thr Gln Thr Phe Thr His Ser Ser Thr Ser Ala Thr Ser Ser Ala
        115                 120                 125

Ser Ser Ser Val Ser Ser Ser Val Ser Ser Ser Gly Ser Ser Ser Ser
    130                 135                 140

Val Lys Thr Thr Thr Ser Thr Gly Ser Ala Val Ala Glu Thr Gly Trp
145                 150                 155                 160

Asp Pro Ser Thr Asp Phe Thr Glu Pro Pro Val Ser Ala Val Thr Ser
                165                 170                 175

Leu Ser Ile Asp Ser Tyr Ile Thr Ile Thr Glu Gly Thr Thr Ser Thr
            180                 185                 190

Tyr Thr Thr Thr Arg Ala Pro Thr Ser Met Trp Val Thr Val Val Arg
        195                 200                 205

Gln Gly Asn Thr Ile Thr Val Gln Thr Thr Phe Val Gln Arg Phe Ser
    210                 215                 220

Ser Gln Tyr Val Thr Val Asp Ser Val Gly Ser Ile Gly Met Gly Thr
225                 230                 235                 240

Leu Thr Gly Thr Val Gly Val Ile Lys Ser Ala Ile Lys Lys Thr Val
                245                 250                 255

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

Leu Gly Gly Leu Leu Thr Val Leu Ile Trp Phe Leu
        275                 280
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<210> SEQ ID NO 3
<211> LENGTH: 4065
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(4065)
<223> OTHER INFORMATION: Saccharomyces cerevisiae mature KRE2 protein
(codon optimized)

<400> SEQUENCE: 3

```
atg cgc ctt ctt gcc ctt gtc ttg ttg ctt ctc tgt gca ccg ctt cgc       48
Met Arg Leu Leu Ala Leu Val Leu Leu Leu Cys Ala Pro Leu Arg
1               5                  10                  15

gcc tgg acc tat tcg ctc cgc tat ggt atc ccc gag tcc gcc cag gtg       96
Ala Trp Thr Tyr Ser Leu Arg Tyr Gly Ile Pro Glu Ser Ala Gln Val
            20                  25                  30

tgg tcg atc ctc gtt cat ctg ctc ggc gac gtg gac aac caa ctc ctt      144
Trp Ser Ile Leu Val His Leu Leu Gly Asp Val Asp Asn Gln Leu Leu
        35                  40                  45

act aac ctg tat ccc ctg gtg acc ggg ctc gac gat gag atc gac atc      192
Thr Asn Leu Tyr Pro Leu Val Thr Gly Leu Asp Asp Glu Ile Asp Ile
    50                  55                  60

cag gag aac ctc gtt acg tcc aac gtg ctg cgc gag cgc tac gat aaa      240
Gln Glu Asn Leu Val Thr Ser Asn Val Leu Arg Glu Arg Tyr Asp Lys
65                  70                  75                  80

gag gac gtc gcg gat ctg ctg gaa ctc tac gca tcg ctc tac ccc atg      288
Glu Asp Val Ala Asp Leu Leu Glu Leu Tyr Ala Ser Leu Tyr Pro Met
                85                  90                  95

ggg atg atc caa cac gac atc tcg tcg aat gcc gag caa gac gac gcg      336
Gly Met Ile Gln His Asp Ile Ser Ser Asn Ala Glu Gln Asp Asp Ala
            100                 105                 110

aat tcc tcc tat ttc gtc ctg aac ggc aat cgg tat gag aaa ccc gac      384
Asn Ser Ser Tyr Phe Val Leu Asn Gly Asn Arg Tyr Glu Lys Pro Asp
        115                 120                 125

gac gtc ttt tac ctg aag tcg aag gac ctg acc atc cag cag aaa gtg      432
Asp Val Phe Tyr Leu Lys Ser Lys Asp Leu Thr Ile Gln Gln Lys Val
    130                 135                 140

ccc gat gtc gac gtc atc caa ccg tac gac gtc gtg att gga acc aac      480
Pro Asp Val Asp Val Ile Gln Pro Tyr Asp Val Val Ile Gly Thr Asn
145                 150                 155                 160

tcc gag gcg ccc ata ctg atc ctc tac ggc tgc ccg acc gtc atc gac      528
Ser Glu Ala Pro Ile Leu Ile Leu Tyr Gly Cys Pro Thr Val Ile Asp
                165                 170                 175

agc gac ttc gag gag ttc aat cgg aat ctc ttc atg gag gct atg aac      576
Ser Asp Phe Glu Glu Phe Asn Arg Asn Leu Phe Met Glu Ala Met Asn
            180                 185                 190

ggc gag ggc aag ttc cgc ttc att tgg cgg agc acg tgt agc ctg gac      624
Gly Glu Gly Lys Phe Arg Phe Ile Trp Arg Ser Thr Cys Ser Leu Asp
        195                 200                 205

ggc aag tcc gtg gag tac ccg ctg acc cac ccc ctg gag atc acc ctg      672
Gly Lys Ser Val Glu Tyr Pro Leu Thr His Pro Leu Glu Ile Thr Leu
    210                 215                 220

cag aac ggc agc cgc atg tcc tcc atc cct cag ctc aag aag atc ctg      720
Gln Asn Gly Ser Arg Met Ser Ser Ile Pro Gln Leu Lys Lys Ile Leu
225                 230                 235                 240
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tac acc gtt ccg aaa gaa atc ctc gtg ggc gca gat aac gac gac cag      768
Tyr Thr Val Pro Lys Glu Ile Leu Val Gly Ala Asp Asn Asp Asp Gln
                245                 250                 255

ctg cac gac ctg gag ccc gag gag ctg cgc gag ctg gac ctc cgc gtg      816
Leu His Asp Leu Glu Pro Glu Glu Leu Arg Glu Leu Asp Leu Arg Val
            260                 265                 270

acc tcg ctc att tcc gag ttc tat cag tat aag aaa gac att acg gcc      864
Thr Ser Leu Ile Ser Glu Phe Tyr Gln Tyr Lys Lys Asp Ile Thr Ala
        275                 280                 285

acc ctg aat ttc acc aaa agt atc gtc aac aat ttc ccg ctg att tcg      912
Thr Leu Asn Phe Thr Lys Ser Ile Val Asn Asn Phe Pro Leu Ile Ser
    290                 295                 300

aag cag ctg atc aag gtt tcg tcg gtc aat aaa gac atc atc acc tcc      960
Lys Gln Leu Ile Lys Val Ser Ser Val Asn Lys Asp Ile Ile Thr Ser
305                 310                 315                 320

aac gag gag ttg aat tcc aag ggc ttc gac tac aac atg ctg ggc atc     1008
Asn Glu Glu Leu Asn Ser Lys Gly Phe Asp Tyr Asn Met Leu Gly Ile
                325                 330                 335

aac ggc cag aac tgg aag atc acc tcc ctg acg ccc tac aat ctt ctc     1056
Asn Gly Gln Asn Trp Lys Ile Thr Ser Leu Thr Pro Tyr Asn Leu Leu
            340                 345                 350

acg gcc ctg aaa acg gag tac cag agt ctg ctg aag atc acc aac ctc     1104
Thr Ala Leu Lys Thr Glu Tyr Gln Ser Leu Leu Lys Ile Thr Asn Leu
        355                 360                 365

ctc cag gag ctg gag ccc tcc aag tgc atc ctc gac tcc aag ttc ctg     1152
Leu Gln Glu Leu Glu Pro Ser Lys Cys Ile Leu Asp Ser Lys Phe Leu
    370                 375                 380

ctc aat aag ttc tcg cag ttc agc ctg ggt aaa ctg cag aat ctg caa     1200
Leu Asn Lys Phe Ser Gln Phe Ser Leu Gly Lys Leu Gln Asn Leu Gln
385                 390                 395                 400

ccg atc aaa atg gac ctc cat acc atc ccg ggt ttt agc gag tcc gtc     1248
Pro Ile Lys Met Asp Leu His Thr Ile Pro Gly Phe Ser Glu Ser Val
                405                 410                 415

atc tac ttc aat gat att gag agt gac ccg cag tac gac gag ctc gtc     1296
Ile Tyr Phe Asn Asp Ile Glu Ser Asp Pro Gln Tyr Asp Glu Leu Val
            420                 425                 430

aac tcg gtg caa gca ttc ttc gac aag tcg aag ttc ggc gag ctg ccc     1344
Asn Ser Val Gln Ala Phe Phe Asp Lys Ser Lys Phe Gly Glu Leu Pro
        435                 440                 445

gag atc aag cag aac tgg tcc gag att atc ttc gtc ata gat ttt gcc     1392
Glu Ile Lys Gln Asn Trp Ser Glu Ile Ile Phe Val Ile Asp Phe Ala
    450                 455                 460

cgg ctg gag gac tcg gaa gtc aaa gag gcc ctc ggc gga ctg gtg agg     1440
Arg Leu Glu Asp Ser Glu Val Lys Glu Ala Leu Gly Gly Leu Val Arg
465                 470                 475                 480

gct gtg aac gtc gtg agc cag ggg tac ccc cag cgc gtg gga ctc ctc     1488
Ala Val Asn Val Val Ser Gln Gly Tyr Pro Gln Arg Val Gly Leu Leu
                485                 490                 495

ccg ttc agc agt gat agc gac aag agc gtc gtc aat aag atc tac gag     1536
Pro Phe Ser Ser Asp Ser Asp Lys Ser Val Val Asn Lys Ile Tyr Glu
            500                 505                 510

ctg aag aac tcg acc gac aat ctc acc gag ctg aag tcg ttc ctg gaa     1584
Leu Lys Asn Ser Thr Asp Asn Leu Thr Glu Leu Lys Ser Phe Leu Glu
        515                 520                 525

acc atg ttg ctg gcc gac ggc ctg tcc gcc aac gcg aag cat agt aag     1632
Thr Met Leu Leu Ala Asp Gly Leu Ser Ala Asn Ala Lys His Ser Lys
    530                 535                 540
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cat atc ccc gtg ccg gac gtg ttc cac ctc ctc gac gag ctg cag atc     1680
His Ile Pro Val Pro Asp Val Phe His Leu Leu Asp Glu Leu Gln Ile
545                 550                 555                 560

gac gaa acg tcc atc atc atc aac ggc gag ata tac ccg ttc cgc aag     1728
Asp Glu Thr Ser Ile Ile Ile Asn Gly Glu Ile Tyr Pro Phe Arg Lys
                565                 570                 575

aat tgg aac tac ctc atc gcc aag gtc atc aag aaa gac acc gaa ttc     1776
Asn Trp Asn Tyr Leu Ile Ala Lys Val Ile Lys Lys Asp Thr Glu Phe
            580                 585                 590

atc cgc aag gag ctg tcg aac tcg tcg ccg aag aac aag cag att agt     1824
Ile Arg Lys Glu Leu Ser Asn Ser Ser Pro Lys Asn Lys Gln Ile Ser
        595                 600                 605

gtg cgc gac ctg ttg cac tat aag agc gcg aac ctc cgc cat aac aag     1872
Val Arg Asp Leu Leu His Tyr Lys Ser Ala Asn Leu Arg His Asn Lys
    610                 615                 620

tat acg ccg aac tat ttc gcg gat agt gtg tat tcc tcg gtc aac aat     1920
Tyr Thr Pro Asn Tyr Phe Ala Asp Ser Val Tyr Ser Ser Val Asn Asn
625                 630                 635                 640

acc gct ctg gaa agc gtc tgc tcg atc ggt tac tac acc aaa aac gag     1968
Thr Ala Leu Glu Ser Val Cys Ser Ile Gly Tyr Tyr Thr Lys Asn Glu
                645                 650                 655

gaa tat aac ctc ctg cat acc att acg ctc gtg gat gac ttc ggc tcg     2016
Glu Tyr Asn Leu Leu His Thr Ile Thr Leu Val Asp Asp Phe Gly Ser
            660                 665                 670

atc cat gcg ctg aag cgg ctg cgg aac ctg ttg cat acg tcc ttc gtg     2064
Ile His Ala Leu Lys Arg Leu Arg Asn Leu Leu His Thr Ser Phe Val
        675                 680                 685

ggc gtg cgg atc cgc att atc cat gtc ggc gat atc agc gac atc tgg     2112
Gly Val Arg Ile Arg Ile Ile His Val Gly Asp Ile Ser Asp Ile Trp
    690                 695                 700

tat cag ctc cgc gga tcc ctg agt cag aaa gac ccg atc ggc agc atc     2160
Tyr Gln Leu Arg Gly Ser Leu Ser Gln Lys Asp Pro Ile Gly Ser Ile
705                 710                 715                 720

aac acc ttc atc gac gcc ctg aaa ctc aaa aag gtc aag tcc cat acg     2208
Asn Thr Phe Ile Asp Ala Leu Lys Leu Lys Lys Val Lys Ser His Thr
                725                 730                 735

tat aag aag tcg cag cag ctc ggc ttg cat aag tgg ctc ccc gac atc     2256
Tyr Lys Lys Ser Gln Gln Leu Gly Leu His Lys Trp Leu Pro Asp Ile
            740                 745                 750

ccg ctg ttc gag ctc caa aag ggt tcg ttc atc gcg ctc aac ggc cgg     2304
Pro Leu Phe Glu Leu Gln Lys Gly Ser Phe Ile Ala Leu Asn Gly Arg
        755                 760                 765

ttc atc atc ctg atc aag atg aaa tgc cag aag caa aac atc tcc aaa     2352
Phe Ile Ile Leu Ile Lys Met Lys Cys Gln Lys Gln Asn Ile Ser Lys
    770                 775                 780

gcc aag atc atc aag cgc gag gcc ctt cgg acc ata gat tcg gtg ttc     2400
Ala Lys Ile Ile Lys Arg Glu Ala Leu Arg Thr Ile Asp Ser Val Phe
785                 790                 795                 800

gcg ctg gac ctc ctc ttt cct ggc ttc agc caa gag atc ata aat ccc     2448
Ala Leu Asp Leu Leu Phe Pro Gly Phe Ser Gln Glu Ile Ile Asn Pro
                805                 810                 815

gat ctc atc gag atg atc tcc tcg atc ctt acc cgc ctc ttc tat cag     2496
Asp Leu Ile Glu Met Ile Ser Ser Ile Leu Thr Arg Leu Phe Tyr Gln
            820                 825                 830

ggg acc cac ata tac aac aac ggc att gac tat act acc gag tcg tcg     2544
Gly Thr His Ile Tyr Asn Asn Gly Ile Asp Tyr Thr Thr Glu Ser Ser
        835                 840                 845
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ctg ccg cgc atg gac ttg tcc gag ttc ttc cgc ccg aat aac ctg acc     2592
Leu Pro Arg Met Asp Leu Ser Glu Phe Phe Arg Pro Asn Asn Leu Thr
    850                 855                 860

atg ttc gag gat ggc aaa tcg gcg tcc atc gat ctc ctc ctc atc ctt     2640
Met Phe Glu Asp Gly Lys Ser Ala Ser Ile Asp Leu Leu Leu Ile Leu
865                 870                 875                 880

gac ccg ctg gaa gaa cgg act cag atg att ctt tcc ctc gtg gag caa     2688
Asp Pro Leu Glu Glu Arg Thr Gln Met Ile Leu Ser Leu Val Glu Gln
                885                 890                 895

ttc cgg cca ctg aag ttc gtg aat atc cag gtc atc ctg atg ccg acc     2736
Phe Arg Pro Leu Lys Phe Val Asn Ile Gln Val Ile Leu Met Pro Thr
            900                 905                 910

ctg gag ctg aat att gtc ccg atc cgg cgc atc tac gtg gac gac gcg     2784
Leu Glu Leu Asn Ile Val Pro Ile Arg Arg Ile Tyr Val Asp Asp Ala
        915                 920                 925

gat atc gtc aag tcc atc acg tcc gag gac tcc cgg tcg gac cct gag     2832
Asp Ile Val Lys Ser Ile Thr Ser Glu Asp Ser Arg Ser Asp Pro Glu
    930                 935                 940

gtt gac atc gag atg gat gtg ccg aac tcg ttc atc gtc gac aat aac     2880
Val Asp Ile Glu Met Asp Val Pro Asn Ser Phe Ile Val Asp Asn Asn
945                 950                 955                 960

tac agg att aag aaa ctg ttg att gag ctg cat tcg ttc tcc agt aaa     2928
Tyr Arg Ile Lys Lys Leu Leu Ile Glu Leu His Ser Phe Ser Ser Lys
                965                 970                 975

acc gtg ctg tcc acg ggc aat atc gac ggc atg ggt ggc gtg tgc ctt     2976
Thr Val Leu Ser Thr Gly Asn Ile Asp Gly Met Gly Gly Val Cys Leu
            980                 985                 990

gcg ctc gtc gat tcg gct ggc aac  att atc gac aaa acc  acg acc atg   3024
Ala Leu Val Asp Ser Ala Gly Asn  Ile Ile Asp Lys Thr  Thr Thr Met
        995                 1000                1005

aaa acg  ttc ggg tac ggc cag  ttc cac acc gac aag  ttc ttg aag      3069
Lys Thr  Phe Gly Tyr Gly Gln  Phe His Thr Asp Lys  Phe Leu Lys
    1010                1015                1020

ggt tgc  tac atc aaa agc tgc  gac agc cgc tat acc  gtc cag tcc      3114
Gly Cys  Tyr Ile Lys Ser Cys  Asp Ser Arg Tyr Thr  Val Gln Ser
    1025                1030                1035

ttc agc  act gat ggc cac ccc  gat ttc atc ccg tcc  gac tcc ctc      3159
Phe Ser  Thr Asp Gly His Pro  Asp Phe Ile Pro Ser  Asp Ser Leu
    1040                1045                1050

gac atc  ctg agc tat aac ccg  cag aag att gcg gtt  aag atc tcc      3204
Asp Ile  Leu Ser Tyr Asn Pro  Gln Lys Ile Ala Val  Lys Ile Ser
    1055                1060                1065

gag gag  ccg acg cac gaa gaa  gag tat gaa gag ggt  cgc aat aac      3249
Glu Glu  Pro Thr His Glu Glu  Glu Tyr Glu Glu Gly  Arg Asn Asn
    1070                1075                1080

gac acg  atc atc aat atc ttt  acc att tcg ggt ccc  gat gaa gaa      3294
Asp Thr  Ile Ile Asn Ile Phe  Thr Ile Ser Gly Pro  Asp Glu Glu
    1085                1090                1095

gag agg  tac atg caa atg atc  ctg tcg atc ctc agc  aaa tgc cca      3339
Glu Arg  Tyr Met Gln Met Ile  Leu Ser Ile Leu Ser  Lys Cys Pro
    1100                1105                1110

gaa acc  caa aaa gtg aat ttc  ttt ata ctg gac cag  ccg ttc att      3384
Glu Thr  Gln Lys Val Asn Phe  Phe Ile Leu Asp Gln  Pro Phe Ile
    1115                1120                1125

tcg gac  acc ctg cgc aag tcc  tgc gaa tac atc aat  tcc agt gat      3429
Ser Asp  Thr Leu Arg Lys Ser  Cys Glu Tyr Ile Asn  Ser Ser Asp
    1130                1135                1140
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gag atg  cgc ggc aat gtc ata  ttc ctc aac tat gag  tgg ccc cag      3474
Glu Met  Arg Gly Asn Val Ile  Phe Leu Asn Tyr Glu  Trp Pro Gln
    1145                 1150                 1155

tgg ctg  cgc cct cag cgg ttc  agc agc cgc agg cgc  gac gtc agc      3519
Trp Leu  Arg Pro Gln Arg Phe  Ser Ser Arg Arg Arg  Asp Val Ser
    1160                 1165                 1170

cgg ttc  ctc ttc ctg gac gtg  ctc ctc ccg cag aac  atc agc aag      3564
Arg Phe  Leu Phe Leu Asp Val  Leu Leu Pro Gln Asn  Ile Ser Lys
    1175                 1180                 1185

gtc ctc  tat atg tcg ccg acc  gag gtc ccg ctt gat  ccg ttc gac      3609
Val Leu  Tyr Met Ser Pro Thr  Glu Val Pro Leu Asp  Pro Phe Asp
    1190                 1195                 1200

atc ttc  caa ttc cag ggc ctc  aag cgc gca ccg ctg  ggc ctg ttt      3654
Ile Phe  Gln Phe Gln Gly Leu  Lys Arg Ala Pro Leu  Gly Leu Phe
    1205                 1210                 1215

cgc atg  agc ggt gac ggc tat  tgg aaa gag ggc tac  tgg gag aag      3699
Arg Met  Ser Gly Asp Gly Tyr  Trp Lys Glu Gly Tyr  Trp Glu Lys
    1220                 1225                 1230

atg ctg  cgc gag aac aac ttg  gaa ttc tat agc acc  gag ccg gcg      3744
Met Leu  Arg Glu Asn Asn Leu  Glu Phe Tyr Ser Thr  Glu Pro Ala
    1235                 1240                 1245

ttc ttg  gtc aat ctg gaa cgc  ttc cgc gag ctg gac  gcc ggc gac      3789
Phe Leu  Val Asn Leu Glu Arg  Phe Arg Glu Leu Asp  Ala Gly Asp
    1250                 1255                 1260

aag tac  agg atc cat tac caa  cgc att agc acc gac  gcg atg agc      3834
Lys Tyr  Arg Ile His Tyr Gln  Arg Ile Ser Thr Asp  Ala Met Ser
    1265                 1270                 1275

ctg gtg  aac atc ggg caa gac  ctc gtc aat aat ctg  caa ctt gag      3879
Leu Val  Asn Ile Gly Gln Asp  Leu Val Asn Asn Leu  Gln Leu Glu
    1280                 1285                 1290

gtc ccg  atc cgg ttc ctg aag  ggt agt tat aag aaa  aag ctc gtg      3924
Val Pro  Ile Arg Phe Leu Lys  Gly Ser Tyr Lys Lys  Lys Leu Val
    1295                 1300                 1305

atc aat  gat gag tgc gtc agc  gag tgg aag aaa aag  atc aac aag      3969
Ile Asn  Asp Glu Cys Val Ser  Glu Trp Lys Lys Lys  Ile Asn Lys
    1310                 1315                 1320

ttt gcc  tcg tcc cca ggg gac  gag gac gtt ccc ggc  gag agt gtg      4014
Phe Ala  Ser Ser Pro Gly Asp  Glu Asp Val Pro Gly  Glu Ser Val
    1325                 1330                 1335

agc tcg  aag tat cag gat tcg  gat aac gcc gcg cca  ctc cat gac      4059
Ser Ser  Lys Tyr Gln Asp Ser  Asp Asn Ala Ala Pro  Leu His Asp
    1340                 1345                 1350

gaa ctc                                                          4065
Glu Leu
    1355
```

<210> SEQ ID NO 4
<211> LENGTH: 1355
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 4

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Met Arg Leu Leu Ala Leu Val Leu Leu Leu Leu Cys Ala Pro Leu Arg
1               5                  10                  15

