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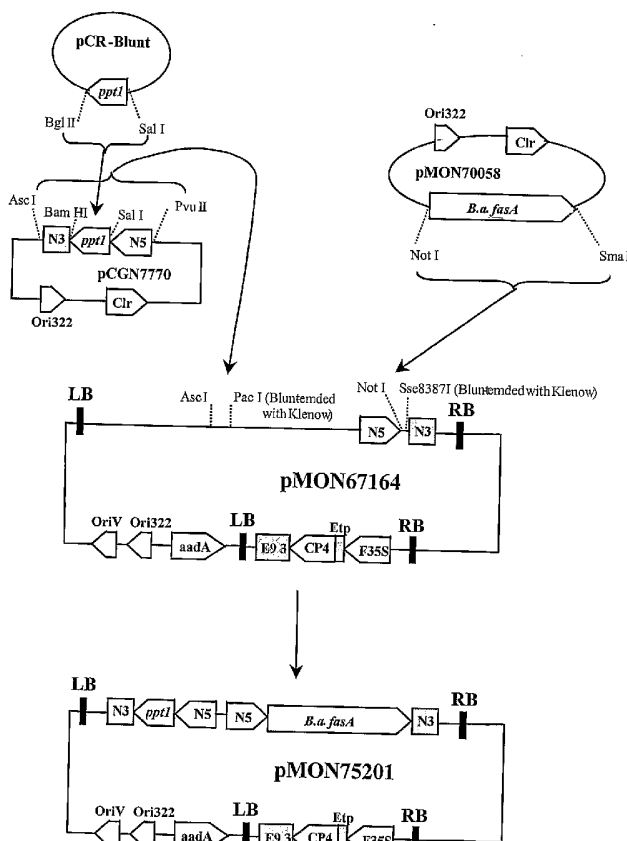
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(54) Title: ELEVATION OF OIL LEVELS IN BRASSICA PLANTS



(57) Abstract: This present invention provides a method for increasing oil levels in the tissues of *Brassica* sp. plants by expression of a heterologous multifunctional fatty acid synthase (mfFAS) within the plant. In one embodiment, the present invention provides isolated nucleic acid molecules encoding mfFAS enzymes from various sources for this purpose, and vectors and plants containing same.



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ELEVATION OF OIL LEVELS IN *BRASSICA* PLANTS

This patent application claims the benefit of U.S. Provisional Patent Application No. 60/435,197, filed December 19, 2002, incorporated herein by reference.

The present invention relates to the fields of nucleic acid chemistry and agricultural biotechnology. In particular, the present invention is directed at the identification of nucleic acids that encode proteins useful for increasing oil levels in *Brassica* plants and creating *Brassica* plants that include such nucleic acids.

Brassica plants are a source of polyunsaturated oils. While tissues of most *Brassica* plant species contain little oil, the cultivation of certain plant types, over many acres, permit large quantities of *Brassica* plant oils to be produced. If the oil content of these *Brassica* plants could be increased, then *Brassica* plant oils could be produced more efficiently.

Higher plants such as *Brassica* synthesize fatty acids via a common metabolic pathway involving the co-factor ACP and the fatty acid synthase (FAS) enzyme complex. The FAS complex consists of about 8 separate enzymes that catalyze 30 or more individual reaction steps, all of which, in plants, are located in the plastids. In developing seeds, for example, where fatty acids are stored, the fatty acid synthase (FAS) enzyme complex is located in the plastids, synthesizes the fatty acids therein, and then the fatty acids are transported to the cytosol in accordance with energy needs there.

Certain workers have attempted to increase or modulate the oil content of plants. For example, U.S. Patent 6,268,550 to Gengenbach *et al.*, provides maize acetyl CoA carboxylase nucleic acids for altering the oil content of plants. Additionally, U.S. Patent 5,925,805 to Ohlrogge *et al.*, provides an *Arabidopsis* acetyl CoA carboxylase gene that can be used to increase the oil content of plants.

SUMMARY OF THE INVENTION

A need exists for a method to increase the oil content of *Brassica* plants and seeds. Moreover, it would be more energy efficient to provide the plant with a capability to synthesize fatty acids in the cytosol directly. This present invention provides a *Brassica* sp. plant comprising a heterologous nucleic acid encoding a multifunctional fatty acid synthase. In one embodiment, the plant further comprises a second nucleic acid encoding a phosphopantetheine:protein transferase. In one preferred embodiment the *Brassica* plant produces increased oil levels in the seed tissue as a result of the multifunctional fatty acid synthase. In another preferred embodiment the multifunctional fatty acid synthase is substantially located in the cytosol of the plant cell.

This present invention further provides a method for increasing oil levels in the tissues of a *Brassica* sp. plant by expressing a gene encoding a multifunctional fatty acid synthase on either a single or multiple polypeptide chains. In one preferred embodiment of this present invention, the gene encodes a cytosol-targeted mfFAS. Preferably, the source of the mfFAS is selected from the group consisting of bacteria, fungus, planta, mycoplasma, and the like; more preferably, the source of the mfFAS is bacteria or fungus; most preferably, the source of the mfFAS is bacteria. In another embodiment of this present invention, the expression of the mfFAS gene is in the seed tissue of the *Brassica* plant, preferably resulting in the accumulation of oil in the seed.

In another embodiment the present invention provides plant transformation vectors for *Brassica* containing a mfFAS gene, as well as transformed *Brassica* plants and seeds are also provided.

In another embodiment, the present invention provides a method of producing a *Brassica* oil, comprising the steps of: a) growing an oilseed *Brassica* plant, the genome of which contains a nucleic acid molecule encoding a multifunctional fatty acid synthase, to produce oil-containing seeds; and b) extracting oil from the seeds. In another embodiment, the present invention provides a method of producing a *Brassica* oil, comprising the steps of: a) growing an oilseed *Brassica* plant, the genome of which contains a nucleic acid molecule encoding a phosphopantetheine:protein transferase, to produce oil-containing seeds; and b) extracting oil from the seeds.

DESCRIPTION OF THE FIGURES

Figure 1 provides a map of the plasmid pMON70058 that contains the 8 KB *fasA* gene from *Brevibacterium ammoniagenes*.

Figure 2 provides an alignment of the *fasA* *Brevibacterium ammoniagenes* nucleic acid sequence [SEQ ID NO: 1] provided herein with a published *fasA* *Brevibacterium ammoniagenes* nucleic acid sequence (Stuible *et al.*, *J. Bacteriol.*, 178:4787, 1996). A number of differences at the DNA level were observed.

Figure 3 provides an alignment of the *fasA* *Brevibacterium ammoniagenes* amino acid sequence [SEQ ID NO: 1] provided herein with a published *fasA* *Brevibacterium ammoniagenes* amino acid sequence (Stuible *et al.*, *J. Bacteriol.*, 178:4787, 1996). A number of differences at the protein level were observed.

Figure 4 illustrates FasA enzyme activity of the cloned *fasA* gene from *B. ammoniagenes*. The FasA enzyme activity was determined as outlined in Kawaguchi *et al.*, *Methods in Enzymology*, 71:120-127 (1981) for partially purified enzyme preparations

from *B. ammoniagenes* (*B.a.*), for an untransformed *E. coli* strain VCS257 (*E.c.*), and for the same strain transformed with the *ppt1* expressing plasmid (*E.c.*+ P), the *fasA* cosmid (*E.c.*+ FA), or the *ppt1* expressing plasmid and the *fasA* cosmid (*E.c.*+ P + FA).

Figure 5 provides a schematic representation of the preparation of pMON75201 as well as a map of pMON75201.

Figure 6 shows the results of the analyses of R2 seed from events generated from the transformation of canola explants with the vector pMON75201.

Figure 7 shows the statistical analysis of the oil results from positive and negative isolines of event BN_G1216.

BRIEF DESCRIPTION OF THE SEQUENCES

SEQ ID NO: 1 is a DNA encoding FasA from *Brevibacterium ammoniagenes*.

SEQ ID NO: 2 is a protein known as FasA from *Brevibacterium ammoniagenes*.

SEQ ID NO: 3 is a DNA encoding a phosphopantetheine:protein transferase (PPT1) enzyme from *B. ammoniagenes*.

SEQ ID NO: 4 is a protein known as phosphopantetheine:protein transferase (PPT1) enzyme from *B. ammoniagenes*.

SEQ ID NO: 5 is a nucleic acid used as a PCR primer.

SEQ ID NO: 6 is a nucleic acid used as a PCR primer.

SEQ ID NO: 7 is a nucleic acid used as a PCR primer.

SEQ ID NO: 8 is a nucleic acid used as a PCR primer.

SEQ ID NO: 9 is a nucleic acid used as a PCR primer.

SEQ ID NO: 10 is a nucleic acid used as a PCR primer.

SEQ ID NO: 11 is a nucleic acid used as a PCR primer.

SEQ ID NO: 12 is a nucleic acid used as a PCR primer.

SEQ ID NO: 13 is a nucleic acid used as a PCR primer.

SEQ ID NO: 14 is a nucleic acid used as a PCR primer.

SEQ ID NO: 15 is a protein known as fatty acid synthase 1 of *Schizosaccharomyces pombe*; NCBI Accession No. CAB54157.

SEQ ID NO: 16 is a DNA encoding fatty acid synthase subunit beta of *Schizosaccharomyces pombe*.

SEQ ID NO: 17 is a protein known as fatty acid synthase subunit alpha of *Schizosaccharomyces pombe*; NCBI Accession No. D83412.

SEQ ID NO: 18 is a protein known as fatty acid synthase subunit beta of *Saccharomyces cerevisiae*; NCBI Accession No. CAA82025.

SEQ ID NO: 19 is a protein known as fatty acid synthase subunit alpha of *Saccharomyces cerevisiae*; NCBI Accession No. CAA97948.

SEQ ID NO: 20 is a protein known as fatty acid synthase subunit beta of *Candida albicans*; NCBI Accession No. CAA52907.

5 SEQ ID NO: 21 is a DNA encoding fatty acid synthase subunit alpha of *Candida albicans*; NCBI Accession No. L29063.

SEQ ID NO: 22 is a protein known as fatty acid synthase subunit alpha of *Candida albicans*; NCBI Accession No. L29063.

10 SEQ ID NO: 23 is a protein known as fatty acid synthase of *Mycobacterium tuberculosis* H37Rv; NCBI Accession No. CAB06201.

SEQ ID NO: 24 is a protein known as fatty acid synthase of *Mycobacterium leprae*; NCBI Accession No. CAB39571.

SEQ ID NO: 25 is a protein known as fatty acid synthase of *Caenorhabditis elegans*; NCBI Accession No. NP492417.

15 SEQ ID NO: 26 is a DNA encoding fatty acid synthase (FAS) of *Rattus norvegicus*; NCBI Accession No. X13415.

SEQ ID NO: 27 is a protein known as fatty acid synthase (FAS) of *Rattus norvegicus*; NCBI Accession No. X13415.

20 SEQ ID NO: 28 is a DNA encoding fatty acid synthase (FAS) of chicken (*Gallus gallus*); NCBI Accession No. J03860 M22987.

SEQ ID NO: 29 is a protein known as fatty acid synthase (FAS) of chicken (*Gallus gallus*); NCBI Accession No. J03860 M22987.

SEQ ID NO: 30 is a DNA encoding fatty acid synthase (FAS) of *Mycobacterium bovis*; NCBI Accession No. U36763.

25 SEQ ID NO: 31 is a protein known as fatty acid synthase (FAS) of *Mycobacterium bovis*; NCBI Accession No. U36763.

SEQ ID NO: 32 is a DNA encoding a phosphopantetheine:protein transferase (*sfp* gene product) enzyme from *Bacillus subtilis*; NCBI Accession No. X63158.

30 SEQ ID NO: 33 is a protein known as phosphopantetheine:protein transferase (*sfp* gene product) enzyme from *Bacillus subtilis*; NCBI Accession No. X63158.

SEQ ID NO: 34 is a DNA encoding a phosphopantetheine:protein transferase (*gsp* gene product) enzyme from *Brevibacillus brevis* (ATCC 9999); NCBI Accession No. X76434.

SEQ ID NO: 35 is a protein known as phosphopantetheine:protein transferase (*gsp* gene product) enzyme from *Brevibacillus brevis* (ATCC 9999); NCBI Accession No. X76434.

SEQ ID NO: 36 is a DNA encoding a phosphopantetheine:protein transferase (*entD* gene product) enzyme from *Escherichia coli*; NCBI Accession No. D90700.

SEQ ID NO: 37 is a protein known as phosphopantetheine:protein transferase (*entD* gene product) enzyme from *Escherichia coli*; NCBI Accession No. D90700.

SEQ ID NO: 38 is a DNA encoding a phosphopantetheine:protein transferase (*pptA* gene product) enzyme from *Streptomyces verticillus*; NCBI Accession No. AF210311.

SEQ ID NO: 39 is a protein known as phosphopantetheine:protein transferase (*pptA* gene product) enzyme from *Streptomyces verticillus*; NCBI Accession No. AF210311.

SEQ ID NO: 40 is a DNA encoding an α -aminoadipate reductase small subunit (*lys5* gene product) enzyme from *Saccharomyces cerevisiae*; NCBI Accession No. U32586.

SEQ ID NO: 41 is a protein known as the small subunit (*lys5* gene product) of an α -aminoadipate reductase from *Saccharomyces cerevisiae*; NCBI Accession No. U32586.

SEQ ID NO: 42 is a DNA encoding an open reading frame o195 from *Escherichia coli*; NCBI Accession No. U00039.

SEQ ID NO: 43 is a protein encoded by open reading frame o195 from *Escherichia coli*; NCBI Accession No. U00039.

DEFINITIONS

The following definitions are provided as an aid to understanding the detailed description of the present invention.

The phrases "coding sequence," "coding region," "structural sequence," and "structural nucleic acid sequence" refer to a physical structure comprising an orderly arrangement of nucleotides. The nucleotides are arranged in a series of triplets that each form a codon. Each codon encodes a specific amino acid. Thus, the coding sequence, coding region, structural sequence, and structural nucleic acid sequence encode a series of amino acids forming a protein, polypeptide, or peptide sequence. The coding sequence, coding region, structural sequence, and structural nucleic acid sequence may be contained within a larger nucleic acid molecule, vector, or the like. In addition, the orderly arrangement of nucleotides in these sequences may be depicted in the form of a sequence listing, figure, table, electronic medium, or the like.

The phrases "DNA sequence," "nucleic acid sequence," and "nucleic acid molecule" refer to a physical structure comprising an orderly arrangement of nucleotides. The DNA

sequence or nucleotide sequence may be contained within a larger nucleotide molecule, vector, or the like. In addition, the orderly arrangement of nucleic acids in these sequences may be depicted in the form of a sequence listing, figure, table, electronic medium, or the like.

5 The term "expression" refers to the transcription of a gene to produce the corresponding mRNA and translation of this mRNA to produce the corresponding gene product (*i.e.*, a peptide, polypeptide, or protein).

The phrase "expression of antisense RNA" refers to the transcription of a DNA to produce a first RNA molecule capable of hybridizing to a second RNA molecule, which second RNA molecule encodes a gene product that is desirably down-regulated.

10 The term "homology" refers to the level of similarity between 2 or more nucleic acid or amino acid sequences in terms of percent of positional identity (*i.e.*, sequence similarity or identity). Homology also refers to the concept of similar functional properties among different nucleic acids or proteins.

15 The term "heterologous" refers to the relationship between 2 or more nucleic acid or protein sequences that are derived from different sources. For example, a promoter is heterologous with respect to a coding sequence if such a combination is not normally found in nature. In addition, a particular nucleic acid molecule may be "heterologous" with respect to a cell or organism into which it is inserted (*i.e.*, does not naturally occur in that particular cell or organism).

20 The term "hybridization" refers to the ability of a first strand of nucleic acid to join with a second strand via hydrogen bond base pairing when the 2 nucleic acid strands have sufficient sequence complementarity. Hybridization occurs when the 2 nucleic acid molecules anneal to one another under appropriate conditions.

25 The phrase "operably linked" refers to the functional spatial arrangement of 2 or more nucleic acid regions or nucleic acid sequences. For example, a promoter region may be positioned relative to a nucleic acid sequence such that transcription of the nucleic acid sequence is directed by the promoter region. Thus, a promoter region is operably linked to the nucleic acid sequence.

30 In the context of the present invention, the terms "plant" or "plants" refer to plants of the species *Brassica*.

The terms "promoter" or "promoter region" refers to a nucleic acid sequence, usually found upstream (5') to a coding sequence, that is capable of directing transcription of a nucleic acid sequence into mRNA. The promoter or promoter region typically provides a recognition site for RNA polymerase and the other factors necessary for proper initiation of transcription.

As contemplated herein, a promoter or promoter region includes variations of promoters derived by inserting or deleting regulatory regions, subjecting the promoter to random or site-directed mutagenesis, and the like. The activity or strength of a promoter may be measured in terms of the amounts of RNA it produces, or the amount of protein accumulation in a cell or tissue, relative to a second promoter that is similarly measured.

The term "5'-UTR" refers to the untranslated region of DNA upstream, or 5', of the coding region of a gene.

The term "3'-UTR" refers to the untranslated region of DNA downstream, or 3', of the coding region of a gene.

The phrase "recombinant vector" refers to any agent by or in which a nucleic acid of interest is amplified, expressed, or stored, such as a plasmid, cosmid, virus, autonomously replicating sequence, phage, or linear single-stranded, circular single-stranded, linear double-stranded, or circular double-stranded DNA or RNA nucleotide sequence. The recombinant vector may be derived from any source and is capable of genomic integration or autonomous replication.

The phrase "regulatory sequence" refers to a nucleotide sequence located upstream (5'), within, or downstream (3') with respect to a coding sequence. Transcription and expression of the coding sequence is typically impacted by the presence or absence of the regulatory sequence.

The phrase "substantially homologous" refers to 2 sequences that are at least about 90% identical in sequence, as measured by the CLUSTAL W method in the Omega program, using default parameters (Version 2.0; Accelrys, San Diego, California).

The term "transformation" refers to the introduction of nucleic acid into a recipient host. The term "host" refers to bacteria cells, fungi, animals or animal cells, plants or seeds, or any plant parts or tissues including plant cells, protoplasts, calli, roots, tubers, seeds, stems, leaves, seedlings, embryos, and pollen.

As used herein, the phrase "transgenic *Brassica* plant" refers to a *Brassica* plant having an introduced nucleic acid stably introduced into a genome of that plant, for example, the nuclear or plastid genomes.

As used herein, the phrase "substantially purified" refers to a molecule separated from substantially all other molecules normally associated with it in its native state. More preferably, a substantially purified molecule is the predominant species present in a preparation. A substantially purified molecule may be greater than about 60% free, preferably about 75% free, more preferably about 90% free, and most preferably about 95% free from

the other molecules (exclusive of solvent) present in the natural mixture. The phrase "substantially purified" is not intended to encompass molecules present in their native state.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides a multifunctional fatty acid synthase ("mfFAS") that
5 encodes the enzymatic functions required to synthesize palmitoyl (16:0) CoA, stearoyl (18:0) CoA, and oleoyl (18:1) CoA, the fatty acids used as precursors for other long chain saturated and unsaturated fatty acids. Obtaining nucleic acid sequences capable of producing increased oil content in *Brassica* plants is problematic because many non-associated, monofunctional enzymes are used to make fatty acids in *Brassica* plants. Accordingly, cloning and genetic
10 manipulation of plant fatty acid synthases ("FASs") would require isolation and coordinated expression of at least 8 separate genes. In particular, plant fatty acid synthesis depends on availability of the following plastid-localized FAS enzymes: Malonyl-CoA:ACP transacylase, β -ketoacyl-ACP synthase III, β -ketoacyl-ACP synthase I, β -ketoacyl-ACP synthase II, β -ketoacyl-ACP reductase, β -hydroxyacyl-ACP dehydratase, enoyl-ACP reductase, and
15 stearoyl-ACP desaturase. For movement of the end-product, acyl-ACP, from the plastid to the cytosol of the cell, two more enzymatic activities are required: acyl-ACP thioesterase and acyl-CoA synthase.