Ala Trp Thr Tyr Ser Leu Arg Tyr Gly Ile Pro Glu Ser Ala Gln Val
            20                  25                  30
```

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Trp Ser Ile Leu Val His Leu Leu Gly Asp Val Asp Asn Gln Leu Leu
        35                  40                  45

Thr Asn Leu Tyr Pro Leu Val Thr Gly Leu Asp Asp Glu Ile Asp Ile
    50                  55                  60

Gln Glu Asn Leu Val Thr Ser Asn Val Leu Arg Glu Arg Tyr Asp Lys
65                  70                  75                  80

Glu Asp Val Ala Asp Leu Leu Glu Leu Tyr Ala Ser Leu Tyr Pro Met
                85                  90                  95

Gly Met Ile Gln His Asp Ile Ser Ser Asn Ala Glu Gln Asp Asp Ala
            100                 105                 110

Asn Ser Ser Tyr Phe Val Leu Asn Gly Asn Arg Tyr Glu Lys Pro Asp
        115                 120                 125

Asp Val Phe Tyr Leu Lys Ser Lys Asp Leu Thr Ile Gln Gln Lys Val
    130                 135                 140

Pro Asp Val Asp Val Ile Gln Pro Tyr Asp Val Val Ile Gly Thr Asn
145                 150                 155                 160

Ser Glu Ala Pro Ile Leu Ile Leu Tyr Gly Cys Pro Thr Val Ile Asp
                165                 170                 175

Ser Asp Phe Glu Glu Phe Asn Arg Asn Leu Phe Met Glu Ala Met Asn
            180                 185                 190

Gly Glu Gly Lys Phe Arg Phe Ile Trp Arg Ser Thr Cys Ser Leu Asp
        195                 200                 205

Gly Lys Ser Val Glu Tyr Pro Leu Thr His Pro Leu Glu Ile Thr Leu
    210                 215                 220

Gln Asn Gly Ser Arg Met Ser Ser Ile Pro Gln Leu Lys Lys Ile Leu
225                 230                 235                 240

Tyr Thr Val Pro Lys Glu Ile Leu Val Gly Ala Asp Asn Asp Asp Gln
                245                 250                 255

Leu His Asp Leu Glu Pro Glu Glu Leu Arg Glu Leu Asp Leu Arg Val
            260                 265                 270

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

Thr Leu Asn Phe Thr Lys Ser Ile Val Asn Asn Phe Pro Leu Ile Ser
    290                 295                 300

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

Asn Glu Glu Leu Asn Ser Lys Gly Phe Asp Tyr Asn Met Leu Gly Ile
                325                 330                 335

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

Thr Ala Leu Lys Thr Glu Tyr Gln Ser Leu Leu Lys Ile Thr Asn Leu
        355                 360                 365

Leu Gln Glu Leu Glu Pro Ser Lys Cys Ile Leu Asp Ser Lys Phe Leu
    370                 375                 380

Leu Asn Lys Phe Ser Gln Phe Ser Leu Gly Lys Leu Gln Asn Leu Gln
385                 390                 395                 400

Pro Ile Lys Met Asp Leu His Thr Ile Pro Gly Phe Ser Glu Ser Val
                405                 410                 415

Ile Tyr Phe Asn Asp Ile Glu Ser Asp Pro Gln Tyr Asp Glu Leu Val
            420                 425                 430

Asn Ser Val Gln Ala Phe Phe Asp Lys Ser Lys Phe Gly Glu Leu Pro
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        435                 440                 445

Glu Ile Lys Gln Asn Trp Ser Glu Ile Ile Phe Val Ile Asp Phe Ala
    450                 455                 460

Arg Leu Glu Asp Ser Glu Val Lys Glu Ala Leu Gly Gly Leu Val Arg
465                 470                 475                 480

Ala Val Asn Val Val Ser Gln Gly Tyr Pro Gln Arg Val Gly Leu Leu
                485                 490                 495

Pro Phe Ser Ser Asp Ser Asp Lys Ser Val Val Asn Lys Ile Tyr Glu
            500                 505                 510

Leu Lys Asn Ser Thr Asp Asn Leu Thr Glu Leu Lys Ser Phe Leu Glu
        515                 520                 525

Thr Met Leu Leu Ala Asp Gly Leu Ser Ala Asn Ala Lys His Ser Lys
    530                 535                 540

His Ile Pro Val Pro Asp Val Phe His Leu Leu Asp Glu Leu Gln Ile
545                 550                 555                 560

Asp Glu Thr Ser Ile Ile Ile Asn Gly Glu Ile Tyr Pro Phe Arg Lys
                565                 570                 575

Asn Trp Asn Tyr Leu Ile Ala Lys Val Ile Lys Lys Asp Thr Glu Phe
            580                 585                 590

Ile Arg Lys Glu Leu Ser Asn Ser Ser Pro Lys Asn Lys Gln Ile Ser
        595                 600                 605

Val Arg Asp Leu Leu His Tyr Lys Ser Ala Asn Leu Arg His Asn Lys
    610                 615                 620

Tyr Thr Pro Asn Tyr Phe Ala Asp Ser Val Tyr Ser Ser Val Asn Asn
625                 630                 635                 640

Thr Ala Leu Glu Ser Val Cys Ser Ile Gly Tyr Tyr Thr Lys Asn Glu
                645                 650                 655

Glu Tyr Asn Leu Leu His Thr Ile Thr Leu Val Asp Asp Phe Gly Ser
            660                 665                 670

Ile His Ala Leu Lys Arg Leu Arg Asn Leu Leu His Thr Ser Phe Val
        675                 680                 685

Gly Val Arg Ile Arg Ile Ile His Val Gly Asp Ile Ser Asp Ile Trp
    690                 695                 700

Tyr Gln Leu Arg Gly Ser Leu Ser Gln Lys Asp Pro Ile Gly Ser Ile
705                 710                 715                 720

Asn Thr Phe Ile Asp Ala Leu Lys Leu Lys Lys Val Lys Ser His Thr
                725                 730                 735

Tyr Lys Lys Ser Gln Gln Leu Gly Leu His Lys Trp Leu Pro Asp Ile
            740                 745                 750

Pro Leu Phe Glu Leu Gln Lys Gly Ser Phe Ile Ala Leu Asn Gly Arg
        755                 760                 765

Phe Ile Ile Leu Ile Lys Met Lys Cys Gln Lys Gln Asn Ile Ser Lys
    770                 775                 780

Ala Lys Ile Ile Lys Arg Glu Ala Leu Arg Thr Ile Asp Ser Val Phe
785                 790                 795                 800

Ala Leu Asp Leu Leu Phe Pro Gly Phe Ser Gln Glu Ile Ile Asn Pro
                805                 810                 815

Asp Leu Ile Glu Met Ile Ser Ser Ile Leu Thr Arg Leu Phe Tyr Gln
            820                 825                 830

Gly Thr His Ile Tyr Asn Asn Gly Ile Asp Tyr Thr Thr Glu Ser Ser
        835                 840                 845
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Leu Pro Arg Met Asp Leu Ser Glu Phe Phe Arg Pro Asn Asn Leu Thr
    850                 855                 860

Met Phe Glu Asp Gly Lys Ser Ala Ser Ile Asp Leu Leu Leu Ile Leu
865                 870                 875                 880

Asp Pro Leu Glu Glu Arg Thr Gln Met Ile Leu Ser Leu Val Glu Gln
                885                 890                 895

Phe Arg Pro Leu Lys Phe Val Asn Ile Gln Val Ile Leu Met Pro Thr
            900                 905                 910

Leu Glu Leu Asn Ile Val Pro Ile Arg Arg Ile Tyr Val Asp Asp Ala
        915                 920                 925

Asp Ile Val Lys Ser Ile Thr Ser Glu Asp Ser Arg Ser Asp Pro Glu
    930                 935                 940

Val Asp Ile Glu Met Asp Val Pro Asn Ser Phe Ile Val Asp Asn Asn
945                 950                 955                 960

Tyr Arg Ile Lys Lys Leu Leu Ile Glu Leu His Ser Phe Ser Ser Lys
                965                 970                 975

Thr Val Leu Ser Thr Gly Asn Ile Asp Gly Met Gly Gly Val Cys Leu
            980                 985                 990

Ala Leu Val Asp Ser Ala Gly Asn  Ile Ile Asp Lys Thr  Thr Thr Met
        995                 1000                1005

Lys Thr  Phe Gly Tyr Gly Gln  Phe His Thr Asp Lys  Phe Leu Lys
    1010                1015                1020

Gly Cys  Tyr Ile Lys Ser Cys  Asp Ser Arg Tyr Thr  Val Gln Ser
    1025                1030                1035

Phe Ser  Thr Asp Gly His Pro  Asp Phe Ile Pro Ser  Asp Ser Leu
    1040                1045                1050

Asp Ile  Leu Ser Tyr Asn Pro  Gln Lys Ile Ala Val  Lys Ile Ser
    1055                1060                1065

Glu Glu  Pro Thr His Glu Glu  Glu Tyr Glu Glu Gly  Arg Asn Asn
    1070                1075                1080

Asp Thr  Ile Ile Asn Ile Phe  Thr Ile Ser Gly Pro  Asp Glu Glu
    1085                1090                1095

Glu Arg  Tyr Met Gln Met Ile  Leu Ser Ile Leu Ser  Lys Cys Pro
    1100                1105                1110

Glu Thr  Gln Lys Val Asn Phe  Phe Ile Leu Asp Gln  Pro Phe Ile
    1115                1120                1125

Ser Asp  Thr Leu Arg Lys Ser  Cys Glu Tyr Ile Asn  Ser Ser Asp
    1130                1135                1140

Glu Met  Arg Gly Asn Val Ile  Phe Leu Asn Tyr Glu  Trp Pro Gln
    1145                1150                1155

Trp Leu  Arg Pro Gln Arg Phe  Ser Ser Arg Arg Arg  Asp Val Ser
    1160                1165                1170

Arg Phe  Leu Phe Leu Asp Val  Leu Leu Pro Gln Asn  Ile Ser Lys
    1175                1180                1185

Val Leu  Tyr Met Ser Pro Thr  Glu Val Pro Leu Asp  Pro Phe Asp
    1190                1195                1200

Ile Phe  Gln Phe Gln Gly Leu  Lys Arg Ala Pro Leu  Gly Leu Phe
    1205                1210                1215

Arg Met  Ser Gly Asp Gly Tyr  Trp Lys Glu Gly Tyr  Trp Glu Lys
    1220                1225                1230
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Met Leu  Arg Glu Asn Asn Leu  Glu Phe Tyr Ser Thr  Glu Pro Ala
    1235                 1240                 1245

Phe Leu  Val Asn Leu Glu Arg  Phe Arg Glu Leu Asp  Ala Gly Asp
    1250                 1255                 1260

Lys Tyr  Arg Ile His Tyr Gln  Arg Ile Ser Thr Asp  Ala Met Ser
    1265                 1270                 1275

Leu Val  Asn Ile Gly Gln Asp  Leu Val Asn Asn Leu  Gln Leu Glu
    1280                 1285                 1290

Val Pro  Ile Arg Phe Leu Lys  Gly Ser Tyr Lys Lys  Lys Leu Val
    1295                 1300                 1305

Ile Asn  Asp Glu Cys Val Ser  Glu Trp Lys Lys Lys  Ile Asn Lys
    1310                 1315                 1320

Phe Ala  Ser Ser Pro Gly Asp  Glu Asp Val Pro Gly  Glu Ser Val
    1325                 1330                 1335

Ser Ser  Lys Tyr Gln Asp Ser  Asp Asn Ala Ala Pro  Leu His Asp
    1340                 1345                 1350

Glu Leu
    1355


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<211> LENGTH: 5616
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(5616)
<223> OTHER INFORMATION: Saccharomyces cerevisiae s288c FKS1 (codon
      optimized)

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atg aat acc gac cag caa ccg tac caa gga cag acc gac tat acc caa       48
Met Asn Thr Asp Gln Gln Pro Tyr Gln Gly Gln Thr Asp Tyr Thr Gln
1               5                  10                  15

ggc cca gga aac gga cag agc caa gag caa gac tac gat caa tac ggg       96
Gly Pro Gly Asn Gly Gln Ser Gln Glu Gln Asp Tyr Asp Gln Tyr Gly
            20                  25                  30

cag ccg ctg tat ccg agt caa gcg gat ggc tac tac gac ccg aac gtt      144
Gln Pro Leu Tyr Pro Ser Gln Ala Asp Gly Tyr Tyr Asp Pro Asn Val
        35                  40                  45

gcc gca ggc acg gaa gcc gac atg tat ggc cag cag ccc ccg aac gag      192
Ala Ala Gly Thr Glu Ala Asp Met Tyr Gly Gln Gln Pro Pro Asn Glu
    50                  55                  60

tcg tat gac cag gat tat acc aac ggc gag tat tat ggc cag ccg ccc      240
Ser Tyr Asp Gln Asp Tyr Thr Asn Gly Glu Tyr Tyr Gly Gln Pro Pro
65                  70                  75                  80

aac atg gcc gct caa gac ggc gag aat ttc agc gac ttc tcc tcg tat      288
Asn Met Ala Ala Gln Asp Gly Glu Asn Phe Ser Asp Phe Ser Ser Tyr
                85                  90                  95

ggt ccg cct ggt acc ccg ggg tac gat tcc tat ggc ggg cag tac acg      336
Gly Pro Pro Gly Thr Pro Gly Tyr Asp Ser Tyr Gly Gly Gln Tyr Thr
            100                 105                 110

gca tcg caa atg tcc tat ggc gag ccg aat agc tcg ggc acc agt acg      384
Ala Ser Gln Met Ser Tyr Gly Glu Pro Asn Ser Ser Gly Thr Ser Thr
        115                 120                 125

ccg ata tac ggc aac tac gat ccg aac gcc atc gca atg gca ctg ccc      432
Pro Ile Tyr Gly Asn Tyr Asp Pro Asn Ala Ile Ala Met Ala Leu Pro
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    130                 135                 140

aac gag ccg tac ccc gcg tgg acg gcc gac tcg cag agc ccg gtc agc      480
Asn Glu Pro Tyr Pro Ala Trp Thr Ala Asp Ser Gln Ser Pro Val Ser
145                 150                 155                 160

atc gaa cag atc gag gac ata ttc atc gac ctc acc aat cgc ctc ggc      528
Ile Glu Gln Ile Glu Asp Ile Phe Ile Asp Leu Thr Asn Arg Leu Gly
                165                 170                 175

ttc cag cgc gac tcc atg cgc aac atg ttc gac cat ttc atg gtc ctc      576
Phe Gln Arg Asp Ser Met Arg Asn Met Phe Asp His Phe Met Val Leu
            180                 185                 190

ctc gac tcc cgc tcc tcg cgc atg agc ccg gac caa gcg ctc ctg tcc      624
Leu Asp Ser Arg Ser Ser Arg Met Ser Pro Asp Gln Ala Leu Leu Ser
        195                 200                 205

ttg cat gct gac tat att ggc ggc gac acc gcc aac tat aag aaa tgg      672
Leu His Ala Asp Tyr Ile Gly Gly Asp Thr Ala Asn Tyr Lys Lys Trp
    210                 215                 220

tat ttc gcc gcc cag ctc gac atg gac gac gag att ggc ttc cgg aat      720
Tyr Phe Ala Ala Gln Leu Asp Met Asp Asp Glu Ile Gly Phe Arg Asn
225                 230                 235                 240

atg tcc ctc ggg aag ctc tcg cgc aag gcc cgc aag gca aag aaa aag      768
Met Ser Leu Gly Lys Leu Ser Arg Lys Ala Arg Lys Ala Lys Lys Lys
                245                 250                 255

aac aag aag gca atg gaa gag gcg aat ccc gag gat acc gag gaa acc      816
Asn Lys Lys Ala Met Glu Glu Ala Asn Pro Glu Asp Thr Glu Glu Thr
            260                 265                 270

ctc aat aag att gag ggc gac aac agc ctt gag gct gcg gac ttc cgc      864
Leu Asn Lys Ile Glu Gly Asp Asn Ser Leu Glu Ala Ala Asp Phe Arg
        275                 280                 285

tgg aaa gcg aag atg aat cag ctg tcg ccc ctt gag cgc gtc cgc cac      912
Trp Lys Ala Lys Met Asn Gln Leu Ser Pro Leu Glu Arg Val Arg His
    290                 295                 300

atc gcg ctc tat ctc ctg tgt tgg ggg gaa gcc aat cag gtc cgc ttc      960
Ile Ala Leu Tyr Leu Leu Cys Trp Gly Glu Ala Asn Gln Val Arg Phe
305                 310                 315                 320

acc gcc gaa tgc ctc tgc ttc atc tac aag tgc gcg ctc gat tac ctg     1008
Thr Ala Glu Cys Leu Cys Phe Ile Tyr Lys Cys Ala Leu Asp Tyr Leu
                325                 330                 335

gac agc ccg ctc tgc cag cag cgg caa gaa ccc atg ccc gag ggt gac     1056
Asp Ser Pro Leu Cys Gln Gln Arg Gln Glu Pro Met Pro Glu Gly Asp
            340                 345                 350

ttc ctg aat cgc gtg atc acc ccg atc tat cac ttc ata cgc aac cag     1104
Phe Leu Asn Arg Val Ile Thr Pro Ile Tyr His Phe Ile Arg Asn Gln
        355                 360                 365

gtg tac gag att gtg gat ggc cgg ttc gtc aag cgc gag cgc gat cac     1152
Val Tyr Glu Ile Val Asp Gly Arg Phe Val Lys Arg Glu Arg Asp His
    370                 375                 380

aat aag atc gtg ggc tat gat gac ctg aac cag ctc ttt tgg tac ccg     1200
Asn Lys Ile Val Gly Tyr Asp Asp Leu Asn Gln Leu Phe Trp Tyr Pro
385                 390                 395                 400

gaa gga atc gcg aag ata gtt ctg gaa gat ggc acc aag ctt atc gag     1248
Glu Gly Ile Ala Lys Ile Val Leu Glu Asp Gly Thr Lys Leu Ile Glu
                405                 410                 415

ctc ccg ctt gag gag cgc tat ctg cgg ctg ggt gac gtc gtg tgg gac     1296
Leu Pro Leu Glu Glu Arg Tyr Leu Arg Leu Gly Asp Val Val Trp Asp
            420                 425                 430

gac gtg ttc ttc aaa acg tac aag gaa acg cgc acc tgg ctg cac ctt     1344
Asp Val Phe Phe Lys Thr Tyr Lys Glu Thr Arg Thr Trp Leu His Leu
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        435                 440                 445

gtc acg aac ttc aat cgc atc tgg gtg atg cat atc tcg att ttc tgg     1392
Val Thr Asn Phe Asn Arg Ile Trp Val Met His Ile Ser Ile Phe Trp
    450                 455                 460

atg tac ttc gca tac aac tcg ccg acg ttc tat acc cac aat tat cag     1440
Met Tyr Phe Ala Tyr Asn Ser Pro Thr Phe Tyr Thr His Asn Tyr Gln
465                 470                 475                 480

caa ctc gtc gac aat caa ccg ctg gcc gcg tac aag tgg gcg tcg tgc     1488
Gln Leu Val Asp Asn Gln Pro Leu Ala Ala Tyr Lys Trp Ala Ser Cys
                485                 490                 495

gct ctg ggc ggc acc gtg gcg tcc ctc atc cag att gtc gcc acg ctc     1536
Ala Leu Gly Gly Thr Val Ala Ser Leu Ile Gln Ile Val Ala Thr Leu
            500                 505                 510

tgt gag tgg tcc ttc gtc ccg cgg aaa tgg gcg gga gcc cag cat ctg     1584
Cys Glu Trp Ser Phe Val Pro Arg Lys Trp Ala Gly Ala Gln His Leu
        515                 520                 525

tcg cgc cgg ttc tgg ttc ctg tgc atc atc ttc ggg atc aac ctg ggc     1632
Ser Arg Arg Phe Trp Phe Leu Cys Ile Ile Phe Gly Ile Asn Leu Gly
    530                 535                 540

ccg atc atc ttc gtg ttc gcc tac gac aag gac acg gtc tat tcc acc     1680
Pro Ile Ile Phe Val Phe Ala Tyr Asp Lys Asp Thr Val Tyr Ser Thr
545                 550                 555                 560

gca gcg cat gtc gtc gca gcg gtc atg ttc ttc gtt gcg gtc gcg acc     1728
Ala Ala His Val Val Ala Ala Val Met Phe Phe Val Ala Val Ala Thr
                565                 570                 575

atc atc ttt ttc tcc atc atg cca ctg ggt ggc ctc ttc acc agc tat     1776
Ile Ile Phe Phe Ser Ile Met Pro Leu Gly Gly Leu Phe Thr Ser Tyr
            580                 585                 590

atg aag aaa tcg act cgc cgg tac gtc gct agc cag acc ttc acg gca     1824
Met Lys Lys Ser Thr Arg Arg Tyr Val Ala Ser Gln Thr Phe Thr Ala
        595                 600                 605

gcg ttc gca ccc ctg cat ggc ctc gac cgc tgg atg agc tac ttg gtg     1872
Ala Phe Ala Pro Leu His Gly Leu Asp Arg Trp Met Ser Tyr Leu Val
    610                 615                 620

tgg gtc acg gtg ttc gcg gcc aag tat tcc gag tcc tac tat ttc ctc     1920
Trp Val Thr Val Phe Ala Ala Lys Tyr Ser Glu Ser Tyr Tyr Phe Leu
625                 630                 635                 640

gtg ctg tcc ctc cgc gac ccg atc cgc atc ctg agc acc acc gcc atg     1968
Val Leu Ser Leu Arg Asp Pro Ile Arg Ile Leu Ser Thr Thr Ala Met
                645                 650                 655

cgc tgc acc ggg gag tac tgg tgg ggt gcg gtg ctc tgc aaa gtc cag     2016
Arg Cys Thr Gly Glu Tyr Trp Trp Gly Ala Val Leu Cys Lys Val Gln
            660                 665                 670

ccc aag atc gtt ctt ggc ctg gtg atc gcg acg gac ttc atc ctc ttt     2064
Pro Lys Ile Val Leu Gly Leu Val Ile Ala Thr Asp Phe Ile Leu Phe
        675                 680                 685

ttc ctt gac acc tat ctg tgg tac att atc gtc aac acc att ttc agc     2112
Phe Leu Asp Thr Tyr Leu Trp Tyr Ile Ile Val Asn Thr Ile Phe Ser
    690                 695                 700

gtg ggc aag tcg ttc tac ctc ggc atc agt atc ctg acc ccg tgg cgc     2160
Val Gly Lys Ser Phe Tyr Leu Gly Ile Ser Ile Leu Thr Pro Trp Arg
705                 710                 715                 720

aac atc ttc acc cgg ctc ccc aag cgc ata tac tcg aag att ctg gcc     2208
Asn Ile Phe Thr Arg Leu Pro Lys Arg Ile Tyr Ser Lys Ile Leu Ala
                725                 730                 735

acc act gac atg gag atc aag tat aag ccg aag gtc ctc att agc cag     2256
Thr Thr Asp Met Glu Ile Lys Tyr Lys Pro Lys Val Leu Ile Ser Gln
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            740                 745                 750

gtg tgg aac gcg atc ata atc tcg atg tat cgg gag cac ttg ctg gct     2304
Val Trp Asn Ala Ile Ile Ile Ser Met Tyr Arg Glu His Leu Leu Ala
        755                 760                 765

atc gac cac gtg cag aaa ctg ctg tat cat caa gtg ccc agt gag atc     2352
Ile Asp His Val Gln Lys Leu Leu Tyr His Gln Val Pro Ser Glu Ile
    770                 775                 780

gag ggt aaa cgg acg ctg agg gca ccc acc ttc ttt gtg agc cag gat     2400
Glu Gly Lys Arg Thr Leu Arg Ala Pro Thr Phe Phe Val Ser Gln Asp
785                 790                 795                 800

gac aat aat ttt gaa acc gaa ttc ttc cct cgc gat tcc gag gcc gag     2448
Asp Asn Asn Phe Glu Thr Glu Phe Phe Pro Arg Asp Ser Glu Ala Glu
                805                 810                 815

cgg cgc atc agc ttc ttt gcc caa tcc ctg tcg acg ccc atc ccg gag     2496
Arg Arg Ile Ser Phe Phe Ala Gln Ser Leu Ser Thr Pro Ile Pro Glu
            820                 825                 830

ccc ctg ccg gtg gac aac atg ccg acc ttt acc gtg ctc acg ccc cat     2544
Pro Leu Pro Val Asp Asn Met Pro Thr Phe Thr Val Leu Thr Pro His
        835                 840                 845

tat gcc gag cgc atc ctc ctg agc ttg cgc gag atc atc cgc gag gac     2592
Tyr Ala Glu Arg Ile Leu Leu Ser Leu Arg Glu Ile Ile Arg Glu Asp
    850                 855                 860

gac cag ttc tcg cgg gtt acg ctc ctg gag tac ctc aag caa ctg cat     2640
Asp Gln Phe Ser Arg Val Thr Leu Leu Glu Tyr Leu Lys Gln Leu His
865                 870                 875                 880

ccg gtg gag tgg gag tgc ttc gtc aaa gac acc aaa atc ctg gcc gag     2688
Pro Val Glu Trp Glu Cys Phe Val Lys Asp Thr Lys Ile Leu Ala Glu
                885                 890                 895

gaa act gct gcg tac gag ggc aat gag aac gag gcc gag aag gaa gat     2736
Glu Thr Ala Ala Tyr Glu Gly Asn Glu Asn Glu Ala Glu Lys Glu Asp
            900                 905                 910

gca ctg aaa tcc cag atc gac gat ttg cct ttc tat tgt atc ggc ttc     2784
Ala Leu Lys Ser Gln Ile Asp Asp Leu Pro Phe Tyr Cys Ile Gly Phe
        915                 920                 925

aag agt gcg gcc ccg gag tac acg ctc cgc acc cgg atc tgg gcg agt     2832
Lys Ser Ala Ala Pro Glu Tyr Thr Leu Arg Thr Arg Ile Trp Ala Ser
    930                 935                 940

ctg cgc tcc cag acc ctc tac cgc acc atc tcg ggc ttc atg aac tat     2880
Leu Arg Ser Gln Thr Leu Tyr Arg Thr Ile Ser Gly Phe Met Asn Tyr
945                 950                 955                 960

tcg cgc gct atc aag ctg ctt tat cgg gtc gag aac ccc gag atc gtg     2928
Ser Arg Ala Ile Lys Leu Leu Tyr Arg Val Glu Asn Pro Glu Ile Val
                965                 970                 975

caa atg ttc ggt ggc aat gcc gag ggc ctt gag cgc gag ctg gag aaa     2976
Gln Met Phe Gly Gly Asn Ala Glu Gly Leu Glu Arg Glu Leu Glu Lys
            980                 985                 990

atg gcg agg cgc aag ttc aag ttc  ctg gtg tcc atg cag  cgg ctg gcg   3024
Met Ala Arg Arg Lys Phe Lys Phe  Leu Val Ser Met Gln  Arg Leu Ala
        995                 1000                1005

aag ttt  aag ttc ctc gaa aat  gcc gag ttc ctc ctc  cgg gcg tac      3069
Lys Phe  Lys Phe Leu Glu Asn  Ala Glu Phe Leu Leu  Arg Ala Tyr
    1010                1015                1020

ccg gac  ctc cag atc gcc tat  ctt gac gag gaa ccc  ccg ctg acg      3114
Pro Asp  Leu Gln Ile Ala Tyr  Leu Asp Glu Glu Pro  Pro Leu Thr
    1025                1030                1035

gag ggc  gag gag ccg cgg atc  tat tcg gcg ctc att  gac ggc cac      3159
Glu Gly  Glu Glu Pro Arg Ile  Tyr Ser Ala Leu Ile  Asp Gly His
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    1040                1045                1050

tgc gag  atc ctc gac aac ggt  cgg cgc agg cca aag  ttc cgc gtg      3204
Cys Glu  Ile Leu Asp Asn Gly  Arg Arg Arg Pro Lys  Phe Arg Val
    1055                1060                1065

caa ctc  agc ggc aat ccc att  ctg ggc gac ggc aaa  tcc gac aac      3249
Gln Leu  Ser Gly Asn Pro Ile  Leu Gly Asp Gly Lys  Ser Asp Asn
    1070                1075                1080

caa aac  cat gcc ctg atc ttc  tat agg ggt gag tat  att cag ctg      3294
Gln Asn  His Ala Leu Ile Phe  Tyr Arg Gly Glu Tyr  Ile Gln Leu
    1085                1090                1095

atc gac  gcg aac cag gac aat  tat ctt gag gaa tgc  ctc aag atc      3339
Ile Asp  Ala Asn Gln Asp Asn  Tyr Leu Glu Glu Cys  Leu Lys Ile
    1100                1105                1110

cgc tcg  gtc ctg gcc gag ttc  gag gag ctc aac gtc  gaa cag gtc      3384
Arg Ser  Val Leu Ala Glu Phe  Glu Glu Leu Asn Val  Glu Gln Val
    1115                1120                1125

aac cct  tat gct ccg ggc ctg  cgg tac gaa gaa cag  acc acg aac      3429
Asn Pro  Tyr Ala Pro Gly Leu  Arg Tyr Glu Glu Gln  Thr Thr Asn
    1130                1135                1140

cat ccg  gtc gcc atc gtc gga  gcg cgc gag tac att  ttc tcg gag      3474
His Pro  Val Ala Ile Val Gly  Ala Arg Glu Tyr Ile  Phe Ser Glu
    1145                1150                1155

aat tcc  ggc gtc ctc ggc gat  gtg gcg gca ggc aag  gag cag acc      3519
Asn Ser  Gly Val Leu Gly Asp  Val Ala Ala Gly Lys  Glu Gln Thr
    1160                1165                1170

ttc ggc  acc ctg ttc gcc cgc  acc ctc tcc cag att  ggt ggc aaa      3564
Phe Gly  Thr Leu Phe Ala Arg  Thr Leu Ser Gln Ile  Gly Gly Lys
    1175                1180                1185

ctg cat  tac ggc cat ccg gac  ttc ata aac gcg acc  ttc atg acc      3609
Leu His  Tyr Gly His Pro Asp  Phe Ile Asn Ala Thr  Phe Met Thr
    1190                1195                1200

acc cgg  ggt ggc gtc agc aag  gcc caa aag ggc ctc  cat ctt aac      3654
Thr Arg  Gly Gly Val Ser Lys  Ala Gln Lys Gly Leu  His Leu Asn
    1205                1210                1215

gaa gat  atc tac gcg ggt atg  aat gcc atg ctc agg  ggc ggt cgg      3699
Glu Asp  Ile Tyr Ala Gly Met  Asn Ala Met Leu Arg  Gly Gly Arg
    1220                1225                1230

atc aag  cat tgt gag tat tac  cag tgc gga aag ggc  agg gat ctg      3744
Ile Lys  His Cys Glu Tyr Tyr  Gln Cys Gly Lys Gly  Arg Asp Leu
    1235                1240                1245

ggc ttc  ggc acc atc ctc aat  ttc acc acc aag atc  ggg gca ggc      3789
Gly Phe  Gly Thr Ile Leu Asn  Phe Thr Thr Lys Ile  Gly Ala Gly
    1250                1255                1260

atg gga  gaa cag atg ttg agc  cgg gag tac tat tac  ctc ggg acg      3834
Met Gly  Glu Gln Met Leu Ser  Arg Glu Tyr Tyr Tyr  Leu Gly Thr
    1265                1270                1275

cag ctc  ccg gtc gat cgg ttc  ctg acc ttc tac tat  gcc cat ccg      3879
Gln Leu  Pro Val Asp Arg Phe  Leu Thr Phe Tyr Tyr  Ala His Pro
    1280                1285                1290

ggt ttc  cat ctg aat aac ctc  ttc atc caa ctg tcc  ctt cag atg      3924
Gly Phe  His Leu Asn Asn Leu  Phe Ile Gln Leu Ser  Leu Gln Met
    1295                1300                1305

ttc atg  ttg acg ctc gtg aac  ctg agt agc ctc gca  cat gag tcg      3969
Phe Met  Leu Thr Leu Val Asn  Leu Ser Ser Leu Ala  His Glu Ser
    1310                1315                1320

atc atg  tgc atc tac gat cgg  aat aag ccg aaa acc  gac gtc ctg      4014
Ile Met  Cys Ile Tyr Asp Arg  Asn Lys Pro Lys Thr  Asp Val Leu
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    1325                1330                1335

gtg ccg  att ggc tgc tac aac  ttc cag ccc gcg gtc  gac tgg gtc      4059
Val Pro  Ile Gly Cys Tyr Asn  Phe Gln Pro Ala Val  Asp Trp Val
    1340                1345                1350

cgc cgc  tat acg ctt agc atc  ttt atc gtg ttc tgg  atc gcg ttc      4104
Arg Arg  Tyr Thr Leu Ser Ile  Phe Ile Val Phe Trp  Ile Ala Phe
    1355                1360                1365

gtg ccg  atc gtt gtg cag gag  ctg atc gag cgc ggt  ctg tgg aag      4149
Val Pro  Ile Val Val Gln Glu  Leu Ile Glu Arg Gly  Leu Trp Lys
    1370                1375                1380

gcc acg  cag cgc ttc ttc tgc  cat ctg ctg tcg ctg  agt ccg atg      4194
Ala Thr  Gln Arg Phe Phe Cys  His Leu Leu Ser Leu  Ser Pro Met
    1385                1390                1395

ttc gag  gtc ttt gcg ggc caa  atc tat tcg agc gcg  ctc ctg agc      4239
Phe Glu  Val Phe Ala Gly Gln  Ile Tyr Ser Ser Ala  Leu Leu Ser
    1400                1405                1410

gat ttg  gcg atc ggg gga gcg  cgc tac atc tcg acg  ggt cgg ggc      4284
Asp Leu  Ala Ile Gly Gly Ala  Arg Tyr Ile Ser Thr  Gly Arg Gly
    1415                1420                1425

ttc gcc  acc tcc cgc att cca  ttc agc atc aag cgc  ttc gcg ggc      4329
Phe Ala  Thr Ser Arg Ile Pro  Phe Ser Ile Lys Arg  Phe Ala Gly
    1430                1435                1440

tcg gcg  atc tac atg ggc gca  cgc tcg atg ttg atg  ctg ctg ttc      4374
Ser Ala  Ile Tyr Met Gly Ala  Arg Ser Met Leu Met  Leu Leu Phe
    1445                1450                1455

ggc acc  gtg gct cat tgg cag  gcg ccg ctc ctg tgg  ttc tgg gcg      4419
Gly Thr  Val Ala His Trp Gln  Ala Pro Leu Leu Trp  Phe Trp Ala
    1460                1465                1470

tcc ctg  agc agc ctc atc ttc  gcc ccc ttc gtg ttc  aac ccg cat      4464
Ser Leu  Ser Ser Leu Ile Phe  Ala Pro Phe Val Phe  Asn Pro His
    1475                1480                1485

cag ttt  gcg tgg gag gac ttt  ttc ctg gac tac cgc  gac tac atc      4509
Gln Phe  Ala Trp Glu Asp Phe  Phe Leu Asp Tyr Arg  Asp Tyr Ile
    1490                1495                1500

cgg tgg  ctc tcc cgg gga aat  aac cag tac cac cgc  aat tcc tgg      4554
Arg Trp  Leu Ser Arg Gly Asn  Asn Gln Tyr His Arg  Asn Ser Trp
    1505                1510                1515

att ggc  tat gtg cgg atg agc  cgc gct cgc atc acc  ggc ttc aag      4599
Ile Gly  Tyr Val Arg Met Ser  Arg Ala Arg Ile Thr  Gly Phe Lys
    1520                1525                1530

cgg aaa  ctg gtc ggt gac gaa  agc gag aaa gcc gcg  ggc gac gcc      4644
Arg Lys  Leu Val Gly Asp Glu  Ser Glu Lys Ala Ala  Gly Asp Ala
    1535                1540                1545

tcg cgg  gcc cac cgc acc aac  ctg atc atg gcc gag  atc atc ccc      4689
Ser Arg  Ala His Arg Thr Asn  Leu Ile Met Ala Glu  Ile Ile Pro
    1550                1555                1560

tgc gcc  atc tat gcg gca ggg  tgc ttc ata gcg ttc  acc ttc atc      4734
Cys Ala  Ile Tyr Ala Ala Gly  Cys Phe Ile Ala Phe  Thr Phe Ile
    1565                1570                1575

aac gcc  cag act ggc gtc aag  acc acc gac gac gac  cgg gtc aac      4779
Asn Ala  Gln Thr Gly Val Lys  Thr Thr Asp Asp Asp  Arg Val Asn
    1580                1585                1590

tcg gtg  ctc cgc atc atc atc  tgc acg ctg gcg ccg  att gcg gtc      4824
Ser Val  Leu Arg Ile Ile Ile  Cys Thr Leu Ala Pro  Ile Ala Val
    1595                1600                1605

aat ctc  ggg gtc ctc ttc ttc  tgc atg ggc atg tcg  tgc tgc tcc      4869
Asn Leu  Gly Val Leu Phe Phe  Cys Met Gly Met Ser  Cys Cys Ser
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    1610                1615                1620

ggc cca  ctg ttc ggc atg tgc  tgc aag aaa acg ggc  tcg gtc atg      4914
Gly Pro  Leu Phe Gly Met Cys  Cys Lys Lys Thr Gly  Ser Val Met
    1625                1630                1635

gcc ggc  atc gcc cac ggc gtc  gcg gtc att gtg cat  atc gct ttc      4959
Ala Gly  Ile Ala His Gly Val  Ala Val Ile Val His  Ile Ala Phe
    1640                1645                1650

ttc atc  gtg atg tgg gtt ctg  gag tcc ttc aat ttc  gtc cgg atg      5004
Phe Ile  Val Met Trp Val Leu  Glu Ser Phe Asn Phe  Val Arg Met
    1655                1660                1665

ctg atc  ggc gtg gtg acg tgc  atc cag tgc cag cgc  ctc atc ttc      5049
Leu Ile  Gly Val Val Thr Cys  Ile Gln Cys Gln Arg  Leu Ile Phe
    1670                1675                1680

cac tgc  atg acc gcc ctc atg  ctc acg cgg gag ttc  aaa aat gat      5094
His Cys  Met Thr Ala Leu Met  Leu Thr Arg Glu Phe  Lys Asn Asp
    1685                1690                1695

cat gcg  aat acg gcc ttc tgg  acc ggc aaa tgg tac  ggc aag ggc      5139
His Ala  Asn Thr Ala Phe Trp  Thr Gly Lys Trp Tyr  Gly Lys Gly
    1700                1705                1710

atg ggc  tat atg gcc tgg acg  caa ccc tcg cgc gag  ctg acg gcc      5184
Met Gly  Tyr Met Ala Trp Thr  Gln Pro Ser Arg Glu  Leu Thr Ala
    1715                1720                1725

aag gtc  atc gag ttg tcc gag  ttt gcc gct gac ttc  gtc ctc ggc      5229
Lys Val  Ile Glu Leu Ser Glu  Phe Ala Ala Asp Phe  Val Leu Gly
    1730                1735                1740

cat gtt  atc ttg atc tgc cag  ctg ccg ctg ata atc  ata ccg aag      5274
His Val  Ile Leu Ile Cys Gln  Leu Pro Leu Ile Ile  Ile Pro Lys
    1745                1750                1755

atc gac  aag ttt cat tcc atc  atg ctg ttc tgg ctg  aaa ccg tcg      5319
Ile Asp  Lys Phe His Ser Ile  Met Leu Phe Trp Leu  Lys Pro Ser
    1760                1765                1770

cgc cag  att agg ccc cct atc  tac tcg ctc aaa cag  act agg ctc      5364
Arg Gln  Ile Arg Pro Pro Ile  Tyr Ser Leu Lys Gln  Thr Arg Leu
    1775                1780                1785

cgg aaa  cgc atg gtc aag aaa  tac tgc tcg ctg tat  ttc ctc gtg      5409
Arg Lys  Arg Met Val Lys Lys  Tyr Cys Ser Leu Tyr  Phe Leu Val
    1790                1795                1800

ctg gcc  ata ttc gcg ggc tgc  atc atc gga ccg gcc  gtg gcg agc      5454
Leu Ala  Ile Phe Ala Gly Cys  Ile Ile Gly Pro Ala  Val Ala Ser
    1805                1810                1815

gcc aag  atc cat aag cat atc  ggg gat tcc ctg gac  ggt gtc gtc      5499
Ala Lys  Ile His Lys His Ile  Gly Asp Ser Leu Asp  Gly Val Val
    1820                1825                1830

cac aac  ctg ttc cag ccg atc  aac act acc aac aac  gac acc ggc      5544
His Asn  Leu Phe Gln Pro Ile  Asn Thr Thr Asn Asn  Asp Thr Gly
    1835                1840                1845

tcc cag  atg tcg acc tac cag  tcg cac tac tac acc  cac acc ccg      5589
Ser Gln  Met Ser Thr Tyr Gln  Ser His Tyr Tyr Thr  His Thr Pro
    1850                1855                1860

tcc ctt  aag acc tgg agc acc  ata aag                            5616
Ser Leu  Lys Thr Trp Ser Thr  Ile Lys
    1865                1870
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<210> SEQ ID NO 6
<211> LENGTH: 1872
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 6

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Met Asn Thr Asp Gln Gln Pro Tyr Gln Gly Gln Thr Asp Tyr Thr Gln
1               5                  10                  15

Gly Pro Gly Asn Gly Gln Ser Gln Glu Gln Asp Tyr Asp Gln Tyr Gly
            20                  25                  30

Gln Pro Leu Tyr Pro Ser Gln Ala Asp Gly Tyr Tyr Asp Pro Asn Val
        35                  40                  45

Ala Ala Gly Thr Glu Ala Asp Met Tyr Gly Gln Gln Pro Pro Asn Glu
    50                  55                  60

Ser Tyr Asp Gln Asp Tyr Thr Asn Gly Glu Tyr Tyr Gly Gln Pro Pro
65                  70                  75                  80

Asn Met Ala Ala Gln Asp Gly Glu Asn Phe Ser Asp Phe Ser Ser Tyr
                85                  90                  95

Gly Pro Pro Gly Thr Pro Gly Tyr Asp Ser Tyr Gly Gly Gln Tyr Thr
            100                 105                 110

Ala Ser Gln Met Ser Tyr Gly Glu Pro Asn Ser Ser Gly Thr Ser Thr
        115                 120                 125

Pro Ile Tyr Gly Asn Tyr Asp Pro Asn Ala Ile Ala Met Ala Leu Pro
    130                 135                 140

Asn Glu Pro Tyr Pro Ala Trp Thr Ala Asp Ser Gln Ser Pro Val Ser
145                 150                 155                 160

Ile Glu Gln Ile Glu Asp Ile Phe Ile Asp Leu Thr Asn Arg Leu Gly
                165                 170                 175

Phe Gln Arg Asp Ser Met Arg Asn Met Phe Asp His Phe Met Val Leu
            180                 185                 190

Leu Asp Ser Arg Ser Ser Arg Met Ser Pro Asp Gln Ala Leu Leu Ser
        195                 200                 205

Leu His Ala Asp Tyr Ile Gly Gly Asp Thr Ala Asn Tyr Lys Lys Trp
    210                 215                 220

Tyr Phe Ala Ala Gln Leu Asp Met Asp Asp Glu Ile Gly Phe Arg Asn
225                 230                 235                 240

Met Ser Leu Gly Lys Leu Ser Arg Lys Ala Arg Lys Ala Lys Lys Lys
                245                 250                 255

Asn Lys Lys Ala Met Glu Glu Ala Asn Pro Glu Asp Thr Glu Glu Thr
            260                 265                 270

Leu Asn Lys Ile Glu Gly Asp Asn Ser Leu Glu Ala Ala Asp Phe Arg
        275                 280                 285

Trp Lys Ala Lys Met Asn Gln Leu Ser Pro Leu Glu Arg Val Arg His
    290                 295                 300

Ile Ala Leu Tyr Leu Leu Cys Trp Gly Glu Ala Asn Gln Val Arg Phe
305                 310                 315                 320

Thr Ala Glu Cys Leu Cys Phe Ile Tyr Lys Cys Ala Leu Asp Tyr Leu
                325                 330                 335

Asp Ser Pro Leu Cys Gln Gln Arg Gln Glu Pro Met Pro Glu Gly Asp
            340                 345                 350

Phe Leu Asn Arg Val Ile Thr Pro Ile Tyr His Phe Ile Arg Asn Gln
        355                 360                 365

Val Tyr Glu Ile Val Asp Gly Arg Phe Val Lys Arg Glu Arg Asp His
    370                 375                 380
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Asn Lys Ile Val Gly Tyr Asp Asp Leu Asn Gln Leu Phe Trp Tyr Pro
385                 390                 395                 400

Glu Gly Ile Ala Lys Ile Val Leu Glu Asp Gly Thr Lys Leu Ile Glu
                405                 410                 415

Leu Pro Leu Glu Glu Arg Tyr Leu Arg Leu Gly Asp Val Val Trp Asp
            420                 425                 430

Asp Val Phe Phe Lys Thr Tyr Lys Glu Thr Arg Thr Trp Leu His Leu
        435                 440                 445

Val Thr Asn Phe Asn Arg Ile Trp Val Met His Ile Ser Ile Phe Trp
    450                 455                 460

Met Tyr Phe Ala Tyr Asn Ser Pro Thr Phe Tyr Thr His Asn Tyr Gln
465                 470                 475                 480

Gln Leu Val Asp Asn Gln Pro Leu Ala Ala Tyr Lys Trp Ala Ser Cys
                485                 490                 495

Ala Leu Gly Gly Thr Val Ala Ser Leu Ile Gln Ile Val Ala Thr Leu
            500                 505                 510

Cys Glu Trp Ser Phe Val Pro Arg Lys Trp Ala Gly Ala Gln His Leu
        515                 520                 525

Ser Arg Arg Phe Trp Phe Leu Cys Ile Ile Phe Gly Ile Asn Leu Gly
    530                 535                 540

Pro Ile Ile Phe Val Phe Ala Tyr Asp Lys Asp Thr Val Tyr Ser Thr
545                 550                 555                 560

Ala Ala His Val Val Ala Ala Val Met Phe Phe Val Ala Val Ala Thr
                565                 570                 575

Ile Ile Phe Phe Ser Ile Met Pro Leu Gly Gly Leu Phe Thr Ser Tyr
            580                 585                 590

Met Lys Lys Ser Thr Arg Arg Tyr Val Ala Ser Gln Thr Phe Thr Ala
        595                 600                 605

Ala Phe Ala Pro Leu His Gly Leu Asp Arg Trp Met Ser Tyr Leu Val
    610                 615                 620

Trp Val Thr Val Phe Ala Ala Lys Tyr Ser Glu Ser Tyr Tyr Phe Leu
625                 630                 635                 640

Val Leu Ser Leu Arg Asp Pro Ile Arg Ile Leu Ser Thr Thr Ala Met
                645                 650                 655

Arg Cys Thr Gly Glu Tyr Trp Trp Gly Ala Val Leu Cys Lys Val Gln
            660                 665                 670

Pro Lys Ile Val Leu Gly Leu Val Ile Ala Thr Asp Phe Ile Leu Phe
        675                 680                 685

Phe Leu Asp Thr Tyr Leu Trp Tyr Ile Ile Val Asn Thr Ile Phe Ser
    690                 695                 700

Val Gly Lys Ser Phe Tyr Leu Gly Ile Ser Ile Leu Thr Pro Trp Arg
705                 710                 715                 720

Asn Ile Phe Thr Arg Leu Pro Lys Arg Ile Tyr Ser Lys Ile Leu Ala
                725                 730                 735

Thr Thr Asp Met Glu Ile Lys Tyr Lys Pro Lys Val Leu Ile Ser Gln
            740                 745                 750

Val Trp Asn Ala Ile Ile Ile Ser Met Tyr Arg Glu His Leu Leu Ala
        755                 760                 765

Ile Asp His Val Gln Lys Leu Leu Tyr His Gln Val Pro Ser Glu Ile
    770                 775                 780

Glu Gly Lys Arg Thr Leu Arg Ala Pro Thr Phe Phe Val Ser Gln Asp
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785                 790                 795                 800

Asp Asn Asn Phe Glu Thr Glu Phe Phe Pro Arg Asp Ser Glu Ala Glu
                805                 810                 815

Arg Arg Ile Ser Phe Phe Ala Gln Ser Leu Ser Thr Pro Ile Pro Glu
            820                 825                 830

Pro Leu Pro Val Asp Asn Met Pro Thr Phe Thr Val Leu Thr Pro His
        835                 840                 845

Tyr Ala Glu Arg Ile Leu Leu Ser Leu Arg Glu Ile Ile Arg Glu Asp
    850                 855                 860

Asp Gln Phe Ser Arg Val Thr Leu Leu Glu Tyr Leu Lys Gln Leu His
865                 870                 875                 880

Pro Val Glu Trp Glu Cys Phe Val Lys Asp Thr Lys Ile Leu Ala Glu
                885                 890                 895

Glu Thr Ala Ala Tyr Glu Gly Asn Glu Asn Glu Ala Glu Lys Glu Asp
            900                 905                 910

Ala Leu Lys Ser Gln Ile Asp Asp Leu Pro Phe Tyr Cys Ile Gly Phe
        915                 920                 925

Lys Ser Ala Ala Pro Glu Tyr Thr Leu Arg Thr Arg Ile Trp Ala Ser
    930                 935                 940

Leu Arg Ser Gln Thr Leu Tyr Arg Thr Ile Ser Gly Phe Met Asn Tyr
945                 950                 955                 960

Ser Arg Ala Ile Lys Leu Leu Tyr Arg Val Glu Asn Pro Glu Ile Val
                965                 970                 975

Gln Met Phe Gly Gly Asn Ala Glu Gly Leu Glu Arg Glu Leu Glu Lys