However, the present invention solves this problem by providing a multifunctional fatty acid synthase that encodes all of the FAS enzymatic functions in a single, long
20 polypeptide chain or in two chains that combine together, which may be employed in the cytosol or plastid, preferably in both, more preferably in the cytosol. Such a multifunctional fatty acid synthase is surprisingly effective in *Brassica* plants even though its structure is so dissimilar from plant endogenous fatty acid synthases. Most preferably, the mfFAS of the present invention is employed in the cytosol of a *Brassica* plant, and in this way the need for
25 an acyl carrier protein ("ACP") in fatty acid synthesis and the enzymes acyl-ACP thioesterase and acyl-CoA synthase is removed. Accordingly, not only does the present invention remove the need to clone at least 8 different genes to accomplish altered fatty acid synthesis in a *Brassica* plant, but when the mfFAS is employed in the cytosol, it replaces the function of 11 different plant gene products.

30 **Fatty Acid Synthases:** Fatty acid synthases are among the functionally most complex multienzyme systems known, which can be formed from a single polypeptide or multiple polypeptides. For mfFASs formed of a single polypeptide, there are multiple regions included thereon that perform the various enzymatic activities; such regions are referred to as "domains." Multifunctional fatty acid synthases formed of multiple polypeptides include

various FAS domains as well, which require the interaction of the constituent polypeptides to function. Such polypeptides, whether a multi-domain or single-domain polypeptide, can be isolated from an organism, or can be generated by combining domains or parts of domains together at the nucleic acid level using conventional recombinant technology. Accordingly, 5 recombinant chimeric nucleic acids that combine some mfFAS domains from one source with the remainder of the mfFAS domains from one or more second sources are preferred embodiments of the present invention. In the same fashion, the nucleic acid sequences in a mfFAS gene that encodes a particular domain can be replaced with a homologous nucleic acid sequence from a second source that encodes the same domain.

10 Fatty acid synthases usually comprise a set of 8 different functional domains and catalyze more than about 30 individual reaction steps. Two structurally distinct classes of fatty acid synthases exist. Type I fatty acid synthases are multifunctional synthases, commonly found in non-plant eukaryotes and in a few bacterial species. Type II fatty acid synthases constitute a set of separate, monofunctional polypeptides that are found in most 15 bacteria and in the plastids of higher plants. These polypeptides must properly assemble into a multimeric complex before the synthase becomes active. The fatty acid synthase from some bacteria, such as *Brevibacterium ammoniagenes*, is unlike plant and animal synthases in that it has a ninth catalytic activity (Seyama and Kawaguchi (1987), in Dolthin *et al.*, (eds.), Pyridine Nucleotide Coenzymes: Chemical, Biochemical and Medical Aspects, vol. 2B, Wiley, NY, 20 pp. 381-431), the 3-hydroxydecanoyl β,γ -dehydratase, which enables synthesis of both saturated and unsaturated fatty acids.

For transgenic purposes, type I multifunctional fatty acid synthases may have certain advantages over the type II "monofunctional" fatty acid synthases. For example, the type I multifunctional fatty acid synthases may have greater stability and/or better-coordinated 25 expression. Addition of a single polypeptide specific for one of the enzymatic fatty acid synthase activities to a plant by transgenic means may not provide overproduction of the entire fatty acid synthase complex because there may not be sufficient endogenous amounts of the other non-transgenic FAS polypeptides to substantially increase levels of the functional complex. In contrast, nucleic acids encoding a type I multifunctional fatty acid synthase can 30 reliably be used to overproduce all of the enzymatic functions of fatty acid synthase.

According to the present invention, nucleic acids encoding one or more of the separate domains from a type II monofunctional fatty acid synthase can be fused or linked to provide a synthetic multifunctional fatty acid synthase that can generate high oil levels when expressed within a host, such as, for example, a *Brassica* plant cell, plant tissue, or seed. Such a fused,

synthetic multifunctional fatty acid synthase can be made by fusing or linking the separate enzymatic functions associated with the various polypeptides of type II fatty acid synthases by chemically linking the nucleic acids that encode the various polypeptides. The overall sequence of such a synthetic gene generally aligns with that of a type I multifunctional fatty acid synthase. Using such sequence alignments, the spacing and orientation of polypeptides that contain the various fatty acid synthase activities can be adjusted or modified by altering the lengths of linking DNA between coding regions to generate a synthetic multifunctional fatty acid synthase DNA construct that optimally aligns with a natural type I multifunctional fatty acid synthase gene.

The fatty acid synthase polypeptides of the present invention can therefore encode more than one of the enzymes associated with fatty acid synthase, such as, for example, 2 through and including 9, thereby enabling up to the same 9 catalytic activities as are found in the mfFAS of *Brevibacterium ammoniagenes*. Any of the enzymes involved in the various steps of fatty acid synthesis can be joined. The first step in initiation stage of fatty acid synthesis is the carboxylation of the 2-carbon acetyl-CoA to form the 3-carbon β -ketoacid malonyl-CoA by acetyl-CoA carboxylase (ACCase). The ACCase step is irreversible, so once this step is accomplished, the resultant carbon compound is committed to fatty acid synthesis. All subsequent steps are catalyzed by the FAS. Malonyl-ACP is synthesized from malonyl-CoA and ACP by the enzyme malonyl-CoA:ACP transacylase. An acetyl moiety from acetyl-CoA is joined to a malonyl-ACP in a condensation reaction catalyzed by β -ketoacyl-ACP synthase III. Elongation of acetyl-ACP to 16- and 18-carbon fatty acids involves the cyclical action of the following sequence of reactions. After acetyl-CoA is condensed with malonyl-ACP using β -ketoacyl-ACP synthase, a β -ketoacyl-ACP is formed. The keto group on the β -ketoacyl-ACP is then reduced to an alcohol by β -ketoacyl-ACP reductase. The alcohol is removed in a dehydration reaction to form an enoyl-ACP by β -hydroxyacyl-ACP dehydratase. Finally, the enoyl-ACP is reduced to form the elongated saturated acyl-ACP by enoyl-ACP reductase.

The enzyme β -ketoacyl-ACP synthase I catalyzes elongation up to palmitoyl-ACP (C16:0), which is generally the end product from which other types of fatty acids are made.

The enzyme β -ketoacyl-ACP synthase II catalyzes the final elongation of palmitoyl-ACP to stearoyl-ACP (C18:0).

Common plant unsaturated fatty acids, such as oleic, linoleic, and α -linolenic acids, originate from the desaturation of stearoyl-ACP to form oleoyl-ACP (C18:1) in a reaction

catalyzed by a soluble plastid enzyme, Δ -9 desaturase (also often referred to as "stearoyl-ACP desaturase"). Molecular oxygen is required for desaturation and reduced ferredoxin serves as an electron co-donor.

Hence, the present invention contemplates polypeptides encoding several functions, for example, those relating to acyl carrier protein, malonyl CoA-ACP acyltransferase, β -ketoacyl-ACP synthase III, β -ketoacyl-ACP reductase, β -hydroxyacyl-ACP dehydratase, enoyl-ACP reductase, β -ketoacyl-ACP synthase I, β -ketoacyl-ACP synthase II, and Δ -9 desaturase.

In one embodiment, the present invention provides an isolated mfFAS polypeptide from a species of the group consisting of *Brevibacterium ammoniagenes*, *Schizosaccharomyces pombe*, *Saccharomyces cerevesiae*, *Candida albicans*, *Mycobacterium tuberculosis*, *Caenorhabditis elegans*, *Rattus norvegicus*, *Gallus gallus*, *Lipomyces starkeyi*, *Rhodospiridium toruloides*, and *Mycobacterium bovis*. Preferably, the mfFAS polypeptide is isolated from *Brevibacterium ammoniagenes*, *Schizosaccharomyces pombe*, *Saccharomyces cerevesiae*, *Candida albicans*; more preferably, the mfFAS polypeptides is isolated from *Brevibacterium ammoniagenes*. Such mfFAS polypeptides include one selected from the group consisting of SEQ ID NOs: 2, 15, 17, 18, 19, 20, 22, 23, 24, 25, 27, 29, and 31. Preferably, the mfFAS polypeptide used in the context of the present invention is one selected from the group consisting of SEQ ID NOs: 2, 15, 17, 18, 19, 20, and 22; more preferably, the mfFAS is SEQ ID NO: 2. Any of the aforementioned mfFAS polypeptides functions to increase the oil content of *Brassica* plant tissues.

mfFAS Nucleic Acids: The present invention uses nucleic acids that encode multifunctional fatty acid synthases, which are used in the context of the present invention for increasing the oil content of *Brassica* plant tissues. Such nucleic acids can encode a type I multifunctional fatty acid synthase that has been isolated from an organism. Preferred organisms from which nucleic acids encoding mfFAS can be isolated include, without limitation: bacteria, preferably *Brevibacteria* and *Bacilli*; fungi, preferably *Saccharomycetes*, *Schizosaccharomycetes*, *Lipomyces starkeyi*, *Rhodospiridium toruloides*, or *Candidae*; mycobacteria; nematodes, preferably *Caenorhabditis*; and mammals, preferably rat or chicken. Alternatively, the nucleic acids can encode a multifunctional fatty acid synthase that has been recombinantly generated to contain a fusion of 2 or more regions that encode monofunctional enzymatic domains that facilitate 2 or more of the steps required to make a fatty acid.

In one embodiment, the present invention uses an isolated nucleic acid that encodes a protein having mfFAS activity, which nucleic acid is selected from the group consisting of SEQ ID NOs: 1, 16, 21, 26, 28, and 30, and complements thereof, and nucleic acids having at least about 70% sequence identity thereof. Preferred nucleic acid is SEQ ID NO: 1, 16, 21, 26, 28, or 30; more preferred is SEQ ID NO: 1. The percent sequence identity of included nucleic acids in the group is preferably at least about 75%, more preferably at least about 80%, yet more preferably at least about 85%, and yet more preferably at least about 90%; even more preferably at least about 95%; and most preferably at least about 98%. The nucleic acids of the present invention can be isolated from any species that has a multifunctional fatty acid synthase, including without limitation *Brevibacterium ammoniagenes* (source of SEQ ID NO: 1), *Schizosaccharomyces pombe* (source of SEQ ID NO: 16), *Saccharomyces cerevesiae*, *Candida albicans* (source of SEQ ID NO: 21), *Mycobacterium tuberculosis*, *Mycobacterium leprae*, *Mycobacterium bovis* (source of SEQ ID NO: 30), *Caenorhabditis elegans*, rat (source of SEQ ID NO: 26), and chicken (source of SEQ ID NO: 28). In a preferred embodiment, the present invention provides a nucleic acid that encodes mfFAS from *Brevibacterium ammoniagenes*, *Schizosaccharomyces pombe*, *Saccharomyces cerevesiae*, or *Candida albicans*; more preferably, the mfFAS polypeptides are isolated from *Brevibacterium ammoniagenes*.

In yet another embodiment, the present invention uses a nucleic acid that encodes a multifunctional fatty acid synthase having an amino acid sequence comprising a protein selected from the group consisting of SEQ ID NOs: 2, 15, 17, 18, 19, 20, 22, 23, 24, 25, 27, 29, and 31. Preferably, the protein is SEQ ID NO: 2. The present invention also uses the set of nucleic acids that includes those nucleic acids that are at least about 80% identical to those that encode SEQ ID NO: 2, 15, 17, 18, 19, 20, 22, 23, 24, 25, 27, 29, or 31; more preferably, the set of nucleic acids are at least about 85% identical to one or more of the nucleic acids that encode one or more of the identified SEQ ID NOs; yet more preferably, at least about 90% identical; even more preferably, at least about 95% identical; and most preferably, at least about 98% identical.

The present invention also uses vectors containing such multifunctional fatty acid synthase nucleic acids. As set forth in further detail hereinbelow, preferred nucleic acids include appropriate regulatory elements operably linked thereto that facilitate efficient expression of the inventive nucleic acids in a host, including without limitation, *Brassica* plant hosts. Vectors useful in the context of the present invention can include such regulatory elements.

In a preferred embodiment of the present invention, the nucleic acid molecules of the present invention encode enzymes that are allelic to those defined. As used herein, a mutant enzyme is any enzyme that contains an amino acid that is different from the amino acid in the same position of an enzyme of the same type.

5 The nucleic acids and vectors described herein need not have the exact nucleic acid sequences described herein. Instead, the sequences of these nucleic acids and vectors can vary, so long as the nucleic acid either performs the function for which it is intended or has some other utility, for example, as a nucleic acid probe for complementary nucleic acids. For example, some sequence variability in any part of a multifunctional fatty acid synthase nucleic
10 acid is permitted so long as the mutant or variant polypeptide or polypeptides retains at least about 10% of the fatty acid synthase (FasA) activity observed under similar conditions for an analogous wild type fatty acid synthase enzyme, more preferably, the polypeptide(s) retain at least about 25% of the FasA activity; more preferably at least about 50% of the FasA activity; even more preferably, at least about 75% of the FasA activity; and yet more preferably, at
15 least about 90% of the FasA activity. Most preferably, the aforementioned sequence variability results in increased FasA activity. In a preferred embodiment, the comparison of enzymatic activity is with the wild type *Brevibacterium ammoniagenes* fatty acid synthase [SEQ ID NO: 2].

Fragment and variant nucleic acids, for example, of SEQ ID NO: 1, are also
20 encompassed by the present invention. Nucleic acid "fragments" encompassed by the present invention are of 3 general types. First, fragment nucleic acids that are not full length but do perform their intended function (fatty acid synthesis) are encompassed within the present invention. Second, fragments of nucleic acids identified herein that are useful as hybridization probes, but generally are not functional for fatty acid synthesis, are also
25 included in the present invention. And, third, fragments of nucleic acids identified herein can be used in suppression technologies known in the art, such as, for example, anti-sense technology or RNA inhibition (RNAi), which provides for reducing carbon flow in a plant into oil, making more carbon available for protein or starch accumulation, for example. Thus, fragments of a nucleotide sequence, such as SEQ ID NO: 1, 16, 21, 26, 28, or 30, without
30 limitation, may range from at least about 15 nucleotides, at least about 17 nucleotides, at least about 18 nucleotides, at least about 20 nucleotides, at least about 50 nucleotides, at least about 100 nucleotides, or more. In general, a fragment nucleic acid of the present invention can have any upper size limit so long as it is related in sequence to the nucleic acids of the present invention but does not include the full length.

In another embodiment, the present invention provides DNA molecules comprising a sequence encoding a consensus amino acid sequence, and complements thereof. In another aspect, the present invention provides DNA molecules comprising a sequence encoding a polypeptide comprising a conserved fragment of an amino acid consensus sequence. The present invention includes the use of consensus sequence and fragments thereof in transgenic *Brassica* plants, other organisms, and for other uses including those described below.

As used herein, "variants" have substantially similar or substantially homologous sequences when compared to reference or wild type sequence. For nucleotide sequences that encode proteins, variants also include those sequences that, because of the degeneracy of the genetic code, encode the identical amino acid sequence of the reference protein. Variant nucleic acids also include those that encode polypeptides that do not have amino acid sequences identical to that of the proteins identified herein, but which encode an active protein with conservative changes in the amino acid sequence.

As is known by one of skill in the art, the genetic code is "degenerate," meaning that several trinucleotide codons can encode the same amino acid. This degeneracy is apparent from Table 1.

Table 1

1 st Position	2 nd Position				3 rd Position
	T	C	A	G	
T	TTT = Phe	TCT = Ser	TAT = Tyr	TGT = Cys	T
T	TTC = Phe	TCC = Ser	TAC = Tyr	TGC = Cys	C
T	TTA = Leu	TCA = Ser	TAA = Stop	TGA = Stop	A
T	TTG = Leu	TCG = Ser	TAG = Stop	TGG = Trp	G
C	CTT = Leu	CCT = Pro	CAT = His	CGT = Arg	T
C	CTC = Leu	CCC = Pro	CAC = His	CGC = Arg	C
C	CTA = Leu	CCA = Pro	CAA = Gln	CGA = Arg	A
C	CTG = Leu	CCG = Pro	CAG = Gln	CGG = Arg	G
A	ATT = Ile	ACT = Thr	AAT = Asn	AGT = Ser	T
A	ATC = Ile	ACC = Thr	AAC = Asn	AGC = Ser	C
A	ATA = Ile	ACA = Thr	AAA = Lys	AGA = Arg	A
A	ATG = Met	ACG = Thr	AAG = Lys	AGG = Arg	G
G	GTT = Val	GCT = Ala	GAT = Asp	GGT = Gly	T
G	GTC = Val	GCC = Ala	GAC = Asp	GGC = Gly	C
G	GTA = Val	GCA = Ala	GAA = Gln	GGA = Gly	A
G	GTG = Val	GCG = Ala	GAG = Gln	GGG = Gly	G

Hence, many changes in the nucleotide sequence of the variant may be silent and may not alter the amino acid sequence encoded by the nucleic acid. Where nucleic acid sequence alterations are silent, a variant nucleic acid will encode a polypeptide with the same amino acid sequence as the reference nucleic acid. Therefore, a particular nucleic acid of the present invention also encompasses variants with degenerate codon substitutions, and complementary sequences thereof, as well as the sequence explicitly specified by a SEQ ID NO as set forth herein. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the reference codon is replaced by any of the codons for the amino acid specified by the reference codon. In general, the third position of one or more selected codons can be substituted with mixed-base and/or deoxyinosine residues as disclosed by Batzer *et al.*, *Nucleic Acid Res.*, 19:5081 (1991) and/or Ohtsuka *et al.*, *J. Biol. Chem.*, 260:2605 (1985); Rossolini *et al.*, *Mol. Cell. Probes*, 8:91 (1994).

A host cell often displays a preferred pattern of codon usage. Structural nucleic acid sequences are preferably constructed to utilize the codon usage pattern of the particular host cell. This generally enhances the expression of the structural nucleic acid sequence in a transformed host cell. Any disclosed nucleic acid or amino acid sequence may be modified to reflect the preferred codon usage of a host cell or organism in which they are contained. Modification of a structural nucleic acid sequence for optimal codon usage in plants is described in U.S. Patent 5,689,052, which is incorporated herein by reference. In a preferred embodiment, the present invention includes nucleic acids that encode mfFAS and that are codon-optimized in a *Brassica* plant. In a preferred embodiment the plants are of the *Brassica* species, and most preferably *Brassica napus* (canola).

However, the present invention is not limited to silent changes in the present nucleotide sequences but also includes variant nucleic acid sequences that conservatively alter the amino acid sequence of a polypeptide of the present invention. Because it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence and, of course, its underlying DNA coding sequence and, nevertheless, a protein with like properties can still be obtained. It is thus contemplated by the inventors that various changes may be made in the peptide sequences of the proteins or fragments of the present invention, or corresponding DNA sequences that encode the peptides, without appreciable loss of their biological utility or activity. According to the present invention, then, variant and reference nucleic acids of the present invention may differ in the encoded amino acid sequence by one or more substitutions, additions, insertions, deletions, fusions, and truncations, which may be

present in any combination, so long as an active mfFAS protein is encoded by the variant nucleic acid. Such variant nucleic acids will not encode exactly the same amino acid sequence as the reference nucleic acid, but have conservative sequence changes. It is known that codons capable of coding for such conservative amino acid substitutions are known in the art.

Another approach to identifying conservative amino acid substitutions require analysis of the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biological function on a protein is generally understood in the art (Kyte and Doolittle, *J. Mol. Biol.*, 157:105-132, 1982). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant polypeptide, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like.

Each amino acid has been assigned a hydropathic index on the basis of its hydrophobicity and charge characteristics (Kyte and Doolittle, *J. Mol. Biol.*, 157:105-132, 1982); these are isoleucine (+4.5), valine (+4.2), leucine (+3.8), phenylalanine (+2.8), cysteine/cystine (+2.5), methionine (+1.9), alanine (+1.8), glycine (-0.4), threonine (-0.7), serine (-0.8), tryptophan (-0.9), tyrosine (-1.3), proline (-1.6), histidine (-3.2), glutamate (-3.5), glutamine (-3.5), aspartate (-3.5), asparagine (-3.5), lysine (-3.9), and arginine (-4.5).

In making such changes, the substitution of amino acids whose hydropathic indices are within ± 2 is preferred, those that are within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred.

It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U.S. Patent 4,554,101, states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein.

As detailed in U.S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0), lysine (+3.0), aspartate (+3.0 $\pm$ 1), glutamate (+3.0 $\pm$ 1), serine (+0.3), asparagine (+0.2), glutamine (+0.2), glycine (0), threonine (-0.4), proline (-0.5 $\pm$ 1), alanine (-0.5), histidine (-0.5), cysteine (-1.0), methionine (-1.3), valine (-1.5), leucine (-1.8), isoleucine (-1.8), tyrosine (-2.3), phenylalanine (-2.5), and tryptophan (-3.4).

In making such changes, the substitution of amino acids whose hydrophilicity values are within ± 2 is preferred, those that are within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred.

Variant nucleic acids with silent and conservative changes can be defined and characterized by the degree of homology to the reference nucleic acid. Preferred variant nucleic acids are "substantially homologous" to the reference nucleic acids of the present invention. As recognized by one of skill in the art, such substantially similar nucleic acids can hybridize under stringent conditions with the reference nucleic acids identified by SEQ ID NO herein. These types of substantially homologous nucleic acids are encompassed by this present invention.

Generally, nucleic acid derivatives and variants of the present invention will have at least about 90%, at least about 91%, at least about 92%, at least about 93%, or at least about 94% sequence identity to the reference nucleotide sequence defined herein. Preferably, nucleic acids of the present invention will have at least about 95%, at least about 96%, at least about 97%, or at least about 98% sequence identity to the reference nucleotide sequence defined herein.

Variant nucleic acids can be detected and isolated by standard hybridization procedures. Hybridization to detect or isolate such sequences is generally carried out under "moderately stringent" and preferably under "stringent" conditions. Moderately stringent hybridization conditions and associated moderately stringent and stringent hybridization wash conditions used in the context of nucleic acid hybridization experiments, such as Southern and Northern hybridization, are sequence dependent, and are different under different environmental parameters. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, Laboratory Techniques in Biochemistry and Molecular biology-Hybridization with Nucleic Acid Probes, page 1, Chapter 2, *Overview of principles of hybridization and the strategy of nucleic acid probe assays*, Elsevier, NY (1993). See also, J. Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, NY, pp. 9.31-9.58 (1989); J. Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, NY (3rd ed. 2001).

The present invention also provides methods for detection and isolation of derivative or variant nucleic acids encoding the proteins provided herein. The methods involve hybridizing at least a portion of a nucleic acid comprising any part of SEQ ID NO: 1, 16, 21, 26, 28, or 30, with respect to FAS-related sequences; and any part of SEQ ID NO: 3, 32, 34, 36, 38, 40, or 42, with respect to phosphopantetheine:protein transferase to a sample nucleic

acid, thereby forming a hybridization complex; and detecting the hybridization complex. The presence of the complex correlates with the presence of a derivative or variant nucleic acid that can be further characterized by nucleic acid sequencing, expression of RNA and/or protein and testing to determine whether the derivative or variant retains activity. In general, the portion of a nucleic acid comprising any part of the aforementioned DNAs identified by SEQ ID NO used for hybridization is preferably at least about 15 nucleotides, and hybridization is under hybridization conditions that are sufficiently stringent to permit detection and isolation of substantially homologous nucleic acids; preferably, the hybridization conditions are "moderately stringent"; more preferably the hybridization conditions are "stringent", as defined herein and in the context of conventional molecular biological techniques well known in the art.

Generally, highly stringent hybridization and wash conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific double-stranded sequence at a defined ionic strength and pH. For example, under "highly stringent conditions" or "highly stringent hybridization conditions" a nucleic acid will hybridize to its complement to a detectably greater degree than to other sequences (*e.g.*, at least 2-fold over background). By controlling the stringency of the hybridization and/or the washing conditions, nucleic acids having 100% complementary can be identified and isolated.

Alternatively, stringency conditions can be adjusted to allow some mismatching in sequences so that lower degrees of similarity are detected (heterologous probing) using, for example, moderately stringent conditions. Appropriate stringency conditions that promote DNA hybridization under moderately stringent conditions are, for example, about 2X sodium chloride/sodium citrate (SSC) at about 65°C, followed by a wash of 2X SSC at 20-25°C, are known to those skilled in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, NY, 6.3.1-6.3.6 (1989). Both temperature and salt may be varied, or either the temperature or the salt concentration may be held constant while the other variable is changed.

Typically, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (*e.g.*, 10 to 50 nucleotides) and at least about 60°C for long probes (*e.g.*, greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide, in which case hybridization temperatures can be decreased. Dextran sulfate

and/or Denhardt's solution (50X Denhardt's is 5% Ficoll, 5% polyvinylpyrrolidone, 5% BSA) can also be included in the hybridization reactions.

Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 50% formamide, 5X SSC (20X SSC is 3M NaCl, 0.3 M trisodium citrate), 50mM sodium phosphate, pH7, 5mM EDTA, 0.1% SDS (sodium dodecyl sulfate), 5X Denhardt's with 100 μ g/ml denatured salmon sperm DNA at 37°C, and a wash in 1X to 5X SSC (20X SSC = 3.0 M NaCl and 0.3 M trisodium citrate), 0.1% SDS at 37°C. Exemplary moderate stringency conditions include hybridization in 40 to 50% formamide, 5X SSC 50mM sodium phosphate, pH 7, 5mM EDTA, 0.1% SDS, 5X Denhardt's with 100 μ g/ml denatured salmon sperm DNA at 42°C, and a wash in 0.1X to 2X SSC, 0.1% SDS at 42 to 55°C. Exemplary high stringency conditions include hybridization in 50% formamide, 5X SSC, 50mM sodium phosphate, pH 7.0, 5mM EDTA, 0.1% SDS, 5X Denhardt's with 100 μ g/ml denatured salmon sperm DNA at 42°C, and a wash in 0.1X SSC, 0.1% SDS at 60 to 65°C.

The degree of complementarity or homology of hybrids obtained during hybridization is typically a function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. The type and length of hybridizing nucleic acids also affects whether hybridization will occur and whether any hybrids formed will be stable under a given set of hybridization and wash conditions. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl, *Anal. Biochem.*, 138:267-284 (1984);

$$T_m = 81.5^\circ\text{C} + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\% \text{ form}) - 500/L$$

where M is the molarity of monovalent cations, %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. The T_m is the temperature (under defined ionic strength and pH) at which 50% of a complementary target sequence hybridizes to a perfectly matched probe. Very stringent conditions are selected for hybridization to derivative and variant nucleic acids having a T_m equal to the exact complement of a particular probe, less stringent conditions are selected for hybridization to derivative and variant nucleic acids having a T_m less than the exact complement of the probe.

In general, T_m is reduced by about 1°C for each 1% of mismatching. Thus, T_m , hybridization, and/or wash conditions can be adjusted to hybridize to sequences of the desired sequence identity. For example, if sequences with greater than about 90% identity are sought,

the T_m can be decreased by about 10°C. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at about 1, about 2, about 3, or about 4°C lower than the thermal melting point (T_m); moderately stringent conditions can utilize a hybridization and/or wash at about 6, about 7, about 8, about 9, or about 10°C lower than the thermal melting point (T_m); low stringency conditions can utilize a hybridization and/or wash at about 11, about 12, about 13, about 14, about 15, or about 20°C lower than the thermal melting point (T_m).

If the desired degree of mismatching results in a T_m of less than 45°C (aqueous solution) or 32°C (formamide solution), it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen (1993) *Laboratory Techniques in Biochemistry and Molecular Biology-Hybridization with Nucleic Acid Probes*, Part 1, Chapter 2, Elsevier, NY; Ausubel *et al.*, eds. (1995) *Current Protocols in Molecular Biology*, Chapter 2, Greene Publishing and Wiley - Interscience, NY. See Sambrook *et al.*, (1989) *Molecular Cloning: A Laboratory Manual*, 2d ed., Cold Spring Harbor Laboratory Press, Plainview, NY. Using these references and the teachings herein on the relationship between T_m , mismatch, and hybridization and wash conditions, those of ordinary skill can generate variants of the present nucleic acids.

In another preferred embodiment of the present invention, the inventive nucleic acids are defined by the percent identity relationship between particular nucleic acids and other members of the class using analytic protocols well known in the art. Such analytic protocols include, but are not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, California, or in the Omiga program version 2.0 Accelrys Inc., San Diego, California); the ALIGN program (Version 2.0) and GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Version 8 (available from Genetics Computer Group (GCG), 575 Science Drive, Madison, WI). Alignments using these programs can be performed using the default parameters. The CLUSTAL program is well described by Higgins *et al.*, *Gene*, 73:237- 244 (1988); Higgins *et al.*, *CABIOS*, 5:151-153 (1989); Corpet *et al.*, *Nucleic Acids Res.*, 16:10881-90 (1988); Huang *et al.*, *CABIOS*, 8:155-65 (1992); and Pearson *et al.*, *Meth. Mol. Biol.*, 24:307-331 (1994). The ALIGN program is based on the algorithm of Meyers and Miller, *Computer Applic. Biol. Sci.*, 4:11-17 (1988). The BLAST programs of Altschul *et al.*, *J. Mol. Biol.*, 215:403 (1990), are based on the algorithm of Karlin and Altschul *Proc. Natl. Acad. Sci. (U.S.A.)*, 87:2264-2268 (1990). To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST 2.0) can

be utilized as described in Altschul *et al.*, *Nucleic Acids Res.*, 25:3389 (1997). Alternatively, PSI-BLAST (in BLAST 2.0) can be used to perform an iterated search that detects distant relationships between molecules. *See*, Altschul *et al.*, *supra*. When utilizing BLAST, Gapped BLAST, PSI-BLAST, the default parameters of the respective programs (*e.g.*, BLASTN for nucleotide sequences, BLASTX for proteins) can be used. The BLASTN program (for nucleotide sequences) uses as defaults a word length (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a word length (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (*see*, Henikoff & Henikoff, *Proc. Natl. Acad. Sci. (U.S.A.)*, 89:10915, 1989). Alignment may also be performed manually by inspection.

For purposes of the present invention, comparison of nucleotide sequences for determination of percent sequence identity to the nucleic acid sequences disclosed herein is preferably made using the BLASTN program (version 1.4.7 or later) with its default parameters or any equivalent program. By "equivalent program" is intended any sequence comparison program that, for any 2 sequences in question, generates an alignment having identical nucleotide or amino acid residue matches and an identical percent sequence identity when compared to the corresponding alignment generated by the preferred program.

Isolation of Nucleic Acids Encoding Multifunctional Fatty Acid Synthases:

Nucleic acids encoding a multifunctional fatty acid synthase can be identified and isolated by standard methods, as described by Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor, NY (1989). For example, a DNA sequence encoding a type I multifunctional fatty acid synthase can be identified by screening of a DNA or cDNA library generated from nucleic acid derived from a particular cell type, cell line, primary cells, or tissue. Examples of libraries useful for identifying and isolating a multifunctional fatty acid synthase include libraries made from the genomic DNA or cDNA of any organism encoding a type I fatty acid synthase, preferably a bacteria or non-plant eukaryote.

Screening for DNA fragments that encode a multifunctional fatty acid synthase can be accomplished by screening colonies or plaques from a genomic or cDNA library for hybridization to a probe of an available multifunctional fatty acid synthase from other organisms or by screening colonies or plaques from a cDNA expression library for binding to antibodies that specifically recognize a multifunctional fatty acid synthase. DNA fragments that hybridize to multifunctional fatty acid synthase probes from other organisms and/or colonies or plaques carrying DNA fragments that are immunoreactive with antibodies to multifunctional fatty acid synthase can be subcloned into a vector and sequenced and/or used

as probes to identify other cDNA or genomic sequences encoding all or a portion of the desired multifunctional fatty acid synthase gene. Probes for isolation of multifunctional fatty acid synthase genes can also include DNA fragments of type II fatty acid synthase genes or antibodies to the type II proteins, as noted herein above.

5 A cDNA library can be prepared, for example, by random oligo priming or oligo dT priming. Plaques containing DNA fragments can be screened with probes or antibodies specific for multifunctional fatty acid synthase. DNA fragments encoding a portion of a multifunctional fatty acid synthase gene can be subcloned and sequenced and used as probes to identify a genomic multifunctional fatty acid synthase gene. DNA fragments encoding a
10 portion of a multifunctional fatty acid synthase can be verified by determining sequence homology with other known multifunctional fatty acid synthase genes or by hybridization to multifunctional fatty acid synthase-specific messenger RNA. Once cDNA fragments encoding portions of the 5', middle and 3' ends of a multifunctional fatty acid synthase are obtained, they can be used as probes to identify and clone a complete genomic copy of the
15 multifunctional fatty acid synthase gene from a genomic library.

Portions of the genomic copy or copies of an multifunctional fatty acid synthase gene can be sequenced and the 5' end of the gene identified by standard methods, including either DNA sequence homology to other multifunctional fatty acid synthase genes or by RNAase protection analysis, as described by Sambrook *et al.*, Molecular Cloning: A Laboratory
20 Manual, Cold Spring Harbor Press, Cold Spring Harbor, NY (1989). The 3' and 5' ends of the target gene can also be located by computer searches of genomic sequence databases using known fatty acid synthase coding regions. Once portions of the 5' end of the gene are identified, complete copies of the multifunctional fatty acid synthase gene can be obtained by standard methods, including cloning or polymerase chain reaction (PCR) synthesis using
25 oligonucleotide primers complementary to the DNA sequence at the 5' end of the gene. The presence of an isolated full-length copy of the multifunctional fatty acid synthase gene can be verified by hybridization, partial sequence analysis, or by expression of the multifunctional fatty acid synthase enzyme.

Phosphopantetheine:Protein Transferases: During the process of fatty acid
30 synthesis, the growing acyl chain is preferably covalently linked by a thioester bond to the cysteamine thiol of a phosphopantetheinyl (P-Pan) moiety, which is preferably attached at the other end to a specific serine residue of acyl carrier protein (ACP), in the case of type II FAS systems, or the ACP-domain of a type I FAS. This P-Pan moiety acts as a "swinging arm," carrying the growing acyl chain between the active sites of the different enzymes or domains

of the FAS complex. Accordingly, the transgenic mfFAS used in the context of the present invention is preferably phosphopantetheinylated, which phosphopantetheinylation is accomplished by a co-transformed gene that encodes a suitable PPTase or by a host PPTase that has sufficient substrate range of activity for the purpose of modifying the transgenic
5 mfFAS.

The enzymatic post-translational attachment of the P-Pan group to an ACP protein or domain is carried out by a phosphopantetheinyl transferase (PPTase). Any suitable PPTase can be used in the context of the present invention, the suitability of which is determined by the ability of the PPTase to phosphopantetheinylate a mfFAS used herein. For example, the
10 *Brevibacterium ammoniagenes* FasA protein [SEQ ID NO: 2] can be suitably combined with the PPTase from the same species, which is identified herein as SEQ ID NO: 4. In another embodiment of the present invention, the gene encoding the mfFAS includes its own PPTase activity, such as the mfFAS derived from yeast (*e.g.*, SEQ ID NOs: 15-19), and thus the transgenic mfFAS is suitably modified to be active upon expression in the host. Particularly
15 preferred PPTases have broad specificity, such as, for example, those referred to as being of the *sfp*-type, as further discussed hereinbelow. More preferred, the mfFAS employed in the context of the present invention is pantethenylated by an enzyme having PPTase activity that is native to the host *Brassica* plant into which the mfFAS transgene has been inserted.

A PPTase from *Bacillus subtilis*, the *sfp* gene product, has a remarkably broad range
20 of substrate specificity, being able to phosphopantetheinylate non-native substrates both *in vitro* (Lambalot *et al.*, *Chem. Biol.*, 3:923-936, 1996) and *in vivo* (Mootz *et al.*, *J. Biol. Chem.*, 276:37389-37298, 2001); *see* Figure 23 for recital of the sequences of the *sfp* gene and its product. Mootz and co-workers have shown that the *sfp* gene product not only complements heterologous PPTases, such as *E. coli* ACPS, but it *in vivo* phosphopantetheinylates all the
25 different acceptor domains in natural host cells (*e.g.*, *Bacillus subtilis*) that include ACP and PCP (petide carrier protein) of type I polyketide synthases (PKS) and non-ribosomal peptide synthetases (NRPS) involved in secondary metabolism as well as the type II ACP protein required for fatty acid synthesis (primary metabolism). Indeed, this broad range of specificity appears to be a general feature of many *sfp*-type PPTases. *Streptomyces verticillus svp*
30 PPTase (*see* Figure 26), another *sfp*-type enzyme, was also found to be able to phosphopantetheinylate a broad range of substrates, including type I and II ACP and PCP domains from various *Streptomyces* species (Sánchez *et al.*, *Chem. Biol.*, 8:725-728, 2001). Other useful *sfp*-type PPTases include those found in *Brevibacillus brevis* (SEQ ID NO: 35), and *Escherichia coli* (SEQ ID NO: 36), which are listed here without any intention to limit the

sfp-type PPTases that are usefully employed in the context of the present invention. Preferably, the *Bacillus subtilis* PPTase, that is the gene that encodes it, is used.

In the case of the multifunctional FasA and FasB proteins from *Brevibacterium ammoniagenes*, Stuible and co-workers found that the *E. coli* ACPS was unable to
5 phosphopantetheinylate these type I FAS proteins either *in vivo* when the genes were introduced into *E. coli* or *in vitro* when mixed with the proteins. The *B. ammoniagenes* PPT1 protein was required to phosphopantetheinylate both of these type I FAS proteins (Stuible *et al.*, *Eur. J. Biochem.*, 248:481-487, 1997).

A preferred embodiment of the present invention relates to the use of an mfFAS that
10 can be phosphopantetheinylated by a PPTase that is innate to a *Brassica* plant. An alternative preferred embodiment relates to the use of a PPTase specific for the introduced multifunctional FAS that is inserted in a *Brassica* plant, such as *ppt1* in the case of the *B. ammoniagenes* *fasA* and *fasB* genes, which specific PPTase could be co-expressed in order to engineer functional multifunctional FAS expression in *Brassica* plants. As a further
15 embodiment of the present invention, a PPTase of broad specificity, such as a *sfp*-type PPTase, may be co-expressed with a type II FAS gene in order to engineer functional multifunctional FAS expression in *Brassica* plants.

Expression Vectors and Cassettes: The expression vectors and cassettes of the present invention include nucleic acids encoding multifunctional fatty acid synthases. When
20 inclusion of a heterologous phosphopantetheine protein transferase enzyme (PPTase) is desired, such expression vectors and cassettes can also include a nucleic acid encoding a PPTase that can post-translationally activate the multifunctional fatty acid synthase polypeptide. Alternatively, a separate expression vector or cassette can encode a phosphopantetheine protein transferase enzyme. One such PPTase is encoded by the
25 *B. ammoniagenes* *ppt1* gene. Other sources of PPTase having broad spectrum activity include: *Bacillus subtilis*, *Brevibacillus brevis*, *Escherichia coli*, *Streptomyces verticillus*, and *Saccharomyces cerevisiae*.

A transgene comprising a multifunctional fatty acid synthase can be subcloned into an expression vector or cassette, and fatty acid synthase expression can be detected and/or
30 quantified. This method of screening is useful to identify transgenes providing for an expression of a multifunctional fatty acid synthase, and expression of a multifunctional fatty acid synthase in a transformed *Brassica* plant cell.