            980                 985                 990

Met Ala Arg Arg Lys Phe Lys Phe  Leu Val Ser Met Gln  Arg Leu Ala
        995                 1000                1005

Lys Phe  Lys Phe Leu Glu Asn  Ala Glu Phe Leu Leu  Arg Ala Tyr
    1010                1015                1020

Pro Asp  Leu Gln Ile Ala Tyr  Leu Asp Glu Glu Pro  Pro Leu Thr
    1025                1030                1035

Glu Gly  Glu Glu Pro Arg Ile  Tyr Ser Ala Leu Ile  Asp Gly His
    1040                1045                1050

Cys Glu  Ile Leu Asp Asn Gly  Arg Arg Arg Pro Lys  Phe Arg Val
    1055                1060                1065

Gln Leu  Ser Gly Asn Pro Ile  Leu Gly Asp Gly Lys  Ser Asp Asn
    1070                1075                1080

Gln Asn  His Ala Leu Ile Phe  Tyr Arg Gly Glu Tyr  Ile Gln Leu
    1085                1090                1095

Ile Asp  Ala Asn Gln Asp Asn  Tyr Leu Glu Glu Cys  Leu Lys Ile
    1100                1105                1110

Arg Ser  Val Leu Ala Glu Phe  Glu Glu Leu Asn Val  Glu Gln Val
    1115                1120                1125

Asn Pro  Tyr Ala Pro Gly Leu  Arg Tyr Glu Glu Gln  Thr Thr Asn
    1130                1135                1140

His Pro  Val Ala Ile Val Gly  Ala Arg Glu Tyr Ile  Phe Ser Glu
    1145                1150                1155

Asn Ser  Gly Val Leu Gly Asp  Val Ala Ala Gly Lys  Glu Gln Thr
    1160                1165                1170

Phe Gly  Thr Leu Phe Ala Arg  Thr Leu Ser Gln Ile  Gly Gly Lys
    1175                1180                1185
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Leu His  Tyr Gly His Pro Asp  Phe Ile Asn Ala Thr  Phe Met Thr
    1190                 1195                 1200

Thr Arg  Gly Gly Val Ser Lys  Ala Gln Lys Gly Leu  His Leu Asn
    1205                 1210                 1215

Glu Asp  Ile Tyr Ala Gly Met  Asn Ala Met Leu Arg  Gly Gly Arg
    1220                 1225                 1230

Ile Lys  His Cys Glu Tyr Tyr  Gln Cys Gly Lys Gly  Arg Asp Leu
    1235                 1240                 1245

Gly Phe  Gly Thr Ile Leu Asn  Phe Thr Thr Lys Ile  Gly Ala Gly
    1250                 1255                 1260

Met Gly  Glu Gln Met Leu Ser  Arg Glu Tyr Tyr Tyr  Leu Gly Thr
    1265                 1270                 1275

Gln Leu  Pro Val Asp Arg Phe  Leu Thr Phe Tyr Tyr  Ala His Pro
    1280                 1285                 1290

Gly Phe  His Leu Asn Asn Leu  Phe Ile Gln Leu Ser  Leu Gln Met
    1295                 1300                 1305

Phe Met  Leu Thr Leu Val Asn  Leu Ser Ser Leu Ala  His Glu Ser
    1310                 1315                 1320

Ile Met  Cys Ile Tyr Asp Arg  Asn Lys Pro Lys Thr  Asp Val Leu
    1325                 1330                 1335

Val Pro  Ile Gly Cys Tyr Asn  Phe Gln Pro Ala Val  Asp Trp Val
    1340                 1345                 1350

Arg Arg  Tyr Thr Leu Ser Ile  Phe Ile Val Phe Trp  Ile Ala Phe
    1355                 1360                 1365

Val Pro  Ile Val Val Gln Glu  Leu Ile Glu Arg Gly  Leu Trp Lys
    1370                 1375                 1380

Ala Thr  Gln Arg Phe Phe Cys  His Leu Leu Ser Leu  Ser Pro Met
    1385                 1390                 1395

Phe Glu  Val Phe Ala Gly Gln  Ile Tyr Ser Ser Ala  Leu Leu Ser
    1400                 1405                 1410

Asp Leu  Ala Ile Gly Gly Ala  Arg Tyr Ile Ser Thr  Gly Arg Gly
    1415                 1420                 1425

Phe Ala  Thr Ser Arg Ile Pro  Phe Ser Ile Lys Arg  Phe Ala Gly
    1430                 1435                 1440

Ser Ala  Ile Tyr Met Gly Ala  Arg Ser Met Leu Met  Leu Leu Phe
    1445                 1450                 1455

Gly Thr  Val Ala His Trp Gln  Ala Pro Leu Leu Trp  Phe Trp Ala
    1460                 1465                 1470

Ser Leu  Ser Ser Leu Ile Phe  Ala Pro Phe Val Phe  Asn Pro His
    1475                 1480                 1485

Gln Phe  Ala Trp Glu Asp Phe  Phe Leu Asp Tyr Arg  Asp Tyr Ile
    1490                 1495                 1500

Arg Trp  Leu Ser Arg Gly Asn  Asn Gln Tyr His Arg  Asn Ser Trp
    1505                 1510                 1515

Ile Gly  Tyr Val Arg Met Ser  Arg Ala Arg Ile Thr  Gly Phe Lys
    1520                 1525                 1530

Arg Lys  Leu Val Gly Asp Glu  Ser Glu Lys Ala Ala  Gly Asp Ala
    1535                 1540                 1545

Ser Arg  Ala His Arg Thr Asn  Leu Ile Met Ala Glu  Ile Ile Pro
    1550                 1555                 1560
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Cys Ala  Ile Tyr Ala Ala Gly  Cys Phe Ile Ala Phe  Thr Phe Ile
    1565                 1570                 1575

Asn Ala  Gln Thr Gly Val Lys  Thr Thr Asp Asp Asp  Arg Val Asn
    1580                 1585                 1590

Ser Val  Leu Arg Ile Ile Ile  Cys Thr Leu Ala Pro  Ile Ala Val
    1595                 1600                 1605

Asn Leu  Gly Val Leu Phe Phe  Cys Met Gly Met Ser  Cys Cys Ser
    1610                 1615                 1620

Gly Pro  Leu Phe Gly Met Cys  Cys Lys Lys Thr Gly  Ser Val Met
    1625                 1630                 1635

Ala Gly  Ile Ala His Gly Val  Ala Val Ile Val His  Ile Ala Phe
    1640                 1645                 1650

Phe Ile  Val Met Trp Val Leu  Glu Ser Phe Asn Phe  Val Arg Met
    1655                 1660                 1665

Leu Ile  Gly Val Val Thr Cys  Ile Gln Cys Gln Arg  Leu Ile Phe
    1670                 1675                 1680

His Cys  Met Thr Ala Leu Met  Leu Thr Arg Glu Phe  Lys Asn Asp
    1685                 1690                 1695

His Ala  Asn Thr Ala Phe Trp  Thr Gly Lys Trp Tyr  Gly Lys Gly
    1700                 1705                 1710

Met Gly  Tyr Met Ala Trp Thr  Gln Pro Ser Arg Glu  Leu Thr Ala
    1715                 1720                 1725

Lys Val  Ile Glu Leu Ser Glu  Phe Ala Ala Asp Phe  Val Leu Gly
    1730                 1735                 1740

His Val  Ile Leu Ile Cys Gln  Leu Pro Leu Ile Ile  Ile Pro Lys
    1745                 1750                 1755

Ile Asp  Lys Phe His Ser Ile  Met Leu Phe Trp Leu  Lys Pro Ser
    1760                 1765                 1770

Arg Gln  Ile Arg Pro Pro Ile  Tyr Ser Leu Lys Gln  Thr Arg Leu
    1775                 1780                 1785

Arg Lys  Arg Met Val Lys Lys  Tyr Cys Ser Leu Tyr  Phe Leu Val
    1790                 1795                 1800

Leu Ala  Ile Phe Ala Gly Cys  Ile Ile Gly Pro Ala  Val Ala Ser
    1805                 1810                 1815

Ala Lys  Ile His Lys His Ile  Gly Asp Ser Leu Asp  Gly Val Val
    1820                 1825                 1830

His Asn  Leu Phe Gln Pro Ile  Asn Thr Thr Asn Asn  Asp Thr Gly
    1835                 1840                 1845

Ser Gln  Met Ser Thr Tyr Gln  Ser His Tyr Tyr Thr  His Thr Pro
    1850                 1855                 1860

Ser Leu  Lys Thr Trp Ser Thr  Ile Lys
    1865                 1870


<210> SEQ ID NO 7
<211> LENGTH: 5661
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(5661)
<223> OTHER INFORMATION: Saccharomyces cerevisiae FKS2 (codon optimized)

<400> SEQUENCE: 7
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atg tcc tac aac gat ccc aat ctc aat ggc cag tat tac tcc aac ggc       48
Met Ser Tyr Asn Asp Pro Asn Leu Asn Gly Gln Tyr Tyr Ser Asn Gly
1               5                  10                  15

gac ggc acc ggc gat ggc aat tat ccg acc tac cag gtg acc cag gat       96
Asp Gly Thr Gly Asp Gly Asn Tyr Pro Thr Tyr Gln Val Thr Gln Asp
            20                  25                  30

caa agc gcg tac gac gag tac ggc cag ccc atc tat acc caa aat caa      144
Gln Ser Ala Tyr Asp Glu Tyr Gly Gln Pro Ile Tyr Thr Gln Asn Gln
        35                  40                  45

ctg gac gat ggc tac tat gac ccg aat gaa caa tac gtg gat ggc acc      192
Leu Asp Asp Gly Tyr Tyr Asp Pro Asn Glu Gln Tyr Val Asp Gly Thr
    50                  55                  60

cag ttc ccg cag ggc cag gac ccg tcg cag gac caa ggc ccg tat aac      240
Gln Phe Pro Gln Gly Gln Asp Pro Ser Gln Asp Gln Gly Pro Tyr Asn
65                  70                  75                  80

aat gac gcc agc tat tac aac cag ccg ccg aac atg atg aac ccg tcg      288
Asn Asp Ala Ser Tyr Tyr Asn Gln Pro Pro Asn Met Met Asn Pro Ser
                85                  90                  95

tcc cag gac ggt gag aat ttc tcg gac ttc agc tcg tat gga ccg ccc      336
Ser Gln Asp Gly Glu Asn Phe Ser Asp Phe Ser Ser Tyr Gly Pro Pro
            100                 105                 110

tcg gga acg tac cct aat gac cag tat acg ccc agt cag atg tcc tac      384
Ser Gly Thr Tyr Pro Asn Asp Gln Tyr Thr Pro Ser Gln Met Ser Tyr
        115                 120                 125

ccg gat cag gac ggc tcg tcg ggt gcg tcg acg ccg tat ggc aac ggc      432
Pro Asp Gln Asp Gly Ser Ser Gly Ala Ser Thr Pro Tyr Gly Asn Gly
    130                 135                 140

gtc gtc aat ggg aac ggc cag tat tat gat ccg aat gcg atc gag atg      480
Val Val Asn Gly Asn Gly Gln Tyr Tyr Asp Pro Asn Ala Ile Glu Met
145                 150                 155                 160

gcg ctg ccc aat gac ccg tat ccg gcg tgg acc gcc gat ccc cag tcc      528
Ala Leu Pro Asn Asp Pro Tyr Pro Ala Trp Thr Ala Asp Pro Gln Ser
                165                 170                 175

cct ctc ccc atc gag caa att gag gac atc ttc ata gat ctc acc aat      576
Pro Leu Pro Ile Glu Gln Ile Glu Asp Ile Phe Ile Asp Leu Thr Asn
            180                 185                 190

aag ttc ggc ttc cag cgc gac tcg atg cgg aac atg ttc gac cac ttc      624
Lys Phe Gly Phe Gln Arg Asp Ser Met Arg Asn Met Phe Asp His Phe
        195                 200                 205

atg acc ctg ctg gat tcg cgc agc tcg cgc atg tcg ccg gaa cag gcc      672
Met Thr Leu Leu Asp Ser Arg Ser Ser Arg Met Ser Pro Glu Gln Ala
    210                 215                 220

ttg ctc tcc ctc cat gcc gac tac att ggc ggc gac acc gcc aac tac      720
Leu Leu Ser Leu His Ala Asp Tyr Ile Gly Gly Asp Thr Ala Asn Tyr
225                 230                 235                 240

aag aaa tgg tat ttt gcg gcc caa ctg gat atg gac gat gag atc ggc      768
Lys Lys Trp Tyr Phe Ala Ala Gln Leu Asp Met Asp Asp Glu Ile Gly
                245                 250                 255

ttc cgg aac atg aaa ctc ggc aag ctg tcc cgc aaa gcg cgc aaa gcg      816
Phe Arg Asn Met Lys Leu Gly Lys Leu Ser Arg Lys Ala Arg Lys Ala
            260                 265                 270

aag aag aaa aac aaa aag gcc atg caa gag gat gag gac act gaa gag      864
Lys Lys Lys Asn Lys Lys Ala Met Gln Glu Asp Glu Asp Thr Glu Glu
        275                 280                 285

act ctg aac cag atc gag ggc gat aac tcc ctc gaa gcc gct gac ttc      912
Thr Leu Asn Gln Ile Glu Gly Asp Asn Ser Leu Glu Ala Ala Asp Phe
    290                 295                 300
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cgg tgg aag agt aaa atg aat caa ctc agc ccc ttc gag atg gtg cgg      960
Arg Trp Lys Ser Lys Met Asn Gln Leu Ser Pro Phe Glu Met Val Arg
305                 310                 315                 320

caa atc gcc ctc ttc ctc ctg tgc tgg ggc gag gcc aat caa gtg cgg     1008
Gln Ile Ala Leu Phe Leu Leu Cys Trp Gly Glu Ala Asn Gln Val Arg
                325                 330                 335

ttc acc ccg gag tgc ctg tgc ttt atc tac aag tgc gcg agc gac tac     1056
Phe Thr Pro Glu Cys Leu Cys Phe Ile Tyr Lys Cys Ala Ser Asp Tyr
            340                 345                 350

ctg gac tcc gcc caa tgc cag cag cgg ccc gac ccc ctg ccc gag ggc     1104
Leu Asp Ser Ala Gln Cys Gln Gln Arg Pro Asp Pro Leu Pro Glu Gly
        355                 360                 365

gac ttt ctc aat cgg gtg atc acg ccc ttg tac cgc ttc att cgc agc     1152
Asp Phe Leu Asn Arg Val Ile Thr Pro Leu Tyr Arg Phe Ile Arg Ser
    370                 375                 380

cag gtg tac gag atc gtc gac ggc cgc tac gtg aag tcc gag aag gac     1200
Gln Val Tyr Glu Ile Val Asp Gly Arg Tyr Val Lys Ser Glu Lys Asp
385                 390                 395                 400

cat aac aag gtc att ggt tat gac gac gtc aac caa ctt ttc tgg tat     1248
His Asn Lys Val Ile Gly Tyr Asp Asp Val Asn Gln Leu Phe Trp Tyr
                405                 410                 415

ccg gaa ggc atc gcc aag atc gtg atg gag gac ggc acg cgc ctt atc     1296
Pro Glu Gly Ile Ala Lys Ile Val Met Glu Asp Gly Thr Arg Leu Ile
            420                 425                 430

gac ctc ccc gct gag gaa cgg tac ctc aag ctc ggc gag atc ccc tgg     1344
Asp Leu Pro Ala Glu Glu Arg Tyr Leu Lys Leu Gly Glu Ile Pro Trp
        435                 440                 445

gac gat gtg ttc ttc aag acc tat aag gaa acc cgc tcc tgg ctc cat     1392
Asp Asp Val Phe Phe Lys Thr Tyr Lys Glu Thr Arg Ser Trp Leu His
    450                 455                 460

ctg gtg acc aac ttc aat cgg att tgg att atg cac gtg tat tgg atg     1440
Leu Val Thr Asn Phe Asn Arg Ile Trp Ile Met His Val Tyr Trp Met
465                 470                 475                 480

tat tgt gca tac aat gcc ccc acc ttc tat acg cac aat tac caa cag     1488
Tyr Cys Ala Tyr Asn Ala Pro Thr Phe Tyr Thr His Asn Tyr Gln Gln
                485                 490                 495

ctt gtc gac aac cag ccg ctc gcc gca tac aag tgg gcc acc gct gcc     1536
Leu Val Asp Asn Gln Pro Leu Ala Ala Tyr Lys Trp Ala Thr Ala Ala
            500                 505                 510

ctc ggg ggg acg gtc gcg tcg ttg atc cag gtc gcg gcg acg ctg tgc     1584
Leu Gly Gly Thr Val Ala Ser Leu Ile Gln Val Ala Ala Thr Leu Cys
        515                 520                 525

gag tgg tcc ttc gtg ccg cgg aaa tgg gca ggc gcg cag cac ctg tcc     1632
Glu Trp Ser Phe Val Pro Arg Lys Trp Ala Gly Ala Gln His Leu Ser
    530                 535                 540

cgg cgc ttc tgg ttc ctg tgc gtc atc atg ggc atc aat ctt ggc ccc     1680
Arg Arg Phe Trp Phe Leu Cys Val Ile Met Gly Ile Asn Leu Gly Pro
545                 550                 555                 560

gtc atc ttc gtg ttc gcc tat gac aaa gat acg gtc tac tcg acg gcc     1728
Val Ile Phe Val Phe Ala Tyr Asp Lys Asp Thr Val Tyr Ser Thr Ala
                565                 570                 575

gca cac gtc gtg ggc gca gtt atg ttc ttt gtc gcc gtg gcg act ctg     1776
Ala His Val Val Gly Ala Val Met Phe Phe Val Ala Val Ala Thr Leu
            580                 585                 590

gtc ttt ttc agc gtc atg ccg ctg ggt ggc ctg ttc acc agt tat atg     1824
Val Phe Phe Ser Val Met Pro Leu Gly Gly Leu Phe Thr Ser Tyr Met
        595                 600                 605
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aag aaa agt acc cgg tcg tac gtc gcg agt cag acc ttc acc gcc agc     1872
Lys Lys Ser Thr Arg Ser Tyr Val Ala Ser Gln Thr Phe Thr Ala Ser
    610                 615                 620

ttc gcg cca ctg cat ggg ctg gac cgg tgg atg agt tac ctc gtg tgg     1920
Phe Ala Pro Leu His Gly Leu Asp Arg Trp Met Ser Tyr Leu Val Trp
625                 630                 635                 640

gtg acc gtt ttc gcc gcc aaa tat gcg gag tcg tac ttc ttc ctg atc     1968
Val Thr Val Phe Ala Ala Lys Tyr Ala Glu Ser Tyr Phe Phe Leu Ile
                645                 650                 655

ctt tcg ctc cgc gat ccg att cgc atc ctg tcg acg acc tcg atg cgc     2016
Leu Ser Leu Arg Asp Pro Ile Arg Ile Leu Ser Thr Thr Ser Met Arg
            660                 665                 670

tgc acg ggc gag tac tgg tgg gga aac aag atc tgc aag gtc caa ccg     2064
Cys Thr Gly Glu Tyr Trp Trp Gly Asn Lys Ile Cys Lys Val Gln Pro
        675                 680                 685

aag atc gtc ttg ggc ctc atg atc gcc acg gac ttc atc ctg ttc ttc     2112
Lys Ile Val Leu Gly Leu Met Ile Ala Thr Asp Phe Ile Leu Phe Phe
    690                 695                 700

ctg gac acc tac ctc tgg tac atc gtc gtg aac acg gtt ttc agc gtc     2160
Leu Asp Thr Tyr Leu Trp Tyr Ile Val Val Asn Thr Val Phe Ser Val
705                 710                 715                 720

gga aaa tcg ttc tac ctg ggc atc tcc att ctc acc ccg tgg cgc aac     2208
Gly Lys Ser Phe Tyr Leu Gly Ile Ser Ile Leu Thr Pro Trp Arg Asn
                725                 730                 735

atc ttt acc cgg ctg ccc aag cgc ata tac agc aag atc ctg gcc acc     2256
Ile Phe Thr Arg Leu Pro Lys Arg Ile Tyr Ser Lys Ile Leu Ala Thr
            740                 745                 750

acc gac atg gag atc aag tac aaa ccc aag gtc ctc atc agc cag atc     2304
Thr Asp Met Glu Ile Lys Tyr Lys Pro Lys Val Leu Ile Ser Gln Ile
        755                 760                 765

tgg aat gcg ata atc ata tcc atg tat cgc gag cat ctt ctg gcg atc     2352
Trp Asn Ala Ile Ile Ile Ser Met Tyr Arg Glu His Leu Leu Ala Ile
    770                 775                 780

gac cat gtc caa aag ctg ctg tat cat cag gtg ccg agc gag atc gag     2400
Asp His Val Gln Lys Leu Leu Tyr His Gln Val Pro Ser Glu Ile Glu
785                 790                 795                 800

ggt aag cgc acc ttg cgc gct ccg acc ttc ttc gtt tcg caa gac gat     2448
Gly Lys Arg Thr Leu Arg Ala Pro Thr Phe Phe Val Ser Gln Asp Asp
                805                 810                 815

aac aac ttc gag act gag ttc ttc cca agg gat tcc gag gcc gag cgc     2496
Asn Asn Phe Glu Thr Glu Phe Phe Pro Arg Asp Ser Glu Ala Glu Arg
            820                 825                 830

cgg atc agc ttt ttc gcg cag agc ctt tcc acc ccc atc ccc gag ccg     2544
Arg Ile Ser Phe Phe Ala Gln Ser Leu Ser Thr Pro Ile Pro Glu Pro
        835                 840                 845

ctg ccg gtg gac aac atg ccc acg ttc acg gtt ctg acc ccg cat tac     2592
Leu Pro Val Asp Asn Met Pro Thr Phe Thr Val Leu Thr Pro His Tyr
    850                 855                 860

gcc gag cgc atc ttg ctg agc ctg cgg gaa atc atc cgc gag gac gac     2640
Ala Glu Arg Ile Leu Leu Ser Leu Arg Glu Ile Ile Arg Glu Asp Asp
865                 870                 875                 880

cag ttc agc cgc gtg acc ctc ctg gag tat ctg aag caa ctc cat ccc     2688
Gln Phe Ser Arg Val Thr Leu Leu Glu Tyr Leu Lys Gln Leu His Pro
                885                 890                 895

gtg gag tgg gat tgc ttc gtc aaa gac acc aag atc ctg gcc gag gaa     2736
Val Glu Trp Asp Cys Phe Val Lys Asp Thr Lys Ile Leu Ala Glu Glu
            900                 905                 910
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acc gcc gct tac gaa aac aac gag gac gag cct gag aag gag gac gcg     2784
Thr Ala Ala Tyr Glu Asn Asn Glu Asp Glu Pro Glu Lys Glu Asp Ala
        915                 920                 925

ctc aaa agt cag atc gac gac ttg ccg ttc tac tgc att gga ttc aaa     2832
Leu Lys Ser Gln Ile Asp Asp Leu Pro Phe Tyr Cys Ile Gly Phe Lys
    930                 935                 940

tcg gcg gca ccg gag tac acg ctt cgg acc cgg atc tgg gcg agc ctc     2880
Ser Ala Ala Pro Glu Tyr Thr Leu Arg Thr Arg Ile Trp Ala Ser Leu
945                 950                 955                 960

cgc tcg cag acc ctc tat cgg acc atc tcg gga ttc atg aat tac tcc     2928
Arg Ser Gln Thr Leu Tyr Arg Thr Ile Ser Gly Phe Met Asn Tyr Ser
                965                 970                 975

cgg gca atc aag ctg ctg tat cgc gtg gag aac ccg gag atc gtg caa     2976
Arg Ala Ile Lys Leu Leu Tyr Arg Val Glu Asn Pro Glu Ile Val Gln
            980                 985                 990

atg ttc ggc ggc aat gcc gac ggc  ctg gag cgc gag ctt  gag aag atg   3024
Met Phe Gly Gly Asn Ala Asp Gly  Leu Glu Arg Glu Leu  Glu Lys Met
        995                 1000                1005

gcg agg  cgc aag ttc aag ttc  ctc gtg agt atg cag  cgc ctg gca      3069
Ala Arg  Arg Lys Phe Lys Phe  Leu Val Ser Met Gln  Arg Leu Ala
    1010                1015                1020

aag ttc  aag ttc ctg gag aac  gcc gag ttc ctg ctt  cgg gcg tat      3114
Lys Phe  Lys Phe Leu Glu Asn  Ala Glu Phe Leu Leu  Arg Ala Tyr
    1025                1030                1035

ccg gac  ctc cag atc gcc tac  ctg gac gaa gaa ccg  ccc ctg aat      3159
Pro Asp  Leu Gln Ile Ala Tyr  Leu Asp Glu Glu Pro  Pro Leu Asn
    1040                1045                1050

gag ggc  gag gag cca cgc atc  tat tcc gcg ctc atc  gac ggc cac      3204
Glu Gly  Glu Glu Pro Arg Ile  Tyr Ser Ala Leu Ile  Asp Gly His
    1055                1060                1065

tgc gag  att aat ggc cgc cgg  cgc ccg aag ttc agg  gtc cag ctc      3249
Cys Glu  Ile Asn Gly Arg Arg  Arg Pro Lys Phe Arg  Val Gln Leu
    1070                1075                1080

tcc ggc  aac ccg att ttg ggc  gat ggg aaa tcg gac  aac cag aat      3294
Ser Gly  Asn Pro Ile Leu Gly  Asp Gly Lys Ser Asp  Asn Gln Asn
    1085                1090                1095

cat gcg  ctc atc ttc tat cgc  ggc gag tac att cag  ctg atc gac      3339
His Ala  Leu Ile Phe Tyr Arg  Gly Glu Tyr Ile Gln  Leu Ile Asp
    1100                1105                1110

gcc aac  caa gat aac tat ctt  gag gag tgc ctg aag  atc cgc tcg      3384
Ala Asn  Gln Asp Asn Tyr Leu  Glu Glu Cys Leu Lys  Ile Arg Ser
    1115                1120                1125

gtg ctg  gcg gag ttt gag gaa  ctc ggt att gaa cag  ata cac ccg      3429
Val Leu  Ala Glu Phe Glu Glu  Leu Gly Ile Glu Gln  Ile His Pro
    1130                1135                1140

tat acc  ccc gga ctc aag tac  gag gac cag tcg acg  aat cat cca      3474
Tyr Thr  Pro Gly Leu Lys Tyr  Glu Asp Gln Ser Thr  Asn His Pro
    1145                1150                1155

gtg gct  atc gtc ggt gcc cgc  gag tat atc ttc agc  gag aac tcc      3519
Val Ala  Ile Val Gly Ala Arg  Glu Tyr Ile Phe Ser  Glu Asn Ser
    1160                1165                1170

ggt gtc  ctc ggc gac gtg gcg  gct ggc aag gaa cag  acc ttc ggc      3564
Gly Val  Leu Gly Asp Val Ala  Ala Gly Lys Glu Gln  Thr Phe Gly
    1175                1180                1185

acc ctc  ttc gcc cgg acc ctc  gcg cag atc ggc ggc  aag ctg cac      3609
Thr Leu  Phe Ala Arg Thr Leu  Ala Gln Ile Gly Gly  Lys Leu His
    1190                1195                1200
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tac ggc  cat ccg gac ttc atc  aac gcg acc ttc atg  acg acc cgg      3654
Tyr Gly  His Pro Asp Phe Ile  Asn Ala Thr Phe Met  Thr Thr Arg
    1205                 1210                 1215

ggt ggg  gtc agc aag gcc cag  aaa ggg ctg cat ctc  aat gaa gat      3699
Gly Gly  Val Ser Lys Ala Gln  Lys Gly Leu His Leu  Asn Glu Asp
    1220                 1225                 1230

atc tac  gcg ggg atg aac gct  gtc ctc cgc ggt ggc  cgc att aag      3744
Ile Tyr  Ala Gly Met Asn Ala  Val Leu Arg Gly Gly  Arg Ile Lys
    1235                 1240                 1245

cac tgc  gag tat tac cag tgc  ggc aag ggt cgc gac  ttg ggc ttt      3789
His Cys  Glu Tyr Tyr Gln Cys  Gly Lys Gly Arg Asp  Leu Gly Phe
    1250                 1255                 1260

ggc acc  atc ctc aac ttc acg  acg aaa atc ggc gct  ggc atg ggc      3834
Gly Thr  Ile Leu Asn Phe Thr  Thr Lys Ile Gly Ala  Gly Met Gly
    1265                 1270                 1275

gag caa  atg ctg agt cgg gag  tac tat tac ctg ggc  acc cag ctg      3879
Glu Gln  Met Leu Ser Arg Glu  Tyr Tyr Tyr Leu Gly  Thr Gln Leu
    1280                 1285                 1290

cca atc  gac cgc ttc ctc acc  ttc tac tat gcg cat  ccc ggc ttc      3924
Pro Ile  Asp Arg Phe Leu Thr  Phe Tyr Tyr Ala His  Pro Gly Phe
    1295                 1300                 1305

cat ctg  aat aac ctg ttc ata  cag ctg tcg ctg cag  atg ttc atg      3969
His Leu  Asn Asn Leu Phe Ile  Gln Leu Ser Leu Gln  Met Phe Met
    1310                 1315                 1320

ctg act  ctg gtc aac ctc cac  gca ctc gcg cat gag  agc att ttg      4014
Leu Thr  Leu Val Asn Leu His  Ala Leu Ala His Glu  Ser Ile Leu
    1325                 1330                 1335

tgc gtg  tat gac agg gat aaa  ccg atc acc gac gtc  ctc tat cct      4059
Cys Val  Tyr Asp Arg Asp Lys  Pro Ile Thr Asp Val  Leu Tyr Pro
    1340                 1345                 1350

atc ggt  tgc tat aac ttc cat  ccg gcg atc gac tgg  gtt cgc cgc      4104
Ile Gly  Cys Tyr Asn Phe His  Pro Ala Ile Asp Trp  Val Arg Arg
    1355                 1360                 1365

tac acc  ctg agc atc ttt atc  gtg ttc tgg ata gcg  ttc gtc ccg      4149
Tyr Thr  Leu Ser Ile Phe Ile  Val Phe Trp Ile Ala  Phe Val Pro
    1370                 1375                 1380

atc gtc  gtc cag gag ctg atc  gag agg ggc ctg tgg  aag gcc acg      4194
Ile Val  Val Gln Glu Leu Ile  Glu Arg Gly Leu Trp  Lys Ala Thr
    1385                 1390                 1395

cag cgg  ttc ttc agg cac atc  ttg tcg ctc agc ccg  atg ttc gaa      4239
Gln Arg  Phe Phe Arg His Ile  Leu Ser Leu Ser Pro  Met Phe Glu
    1400                 1405                 1410

gtg ttc  gcg ggt cag atc tat  tcc agc gcg ctc ctg  agc gac att      4284
Val Phe  Ala Gly Gln Ile Tyr  Ser Ser Ala Leu Leu  Ser Asp Ile
    1415                 1420                 1425

gcc gtg  ggc ggc gcc cgg tac  atc tcc acg ggc cgc  ggt ttc gcg      4329
Ala Val  Gly Gly Ala Arg Tyr  Ile Ser Thr Gly Arg  Gly Phe Ala
    1430                 1435                 1440

acc tcc  cgc atc ccg ttc tcg  atc ctc tat tcg cgc  ttc gcg ggc      4374
Thr Ser  Arg Ile Pro Phe Ser  Ile Leu Tyr Ser Arg  Phe Ala Gly
    1445                 1450                 1455

agc gcg  atc tac atg ggt tcc  cgg agc atg ctc atg  ctc ctg ttc      4419
Ser Ala  Ile Tyr Met Gly Ser  Arg Ser Met Leu Met  Leu Leu Phe
    1460                 1465                 1470

ggc acc  gtc gcc cac tgg cag  gct ccc ctg ctt tgg  ttc tgg gcg      4464
Gly Thr  Val Ala His Trp Gln  Ala Pro Leu Leu Trp  Phe Trp Ala
    1475                 1480                 1485
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agc ctt  agc gcg ctg atc ttc  gcc ccg ttc atc ttc  aat ccg cat      4509
Ser Leu  Ser Ala Leu Ile Phe  Ala Pro Phe Ile Phe  Asn Pro His
    1490                 1495                 1500

cag ttc  gcc tgg gag gac ttc  ttc ctc gac tat agg  gac tac atc      4554
Gln Phe  Ala Trp Glu Asp Phe  Phe Leu Asp Tyr Arg  Asp Tyr Ile
    1505                 1510                 1515

cgc tgg  ctg tcc cgc gga aac  aac aag tat cac cgc  aac tcg tgg      4599
Arg Trp  Leu Ser Arg Gly Asn  Asn Lys Tyr His Arg  Asn Ser Trp
    1520                 1525                 1530

atc ggt  tac gtg cgc atg tcg  cgg tcc cgg gtg acg  ggt ttc aag      4644
Ile Gly  Tyr Val Arg Met Ser  Arg Ser Arg Val Thr  Gly Phe Lys
    1535                 1540                 1545

cgc aag  ctc gtc ggc gat gag  tcg gag aag agt gcc  ggg gac gcc      4689
Arg Lys  Leu Val Gly Asp Glu  Ser Glu Lys Ser Ala  Gly Asp Ala
    1550                 1555                 1560

tcc cgc  gcc cat cgc acc aac  ctc atc atg gcc gag  atc atc ccg      4734
Ser Arg  Ala His Arg Thr Asn  Leu Ile Met Ala Glu  Ile Ile Pro
    1565                 1570                 1575

tgc gcc  atc tac gcg gca ggc  tgc ttc atc gcc ttc  acc ttt atc      4779
Cys Ala  Ile Tyr Ala Ala Gly  Cys Phe Ile Ala Phe  Thr Phe Ile
    1580                 1585                 1590

aac gcg  cag acc ggc gtc aag  acc acc gat gag gac  cgc gtg aac      4824
Asn Ala  Gln Thr Gly Val Lys  Thr Thr Asp Glu Asp  Arg Val Asn
    1595                 1600                 1605

tcc acg  ctg cgc atc atc atc  tgt acc ctg gca ccg  atc gtc ata      4869
Ser Thr  Leu Arg Ile Ile Ile  Cys Thr Leu Ala Pro  Ile Val Ile
    1610                 1615                 1620

gac atc  ggg gtg ctg ttc ttc  tgc atg ggc ttg agc  tgt tgc tcg      4914
Asp Ile  Gly Val Leu Phe Phe  Cys Met Gly Leu Ser  Cys Cys Ser
    1625                 1630                 1635

gga ccg  ctg ctc ggc atg tgc  tgc aag aaa act ggc  agc gtc atg      4959
Gly Pro  Leu Leu Gly Met Cys  Cys Lys Lys Thr Gly  Ser Val Met
    1640                 1645                 1650

gcc ggc  att gcc cat ggc atc  gcc gtc gtc gtc cat  att gtc ttt      5004
Ala Gly  Ile Ala His Gly Ile  Ala Val Val Val His  Ile Val Phe
    1655                 1660                 1665

ttc atc  gtc atg tgg gtg ctc  gaa ggc ttc tcc ttc  gtc cgc atg      5049
Phe Ile  Val Met Trp Val Leu  Glu Gly Phe Ser Phe  Val Arg Met
    1670                 1675                 1680

ctg atc  ggt gtc gtg acg tgc  atc cag tgt cag cgg  ctt atc ttt      5094
Leu Ile  Gly Val Val Thr Cys  Ile Gln Cys Gln Arg  Leu Ile Phe
    1685                 1690                 1695

cat tgc  atg acc gtg ctc ctc  ctc acg cgg gaa ttc  aag aat gac      5139
His Cys  Met Thr Val Leu Leu  Leu Thr Arg Glu Phe  Lys Asn Asp
    1700                 1705                 1710

cac gcc  aac acc gcg ttc tgg  acc ggc aag tgg tat  tcg acg gga      5184
His Ala  Asn Thr Ala Phe Trp  Thr Gly Lys Trp Tyr  Ser Thr Gly
    1715                 1720                 1725

ctc ggt  tat atg gcc tgg acg  cag cca acg cgc gag  ctg acg gca      5229
Leu Gly  Tyr Met Ala Trp Thr  Gln Pro Thr Arg Glu  Leu Thr Ala
    1730                 1735                 1740

aag gtt  atc gag ctg agc gaa  ttc gcg gct gac ttc  gtg ctg ggc      5274
Lys Val  Ile Glu Leu Ser Glu  Phe Ala Ala Asp Phe  Val Leu Gly
    1745                 1750                 1755

cat gtc  atc ctc atc ttc cag  ctc ccg gtt atc tgc  atc ccg aag      5319
His Val  Ile Leu Ile Phe Gln  Leu Pro Val Ile Cys  Ile Pro Lys
    1760                 1765                 1770
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atc gac  aaa ttc cac tcg att  atg ctc ttt tgg ctg  aag ccg tcg      5364
Ile Asp  Lys Phe His Ser Ile  Met Leu Phe Trp Leu  Lys Pro Ser
    1775                 1780                 1785

cgc caa  atc cgc cct ccg atc  tac tcc ctg aaa cag  gcg cgc ctg      5409
Arg Gln  Ile Arg Pro Pro Ile  Tyr Ser Leu Lys Gln  Ala Arg Leu
    1790                 1795                 1800

cgc aag  cgc atg gtc cgg cgc  tac tgc tcc ctc tac  ttc ctg gtg      5454
Arg Lys  Arg Met Val Arg Arg  Tyr Cys Ser Leu Tyr  Phe Leu Val
    1805                 1810                 1815

ctg atc  atc ttc gcg ggt tgc  atc gtg ggt ccc gcc  gtg gcg tcg      5499
Leu Ile  Ile Phe Ala Gly Cys  Ile Val Gly Pro Ala  Val Ala Ser
    1820                 1825                 1830

gct cac  gtg ccg aaa gac ctg  ggc tcc ggg ctg acc  ggc acc ttt      5544
Ala His  Val Pro Lys Asp Leu  Gly Ser Gly Leu Thr  Gly Thr Phe
    1835                 1840                 1845

cat aac  ctg gtg cag ccg cgc  aac gtc agc aat aat  gac acg ggc      5589
His Asn  Leu Val Gln Pro Arg  Asn Val Ser Asn Asn  Asp Thr Gly
    1850                 1855                 1860

tcg caa  atg tcc acc tat aag  tcg cat tac tac acc  cat acc ccg      5634
Ser Gln  Met Ser Thr Tyr Lys  Ser His Tyr Tyr Thr  His Thr Pro
    1865                 1870                 1875

tcg ctc  aaa acc tgg tcg acc  att aaa                              5661
Ser Leu  Lys Thr Trp Ser Thr  Ile Lys
    1880                 1885
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<210> SEQ ID NO 8
<211> LENGTH: 1887
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 8

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Asp Gly Thr Gly Asp Gly Asn Tyr Pro Thr Tyr Gln Val Thr Gln Asp
            20                  25                  30

Gln Ser Ala Tyr Asp Glu Tyr Gly Gln Pro Ile Tyr Thr Gln Asn Gln
        35                  40                  45

Leu Asp Asp Gly Tyr Tyr Asp Pro Asn Glu Gln Tyr Val Asp Gly Thr
    50                  55                  60

Gln Phe Pro Gln Gly Gln Asp Pro Ser Gln Asp Gln Gly Pro Tyr Asn
65                  70                  75                  80

Asn Asp Ala Ser Tyr Tyr Asn Gln Pro Pro Asn Met Met Asn Pro Ser
                85                  90                  95

Ser Gln Asp Gly Glu Asn Phe Ser Asp Phe Ser Ser Tyr Gly Pro Pro
            100                 105                 110

Ser Gly Thr Tyr Pro Asn Asp Gln Tyr Thr Pro Ser Gln Met Ser Tyr
        115                 120                 125

Pro Asp Gln Asp Gly Ser Ser Gly Ala Ser Thr Pro Tyr Gly Asn Gly
    130                 135                 140

Val Val Asn Gly Asn Gly Gln Tyr Tyr Asp Pro Asn Ala Ile Glu Met
145                 150                 155                 160

Ala Leu Pro Asn Asp Pro Tyr Pro Ala Trp Thr Ala Asp Pro Gln Ser
                165                 170                 175
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Pro Leu Pro Ile Glu Gln Ile Glu Asp Ile Phe Ile Asp Leu Thr Asn
            180                 185                 190

Lys Phe Gly Phe Gln Arg Asp Ser Met Arg Asn Met Phe Asp His Phe
        195                 200                 205

Met Thr Leu Leu Asp Ser Arg Ser Ser Arg Met Ser Pro Glu Gln Ala
    210                 215                 220

Leu Leu Ser Leu His Ala Asp Tyr Ile Gly Gly Asp Thr Ala Asn Tyr
225                 230                 235                 240

Lys Lys Trp Tyr Phe Ala Ala Gln Leu Asp Met Asp Asp Glu Ile Gly
                245                 250                 255

Phe Arg Asn Met Lys Leu Gly Lys Leu Ser Arg Lys Ala Arg Lys Ala
            260                 265                 270

Lys Lys Lys Asn Lys Lys Ala Met Gln Glu Asp Glu Asp Thr Glu Glu
        275                 280                 285

Thr Leu Asn Gln Ile Glu Gly Asp Asn Ser Leu Glu Ala Ala Asp Phe
    290                 295                 300

Arg Trp Lys Ser Lys Met Asn Gln Leu Ser Pro Phe Glu Met Val Arg
305                 310                 315                 320

Gln Ile Ala Leu Phe Leu Leu Cys Trp Gly Glu Ala Asn Gln Val Arg
                325                 330                 335

Phe Thr Pro Glu Cys Leu Cys Phe Ile Tyr Lys Cys Ala Ser Asp Tyr
            340                 345                 350

Leu Asp Ser Ala Gln Cys Gln Gln Arg Pro Asp Pro Leu Pro Glu Gly
        355                 360                 365

Asp Phe Leu Asn Arg Val Ile Thr Pro Leu Tyr Arg Phe Ile Arg Ser
    370                 375                 380

Gln Val Tyr Glu Ile Val Asp Gly Arg Tyr Val Lys Ser Glu Lys Asp
385                 390                 395                 400

His Asn Lys Val Ile Gly Tyr Asp Asp Val Asn Gln Leu Phe Trp Tyr
                405                 410                 415

Pro Glu Gly Ile Ala Lys Ile Val Met Glu Asp Gly Thr Arg Leu Ile
            420                 425                 430

Asp Leu Pro Ala Glu Glu Arg Tyr Leu Lys Leu Gly Glu Ile Pro Trp
        435                 440                 445

Asp Asp Val Phe Phe Lys Thr Tyr Lys Glu Thr Arg Ser Trp Leu His
    450                 455                 460

Leu Val Thr Asn Phe Asn Arg Ile Trp Ile Met His Val Tyr Trp Met
465                 470                 475                 480

Tyr Cys Ala Tyr Asn Ala Pro Thr Phe Tyr Thr His Asn Tyr Gln Gln
                485                 490                 495

Leu Val Asp Asn Gln Pro Leu Ala Ala Tyr Lys Trp Ala Thr Ala Ala
            500                 505                 510

Leu Gly Gly Thr Val Ala Ser Leu Ile Gln Val Ala Ala Thr Leu Cys
        515                 520                 525

Glu Trp Ser Phe Val Pro Arg Lys Trp Ala Gly Ala Gln His Leu Ser
    530                 535                 540

Arg Arg Phe Trp Phe Leu Cys Val Ile Met Gly Ile Asn Leu Gly Pro
545                 550                 555                 560

Val Ile Phe Val Phe Ala Tyr Asp Lys Asp Thr Val Tyr Ser Thr Ala
                565                 570                 575

Ala His Val Val Gly Ala Val Met Phe Phe Val Ala Val Ala Thr Leu
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            580                 585                 590

Val Phe Phe Ser Val Met Pro Leu Gly Gly Leu Phe Thr Ser Tyr Met
        595                 600                 605

Lys Lys Ser Thr Arg Ser Tyr Val Ala Ser Gln Thr Phe Thr Ala Ser
    610                 615                 620

Phe Ala Pro Leu His Gly Leu Asp Arg Trp Met Ser Tyr Leu Val Trp
625                 630                 635                 640

Val Thr Val Phe Ala Ala Lys Tyr Ala Glu Ser Tyr Phe Phe Leu Ile
                645                 650                 655

Leu Ser Leu Arg Asp Pro Ile Arg Ile Leu Ser Thr Thr Ser Met Arg
            660                 665                 670

Cys Thr Gly Glu Tyr Trp Trp Gly Asn Lys Ile Cys Lys Val Gln Pro
        675                 680                 685

Lys Ile Val Leu Gly Leu Met Ile Ala Thr Asp Phe Ile Leu Phe Phe
    690                 695                 700

Leu Asp Thr Tyr Leu Trp Tyr Ile Val Val Asn Thr Val Phe Ser Val
705                 710                 715                 720

Gly Lys Ser Phe Tyr Leu Gly Ile Ser Ile Leu Thr Pro Trp Arg Asn
                725                 730                 735

Ile Phe Thr Arg Leu Pro Lys Arg Ile Tyr Ser Lys Ile Leu Ala Thr
            740                 745                 750

Thr Asp Met Glu Ile Lys Tyr Lys Pro Lys Val Leu Ile Ser Gln Ile
        755                 760                 765

Trp Asn Ala Ile Ile Ile Ser Met Tyr Arg Glu His Leu Leu Ala Ile
    770                 775                 780

Asp His Val Gln Lys Leu Leu Tyr His Gln Val Pro Ser Glu Ile Glu
785                 790                 795                 800

Gly Lys Arg Thr Leu Arg Ala Pro Thr Phe Phe Val Ser Gln Asp Asp
                805                 810                 815

Asn Asn Phe Glu Thr Glu Phe Phe Pro Arg Asp Ser Glu Ala Glu Arg
            820                 825                 830

Arg Ile Ser Phe Phe Ala Gln Ser Leu Ser Thr Pro Ile Pro Glu Pro
        835                 840                 845

Leu Pro Val Asp Asn Met Pro Thr Phe Thr Val Leu Thr Pro His Tyr
    850                 855                 860

Ala Glu Arg Ile Leu Leu Ser Leu Arg Glu Ile Ile Arg Glu Asp Asp
865                 870                 875                 880

Gln Phe Ser Arg Val Thr Leu Leu Glu Tyr Leu Lys Gln Leu His Pro
                885                 890                 895

Val Glu Trp Asp Cys Phe Val Lys Asp Thr Lys Ile Leu Ala Glu Glu
            900                 905                 910

Thr Ala Ala Tyr Glu Asn Asn Glu Asp Glu Pro Glu Lys Glu Asp Ala
        915                 920                 925

Leu Lys Ser Gln Ile Asp Asp Leu Pro Phe Tyr Cys Ile Gly Phe Lys
    930                 935                 940

Ser Ala Ala Pro Glu Tyr Thr Leu Arg Thr Arg Ile Trp Ala Ser Leu
945                 950                 955                 960

Arg Ser Gln Thr Leu Tyr Arg Thr Ile Ser Gly Phe Met Asn Tyr Ser
                965                 970                 975

Arg Ala Ile Lys Leu Leu Tyr Arg Val Glu Asn Pro Glu Ile Val Gln
            980                 985                 990
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Met Phe Gly Gly Asn Ala Asp Gly  Leu Glu Arg Glu Leu  Glu Lys Met
        995                1000                1005

Ala Arg  Arg Lys Phe Lys Phe  Leu Val Ser Met Gln  Arg Leu Ala
    1010                1015                1020

Lys Phe  Lys Phe Leu Glu Asn  Ala Glu Phe Leu Leu  Arg Ala Tyr
    1025                1030                1035

Pro Asp  Leu Gln Ile Ala Tyr  Leu Asp Glu Glu Pro  Pro Leu Asn
    1040                1045                1050

Glu Gly  Glu Glu Pro Arg Ile  Tyr Ser Ala Leu Ile  Asp Gly His
    1055                1060                1065

Cys Glu  Ile Asn Gly Arg Arg  Arg Pro Lys Phe Arg  Val Gln Leu
    1070                1075                1080

Ser Gly  Asn Pro Ile Leu Gly  Asp Gly Lys Ser Asp  Asn Gln Asn
    1085                1090                1095

His Ala  Leu Ile Phe Tyr Arg  Gly Glu Tyr Ile Gln  Leu Ile Asp
    1100                1105                1110

Ala Asn  Gln Asp Asn Tyr Leu  Glu Glu Cys Leu Lys  Ile Arg Ser
    1115                1120                1125

Val Leu  Ala Glu Phe Glu Glu  Leu Gly Ile Glu Gln  Ile His Pro
    1130                1135                1140

Tyr Thr  Pro Gly Leu Lys Tyr  Glu Asp Gln Ser Thr  Asn His Pro
    1145                1150                1155

Val Ala  Ile Val Gly Ala Arg  Glu Tyr Ile Phe Ser  Glu Asn Ser
    1160                1165                1170

Gly Val  Leu Gly Asp Val Ala  Ala Gly Lys Glu Gln  Thr Phe Gly
    1175                1180                1185

Thr Leu  Phe Ala Arg Thr Leu  Ala Gln Ile Gly Gly  Lys Leu His
    1190                1195                1200

Tyr Gly  His Pro Asp Phe Ile  Asn Ala Thr Phe Met  Thr Thr Arg
    1205                1210                1215

Gly Gly  Val Ser Lys Ala Gln  Lys Gly Leu His Leu  Asn Glu Asp
    1220                1225                1230

Ile Tyr  Ala Gly Met Asn Ala  Val Leu Arg Gly Gly  Arg Ile Lys
    1235                1240                1245

His Cys  Glu Tyr Tyr Gln Cys  Gly Lys Gly Arg Asp  Leu Gly Phe
    1250                1255                1260

Gly Thr  Ile Leu Asn Phe Thr  Thr Lys Ile Gly Ala  Gly Met Gly
    1265                1270                1275

Glu Gln  Met Leu Ser Arg Glu  Tyr Tyr Tyr Leu Gly  Thr Gln Leu
    1280                1285                1290

Pro Ile  Asp Arg Phe Leu Thr  Phe Tyr Tyr Ala His  Pro Gly Phe
    1295                1300                1305

His Leu  Asn Asn Leu Phe Ile  Gln Leu Ser Leu Gln  Met Phe Met
    1310                1315                1320

Leu Thr  Leu Val Asn Leu His  Ala Leu Ala His Glu  Ser Ile Leu
    1325                1330                1335

Cys Val  Tyr Asp Arg Asp Lys  Pro Ile Thr Asp Val  Leu Tyr Pro
    1340                1345                1350

Ile Gly  Cys Tyr Asn Phe His  Pro Ala Ile Asp Trp  Val Arg Arg
    1355                1360                1365
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Tyr Thr  Leu Ser Ile Phe Ile  Val Phe Trp Ile Ala  Phe Val Pro
    1370                1375                1380

Ile Val  Val Gln Glu Leu Ile  Glu Arg Gly Leu Trp  Lys Ala Thr
    1385                1390                1395

Gln Arg  Phe Phe Arg His Ile  Leu Ser Leu Ser Pro  Met Phe Glu
    1400                1405                1410

Val Phe  Ala Gly Gln Ile Tyr  Ser Ser Ala Leu Leu  Ser Asp Ile
    1415                1420                1425

Ala Val  Gly Gly Ala Arg Tyr  Ile Ser Thr Gly Arg  Gly Phe Ala
    1430                1435                1440

Thr Ser  Arg Ile Pro Phe Ser  Ile Leu Tyr Ser Arg  Phe Ala Gly
    1445                1450                1455

Ser Ala  Ile Tyr Met Gly Ser  Arg Ser Met Leu Met  Leu Leu Phe
    1460                1465                1470

Gly Thr  Val Ala His Trp Gln  Ala Pro Leu Leu Trp  Phe Trp Ala
    1475                1480                1485

Ser Leu  Ser Ala Leu Ile Phe  Ala Pro Phe Ile Phe  Asn Pro His
    1490                1495                1500

Gln Phe  Ala Trp Glu Asp Phe  Phe Leu Asp Tyr Arg  Asp Tyr Ile
    1505                1510                1515

Arg Trp  Leu Ser Arg Gly Asn  Asn Lys Tyr His Arg  Asn Ser Trp
    1520                1525                1530

Ile Gly  Tyr Val Arg Met Ser  Arg Ser Arg Val Thr  Gly Phe Lys
    1535                1540                1545

Arg Lys  Leu Val Gly Asp Glu  Ser Glu Lys Ser Ala  Gly Asp Ala
    1550                1555                1560

Ser Arg  Ala His Arg Thr Asn  Leu Ile Met Ala Glu  Ile Ile Pro
    1565                1570                1575

Cys Ala  Ile Tyr Ala Ala Gly  Cys Phe Ile Ala Phe  Thr Phe Ile
    1580                1585                1590

Asn Ala  Gln Thr Gly Val Lys  Thr Thr Asp Glu Asp  Arg Val Asn
    1595                1600                1605

Ser Thr  Leu Arg Ile Ile Ile  Cys Thr Leu Ala Pro  Ile Val Ile
    1610                1615                1620

Asp Ile  Gly Val Leu Phe Phe  Cys Met Gly Leu Ser  Cys Cys Ser
    1625                1630                1635

Gly Pro  Leu Leu Gly Met Cys  Cys Lys Lys Thr Gly  Ser Val Met
    1640                1645                1650

Ala Gly  Ile Ala His Gly Ile  Ala Val Val Val His  Ile Val Phe
    1655                1660                1665

Phe Ile  Val Met Trp Val Leu  Glu Gly Phe Ser Phe  Val Arg Met
    1670                1675                1680

Leu Ile  Gly Val Val Thr Cys  Ile Gln Cys Gln Arg  Leu Ile Phe
    1685                1690                1695

His Cys  Met Thr Val Leu Leu  Leu Thr Arg Glu Phe  Lys Asn Asp
    1700                1705                1710

His Ala  Asn Thr Ala Phe Trp  Thr Gly Lys Trp Tyr  Ser Thr Gly
    1715                1720                1725

Leu Gly  Tyr Met Ala Trp Thr  Gln Pro Thr Arg Glu  Leu Thr Ala
    1730                1735                1740

Lys Val  Ile Glu Leu Ser Glu  Phe Ala Ala Asp Phe  Val Leu Gly
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    1745                1750                1755

His Val  Ile Leu Ile Phe Gln  Leu Pro Val Ile Cys  Ile Pro Lys
    1760                1765                1770

Ile Asp  Lys Phe His Ser Ile  Met Leu Phe Trp Leu  Lys Pro Ser
    1775                1780                1785

Arg Gln  Ile Arg Pro Pro Ile  Tyr Ser Leu Lys Gln  Ala Arg Leu
    1790                1795                1800

Arg Lys  Arg Met Val Arg Arg  Tyr Cys Ser Leu Tyr  Phe Leu Val
    1805                1810                1815

Leu Ile  Ile Phe Ala Gly Cys  Ile Val Gly Pro Ala  Val Ala Ser
    1820                1825                1830

Ala His  Val Pro Lys Asp Leu  Gly Ser Gly Leu Thr  Gly Thr Phe
    1835                1840                1845

His Asn  Leu Val Gln Pro Arg  Asn Val Ser Asn Asn  Asp Thr Gly
    1850                1855                1860

Ser Gln  Met Ser Thr Tyr Lys  Ser His Tyr Tyr Thr  His Thr Pro
    1865                1870                1875

Ser Leu  Lys Thr Trp Ser Thr  Ile Lys
    1880                1885


<210> SEQ ID NO 9
<211> LENGTH: 5679
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(5679)
<223> OTHER INFORMATION: Candida albicans FKS1 (codon optimized)

<400> SEQUENCE: 9

atg agc tac aac gac aac aat aat cac tat tac gac ccg aat cag caa       48
Met Ser Tyr Asn Asp Asn Asn Asn His Tyr Tyr Asp Pro Asn Gln Gln
1               5                   10                  15

ggc gga atg ccc cct cat caa ggc gga gag ggg tat tac cag cag cag       96
Gly Gly Met Pro Pro His Gln Gly Gly Glu Gly Tyr Tyr Gln Gln Gln
            20                  25                  30

tat gat gac atg ggc caa caa ccg cac caa cag gac tac tac gat ccg      144
Tyr Asp Asp Met Gly Gln Gln Pro His Gln Gln Asp Tyr Tyr Asp Pro
        35                  40                  45

aat gct cag tat cag cag cag ccg tat gac atg gac ggt tat cag gac      192
Asn Ala Gln Tyr Gln Gln Gln Pro Tyr Asp Met Asp Gly Tyr Gln Asp
    50                  55                  60

caa gcg aac tac ggc ggt cag ccg atg aat gcg caa ggc tac aac gcc      240
Gln Ala Asn Tyr Gly Gly Gln Pro Met Asn Ala Gln Gly Tyr Asn Ala
65                  70                  75                  80

gat ccc gag gcc ttt tcc gac ttc agc tac ggt ggc cag acc ccg ggt      288
Asp Pro Glu Ala Phe Ser Asp Phe Ser Tyr Gly Gly Gln Thr Pro Gly
                85                  90                  95

acc cca ggc tac gac cag tac ggt acc cag tac acc ccg agc cag atg      336
Thr Pro Gly Tyr Asp Gln Tyr Gly Thr Gln Tyr Thr Pro Ser Gln Met
            100                 105                 110

tcc tat ggc ggc gac ccc cgg tcc tcg ggt gca agc act ccc att tat      384
Ser Tyr Gly Gly Asp Pro Arg Ser Ser Gly Ala Ser Thr Pro Ile Tyr
        115                 120                 125

ggc ggc cag ggc cag ggt tac gac cct acc cag ttc aac atg tcc tcc      432
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Gly Gly Gln Gly Gln Gly Tyr Asp Pro Thr Gln Phe Asn Met Ser Ser
    130                 135                 140

aac ctc ccc tac ccc gcc tgg agc gcg gac ccc cag gcc ccg atc aag      480
Asn Leu Pro Tyr Pro Ala Trp Ser Ala Asp Pro Gln Ala Pro Ile Lys
145                 150                 155                 160

ata gag cat atc gaa gat atc ttc atc gac ctc acc aac aag ttc ggg      528
Ile Glu His Ile Glu Asp Ile Phe Ile Asp Leu Thr Asn Lys Phe Gly
                165                 170                 175

ttc cag cgg gac tcg atg cgc aat atg ttc gac tac ttc atg acg ctg      576
Phe Gln Arg Asp Ser Met Arg Asn Met Phe Asp Tyr Phe Met Thr Leu
            180                 185                 190

ttg gat tcc cgc agc tcg cgc atg agc ccg gct cag gcc ctc ctc agc      624
Leu Asp Ser Arg Ser Ser Arg Met Ser Pro Ala Gln Ala Leu Leu Ser
        195                 200                 205

ctg cat gcg gac tat att ggc ggg gat aac gcg aac tac cgg aaa tgg      672
Leu His Ala Asp Tyr Ile Gly Gly Asp Asn Ala Asn Tyr Arg Lys Trp
    210                 215                 220

tac ttc agt tcg cag caa gat ctc gac gac tcg ctg ggc ttc gcg aac      720
Tyr Phe Ser Ser Gln Gln Asp Leu Asp Asp Ser Leu Gly Phe Ala Asn
225                 230                 235                 240

atg acc ctg ggg aag atc gga cgc aag gcc cgg aag gcc agc aag aaa      768
Met Thr Leu Gly Lys Ile Gly Arg Lys Ala Arg Lys Ala Ser Lys Lys
                245                 250                 255

tcc aag aag gcc cgc aaa gcg gcc gag gag cac ggc cag gac gtg gac      816
Ser Lys Lys Ala Arg Lys Ala Ala Glu Glu His Gly Gln Asp Val Asp
            260                 265                 270

gcg aac gag ctg gaa ggc gac tat tcg ctt gag gcc gca gag atc cgc      864
Ala Asn Glu Leu Glu Gly Asp Tyr Ser Leu Glu Ala Ala Glu Ile Arg
        275                 280                 285

tgg aag gcc aag atg aat tcg ctg acc ccg gaa gaa cgc gtg cgg gac      912
Trp Lys Ala Lys Met Asn Ser Leu Thr Pro Glu Glu Arg Val Arg Asp
    290                 295                 300

ctg gcg ctg tat ctc ctg atc tgg ggc gaa gcg aat cag gtc agg ttt      960
Leu Ala Leu Tyr Leu Leu Ile Trp Gly Glu Ala Asn Gln Val Arg Phe
305                 310                 315                 320

acg ccc gag tgt ctc tgc tac atc tac aaa tcg gcc acc gat tat ctg     1008
Thr Pro Glu Cys Leu Cys Tyr Ile Tyr Lys Ser Ala Thr Asp Tyr Leu
                325                 330                 335

aat tcg ccc ctt tgc cag cag cgc cag gaa ccc gtc ccg gaa ggc gac     1056
Asn Ser Pro Leu Cys Gln Gln Arg Gln Glu Pro Val Pro Glu Gly Asp
            340                 345                 350

tat ctg aac cgc gtg att acc ccc ctt tac cgc ttc atc cgg tcc caa     1104
Tyr Leu Asn Arg Val Ile Thr Pro Leu Tyr Arg Phe Ile Arg Ser Gln
        355                 360                 365

gtc tat gag atc tac gac ggc cgg ttc gtc aag cgc gag aag gac cac     1152
Val Tyr Glu Ile Tyr Asp Gly Arg Phe Val Lys Arg Glu Lys Asp His
    370                 375                 380

aat aag gtc att gga tac gac gac gtg aac caa ttg ttc tgg tat ccc     1200
Asn Lys Val Ile Gly Tyr Asp Asp Val Asn Gln Leu Phe Trp Tyr Pro
385                 390                 395                 400

gag ggc atc agc cgc atc atc ttc gag gat ggc acg cgc ctg gtg gac     1248
Glu Gly Ile Ser Arg Ile Ile Phe Glu Asp Gly Thr Arg Leu Val Asp
                405                 410                 415

atc ccg cag gag gag cgg ttc ttg aag ctc gga gag gtc gag tgg aaa     1296
Ile Pro Gln Glu Glu Arg Phe Leu Lys Leu Gly Glu Val Glu Trp Lys
            420                 425                 430

aat gtg ttc ttc aag acc tat aaa gaa atc cgc acc tgg ctg cac ttc     1344
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Asn Val Phe Phe Lys Thr Tyr Lys Glu Ile Arg Thr Trp Leu His Phe
        435                 440                 445

gtg acc aat ttc aac cgg atc tgg atc atc cat ggc acg atc tat tgg     1392
Val Thr Asn Phe Asn Arg Ile Trp Ile Ile His Gly Thr Ile Tyr Trp
    450                 455                 460

atg tat acg gcc tac aac tcg ccg acc ctg tat acc aag cat tat gtg     1440
Met Tyr Thr Ala Tyr Asn Ser Pro Thr Leu Tyr Thr Lys His Tyr Val
465                 470                 475                 480

cag acg atc aat cag cag ccg ctg gcc tcc agc cgc tgg gcc gcc tgc     1488
Gln Thr Ile Asn Gln Gln Pro Leu Ala Ser Ser Arg Trp Ala Ala Cys
                485                 490                 495

gcc att ggc ggc gtg ctc gcc tcc ttc atc caa att ctg gcc acc ctc     1536
Ala Ile Gly Gly Val Leu Ala Ser Phe Ile Gln Ile Leu Ala Thr Leu
            500                 505                 510

ttc gag tgg att ttc gtt ccg cgg gag tgg gcg ggt gcg cag cat ctg     1584
Phe Glu Trp Ile Phe Val Pro Arg Glu Trp Ala Gly Ala Gln His Leu
        515                 520                 525

tcg agg cgc atg ctg ttc ctg gtc ctc atc ttt ctg ctt aac ctg gtc     1632
Ser Arg Arg Met Leu Phe Leu Val Leu Ile Phe Leu Leu Asn Leu Val
    530                 535                 540

cct ccg gtc tat acc ttc cag ata acc aag ctc gtc atc tac tcg aag     1680
Pro Pro Val Tyr Thr Phe Gln Ile Thr Lys Leu Val Ile Tyr Ser Lys
545                 550                 555                 560

agt gcg tac gct gtg tcc atc gtg ggc ttc ttc att gcc gtg gct acc     1728
Ser Ala Tyr Ala Val Ser Ile Val Gly Phe Phe Ile Ala Val Ala Thr
                565                 570                 575

ctg gtc ttt ttc gcg gtc atg ccg ctc ggg ggc ctc ttc acg tcc tat     1776
Leu Val Phe Phe Ala Val Met Pro Leu Gly Gly Leu Phe Thr Ser Tyr
            580                 585                 590

atg aac aag cgg agt cgc cgg tat atc gcg agt cag acg ttc act gcg     1824
Met Asn Lys Arg Ser Arg Arg Tyr Ile Ala Ser Gln Thr Phe Thr Ala
        595                 600                 605

aac tat atc aag ctc aag ggc ctc gac atg tgg atg agt tac ctc ctg     1872
Asn Tyr Ile Lys Leu Lys Gly Leu Asp Met Trp Met Ser Tyr Leu Leu
    610                 615                 620

tgg ttc ctg gtt ttc ctc gcc aag ctc gtt gag tcc tac ttc ttc agc     1920
Trp Phe Leu Val Phe Leu Ala Lys Leu Val Glu Ser Tyr Phe Phe Ser
625                 630                 635                 640

acc ctg tcg ctg cgc gac ccc atc cgc aac ctg tcc acg atg acg atg     1968
Thr Leu Ser Leu Arg Asp Pro Ile Arg Asn Leu Ser Thr Met Thr Met
                645                 650                 655

cgc tgc gtc ggc gag gtc tgg tac aag gac atc gtg tgc cgc aac caa     2016
Arg Cys Val Gly Glu Val Trp Tyr Lys Asp Ile Val Cys Arg Asn Gln
            660                 665                 670

gcc aag atc gtc ctc ggc ctc atg tat ctg gtc gat ctg ctc ctc ttc     2064
Ala Lys Ile Val Leu Gly Leu Met Tyr Leu Val Asp Leu Leu Leu Phe
        675                 680                 685

ttc ctc gat acc tac atg tgg tac atc atc tgc aac tgc atc ttc tcc     2112
Phe Leu Asp Thr Tyr Met Trp Tyr Ile Ile Cys Asn Cys Ile Phe Ser
    690                 695                 700

ata ggc cgc agc ttc tat ctg gga att agt atc ctc acc ccg tgg cgg     2160
Ile Gly Arg Ser Phe Tyr Leu Gly Ile Ser Ile Leu Thr Pro Trp Arg
705                 710                 715                 720

aac atc ttc acg cgc ctg ccg aag cgg att tac agc aag atc ttg gcg     2208
Asn Ile Phe Thr Arg Leu Pro Lys Arg Ile Tyr Ser Lys Ile Leu Ala
                725                 730                 735

acc acc gag atg gag atc aaa tac aaa ccc aag gtc ctt atc agc cag     2256
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Thr Thr Glu Met Glu Ile Lys Tyr Lys Pro Lys Val Leu Ile Ser Gln
            740                 745                 750

atc tgg aat gcg att gtt atc tcc atg tat cgc gag cat ctc ctg gcc     2304
Ile Trp Asn Ala Ile Val Ile Ser Met Tyr Arg Glu His Leu Leu Ala
        755                 760                 765

atc gac cac gtc cag aaa ctg ctg tat cat caa gtg cca agc gag atc     2352
Ile Asp His Val Gln Lys Leu Leu Tyr His Gln Val Pro Ser Glu Ile
    770                 775                 780

gaa ggc aag cgc acg ctg cgg gcg ccg acg ttc ttc gtg tcg caa gac     2400
Glu Gly Lys Arg Thr Leu Arg Ala Pro Thr Phe Phe Val Ser Gln Asp
785                 790                 795                 800

gac aat aat ttc gag act gag ttc ttc ccg cgc aac tcc gag gcc gag     2448
Asp Asn Asn Phe Glu Thr Glu Phe Phe Pro Arg Asn Ser Glu Ala Glu
                805                 810                 815

cgg cgc att agt ttc ttc gcc caa tcc ctt gcg acc ccg atg ccg gag     2496
Arg Arg Ile Ser Phe Phe Ala Gln Ser Leu Ala Thr Pro Met Pro Glu
            820                 825                 830

ccc ctc ccg gtc gat aac atg ccc acg ttt acc gtg ttc acc cct cat     2544
Pro Leu Pro Val Asp Asn Met Pro Thr Phe Thr Val Phe Thr Pro His
        835                 840                 845

tac agc gag aag atc ctg ctc agc ctg cgc gag atc att cgc gag gac     2592
Tyr Ser Glu Lys Ile Leu Leu Ser Leu Arg Glu Ile Ile Arg Glu Asp
    850                 855                 860

gac caa ttc tcg cgc gtc acg ctg ctg gag tat ctc aag cag ctg cat     2640
Asp Gln Phe Ser Arg Val Thr Leu Leu Glu Tyr Leu Lys Gln Leu His
865                 870                 875                 880

ccg gtc gag tgg gac tgc ttc gtt aag gac acg aag atc ctc gcc gaa     2688
Pro Val Glu Trp Asp Cys Phe Val Lys Asp Thr Lys Ile Leu Ala Glu
                885                 890                 895

gaa acc gct gcc tac gag aac ggc gac gac tcg gag aaa ttg tcc gag     2736
Glu Thr Ala Ala Tyr Glu Asn Gly Asp Asp Ser Glu Lys Leu Ser Glu
            900                 905                 910

gac ggc ctc aag tcg aag atc gat gac ctc cca ttc tac tgc atc ggc     2784
Asp Gly Leu Lys Ser Lys Ile Asp Asp Leu Pro Phe Tyr Cys Ile Gly
        915                 920                 925

ttc aaa tcc gca gca ccc gag tat acg ctc cgg acg cgc atc tgg gcg     2832
Phe Lys Ser Ala Ala Pro Glu Tyr Thr Leu Arg Thr Arg Ile Trp Ala
    930                 935                 940

agc ctg cgc agc caa acc ttg tac cgg acg gtc agc ggc ttc atg aat     2880
Ser Leu Arg Ser Gln Thr Leu Tyr Arg Thr Val Ser Gly Phe Met Asn
945                 950                 955                 960

tac gcc cgc gcg ata aaa ctg ctc tat agg gtc gag aac ccg gag ctc     2928
Tyr Ala Arg Ala Ile Lys Leu Leu Tyr Arg Val Glu Asn Pro Glu Leu
                965                 970                 975

gtc cag tat ttt ggc ggc gac ccc gag ggc ctg gag ctg gcg ctg gag     2976
Val Gln Tyr Phe Gly Gly Asp Pro Glu Gly Leu Glu Leu Ala Leu Glu
            980                 985                 990

cgc atg gcg cgc cgc aaa ttc cgc  ttc ctc gtg agc atg  cag cgc ctg   3024
Arg Met Ala Arg Arg Lys Phe Arg  Phe Leu Val Ser Met  Gln Arg Leu
        995                 1000                1005

tcg aag  ttc aaa gac gat gag  atg gag aat gct gaa  ttc ctc ctg      3069
Ser Lys  Phe Lys Asp Asp Glu  Met Glu Asn Ala Glu  Phe Leu Leu
    1010                1015                1020

cgg gcc  tac ccg gac ctc cag  atc gcg tat ctc gac  gaa gaa ccg      3114
Arg Ala  Tyr Pro Asp Leu Gln  Ile Ala Tyr Leu Asp  Glu Glu Pro
    1025                1030                1035

gcg ctg  aat gag gac gag gaa  ccg cgc gtg tac agc  gca ctg atc      3159
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Ala Leu  Asn Glu Asp Glu Glu  Pro Arg Val Tyr Ser  Ala Leu Ile
    1040                1045                1050

gac gga  cac tgc gag atg ctg  gag aac ggc agg cgc  agg ccg aag      3204
Asp Gly  His Cys Glu Met Leu  Glu Asn Gly Arg Arg  Arg Pro Lys
    1055                1060                1065

ttt cgc  gtc cag ttg tcg ggc  aac ccg atc ctc ggc  gat ggt aag      3249
Phe Arg  Val Gln Leu Ser Gly  Asn Pro Ile Leu Gly  Asp Gly Lys
    1070                1075                1080

tcc gac  aac cag aat cac gcc  gtc atc ttc cat cgc  ggc gag tat      3294
Ser Asp  Asn Gln Asn His Ala  Val Ile Phe His Arg  Gly Glu Tyr
    1085                1090                1095

atc cag  ctg atc gac gcg aac  cag gac aac tat ctg  gaa gag tgc      3339
Ile Gln  Leu Ile Asp Ala Asn  Gln Asp Asn Tyr Leu  Glu Glu Cys
    1100                1105                1110

ctg aag  atc cgc tcg gtc ctg  gct gaa ttc gaa gag  atg aac gtc      3384
Leu Lys  Ile Arg Ser Val Leu  Ala Glu Phe Glu Glu  Met Asn Val
    1115                1120                1125

gag cat  gtt aat ccg tac gcc  ccg aat ttg aaa tcc  gag gac aac      3429
Glu His  Val Asn Pro Tyr Ala  Pro Asn Leu Lys Ser  Glu Asp Asn
    1130                1135                1140

aac acg  aag aaa gac ccg gtc  gcc ttc ctg ggc gca  cgc gag tac      3474
Asn Thr  Lys Lys Asp Pro Val  Ala Phe Leu Gly Ala  Arg Glu Tyr
    1145                1150                1155

atc ttc  agt gag aac tcg ggc  gtg ctg ggc gac gtg  gct gcg ggc      3519
Ile Phe  Ser Glu Asn Ser Gly  Val Leu Gly Asp Val  Ala Ala Gly
    1160                1165                1170

aaa gag  cag acg ttt ggc acc  ctg ttc gcc cgg acc  ctc gcg cag      3564
Lys Glu  Gln Thr Phe Gly Thr  Leu Phe Ala Arg Thr  Leu Ala Gln
    1175                1180                1185

atc ggc  ggg aag ctc cac tat  ggc cat ccc gac ttc  ctg aat gcg      3609
Ile Gly  Gly Lys Leu His Tyr  Gly His Pro Asp Phe  Leu Asn Ala
    1190                1195                1200

acg ttc  atg ctc acg cgc ggg  ggc gtg tcc aaa gcc  cag aag ggc      3654
Thr Phe  Met Leu Thr Arg Gly  Gly Val Ser Lys Ala  Gln Lys Gly
    1205                1210                1215

ctg cac  ctc aac gaa gat atc  tat gcg ggt atg aat  gcg atg atg      3699
Leu His  Leu Asn Glu Asp Ile  Tyr Ala Gly Met Asn  Ala Met Met
    1220                1225                1230

cgg ggt  ggc aag atc aag cac  tgc gag tac tac cag  tgc ggt aag      3744
Arg Gly  Gly Lys Ile Lys His  Cys Glu Tyr Tyr Gln  Cys Gly Lys
    1235                1240                1245

ggc agg  gat ctt ggc ttc ggc  tcc atc ctc aac ttc  acc acc aag      3789
Gly Arg  Asp Leu Gly Phe Gly  Ser Ile Leu Asn Phe  Thr Thr Lys
    1250                1255                1260

atc ggg  gcc ggc atg ggc gag  caa atg ctc tcg cgg  gag tac ttt      3834
Ile Gly  Ala Gly Met Gly Glu  Gln Met Leu Ser Arg  Glu Tyr Phe
    1265                1270                1275

tat ctg  ggt acc cag ctt ccc  ctt gac cgc ttc ctc  tcg ttc tac      3879
Tyr Leu  Gly Thr Gln Leu Pro  Leu Asp Arg Phe Leu  Ser Phe Tyr
    1280                1285                1290

tac ggg  cat ccg gga ttc cac  atc aac aac ctc ttc  atc caa ctg      3924
Tyr Gly  His Pro Gly Phe His  Ile Asn Asn Leu Phe  Ile Gln Leu
    1295                1300                1305

agc ctc  caa gtg ttc atc ctt  gtg ctt ggc aat ctg  aat tcg ctg      3969
Ser Leu  Gln Val Phe Ile Leu  Val Leu Gly Asn Leu  Asn Ser Leu
    1310                1315                1320

gcc cac  gag gcc atc atg tgt  tcg tac aac aaa gac  gtg ccc gtc      4014
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Ala His  Glu Ala Ile Met Cys  Ser Tyr Asn Lys Asp  Val Pro Val
    1325                 1330                 1335

act gac  gtg ctc tac ccc ttc  ggc tgt tac aat atc  gct ccc gcg      4059
Thr Asp  Val Leu Tyr Pro Phe  Gly Cys Tyr Asn Ile  Ala Pro Ala
    1340                 1345                 1350

gtg gat  tgg atc cgc cgg tat  acc ctc tcg atc ttc  att gtc ttt      4104
Val Asp  Trp Ile Arg Arg Tyr  Thr Leu Ser Ile Phe  Ile Val Phe
    1355                 1360                 1365

ttc atc  tcg ttc atc ccg ctg  gtc gtc cag gag ctc  ata gag cgg      4149
Phe Ile  Ser Phe Ile Pro Leu  Val Val Gln Glu Leu  Ile Glu Arg
    1370                 1375                 1380

gga gtg  tgg aag gct ttc cag  cgg ttc gtc cgg cat  ttc atc tcg      4194
Gly Val  Trp Lys Ala Phe Gln  Arg Phe Val Arg His  Phe Ile Ser
    1385                 1390                 1395

atg tcc  ccg ttc ttc gag gtg  ttc gtg gcg cag ata  tat tcg agc      4239
Met Ser  Pro Phe Phe Glu Val  Phe Val Ala Gln Ile  Tyr Ser Ser
    1400                 1405                 1410

tcc gtg  ttc acg gac ctc acc  gtg ggt ggg gcg agg  tat atc agc      4284
Ser Val  Phe Thr Asp Leu Thr  Val Gly Gly Ala Arg  Tyr Ile Ser
    1415                 1420                 1425

acc ggg  cgc ggg ttc gcc acc  tcg cgc atc ccg ttt  tcg atc aag      4329
Thr Gly  Arg Gly Phe Ala Thr  Ser Arg Ile Pro Phe  Ser Ile Lys
    1430                 1435                 1440

cgc ttt  gcg gat tcg agt atc  tat atg ggc gct cgg  ctc atg ctc      4374
Arg Phe  Ala Asp Ser Ser Ile  Tyr Met Gly Ala Arg  Leu Met Leu
    1445                 1450                 1455

atc ctg  ctt ttc ggt acc gtg  agc cac tgg caa gcg  ccg ctt ctc      4419
Ile Leu  Leu Phe Gly Thr Val  Ser His Trp Gln Ala  Pro Leu Leu
    1460                 1465                 1470

tgg ttc  tgg gcc tcg ctc tcc  gcg ttg atg ttc tcc  ccg ttc atc      4464
Trp Phe  Trp Ala Ser Leu Ser  Ala Leu Met Phe Ser  Pro Phe Ile
    1475                 1480                 1485

ttt aac  ccg cat cag ttc gcg  tgg gaa gat ttc ttt  ctc gac tat      4509
Phe Asn  Pro His Gln Phe Ala  Trp Glu Asp Phe Phe  Leu Asp Tyr
    1490                 1495                 1500

cgc gat  ttc atc cgc tgg ctg  tcc cgc gga aac acc  aag tgg cat      4554
Arg Asp  Phe Ile Arg Trp Leu  Ser Arg Gly Asn Thr  Lys Trp His
    1505                 1510                 1515

cgg aac  agc tgg atc ggc tac  gtt cgc ctc tcg cgg  tcg cgc ata      4599
Arg Asn  Ser Trp Ile Gly Tyr  Val Arg Leu Ser Arg  Ser Arg Ile
    1520                 1525                 1530

acg ggc  ttc aag cgg aaa ctc  acc ggc gac gtg agc  gag aaa gcc      4644
Thr Gly  Phe Lys Arg Lys Leu  Thr Gly Asp Val Ser  Glu Lys Ala
    1535                 1540                 1545

gct ggc  gat gcc tcc agg gct  cat cgc tcg aat gtg  ctg ttc gcg      4689
Ala Gly  Asp Ala Ser Arg Ala  His Arg Ser Asn Val  Leu Phe Ala
    1550                 1555                 1560

gac ttc  ctg ccg acc ctg ata  tac act gcg ggc ctc  tac gtc gcc      4734
Asp Phe  Leu Pro Thr Leu Ile  Tyr Thr Ala Gly Leu  Tyr Val Ala
    1565                 1570                 1575

tat acc  ttc atc aac gcc cag  acg ggc gtc acc agc  tat ccc tac      4779
Tyr Thr  Phe Ile Asn Ala Gln  Thr Gly Val Thr Ser  Tyr Pro Tyr
    1580                 1585                 1590

gag atc  aat ggc tcg acg gac  ccg caa cca gtt aac  tcc acg ctg      4824
Glu Ile  Asn Gly Ser Thr Asp  Pro Gln Pro Val Asn  Ser Thr Leu
    1595                 1600                 1605

agg ctc  atc atc tgc gcc ctg  gca cct gtc gtc atc  gac atg ggc      4869
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Arg Leu  Ile Ile Cys Ala Leu  Ala Pro Val Val Ile  Asp Met Gly
    1610                 1615                 1620

tgc ctg  ggt gtg tgc ctc gcc  atg gcg tgc tgc gcc  ggc ccg atg      4914
Cys Leu  Gly Val Cys Leu Ala  Met Ala Cys Cys Ala  Gly Pro Met
    1625                 1630                 1635

ctg ggc  ctg tgc tgc aag aaa  acc ggc gca gtc atc  gcc ggt gtc      4959
Leu Gly  Leu Cys Cys Lys Lys  Thr Gly Ala Val Ile  Ala Gly Val
    1640                 1645                 1650

gcg cac  ggc gtc gcc gtc atc  gtc cat atc atc ttc  ttc atc gtg      5004
Ala His  Gly Val Ala Val Ile  Val His Ile Ile Phe  Phe Ile Val
    1655                 1660                 1665

atg tgg  gtg act gag ggt ttc  aat ttc gca cgc ctg  atg ctt ggc      5049
Met Trp  Val Thr Glu Gly Phe  Asn Phe Ala Arg Leu  Met Leu Gly
    1670                 1675                 1680

atc gcg  acc atg atc tat gtg  cag agg ctg ctt ttc  aag ttc ctg      5094
Ile Ala  Thr Met Ile Tyr Val  Gln Arg Leu Leu Phe  Lys Phe Leu
    1685                 1690                 1695

acg ctg  tgc ttc ctc acc cgg  gag ttc aag aac gac  aaa gcc aac      5139
Thr Leu  Cys Phe Leu Thr Arg  Glu Phe Lys Asn Asp  Lys Ala Asn
    1700                 1705                 1710

acc gcg  ttt tgg acg ggt aag  tgg tat aac acc ggc  atg ggc tgg      5184
Thr Ala  Phe Trp Thr Gly Lys  Trp Tyr Asn Thr Gly  Met Gly Trp
    1715                 1720                 1725

atg gcc  ttc acg cag ccg agc  cgc gag ttc gtg gcc  aag atc atc      5229
Met Ala  Phe Thr Gln Pro Ser  Arg Glu Phe Val Ala  Lys Ile Ile
    1730                 1735                 1740

gag atg  agc gag ttc gcg ggt  gat ttc gtc ctt gcc  cac ata atc      5274
Glu Met  Ser Glu Phe Ala Gly  Asp Phe Val Leu Ala  His Ile Ile
    1745                 1750                 1755

ctg ttc  tgc cag ctg ccg ctc  ctg ttc att ccg ttg  gtc gac cgc      5319
Leu Phe  Cys Gln Leu Pro Leu  Leu Phe Ile Pro Leu  Val Asp Arg
    1760                 1765                 1770

tgg cat  agc atg atg ctg ttc  tgg ctg aag ccg tcc  cgc ctc att      5364
Trp His  Ser Met Met Leu Phe  Trp Leu Lys Pro Ser  Arg Leu Ile
    1775                 1780                 1785

cgg cca  cct atc tac tcg ctc  aaa caa gcg cgc ctg  cgc aag cgg      5409
Arg Pro  Pro Ile Tyr Ser Leu  Lys Gln Ala Arg Leu  Arg Lys Arg
    1790                 1795                 1800

atg gtc  cgc aaa tac tgt gtc  ctg tat ttc gca gtg  ctt atc ctg      5454
Met Val  Arg Lys Tyr Cys Val  Leu Tyr Phe Ala Val  Leu Ile Leu
    1805                 1810                 1815

ttc atc  gtt atc atc gtc gcg  cct gcg gtc gca tcg  ggg cag atc      5499
Phe Ile  Val Ile Ile Val Ala  Pro Ala Val Ala Ser  Gly Gln Ile
    1820                 1825                 1830

gcg gtg  gac cag ttc gcc aac  att ggc ggc agc ggc  tcc ata gca      5544
Ala Val  Asp Gln Phe Ala Asn  Ile Gly Gly Ser Gly  Ser Ile Ala
    1835                 1840                 1845

gac ggc  ttg ttc caa ccc cgg  aat gtg agc aac aac  gac acc ggg      5589
Asp Gly  Leu Phe Gln Pro Arg  Asn Val Ser Asn Asn  Asp Thr Gly
    1850                 1855                 1860

aat cat  cgc cca aag acc tac  acc tgg tcc tac ctc  tcg acc cgc      5634
Asn His  Arg Pro Lys Thr Tyr  Thr Trp Ser Tyr Leu  Ser Thr Arg
    1865                 1870                 1875

ttc acc  ggc tcg acc acc ccc  tac tcc acc aat ccc  ttc agg gtg      5679
Phe Thr  Gly Ser Thr Thr Pro  Tyr Ser Thr Asn Pro  Phe Arg Val
    1880                 1885                 1890
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<210> SEQ ID NO 10
<211> LENGTH: 1893
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 10

Met Ser Tyr Asn Asp Asn Asn Asn His Tyr Tyr Asp Pro Asn Gln Gln
1 5 10 15

Gly Gly Met Pro Pro His Gln Gly Gly Glu Gly Tyr Tyr Gln Gln Gln
20 25 30

Tyr Asp Asp Met Gly Gln Gln Pro His Gln Gln Asp Tyr Tyr Asp Pro
35 40 45

Asn Ala Gln Tyr Gln Gln Gln Pro Tyr Asp Met Asp Gly Tyr Gln Asp
50 55 60

Gln Ala Asn Tyr Gly Gly Gln Pro Met Asn Ala Gln Gly Tyr Asn Ala
65 70 75 80

Asp Pro Glu Ala Phe Ser Asp Phe Ser Tyr Gly Gly Gln Thr Pro Gly
85 90 95

Thr Pro Gly Tyr Asp Gln Tyr Gly Thr Gln Tyr Thr Pro Ser Gln Met
100 105 110

Ser Tyr Gly Gly Asp Pro Arg Ser Ser Gly Ala Ser Thr Pro Ile Tyr
115 120 125

Gly Gly Gln Gly Gln Gly Tyr Asp Pro Thr Gln Phe Asn Met Ser Ser
130 135 140

Asn Leu Pro Tyr Pro Ala Trp Ser Ala Asp Pro Gln Ala Pro Ile Lys
145 150 155 160

Ile Glu His Ile Glu Asp Ile Phe Ile Asp Leu Thr Asn Lys Phe Gly
165 170 175

Phe Gln Arg Asp Ser Met Arg Asn Met Phe Asp Tyr Phe Met Thr Leu
180 185 190

Leu Asp Ser Arg Ser Ser Arg Met Ser Pro Ala Gln Ala Leu Leu Ser
195 200 205

Leu His Ala Asp Tyr Ile Gly Gly Asp Asn Ala Asn Tyr Arg Lys Trp
210 215 220

Tyr Phe Ser Ser Gln Gln Asp Leu Asp Asp Ser Leu Gly Phe Ala Asn
225 230 235 240

Met Thr Leu Gly Lys Ile Gly Arg Lys Ala Arg Lys Ala Ser Lys Lys
245 250 255

Ser Lys Lys Ala Arg Lys Ala Ala Glu Glu His Gly Gln Asp Val Asp
260 265 270

Ala Asn Glu Leu Glu Gly Asp Tyr Ser Leu Glu Ala Ala Glu Ile Arg
275 280 285

Trp Lys Ala Lys Met Asn Ser Leu Thr Pro Glu Glu Arg Val Arg Asp
290 295 300

Leu Ala Leu Tyr Leu Leu Ile Trp Gly Glu Ala Asn Gln Val Arg Phe
305 310 315 320

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

Asn Ser Pro Leu Cys Gln Gln Arg Gln Glu Pro Val Pro Glu Gly Asp
340 345 350

Tyr Leu Asn Arg Val Ile Thr Pro Leu Tyr Arg Phe Ile Arg Ser Gln

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        355                 360                 365

Val Tyr Glu Ile Tyr Asp Gly Arg Phe Val Lys Arg Glu Lys Asp His
    370                 375                 380

Asn Lys Val Ile Gly Tyr Asp Asp Val Asn Gln Leu Phe Trp Tyr Pro
385                 390                 395                 400

Glu Gly Ile Ser Arg Ile Ile Phe Glu Asp Gly Thr Arg Leu Val Asp
                405                 410                 415

Ile Pro Gln Glu Glu Arg Phe Leu Lys Leu Gly Glu Val Glu Trp Lys
            420                 425                 430

Asn Val Phe Phe Lys Thr Tyr Lys Glu Ile Arg Thr Trp Leu His Phe
        435                 440                 445

Val Thr Asn Phe Asn Arg Ile Trp Ile Ile His Gly Thr Ile Tyr Trp
    450                 455                 460

Met Tyr Thr Ala Tyr Asn Ser Pro Thr Leu Tyr Thr Lys His Tyr Val
465                 470                 475                 480

Gln Thr Ile Asn Gln Gln Pro Leu Ala Ser Ser Arg Trp Ala Ala Cys
                485                 490                 495

Ala Ile Gly Gly Val Leu Ala Ser Phe Ile Gln Ile Leu Ala Thr Leu
            500                 505                 510

Phe Glu Trp Ile Phe Val Pro Arg Glu Trp Ala Gly Ala Gln His Leu
        515                 520                 525

Ser Arg Arg Met Leu Phe Leu Val Leu Ile Phe Leu Leu Asn Leu Val
    530                 535                 540

Pro Pro Val Tyr Thr Phe Gln Ile Thr Lys Leu Val Ile Tyr Ser Lys
545                 550                 555                 560

Ser Ala Tyr Ala Val Ser Ile Val Gly Phe Phe Ile Ala Val Ala Thr
                565                 570                 575

Leu Val Phe Phe Ala Val Met Pro Leu Gly Gly Leu Phe Thr Ser Tyr
            580                 585                 590

Met Asn Lys Arg Ser Arg Arg Tyr Ile Ala Ser Gln Thr Phe Thr Ala
        595                 600                 605

Asn Tyr Ile Lys Leu Lys Gly Leu Asp Met Trp Met Ser Tyr Leu Leu
    610                 615                 620

Trp Phe Leu Val Phe Leu Ala Lys Leu Val Glu Ser Tyr Phe Phe Ser
625                 630                 635                 640

Thr Leu Ser Leu Arg Asp Pro Ile Arg Asn Leu Ser Thr Met Thr Met
                645                 650                 655

Arg Cys Val Gly Glu Val Trp Tyr Lys Asp Ile Val Cys Arg Asn Gln
            660                 665                 670

Ala Lys Ile Val Leu Gly Leu Met Tyr Leu Val Asp Leu Leu Leu Phe
        675                 680                 685

Phe Leu Asp Thr Tyr Met Trp Tyr Ile Ile Cys Asn Cys Ile Phe Ser
    690                 695                 700

Ile Gly Arg Ser Phe Tyr Leu Gly Ile Ser Ile Leu Thr Pro Trp Arg
705                 710                 715                 720

Asn Ile Phe Thr Arg Leu Pro Lys Arg Ile Tyr Ser Lys Ile Leu Ala
                725                 730                 735

Thr Thr Glu Met Glu Ile Lys Tyr Lys Pro Lys Val Leu Ile Ser Gln
            740                 745                 750

Ile Trp Asn Ala Ile Val Ile Ser Met Tyr Arg Glu His Leu Leu Ala
        755                 760                 765
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Ile Asp His Val Gln Lys Leu Leu Tyr His Gln Val Pro Ser Glu Ile
    770                 775                 780

Glu Gly Lys Arg Thr Leu Arg Ala Pro Thr Phe Phe Val Ser Gln Asp
785                 790                 795                 800

Asp Asn Asn Phe Glu Thr Glu Phe Phe Pro Arg Asn Ser Glu Ala Glu
                805                 810                 815

Arg Arg Ile Ser Phe Phe Ala Gln Ser Leu Ala Thr Pro Met Pro Glu
            820                 825                 830

Pro Leu Pro Val Asp Asn Met Pro Thr Phe Thr Val Phe Thr Pro His
        835                 840                 845

Tyr Ser Glu Lys Ile Leu Leu Ser Leu Arg Glu Ile Ile Arg Glu Asp
    850                 855                 860

Asp Gln Phe Ser Arg Val Thr Leu Leu Glu Tyr Leu Lys Gln Leu His
865                 870                 875                 880

Pro Val Glu Trp Asp Cys Phe Val Lys Asp Thr Lys Ile Leu Ala Glu
                885                 890                 895

Glu Thr Ala Ala Tyr Glu Asn Gly Asp Asp Ser Glu Lys Leu Ser Glu
            900                 905                 910

Asp Gly Leu Lys Ser Lys Ile Asp Asp Leu Pro Phe Tyr Cys Ile Gly
        915                 920                 925

Phe Lys Ser Ala Ala Pro Glu Tyr Thr Leu Arg Thr Arg Ile Trp Ala
    930                 935                 940

Ser Leu Arg Ser Gln Thr Leu Tyr Arg Thr Val Ser Gly Phe Met Asn
945                 950                 955                 960

Tyr Ala Arg Ala Ile Lys Leu Leu Tyr Arg Val Glu Asn Pro Glu Leu
                965                 970                 975

Val Gln Tyr Phe Gly Gly Asp Pro Glu Gly Leu Glu Leu Ala Leu Glu
            980                 985                 990

Arg Met Ala Arg Arg Lys Phe Arg  Phe Leu Val Ser Met  Gln Arg Leu
        995                 1000                1005

Ser Lys  Phe Lys Asp Asp Glu  Met Glu Asn Ala Glu  Phe Leu Leu
    1010                1015                1020

Arg Ala  Tyr Pro Asp Leu Gln  Ile Ala Tyr Leu Asp  Glu Glu Pro
    1025                1030                1035

Ala Leu  Asn Glu Asp Glu Glu  Pro Arg Val Tyr Ser  Ala Leu Ile
    1040                1045                1050

Asp Gly  His Cys Glu Met Leu  Glu Asn Gly Arg Arg  Arg Pro Lys
    1055                1060                1065

Phe Arg  Val Gln Leu Ser Gly  Asn Pro Ile Leu Gly  Asp Gly Lys
    1070                1075                1080

Ser Asp  Asn Gln Asn His Ala  Val Ile Phe His Arg  Gly Glu Tyr
    1085                1090                1095

Ile Gln  Leu Ile Asp Ala Asn  Gln Asp Asn Tyr Leu  Glu Glu Cys
    1100                1105                1110

Leu Lys  Ile Arg Ser Val Leu  Ala Glu Phe Glu Glu  Met Asn Val
    1115                1120                1125

Glu His  Val Asn Pro Tyr Ala  Pro Asn Leu Lys Ser  Glu Asp Asn
    1130                1135                1140

Asn Thr  Lys Lys Asp Pro Val  Ala Phe Leu Gly Ala  Arg Glu Tyr
    1145                1150                1155
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Ile Phe  Ser Glu Asn Ser Gly  Val Leu Gly Asp Val  Ala Ala Gly
    1160                 1165                 1170

Lys Glu  Gln Thr Phe Gly Thr  Leu Phe Ala Arg Thr  Leu Ala Gln
    1175                 1180                 1185

Ile Gly  Gly Lys Leu His Tyr  Gly His Pro Asp Phe  Leu Asn Ala
    1190                 1195                 1200

Thr Phe  Met Leu Thr Arg Gly  Gly Val Ser Lys Ala  Gln Lys Gly
    1205                 1210                 1215

Leu His  Leu Asn Glu Asp Ile  Tyr Ala Gly Met Asn  Ala Met Met
    1220                 1225                 1230

Arg Gly  Gly Lys Ile Lys His  Cys Glu Tyr Tyr Gln  Cys Gly Lys
    1235                 1240                 1245

Gly Arg  Asp Leu Gly Phe Gly  Ser Ile Leu Asn Phe  Thr Thr Lys
    1250                 1255                 1260

Ile Gly  Ala Gly Met Gly Glu  Gln Met Leu Ser Arg  Glu Tyr Phe
    1265                 1270                 1275

Tyr Leu  Gly Thr Gln Leu Pro  Leu Asp Arg Phe Leu  Ser Phe Tyr
    1280                 1285                 1290

Tyr Gly  His Pro Gly Phe His  Ile Asn Asn Leu Phe  Ile Gln Leu
    1295                 1300                 1305

Ser Leu  Gln Val Phe Ile Leu  Val Leu Gly Asn Leu  Asn Ser Leu
    1310                 1315                 1320

Ala His  Glu Ala Ile Met Cys  Ser Tyr Asn Lys Asp  Val Pro Val
    1325                 1330                 1335

Thr Asp  Val Leu Tyr Pro Phe  Gly Cys Tyr Asn Ile  Ala Pro Ala
    1340                 1345                 1350

Val Asp  Trp Ile Arg Arg Tyr  Thr Leu Ser Ile Phe  Ile Val Phe
    1355                 1360                 1365

Phe Ile  Ser Phe Ile Pro Leu  Val Val Gln Glu Leu  Ile Glu Arg
    1370                 1375                 1380

Gly Val  Trp Lys Ala Phe Gln  Arg Phe Val Arg His  Phe Ile Ser
    1385                 1390                 1395

Met Ser  Pro Phe Phe Glu Val  Phe Val Ala Gln Ile  Tyr Ser Ser
    1400                 1405                 1410

Ser Val  Phe Thr Asp Leu Thr  Val Gly Gly Ala Arg  Tyr Ile Ser
    1415                 1420                 1425

Thr Gly  Arg Gly Phe Ala Thr  Ser Arg Ile Pro Phe  Ser Ile Lys
    1430                 1435                 1440

Arg Phe  Ala Asp Ser Ser Ile  Tyr Met Gly Ala Arg  Leu Met Leu
    1445                 1450                 1455

Ile Leu  Leu Phe Gly Thr Val  Ser His Trp Gln Ala  Pro Leu Leu
    1460                 1465                 1470

Trp Phe  Trp Ala Ser Leu Ser  Ala Leu Met Phe Ser  Pro Phe Ile
    1475                 1480                 1485

Phe Asn  Pro His Gln Phe Ala  Trp Glu Asp Phe Phe  Leu Asp Tyr
    1490                 1495                 1500

Arg Asp  Phe Ile Arg Trp Leu  Ser Arg Gly Asn Thr  Lys Trp His
    1505                 1510                 1515

Arg Asn  Ser Trp Ile Gly Tyr  Val Arg Leu Ser Arg  Ser Arg Ile
    1520                 1525                 1530

Thr Gly  Phe Lys Arg Lys Leu  Thr Gly Asp Val Ser  Glu Lys Ala
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    1535                1540                1545

Ala Gly  Asp Ala Ser Arg Ala  His Arg Ser Asn Val  Leu Phe Ala
    1550                1555                1560

Asp Phe  Leu Pro Thr Leu Ile  Tyr Thr Ala Gly Leu  Tyr Val Ala
    1565                1570                1575

Tyr Thr  Phe Ile Asn Ala Gln  Thr Gly Val Thr Ser  Tyr Pro Tyr
    1580                1585                1590

Glu Ile  Asn Gly Ser Thr Asp  Pro Gln Pro Val Asn  Ser Thr Leu
    1595                1600                1605

Arg Leu  Ile Ile Cys Ala Leu  Ala Pro Val Val Ile  Asp Met Gly
    1610                1615                1620

Cys Leu  Gly Val Cys Leu Ala  Met Ala Cys Cys Ala  Gly Pro Met
    1625                1630                1635

Leu Gly  Leu Cys Cys Lys Lys  Thr Gly Ala Val Ile  Ala Gly Val
    1640                1645                1650

Ala His  Gly Val Ala Val Ile  Val His Ile Ile Phe  Phe Ile Val
    1655                1660                1665

Met Trp  Val Thr Glu Gly Phe  Asn Phe Ala Arg Leu  Met Leu Gly
    1670                1675                1680

Ile Ala  Thr Met Ile Tyr Val  Gln Arg Leu Leu Phe  Lys Phe Leu
    1685                1690                1695

Thr Leu  Cys Phe Leu Thr Arg  Glu Phe Lys Asn Asp  Lys Ala Asn
    1700                1705                1710

Thr Ala  Phe Trp Thr Gly Lys  Trp Tyr Asn Thr Gly  Met Gly Trp
    1715                1720                1725

Met Ala  Phe Thr Gln Pro Ser  Arg Glu Phe Val Ala  Lys Ile Ile
    1730                1735                1740

Glu Met  Ser Glu Phe Ala Gly  Asp Phe Val Leu Ala  His Ile Ile
    1745                1750                1755

Leu Phe  Cys Gln Leu Pro Leu  Leu Phe Ile Pro Leu  Val Asp Arg
    1760                1765                1770

Trp His  Ser Met Met Leu Phe  Trp Leu Lys Pro Ser  Arg Leu Ile
    1775                1780                1785

Arg Pro  Pro Ile Tyr Ser Leu  Lys Gln Ala Arg Leu  Arg Lys Arg
    1790                1795                1800

Met Val  Arg Lys Tyr Cys Val  Leu Tyr Phe Ala Val  Leu Ile Leu
    1805                1810                1815

Phe Ile  Val Ile Ile Val Ala  Pro Ala Val Ala Ser  Gly Gln Ile
    1820                1825                1830

Ala Val  Asp Gln Phe Ala Asn  Ile Gly Gly Ser Gly  Ser Ile Ala
    1835                1840                1845

Asp Gly  Leu Phe Gln Pro Arg  Asn Val Ser Asn Asn  Asp Thr Gly
    1850                1855                1860

Asn His  Arg Pro Lys Thr Tyr  Thr Trp Ser Tyr Leu  Ser Thr Arg
    1865                1870                1875

Phe Thr  Gly Ser Thr Thr Pro  Tyr Ser Thr Asn Pro  Phe Arg Val
    1880                1885                1890


<210> SEQ ID NO 11
<211> LENGTH: 171
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
```