Plasmid vectors that provide for easy selection, amplification, and transformation of the transgene in prokaryotic and eukaryotic cells include, for example, pUC-derived vectors,

pSK-derived vectors, pGEM-derived vectors, pSP-derived vectors, pBS-derived vectors, pFastBac (Invitrogen) for baculovirus expression and pYES2 (Invitrogen) for yeast expression. Additional elements may be present in such vectors, including origins of replication to provide for autonomous replication of the vector, selectable marker genes, preferably encoding antibiotic or herbicide resistance, unique multiple cloning sites providing for multiple sites to insert DNA sequences or genes encoded in the transgene, and sequences that enhance transformation of prokaryotic and eukaryotic cells. One vector that is useful for expression in both plant and prokaryotic cells is the binary Ti plasmid (as disclosed in Schilperoot *et al.*, U.S. Patent 4,940,838), as exemplified by vector pGA582. This binary Ti plasmid vector has been previously characterized by An, *Methods in Enzymology*, 153:292 (1987). This binary Ti vector can be replicated in prokaryotic bacteria, such as *E. coli* and *Agrobacterium*. The *Agrobacterium* plasmid vectors can also be used to transfer the transgene to *Brassica* plant cells. The binary Ti vectors preferably include the nopaline T DNA right and left borders to provide for efficient *Brassica* plant cell transformation, a selectable marker gene, unique multiple cloning sites in the T border regions, the *colE1* replication of origin and a wide host range replicon. The binary Ti vectors carrying a transgene of the present invention can be used to transform both prokaryotic and eukaryotic cells, but is preferably used to transform plant cells. See, for example, Glassman *et al.*, U.S. Patent 5,258,300.

In general, the expression vectors and cassettes of the present invention contain at least a promoter capable of expressing RNA in a *Brassica* plant cell and a terminator, in addition to a nucleic acid encoding a multifunctional fatty acid synthase. Other elements may also be present in the expression cassettes of the present invention. For example, expression cassettes can also contain enhancers, introns, untranslated leader sequences, cloning sites, matrix attachment regions for silencing the effects of chromosomal control elements, and other elements known to one of skill in the art.

Nucleic acids encoding fatty acid synthases are operably linked to regulatory elements, such as a promoter, termination signals, and the like. Operably linking a nucleic acid under the regulatory control of a promoter or a regulatory element means positioning the nucleic acid such that the expression of the nucleic acid is controlled by these sequences. In general, promoters are found positioned 5' (upstream) to the nucleic acid that they control. Thus, in the construction of heterologous promoter/nucleic acid combinations, the promoter is preferably positioned upstream to the nucleic acid and at a distance from the transcription start site of the nucleic acid that the distance between the promoter and the transcription start site

approximates the distance observed in the natural setting. As is known in the art, some variation in this distance can be tolerated without loss of promoter function. Similarly, the preferred positioning of a regulatory element with respect to a heterologous nucleic acid placed under its control is the natural position of the regulatory element relative to the structural gene it naturally regulates. Again, as is known in the art, some variation in this distance can be accommodated.

Expression cassettes have promoters that can regulate gene expression. Promoter regions are typically found in the flanking DNA sequence upstream from coding regions in both prokaryotic and eukaryotic cells. A promoter sequence provides for regulation of transcription of the downstream gene sequence and typically includes from about 50 to about 2,000 nucleotide base pairs. Promoter sequences also contain regulatory sequences, such as enhancer sequences that can influence the level of gene expression. Some isolated promoter sequences can provide for gene expression of heterologous genes, that is, a gene different from the native or homologous gene. Promoter sequences are also known to be strong or weak or inducible. A strong promoter provides for a high level of gene expression, whereas a weak promoter provides for a very low level of gene expression. An inducible promoter is a promoter that provides for turning on and off of gene expression in response to an exogenously added agent or to an environmental or developmental stimulus. Promoters can also provide for tissue specific or developmental regulation. An isolated promoter sequence that is a strong promoter for heterologous genes is advantageous because it provides for a sufficient level of gene expression to allow for easy detection and selection of transformed cells and provides for a high level of gene expression when desired. Transcription initiation regions that are preferentially expressed in seed tissue, and that are undetectable in other *Brassica* plant parts, are considered desirable for seed oil modifications in order to minimize any disruptive or adverse effects of the gene product.

Promoters of the present invention will generally include, but are not limited to, promoters that function in bacteria, bacteriophage, plastids, or plant cells. Useful promoters include the globulin promoter (*see*, for example, Belanger and Kriz, *Genet.*, 129:863-872, 1991), gamma zein Z27 promoter (*see*, for example, U.S. Serial Number 08/763,705; also Lopes *et al.*, *Mol Gen Genet.*, 247:603-613, 1995), L3 oleosin promoter (U.S. Patent 6,433,252), USP promoter and 7Sa promoter (U.S. Serial Number 10/235,618), 7Sa' promoter (*see*, for example, Beachy *et al.*, *EMBO J.*, 4:3047, 1985; Schuler *et al.*, *Nucleic Acid Res.*, 10(24):8225-8244, 1982), CaMV 35S promoter (Odell *et al.*, *Nature*, 313:810, 1985), the CaMV 19S (Lawton *et al.*, *Plant Mol. Biol.*, 9:31F, 1987), *nos* (Ebert *et al.*, *Proc.*

Natl. Acad. Sci. (U.S.A.), 84:5745, 1987), Adh (Walker *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)*, 84:6624, 1987), sucrose synthase (Yang *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)*, 87:4144, 1990), tubulin, actin (Wang *et al.*, *Mol. Cell. Biol.*, 12:3399, 1992), *cab* (Sullivan *et al.*, *Mol. Gen. Genet.*, 215:431, 1989), PEPCase promoter (Hudspeth *et al.*, *Plant Mol. Biol.*, 12:579, 1989),
5 or those associated with the R gene complex (Chandler *et al.*, *The Plant Cell*, 1:1175, 1989). Other useful promoters include the Figwort Mosaic Virus (FMV) promoter (Richins *et al.*, *Nucleic Acids Res.*, 20:8451, 1987), arcelin, tomato E8, patatin, ubiquitin, mannopine synthase (mas), soybean seed protein glycinin (Gly), soybean vegetative storage protein (vsp), bacteriophage SP6, T3, and T7 promoters.

10 Indeed, in a preferred embodiment, the promoter used is a seed-specific promoter. Examples of seed regulated genes and transcriptional regions are disclosed in U.S. Patents 5,420,034; 5,608,152; and 5,530,194. Examples of such promoters include the 5' regulatory regions from such genes as napin (Kridl *et al.*, *Seed Sci. Res.*, 1:209-219, 1991), phaseolin (Bustos *et al.*, *Plant Cell*, 1(9):839-853, 1989), soybean trypsin inhibitor (Riggs *et al.*, *Plant*
15 *Cell*, 1(6):609-621, 1989), ACP (Baerson *et al.*, *Plant Mol. Biol.*, 22(2):255-267, 1993), stearyl-ACP desaturase (Slocombe *et al.*, *Plant Physiol.*, 104(4):167-176, 1994), soybean α' subunit of β -conglycinin (Chen *et al.*, *Proc. Natl. Acad. Sci.*, 83:8560-8564, 1986), *Lesquerella* hydroxylase promoter (described in Broun *et al.*, *Plant Journal*, 12(2):201-210, 1998; U.S. Patent 5,965,793), delta 12 desaturase and oleosin (Hong *et al.*, *Plant Mol. Biol.*,
20 34(3):549-555, 1997). Further examples include the promoter for β -conglycinin (Chen *et al.*, *Dev. Genet.*, 10:112-122, 1989), the GL2 promoter (Szymanski *et al.*, *Development*, 125:1161-1171, 1998), the tt2 promoter (Nesi *et al.*, *The Plant Cell*, 13:2099-114, 2001), the LDOX promoter (Pelletier *et al.*, *Plant Physiology*, 113:1437-1445, 1997), the CPC promoter (Wada *et al.*, *Science*, 277:1113-1116, 1997).

25 Plastid promoters can also be used. Most plastid genes contain a promoter for the multi-subunit plastid-encoded RNA polymerase (PEP) as well as the single-subunit nuclear-encoded RNA polymerase. A consensus sequence for the nuclear-encoded polymerase (NEP) promoters and listing of specific promoter sequences for several native plastid genes can be found in Hajdukiewicz *et al.*, *EMBO J.*, 16:4041-4048 (1997), which is hereby in its entirety
30 incorporated by reference.

Examples of plastid promoters that can be used include the *Zea mays* plastid RRN (ZMRRN) promoter. The ZMRRN promoter can drive expression of a gene when the *Arabidopsis thaliana* plastid RNA polymerase is present. Similar promoters that can be used in the present invention are the Glycine max plastid RRN (SOYRRN) and the *Nicotiana*

tabacum plastid RRN (NTRRN) promoters. All three promoters can be recognized by the *Arabidopsis* plastid RNA polymerase. The general features of RRN promoters are described by Hajdukiewicz *et al.*, *supra*, and U.S. Patent 6,218,145.

Moreover, transcription enhancers or duplications of enhancers can be used to increase expression from a particular promoter. Examples of such enhancers include, but are not limited to, elements from the CaMV 35S promoter and octopine synthase genes (Last *et al.*, U.S. Patent 5,290,924). As the DNA sequence between the transcription initiation site and the start of the coding sequence, *i.e.*, the untranslated leader sequence, can influence gene expression, one may also wish to employ a particular leader sequence. Any leader sequence available to one of skill in the art may be employed. Preferred leader sequences direct optimum levels of expression of the attached gene, for example, by increasing or maintaining mRNA stability and/or by preventing inappropriate initiation of translation (Joshi, *Nucl. Acid Res.*, 15:6643, 1987). The choice of such sequences is at the discretion of those of skill in the art. Sequences that are derived from genes that are highly expressed in *Brassica* in particular are contemplated.

An inducible promoter can be turned on or off by an exogenously added agent so that expression of an operably linked nucleic acid is also turned on or off. For example, a bacterial promoter, such as the P_{tac}, promoter can be induced to varying levels of gene expression depending on the level of isothiopyrogalactoside added to the transformed bacterial cells. It may also be preferable to combine the nucleic acid encoding the polypeptide of interest with a promoter that provides tissue specific expression or developmentally regulated gene expression in plants.

Expression cassettes of the present invention will also include a sequence near the 3' end of the cassette that acts as a signal to terminate transcription from a heterologous nucleic acid and that directs polyadenylation of the resultant mRNA. Some 3' elements that can act as termination signals include those from the nopaline synthase gene of *Agrobacterium tumefaciens* (Bevan *et al.*, *Nucl. Acid Res.*, 11:369, 1983), a napin 3' untranslated region (Kridl *et al.*, *Seed Sci Res.*, 1:209-219, 1991), a globulin 3' untranslated region (Belanger and Kriz, *Genetics*, 129:863-872, 1991), or one from a zein gene, such as Z27 (Lopes *et al.*, *Mol Gen Genet.*, 247:603-613, 1995). Other 3' elements known by one of skill in the art also can be used in the vectors of the present invention.

Regulatory elements, such as Adh intron 1 (Callis *et al.*, *Genes Develop.*, 1:1183, 1987), a rice actin intron (McElroy *et al.*, *Mol. Gen. Genet.*, 231(1):150-160, 1991), sucrose synthase intron (Vasil *et al.*, *Plant Physiol.*, 91:5175, 1989), the maize HSP70 intron

(Rochester *et al.*, *EMBO J.*, 5:451-458, 1986), or TMV omega element (Gallie *et al.*, *The Plant Cell*, 1:301, 1989) may further be included where desired. These 3' nontranslated regulatory sequences can be obtained as described in An, *Methods in Enzymology*, 153:292 (1987) or are already present in plasmids available from commercial sources, such as

5 Clontech, Palo Alto, California. The 3' nontranslated regulatory sequences can be operably linked to the 3' terminus of any heterologous nucleic acid to be expressed by the expression cassettes contained within the present vectors. Other such regulatory elements useful in the practice of the present invention are known by one of skill in the art and can also be placed in the vectors of the present invention.

10 The vectors of the present invention, as well as the coding regions claimed herein, can be optimized for expression in *Brassica* plants by having one or more codons replaced by other codons encoding the same amino acids so that the polypeptide is optimally translated by the translation machinery of the *Brassica* plant species in which the vector is used.

Selectable Markers: Selectable marker genes or reporter genes are also useful in the
15 present invention. Such genes can impart a distinct phenotype to cells expressing the marker gene and thus allow such transformed cells to be distinguished from cells that do not have the marker. Selectable marker genes confer a trait that one can 'select' for by chemical means, *i.e.*, through the use of a selective agent (*e.g.*, a herbicide, antibiotic, or the like). Reporter genes or screenable genes, confer a trait that one can identify through observation or testing,
20 *i.e.*, by 'screening' (*e.g.*, the R-locus trait). Of course, many examples of suitable marker genes are known to the art and can be employed in the practice of the present invention.

Possible selectable markers for use in connection with the present invention include, but are not limited to, a *neo* gene (Potrykus *et al.*, *Mol. Gen. Genet.*, 199:183, 1985) which codes for kanamycin resistance and can be selected for by applying kanamycin, a kanamycin
25 analog such as geneticin (Sigma Chemical Company, St. Louis, MO), and the like; a *bar* gene that codes for bialaphos resistance; a gene that encodes an altered EPSP synthase protein (Hinchee *et al.*, *Biotech.*, 6:915, 1988) thus conferring glyphosate resistance; a nitrilase gene, such as *bxn* from *Klebsiella ozaenae*, which confers resistance to bromoxynil (Stalker *et al.*, *Science*, 242:419, 1988); a mutant acetolactate synthase gene (ALS) that confers resistance to
30 imidazolinone, sulfonylurea, or other ALS-inhibiting chemicals (EP 154 204A1, 1985); a methotrexate-resistant DHFR gene (Thillet *et al.*, *J. Biol. Chem.*, 263:12500, 1988); a dalapon dehalogenase gene that confers resistance to the herbicide dalapon. Where a mutant EPSP synthase gene is employed, additional benefit may be realized through the incorporation of a suitable plastid transit peptide (CTP).

An illustrative embodiment of a selectable marker gene capable of being used in systems to select transformants is the genes that encode the enzyme phosphinothricin acetyltransferase, such as the *bar* gene from *Streptomyces hygrosopicus* or the *pat* gene from *Streptomyces viridochromogenes* (U.S. Patent 5,550,318, which is incorporated by reference
5 herein). The enzyme phosphinothricin acetyl transferase (PAT) inactivates the active ingredient in the herbicide bialaphos, phosphinothricin that inhibits glutamine synthetase, (Murakami *et al.*, *Mol. Gen. Genet.*, 205:42, 1986; Twell *et al.*, *Plant Physiol.*, 91:1270, 1989) causing rapid accumulation of ammonia and cell death.

Screenable markers that may be employed include, but are not limited to, a
10 β -glucuronidase or *uidA* gene (GUS), which encodes an enzyme for which various chromogenic substrates are known; an R-locus gene, which encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues (Dellaporta *et al.*, *Chromosome Structure and Function*, 263-282, 1988); a β -lactamase gene (Sutcliffe, *Proc. Natl. Acad. Sci. (U.S.A.)*, 75:3737, 1978), which encodes an enzyme for which various
15 chromogenic substrates are known (*e.g.*, PADAC, a chromogenic cephalosporin); a *xyIE* gene (Zukowsky *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)*, 80:1101, 1983) that encodes a catechol dioxygenase that can convert chromogenic catechols; an α -amylase gene (Ikuta *et al.*, *Biotech.*, 8:241, 1990); a tyrosinase gene (Katz *et al.*, *J. Gen. Microbiol.*, 129:2703, 1983) that encodes an enzyme capable of oxidizing tyrosine to DOPA and dopaquinone, which in turn
20 condenses to form the easily detectable compound melanin; a β -galactosidase gene, which encodes an enzyme for which there are chromogenic substrates; a luciferase (*lux*) gene (Ow *et al.*, *Science*, 234:856, 1986), which allows for bioluminescence detection; or an aequorin gene (Prasher *et al.*, *Biochem. Biophys. Res. Comm.*, 126:1259, 1985), which may be employed in calcium-sensitive bioluminescence detection, or a green fluorescent protein gene (Niedz *et al.*,
25 *Plant Cell Reports*, 14:403, 1995). The presence of the *lux* gene in transformed cells may be detected using, for example, X-ray film, scintillation counting, fluorescent spectrophotometry, low-light video cameras, photon-counting cameras, or multiwell luminometry. It is also envisioned that this system may be developed for populational screening for bioluminescence, such as on tissue culture plates, or even for whole plant screening.

30 **Transit Peptides:** Additionally, transgenes may be constructed and employed to provide targeting of the gene product to an intracellular compartment within plant cells or in directing a protein to the extracellular environment. This will generally be achieved by joining a DNA sequence encoding a transit or signal peptide sequence to the coding sequence of a particular gene. The resultant transit or signal peptide will transport the protein to a

particular intracellular, or extracellular destination, respectively, and may then be post-translationally removed. Transit or signal peptides act by facilitating the transport of proteins through intracellular membranes, *e.g.*, vacuole, vesicle, plastid, and mitochondrial membranes, whereas signal peptides direct proteins through the extracellular membrane. By
5 facilitating transport of the protein into compartments inside or outside the cell, these sequences may increase the accumulation of gene product.

An example of such a use concerns the direction of a fatty acid synthase to a particular organelle, such as to a plastid rather than to the cytoplasm. This is exemplified by the use of the *Arabidopsis* SSU1A transit peptide that confers plastid-specific targeting of proteins.

10 Alternatively, the transgene can comprise a plastid transit peptide-encoding DNA sequence or a DNA sequence encoding the *rbcS* (RuBISCO) transit peptide operably linked between a promoter and the DNA sequence encoding a fatty acid synthase (for a review of plastid targeting peptides, *see* Heijne *et al.*, *Eur. J. Biochem.*, 180:535, 1989; Keegstra *et al.*, *Ann. Rev. Plant Physiol. Plant Mol. Biol.*, 40:471, 1989). If the transgene is to be introduced into a
15 plant cell, the transgene can also contain plant transcriptional termination and polyadenylation signals and translational signals linked to the 3' terminus of a plant fatty acid synthase gene.

A heterologous plastid transit peptide can be linked to a multifunctional fatty acid synthase gene. A plastid transit peptide is typically 40 to 70 amino acids in length and functions post-translationally to direct a protein to the plastid. The transit peptide is cleaved
20 either during or just after import into the plastid to yield the mature protein.

Heterologous plastid transit peptide encoding sequences can be obtained from a variety of plant nuclear genes, so long as the products of the genes are expressed as preproteins comprising an amino terminal transit peptide and transported into plastid. Examples of plant gene products known to include such transit peptide sequences include, but
25 are not limited to, the small subunit of ribulose biphosphate carboxylase, chlorophyll a/b binding protein, plastid ribosomal proteins encoded by nuclear genes, certain heat shock proteins, amino acid biosynthetic enzymes, such as acetolactate acid synthase, 3-enolpyruvylphosphoshikimate synthase, dihydrodipicolinate synthase, fatty acid synthase, and the like. In some instances, a plastid transport protein already may be encoded in the fatty
30 acid synthase gene of interest, in which case there may be no need to add such plastid transit sequences. Alternatively, the DNA fragment coding for the transit peptide may be chemically synthesized either wholly or in part from the known sequences of transit peptides such as those listed above.

Regardless of the source of the DNA fragment coding for the transit peptide, it should include a translation initiation codon, for example, an ATG codon, and be expressed as an amino acid sequence that is recognized by and will function properly in plastids of the host plant. Attention should also be given to the amino acid sequence at the junction between the transit peptide and the fatty acid synthase enzyme, where it is cleaved to yield the mature enzyme. Certain conserved amino acid sequences have been identified and may serve as a guideline. Precise fusion of the transit peptide coding sequence with the fatty acid synthase coding sequence may require manipulation of one or both DNA sequences to introduce, for example, a convenient restriction site. This may be accomplished by methods including site-directed mutagenesis, insertion of chemically synthesized oligonucleotide linkers, and the like.

Precise fusion of the nucleic acids encoding the plastid transport protein may not be necessary so long as the coding sequence of the plastid transport protein is in-frame with that of the fatty acid synthase. For example, additional peptidyl or amino acids can often be included without adversely affecting the expression or localization of the protein of interest.

Once obtained, and when desired, the plastid transit peptide sequence can be appropriately linked to the promoter and a fatty acid synthase coding region in a transgene using standard methods. A plasmid containing a promoter functional in plant cells and having multiple cloning sites downstream can be constructed or obtained from commercial sources. The plastid transit peptide sequence can be inserted downstream from the promoter using restriction enzymes. A fatty acid synthase coding region can then be translationally fused or inserted immediately downstream from and in frame with the 3' terminus of the plastid transit peptide sequence. Hence, the plastid transit peptide is preferably linked to the amino terminus of the fatty acid synthase. Once formed, the transgene can be subcloned into other plasmids or vectors.