-continued

<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(171)
<223> OTHER INFORMATION: Zea mays (corn) portion of 1,3-D-glucan synthase (codon optimized)

<400> SEQUENCE: 11

```
ttc aac tgt acc ctc cgc ggc ggc aat gtt acc cat cac gaa tat atc       48
Phe Asn Cys Thr Leu Arg Gly Gly Asn Val Thr His His Glu Tyr Ile
1               5                   10                  15

caa gtc ggc aaa gga cgc gac gtc ggc ctg aat caa gtg tcg atg ttc       96
Gln Val Gly Lys Gly Arg Asp Val Gly Leu Asn Gln Val Ser Met Phe
            20                  25                  30

gag gcg aaa gtc gcc tcc ggt aac ggc gag cag acg ctg agc cgc gac      144
Glu Ala Lys Val Ala Ser Gly Asn Gly Glu Gln Thr Leu Ser Arg Asp
        35                  40                  45

gtg tac cgg ctc ggg cat cgg ctg gat                                  171
Val Tyr Arg Leu Gly His Arg Leu Asp
    50                  55
```

<210> SEQ ID NO 12
<211> LENGTH: 57
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 12

```
Phe Asn Cys Thr Leu Arg Gly Gly Asn Val Thr His His Glu Tyr Ile
1               5                   10                  15

Gln Val Gly Lys Gly Arg Asp Val Gly Leu Asn Gln Val Ser Met Phe
            20                  25                  30

Glu Ala Lys Val Ala Ser Gly Asn Gly Glu Gln Thr Leu Ser Arg Asp
        35                  40                  45

Val Tyr Arg Leu Gly His Arg Leu Asp
    50                  55
```

<210> SEQ ID NO 13
<211> LENGTH: 450
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(450)
<223> OTHER INFORMATION: Zea mays (corn): portion of 1,3-D-glucan synthase (codon optimized)

<400> SEQUENCE: 13

```
cag ctg aag cgc ctg cat ctc ctc ctc acc gtc aaa gac agc gcc acc       48
Gln Leu Lys Arg Leu His Leu Leu Leu Thr Val Lys Asp Ser Ala Thr
1               5                   10                  15

aac atc ccg aag aat ctt gag gcc cgg cgg cgc ctg cag ttc ttc acg       96
Asn Ile Pro Lys Asn Leu Glu Ala Arg Arg Arg Leu Gln Phe Phe Thr
            20                  25                  30

aac agc ctg ttc atg gat atc ccg caa gcg aag ccc gtg tcc gag atg      144
Asn Ser Leu Phe Met Asp Ile Pro Gln Ala Lys Pro Val Ser Glu Met
        35                  40                  45

atc ccg ttt tcg gtg ttc acc ccg tac tac tcg gag act gtt ctc tat      192
```

-continued

```
Ile Pro Phe Ser Val Phe Thr Pro Tyr Tyr Ser Glu Thr Val Leu Tyr
    50                  55                  60

tcc atg tcc gag ctg tgc gtc gag aat gag gac ggc atc agt att ctg      240
Ser Met Ser Glu Leu Cys Val Glu Asn Glu Asp Gly Ile Ser Ile Leu
65                  70                  75                  80

ttc tac ctc caa aag atc tat ccc gac gag tgg gca aac ttc ctg gag      288
Phe Tyr Leu Gln Lys Ile Tyr Pro Asp Glu Trp Ala Asn Phe Leu Glu
                85                  90                  95

cgc atc ggg tgc ggc gag tcg agc gaa gat gac ttc aaa gaa tcg ccg      336
Arg Ile Gly Cys Gly Glu Ser Ser Glu Asp Asp Phe Lys Glu Ser Pro
            100                 105                 110

tcc gac acg atg gaa ttg cgg ttc tgg gtg agc tac cgc ggt cag acc      384
Ser Asp Thr Met Glu Leu Arg Phe Trp Val Ser Tyr Arg Gly Gln Thr
        115                 120                 125

ctc ggc cgc acc gtc cgg ggc atg atg tat tac cgc agg gcg ctg atg      432
Leu Gly Arg Thr Val Arg Gly Met Met Tyr Tyr Arg Arg Ala Leu Met
    130                 135                 140

ctc cag tcg tat ctg gag                                             450
Leu Gln Ser Tyr Leu Glu
145                 150


<210> SEQ ID NO 14
<211> LENGTH: 150
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 14

Gln Leu Lys Arg Leu His Leu Leu Leu Thr Val Lys Asp Ser Ala Thr
1               5                   10                  15

Asn Ile Pro Lys Asn Leu Glu Ala Arg Arg Arg Leu Gln Phe Phe Thr
            20                  25                  30

Asn Ser Leu Phe Met Asp Ile Pro Gln Ala Lys Pro Val Ser Glu Met
        35                  40                  45

Ile Pro Phe Ser Val Phe Thr Pro Tyr Tyr Ser Glu Thr Val Leu Tyr
    50                  55                  60

Ser Met Ser Glu Leu Cys Val Glu Asn Glu Asp Gly Ile Ser Ile Leu
65                  70                  75                  80

Phe Tyr Leu Gln Lys Ile Tyr Pro Asp Glu Trp Ala Asn Phe Leu Glu
                85                  90                  95

Arg Ile Gly Cys Gly Glu Ser Ser Glu Asp Asp Phe Lys Glu Ser Pro
            100                 105                 110

Ser Asp Thr Met Glu Leu Arg Phe Trp Val Ser Tyr Arg Gly Gln Thr
        115                 120                 125

Leu Gly Arg Thr Val Arg Gly Met Met Tyr Tyr Arg Arg Ala Leu Met
    130                 135                 140

Leu Gln Ser Tyr Leu Glu
145                 150


<210> SEQ ID NO 15
<211> LENGTH: 405
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: CDS
```

-continued

<222> LOCATION: (1)..(405)
<223> OTHER INFORMATION: Oryza sativa (rice) portion of 1,3-beta-D-glucan synthase (codon optimized)

<400> SEQUENCE: 15

```
gag aac tat cgc ctc tac tcg cgc tcc cat ttc gtc aaa gca ctc gaa       48
Glu Asn Tyr Arg Leu Tyr Ser Arg Ser His Phe Val Lys Ala Leu Glu
1               5                   10                  15

gtt gcc ctg ctg ctc atc atc tat att gcg tac ggc tat acc cgg ggg       96
Val Ala Leu Leu Leu Ile Ile Tyr Ile Ala Tyr Gly Tyr Thr Arg Gly
            20                  25                  30

ggc tcc tcc agc ttc atc ctg ttg acc att agt tcg tgg ttc ctc gtc      144
Gly Ser Ser Ser Phe Ile Leu Leu Thr Ile Ser Ser Trp Phe Leu Val
        35                  40                  45

gtg tcg tgg ctg ttc gct ccc tac ata ttc aac ccg agc ggc ttt gag      192
Val Ser Trp Leu Phe Ala Pro Tyr Ile Phe Asn Pro Ser Gly Phe Glu
    50                  55                  60

tgg cag aaa acc gtc gag gac ttc gac gat tgg acg aat tgg ctc ctg      240
Trp Gln Lys Thr Val Glu Asp Phe Asp Asp Trp Thr Asn Trp Leu Leu
65                  70                  75                  80

tac aag ggc gga gtg ggc gtg aag ggt gag aat agc tgg gag tcc tgg      288
Tyr Lys Gly Gly Val Gly Val Lys Gly Glu Asn Ser Trp Glu Ser Trp
                85                  90                  95

tgg gac gag gaa cag gcg cat atc caa acg ctg agg ggt cgg atc ctt      336
Trp Asp Glu Glu Gln Ala His Ile Gln Thr Leu Arg Gly Arg Ile Leu
            100                 105                 110

gag act atc ctg tcg ctg cgc ttc ctc atc ttc cag tac ggc atc gtc      384
Glu Thr Ile Leu Ser Leu Arg Phe Leu Ile Phe Gln Tyr Gly Ile Val
        115                 120                 125

tat aag ctc aag atc gcc cac                                         405
Tyr Lys Leu Lys Ile Ala His
    130                 135
```

<210> SEQ ID NO 16
<211> LENGTH: 135
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 16

```
Glu Asn Tyr Arg Leu Tyr Ser Arg Ser His Phe Val Lys Ala Leu Glu
1               5                   10                  15

Val Ala Leu Leu Leu Ile Ile Tyr Ile Ala Tyr Gly Tyr Thr Arg Gly
            20                  25                  30

Gly Ser Ser Ser Phe Ile Leu Leu Thr Ile Ser Ser Trp Phe Leu Val
        35                  40                  45

Val Ser Trp Leu Phe Ala Pro Tyr Ile Phe Asn Pro Ser Gly Phe Glu
    50                  55                  60

Trp Gln Lys Thr Val Glu Asp Phe Asp Asp Trp Thr Asn Trp Leu Leu
65                  70                  75                  80

Tyr Lys Gly Gly Val Gly Val Lys Gly Glu Asn Ser Trp Glu Ser Trp
                85                  90                  95

Trp Asp Glu Glu Gln Ala His Ile Gln Thr Leu Arg Gly Arg Ile Leu
            100                 105                 110

Glu Thr Ile Leu Ser Leu Arg Phe Leu Ile Phe Gln Tyr Gly Ile Val
        115                 120                 125
```

-continued

```
Tyr Lys Leu Lys Ile Ala His
    130                 135


<210> SEQ ID NO 17
<211> LENGTH: 306
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(306)
<223> OTHER INFORMATION: Oryza sativa (rice)  portion of 1,3-beta-D-
      glucan synthase (codon optimized)

<400> SEQUENCE: 17

tgg gtc gtt gct ttc gcc atc ctg tac aaa gaa gcc tgg aac aac cgc       48
Trp Val Val Ala Phe Ala Ile Leu Tyr Lys Glu Ala Trp Asn Asn Arg
1               5                   10                  15

aat tcg aat agc caa atc atg cgc ttt ttg tat gca gcc gcg gtg ttc       96
Asn Ser Asn Ser Gln Ile Met Arg Phe Leu Tyr Ala Ala Ala Val Phe
            20                  25                  30

atg atc ccc gag gtc ctg gcg atc gtg ctg ttc atc gtc ccg tgg gtc      144
Met Ile Pro Glu Val Leu Ala Ile Val Leu Phe Ile Val Pro Trp Val
        35                  40                  45

cgg aac gcc ctg gag aaa acc aat tgg aag att tgc tat gcg ctc acc      192
Arg Asn Ala Leu Glu Lys Thr Asn Trp Lys Ile Cys Tyr Ala Leu Thr
    50                  55                  60

tgg tgg ttc cag agc cgc tcg ttc gtg ggt cgg ggc ctc cgc gag ggc      240
Trp Trp Phe Gln Ser Arg Ser Phe Val Gly Arg Gly Leu Arg Glu Gly
65                  70                  75                  80

acg ttc gac aac gtg aag tac tcc gtg ttc tgg gtc ctt ctc ctc gcg      288
Thr Phe Asp Asn Val Lys Tyr Ser Val Phe Trp Val Leu Leu Leu Ala
                85                  90                  95

gtc aag ttc gcg ttc tcc                                             306
Val Lys Phe Ala Phe Ser
            100


<210> SEQ ID NO 18
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 18

Trp Val Val Ala Phe Ala Ile Leu Tyr Lys Glu Ala Trp Asn Asn Arg
1               5                   10                  15

Asn Ser Asn Ser Gln Ile Met Arg Phe Leu Tyr Ala Ala Ala Val Phe
            20                  25                  30

Met Ile Pro Glu Val Leu Ala Ile Val Leu Phe Ile Val Pro Trp Val
        35                  40                  45

Arg Asn Ala Leu Glu Lys Thr Asn Trp Lys Ile Cys Tyr Ala Leu Thr
    50                  55                  60

Trp Trp Phe Gln Ser Arg Ser Phe Val Gly Arg Gly Leu Arg Glu Gly
65                  70                  75                  80

Thr Phe Asp Asn Val Lys Tyr Ser Val Phe Trp Val Leu Leu Leu Ala
                85                  90                  95

Val Lys Phe Ala Phe Ser
            100
```

-continued

<210> SEQ ID NO 19
<211> LENGTH: 435
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(435)
<223> OTHER INFORMATION: Gycine max (soy) portion of 1,3-beta-D-glucan synthase (codon optimized)

<400> SEQUENCE: 19

```
ttg agg tcc tcg gaa atg cgg aaa att ata gcc acg ctg cgc gct ctt       48
Leu Arg Ser Ser Glu Met Arg Lys Ile Ile Ala Thr Leu Arg Ala Leu
1               5                   10                  15

gtt gaa gtc ttg gaa tcc ctg tcg aag gac gcg gat ccg ggt ggc gtc       96
Val Glu Val Leu Glu Ser Leu Ser Lys Asp Ala Asp Pro Gly Gly Val
            20                  25                  30

ggt ggc ctg atc atg gaa gaa ctc cgg aag atc aag aaa tcg agt gtg      144
Gly Gly Leu Ile Met Glu Glu Leu Arg Lys Ile Lys Lys Ser Ser Val
        35                  40                  45

acc ctg tcg ggc gag ctc acc ccc tat aac atc att ccg ctt gag gcg      192
Thr Leu Ser Gly Glu Leu Thr Pro Tyr Asn Ile Ile Pro Leu Glu Ala
    50                  55                  60

ccg tcc ctc acc aat ccc atc cgg atc ttc ccc gag gtg aag gcc gcg      240
Pro Ser Leu Thr Asn Pro Ile Arg Ile Phe Pro Glu Val Lys Ala Ala
65                  70                  75                  80

atc agc gcg atc cgc tac acg gac cag ttc cca cgc ctc cct gcc ggc      288
Ile Ser Ala Ile Arg Tyr Thr Asp Gln Phe Pro Arg Leu Pro Ala Gly
                85                  90                  95

ttc aag atc agc ggg cag cgc gac gcg gat atg ttc gac ctc ctg gag      336
Phe Lys Ile Ser Gly Gln Arg Asp Ala Asp Met Phe Asp Leu Leu Glu
            100                 105                 110

ttc gtc ttt gga ttc cag aaa gac aac gtg cgc aac cag cgg gag aat      384
Phe Val Phe Gly Phe Gln Lys Asp Asn Val Arg Asn Gln Arg Glu Asn
        115                 120                 125

gtc gtg ctg atg atc gcc aac aag caa agc cgc ctc ggc atc ccg gca      432
Val Val Leu Met Ile Ala Asn Lys Gln Ser Arg Leu Gly Ile Pro Ala
    130                 135                 140

gag                                                                  435
Glu
145
```

<210> SEQ ID NO 20
<211> LENGTH: 145
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 20

```
Leu Arg Ser Ser Glu Met Arg Lys Ile Ile Ala Thr Leu Arg Ala Leu
1               5                   10                  15

Val Glu Val Leu Glu Ser Leu Ser Lys Asp Ala Asp Pro Gly Gly Val
            20                  25                  30

Gly Gly Leu Ile Met Glu Glu Leu Arg Lys Ile Lys Lys Ser Ser Val
        35                  40                  45

Thr Leu Ser Gly Glu Leu Thr Pro Tyr Asn Ile Ile Pro Leu Glu Ala
```

-continued

```
    50                  55                  60

Pro Ser Leu Thr Asn Pro Ile Arg Ile Phe Pro Glu Val Lys Ala Ala
65                  70                  75                  80

Ile Ser Ala Ile Arg Tyr Thr Asp Gln Phe Pro Arg Leu Pro Ala Gly
                85                  90                  95

Phe Lys Ile Ser Gly Gln Arg Asp Ala Asp Met Phe Asp Leu Leu Glu
            100                 105                 110

Phe Val Phe Gly Phe Gln Lys Asp Asn Val Arg Asn Gln Arg Glu Asn
        115                 120                 125

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

Glu
145
```

<210> SEQ ID NO 21
<211> LENGTH: 489
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(489)
<223> OTHER INFORMATION: Veronia mespilifolia 1,3-beta-D-glucan synthase (codon optimized)

<400> SEQUENCE: 21

```
tat ggc cat cca gat gtc ttt gac cgc gtt ttt cat att acc agg gga       48
Tyr Gly His Pro Asp Val Phe Asp Arg Val Phe His Ile Thr Arg Gly
1               5                   10                  15

gga atc agt aaa gct agc cgc gtg atc aat atc tcc gaa gat atc tat       96
Gly Ile Ser Lys Ala Ser Arg Val Ile Asn Ile Ser Glu Asp Ile Tyr
            20                  25                  30

gcc ggc ttc aat tcc acc ctg cgg caa ggc aat atc acc cac cac gag      144
Ala Gly Phe Asn Ser Thr Leu Arg Gln Gly Asn Ile Thr His His Glu
        35                  40                  45

tat atc cag gtc ggt aag ggc cgc gac gtc ggc ctg aac cag att gcc      192
Tyr Ile Gln Val Gly Lys Gly Arg Asp Val Gly Leu Asn Gln Ile Ala
    50                  55                  60

ctc ttc gag ggc aag gtc gcg ggc ggg aac ggc gag caa gtc ctc tcg      240
Leu Phe Glu Gly Lys Val Ala Gly Gly Asn Gly Glu Gln Val Leu Ser
65                  70                  75                  80

cgc gac atc tac cgc ctc ggc cag ctg ttc gac ttc ttc cgg atg ctg      288
Arg Asp Ile Tyr Arg Leu Gly Gln Leu Phe Asp Phe Phe Arg Met Leu
                85                  90                  95

tcg ttc tac ttc acg acc gtg ggg tac tat ttc tgc acc atg ctg acc      336
Ser Phe Tyr Phe Thr Thr Val Gly Tyr Tyr Phe Cys Thr Met Leu Thr
            100                 105                 110

gtg acg act gtg tac ata ttc ctc tat ggt aag acc tac ttg gcc ctg      384
Val Thr Thr Val Tyr Ile Phe Leu Tyr Gly Lys Thr Tyr Leu Ala Leu
        115                 120                 125

tcg ggt gtc ggc gag gac atc cag aac cgg agc gaa gtc ctc gac aac      432
Ser Gly Val Gly Glu Asp Ile Gln Asn Arg Ser Glu Val Leu Asp Asn
    130                 135                 140

aaa gcg ctt acc gca gcg ctg aac acg cag ttc ctc ttc cag atc ggc      480
Lys Ala Leu Thr Ala Ala Leu Asn Thr Gln Phe Leu Phe Gln Ile Gly
145                 150                 155                 160

gtg ttc acg                                                          489
```

-continued

```
Val Phe Thr

<210> SEQ ID NO 22
<211> LENGTH: 163
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 22

Tyr Gly His Pro Asp Val Phe Asp Arg Val Phe His Ile Thr Arg Gly
1               5                   10                  15

Gly Ile Ser Lys Ala Ser Arg Val Ile Asn Ile Ser Glu Asp Ile Tyr
            20                  25                  30

Ala Gly Phe Asn Ser Thr Leu Arg Gln Gly Asn Ile Thr His His Glu
        35                  40                  45

Tyr Ile Gln Val Gly Lys Gly Arg Asp Val Gly Leu Asn Gln Ile Ala
    50                  55                  60

Leu Phe Glu Gly Lys Val Ala Gly Gly Asn Gly Glu Gln Val Leu Ser
65                  70                  75                  80

Arg Asp Ile Tyr Arg Leu Gly Gln Leu Phe Asp Phe Phe Arg Met Leu
                85                  90                  95

Ser Phe Tyr Phe Thr Thr Val Gly Tyr Tyr Phe Cys Thr Met Leu Thr
            100                 105                 110

Val Thr Thr Val Tyr Ile Phe Leu Tyr Gly Lys Thr Tyr Leu Ala Leu
        115                 120                 125

Ser Gly Val Gly Glu Asp Ile Gln Asn Arg Ser Glu Val Leu Asp Asn
    130                 135                 140

Lys Ala Leu Thr Ala Ala Leu Asn Thr Gln Phe Leu Phe Gln Ile Gly
145                 150                 155                 160

Val Phe Thr


<210> SEQ ID NO 23
<211> LENGTH: 1467
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1467)
<223> OTHER INFORMATION: Triticum aestivum (wheat) 1,3-beta-D-glucan
      synthase (codon optimized)

<400> SEQUENCE: 23

cgc gtg ggg aag ggt agg gat gtc ggc ttg aat caa atc agt atg ttc       48
Arg Val Gly Lys Gly Arg Asp Val Gly Leu Asn Gln Ile Ser Met Phe
1               5                   10                  15

gaa gca aaa gtg gct ggg gga aat ggt gag cag act ctg tcc cgc gac       96
Glu Ala Lys Val Ala Gly Gly Asn Gly Glu Gln Thr Leu Ser Arg Asp
            20                  25                  30

gtc tac cgc ctt ggc cat ggc ctg gac ttc ttc cgg atg ctg agc ttc      144
Val Tyr Arg Leu Gly His Gly Leu Asp Phe Phe Arg Met Leu Ser Phe
        35                  40                  45

ttc tac acg acc atc ggc ttt tac ctc aat acc atg atg gtc gtc ctc      192
Phe Tyr Thr Thr Ile Gly Phe Tyr Leu Asn Thr Met Met Val Val Leu
    50                  55                  60

acg gtg tac gcc ttc gtg tgg ggt cgg ttc tac ctc gcg ctg tcg ggc      240
Thr Val Tyr Ala Phe Val Trp Gly Arg Phe Tyr Leu Ala Leu Ser Gly
```

-continued

```
65                  70                  75                  80

ctt gag gcc gac tat atc acc aat aac acc tcc tcg acc gat aat gcc      288
Leu Glu Ala Asp Tyr Ile Thr Asn Asn Thr Ser Ser Thr Asp Asn Ala
                85                  90                  95

gcg ctg tgg gca gtg ctc aac caa cag ttc ttc atc caa ttc ggc ctc      336
Ala Leu Trp Ala Val Leu Asn Gln Gln Phe Phe Ile Gln Phe Gly Leu
            100                 105                 110

ttc acg gcc ctc ccc atg atc atc gag aac tcc ctt gag cat ggc ttc      384
Phe Thr Ala Leu Pro Met Ile Ile Glu Asn Ser Leu Glu His Gly Phe
        115                 120                 125

ctc ata gcc gtc tgg gac ttc atc gtc atg cag ctg cag tgc gcg tcg      432
Leu Ile Ala Val Trp Asp Phe Ile Val Met Gln Leu Gln Cys Ala Ser
    130                 135                 140

gtg ttc tat acc ttc tgc atg ggc acc aag act cac tat tat ggc cgc      480
Val Phe Tyr Thr Phe Cys Met Gly Thr Lys Thr His Tyr Tyr Gly Arg
145                 150                 155                 160

acg ctg ctg cat ggt ggg gcc aag tac cgc cca acc ggt cgg ggc ttc      528
Thr Leu Leu His Gly Gly Ala Lys Tyr Arg Pro Thr Gly Arg Gly Phe
                165                 170                 175

gtg gtc gag cac aag aaa ttc gcc gag aac tac cgg ctg tat gcg cgc      576
Val Val Glu His Lys Lys Phe Ala Glu Asn Tyr Arg Leu Tyr Ala Arg
            180                 185                 190

agc cat ttc acc aag gct atc gag ctg ggc gtg atc ttg tgt ttg tat      624
Ser His Phe Thr Lys Ala Ile Glu Leu Gly Val Ile Leu Cys Leu Tyr
        195                 200                 205

tcc tcg tac agc aac atc gct ggc gac acc ctg gtg tat att ctg ctg      672
Ser Ser Tyr Ser Asn Ile Ala Gly Asp Thr Leu Val Tyr Ile Leu Leu
    210                 215                 220

acc ctc tcg tcg tgg ttt ctc gtc tgc tcc tgg atc ctc gcg ccg ttc      720
Thr Leu Ser Ser Trp Phe Leu Val Cys Ser Trp Ile Leu Ala Pro Phe
225                 230                 235                 240

atc ttc aac ccg agc gga ctc gat tgg cag aag aat tcc aac gac ttc      768
Ile Phe Asn Pro Ser Gly Leu Asp Trp Gln Lys Asn Ser Asn Asp Phe
                245                 250                 255

gag gat ttc ttc tcg tgg atc tgg ttt cag ggc ggc ggc atc agt gtc      816
Glu Asp Phe Phe Ser Trp Ile Trp Phe Gln Gly Gly Gly Ile Ser Val
            260                 265                 270

aag tcc gac cag agc tgg gag aag tgg tgg gag gaa gaa acc gac cat      864
Lys Ser Asp Gln Ser Trp Glu Lys Trp Trp Glu Glu Glu Thr Asp His
        275                 280                 285

ctg gcg cgg acg acg acc ggc ctg tgg ggc agc atc atc gag ata att      912
Leu Ala Arg Thr Thr Thr Gly Leu Trp Gly Ser Ile Ile Glu Ile Ile
    290                 295                 300

ctg gac ctg gcg cgc acc tac ttt ttc ttc cag tat gcg atc gtt tat      960
Leu Asp Leu Ala Arg Thr Tyr Phe Phe Phe Gln Tyr Ala Ile Val Tyr
305                 310                 315                 320

cgc ctc cac atg gcc ggt ggc agc cgc tcc atc ctg gtc tat gtg ctc     1008
Arg Leu His Met Ala Gly Gly Ser Arg Ser Ile Leu Val Tyr Val Leu
                325                 330                 335

tcg tgg gcg tgc atc ccg ctc ccg ttc ctg gcg ctg gtc acc gtg acg     1056
Ser Trp Ala Cys Ile Pro Leu Pro Phe Leu Ala Leu Val Thr Val Thr
            340                 345                 350

tac ttc cgc gac aag tac tcg gcc aag aaa cat atc cgg tac cgc ctt     1104
Tyr Phe Arg Asp Lys Tyr Ser Ala Lys Lys His Ile Arg Tyr Arg Leu
        355                 360                 365

gtt caa tcg gtg att gtc tgc gca agc ctg gcg gcg att atc gtg ctc     1152
Val Gln Ser Val Ile Val Cys Ala Ser Leu Ala Ala Ile Ile Val Leu
```

-continued

```
    370                 375                 380

ctc acc ctc acc aag ttc cag ttc atc gac acc ttc acc agc ctc ctg     1200
Leu Thr Leu Thr Lys Phe Gln Phe Ile Asp Thr Phe Thr Ser Leu Leu
385                 390                 395                 400

gcc ttt ctg ccc acc ggc tgg ggc atc atc tcc atc gcc ctg gtg ttc     1248
Ala Phe Leu Pro Thr Gly Trp Gly Ile Ile Ser Ile Ala Leu Val Phe
                405                 410                 415

cgc caa tat ctg aag aaa agc gac acg gtg tgg aaa acc gtc gtc gtg     1296
Arg Gln Tyr Leu Lys Lys Ser Asp Thr Val Trp Lys Thr Val Val Val
            420                 425                 430

gtc gcg cgg ttc tac gac atc acc ctc ggc ctg att gtt atg gcg ccg     1344
Val Ala Arg Phe Tyr Asp Ile Thr Leu Gly Leu Ile Val Met Ala Pro
        435                 440                 445

atc gtc gtc ctg tcg tgg ctc cct ggc ctc cgc gag ctg cag acg cgg     1392
Ile Val Val Leu Ser Trp Leu Pro Gly Leu Arg Glu Leu Gln Thr Arg
    450                 455                 460

atc ttg ttc aac gaa gcc ttc tcc aag ggc ctc cac atc tcg cag atg     1440
Ile Leu Phe Asn Glu Ala Phe Ser Lys Gly Leu His Ile Ser Gln Met
465                 470                 475                 480

atc acg cgc agg aaa acg cat cgc gcc                                 1467
Ile Thr Arg Arg Lys Thr His Arg Ala
                485


<210> SEQ ID NO 24
<211> LENGTH: 489
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 24

Arg Val Gly Lys Gly Arg Asp Val Gly Leu Asn Gln Ile Ser Met Phe
1               5                   10                  15

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

Val Tyr Arg Leu Gly His Gly Leu Asp Phe Phe Arg Met Leu Ser Phe
        35                  40                  45

Phe Tyr Thr Thr Ile Gly Phe Tyr Leu Asn Thr Met Met Val Val Leu
    50                  55                  60

Thr Val Tyr Ala Phe Val Trp Gly Arg Phe Tyr Leu Ala Leu Ser Gly
65                  70                  75                  80

Leu Glu Ala Asp Tyr Ile Thr Asn Asn Thr Ser Ser Thr Asp Asn Ala
                85                  90                  95

Ala Leu Trp Ala Val Leu Asn Gln Gln Phe Phe Ile Gln Phe Gly Leu
            100                 105                 110

Phe Thr Ala Leu Pro Met Ile Ile Glu Asn Ser Leu Glu His Gly Phe
        115                 120                 125

Leu Ile Ala Val Trp Asp Phe Ile Val Met Gln Leu Gln Cys Ala Ser
    130                 135                 140

Val Phe Tyr Thr Phe Cys Met Gly Thr Lys Thr His Tyr Tyr Gly Arg
145                 150                 155                 160

Thr Leu Leu His Gly Gly Ala Lys Tyr Arg Pro Thr Gly Arg Gly Phe
                165                 170                 175

Val Val Glu His Lys Lys Phe Ala Glu Asn Tyr Arg Leu Tyr Ala Arg
            180                 185                 190
```

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```
Ser His Phe Thr Lys Ala Ile Glu Leu Gly Val Ile Leu Cys Leu Tyr
        195                 200                 205

Ser Ser Tyr Ser Asn Ile Ala Gly Asp Thr Leu Val Tyr Ile Leu Leu
    210                 215                 220

Thr Leu Ser Ser Trp Phe Leu Val Cys Ser Trp Ile Leu Ala Pro Phe
225                 230                 235                 240

Ile Phe Asn Pro Ser Gly Leu Asp Trp Gln Lys Asn Ser Asn Asp Phe
                245                 250                 255

Glu Asp Phe Phe Ser Trp Ile Trp Phe Gln Gly Gly Gly Ile Ser Val
            260                 265                 270

Lys Ser Asp Gln Ser Trp Glu Lys Trp Trp Glu Glu Glu Thr Asp His
        275                 280                 285

Leu Ala Arg Thr Thr Thr Gly Leu Trp Gly Ser Ile Ile Glu Ile Ile
    290                 295                 300

Leu Asp Leu Ala Arg Thr Tyr Phe Phe Phe Gln Tyr Ala Ile Val Tyr
305                 310                 315                 320

Arg Leu His Met Ala Gly Gly Ser Arg Ser Ile Leu Val Tyr Val Leu
                325                 330                 335

Ser Trp Ala Cys Ile Pro Leu Pro Phe Leu Ala Leu Val Thr Val Thr
            340                 345                 350

Tyr Phe Arg Asp Lys Tyr Ser Ala Lys Lys His Ile Arg Tyr Arg Leu
        355                 360                 365

Val Gln Ser Val Ile Val Cys Ala Ser Leu Ala Ala Ile Ile Val Leu
    370                 375                 380

Leu Thr Leu Thr Lys Phe Gln Phe Ile Asp Thr Phe Thr Ser Leu Leu
385                 390                 395                 400

Ala Phe Leu Pro Thr Gly Trp Gly Ile Ile Ser Ile Ala Leu Val Phe
                405                 410                 415

Arg Gln Tyr Leu Lys Lys Ser Asp Thr Val Trp Lys Thr Val Val Val
            420                 425                 430

Val Ala Arg Phe Tyr Asp Ile Thr Leu Gly Leu Ile Val Met Ala Pro
        435                 440                 445

Ile Val Val Leu Ser Trp Leu Pro Gly Leu Arg Glu Leu Gln Thr Arg
    450                 455                 460

Ile Leu Phe Asn Glu Ala Phe Ser Lys Gly Leu His Ile Ser Gln Met
465                 470                 475                 480

Ile Thr Arg Arg Lys Thr His Arg Ala
                485
```

<210> SEQ ID NO 25
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(336)
<223> OTHER INFORMATION: Horderum vulgars (barley) 1,3-beta-D-glucan synthase (codon optimized)

<400> SEQUENCE: 25

```
att gcc gga gca gcc gct gga atc gct gga acc ctc atg tgt cac ccc       48
Ile Ala Gly Ala Ala Ala Gly Ile Ala Gly Thr Leu Met Cys His Pro
1               5                   10                  15
```

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```
ctc gaa gtc ata aaa gat cgc ttg acc gtc gac agg gtg acg tat ccg       96
Leu Glu Val Ile Lys Asp Arg Leu Thr Val Asp Arg Val Thr Tyr Pro
            20                  25                  30

tcg atc agc atc gcg ttc tcg aag atc tac cgg acc gag ggc atc cgc      144
Ser Ile Ser Ile Ala Phe Ser Lys Ile Tyr Arg Thr Glu Gly Ile Arg
        35                  40                  45

ggc ctg tat agc ggc ctg tgc ccc acc ctc att ggc atg ctg ccg tac      192
Gly Leu Tyr Ser Gly Leu Cys Pro Thr Leu Ile Gly Met Leu Pro Tyr
    50                  55                  60

tcg act tgc tac tat ttc atg tat gac acg atc aag acc tcc tac tgc      240
Ser Thr Cys Tyr Tyr Phe Met Tyr Asp Thr Ile Lys Thr Ser Tyr Cys
65                  70                  75                  80

cgg ctc cat aag aaa aag tcg ctg agt cgc cct gag ctg ctg atc atc      288
Arg Leu His Lys Lys Lys Ser Leu Ser Arg Pro Glu Leu Leu Ile Ile
                85                  90                  95

ggt gcg ctt acc agc ctc acc gcg tcc acg atc tcc ttc ccg ctg gag      336
Gly Ala Leu Thr Ser Leu Thr Ala Ser Thr Ile Ser Phe Pro Leu Glu
            100                 105                 110


<210> SEQ ID NO 26
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 26

Ile Ala Gly Ala Ala Ala Gly Ile Ala Gly Thr Leu Met Cys His Pro
1               5                   10                  15

Leu Glu Val Ile Lys Asp Arg Leu Thr Val Asp Arg Val Thr Tyr Pro
            20                  25                  30

Ser Ile Ser Ile Ala Phe Ser Lys Ile Tyr Arg Thr Glu Gly Ile Arg
        35                  40                  45

Gly Leu Tyr Ser Gly Leu Cys Pro Thr Leu Ile Gly Met Leu Pro Tyr
    50                  55                  60

Ser Thr Cys Tyr Tyr Phe Met Tyr Asp Thr Ile Lys Thr Ser Tyr Cys
65                  70                  75                  80

Arg Leu His Lys Lys Lys Ser Leu Ser Arg Pro Glu Leu Leu Ile Ile
                85                  90                  95

Gly Ala Leu Thr Ser Leu Thr Ala Ser Thr Ile Ser Phe Pro Leu Glu
            100                 105                 110


<210> SEQ ID NO 27
<211> LENGTH: 1293
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1293)
<223> OTHER INFORMATION: E.coli Glucose-1-phosphate adenyltransfersase
      (Acc. No. YP 49003.1) (codon optimized)

<400> SEQUENCE: 27

atg gtt tcc ctg gag aaa aat gac cac ctg atg ctc gca cgc caa ctc       48
Met Val Ser Leu Glu Lys Asn Asp His Leu Met Leu Ala Arg Gln Leu
1               5                   10                  15

ccg ctt aag tcc gtc gcc ctg atc ctc gcc ggc gga cgc ggc acg cgg       96
Pro Leu Lys Ser Val Ala Leu Ile Leu Ala Gly Gly Arg Gly Thr Arg
```

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```
            20                  25                  30

ctc aaa gac ctc acc aac aag cgc gcg aaa ccg gct gtc cat ttc ggt      144
Leu Lys Asp Leu Thr Asn Lys Arg Ala Lys Pro Ala Val His Phe Gly
        35                  40                  45

ggc aag ttc agg atc ata gac ttc gcg ctg tcg aac tgc atc aat tcc      192
Gly Lys Phe Arg Ile Ile Asp Phe Ala Leu Ser Asn Cys Ile Asn Ser
    50                  55                  60

ggc att agg cgc atg gga gtc att acc cag tac caa tcg cat acg ctc      240
Gly Ile Arg Arg Met Gly Val Ile Thr Gln Tyr Gln Ser His Thr Leu
65                  70                  75                  80

gtc cag cat atc cag cgg ggc tgg tcg ttc ttc aac gaa gag atg aac      288
Val Gln His Ile Gln Arg Gly Trp Ser Phe Phe Asn Glu Glu Met Asn
                85                  90                  95

gag ttc gtc gac ctc ctc ccg gcg cag cag cgg atg aaa ggc gag aac      336
Glu Phe Val Asp Leu Leu Pro Ala Gln Gln Arg Met Lys Gly Glu Asn
            100                 105                 110

tgg tac cgc ggc acg gct gat gcc gtt acc cag aac ctg gac att att      384
Trp Tyr Arg Gly Thr Ala Asp Ala Val Thr Gln Asn Leu Asp Ile Ile
        115                 120                 125

cgc cgc tat aaa gcc gag tat gtt gtg atc ctg gcc ggt gac cac atc      432
Arg Arg Tyr Lys Ala Glu Tyr Val Val Ile Leu Ala Gly Asp His Ile
    130                 135                 140

tac aaa caa gac tat agt cgg atg ctc atc gac cat gtg gaa aag ggc      480
Tyr Lys Gln Asp Tyr Ser Arg Met Leu Ile Asp His Val Glu Lys Gly
145                 150                 155                 160

gct cgc tgc acc gtg gcg tgc atg cca gtg ccg atc gaa gag gcc tcc      528
Ala Arg Cys Thr Val Ala Cys Met Pro Val Pro Ile Glu Glu Ala Ser
                165                 170                 175

gcg ttc ggc gtg atg gcc gtg gat gag aac gac aag atc atc gag ttc      576
Ala Phe Gly Val Met Ala Val Asp Glu Asn Asp Lys Ile Ile Glu Phe
            180                 185                 190

gtg gag aag ccc gcg aac ccg ccg tcg atg ccc aac gac ccg agc aag      624
Val Glu Lys Pro Ala Asn Pro Pro Ser Met Pro Asn Asp Pro Ser Lys
        195                 200                 205

agc ctg gcg tcc atg ggc atc tac gtc ttt gac gcg gat tat ctg tac      672
Ser Leu Ala Ser Met Gly Ile Tyr Val Phe Asp Ala Asp Tyr Leu Tyr
    210                 215                 220

gag ctt ttg gaa gag gat gat cgg gac gag aat agc tcg cac gac ttc      720
Glu Leu Leu Glu Glu Asp Asp Arg Asp Glu Asn Ser Ser His Asp Phe
225                 230                 235                 240

ggc aaa gac ctg atc ccg aag atc acc gaa gcc ggg ctg gcg tat gcc      768
Gly Lys Asp Leu Ile Pro Lys Ile Thr Glu Ala Gly Leu Ala Tyr Ala
                245                 250                 255

cat cct ttt ccg ctc agc tgc gtg cag tcg gac ccc gat gcg gag ccg      816
His Pro Phe Pro Leu Ser Cys Val Gln Ser Asp Pro Asp Ala Glu Pro
            260                 265                 270

tat tgg cgc gac gtg ggt acc ctg gaa gcg tac tgg aag gcc aat ctc      864
Tyr Trp Arg Asp Val Gly Thr Leu Glu Ala Tyr Trp Lys Ala Asn Leu
        275                 280                 285

gac ctc gcc agc gtg gtg ccg gaa ctg gac atg tac gac cgc aat tgg      912
Asp Leu Ala Ser Val Val Pro Glu Leu Asp Met Tyr Asp Arg Asn Trp
    290                 295                 300

ccg atc cgc act tac aac gag agc ctg ccc ccg gcg aag ttc gtc cag      960
Pro Ile Arg Thr Tyr Asn Glu Ser Leu Pro Pro Ala Lys Phe Val Gln
305                 310                 315                 320

gac cgg agt ggc agc cac ggc atg acg ctc aat tcc ctt gtg tcg ggg     1008
Asp Arg Ser Gly Ser His Gly Met Thr Leu Asn Ser Leu Val Ser Gly
```

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```
                325                 330                 335

ggc tgc gtc atc tcg ggt tcg gtc gtc gtc cag tcc gtc ctc ttc agc     1056
Gly Cys Val Ile Ser Gly Ser Val Val Val Gln Ser Val Leu Phe Ser
            340                 345                 350

cgg gtc agg gtc aat tcc ttc tgc aac atc gat agc gca gtg ctg ttg     1104
Arg Val Arg Val Asn Ser Phe Cys Asn Ile Asp Ser Ala Val Leu Leu
        355                 360                 365

ccc gag gtc tgg gtg ggc cgc tcg tgt cgg ctg cgc cgc tgc gtg atc     1152
Pro Glu Val Trp Val Gly Arg Ser Cys Arg Leu Arg Arg Cys Val Ile
    370                 375                 380

gac cgc gcc tgc gtc atc ccc gag ggc atg gtc ata ggc gag aat gcc     1200
Asp Arg Ala Cys Val Ile Pro Glu Gly Met Val Ile Gly Glu Asn Ala
385                 390                 395                 400

gaa gag gac gcg cgg cgc ttc tat cgg tcc gag gag ggc atc gtg ctg     1248
Glu Glu Asp Ala Arg Arg Phe Tyr Arg Ser Glu Glu Gly Ile Val Leu
                405                 410                 415

gtc acc cgc gag atg ctg cgc aag ctc ggg cat aag caa gag cgc         1293
Val Thr Arg Glu Met Leu Arg Lys Leu Gly His Lys Gln Glu Arg
            420                 425                 430


<210> SEQ ID NO 28
<211> LENGTH: 431
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 28

Met Val Ser Leu Glu Lys Asn Asp His Leu Met Leu Ala Arg Gln Leu
1               5                   10                  15

Pro Leu Lys Ser Val Ala Leu Ile Leu Ala Gly Gly Arg Gly Thr Arg
            20                  25                  30

Leu Lys Asp Leu Thr Asn Lys Arg Ala Lys Pro Ala Val His Phe Gly
        35                  40                  45

Gly Lys Phe Arg Ile Ile Asp Phe Ala Leu Ser Asn Cys Ile Asn Ser
    50                  55                  60

Gly Ile Arg Arg Met Gly Val Ile Thr Gln Tyr Gln Ser His Thr Leu
65                  70                  75                  80

Val Gln His Ile Gln Arg Gly Trp Ser Phe Phe Asn Glu Glu Met Asn
                85                  90                  95

Glu Phe Val Asp Leu Leu Pro Ala Gln Gln Arg Met Lys Gly Glu Asn
            100                 105                 110

Trp Tyr Arg Gly Thr Ala Asp Ala Val Thr Gln Asn Leu Asp Ile Ile
        115                 120                 125

Arg Arg Tyr Lys Ala Glu Tyr Val Val Ile Leu Ala Gly Asp His Ile
    130                 135                 140

Tyr Lys Gln Asp Tyr Ser Arg Met Leu Ile Asp His Val Glu Lys Gly
145                 150                 155                 160

Ala Arg Cys Thr Val Ala Cys Met Pro Val Pro Ile Glu Glu Ala Ser
                165                 170                 175

Ala Phe Gly Val Met Ala Val Asp Glu Asn Asp Lys Ile Ile Glu Phe
            180                 185                 190

Val Glu Lys Pro Ala Asn Pro Pro Ser Met Pro Asn Asp Pro Ser Lys
        195                 200                 205

Ser Leu Ala Ser Met Gly Ile Tyr Val Phe Asp Ala Asp Tyr Leu Tyr
```

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    210                 215                 220

Glu Leu Leu Glu Glu Asp Asp Arg Asp Glu Asn Ser Ser His Asp Phe
225                 230                 235                 240

Gly Lys Asp Leu Ile Pro Lys Ile Thr Glu Ala Gly Leu Ala Tyr Ala
                245                 250                 255