In addition to nuclear plant transformation, the present invention also extends to direct transformation of the plastid genome of *Brassica* plants. Hence, targeting of the gene product to an intracellular compartment within plant cells may also be achieved by direct delivery of a gene to the intracellular compartment. In some embodiments, direct transformation of plastid genome may provide additional benefits over nuclear transformation. For example, direct plastid transformation of fatty acid synthase eliminates the requirement for a plastid targeting peptide and post-translational transport and processing of the pre-protein derived from the corresponding nuclear transformants. Plastid transformation of plants has been described by Maliga, *Current Opinion in Plant Biology*, 5:164-172 (2002); Heifetz, *Biochimie*, 82:655-666

(2000); Bock, *J. Mol. Biol.*, 312:425-438 (2001); and Daniell *et al.*, *Trends in Plant Science*, 7:84-91 (2002), and references cited therein.

After constructing a transgene containing a multifunctional fatty acid synthase, the expression vector or cassette can then be introduced into a *Brassica* plant cell. Depending on the type of plant cell, the level of gene expression, and the activity of the enzyme encoded by the gene, introduction of DNA encoding a multifunctional fatty acid synthase into the plant cell can lead to increased oil content in *Brassica* plant tissues.

Plant Transformation: There are many methods for introducing transforming nucleic acid molecules into plant cells. Suitable methods are believed to include virtually any method by which nucleic acid molecules may be introduced into a cell, such as by *Agrobacterium* infection or direct delivery of nucleic acid molecules, such as, for example, by PEG-mediated transformation, by electroporation or by acceleration of DNA coated particles, and the like. (Potrykus, *Ann. Rev. Plant Physiol. Plant Mol. Biol.*, 42:205-225, 1991; Vasil, *Plant Mol. Biol.*, 25:925-937, 1994). For example, electroporation has been used to transform maize protoplasts (Fromm *et al.*, *Nature*, 312:791-793, 1986).

Other vector systems suitable for introducing transforming DNA into a host plant cell include but are not limited to binary artificial chromosome (BIBAC) vectors (Hamilton *et al.*, *Gene*, 200:107-116, 1997); and transfection with RNA viral vectors (Della-Cioppa *et al.*, *Ann. N.Y. Acad. Sci.*, (1996), 792 (Engineering Plants for Commercial Products and Applications, 57-61)). Additional vector systems also include plant selectable YAC vectors, such as those described in Mullen *et al.*, *Molecular Breeding*, 4:449-457 (1988).

Technology for introduction of DNA into cells is well known by one of skill in the art. Four general methods for delivering a gene into cells have been described: (1) chemical methods (Graham and van der Eb, *Virology*, 54:536-539, 1973); (2) physical methods, such as microinjection (Capecchi, *Cell*, 22:479-488, 1980), electroporation (Wong and Neumann, *Biochem. Biophys. Res. Commun.*, 107:584-587, 1982; Fromm *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)*, 82:5824-5828, 1985; U.S. Patent 5,384,253); the gene gun (Johnston and Tang, *Methods Cell Biol.*, 43:353-365, 1994); and vacuum infiltration (Bechtold *et al.*, *C.R. Acad. Sci. Paris, Life Sci.*, 316:1194-1199, 1993); (3) viral vectors (Clapp, *Clin. Perinatol.*, 20:155-168, 1993; Lu *et al.*, *J. Exp. Med.*, 178:2089-2096, 1993; Eglitis and Anderson, *Biotechniques*, 6:608-614, 1988); and (4) receptor-mediated mechanisms (Curiel *et al.*, *Hum. Gen. Ther.*, 3:147-154, 1992; Wagner *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)*, 89:6099-6103, 1992).

Acceleration methods that may be used include, for example, microprojectile bombardment and the like. One example of a method for delivering transforming nucleic acid molecules into plant cells is microprojectile bombardment. This method has been reviewed by Yang and Christou (eds.), *Particle Bombardment Technology for Gene Transfer*, Oxford Press, Oxford, England (1994). Non-biological particles (microprojectiles) may be coated with nucleic acids and delivered into cells by a propelling force. Exemplary particles include those comprised of tungsten, gold, platinum, and the like.

A particular advantage of microprojectile bombardment, in addition to it being an effective means of reproducibly transforming monocots, is that neither the isolation of protoplasts (Cristou *et al.*, *Plant Physiol.*, 87:671-674, 1988) nor the susceptibility to *Agrobacterium* infection is required. An illustrative embodiment of a method for delivering DNA into maize cells by acceleration is a biolistics α -particle delivery system, which can be used to propel particles coated with DNA through a screen, such as a stainless steel or Nytex screen, onto a filter surface covered with maize cells cultured in suspension. Gordon-Kamm *et al.*, describes the basic procedure for coating tungsten particles with DNA (Gordon-Kamm *et al.*, *Plant Cell*, 2:603-618, 1990). The screen disperses the tungsten nucleic acid particles so that they are not delivered to the recipient cells in large aggregates. A particle delivery system suitable for use with the present invention is the helium acceleration PDS-1000/He gun, which is available from Bio-Rad Laboratories (Bio-Rad, Hercules, California) (also, *see*, Sanford *et al.*, *Technique*, 3:3-16, 1991).

For the bombardment, cells in suspension may be concentrated on filters. Filters containing the cells to be bombarded are positioned at an appropriate distance below the microprojectile stopping plate. If desired, one or more screens are also positioned between the gun and the cells to be bombarded.

Alternatively, immature embryos or other target cells may be arranged on solid culture medium. The cells to be bombarded are positioned at an appropriate distance below the microprojectile stopping plate. If desired, one or more screens are also positioned between the acceleration device and the cells to be bombarded. Through the use of techniques set forth herein one may obtain 1000 or more loci of cells transiently expressing a marker gene. The number of cells in a focus that express the exogenous gene product 48 hours post-bombardment often ranges from 1 to 10, and average 1 to 3.

In bombardment transformation, one may optimize the pre-bombardment culturing conditions and the bombardment parameters to yield the maximum numbers of stable transformants. Both the physical and biological parameters for bombardment are important in

this technology. Physical factors are those that involve manipulating the DNA/microprojectile precipitate or those that affect the flight and velocity of the microprojectiles. Biological factors include all steps involved in manipulation of cells before and immediately after bombardment, the osmotic adjustment of target cells to help alleviate the trauma associated with bombardment and, also, the nature of the transforming DNA, such as linearized DNA or intact supercoiled plasmids. It is believed that pre-bombardment manipulations are especially important for successful transformation of immature embryos.

In another alternative embodiment, plastids can be stably transformed. Methods disclosed for plastid transformation in higher plants include the particle gun delivery of DNA containing a selectable marker and targeting of the DNA to the plastid genome through homologous recombination (Svab *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)*, 87:8526-8530, 1990; Svab and Maliga, *Proc. Natl. Acad. Sci. (U.S.A.)*, 90:913-917, 1993; Staub and Maliga, *EMBO J.*, 12:601-606, 1993; U.S. Patents 5,451,513 and 5,545,818).

Accordingly, it is contemplated that one may wish to adjust various aspects of the bombardment parameters in small scale studies to fully optimize the conditions. One may particularly wish to adjust physical parameters such as gap distance, flight distance, tissue distance, and helium pressure. One may also minimize the trauma reduction factors by modifying conditions that influence the physiological state of the recipient cells and which may therefore influence transformation and integration efficiencies. For example, the osmotic state, tissue hydration, and the subculture stage or cell cycle of the recipient cells may be adjusted for optimum transformation. The execution of other routine adjustments will be known by one of skill in the art in light of the present invention.

Agrobacterium-mediated transfer is a widely applicable system for introducing genes into plant cells because the DNA can be introduced into whole plant tissues, thereby bypassing the need for regeneration of an intact plant from a protoplast. The use of *Agrobacterium*-mediated plant integrating vectors to introduce DNA into plant cells is well known in the art. See, for example the methods described by Fraley *et al.*, *Bio/Technology*, 3:629-635 (1985) and Rogers *et al.*, *Methods Enzymol.*, 153:253-277 (1987). Further, the integration of the Ti-DNA is a relatively precise process resulting in few rearrangements. The region of DNA to be transferred is defined by the border sequences and intervening DNA is usually inserted into the plant genome as described (Spielmann *et al.*, *Mol. Gen. Genet.*, 205:34, 1986).

Modern *Agrobacterium* transformation vectors are capable of replication in *E. coli* as well as *Agrobacterium*, allowing for convenient manipulations as described (Klee *et al.*, In:

Plant DNA Infectious Agents, Hohn and Schell (eds.), Springer-Verlag, NY, pp. 179-203, 1985). Moreover, technological advances in vectors for *Agrobacterium*-mediated gene transfer have improved the arrangement of genes and restriction sites in the vectors to facilitate construction of vectors capable of expressing various polypeptide coding genes. The
5 vectors described have convenient multi-linker regions flanked by a promoter and a polyadenylation site for direct expression of inserted polypeptide coding genes and are suitable for present purposes (Rogers *et al.*, *Methods Enzymol.*, 153:253-277, 1987). In addition, *Agrobacterium* containing both armed and disarmed Ti genes can be used for the transformations. In those plant strains where *Agrobacterium*-mediated transformation is
10 efficient, it is the method of choice because of the facile and defined nature of the gene transfer.

A transgenic plant formed using *Agrobacterium* transformation methods typically contains a single gene on one chromosome. Such transgenic plants can be referred to as being heterozygous for the added gene. More preferred is a transgenic plant that is homozygous for
15 the added structural gene; *i.e.*, a transgenic plant that contains 2 added genes, one gene at the same locus on each chromosome of a chromosome pair. A homozygous transgenic plant can be obtained by sexually mating (selfing) an independent segregant, transgenic plant that contains a single added gene, germinating some of the seed produced and analyzing the resulting plants produced for the gene of interest.

20 It is also to be understood that two different transgenic plants can also be mated to produce offspring that contain two independently segregating, exogenous genes. Selfing of appropriate progeny can produce plants that are homozygous for both added, exogenous genes that encode a polypeptide of interest. Back-crossing to a parental plant and out-crossing with a non-transgenic plant are also contemplated, as is vegetative propagation.

25 Transformation of plant protoplasts can be achieved using methods based on calcium phosphate precipitation, polyethylene glycol treatment, electroporation, and combinations of these treatments (*see*, for example, Potrykus *et al.*, *Mol. Gen. Genet.*, 205:193-200, 1986; Lorz *et al.*, *Mol. Gen. Genet.*, 199:178, 1985; Fromm *et al.*, *Nature*, 319:791, 1986; Uchimiya *et al.*, *Mol. Gen. Genet.*, 204:204, 1986; Marcotte *et al.*, *Nature*, 335:454-457, 1988).

30 Application of these systems to different plant strains depends upon the ability to regenerate that particular plant strain from protoplasts. Illustrative methods for the regeneration of cereals from protoplasts are described (Fujimura *et al.*, *Plant Tissue Culture Letters*, 2:74, 1985; Toriyama *et al.*, *Theor. Appl. Genet.*, 205:34, 1986; Yamada *et al.*, *Plant Cell Rep.*, 4:85, 1986; Abdullah *et al.*, *Biotechnology*, 4:1087, 1986).

To transform plant strains that cannot be successfully regenerated from protoplasts, other ways to introduce DNA into intact cells or tissues can be utilized. For example, regeneration of cereals from immature embryos or explants can be effected as described (Vasil, *Biotechnology*, 6:397, 1988). In addition, "particle gun" or high-velocity microprojectile technology can be utilized (Vasil *et al.*, *Bio/Technology*, 10:667, 1992).

Using the latter technology, DNA is carried through the cell wall and into the cytoplasm on the surface of small metal particles as described (Klein *et al.*, *Nature*, 328:70, 1987; Klein *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)*, 85:8502-8505, 1988; McCabe *et al.*, *Bio/Technology*, 6:923, 1988). The metal particles penetrate through several layers of cells and thus allow the transformation of cells within tissue explants.

Other methods of cell transformation can also be used and include but are not limited to introduction of DNA into plants by direct DNA transfer into pollen (Hess *et al.*, *Intern Rev. Cytol.*, 107:367, 1987; Luo *et al.*, *Plant Mol Biol. Reporter*, 6:165, 1988), by direct injection of DNA into reproductive organs of a plant (Pena *et al.*, *Nature*, 325:274, 1987), or by direct injection of DNA into the cells of immature embryos followed by the rehydration of desiccated embryos (Neuhaus *et al.*, *Theor. Appl. Genet.*, 75:30, 1987).

The regeneration, development, and cultivation of plants from single plant protoplast transformants or from various transformed explants is well known in the art (Weissbach and Weissbach, In: *Methods for Plant Molecular Biology*, Academic Press, San Diego, California, 1988). This regeneration and growth process typically includes the steps of selection of transformed cells, culturing those individualized cells through the usual stages of embryonic development through the rooted plantlet stage. Transgenic embryos and seeds are similarly regenerated. The resulting transgenic rooted shoots are thereafter planted in an appropriate plant growth medium such as soil.

The development or regeneration of plants containing the foreign, exogenous gene that encodes a protein of interest is well known in the art. Preferably, the regenerated plants are self-pollinated to provide homozygous transgenic plants. Otherwise, pollen obtained from the regenerated plants is crossed to seed-grown plants of agronomically important lines. Conversely, pollen from plants of these important lines is used to pollinate regenerated plants. A transgenic plant of the present invention containing a desired polypeptide is cultivated using methods well known to one skilled in the art.

There are a variety of methods for the regeneration of plants from plant tissue. The particular method of regeneration will depend on the starting plant tissue and the particular plant species to be regenerated.

Methods for transforming dicots, primarily by use of *Agrobacterium tumefaciens* and obtaining transgenic plants have been published for cotton (U.S. Patents 5,004,863; 5,159,135; and 5,518,908); soybean (U.S. Patents 6,384,301; 5,569,834; and 5,416,011; McCabe *et al.*, *Biotechnology*, 6:923, 1988; Christou *et al.*, *Plant Physiol.*, 87:671-674, 1988);
 5 *Brassica* (U.S. Patent 5,463,174); peanut (Cheng *et al.*, *Plant Cell Rep.*, 15:653-657, 1996; McKently *et al.*, *Plant Cell Rep.*, 14:699-703, 1995); papaya; pea (Grant *et al.*, *Plant Cell Rep.*, 15:254-258, 1995); and *Arabidopsis thaliana* (Bechtold *et al.*, *C.R. Acad. Sci. Paris, Life Sci.*, 316:1194-1199, 1993). The latter method for transforming *Arabidopsis thaliana* is commonly called "dipping" or vacuum infiltration or germplasm transformation.

10 Transformation of monocotyledons using electroporation, particle bombardment and *Agrobacterium* have also been reported. Transformation and plant regeneration have been achieved in asparagus (Bytebier *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)*, 84:5354, 1987); barley (Wan and Lemaux, *Plant Physiol.*, 104:37, 1994); maize (Rhodes *et al.*, *Science*, 240:204, 1988; Gordon-Kamm *et al.*, *Plant Cell*, 2:603-618, 1990; Fromm *et al.*, *Bio/Technology*,
 15 8:833, 1990; Koziel *et al.*, *Bio/Technology*, 11:194, 1993; Armstrong *et al.*, *Crop Science*, 35:550-557, 1995); oat (Somers *et al.*, *Bio/Technology*, 10:1589, 1992); orchard grass (Horn *et al.*, *Plant Cell Rep.*, 7:469, 1988); rice (Toriyama *et al.*, *Theor Appl. Genet.*, 205:34, 1986; Part *et al.*, *Plant Mol. Biol.*, 32:1135-1148, 1996; Abedinia *et al.*, *Aust. J. Plant Physiol.*, 24:133-141, 1997; Zhang and Wu, *Theor. Appl. Genet.*, 76:835, 1988; Zhang *et al.*, *Plant Cell Rep.*, 7:379, 1988; Battraw and Hall, *Plant Sci.*, 86:191-202, 1992; Christou *et al.*,
 20 *Bio/Technology*, 9:957, 1991); rye (DelaPena *et al.*, *Nature*, 325:274, 1987); sugarcane (Bower and Birch, *Plant J.*, 2:409, 1992); tall fescue (Wang *et al.*, *Bio/Technology*, 10:691, 1992); and wheat (Vasil *et al.*, *Bio/Technology*, 10:667, 1992; U.S. Patent 5,631,152).

Assays for gene expression based on the transient expression of cloned nucleic acid
 25 constructs have been developed by introducing the nucleic acid molecules into plant cells by polyethylene glycol treatment, electroporation, or particle bombardment (Marcotte *et al.*, *Nature*, 335:454-457, 1988; Marcotte *et al.*, *Plant Cell*, 1:523-532, 1989; McCarty *et al.*, *Cell*, 66:895-905, 1991; Hattori *et al.*, *Genes Dev.*, 6:609-618, 1992; Goff *et al.*, *EMBO J.*, 9:2517-2522, 1990). Transient expression systems may be used to functionally dissect gene
 30 constructs (*see generally*, Maliga *et al.*, *Methods in Plant Molecular Biology*, Cold Spring Harbor Press, 1995).

Any of the nucleic acid molecules of the present invention may be introduced into a plant cell in a permanent or transient manner in combination with other genetic elements such as vectors, promoters, enhancers, *etc.* Further, any of the nucleic acid molecules of the

present invention may be introduced into a plant cell in a manner that allows for expression or overexpression of the protein or fragment thereof encoded by the nucleic acid molecule.

It is also to be understood that 2 different transgenic *Brassica* plants can also be mated to produce offspring that contain 2 independently segregating added, exogenous genes.

- 5 Selfing of appropriate progeny can produce plants that are homozygous for both added, exogenous genes that encode a polypeptide of interest. Backcrossing to a parental plant and out-crossing with a non-transgenic plant are also contemplated, as is vegetative propagation.

Transgenic *Brassica* plants may find use in the commercial manufacture of proteins or other molecules, where the molecule of interest is extracted or purified from plant parts, seeds, and the like. Cells or tissue from the plants may also be cultured, grown *in vitro*, or fermented to manufacture such molecules.

The transgenic *Brassica* plants may also be used in commercial breeding programs, or may be crossed or bred to plants of related crop species. Improvements encoded by the recombinant DNA may be transferred, *e.g.*, from cells of one species to cells of other species, *e.g.*, by protoplast fusion.

The present invention also provides for a method of stably expressing a fatty acid synthase of interest in a *Brassica* plant, which includes, contacting the plant cell with a vector of the present invention that has a selectable marker gene and a nucleic acid encoding the fatty acid synthase of interest, under conditions effective to transform the plant cell. A promoter within the expression cassette can be any of the promoters provided herein, for example, a constitutive promoter, an inducible promoter, a tissue-specific promoter or a seed specific promoter. Such promoters can provide expression of an encoded fatty acid synthase at a desired time, or at a desired developmental stage, or in a desired tissue.

The present invention also provides for a method of stably expressing a fatty acid synthase of interest in a plant, which includes, contacting the plant cell with a vector of the present invention that has a nucleic acid encoding the fatty acid synthase of interest, under conditions effective to transfer and integrate the vector into the nuclear genome of the cell. The vector can also include a selectable marker gene. When using the vector with *Agrobacterium tumefaciens*, the vector can have an *Agrobacterium tumefaciens* origin of replication.

In another embodiment, the present invention provides a method of producing a *Brassica* oil, comprising the steps of: a) growing an oilseed *Brassica* plant, the genome of which contains a nucleic acid molecule encoding a multifunctional fatty acid synthase, to produce oil-containing seeds; and b) extracting oil from the seeds. In another embodiment,

Plants: Plants for use with the vectors of the present invention include *Brassica* sp., particularly those *Brassica* species useful as sources of seed oil (e.g., *B. napus*, *B. rapa*, *B. juncea*).