His Pro Phe Pro Leu Ser Cys Val Gln Ser Asp Pro Asp Ala Glu Pro
            260                 265                 270

Tyr Trp Arg Asp Val Gly Thr Leu Glu Ala Tyr Trp Lys Ala Asn Leu
        275                 280                 285

Asp Leu Ala Ser Val Val Pro Glu Leu Asp Met Tyr Asp Arg Asn Trp
    290                 295                 300

Pro Ile Arg Thr Tyr Asn Glu Ser Leu Pro Pro Ala Lys Phe Val Gln
305                 310                 315                 320

Asp Arg Ser Gly Ser His Gly Met Thr Leu Asn Ser Leu Val Ser Gly
                325                 330                 335

Gly Cys Val Ile Ser Gly Ser Val Val Val Gln Ser Val Leu Phe Ser
            340                 345                 350

Arg Val Arg Val Asn Ser Phe Cys Asn Ile Asp Ser Ala Val Leu Leu
        355                 360                 365

Pro Glu Val Trp Val Gly Arg Ser Cys Arg Leu Arg Arg Cys Val Ile
    370                 375                 380

Asp Arg Ala Cys Val Ile Pro Glu Gly Met Val Ile Gly Glu Asn Ala
385                 390                 395                 400

Glu Glu Asp Ala Arg Arg Phe Tyr Arg Ser Glu Glu Gly Ile Val Leu
                405                 410                 415

Val Thr Arg Glu Met Leu Arg Lys Leu Gly His Lys Gln Glu Arg
            420                 425                 430


<210> SEQ ID NO 29
<211> LENGTH: 1227
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1227)
<223> OTHER INFORMATION: Cornebacterium glutamicum (ATCC 13032)
      Glucose-1-phosphate adenylyltransferase (codon optimized)

<400> SEQUENCE: 29

atg gtg aag gga gtt aag gga agg cct aat gtt ttg gca ata gtt ctg       48
Met Val Lys Gly Val Lys Gly Arg Pro Asn Val Leu Ala Ile Val Leu
1               5                   10                  15

gcg ggt gga gag ggg aaa cgg ttg ttc ccg ctc acc gag gac cgc gcc       96
Ala Gly Gly Glu Gly Lys Arg Leu Phe Pro Leu Thr Glu Asp Arg Ala
            20                  25                  30

aag ccc gcg gtg ccg ttc ggc ggc acc tac cgc ctg atc gat ttc gtg      144
Lys Pro Ala Val Pro Phe Gly Gly Thr Tyr Arg Leu Ile Asp Phe Val
        35                  40                  45

ctg tcc aat ctg gtc aat tcg ggt ttc ctc aag atc gcg gtc ctc acg      192
Leu Ser Asn Leu Val Asn Ser Gly Phe Leu Lys Ile Ala Val Leu Thr
    50                  55                  60

cag tac aag agc cat agc ctt gac cgg cat atc tcc ctg tcc tgg aac      240
Gln Tyr Lys Ser His Ser Leu Asp Arg His Ile Ser Leu Ser Trp Asn
65                  70                  75                  80
```

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```
gtg tcc ggg ccg acg ggc cag tac atc gcc tcc gtc cca gct cag cag      288
Val Ser Gly Pro Thr Gly Gln Tyr Ile Ala Ser Val Pro Ala Gln Gln
                85                  90                  95

cgg ctc ggc aag cgc tgg ttc acc ggc tcg gcc gac gcc atc ctg cag      336
Arg Leu Gly Lys Arg Trp Phe Thr Gly Ser Ala Asp Ala Ile Leu Gln
            100                 105                 110

agc ctc aac ctg atc tcc gac gag aag ccc gac tat gtc atc gtg ttt      384
Ser Leu Asn Leu Ile Ser Asp Glu Lys Pro Asp Tyr Val Ile Val Phe
        115                 120                 125

ggc gcg gac cac gtg tac cgg atg gat ccc tcc cag atg ctg gat gag      432
Gly Ala Asp His Val Tyr Arg Met Asp Pro Ser Gln Met Leu Asp Glu
    130                 135                 140

cat atc gcg agt ggt cgc gct gtg tcg gtc gcc ggc atc cgc gtc ccg      480
His Ile Ala Ser Gly Arg Ala Val Ser Val Ala Gly Ile Arg Val Pro
145                 150                 155                 160

cgc gaa gag gcg acg gcg ttc ggc tgc atc cag tcc gat gtg gac ggg      528
Arg Glu Glu Ala Thr Ala Phe Gly Cys Ile Gln Ser Asp Val Asp Gly
                165                 170                 175

aac atc acc gag ttc ctc gaa aaa ccc gcc gac ccc ccg ggg acc ccg      576
Asn Ile Thr Glu Phe Leu Glu Lys Pro Ala Asp Pro Pro Gly Thr Pro
            180                 185                 190

gac gac ccc gac atg acc tat gcc agc atg ggc aac tac atc ttc acg      624
Asp Asp Pro Asp Met Thr Tyr Ala Ser Met Gly Asn Tyr Ile Phe Thr
        195                 200                 205

acc gaa gca ctg atc caa gcg ctt aaa gat gat gag aat aac gaa aat      672
Thr Glu Ala Leu Ile Gln Ala Leu Lys Asp Asp Glu Asn Asn Glu Asn
    210                 215                 220

tcg gac cat gac atg ggc ggc gac atc att ccg tat ttc gtg tcg cgc      720
Ser Asp His Asp Met Gly Gly Asp Ile Ile Pro Tyr Phe Val Ser Arg
225                 230                 235                 240

aac gac gcg cat gtc tac gac ttt tcc ggt aac atc gtg ccg ggt gcg      768
Asn Asp Ala His Val Tyr Asp Phe Ser Gly Asn Ile Val Pro Gly Ala
                245                 250                 255

act gag cgc gac aag ggc tat tgg cgc gac gtc ggt acc att gat gcg      816
Thr Glu Arg Asp Lys Gly Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala
            260                 265                 270

ttc tac gag tgc cac atg gac ctg atc tcg gtc cac ccg atc ttc aat      864
Phe Tyr Glu Cys His Met Asp Leu Ile Ser Val His Pro Ile Phe Asn
        275                 280                 285

ctg tat aac agc gag tgg ccg atc cac acc acg tcc gag ggc aac ctc      912
Leu Tyr Asn Ser Glu Trp Pro Ile His Thr Thr Ser Glu Gly Asn Leu
    290                 295                 300

ccg ccg gcc aag ttc gtc cgc ggc ggc ata gcc caa tcg tcg atg gtg      960
Pro Pro Ala Lys Phe Val Arg Gly Gly Ile Ala Gln Ser Ser Met Val
305                 310                 315                 320

agc tcc ggc agc atc atc tcg gct ggc acc gtg agg aat agc gtg ctc     1008
Ser Ser Gly Ser Ile Ile Ser Ala Gly Thr Val Arg Asn Ser Val Leu
                325                 330                 335

tcg aat aat gtc gtc gtc gag gag ggc gcc acg gtc gag ggc gcg gtg     1056
Ser Asn Asn Val Val Val Glu Glu Gly Ala Thr Val Glu Gly Ala Val
            340                 345                 350

ctc atg ccc ggt gtc cgg att ggc aag ggt gcc gtc gtg cgc cat gca     1104
Leu Met Pro Gly Val Arg Ile Gly Lys Gly Ala Val Val Arg His Ala
        355                 360                 365

att ctc gac aaa aac gtc gtc gtg cgc gac ggc gag ctc atc ggc gtg     1152
Ile Leu Asp Lys Asn Val Val Val Arg Asp Gly Glu Leu Ile Gly Val
    370                 375                 380
```

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```
gat cag gtc cgg gac gcc cag cgc ttc aag gtc agt gcg ggc gga gtg     1200
Asp Gln Val Arg Asp Ala Gln Arg Phe Lys Val Ser Ala Gly Gly Val
385                 390                 395                 400

gtc gtg gtc ggc aag aac caa gtc gtg                               1227
Val Val Val Gly Lys Asn Gln Val Val
                405
```

<210> SEQ ID NO 30
<211> LENGTH: 409
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 30

```
Met Val Lys Gly Val Lys Gly Arg Pro Asn Val Leu Ala Ile Val Leu
1               5                   10                  15

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

Lys Pro Ala Val Pro Phe Gly Gly Thr Tyr Arg Leu Ile Asp Phe Val
        35                  40                  45

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

Gln Tyr Lys Ser His Ser Leu Asp Arg His Ile Ser Leu Ser Trp Asn
65                  70                  75                  80

Val Ser Gly Pro Thr Gly Gln Tyr Ile Ala Ser Val Pro Ala Gln Gln
                85                  90                  95

Arg Leu Gly Lys Arg Trp Phe Thr Gly Ser Ala Asp Ala Ile Leu Gln
            100                 105                 110

Ser Leu Asn Leu Ile Ser Asp Glu Lys Pro Asp Tyr Val Ile Val Phe
        115                 120                 125

Gly Ala Asp His Val Tyr Arg Met Asp Pro Ser Gln Met Leu Asp Glu
    130                 135                 140

His Ile Ala Ser Gly Arg Ala Val Ser Val Ala Gly Ile Arg Val Pro
145                 150                 155                 160

Arg Glu Glu Ala Thr Ala Phe Gly Cys Ile Gln Ser Asp Val Asp Gly
                165                 170                 175

Asn Ile Thr Glu Phe Leu Glu Lys Pro Ala Asp Pro Pro Gly Thr Pro
            180                 185                 190

Asp Asp Pro Asp Met Thr Tyr Ala Ser Met Gly Asn Tyr Ile Phe Thr
        195                 200                 205

Thr Glu Ala Leu Ile Gln Ala Leu Lys Asp Asp Glu Asn Asn Glu Asn
    210                 215                 220

Ser Asp His Asp Met Gly Gly Asp Ile Ile Pro Tyr Phe Val Ser Arg
225                 230                 235                 240

Asn Asp Ala His Val Tyr Asp Phe Ser Gly Asn Ile Val Pro Gly Ala
                245                 250                 255

Thr Glu Arg Asp Lys Gly Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala
            260                 265                 270

Phe Tyr Glu Cys His Met Asp Leu Ile Ser Val His Pro Ile Phe Asn
        275                 280                 285

Leu Tyr Asn Ser Glu Trp Pro Ile His Thr Thr Ser Glu Gly Asn Leu
    290                 295                 300

Pro Pro Ala Lys Phe Val Arg Gly Gly Ile Ala Gln Ser Ser Met Val
```

-continued

```
305                 310                 315                 320

Ser Ser Gly Ser Ile Ile Ser Ala Gly Thr Val Arg Asn Ser Val Leu
                325                 330                 335

Ser Asn Asn Val Val Val Glu Glu Gly Ala Thr Val Glu Gly Ala Val
            340                 345                 350

Leu Met Pro Gly Val Arg Ile Gly Lys Gly Ala Val Val Arg His Ala
        355                 360                 365

Ile Leu Asp Lys Asn Val Val Val Arg Asp Gly Glu Leu Ile Gly Val
    370                 375                 380

Asp Gln Val Arg Asp Ala Gln Arg Phe Lys Val Ser Ala Gly Gly Val
385                 390                 395                 400

Val Val Val Gly Lys Asn Gln Val Val
                405


<210> SEQ ID NO 31
<211> LENGTH: 1431
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1431)
<223> OTHER INFORMATION: Escherichia coli str. K-12 substr. W3110
      Glycogen Synthase (codon optimized)

<400> SEQUENCE: 31

atg caa gtt ctt cat gtg tgt tcc gaa atg ttc ccc ctc ctc aaa acc       48
Met Gln Val Leu His Val Cys Ser Glu Met Phe Pro Leu Leu Lys Thr
1               5                   10                  15

ggt ggc ctg gct gat gtc ata ggt gcc ctg ccg gct gcg cag att gcg       96
Gly Gly Leu Ala Asp Val Ile Gly Ala Leu Pro Ala Ala Gln Ile Ala
            20                  25                  30

gac ggc gtg gac gca cgg gtc ctg ctg ccg gcg ttc ccg gat atc cgc      144
Asp Gly Val Asp Ala Arg Val Leu Leu Pro Ala Phe Pro Asp Ile Arg
        35                  40                  45

cgg ggc gtg acc gac gca caa gtc gtg tcg cgc agg gac acc ttt gcc      192
Arg Gly Val Thr Asp Ala Gln Val Val Ser Arg Arg Asp Thr Phe Ala
    50                  55                  60

ggc cac atc acg ctc ttg ttc ggc cac tat aac ggc gtg ggc atc tac      240
Gly His Ile Thr Leu Leu Phe Gly His Tyr Asn Gly Val Gly Ile Tyr
65                  70                  75                  80

ctg atc gat gcg ccg cat ctc tat gac agg ccg ggt tcg ccc tat cat      288
Leu Ile Asp Ala Pro His Leu Tyr Asp Arg Pro Gly Ser Pro Tyr His
                85                  90                  95

gac acg aac ctc ttc gcc tac acg gac aat gtg ctg cgg ttc gca ctt      336
Asp Thr Asn Leu Phe Ala Tyr Thr Asp Asn Val Leu Arg Phe Ala Leu
            100                 105                 110

ctg ggc tgg gtc gga gcc gag atg gca tcc ggc ctc gac ccg ttc tgg      384
Leu Gly Trp Val Gly Ala Glu Met Ala Ser Gly Leu Asp Pro Phe Trp
        115                 120                 125

cgc cct gac gtc gtc cat gcg cat gac tgg cat gcc ggc ctc gca ccc      432
Arg Pro Asp Val Val His Ala His Asp Trp His Ala Gly Leu Ala Pro
    130                 135                 140

gcg tat ttg gcc gcc cgg gga cgg ccg gct aag agc gtg ttt acc gtt      480
Ala Tyr Leu Ala Ala Arg Gly Arg Pro Ala Lys Ser Val Phe Thr Val
145                 150                 155                 160

cat aac ctc gcg tat cag ggc atg ttc tac gcc cat cac atg aat gat      528
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His Asn Leu Ala Tyr Gln Gly Met Phe Tyr Ala His His Met Asn Asp
                165                 170                 175

atc cag ctg ccc tgg tcc ttc ttc aac atc cac ggt ctt gag ttc aat      576
Ile Gln Leu Pro Trp Ser Phe Phe Asn Ile His Gly Leu Glu Phe Asn
            180                 185                 190

ggc caa atc tcg ttc ctg aag gcc ggg ctg tac tac gcg gac cac atc      624
Gly Gln Ile Ser Phe Leu Lys Ala Gly Leu Tyr Tyr Ala Asp His Ile
        195                 200                 205

acc gcg gtg tcg cca acc tac gcc cgc gag atc acc gag ccg cag ttc      672
Thr Ala Val Ser Pro Thr Tyr Ala Arg Glu Ile Thr Glu Pro Gln Phe
    210                 215                 220

gcg tac ggc atg gag ggc ctg ctg caa cag cgc cac cgc gag ggc cgg      720
Ala Tyr Gly Met Glu Gly Leu Leu Gln Gln Arg His Arg Glu Gly Arg
225                 230                 235                 240

ctc agc ggc gtt ctg aac ggc gtc gac gag aaa atc tgg tcg ccc gag      768
Leu Ser Gly Val Leu Asn Gly Val Asp Glu Lys Ile Trp Ser Pro Glu
                245                 250                 255

act gac ttg ctc ctt gcc agc cgc tat acc cgc gac acg ctc gaa gat      816
Thr Asp Leu Leu Leu Ala Ser Arg Tyr Thr Arg Asp Thr Leu Glu Asp
            260                 265                 270

aaa gcc gag aat aag cgc cag ctg cag atc gcc atg ggc ctg aaa gtc      864
Lys Ala Glu Asn Lys Arg Gln Leu Gln Ile Ala Met Gly Leu Lys Val
        275                 280                 285

gac gac aag gtc ccc ctc ttc gcc gtg gtc agc cgc ctg acc tcg caa      912
Asp Asp Lys Val Pro Leu Phe Ala Val Val Ser Arg Leu Thr Ser Gln
    290                 295                 300

aag ggc ctg gac ctg gtg ctc gaa gcc ctc cct ggc ctg ctt gaa cag      960
Lys Gly Leu Asp Leu Val Leu Glu Ala Leu Pro Gly Leu Leu Glu Gln
305                 310                 315                 320

ggt ggc cag ttg gcg ctc ctc ggc gcc ggg gat ccg gtg ttg cag gag     1008
Gly Gly Gln Leu Ala Leu Leu Gly Ala Gly Asp Pro Val Leu Gln Glu
                325                 330                 335

gga ttc ctg gcg gct gcg gcc gag tat ccg ggc cag gtc ggc gtc cag     1056
Gly Phe Leu Ala Ala Ala Ala Glu Tyr Pro Gly Gln Val Gly Val Gln
            340                 345                 350

att ggc tac cat gaa gcg ttc agt cat cgg atc atg ggt ggg gcc gac     1104
Ile Gly Tyr His Glu Ala Phe Ser His Arg Ile Met Gly Gly Ala Asp
        355                 360                 365

gtc atc ctc gtg ccg tcc cgc ttc gag ccg tgc ggc ctc acc cag ctg     1152
Val Ile Leu Val Pro Ser Arg Phe Glu Pro Cys Gly Leu Thr Gln Leu
    370                 375                 380

tac ggc ctc aag tac gga acg ctc ccc ctg gtg cgg cgg acc ggt ggg     1200
Tyr Gly Leu Lys Tyr Gly Thr Leu Pro Leu Val Arg Arg Thr Gly Gly
385                 390                 395                 400

ctc gcc gac acc gtc agc gac tgc tcc ctg gag aac ctg gcg gat ggc     1248
Leu Ala Asp Thr Val Ser Asp Cys Ser Leu Glu Asn Leu Ala Asp Gly
                405                 410                 415

gtc gcg agc ggt ttt gtg ttc gag gac agc aac gcc tgg tcg ctg ctc     1296
Val Ala Ser Gly Phe Val Phe Glu Asp Ser Asn Ala Trp Ser Leu Leu
            420                 425                 430

cgc gcg atc cgc agg gcc ttc gtc ctg tgg agt cgc ccg tcc ctc tgg     1344
Arg Ala Ile Arg Arg Ala Phe Val Leu Trp Ser Arg Pro Ser Leu Trp
        435                 440                 445

cgc ttc gtg cag cgg cag gca atg gcc atg gac ttc tcg tgg caa gtc     1392
Arg Phe Val Gln Arg Gln Ala Met Ala Met Asp Phe Ser Trp Gln Val
    450                 455                 460

gcg gcc aag tcc tat cgc gag ctc tac tat cgc ctg aag                1431
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Ala Ala Lys Ser Tyr Arg Glu Leu Tyr Tyr Arg Leu Lys
465                 470                 475


<210> SEQ ID NO 32
<211> LENGTH: 477
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 32

Met Gln Val Leu His Val Cys Ser Glu Met Phe Pro Leu Leu Lys Thr
1               5                   10                  15

Gly Gly Leu Ala Asp Val Ile Gly Ala Leu Pro Ala Ala Gln Ile Ala
            20                  25                  30

Asp Gly Val Asp Ala Arg Val Leu Leu Pro Ala Phe Pro Asp Ile Arg
        35                  40                  45

Arg Gly Val Thr Asp Ala Gln Val Val Ser Arg Arg Asp Thr Phe Ala
    50                  55                  60

Gly His Ile Thr Leu Leu Phe Gly His Tyr Asn Gly Val Gly Ile Tyr
65                  70                  75                  80

Leu Ile Asp Ala Pro His Leu Tyr Asp Arg Pro Gly Ser Pro Tyr His
                85                  90                  95

Asp Thr Asn Leu Phe Ala Tyr Thr Asp Asn Val Leu Arg Phe Ala Leu
            100                 105                 110

Leu Gly Trp Val Gly Ala Glu Met Ala Ser Gly Leu Asp Pro Phe Trp
        115                 120                 125

Arg Pro Asp Val Val His Ala His Asp Trp His Ala Gly Leu Ala Pro
    130                 135                 140

Ala Tyr Leu Ala Ala Arg Gly Arg Pro Ala Lys Ser Val Phe Thr Val
145                 150                 155                 160

His Asn Leu Ala Tyr Gln Gly Met Phe Tyr Ala His His Met Asn Asp
                165                 170                 175

Ile Gln Leu Pro Trp Ser Phe Phe Asn Ile His Gly Leu Glu Phe Asn
            180                 185                 190

Gly Gln Ile Ser Phe Leu Lys Ala Gly Leu Tyr Tyr Ala Asp His Ile
        195                 200                 205

Thr Ala Val Ser Pro Thr Tyr Ala Arg Glu Ile Thr Glu Pro Gln Phe
    210                 215                 220

Ala Tyr Gly Met Glu Gly Leu Leu Gln Gln Arg His Arg Glu Gly Arg
225                 230                 235                 240

Leu Ser Gly Val Leu Asn Gly Val Asp Glu Lys Ile Trp Ser Pro Glu
                245                 250                 255

Thr Asp Leu Leu Leu Ala Ser Arg Tyr Thr Arg Asp Thr Leu Glu Asp
            260                 265                 270

Lys Ala Glu Asn Lys Arg Gln Leu Gln Ile Ala Met Gly Leu Lys Val
        275                 280                 285

Asp Asp Lys Val Pro Leu Phe Ala Val Val Ser Arg Leu Thr Ser Gln
    290                 295                 300

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

Gly Gly Gln Leu Ala Leu Leu Gly Ala Gly Asp Pro Val Leu Gln Glu
                325                 330                 335
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Gly Phe Leu Ala Ala Ala Ala Glu Tyr Pro Gly Gln Val Gly Val Gln
            340                 345                 350

Ile Gly Tyr His Glu Ala Phe Ser His Arg Ile Met Gly Gly Ala Asp
        355                 360                 365

Val Ile Leu Val Pro Ser Arg Phe Glu Pro Cys Gly Leu Thr Gln Leu
    370                 375                 380

Tyr Gly Leu Lys Tyr Gly Thr Leu Pro Leu Val Arg Arg Thr Gly Gly
385                 390                 395                 400

Leu Ala Asp Thr Val Ser Asp Cys Ser Leu Glu Asn Leu Ala Asp Gly
                405                 410                 415

Val Ala Ser Gly Phe Val Phe Glu Asp Ser Asn Ala Trp Ser Leu Leu
            420                 425                 430

Arg Ala Ile Arg Arg Ala Phe Val Leu Trp Ser Arg Pro Ser Leu Trp
        435                 440                 445

Arg Phe Val Gln Arg Gln Ala Met Ala Met Asp Phe Ser Trp Gln Val
    450                 455                 460

Ala Ala Lys Ser Tyr Arg Glu Leu Tyr Tyr Arg Leu Lys
465                 470                 475


<210> SEQ ID NO 33
<211> LENGTH: 1227
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1227)
<223> OTHER INFORMATION: Cornebacterium glutamicum (ATCC 13032)
      Glycosyltransferase (codon optimized)

<400> SEQUENCE: 33

atg cca cct ttc cgc tat cgc tgt gct act gtt ttc cgc tgg ttg att       48
Met Pro Pro Phe Arg Tyr Arg Cys Ala Thr Val Phe Arg Trp Leu Ile
1               5                   10                  15

ttt gaa ata atg cgc gtc ggg atg atg acc cgc gag tac ccg cct gaa       96
Phe Glu Ile Met Arg Val Gly Met Met Thr Arg Glu Tyr Pro Pro Glu
            20                  25                  30

gtg tac ggt gga gcc ggg gtc cat gtg acc gag ctt acc cgg ttc atg      144
Val Tyr Gly Gly Ala Gly Val His Val Thr Glu Leu Thr Arg Phe Met
        35                  40                  45

cgc gag atc gca gag gtc gac gtg cac tgc atg ggc gca ccg cgc gac      192
Arg Glu Ile Ala Glu Val Asp Val His Cys Met Gly Ala Pro Arg Asp
    50                  55                  60

atg gag ggt gtt ttc gtg cac ggc gtc gac ccg gca ctc gaa tcg gcg      240
Met Glu Gly Val Phe Val His Gly Val Asp Pro Ala Leu Glu Ser Ala
65                  70                  75                  80

aac ccc gcc atc aag acg ctc tcg acg ggc ctg cgg atg gcc gag gcc      288
Asn Pro Ala Ile Lys Thr Leu Ser Thr Gly Leu Arg Met Ala Glu Ala
                85                  90                  95

gcg aat aat gtt gac gtc gtg cat tcg cat acc tgg tat gcg ggc ctg      336
Ala Asn Asn Val Asp Val Val His Ser His Thr Trp Tyr Ala Gly Leu
            100                 105                 110

ggt ggc cat ctc gcg gcc agg ctg cac ggc atc ccg cat gtg gcg acg      384
Gly Gly His Leu Ala Ala Arg Leu His Gly Ile Pro His Val Ala Thr
        115                 120                 125

gcg cat agc ctg gag ccg gac cgg ccc tgg aag cgc gag caa ctc ggc      432
Ala His Ser Leu Glu Pro Asp Arg Pro Trp Lys Arg Glu Gln Leu Gly
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    130                 135                 140

ggc ggc tac gac gtg agc tcc tgg tcg gag aaa aac gcg atg gag tac      480
Gly Gly Tyr Asp Val Ser Ser Trp Ser Glu Lys Asn Ala Met Glu Tyr
145                 150                 155                 160

gcg gac gcc gtg atc gcc gtc agt gcc cgg atg aaa gac tcc atc ctg      528
Ala Asp Ala Val Ile Ala Val Ser Ala Arg Met Lys Asp Ser Ile Leu
                165                 170                 175

gcg gct tat ccg cgc atc gag ccc gat aat gtg cgc gtg gtg ctg aac      576
Ala Ala Tyr Pro Arg Ile Glu Pro Asp Asn Val Arg Val Val Leu Asn
            180                 185                 190

ggc atc gac acc gag ctc tgg cag ccg agg ccg acc ttc gac gac gcc      624
Gly Ile Asp Thr Glu Leu Trp Gln Pro Arg Pro Thr Phe Asp Asp Ala
        195                 200                 205

gag gat tcc gtg ctg cgc agc ctg ggc gtc gac ccg caa cgg ccc atc      672
Glu Asp Ser Val Leu Arg Ser Leu Gly Val Asp Pro Gln Arg Pro Ile
    210                 215                 220

gtc gcg ttt gtc gga cgg att acg cgg cag aaa ggc gtg gag cac ctc      720
Val Ala Phe Val Gly Arg Ile Thr Arg Gln Lys Gly Val Glu His Leu
225                 230                 235                 240

atc aaa gcc gcc gcc ctg ttc gac gag tcc gtc cag ctc gtc ctc tgc      768
Ile Lys Ala Ala Ala Leu Phe Asp Glu Ser Val Gln Leu Val Leu Cys
                245                 250                 255

gcg ggt gcc ccc gac acc ccg gag atc gcg gct cgg acc acg gcg ctg      816
Ala Gly Ala Pro Asp Thr Pro Glu Ile Ala Ala Arg Thr Thr Ala Leu
            260                 265                 270

gtc gag gaa ctc caa gcg aag cgc gag ggc atc ttc tgg gtc cag gat      864
Val Glu Glu Leu Gln Ala Lys Arg Glu Gly Ile Phe Trp Val Gln Asp
        275                 280                 285

atg ctg ggg aag gat aag atc cag gag atc ctc acc gcc gct gac acc      912
Met Leu Gly Lys Asp Lys Ile Gln Glu Ile Leu Thr Ala Ala Asp Thr
    290                 295                 300

ttc gtg tgc ccg tcg atc tat gag ccc ctg ggc atc gtc aac ctc gaa      960
Phe Val Cys Pro Ser Ile Tyr Glu Pro Leu Gly Ile Val Asn Leu Glu
305                 310                 315                 320

gcc atg gcg tgc aat acc gcc gtg gtc gcg agc gac gtc ggc ggc atc     1008
Ala Met Ala Cys Asn Thr Ala Val Val Ala Ser Asp Val Gly Gly Ile
                325                 330                 335

cca gag gtc gtc gtg gac ggc acc acg ggc gca ctg gtg cat tac gat     1056
Pro Glu Val Val Val Asp Gly Thr Thr Gly Ala Leu Val His Tyr Asp
            340                 345                 350

gag aac gat gtg gaa acg ttc gag cgc gac att gcc gaa gcc gtg aac     1104
Glu Asn Asp Val Glu Thr Phe Glu Arg Asp Ile Ala Glu Ala Val Asn
        355                 360                 365

aag atg gtc gcg gat cgc gag act gcc gcg aag ttc ggt ctt gca ggc     1152
Lys Met Val Ala Asp Arg Glu Thr Ala Ala Lys Phe Gly Leu Ala Gly
    370                 375                 380

cgg gag cgg gcg atc aat gac ttc agc tgg gcc acc atc gcc cag cag     1200
Arg Glu Arg Ala Ile Asn Asp Phe Ser Trp Ala Thr Ile Ala Gln Gln
385                 390                 395                 400

acc atc gac gtc tat aag tcg ctg atg                                1227
Thr Ile Asp Val Tyr Lys Ser Leu Met
                405
```

<210> SEQ ID NO 34
<211> LENGTH: 409
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 34

```
Met Pro Pro Phe Arg Tyr Arg Cys Ala Thr Val Phe Arg Trp Leu Ile
1               5                  10                  15

Phe Glu Ile Met Arg Val Gly Met Met Thr Arg Glu Tyr Pro Pro Glu
            20                  25                  30

Val Tyr Gly Gly Ala Gly Val His Val Thr Glu Leu Thr Arg Phe Met
        35                  40                  45

Arg Glu Ile Ala Glu Val Asp Val His Cys Met Gly Ala Pro Arg Asp
    50                  55                  60

Met Glu Gly Val Phe Val His Gly Val Asp Pro Ala Leu Glu Ser Ala
65                  70                  75                  80

Asn Pro Ala Ile Lys Thr Leu Ser Thr Gly Leu Arg Met Ala Glu Ala
                85                  90                  95

Ala Asn Asn Val Asp Val Val His Ser His Thr Trp Tyr Ala Gly Leu
            100                 105                 110

Gly Gly His Leu Ala Ala Arg Leu His Gly Ile Pro His Val Ala Thr
        115                 120                 125

Ala His Ser Leu Glu Pro Asp Arg Pro Trp Lys Arg Glu Gln Leu Gly
    130                 135                 140

Gly Gly Tyr Asp Val Ser Ser Trp Ser Glu Lys Asn Ala Met Glu Tyr
145                 150                 155                 160

Ala Asp Ala Val Ile Ala Val Ser Ala Arg Met Lys Asp Ser Ile Leu
                165                 170                 175

Ala Ala Tyr Pro Arg Ile Glu Pro Asp Asn Val Arg Val Val Leu Asn
            180                 185                 190

Gly Ile Asp Thr Glu Leu Trp Gln Pro Arg Pro Thr Phe Asp Asp Ala
        195                 200                 205

Glu Asp Ser Val Leu Arg Ser Leu Gly Val Asp Pro Gln Arg Pro Ile
    210                 215                 220

Val Ala Phe Val Gly Arg Ile Thr Arg Gln Lys Gly Val Glu His Leu
225                 230                 235                 240

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

Ala Gly Ala Pro Asp Thr Pro Glu Ile Ala Ala Arg Thr Thr Ala Leu
            260                 265                 270

Val Glu Glu Leu Gln Ala Lys Arg Glu Gly Ile Phe Trp Val Gln Asp
        275                 280                 285

Met Leu Gly Lys Asp Lys Ile Gln Glu Ile Leu Thr Ala Ala Asp Thr
    290                 295                 300

Phe Val Cys Pro Ser Ile Tyr Glu Pro Leu Gly Ile Val Asn Leu Glu
305                 310                 315                 320

Ala Met Ala Cys Asn Thr Ala Val Val Ala Ser Asp Val Gly Gly Ile
                325                 330                 335

Pro Glu Val Val Val Asp Gly Thr Thr Gly Ala Leu Val His Tyr Asp
            340                 345                 350

Glu Asn Asp Val Glu Thr Phe Glu Arg Asp Ile Ala Glu Ala Val Asn
        355                 360                 365

Lys Met Val Ala Asp Arg Glu Thr Ala Ala Lys Phe Gly Leu Ala Gly
    370                 375                 380
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Arg Glu Arg Ala Ile Asn Asp Phe Ser Trp Ala Thr Ile Ala Gln Gln
385                 390                 395                 400

Thr Ile Asp Val Tyr Lys Ser Leu Met
                405


<210> SEQ ID NO 35
<211> LENGTH: 2184
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(2184)
<223> OTHER INFORMATION: E. coli  1,4-alpha-glucan branching enzyme
      (Acc.No. YP 492001.1) (codon optimized)