EXAMPLE 1

Genomic DNA was isolated from *B. ammoniagenes* (ATCC 5871) using standard methodologies. A genomic library was prepared by partially digesting *B. ammoniagenes* genomic DNA with the restriction enzyme Sau3A, isolating DNA fragments ranging from 30-42 kb in size and generating the library using the SuperCos 1 Cosmid Vector kit from Stratagene, Inc. (La Jolla, California). The genomic library was screened by hybridization and washing under stringent conditions with a ³²P-labelled 1.1 kb *fasA* PCR fragment generated from isolated genomic DNA using the following PCR primers:

5'-CCAGCTCAACGATGAAGTAG-3' [SEQ ID NO: 5] and

5'-TCGATGATCTGGTCTACTTC-3' [SEQ ID NO: 6]

The full-length *fasA* gene was assembled so as to introduce convenient flanking restriction sites for sub-cloning by using the following basic steps: a) PCR amplification of

the 5' and 3' ends; b) assembling the 5' and 3' ends of the gene together by an overlapping PCR strategy resulting in deletion of the *fasA* sequence between the internal MfeI and XhoI sites; c) cloning the "5'-3' fused" PCR fragment; d) insertion of the 8166 bp *fasA* MfeI / XhoI fragment between the MfeI and XhoI sites in the "5'-3' fused" PCR fragment so as to re-
5 generate the full-length *fasA* gene with convenient flanking cloning sites. The details for each of these steps are outlined below.

A 5' 280 bp *fasA* PCR fragment was generated using the following primers:

16393 (forward)

5'- TCTAGATGCATAGTTAACATGTCGTTGACCCCCTTGC -3' [SEQ ID NO: 9]

10 and

14873 (reverse)

5'-GGTACGCGTCATATTCCTTG -3' [SEQ ID NO: 10]

The forward primer, 16393, introduced XbaI, NsiI, HpaI, and PciI flanking restriction sites.

15 A 3' 946 bp *fasA* PCR fragment was generated using the following primers:

16385 (forward)

5'-CAAGGAATATGACGCGTACCCTCGAGGCAGAAGGCGGCGG- 3' [SEQ ID
NO: 11] and

16394 (reverse)

20 5'-ATGCATGTTAACATGTCTACTTTGTCCTACTTCGCCG-3' [SEQ ID NO: 12]

The reverse primer, 16394, introduced 3' flanking NsiI, HpaI, and PciI restriction sites. The forward primer, 16385, contained 20 bp of sequence matching the 3'-end of the 5' 280 bp restriction fragment described above to allow the 2 fragments to anneal together. The 5' 280 bp *fasA* PCR fragment and the 3' 946 bp *fasA* PCR fragment were fused together by annealing
25 the 2 fragments and PCR amplifying the full length (1206 bp) overlapped fragment using the external primers 16393 (forward) and 16394 (reverse). The 1206 bp 5'-3'- fused PCR fragment was cloned into pCR-Blunt II-TOPO (Invitrogen Corporation, Carlsbad, California) and the correct DNA sequence was confirmed by sequencing. The 1206 bp 5'-3'- fused PCR fragment was then sub-cloned as an SpeI / XbaI fragment into a Bluescript pBC KS+
30 (Stratagene Inc., La Jolla, California) vector which contained a modified multiple cloning sequence (pCGN3686). The full-length *fasA* gene was then obtained by ligation of the 3505 bp MluI / MluI and 4516 bp MluI / XhoI internal *fasA* fragments isolated from the full-length cosmid clone between the MluI and XhoI sites in the 5'-3' fused PCR fragment to make pMON70058 (Figure 1).

The complete double-stranded sequence of the full-length *fasA* gene open reading frame in pMON70058 was determined using a Perkin Elmer ABI 377 DNA sequencer (SEQ ID NO: 1). The corresponding protein sequence (SEQ ID NO: 2) was predicted based on standard genetic code using the program Omega (Accelrys, Inc., Cambridge, UK) and compared with the published *fasA* sequence (Figure 2). Alignment of both the nucleic acid and predicted amino acid sequences to the published sequences (Stuible *et al.*, *J. Bacteriol.*, 178:4787, 1996) revealed a number of differences both at the DNA and protein levels (Figures 2 and 3).

The *B. ammoniagenes ppt1* gene was PCR amplified from isolated genomic DNA using the following primers:

16117 (forward):

5'-GTCGACATGCTCGACAACCGTGAAGCG-3' [SEQ ID NO: 7] and

16118 (reverse):

5'-AGATCTTCACTGGTGGCTTGCCGTAGATCGC-3' [SEQ ID NO: 8]

The PCR-amplified fragment was then cloned into the commercially available cloning vector pCR-Blunt II TOPO (Invitrogen Corporation, Carlsbad, California). The complete double stranded sequence of the full-length *ppt1* gene (SEQ ID NO: 3) was determined using a Perkin Elmer ABI 377 DNA sequencer. The corresponding protein sequence (SEQ ID NO: 4) was predicted based on standard genetic code using the program Omega and compared with the published *ppt1* sequence. Alignment of both the nucleic acid and predicted amino acid sequences to the published sequences (Stuible *et al.*, *J. Bacteriol.*, 178:4787, 1996) revealed that the cloned *ppt1* gene was identical to the published sequence.

EXAMPLE 2

This example describes the transformation of *E. coli* with *fasA* gene constructs for functional testing.

The full-length, sequence-confirmed *B. ammoniagenes ppt1* gene in the pCR-Blunt II TOPO vector described in Example 1 was cut out of the pCR-Blunt II TOPO backbone as a Sal I / Bgl II fragment, and ligated into the Sal I / BamHI sites, respectively, of pSU19 (Bartolome *et al.*, *Gene*, 102(1):75-78, 1991). The Sal I sites of both the *ppt1* and the pSU19 fragments were blunt-ended with the Klenow fragment of DNA polymerase I prior to ligation to enable inframe insertion of the *ppt1* coding sequence into the *lacZ* coding sequence of pSU19. The PPT1 protein was thus expressed in *E. coli* as a lacZ fusion protein upon induction of the lacZ promoter in pSU19 by the use of isopropyl-1-thio- β -D-galactopyranoside (IPTG). This *ppt1*-containing vector was then transformed into *E. coli*

strain VCS257 from Stratagene (cat#200256-51), along with the mfFAS cosmid clone, described in Example 1, for functional testing.

Because the plasmid pSU19 has a pACYC184 origin of replication and conveys chloramphenicol resistance, the *ppt1* expressing plasmid could be stably maintained along with the cosmid (ampicillin resistance) expressing the *fasA* gene.

Based on the published report of Stuible *et al.*, *Eur. J. Biochem.*, 248:481-487 (1997), the endogenous *fasA* promoter was used to express the mfFAS polypeptide encoded by *fasA* in *E. coli*. As a result, *E. coli* transformants containing the *fasA* cosmid alone, the pSU19/*ppt1* construct alone, and both the *fasA* cosmid and the pSU19/*ppt1* construct were made for functional testing. The full-length *fasA* gene was also subcloned as a PciI fragment from pMON70058 into the *E. coli* expression vector pQE60 (QIAGEN, Inc., Valencia, California) to enable inducible expression from an *E. coli* promoter (pMON70081).

EXAMPLE 3

This example sets forth the functional testing of transgene activity in *E. coli* using enzymatic assays.

In order to assay the *E. coli* strains containing the *fasA* cosmid and *ppt1* gene construct the *fasA* gene product was partially purified essentially as outlined in Kawaguchi *et al.*, *Methods in Enzymology*, 71:120-127 (1981). Frozen cells from the strain containing either the *fasA* cosmid alone, the pSU19/*ppt1* construct alone, both the *fasA* cosmid and the pSU19/*ppt1* construct, or the untransformed cell line alone were thawed in 0.1M potassium phosphate buffer (~1ml/1gm) and cells lysed by high speed mixing with glass beads. The supernatant was centrifuged at 105,000 x g for 60 minutes and removed. Ammonium sulphate was slowly added to the supernatant to give a final concentration of 30% w/v followed by 30 minutes of stirring. A second centrifugation step (25,000 x g) was performed and the precipitate was re-suspended in 0.5M potassium phosphate buffer before passing through a Sephadex G-25 column.

The *fasA* activity in each of the extracts was determined by a radiochemical assay at 37°C for 15 minutes using the conditions outlined in Kawaguchi *et al.*, (1981). The results of these assays (shown in Figure 4) demonstrated that only when the *fasA* cosmid (FA) and the pSU19/*ppt1* (P) construct were both present was there any measurable *fasA* activity. Furthermore, they demonstrated that the *fasA* gene that was cloned and used for preparation of *Brassica* transformation constructs did encode a functional *fasA* enzyme.

EXAMPLE 4

This example describes the construction of a plant binary vector for seed-specific expression of the *fasA* gene in canola plants. The construction is shown graphically in Figures 5 and 6. The vector pMON75201 was designed to produce seed-specific expression of the *B. ammoniagenes fasA* and *ppt1* genes in canola.

The full-length, sequence-confirmed *B. ammoniagenes ppt1* gene in the pCR-Blunt II TOPO vector described in Example 1 was cut out of the pCR-Blunt II TOPO backbone using the Sal I and Bgl II sites engineered into the PCR primers 16117 and 16118 (SEQ ID NOs: 7 and 8, respectively) used in the cloning and ligated to the Sal I and BamHI sites between the napin promoter (base pairs 407-2151 of the *Brassica campestris* napin gene, N5, GenBank Accession Number M64632) and the napin 3' untranslated region (UTR), N3, (base pairs 2728-3982 of the *Brassica campestris* napin gene, GenBank Accession Number M64632) found in the plant / *E. coli* binary vector pCGN7770 (Figure 5). The napin promoter / *B. ammoniagenes ppt1* / napin 3' UTR cassette was combined with the *B. ammoniagenes fasA* gene for simultaneous expression in *Brassica* plants as described below.

The full-length, sequence-confirmed *B. ammoniagenes fasA* gene was removed from pMON70058 (described in Example 1 and Figure 1) using the restriction enzymes NotI and SmaI and was ligated into the NotI and blunted Sse8387I restriction sites between a napin promoter and napin 3' UTR (as described above) contained in a two T-DNA binary vector pMON67164. The Sse8387I site was blunt-ended by the action of Klenow fragment of DNA polymerase I. The resultant vector, containing the pMON67164 backbone and the *B. ammoniagenes fasA* gene flanked by the napin expression sequences, was digested with PacI, blunt-ended by the action of Klenow fragment of DNA polymerase I, and then digested with AscI. The AscI / PvuII fragment containing the napin promoter / *B. ammoniagenes ppt1* gene / napin 3' UTR cassette in pCGN7770 (described above) was then inserted into the PacI blunt / AscI sites to form pMON75201. pMON75201 is a two T-DNA vector containing both the *B. ammoniagenes fasA* gene and the *B. ammoniagenes ppt1* gene each under the control of seed-specific napin expression sequences (napin promoter and 3' UTR) and located within one set of T-DNA left and right borders. A selectable marker for plant transformation, containing the FMV 35S promoter, (F35S, base pairs 6927-6474 of the FMV promoter which is the promoter for ORF VII, GenBank Accession Number X06166) driving a CP4 selectable marker gene (a chloroplast targeting sequence from the *Arabidopsis* EPSP gene linked to a synthetic EPSP synthase coding region as described in U.S. Patent 5,633,435) and a

E9 3' UTR (Coruzzi *et al.*, *EMBO J.*, 3(8):1671-1679, 1984) is located within a second set of T-DNA left and right borders.

EXAMPLE 5

This example describes the transformation of canola plants with *fasA* and *ppt1* genes.

5 Canola plants (*Brassica napus*) are transformed using a modification of the protocol described by Radke *et al.*, *Plant Cell Reports*, 11:499-505 (1992). Briefly canola seed of the cultivar 'Ebony' (Monsanto Canada, Inc., Winnipeg, Canada) are disinfected and germinated *in vitro* as described in Radke *et al.*, 1992. Precocultivation with tobacco feeder plates, explant preparation and inoculation of explants with *Agrobacterium tumefaciens* strain ABI
10 (Koncz and Schell, *Mol Gen Genet.*, 204:383-396, 1986) containing the vector pMON75201 are as described with the *Agrobacterium* being maintained in LB media (solid or liquid) containing 75 mg/l spectinomycin, 25 mg/l chloramphenicol, and 50 mg/l kanamycin. For plant transformation including callus induction, shoot regeneration, maturation and rooting, glyphosate selection is used rather than the kanamycin selection as described in Radke *et al.*,
15 1992. Specifically, the B5-1 callus induction medium is supplemented with 500 mg/l carbenicillin and 50 mg/l Timentin (Duchefa Biochemie BV) to inhibit the *Agrobacterium* growth and kanamycin is omitted from the media. B5BZ shoot regeneration medium contains 500 mg/l carbenicillin, 50 mg/l Timentin, and 45 mg/l glyphosate with explants being transferred to fresh medium every 2 weeks. Glyphosate selected shoots are transferred to
20 hormone-free B5-0 shoot maturation medium containing 300 mg/l carbenicillin and 45 mg/l glyphosate for 2 weeks and finally shoots are transferred to B5 root induction medium containing 45 mg/l glyphosate. Rooted green plantlets are transplanted to potting soil and acclimated to green house conditions. Plants are maintained in a greenhouse under standard conditions.

25 Developing seed is harvested at various stages after pollination and stored at -70°C. Mature seed is collected and stored under controlled conditions consisting of about 17°C and 30% humidity.

EXAMPLE 6

This example describes the evaluation and selection of R2 seed from canola
30 plants transformed with the *fasA* and *ppt1* genes as described above in Example 5.

From the transformation of canola ex-plants with pMON75201, as described above, 110 events were generated. These events were analyzed for the presence of the gene of interest (GOI) by PCR, for transcription expression of the GOI by TaqMan methodology, and for the presence of the FasA protein by western blot analysis. The events testing positive for

the GOI by PCR were considered for selection to advance in the development of high oil varieties.

The western blot analysis for the presence of the FasA protein was done using methods well known in the art. Briefly, antibodies were generated by a contract laboratory (Zymed Laboratories Inc., South San Francisco, California) to 4 synthetic peptides located in different regions of the *fasA* gene; *fasA*₂₈₄₃₋₂₈₅₈ = (C)SKHDTSTNANDPNESE (SEQ ID NO: 44), *fasA*₁₇₅₅₋₁₇₆₈ = (C)QNKIRQDQINDSDT (SEQ ID NO: 45), *fasA*₉₁₅₋₉₃₀ = (C)RINSDSYWDNLPEEQR (SEQ ID NO: 46), and *fasA*₁₄₃₁₋₁₄₄₄ = (C)TLVERDENGNSNYG (SEQ ID NO: 47). A protein extract from each of the events was separated using SDS-PAGE according to Laemmli, *Nature*, 227: 680 (1970), and transferred to a polyvinylidene difluoride (PVDF) membrane in Tris buffered saline (TBS; 25mM Tris, 150 mM NaCl) (BioRad, Bulletin #9016). The membrane was blocked with TBST (TBS with 0.05% Tween 20) containing 1% bovine serum albumin (BSA) for 10 minutes then incubated overnight at room temperature with a combined solution of primary antibodies from *fasA*₂₈₄₃₋₂₈₅₈, *fasA*₁₇₅₅₋₁₇₆₈, and *fasA*₁₄₃₁₋₁₄₄₄, at a 1:2000 dilution of each antibody in TBST with 1% BSA. The membrane was washed 3 x 15 minutes with TBST then exposed to a reporting, secondary antibody (Anti-rabbit-AP conjugate, Promega S3731, Madison, WI, 1:5000 in TBST) for one hour. The membrane was washed 3 x 15 minutes with TBST followed by 2 minutes with TBS to remove residual Tween 20. Western Blue Stabilized Substrate for Alkaline Phosphatase (Promega S3841, Madison, WI) was added to visualize protein. Development was stopped by rinsing the membrane with purified water. Of the events tested, 23 were determined to be potentially western positive by exhibiting at least a weak response, and 8 of those confirmed to be positive by exhibiting a strong response. The results are shown in Figure 7.

Mature R1 seed from all 23 events were planted and a selection test was performed to identify gene positive and gene negative lines for each event. For the event selection test, plants from each event were analyzed for the presence of the gene of interest (GOI) by PCR using primers from the GOI and promoter region. DNA for the PCR was isolated from leaf tissue using DNeasy 96 Plant Kit from Qiagen (Cat. No. 69181). The forward primer, located in the promoter region, was primer # 6456 (5'-TTCATAAGATGTCACGCCAGG-3') (SEQ ID NO: 48), and the reverse primer, located in the GOI, was primer # 14873 (5'-GGTACGCGTCATATTCCTTG-3') (SEQ ID NO: 49). PCR protocol was set at 97°C for 1 minute, 40 cycles of [94°C 15 seconds, 60°C 30 seconds, 72°C 30 seconds], and 72°C for

5 minutes. Fourteen events (indicated by ^a in Figure 7) were advanced to the R2 seed stage by growing R1 plants to maturity in the greenhouse under standard conditions. Ten of these events were identified as single locus (indicated by ^b in Figure 7) and were also planted in field trials (Brawley, California) as R1 transplants. The R2 seed from gene positive and null segregants from 4 events (BN_G1193, BN_G1198, BN_G1214, and BN_G1220) as well as commercial control lines, were planted in a randomized complete bloc experiment in field trials (Thief River Falls, Minnesota).

In addition to the PCR gene confirmation and the western blot analysis, developing R1 seed (approximately 20/event) of the 23 events were analyzed for transcript expression of the genes of interest, *fasA* and *ppt1*, by TaqMan. TaqMan analysis was performed using the TaqMan One-Step RT-PCR Master Mix Reagents Kit and Protocol (#4310299 rev. C, Applied Biosystems, Foster City, California). Low, medium, and high GOI-expressing lines are carried forward. Two separate experiments were performed on the same, pooled sample from each event. The results of both experiments are shown in tabular form in Figure 7.

On the occasion when multiple gene copies of the GOI or marker are present, additional work is required to generate a null segregant from which phenotypic comparisons can be made. In addition to the original 14 events that were advanced, two GOI multicopy events (BN_G1223 and BN_G1239) were identified that exhibited a strong response in the western blot analysis. These events were crossed to the variety Ebony in order to produce gene positive as well as null segregants from an F1 population. Event BN_G1216 contained multiple copies of the marker gene, therefore it was out-crossed to Ebony as well. F1 transplants were generated for these events and were planted in the field and greenhouse. These 3 events are identified by ^c in Figure 7. A comparison of the gene positive and null segregant selections is made in the F2 seed generation.

Oil and protein content of the F1 and R2 seed were established by near-infrared reflectance (NIR) spectroscopy (Williams and Norris, eds., *Near-infrared Technology in the Agricultural and Food Industries*, American Association of Cereal Chemists, Inc., St. Paul, MN (1987)), using a standard curve generated from analysis of canola seed with varying oil and protein levels. Briefly, mature canola seeds previously dried to less than 10% moisture were equilibrated to ambient humidity in paper envelopes at room temperature. Single replicate sub-samples (2-3 g) were placed in NIR ring cups (aluminum/quartz; 2 inch diameter by 0.5 inch thick, Foss North America Inc., Silver Springs, MD) and sealed with a paperboard disk. The loaded ring cups were placed in an autoloader and scanned sequentially on a Foss Analytical model 6500 Spectrometer, (Foss North America Inc., Silver Springs, MD). Each

sample was scanned 25 times from 400 to 2500 nm (resolution 2 nm) and the average spectrum was compiled. The averaged spectrum was reduced to second derivative spectra, smoothed, and transformed to a series of principal component scores. The total oil and protein levels were predicted based on a previously prepared calibration models.

- 5 Commercially available software (WinISI ver 1.00, Infrasoft International LLC, State College, PA) was used for calibration development and instrument operation.

One-way analysis of variance and the Student's T-test (JMP software, version 4.04, SAS Institute Inc., Cary, North Carolina) was performed to identify significant differences between transgenic and non-transgenic seed pools as determined by transgene-specific PCR.

- 10 As a result of the statistical analysis of the oil results, R2 seed from event BN_G1216 was determined to have a statistically significant increase in oil content as compared to a negative isoline control. The mean oil content determined by a one-way analysis of variance (ANOVA) for the positive isoline was 44.0%, as compared to 41.8% for the negative isoline control. The results are shown in Figure 8.

15 **EXAMPLE 7**

This example describes the generation and evaluation of R3 seed and F2 seed from canola plants transformed with the *fasA* and *ppt1* genes as described above in Example 5.

- The event that showed a significant increase in oil in the greenhouse (BN_G1216) is included in a randomized complete bloc field test. This event did not show a positive
20 phenotype as an R1 transplant in a first field trial (described above in Example 6). However, because field conditions are variable and have been shown to affect phenotype, and because of the positive phenotype in the greenhouse trial, this second field trial is determined to be warranted. In this second field trial, the gene positive line is compared to its null segregant to determine phenotype. Ebony is included in this experiment as a varietal control. The
25 resulting seed is analyzed for oil and protein and the data is analyzed for statistical differences as described above in Example 6. The results of the R3 seed corroborate the results from the greenhouse grown R2 seed, described above in Example 6.

- Three additional events, BN_G1223, BN_G1216, and BN_G1239, that were Western positive but contained multiple gene copies, are crossed to the variety Ebony in order to
30 produce null segregants from an F1 population of seed that contained gene positive as well as the null segregants. The 3 out-crossed events, BN_G1233xEbony, BN_G1239xEbony, and BN_G1216xEbony, are grown in the field and greenhouse as F1 single plants. They are randomized as positive and negative selections and are grown with Ebony control lines. These events are individually isolated to produce selfed seed. The resulting F2 seed is

harvested and analyzed for oil and protein, and the data is analyzed for statistical differences, as described above. The results of the F2 seed corroborate the results from the greenhouse grown R2 seed, described above in Example 6.

5 The present invention is not limited to the precise details shown and set forth hereinabove, for it should be understood that many variations and modifications may be made while still remaining within the spirit and scope of the present invention defined by the claims.

WHAT IS CLAIMED:

1. A *Brassica* sp. plant comprising a heterologous nucleic acid molecule encoding a multifunctional fatty acid synthase.
- 5 2. The plant of claim 1, further comprising a second heterologous nucleic acid molecule encoding a phosphopantetheine:protein transferase enzyme.
3. The plant of claim 1 or 2, wherein the nucleic acid molecule encodes a multifunctional fatty acid synthase comprising an amino acid sequence selected from the group
10 consisting of SEQ ID NOs: 2, 15, 17, 18, 19, 20, 22-25, 27, 29, and 31.
4. The plant of claim 3, wherein the protein is SEQ ID NO: 2.
5. The plant of claim 2, wherein the nucleic acid molecule encoding a
15 phosphopantetheine:protein transferase enzyme comprises SEQ ID NOs: 4, 33, 35, 37, 39, 41, and 43.
6. The plant of claim 1 or 2, wherein the multifunctional fatty acid synthase increases oil levels in the seed of a plant that has been transformed with said nucleic acid.
20
7. The plant of claim 2, that further comprises a promoter that is operably linked to the nucleic acid encoding a multifunctional fatty acid synthase or the second nucleic acid encoding a phosphopantetheine:protein transferase enzyme, wherein the promoter is functional in a plant cell.
25
8. The plant of claim 7, wherein the promoter provides expression substantially within plant seeds of the multifunctional fatty acid synthase or the phosphopantetheine:protein transferase enzyme.
- 30 9. The plant of claim 1 or 2, wherein the multifunctional fatty acid synthase is substantially located in the cytosol of a plant cell.

10. A method for producing a *Brassica* sp. plant with increased oil content that comprises,
- a. introducing a first nucleic acid molecule encoding a multifunctional fatty acid synthase into a *Brassica* sp. plant cell; and
 - b. regenerating a plant from the plant cell.

5

11. The method of claim 10, further comprising introducing a second nucleic acid molecule encoding a phosphopantetheine:protein transferase enzyme into the plant cell.

10

12. The method of claim 10 or 11, wherein the first nucleic acid molecule is isolated from *Brevibacterium ammoniagenes* (ATCC 5871), *Schizosaccharomyces pombe*, *Saccharomyces cerevisiae*, *Candida albicans*, *Mycobacterium tuberculosis*, *Mycobacterium leprae*, *Mycobacterium bovis*, *Caenorhabditis elegans*, *Lipomyces starkeyi*, rat, or chicken.

15

13. The method of claim 10 or 11, wherein the first nucleic acid molecule encodes a multifunctional fatty acid synthase having an amino acid sequence comprising a protein selected from the group consisting of SEQ ID NOs: 2, 15, 17, 18, 19, 20, 22-25, 27, 29, and 31.

20

14. The method of claim 13, wherein the protein is SEQ ID NO: 2.

25

15. The method of claim 11, wherein the second nucleic acid molecule encoding a phosphopantetheine:protein transferase enzyme encodes an amino acid comprising a protein selected from the group consisting of SEQ ID NOs: 4, 33, 35, 37, 39, 41, and 43.

30

16. The method of claim 10 or 11, wherein the multifunctional fatty acid synthase produces increased oil levels in a seed of the plant.
17. The method of claim 11, wherein the first nucleic acid molecule encoding a multifunctional fatty acid synthase or the second nucleic acid molecule encoding a phosphopantetheine:protein transferase enzyme further comprises a promoter that is operably linked thereto, wherein the promoter is functional in the plant cell.

18. The method of claim 17, wherein the promoter is a globulin promoter, a zein promoter, an oleosin promoter, an ubiquitin promoter, a CaMV 35S promoter, a CaMV 19S promoter, a *nos* promoter, an Adh promoter, a sucrose synthase promoter, a tubulin promoter, a napin promoter, an actin promoter, a *cab* promoter, a PEPCase promoter, a 7S- α' -conglycinin promoter, an R gene complex promoter, a tomato E8 promoter, a patatin promoter, a mannopine synthase promoter, a soybean seed protein glycinin promoter, a soybean vegetative storage protein promoter, or a root-cell promoter.
19. The method of claim 17, wherein the promoter provides expression substantially within plant seeds of the multifunctional fatty acid synthase or the phosphopantetheine:protein transferase enzyme.
20. The method of claim 10 or 11, wherein the multifunctional fatty acid synthase is substantially located in the cytosol of the plant cell.
21. A method of producing a *Brassica* oil, comprising the steps of:
- a) growing an oilseed *Brassica* plant, the genome of which contains a nucleic acid molecule encoding a multifunctional fatty acid synthase, to produce oil-containing seeds; and
 - b) extracting oil from the seeds.
22. A method of producing a *Brassica* oil, comprising the steps of:
- a) growing an oilseed *Brassica* plant, the genome of which contains a nucleic acid molecule encoding a phosphopantetheine:protein transferase, to produce oil-containing seeds; and
 - b) extracting oil from the seeds.

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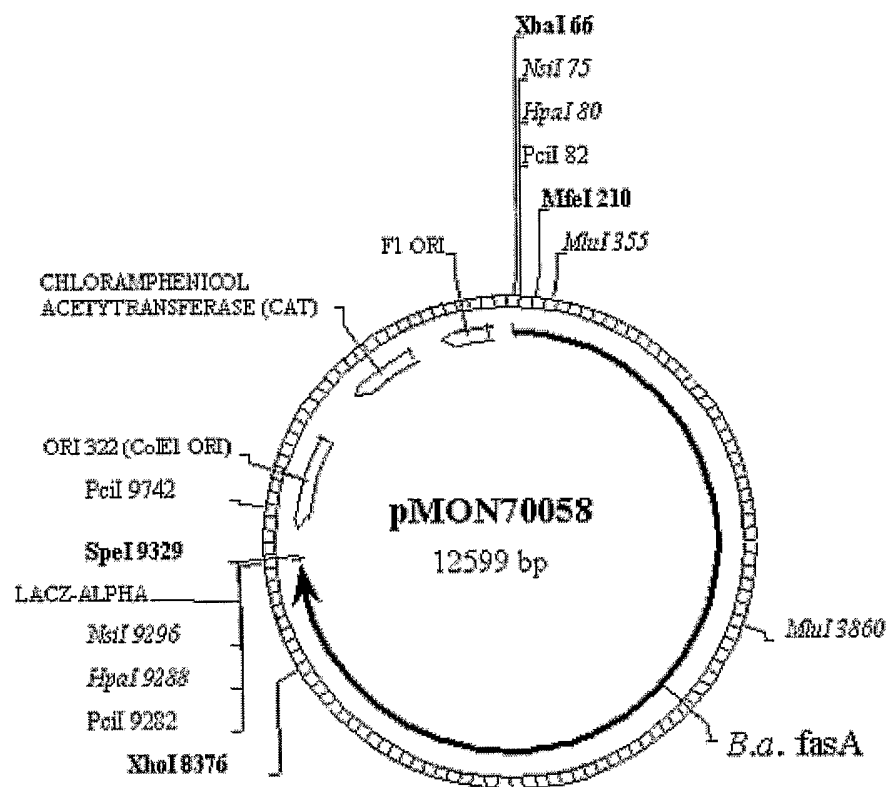


Figure 1

FASA pMON70058.SEQ	A T G T C G T T G A C C C C C T T G C A T A C C T T G T C T A A T G A C A G C A	40
X87822 orf.SEQ	A T G T C G T T G A C C C C C T T G C A T A C C T T G T C T A A T G A C A G C A	40
FASA pMON70058.SEQ	C T G C T C C C G C G G T G C T G T T T G C G G G T C A G G G T T C T G C A T G	80
X87822 orf.SEQ	C T G C T C C C G C G G T G C T G T T T G C G G G T C A G G G T T C T G C A T G	80
FASA pMON70058.SEQ	G C A A A A G G C C A T C G C T G A T G C C G C A G C C A G C C C T C A C C A G	120
X87822 orf.SEQ	G C A A A A G G C C A T C G C T G A T G C C G C A G C C A G C C C T C A C C A G	120
FASA pMON70058.SEQ	G G C G C A C A A T T G C G C G A C A T C C T A A A G A A G T T C G C A C G A	160
X87822 orf.SEQ	G G C G C A C A A T T G C G C G A C A T C C T A A A G A A G T T C G C A C G A	160
FASA pMON70058.SEQ	C C A C C G G C C C A G T A G C A C G C A T C A T T G C G T C G T C G T G C C C	200
X87822 orf.SEQ	C C A C C G G C C C A G T A G C A C G C A T C A T T G C G T C G T C G T G C C C	200
FASA pMON70058.SEQ	T G G C G T T T A T G A A C G C T T G G A A G A A C T T G C T C A G A C C C C C	240
X87822 orf.SEQ	T G G C G T T T A T G A A C G C T T G G A A G A A C T T G C T C A G A C C C C C	240
FASA pMON70058.SEQ	G C T G A C C A A G C A C C G G T G G C C A A G G A A T A T G A C G C G T A C C	280
X87822 orf.SEQ	G C T G A C C A A G C A C C G G T G G C C A A G G A A T A T G A C G C G T A C C	280
FASA pMON70058.SEQ	C G G C T T A C T C C A T C C C C G G C A T C G T C C T G G G A C A A A T T G G	320
X87822 orf.SEQ	C G G C T T A C T C C A T C C C C G G C A T C G T C C T G G G A C A A A T T G G	320
FASA pMON70058.SEQ	T G C C A T T G A G C A C C T T G C G C G A G C T G G G C A T C G A T G T C G A T	360
X87822 orf.SEQ	T G C C A T T G A G C A C C T T C G C G C A G C T G G G C A T C G A T G T C G A T	360
FASA pMON70058.SEQ	T C C G C G C A G T T A G C A G G C C A C T C C C A G G G T T C A T T A G G T G	400
X87822 orf.SEQ	T C C G C G C A G T T A G C A G G C C A C T C C C A G G G T T C A T T A G G T G	400
FASA pMON70058.SEQ	T T G C A G C C G T T A A G G A T G C A C G C C A G G C C C T G G C T A T T G C	440
X87822 orf.SEQ	T T G C A G C C G T T A A G G A T G C A C G C C A G G C C C T G G C T A T T G C	440
FASA pMON70058.SEQ	T G T T T T G A T G G G T A C T G C A G C A G C G G T G A C C C A G G G C G C G	480
X87822 orf.SEQ	T G T T T T G A T G G G T A C T G C A G C A G C G G T G A C C C A G G G C G C G	480
FASA pMON70058.SEQ	A A T G A T T C C C G C T C C C A C A T G C T G T C C G T G C G T G G C G T A C	520
X87822 orf.SEQ	A A T G A T T C C C G C T A C C C A C A T G C T G T C C G T G C G T G G C G T A C	520
FASA pMON70058.SEQ	C A C G T G A G A T G G T C G A A G A A T A C C T C G C T G G T G A C G C T G C	560
X87822 orf.SEQ	C A C G T G A G A T G G T C G A A G A A T A C C T C G C T G G T G A C G C T G C	560
FASA pMON70058.SEQ	G A T T G C C G T G G T C A A C G G C C G C G T G C A C T T T G C A C T G T C G	600
X87822 orf.SEQ	G A T T G C C G T G G T C A A C G G C C G C G T G C A C T T T G C A C T G T C G	600
FASA pMON70058.SEQ	G G T A C C C C A G A G G A T C T G G C T A A G A C C G A G T C C A A C C T C A	640
X87822 orf.SEQ	G G T A C C C C A G A G G A T C T G G C T A A G A C C G A G T C C A A C C T C A	640
FASA pMON70058.SEQ	C C C A G G C T G C C G A G T C C T A C A A C G A C G C G C T G G A A G A A C G	680
X87822 orf.SEQ	C C C A G G C T G C C G A G T C C T A C A A C G A C G C G C T G G A A G A A C G	680
FASA pMON70058.SEQ	C C G C A T C G G C G G C T C C G A A A T T A A C C C A G T C T T C G A C G T A	720
X87822 orf.SEQ	C C G C A T C G G C G G C T C C G A A A T T A A C C C A G T C T T C G A C G T A	720
FASA pMON70058.SEQ	T T G G C C G T G G C A C T T C C T T T C C A C C A C G C A T C A C T G C A G G	760
X87822 orf.SEQ	T T G G C C G T G G C A C T T C C T T T C C A C C A C G C A T C A C T G C A G G	760
FASA pMON70058.SEQ	A T G C A G C G G A T C T G A C C G T G G A C T A C G C C A C C C A G T G T G G	800
X87822 orf.SEQ	A T G C A G C G G A T C T G A C C G T G G A C T A C G C C A C C C A G T G T G G	800
FASA pMON70058.SEQ	C C T G G A C G C T G A G C T T G C A C G C G A G C T G G C A G A T T C C A T C	840
X87822 orf.SEQ	C C T G G A C G C T G A G C T T G C A C G C G A G C T G G C A G A T T C C A T C	840
FASA pMON70058.SEQ	C T G G T T C A G C C A C A T A G C T G G G T T G A G A C C G T G G C C G G T C	880
X87822 orf.SEQ	C T G G T T C A G C C A C A T A G C T G G G T T G A G A C C G T G G C C G G T C	880
FASA pMON70058.SEQ	T C A A C T C C A C C T A C C T G C T C T C C T T A G A C C G T G G T C T G T C	920
X87822 orf.SEQ	T C A A C T C C A C C T A C C T G C T C T C C T T A G A C C G T G G T C T G T C	920
FASA pMON70058.SEQ	T T C G T T G A C T A C A C C T T T G A	940
X87822 orf.SEQ	T T C G T T G A C T A C A C C T T T G A	940

Boxed Residues Differ from pMON70058

Figure 2 (page 1 of 10)

FASA pMON70058.SEQ	T T G C C G G C A C C G G C A A G G T T G T G G T T C C A G C T G C T A C G C C	980
X87822 orf.SEQ	T T G C C G G C A C C G G C A A G G T T G T G G T T C C A G C T G C T A C G C C	980
FASA pMON70058.SEQ	A G C G G A G C G C G A T A A C C T G G C T A C C C C A G G C A C T G A G C T G	1020
X87822 orf.SEQ	A G C G G A G C G C G A T A A C C T G G C T A C C C C A G G C A C T G A G C T G	1020
FASA pMON70058.SEQ	C C T A C C G C G G T G A A C T A C G A G A A G T T C T C A C C A A A G C T C A	1060
X87822 orf.SEQ	C C T A C C G C G G T G A A C T A C G A G A A G T T C T C A C C A A A G C T C A	1060
FASA pMON70058.SEQ	T C T C C T T G C C C A A C G G C A A G T C C T A C A C T C A G A C T C G T T T	1100
X87822 orf.SEQ	T C T C C T T G C C C A A C G G C A A G T C C T A C A C T C A G A C T C G T T T	1100
FASA pMON70058.SEQ	C T C C G A G T G G A C C G G C A T G T C C C C C A T C A T T T T G G G C G G C	1140
X87822 orf.SEQ	C T C C G A G T G G A C C G G C A T G T C C C C C A T C A T T T T G G G C G G C	1140
FASA pMON70058.SEQ	A T G A C G C C G A C C A C G A T G G A T C C G G G C A T C G T T G C C G C A G	1180
X87822 orf.SEQ	A T G A C G C C G A C C A C G A T G G A T C C G G G C A T C G T T G C C G C A G	1180
FASA pMON70058.SEQ	C G G C C A A C G G T G G C T A C T G G T C A G A G A T G G C C G G T G G C G G	1220
X87822 orf.SEQ	C G G C C A A C G G T G G C T A C T G G T C A G A G A T G G C C G G T G G C G G	1220
FASA pMON70058.SEQ	T C A G T A C T C C G A T G A A G C T T T T A C C A T C A A C A A A G A C G G C	1260
X87822 orf.SEQ	T C A G T A C T C C G A T G A A G C T T T T A C C A T C A A C A A A G A C G G C	1260
FASA pMON70058.SEQ	A T G A T G G A G C T G C T G G A G C C A G G T C G C A C C G C A G C A T T T A	1300
X87822 orf.SEQ	A T G A T G G A G C T G C T G G A G C C A G G T C G C A C C G C A G C A T T T A	1300
FASA pMON70058.SEQ	A C A C C A T G T T C T T T G A C C G C T A C C T G T G G A A C C T A C A G T T	1340
X87822 orf.SEQ	A C A C C A T G T T C T T T G A C C G C T A C C T G T G G A A C C T A C A G T T	1340
FASA pMON70058.SEQ	C G G T G T C A C C C G C A T T G T T C C C A A G G C A C G C G C T A A T G G T	1380
X87822 orf.SEQ	C G G T G T C A C C C G C A T T T G T T C C A A G G C A C G C G C T A A T G G T	1380
FASA pMON70058.SEQ	G C T G C G T T T A C C G G C G T G A C C A T C T C C G C T G G T A T C C C A G	1420
X87822 orf.SEQ	G C T G C G T T T A C C G G C G T G A C C A T C T G C G C T G G T A T C C C A G	1420
FASA pMON70058.SEQ	A G C T G G A T G A A G C C A A G G A A T T G C T G G A C C A G C T C A C C T C	1460
X87822 orf.SEQ	A G C T G G A T G A A G C C A A G G A A T T G C T G G A C C A G C T C A C C T C	1460
FASA pMON70058.SEQ	C G A T G G C T T C C C A T A C A T C T C T T T C A A G C C G G G C A C C A C C	1500
X87822 orf.SEQ	C G A T G G C T T T C C A T A C A T C T C T T T C A A G C C G G G C A C C A C C	1500
FASA pMON70058.SEQ	A A G C A G A T T C A A G A C T G C A T C G C T A T C G C A G C G G A T A A C C	1540
X87822 orf.SEQ	A A G C A G A T T C A A G A C T G C G T C G C T A T C G C A G C G G A T A A C C	1540
FASA pMON70058.SEQ	C C A C C C A C C G C G T C A T C A T C C A A A T T G A A G A C G G C C A C G C	1580
X87822 orf.SEQ	C C A C C C A C C G C G T C A T C A T C C A A A T T G A A G A C G C C C A C G C	1580
FASA pMON70058.SEQ	T G G T G G C C A C C A C T C C T G G G T G G A T C T G G A T G A A A T G C T G	1620
X87822 orf.SEQ	T G G T G G C C A C C A C T C C T G G G T G G A T C T G G A T G A A A T G C T G	1620
FASA pMON70058.SEQ	C T G G C T A C C T A C G C A T C T G C C C G T G A G C A C G A C A A C C T G G	1660
X87822 orf.SEQ	C T G G C T A C C T A C G C A T G T G C C C G T G A G C A C G A C A A C C T G G	1660
FASA pMON70058.SEQ	C C A T C A C T G T T G G T G G C G G C A T C C A C T C C C C A G A C C G C G C	1700
X87822 orf.SEQ	C C A T C A C T G T T G G T G G C G G C A T C C A C T C C C C A G A C C G C G C	1700
FASA pMON70058.SEQ	A T C G G A A T A C C T G A C C G G T A C C T G G T C C A C C A A G T A C G G T	1740
X87822 orf.SEQ	A T C G G A A T A C C T G A C C G G T A C C T G G T C C A C C A A G T A C G G T	1740
FASA pMON70058.SEQ	T T G C C C A T C A T G C C G G T T G A T G G T G T C T T C T T G G G C A C C G	1780
X87822 orf.SEQ	T T G C C C A T C A T G C C G G T T G A T G G T G T C T T C T T G G G C A C C G	1780
FASA pMON70058.SEQ	T A G C C A T G G C G A C C A A G G A A G C A A C G G C T A A T G A T G A C G T	1820
X87822 orf.SEQ	T A G C C A T G G C G A C C A A G G A A G C A A C G G C T A A T G A T G A C G T	1820
FASA pMON70058.SEQ	T A A G C A G T T G C T A G T T G A T A C C C A G G T A T T T C C C C A G A G	1860
X87822 orf.SEQ	T A A G C A G T T G C T A G T T G A T A C C C A G G T A T T T C C C C A G A G	1860
FASA pMON70058.SEQ	A C C A A T G G C G G T T G G G T A G G C C G A C T A G A T G C C G A C G G C G	1900
X87822 orf.SEQ	A C C A A T G G C G G T T G G G T A G G C C G A C T A G A T G C C G A C G G C G	1900