<400> SEQUENCE: 35

atg tcc gac cgc att gat agg gac gtc ata aat gca ctg atc gct ggc       48
Met Ser Asp Arg Ile Asp Arg Asp Val Ile Asn Ala Leu Ile Ala Gly
1               5                   10                  15

cac ttt gct gac ccg ttc tcc gtt ctg ggc atg cat aag acc acc gcc       96
His Phe Ala Asp Pro Phe Ser Val Leu Gly Met His Lys Thr Thr Ala
            20                  25                  30

ggt ctg gag gtc cgc gcg ctg ctg ccc gac gcg acc gac gtc tgg gtc      144
Gly Leu Glu Val Arg Ala Leu Leu Pro Asp Ala Thr Asp Val Trp Val
        35                  40                  45

atc gag ccc aag act ggc cgc aaa ctg gcg aaa ctt gag tgc ctc gac      192
Ile Glu Pro Lys Thr Gly Arg Lys Leu Ala Lys Leu Glu Cys Leu Asp
    50                  55                  60

agc cgg gga ttc ttt agc ggc gtg atc ccg cgg cgg aag aac ttc ttt      240
Ser Arg Gly Phe Phe Ser Gly Val Ile Pro Arg Arg Lys Asn Phe Phe
65                  70                  75                  80

agg tat caa ctc gcc gtc gtg tgg cat ggg cag cag aac ctg atc gat      288
Arg Tyr Gln Leu Ala Val Val Trp His Gly Gln Gln Asn Leu Ile Asp
                85                  90                  95

gat ccc tac agg ttc ggt ccc ttg atc caa gag atg gat gcg tgg ctg      336
Asp Pro Tyr Arg Phe Gly Pro Leu Ile Gln Glu Met Asp Ala Trp Leu
            100                 105                 110

ctc tcc gag ggc acc cac ctc cgc ccg tac gag act ctc ggg gca cat      384
Leu Ser Glu Gly Thr His Leu Arg Pro Tyr Glu Thr Leu Gly Ala His
        115                 120                 125

gcg gac acg atg gac ggc gtg acg ggc acc cgc ttc tcg gtc tgg gct      432
Ala Asp Thr Met Asp Gly Val Thr Gly Thr Arg Phe Ser Val Trp Ala
    130                 135                 140

ccg aat gca cgc cgg gtg tcc gtg gtc gga cag ttc aat tac tgg gat      480
Pro Asn Ala Arg Arg Val Ser Val Val Gly Gln Phe Asn Tyr Trp Asp
145                 150                 155                 160

ggt cgg cgc cac ccc atg cgg ctg cgg aag gaa tcg ggt atc tgg gag      528
Gly Arg Arg His Pro Met Arg Leu Arg Lys Glu Ser Gly Ile Trp Glu
                165                 170                 175

ttg ttc atc cca ggc gcc cat aac ggg cag ctc tac aaa tac gaa atg      576
Leu Phe Ile Pro Gly Ala His Asn Gly Gln Leu Tyr Lys Tyr Glu Met
            180                 185                 190

atc gat gcg aat ggc aac ctc cgg ctg aaa agt gac ccg tat gcc ttc      624
Ile Asp Ala Asn Gly Asn Leu Arg Leu Lys Ser Asp Pro Tyr Ala Phe
        195                 200                 205

gaa gcg cag atg cgc ccc gaa acg gcg tcc ctg atc tgc ggc ctc cct      672
Glu Ala Gln Met Arg Pro Glu Thr Ala Ser Leu Ile Cys Gly Leu Pro
    210                 215                 220
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```
gaa aaa gtc gtc cag acc gag gaa cgc aag aag gcc aac caa ttc gac      720
Glu Lys Val Val Gln Thr Glu Glu Arg Lys Lys Ala Asn Gln Phe Asp
225                 230                 235                 240

gcg ccg atc tcg atc tat gag gtc cac ctg ggc tcg tgg cgc agg cac      768
Ala Pro Ile Ser Ile Tyr Glu Val His Leu Gly Ser Trp Arg Arg His
                245                 250                 255

acc gac aac aat ttc tgg ctc tcg tac cgc gag ctg gcg gac caa ctc      816
Thr Asp Asn Asn Phe Trp Leu Ser Tyr Arg Glu Leu Ala Asp Gln Leu
            260                 265                 270

gtg ccg tat gct aag tgg atg gga ttc acg cat ttg gaa ctg ctg ccg      864
Val Pro Tyr Ala Lys Trp Met Gly Phe Thr His Leu Glu Leu Leu Pro
        275                 280                 285

atc aac gaa cat ccc ttc gac ggc agc tgg ggc tat cag ccg acc ggc      912
Ile Asn Glu His Pro Phe Asp Gly Ser Trp Gly Tyr Gln Pro Thr Gly
    290                 295                 300

ctc tac gcc ccg act cgc cgg ttc ggc acg cgg gat gac ttc cgg tac      960
Leu Tyr Ala Pro Thr Arg Arg Phe Gly Thr Arg Asp Asp Phe Arg Tyr
305                 310                 315                 320

ttc atc gat gcc gcg cat gcc gcc ggc ctc aac gtc atc ctg gac tgg     1008
Phe Ile Asp Ala Ala His Ala Ala Gly Leu Asn Val Ile Leu Asp Trp
                325                 330                 335

gtg ccc ggt cac ttt ccc acc gac gac ttc gcg ctg gcc gag ttc gac     1056
Val Pro Gly His Phe Pro Thr Asp Asp Phe Ala Leu Ala Glu Phe Asp
            340                 345                 350

ggc acc aac ctc tac gag cat agt gat ccg cgc gag ggc tac cat cag     1104
Gly Thr Asn Leu Tyr Glu His Ser Asp Pro Arg Glu Gly Tyr His Gln
        355                 360                 365

gac tgg aac acg ctc atc tac aat tac ggt cgc cgc gag gtc agc aac     1152
Asp Trp Asn Thr Leu Ile Tyr Asn Tyr Gly Arg Arg Glu Val Ser Asn
    370                 375                 380

ttc ctg gtt ggg aat gcg ctg tat tgg att gag cgc ttc ggc ata gac     1200
Phe Leu Val Gly Asn Ala Leu Tyr Trp Ile Glu Arg Phe Gly Ile Asp
385                 390                 395                 400

gcc ctg cgc gtc gac gcc gtg gca tcc atg atc tac cgc gat tat tcc     1248
Ala Leu Arg Val Asp Ala Val Ala Ser Met Ile Tyr Arg Asp Tyr Ser
                405                 410                 415

cgc aaa gag ggc gag tgg atc ccc aat gag ttc ggt ggc cgc gag aac     1296
Arg Lys Glu Gly Glu Trp Ile Pro Asn Glu Phe Gly Gly Arg Glu Asn
            420                 425                 430

ctt gag gcc att gag ttc ctt agg aat acg aac cgg atc ctg ggg gaa     1344
Leu Glu Ala Ile Glu Phe Leu Arg Asn Thr Asn Arg Ile Leu Gly Glu
        435                 440                 445

caa gtg tcc ggg gct gtc acc atg gca gag gag agc acc gat ttt ccc     1392
Gln Val Ser Gly Ala Val Thr Met Ala Glu Glu Ser Thr Asp Phe Pro
    450                 455                 460

ggc gtg tcg cgc ccg caa gac atg ggt ggc ctg ggc ttc tgg tac aag     1440
Gly Val Ser Arg Pro Gln Asp Met Gly Gly Leu Gly Phe Trp Tyr Lys
465                 470                 475                 480

tgg aat ctg ggc tgg atg cac gac acc ctc gac tac atg aag ctt gat     1488
Trp Asn Leu Gly Trp Met His Asp Thr Leu Asp Tyr Met Lys Leu Asp
                485                 490                 495

ccg gtc tat cgc cag tat cac cat gac aag ctc acg ttc ggc atc ctg     1536
Pro Val Tyr Arg Gln Tyr His His Asp Lys Leu Thr Phe Gly Ile Leu
            500                 505                 510

tat aac tat acc gag aat ttc gtg ctc ccg ttg agc cat gac gaa gtt     1584
Tyr Asn Tyr Thr Glu Asn Phe Val Leu Pro Leu Ser His Asp Glu Val
        515                 520                 525
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gtc cat ggc aag aag agt att ctg gac cgg atg cca ggc gac gcg tgg     1632
Val His Gly Lys Lys Ser Ile Leu Asp Arg Met Pro Gly Asp Ala Trp
    530                 535                 540

cag aaa ttc gcg aat ctc cgc gcc tat tat ggc tgg atg tgg gcg ttc     1680
Gln Lys Phe Ala Asn Leu Arg Ala Tyr Tyr Gly Trp Met Trp Ala Phe
545                 550                 555                 560

ccg ggc aaa aag ctc ctg ttc atg gga aat gag ttc gcc cag ggc cgg     1728
Pro Gly Lys Lys Leu Leu Phe Met Gly Asn Glu Phe Ala Gln Gly Arg
                565                 570                 575

gag tgg aac cat gac gcg agc ctc gac tgg cat ctc ctt gag ggc gga     1776
Glu Trp Asn His Asp Ala Ser Leu Asp Trp His Leu Leu Glu Gly Gly
            580                 585                 590

gac aac tgg cac cac ggc gtg cag cgc ctc gtg cgg gac ctc aac ctg     1824
Asp Asn Trp His His Gly Val Gln Arg Leu Val Arg Asp Leu Asn Leu
        595                 600                 605

acc tac cgc cat cat aaa gcc atg cac gag ctg gat ttc gac ccg tac     1872
Thr Tyr Arg His His Lys Ala Met His Glu Leu Asp Phe Asp Pro Tyr
    610                 615                 620

ggc ttc gag tgg ctc gtc gtc gac gat aag gag cgc tcg gtc ctc att     1920
Gly Phe Glu Trp Leu Val Val Asp Asp Lys Glu Arg Ser Val Leu Ile
625                 630                 635                 640

ttc gtg cgc agg gac aag gaa ggc aac gag atc atc gtg gcg agc aac     1968
Phe Val Arg Arg Asp Lys Glu Gly Asn Glu Ile Ile Val Ala Ser Asn
                645                 650                 655

ttc acc ccg gtc ccg cgg cac gac tac cgc ttc ggc atc aat cag ccg     2016
Phe Thr Pro Val Pro Arg His Asp Tyr Arg Phe Gly Ile Asn Gln Pro
            660                 665                 670

ggc aag tgg cgc gag atc ctg aac acg gac tcg atg cat tat cat ggt     2064
Gly Lys Trp Arg Glu Ile Leu Asn Thr Asp Ser Met His Tyr His Gly
        675                 680                 685

tcg aac gcc ggg aat ggc ggc acc gtg cac tcg gac gag atc gcc tcc     2112
Ser Asn Ala Gly Asn Gly Gly Thr Val His Ser Asp Glu Ile Ala Ser
    690                 695                 700

cat ggc cgc cag cat agc ttg tcc ctg acc ctg ccc cct ctc gcg acc     2160
His Gly Arg Gln His Ser Leu Ser Leu Thr Leu Pro Pro Leu Ala Thr
705                 710                 715                 720

atc tgg ctg gtg cgc gag gcc gag                                     2184
Ile Trp Leu Val Arg Glu Ala Glu
                725
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<210> SEQ ID NO 36
<211> LENGTH: 728
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 36

```
Met Ser Asp Arg Ile Asp Arg Asp Val Ile Asn Ala Leu Ile Ala Gly
1               5                   10                  15

His Phe Ala Asp Pro Phe Ser Val Leu Gly Met His Lys Thr Thr Ala
            20                  25                  30

Gly Leu Glu Val Arg Ala Leu Leu Pro Asp Ala Thr Asp Val Trp Val
        35                  40                  45

Ile Glu Pro Lys Thr Gly Arg Lys Leu Ala Lys Leu Glu Cys Leu Asp
    50                  55                  60

Ser Arg Gly Phe Phe Ser Gly Val Ile Pro Arg Arg Lys Asn Phe Phe
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65                  70                  75                  80

Arg Tyr Gln Leu Ala Val Val Trp His Gly Gln Gln Asn Leu Ile Asp
                85                  90                  95

Asp Pro Tyr Arg Phe Gly Pro Leu Ile Gln Glu Met Asp Ala Trp Leu
            100                 105                 110

Leu Ser Glu Gly Thr His Leu Arg Pro Tyr Glu Thr Leu Gly Ala His
        115                 120                 125

Ala Asp Thr Met Asp Gly Val Thr Gly Thr Arg Phe Ser Val Trp Ala
    130                 135                 140

Pro Asn Ala Arg Arg Val Ser Val Val Gly Gln Phe Asn Tyr Trp Asp
145                 150                 155                 160

Gly Arg Arg His Pro Met Arg Leu Arg Lys Glu Ser Gly Ile Trp Glu
                165                 170                 175

Leu Phe Ile Pro Gly Ala His Asn Gly Gln Leu Tyr Lys Tyr Glu Met
            180                 185                 190

Ile Asp Ala Asn Gly Asn Leu Arg Leu Lys Ser Asp Pro Tyr Ala Phe
        195                 200                 205

Glu Ala Gln Met Arg Pro Glu Thr Ala Ser Leu Ile Cys Gly Leu Pro
    210                 215                 220

Glu Lys Val Val Gln Thr Glu Glu Arg Lys Lys Ala Asn Gln Phe Asp
225                 230                 235                 240

Ala Pro Ile Ser Ile Tyr Glu Val His Leu Gly Ser Trp Arg Arg His
                245                 250                 255

Thr Asp Asn Asn Phe Trp Leu Ser Tyr Arg Glu Leu Ala Asp Gln Leu
            260                 265                 270

Val Pro Tyr Ala Lys Trp Met Gly Phe Thr His Leu Glu Leu Leu Pro
        275                 280                 285

Ile Asn Glu His Pro Phe Asp Gly Ser Trp Gly Tyr Gln Pro Thr Gly
    290                 295                 300

Leu Tyr Ala Pro Thr Arg Arg Phe Gly Thr Arg Asp Asp Phe Arg Tyr
305                 310                 315                 320

Phe Ile Asp Ala Ala His Ala Ala Gly Leu Asn Val Ile Leu Asp Trp
                325                 330                 335

Val Pro Gly His Phe Pro Thr Asp Asp Phe Ala Leu Ala Glu Phe Asp
            340                 345                 350

Gly Thr Asn Leu Tyr Glu His Ser Asp Pro Arg Glu Gly Tyr His Gln
        355                 360                 365

Asp Trp Asn Thr Leu Ile Tyr Asn Tyr Gly Arg Arg Glu Val Ser Asn
    370                 375                 380

Phe Leu Val Gly Asn Ala Leu Tyr Trp Ile Glu Arg Phe Gly Ile Asp
385                 390                 395                 400

Ala Leu Arg Val Asp Ala Val Ala Ser Met Ile Tyr Arg Asp Tyr Ser
                405                 410                 415

Arg Lys Glu Gly Glu Trp Ile Pro Asn Glu Phe Gly Gly Arg Glu Asn
            420                 425                 430

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

Gln Val Ser Gly Ala Val Thr Met Ala Glu Glu Ser Thr Asp Phe Pro
    450                 455                 460

Gly Val Ser Arg Pro Gln Asp Met Gly Gly Leu Gly Phe Trp Tyr Lys
465                 470                 475                 480
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Trp Asn Leu Gly Trp Met His Asp Thr Leu Asp Tyr Met Lys Leu Asp
                485                 490                 495

Pro Val Tyr Arg Gln Tyr His His Asp Lys Leu Thr Phe Gly Ile Leu
            500                 505                 510

Tyr Asn Tyr Thr Glu Asn Phe Val Leu Pro Leu Ser His Asp Glu Val
        515                 520                 525

Val His Gly Lys Lys Ser Ile Leu Asp Arg Met Pro Gly Asp Ala Trp
    530                 535                 540

Gln Lys Phe Ala Asn Leu Arg Ala Tyr Tyr Gly Trp Met Trp Ala Phe
545                 550                 555                 560

Pro Gly Lys Lys Leu Leu Phe Met Gly Asn Glu Phe Ala Gln Gly Arg
                565                 570                 575

Glu Trp Asn His Asp Ala Ser Leu Asp Trp His Leu Leu Glu Gly Gly
            580                 585                 590

Asp Asn Trp His His Gly Val Gln Arg Leu Val Arg Asp Leu Asn Leu
        595                 600                 605

Thr Tyr Arg His His Lys Ala Met His Glu Leu Asp Phe Asp Pro Tyr
    610                 615                 620

Gly Phe Glu Trp Leu Val Val Asp Asp Lys Glu Arg Ser Val Leu Ile
625                 630                 635                 640

Phe Val Arg Arg Asp Lys Glu Gly Asn Glu Ile Ile Val Ala Ser Asn
                645                 650                 655

Phe Thr Pro Val Pro Arg His Asp Tyr Arg Phe Gly Ile Asn Gln Pro
            660                 665                 670

Gly Lys Trp Arg Glu Ile Leu Asn Thr Asp Ser Met His Tyr His Gly
        675                 680                 685

Ser Asn Ala Gly Asn Gly Gly Thr Val His Ser Asp Glu Ile Ala Ser
    690                 695                 700

His Gly Arg Gln His Ser Leu Ser Leu Thr Leu Pro Pro Leu Ala Thr
705                 710                 715                 720

Ile Trp Leu Val Arg Glu Ala Glu
                725


<210> SEQ ID NO 37
<211> LENGTH: 2193
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(2193)
<223> OTHER INFORMATION: Corynebacterium glutamicum  (ATCC 13032)
      Glycogen branching enzyme (codon optimized)

<400> SEQUENCE: 37

atg acc gtc gac ccc gcg tcc cat atc acg atc ccc gaa gcc gac ctc       48
Met Thr Val Asp Pro Ala Ser His Ile Thr Ile Pro Glu Ala Asp Leu
1               5                   10                  15

gca cgc ctc cgc cac tgc aac cat cac gac ccc cat gga ttc tac ggg       96
Ala Arg Leu Arg His Cys Asn His His Asp Pro His Gly Phe Tyr Gly
            20                  25                  30

tgg cat gaa act gag gcc ggg tcc gtc att cgc acc cgc cag gtc ggc      144
Trp His Glu Thr Glu Ala Gly Ser Val Ile Arg Thr Arg Gln Val Gly
        35                  40                  45
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gcg acc cag gtg aat ctg ctc att gat gac acg agc cat gtc atg acg      192
Ala Thr Gln Val Asn Leu Leu Ile Asp Asp Thr Ser His Val Met Thr
    50                  55                  60

ccc atc ggc gac gac atc ttc gcg atc gac ctc ggg cat cgg gag cgc      240
Pro Ile Gly Asp Asp Ile Phe Ala Ile Asp Leu Gly His Arg Glu Arg
65                  70                  75                  80

gct gat tac cgc ctt gag gtc acg tgg ccg gac caa gag cca cag gtg      288
Ala Asp Tyr Arg Leu Glu Val Thr Trp Pro Asp Gln Glu Pro Gln Val
                85                  90                  95

aaa gct gac ccg tac tat ttc ctc ccc acg gtc ggt gag atg gac atc      336
Lys Ala Asp Pro Tyr Tyr Phe Leu Pro Thr Val Gly Glu Met Asp Ile
            100                 105                 110

tat ctg ttc tcc gag ggt cgg cac gaa cgg ctc tgg gag atc ctc ggc      384
Tyr Leu Phe Ser Glu Gly Arg His Glu Arg Leu Trp Glu Ile Leu Gly
        115                 120                 125

gcc aat atc aag acc tat cag acc gcg ctg ggc acc gtc cgc ggc acg      432
Ala Asn Ile Lys Thr Tyr Gln Thr Ala Leu Gly Thr Val Arg Gly Thr
    130                 135                 140

gcg ttc acc gtc tgg gca ccc aac gcg atc ggc tgc gcg gtc gtg ggg      480
Ala Phe Thr Val Trp Ala Pro Asn Ala Ile Gly Cys Ala Val Val Gly
145                 150                 155                 160

ggc ttc aac ggt tgg aac gcc agt caa cac ccg atg cgg agc atg ggc      528
Gly Phe Asn Gly Trp Asn Ala Ser Gln His Pro Met Arg Ser Met Gly
                165                 170                 175

gga tcc ggc ctt tgg gag ctg ttc atc ccg ggc atc gag gag ggc gag      576
Gly Ser Gly Leu Trp Glu Leu Phe Ile Pro Gly Ile Glu Glu Gly Glu
            180                 185                 190

gtg tac aag ttt gcg gtg cag acc cgc gaa ggc cag cgc agg gat aag      624
Val Tyr Lys Phe Ala Val Gln Thr Arg Glu Gly Gln Arg Arg Asp Lys
        195                 200                 205

gcc gac ccc atg gcg cgg cgc gcc gag ctg gca cca gcc acc ggc agc      672
Ala Asp Pro Met Ala Arg Arg Ala Glu Leu Ala Pro Ala Thr Gly Ser
    210                 215                 220

ata gtt gcc tcg tcc gag tac cag tgg cag gac tcc gag tgg ctg cgc      720
Ile Val Ala Ser Ser Glu Tyr Gln Trp Gln Asp Ser Glu Trp Leu Arg
225                 230                 235                 240

gag cgg agc cag act gac ctc gcc agc aag cct atg tcc gtg tat gag      768
Glu Arg Ser Gln Thr Asp Leu Ala Ser Lys Pro Met Ser Val Tyr Glu
                245                 250                 255

gtg cat ctg ggt tcg tgg cgc tgg ggc aag aac tac gaa gat ctg gcg      816
Val His Leu Gly Ser Trp Arg Trp Gly Lys Asn Tyr Glu Asp Leu Ala
            260                 265                 270

acc gag ctc gtc gat tat gtt gcg gac ctg ggt tat acg cat gtc gag      864
Thr Glu Leu Val Asp Tyr Val Ala Asp Leu Gly Tyr Thr His Val Glu
        275                 280                 285

ttc ctg ccg gtg gcg gag cac ccg ttc ggc ggc tcg tgg ggc tac caa      912
Phe Leu Pro Val Ala Glu His Pro Phe Gly Gly Ser Trp Gly Tyr Gln
    290                 295                 300

gtc acg ggt tat tac gcg ccg acc agc cgc tgg ggc acc ccg gac cag      960
Val Thr Gly Tyr Tyr Ala Pro Thr Ser Arg Trp Gly Thr Pro Asp Gln
305                 310                 315                 320

ttc cgc gcg ttg gtc gac gcg ttc cac gcc agg gga atc ggc gtc atc     1008
Phe Arg Ala Leu Val Asp Ala Phe His Ala Arg Gly Ile Gly Val Ile
                325                 330                 335

atg gac tgg gtt ccc gca cat ttc ccg aaa gat gat tgg gcg ctg gcg     1056
Met Asp Trp Val Pro Ala His Phe Pro Lys Asp Asp Trp Ala Leu Ala
            340                 345                 350
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cgg ttc gac ggc gag gcc ctc tat gag cac ccg gac tgg cgg cgg ggt     1104
Arg Phe Asp Gly Glu Ala Leu Tyr Glu His Pro Asp Trp Arg Arg Gly
        355                 360                 365

gag cag aaa gat tgg ggg acc ctc gtg ttc gat ttt ggc cgg aac gaa     1152
Glu Gln Lys Asp Trp Gly Thr Leu Val Phe Asp Phe Gly Arg Asn Glu
    370                 375                 380

gtc cgc aac ttc ttg gtc gcg aac gcg ctc tat tgg att gaa gag ttc     1200
Val Arg Asn Phe Leu Val Ala Asn Ala Leu Tyr Trp Ile Glu Glu Phe
385                 390                 395                 400

cat att gac ggc ctc cgg gtc gac gcc gtc gcc tcg atg ctc tac ctg     1248
His Ile Asp Gly Leu Arg Val Asp Ala Val Ala Ser Met Leu Tyr Leu
                405                 410                 415

gac tac tcg cgc gag cac ggc gag tgg gag ccg aac atc tat ggc gga     1296
Asp Tyr Ser Arg Glu His Gly Glu Trp Glu Pro Asn Ile Tyr Gly Gly
            420                 425                 430

cgg gag aat ctc gaa gcc gtc cag ttc ctg caa gag atg aac gca acc     1344
Arg Glu Asn Leu Glu Ala Val Gln Phe Leu Gln Glu Met Asn Ala Thr
        435                 440                 445

gtg ctc cgc ctg cat cct ggt gcg ctg acc atc gca gag gaa tcg acc     1392
Val Leu Arg Leu His Pro Gly Ala Leu Thr Ile Ala Glu Glu Ser Thr
    450                 455                 460

tcg tgg ccg ggt gtg acc gct ccg acc tgg gac ggt ggc ctt ggt ttc     1440
Ser Trp Pro Gly Val Thr Ala Pro Thr Trp Asp Gly Gly Leu Gly Phe
465                 470                 475                 480

agc ctg aag tgg aat atg ggc tgg atg cat gac acc ctt gag tat ttc     1488
Ser Leu Lys Trp Asn Met Gly Trp Met His Asp Thr Leu Glu Tyr Phe
                485                 490                 495

tcg aag aat ccg gtg cac agg gcc ttc cac cat tcc gag ctg acg ttc     1536
Ser Lys Asn Pro Val His Arg Ala Phe His His Ser Glu Leu Thr Phe
            500                 505                 510

tcg ctt gtc tac gcc ttc agt gag cgc ttc gtg ctg ccg atc tcc cat     1584
Ser Leu Val Tyr Ala Phe Ser Glu Arg Phe Val Leu Pro Ile Ser His
        515                 520                 525

gac gaa gtc gtc cac ggc aag ggc tcc ctg tgg gac cgg atg ccg ggt     1632
Asp Glu Val Val His Gly Lys Gly Ser Leu Trp Asp Arg Met Pro Gly
    530                 535                 540

gac acc tgg aat aaa gcc gca ggc ctc cgc acg ttc ctg gcg tac atg     1680
Asp Thr Trp Asn Lys Ala Ala Gly Leu Arg Thr Phe Leu Ala Tyr Met
545                 550                 555                 560

tgg agc cac ccg ggc aag aaa ctg ctg ttc atg ggc caa gag ttc ggc     1728
Trp Ser His Pro Gly Lys Lys Leu Leu Phe Met Gly Gln Glu Phe Gly
                565                 570                 575

cag cgc gag gag tgg gcc gag ggc cag ggc ctg ccc tgg gac atc gtg     1776
Gln Arg Glu Glu Trp Ala Glu Gly Gln Gly Leu Pro Trp Asp Ile Val
            580                 585                 590

gac ggg tgg cag ggc gag tat cat gaa gcg atc cgc acc ctc acg cgc     1824
Asp Gly Trp Gln Gly Glu Tyr His Glu Ala Ile Arg Thr Leu Thr Arg
        595                 600                 605

agc ctg aac ggc gtg tac agc gat agt ccg gcg ctc cat acc caa gat     1872
Ser Leu Asn Gly Val Tyr Ser Asp Ser Pro Ala Leu His Thr Gln Asp
    610                 615                 620

ttc acc ggc gag ggc ttc acg tgg aac aaa ggt gac gac gcc acc aat     1920
Phe Thr Gly Glu Gly Phe Thr Trp Asn Lys Gly Asp Asp Ala Thr Asn
625                 630                 635                 640

aac atc ctc gcc ttc acc cgc ttt ggc tcc gac ggc tcg cag atg ctc     1968
Asn Ile Leu Ala Phe Thr Arg Phe Gly Ser Asp Gly Ser Gln Met Leu
                645                 650                 655
```

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tgc gtg ttc aac ctc tcg ggc acc tcg cag ccg gag tac cag ctc ggg     2016
Cys Val Phe Asn Leu Ser Gly Thr Ser Gln Pro Glu Tyr Gln Leu Gly
            660                 665                 670

gtg gcc gct ggg ggc gag tgg aag ctt gtg ctg aat acc gac gac gcc     2064
Val Ala Ala Gly Gly Glu Trp Lys Leu Val Leu Asn Thr Asp Asp Ala
        675                 680                 685

gag ttt ttg gga gcc gaa aac gat atc gcg acg agc gtg caa gct gct     2112
Glu Phe Leu Gly Ala Glu Asn Asp Ile Ala Thr Ser Val Gln Ala Ala
    690                 695                 700

gcc act ccc agg gac aat ttc gcc tat tcc ctg agc ctg cat gtc ccc     2160
Ala Thr Pro Arg Asp Asn Phe Ala Tyr Ser Leu Ser Leu His Val Pro
705                 710                 715                 720

gcc atg tcg gcg cag ttc tac tcg ctc cag aag                         2193
Ala Met Ser Ala Gln Phe Tyr Ser Leu Gln Lys
                725                 730


<210> SEQ ID NO 38
<211> LENGTH: 731
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 38

Met Thr Val Asp Pro Ala Ser His Ile Thr Ile Pro Glu Ala Asp Leu
1               5                   10                  15

Ala Arg Leu Arg His Cys Asn His His Asp Pro His Gly Phe Tyr Gly
            20                  25                  30

Trp His Glu Thr Glu Ala Gly Ser Val Ile Arg Thr Arg Gln Val Gly
        35                  40                  45

Ala Thr Gln Val Asn Leu Leu Ile Asp Asp Thr Ser His Val Met Thr
    50                  55                  60

Pro Ile Gly Asp Asp Ile Phe Ala Ile Asp Leu Gly His Arg Glu Arg
65                  70                  75                  80

Ala Asp Tyr Arg Leu Glu Val Thr Trp Pro Asp Gln Glu Pro Gln Val
                85                  90                  95

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

Tyr Leu Phe Ser Glu Gly Arg His Glu Arg Leu Trp Glu Ile Leu Gly
        115                 120                 125

Ala Asn Ile Lys Thr Tyr Gln Thr Ala Leu Gly Thr Val Arg Gly Thr
    130                 135                 140

Ala Phe Thr Val Trp Ala Pro Asn Ala Ile Gly Cys Ala Val Val Gly
145                 150                 155                 160

Gly Phe Asn Gly Trp Asn Ala Ser Gln His Pro Met Arg Ser Met Gly
                165                 170                 175

Gly Ser Gly Leu Trp Glu Leu Phe Ile Pro Gly Ile Glu Glu Gly Glu
            180                 185                 190

Val Tyr Lys Phe Ala Val Gln Thr Arg Glu Gly Gln Arg Arg Asp Lys
        195                 200                 205

Ala Asp Pro Met Ala Arg Arg Ala Glu Leu Ala Pro Ala Thr Gly Ser
    210                 215                 220

Ile Val Ala Ser Ser Glu Tyr Gln Trp Gln Asp Ser Glu Trp Leu Arg
225                 230                 235                 240

Glu Arg Ser Gln Thr Asp Leu Ala Ser Lys Pro Met Ser Val Tyr Glu
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               245                 250                 255

Val His Leu Gly Ser Trp Arg Trp Gly Lys Asn Tyr Glu Asp Leu Ala
            260                 265                 270

Thr Glu Leu Val Asp Tyr Val Ala Asp Leu Gly Tyr Thr His Val Glu
        275                 280                 285

Phe Leu Pro Val Ala Glu His Pro Phe Gly Gly Ser Trp Gly Tyr Gln
    290                 295                 300

Val Thr Gly Tyr Tyr Ala Pro Thr Ser Arg Trp Gly Thr Pro Asp Gln
305                 310                 315                 320

Phe Arg Ala Leu Val Asp Ala Phe His Ala Arg Gly Ile Gly Val Ile
                325                 330                 335

Met Asp Trp Val Pro Ala His Phe Pro Lys Asp Asp Trp Ala Leu Ala
            340                 345                 350

Arg Phe Asp Gly Glu Ala Leu Tyr Glu His Pro Asp Trp Arg Arg Gly
        355                 360                 365

Glu Gln Lys Asp Trp Gly Thr Leu Val Phe Asp Phe Gly Arg Asn Glu
    370                 375                 380

Val Arg Asn Phe Leu Val Ala Asn Ala Leu Tyr Trp Ile Glu Glu Phe
385                 390                 395                 400

His Ile Asp Gly Leu Arg Val Asp Ala Val Ala Ser Met Leu Tyr Leu
                405                 410                 415

Asp Tyr Ser Arg Glu His Gly Glu Trp Glu Pro Asn Ile Tyr Gly Gly
            420                 425                 430

Arg Glu Asn Leu Glu Ala Val Gln Phe Leu Gln Glu Met Asn Ala Thr
        435                 440                 445

Val Leu Arg Leu His Pro Gly Ala Leu Thr Ile Ala Glu Glu Ser Thr
    450                 455                 460

Ser Trp Pro Gly Val Thr Ala Pro Thr Trp Asp Gly Gly Leu Gly Phe
465                 470                 475                 480

Ser Leu Lys Trp Asn Met Gly Trp Met His Asp Thr Leu Glu Tyr Phe
                485                 490                 495

Ser Lys Asn Pro Val His Arg Ala Phe His His Ser Glu Leu Thr Phe
            500                 505                 510

Ser Leu Val Tyr Ala Phe Ser Glu Arg Phe Val Leu Pro Ile Ser His
        515                 520                 525

Asp Glu Val Val His Gly Lys Gly Ser Leu Trp Asp Arg Met Pro Gly
    530                 535                 540

Asp Thr Trp Asn Lys Ala Ala Gly Leu Arg Thr Phe Leu Ala Tyr Met
545                 550                 555                 560

Trp Ser His Pro Gly Lys Lys Leu Leu Phe Met Gly Gln Glu Phe Gly
                565                 570                 575

Gln Arg Glu Glu Trp Ala Glu Gly Gln Gly Leu Pro Trp Asp Ile Val
            580                 585                 590

Asp Gly Trp Gln Gly Glu Tyr His Glu Ala Ile Arg Thr Leu Thr Arg
        595                 600                 605

Ser Leu Asn Gly Val Tyr Ser Asp Ser Pro Ala Leu His Thr Gln Asp
    610                 615                 620

Phe Thr Gly Glu Gly Phe Thr Trp Asn Lys Gly Asp Asp Ala Thr Asn
625                 630                 635                 640

Asn Ile Leu Ala Phe Thr Arg Phe Gly Ser Asp Gly Ser Gln Met Leu
                645                 650                 655
```

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```
Cys Val Phe Asn Leu Ser Gly Thr Ser Gln Pro Glu Tyr Gln Leu Gly
            660                 665                 670

Val Ala Ala Gly Gly Glu Trp Lys Leu Val Leu Asn Thr Asp Asp Ala
        675                 680                 685

Glu Phe Leu Gly Ala Glu Asn Asp Ile Ala Thr Ser Val Gln Ala Ala
    690                 695                 700

Ala Thr Pro Arg Asp Asn Phe Ala Tyr Ser Leu Ser Leu His Val Pro
705                 710                 715                 720

Ala Met Ser Ala Gln Phe Tyr Ser Leu Gln Lys
                725                 730
```

What is claimed is:

1. A recombinant methanotrophic bacterium, comprising an exogenous nucleic acid that encodes a gluconeogenesis enzyme,

wherein the encoded gluconeogenesis enzyme is one or more of a pyruvate carboxylase, a phosphoenolpyruvate carboxykinase, an enolase, a phosphoglycerate mutase, a phosphoglycerate kinase, a glyceraldehyde-3-phosphate dehydrogenase, a Type A aldolase, a fructose 1,6-bisphosphatase, a phosphofructokinase, a phosphoglucose isomerase, a hexokinase, and a glucose-6-phosphate,

wherein the methanotrophic bacterium is selected from the group consisting of *Methylomonas, Methylobacter, Methylococcus, Methylosinus, Methylocystis, Methylomicrobium, Methanomonas*, and *Methylocella*, and

wherein the recombinant methanotrophic bacterium grown on a C_1 substrate feedstock is capable of producing glucose at a level that is greater than that produced by the parent methanotrophic bacterium.

2. The recombinant methanotrophic bacterium of claim **1**, wherein the C_1 substrate feedstock comprises natural gas or methane.

3. The recombinant methanotrophic bacterium of claim **1**, wherein the methanotrophic bacterium is an obligate methanotrophic bacterium.

4. The recombinant methanotrophic bacterium of claim **1**, wherein the methanotrophic bacterium is a facultative methanotrophic bacterium.

5. The recombinant methanotrophic bacterium of claim **1**, wherein the methanotrophic bacterium is selected from the group consisting of *Methylococcus capsulatus* Bath, *Methylomonas* sp. 16a, *Methylosinus trichosporium* OB3b, *Methylosinus sporium, Methylocystis parvus, Methylomonas methanica, Methylomonas albus, Methylobacter capsulatus* Y, *Methylomonas flagellata* AJ-3670, *Methylacidiphilum infernorum, Methylacidiphdum fumariolicum, Methylomicrobium alcaliphdum*, and *Methyloacida kamchatkensis*.

6. The recombinant methanotrophic bacterium of claim **1**, wherein the exogenous nucleic acid encoding the gluconeogenesis enzyme is endogenous to an organism selected from the group consisting of a bacterium, a yeast, a fungi, and a plant.

7. The recombinant methanotrophic bacterium of claim **1**, wherein the exogenous nucleic acid comprises an expression control sequence that is operably linked to the nucleic acid encoding the gluconeogenesis enzyme.

8. The recombinant methanotrophic bacterium of claim **1**, wherein the exogenous nucleic acid encoding the gluconeogenesis enzyme is endogenous to *Escherichia coli* or *Corynebacterium glutamicum*.

9. The recombinant methanotrophic bacterium of claim **1**, wherein the exogenous nucleic acid encoding the gluconeogenesis enzyme is endogenous to *Saccharomyces cerevisiae*.

10. The recombinant methanotrophic bacterium of claim **1**, wherein the exogenous nucleic acid encoding the gluconeogenesis enzyme is codon optimized for the methanotrophic bacterium.

11. The recombinant methanotrophic bacterium of claim **1**, wherein the carbohydrates of the recombinant methanotrophic bacterium exhibits a $\delta^{13}C$ that is less than −30‰ or is less than −40‰.

12. The recombinant methanotrophic bacterium of claim **1**, wherein the methanotrophic bacterium further comprises an exogenous polynucleotide encoding one or more glycogenesis enzymes selected from the group consisting of a glucose-1-phosphate adenyltransferase, a glycogen synthase, and a 1,4-alpha-glucan-branching protein.

13. The recombinant methanotrophic bacterium of claim **12**, wherein the further exogenous polynucleotide encoding one or more glycogenesis enzymes comprises an expression control sequence that is operably linked to the polynucleotide encoding the one or more glycogenesis enzymes, wherein the one or more glycogenesis enzymes are heterologous glycogenesis enzymes, native glycogenesis enzymes, or a combination thereof.

14. The recombinant methanotrophic bacterium of claim **12**, wherein the exogenous nucleic acid encoding the one or more glycogenesis enzymes is codon optimized for the methanotrophic bacterium.

15. A biomass derived from whole and/or lysed cells of the recombinant methanotrophic bacterium of claim **1**.

16. A carbohydrate composition, comprising carbohydrates extracted from a biomass derived from the methanotrophic bacterium of claim **1**, wherein the composition exhibits a $\delta^{13}C$ that is less than −30‰ or is less than −40‰.

17. An animal feed, comprising the recombinant methanotrophic bacterium of claim **1**, a biomass derived from whole and/or lysed cells of the recombinant methanotrophic bacterium of claim **1**, or a carbohydrate composition comprising carbohydrates extracted from a biomass derived from the recombinant methanotrophic bacterium of claim **1**.

18. The animal feed of claim **17**, further comprising an additive selected from the group consisting of a plant-derived material, an animal-derived material, and a micro-organism-derived material.

19. The animal feed of claim **18**, wherein the additive is plant-derived material and the plant-derived material is selected from the group consisting of corn, soybean meal, pea protein, or a combination thereof.

20. The animal feed of claim **18**, wherein the additive is an animal-derived material and the animal-derived material is fish meal.

21. A method of producing a desired carbohydrate, the method comprising culturing the recombinant methanotrophic bacterium of claim **1** in the presence of a C_1 substrate feedstock comprising methane under conditions sufficient to produce the glucose.

22. The method of claim **21**, wherein the natural gas-derived carbon feedstock is natural gas.

23. The method of claim **21**, wherein the methanotrophic bacterium is selected from the group consisting of *Methylococcus capsulatus* Bath, *Methylomonas* sp. 16a, *Methylosinus trichosporium* OB3b, *Methylosinus sporium, Methylocystis parvus, Methylomonas methanica, Methylomonas albus, Methylobacter capsulatus* Y, *Methylomonas flagellata* AJ-3670, *Methylacidiphilum infernorum, Methylacidiphilum fumariolicum, Methylomicrobium alcaliphilum*, and *Methyloacida kamchatkensis*.

* * * * *