Boxed Residues Differ from pMON70058

FASA pMON70058.SEQ	G C G T C T C C T C C T C C C A G T C C C A C C T G T T G G C T G A C T T G C A	1940
X87822 orf.SEQ	G C G T G T C C T C C T C C C A G T C C C A C C T G T T G G C T G A C T T G C A	1940
FASA pMON70058.SEQ	C G A G A T T G A T A A C T C G T T T G C C A A G G C C T C G C G C A T G A T C	1980
X87822 orf.SEQ	C G A G A T T G A T A A C T C G T T T G C C A A G G C C T C G C G C A T G A T C	1980
FASA pMON70058.SEQ	A C C T C G A T C C C G A T C G A G G A G T A T G A C G A G C G T C G C G A C G	2020
X87822 orf.SEQ	A C C T C G A T C C C G A T C G A G G A G T A T G A C G A G C G T C G C G A C G	2020
FASA pMON70058.SEQ	A G A T C A T T G C T G C T C T G G A C A A G A C C T C C A A G C C A T A C T T	2060
X87822 orf.SEQ	A G A T C A T T G C T G C T C T G G A C A A G A C C T C C A A G C C A T A C T T	2060
FASA pMON70058.SEQ	C G G T G A C C T G T C G G A G A T G A C C T A C G A G G A T T G G G T C G C T	2100
X87822 orf.SEQ	C G G T G A C C T G T C G G A G A T G A C C T A C G A G G A T T G G G T C G C T	2100
FASA pMON70058.SEQ	C G T T T C G C A G A G C G C G C C T A C C C T T G G G T G G A T C C A A C C T	2140
X87822 orf.SEQ	C G T T T C G C A G A G C G C G C C T A C C C T T G G G T G G A T C C A A C C T	2140
FASA pMON70058.SEQ	G G C A C G A T C G T T T C C A C G A T C T G C T C C A G C G C G T A G A A G C	2180
X87822 orf.SEQ	G G C A C G A T C G T T T C C A C G A T C T G C T C C A G C G C G T A G A A G C	2180
FASA pMON70058.SEQ	G C G T C T C A A T G A C G C T G A C C A C G G C G A C A T C G A G A C C C T A	2220
X87822 orf.SEQ	G C G T C T C A A T G A C G C T G A C C A C G G C G A C A T C G A G A C C C T A	2220
FASA pMON70058.SEQ	T T C C C C A C A C T C G A C G A C T C C G A G A A C G C A C C A G A G G C A G	2260
X87822 orf.SEQ	T T C C C C A C A C T C G A C G A C T C C G A G A A C G C A C C A G A G G C A G	2260
FASA pMON70058.SEQ	T A G C C A A G C T G C T G G C T G C C T A C C C G A A T G C A A A G A C C A C	2300
X87822 orf.SEQ	T A G C C A A G C T G C T G G C T G C C T A C C C G A A T G C A A A G A C C A C	2300
FASA pMON70058.SEQ	C A A G G T C A A C A C C C G C G A T G A G G C A T G G T T C C C T A C C C T T	2340
X87822 orf.SEQ	C A A G G T C A A C A C C C G C G A T G A G G C A T G G T T C C C T A C C C T T	2340
FASA pMON70058.SEQ	A T C C G C A A G C A C G T C A A G C C A A T G C C G T G G A C C A C C G C T A	2380
X87822 orf.SEQ	A T C C G C A A G C A C G T C A A G C C A A T G C C G T G G A C C A C C G C T A	2380
FASA pMON70058.SEQ	T T G A C G G T G A C C T G A A G G A A T G G T T T G C C A A G G A C A C C C T	2420
X87822 orf.SEQ	T T G A C G G T G A C C T G A A G G A A T G G T T T G C C A A G G A C A C C C T	2420
FASA pMON70058.SEQ	G T G G C A G G C C C A G G A C C C A C G C T A C G A C G C A G A C G G C G T A	2460
X87822 orf.SEQ	G T G G C A G G C C C A G G A C C C A C G C T A C G A C G C A G A C G G C G T A	2460
FASA pMON70058.SEQ	C G C A T C A T T C C A G G A C C G G T T T C G G T T G C T G G T A T C A C C A	2500
X87822 orf.SEQ	C G C A T C A T T C C A G G A C C G G T T T C G G T T G C T G G T A T C A C C A	2500
FASA pMON70058.SEQ	A G A A G A A T G A G C C C G T C G C A A A C C T G C T C G G T C G C T T C G A	2540
X87822 orf.SEQ	A G A A G A A T G A G C C C G T C G C A A A C C T G C T C G G T C G C T T C G A	2540
FASA pMON70058.SEQ	A G A C G C C A C C A C C G C A G C G C T T A A C G A T G C C G G C G T G G C A	2580
X87822 orf.SEQ	A G A C G C C A C C A C C G C A G C G C T T A A C G A T G C C G G C G T G G C A	2580
FASA pMON70058.SEQ	C C A G T T G A G C T C T A C T C C C G C T T G G C T T C T G C C A A G A A T G	2620
X87822 orf.SEQ	C C A G T T G A G C T C T A C T C C C G C T T G G C T T C T G C C A A G A A T G	2620
FASA pMON70058.SEQ	C A G A A G A G T T C C T G C G C A A T G C A C C A A C C A T C A T G T G G C A	2660
X87822 orf.SEQ	C A G A A G A G T T C C T G C G C A A T G C A C C A A C C A T C A T G T G G C A	2660
FASA pMON70058.SEQ	C G G T C A C C T C A T T G C C A A C C C G G C G T A T G A G C T G C C A G A A	2700
X87822 orf.SEQ	C G G T C A C C T C A T T G C C A A C C C G G C G T A T G A G C T G C C A G A A	2700
FASA pMON70058.SEQ	G A A G C T T T T G A C A T C G T C G A T G A C G G C G A A G G C T T T G C T A	2740
X87822 orf.SEQ	G A A G C T T T T G A C A T C G T C G A T G A C G G C G A A G G C T T T G C T A	2740
FASA pMON70058.SEQ	T T C G C A T C A A C T C T G A C T C C T A C T G G G A T A A C C T C C C A G A	2780
X87822 orf.SEQ	T T C G C A T C A A C T C T G A C T C C T A C A G G G A T A A C C T C C C A G A	2780
FASA pMON70058.SEQ	A G A G C A G C G T C C G T T C T A C G T C A A G C A C G T T G A T A T C C C C	2820
X87822 orf.SEQ	A G A G C A G C G T C C G T T C T A C G T C A A G C A C G T T G A T A T C C C C	2820
FASA pMON70058.SEQ	G T T G C G C T G T C G G A A G C C G T A G C A A C C G G T G C C T C C C C T G	2860
X87822 orf.SEQ	G T T G C G C T G T C G G A A G C C G T A G C A A C C G G T G C C T C C C C T G	2860

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FASA pMON70058.SEQ	T T G T T G A T G A C G C G C G T T T G C C A A A G G C A G T C T T C G A C C T	2900
X87822 orf.SEQ	T T G T T G A T G A C G C G C G T T T G C C A A A G G C A G T C T T C G A C C T	2900
FASA pMON70058.SEQ	G C T C G C A G G C G T T G C T G G T G T C G G G T C T A T C T C T G A G A C C	2940
X87822 orf.SEQ	G C T C G C A G G C G T T G C T G G T G T C G G G T C T A T C T C T G A G A C C	2940
FASA pMON70058.SEQ	G G C G A T A A G A T C A C C G A A C T G C C G A A G G T C A T C G A A G G C T	2980
X87822 orf.SEQ	G G C G A T A A G A T C A C C G A A C T G C C G A A G G T C A T C G A A G G C T	2980
FASA pMON70058.SEQ	C T G T C T C C G A A G A A A A C C C T T A C G G C C T G G T G G A A T A C T C	3020
X87822 orf.SEQ	C T G T C T C C G A A G A A A A C C C T T A C G G C C T G G T G G A A T A C T C	3020
FASA pMON70058.SEQ	C T T T A C C T T G C C T T C T A C C C T G C T G A C C G C A C A C A C C G C G	3060
X87822 orf.SEQ	C T T T A C C T T G C C T T C T A C C C T G C T G A C C G C A C A C A C C G C G	3060
FASA pMON70058.SEQ	G T A A C C G G C G C T G C C T T G G G C A C C G C C A A C G C A G G C A C C C	3100
X87822 orf.SEQ	G T A A C C G G C G C T G C C T T G G G C A C C G C C A A C G C A G G C A C C C	3100
FASA pMON70058.SEQ	C A G A T G C G C T G G T T G G C C C C T G C T G G C C A G C A A T T T A C A C	3140
X87822 orf.SEQ	C A G A T G C G C T G G T T G G C C C C T G C T G G C C A G C A A T T T A C A C	3140
FASA pMON70058.SEQ	C G C G C T G G G C A C C G G T C G A T T G A C C G A A G A A C A C G G T G A G	3180
X87822 orf.SEQ	C G C G C T G G G C A C C G G T C G A T T G A C C G A A G A A C A C G G T G A G	3180
FASA pMON70058.SEQ	C C A G C C G G C A C C G A C T T C C C G G T C A T T G A A G G C C T G C T C A	3220
X87822 orf.SEQ	C C A G C C G G C A C C G A C T T C C C G G T C A T T G A A G G C C T G C T C A	3220
FASA pMON70058.SEQ	A C G C A G T C C A C C T C G A C C A C G T C G T C G A T G T G C G T G T T C C	3260
X87822 orf.SEQ	A C G C A G T C C A C C T C G A C C A C G T C G T C G A T G T G C G T G T T C C	3260
FASA pMON70058.SEQ	T C T T C A C G A A C T C G C A A A G G G T G A A A A G G G C G A A G G C C G T	3300
X87822 orf.SEQ	T C T T C A C G A A C T C G C A A A G G G T G A A A A G G G C G A A G G C G T	3300
FASA pMON70058.SEQ	C G C A T T G A C G T C A C C T C C C G C T G T G C A T C C A T C G C G G A A T	3340
X87822 orf.SEQ	C G C A T T G A C G T C A C C T C C C G C T G T G C A T C C A T C G C G G A A T	3340
FASA pMON70058.SEQ	C C A A C T C C G G T C G C A T T G T C A C C G T G G A A C T T G A G T T G T G	3380
X87822 orf.SEQ	C C A A C T C C G G T C G C A T T G T C A C C G T G G A A C T T G A G T T G T G	3380
FASA pMON70058.SEQ	G G A T G C C G C A A C T C A A G A A G T T G T G G C G A C G C A G A T G C A G	3420
X87822 orf.SEQ	G G A T G C C G C A A C T C A A G A A G T T G T G G C G A C G C A G A T G C A G	3420
FASA pMON70058.SEQ	C G C T T T G C C A T C C G T G G C C G C G C T A C C G G C A C C T C C G T T C	3460
X87822 orf.SEQ	C G C T T T G C C A T C C G T G G C C G C G C T A C C G G C A C C T C C G T T C	3460
FASA pMON70058.SEQ	C G G T T T C T G C A C C A T C C T G G G G C G G C G G C A A G T C T C A G G A	3500
X87822 orf.SEQ	C G G T T T C T G C A C C A T C C T G G G G C G G C G G C A A G T C T C A G G A	3500
FASA pMON70058.SEQ	C A A G A T T G A G A C C A C C C C A C G T T C C T T C G T G G A T C G C G C C	3540
X87822 orf.SEQ	C A A G A T T G A G A C C A C C C C A C G T T C C T T C G T G G A T C G C G C C	3540
FASA pMON70058.SEQ	A T T G T C A C C G C G C C A T C G G A T A T G A C C C C A T T C G C G C T G G	3580
X87822 orf.SEQ	A T T G T C A C C G C G C C A T C G G A T A T G A C C C C A T T C G C G C T G G	3580
FASA pMON70058.SEQ	T C T C C G G T G A C T A C A A C C C A A T T C A C A C C T C C A C C A A C G C	3620
X87822 orf.SEQ	T C T C C G G T G A C T A C A A C C C A A T T C A C A C C T C C A C C A A C G C	3620
FASA pMON70058.SEQ	C G C G C G C T T G G T C A A C C T C G A C G C C C C A C T G G T G C A C G G C	3660
X87822 orf.SEQ	C G C G C G C T T G G T C A A C C T C G A C G C C C C A C T G G T G C A C G G C	3660
FASA pMON70058.SEQ	A T G T G G C T A T C T G C C A C C G C G C A G C A C C T A G C T G G C A A C C	3700
X87822 orf.SEQ	A T G T G G C T A T C T G C C A C C G C G C A G C A C C T A G C T G G C A A C C	3700
FASA pMON70058.SEQ	A C G G C A C C G T G G T G G G T T G G A C C T A T T C C A T G T A C G G C A T	3740
X87822 orf.SEQ	A C G G C A C C G T G G T G G G T T G G A C C T A T T C C A T G T A C G G C A T	3740
FASA pMON70058.SEQ	G G T C C A G C T C A A C G A T G A A G T A G A A A T C A C C G T C G A A C G C	3780
X87822 orf.SEQ	G G T C C A G C T C A A C G A T G A A G T A G A A A T C A C C G T C G A A C G C	3780
FASA pMON70058.SEQ	G T A G G C C G C A A G G G C A T T C A C G C A G C A T T C G A G G T C A C C T	3820
X87822 orf.SEQ	G T A G G C C G C A A G G G C A T T C A C G C A G C A T T C G A G G T C A C C T	3820

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FASA pMON70058.SEQ	G C C G C A T C G A C G G C G A A G T A G T C T C C C G C G G C C A G G C G C T	3860
X87822 orf.SEQ	G C C G C A T C G A C G G C G A A G T A G T C T C C C G C G G C C A G G C G C T	3860
FASA pMON70058.SEQ	C A T G G C A C A G C C A C G C A C C G C T T A T G T C T A C C C A G G C C A G	3900
X87822 orf.SEQ	C A T G G C A C A G C C A C G C A C C G C T T A T G T C T A C C C A G G C C A G	3900
FASA pMON70058.SEQ	G G C A T C C A G G C C G A G G G C A T G G G C C G T G G T G A C C G C G A T G	3940
X87822 orf.SEQ	G G C A T C C A G G C C G A G G G C A T G G G C C G T G G T G A C C G C G A T G	3940
FASA pMON70058.SEQ	C T T C G G C A G C A G C G C G T G A G G T A T G G C G T C G T G C A G A C C G	3980
X87822 orf.SEQ	C T T C G G C A G C A G C G C G T G A G G T A T G G C G T C G T G C A G A C C G	3980
FASA pMON70058.SEQ	C C A C A C C C G C A C C G C A A T G G G C T T T T C T A T T C G C C A G A T C	4020
X87822 orf.SEQ	C C A C A C C C G C A C C G C A C T G G G C T T T T C T A T T C G C C A G A T C	4020
FASA pMON70058.SEQ	A T C G A T G A C A A C C C C A C C G A G C T C G T C G T T C G C G G C A C C A	4060
X87822 orf.SEQ	A T C G A T G A C A A C C C C A C C G A G C T C G T C G T T C G C G G C A C C A	4060
FASA pMON70058.SEQ	A G T T C G T C C A C C C C A A T G G C G T G C T G C A C T T A A C G C A G T T	4100
X87822 orf.SEQ	A G T T C G T C C A C C C C A A T G G C G T G C T G C A C T T A A C G C A G T T	4100
FASA pMON70058.SEQ	C A C T C A G G T T G C C C T C G C A G T C G T T G C T T A T G C A C A A A C C	4140
X87822 orf.SEQ	C A C T C A G G T T G C C C T C G C A G T C G T T G C T T A T G C A C A A A C C	4140
FASA pMON70058.SEQ	G A G C G C C T G C G C G A A G C A G A T G C T C T G G G C A C C A A C T C C A	4180
X87822 orf.SEQ	G A G C G C C T G C G C G A A G C A G A T G C T C T G G G C A C C A A C T C C A	4180
FASA pMON70058.SEQ	T G T A C G C C G G T C A C T C A C T G G G T G A G T A C A C C G C G C T G G C	4220
X87822 orf.SEQ	T G T A C G C C G G T C A C T C A C T G G G T G A G T A C A C C G C G C T G G C	4220
FASA pMON70058.SEQ	A T C G T T G G C G A A T A T C T T T G A C C T C G A A G C G G T T A T C G A C	4260
X87822 orf.SEQ	A T C G T T G G C G A A T A T C T T T G A C C T C G A A G C G G T T A T C G A C	4260
FASA pMON70058.SEQ	A T C G T C T A C T C C C G T G G C T C T G C C A T G G G C A C C T T G G T C G	4300
X87822 orf.SEQ	A T C G T C T A C T C C C G T G G C T C T G C C A T G G G C A C C T T G G T C G	4300
FASA pMON70058.SEQ	A A C G T G A T G A A A A C G G T A A C T C C A A C T A C G G C A T G G G C G C	4340
X87822 orf.SEQ	A A C G T G A T G A A A A C G G T A A C T C C A A C T A C G G C A T G G G C G C	4340
FASA pMON70058.SEQ	G C T G C G T C C A A A C A T G A T T G G T G T T C C C G C A G A C C A G G T T	4380
X87822 orf.SEQ	G C T G C G T C C A A A C A T G A T T G G T G T T C C C G C A G A C C A G G T T	4380
FASA pMON70058.SEQ	G A G G C C T A C A T C G C G C A G A C C G C G G A A G A A A C T G G C G A A T	4420
X87822 orf.SEQ	G A G G C C T A C A T C G C G C A G A C C G C G G A A G A A A C T G G C G A A T	4420
FASA pMON70058.SEQ	T C C T C G A A A T C G T C A A C T A C A A C A T C G C T G G T C A G C A G T A	4460
X87822 orf.SEQ	T C C T C G A A A T C G T C A A C T A C A A C A T C G C T G G T C A G C A G T A	4460
FASA pMON70058.SEQ	C T C C A T C G C G G G T A C C A A G G C T G G T T T G G C C G C C C T G A A G	4500
X87822 orf.SEQ	C T C C A T C G C G G G T A C C A A G G C T G G T T T G G C C G C C C T G A A G	4500
FASA pMON70058.SEQ	A A A A A G G C C A A C T C C G T C A A G G A C C G T G C T T A T G T C A C G G	4540
X87822 orf.SEQ	A A A A A G G C C A A C T C C G T C A A G G A C C G T G C T T A T G T C A C G G	4540
FASA pMON70058.SEQ	T T C C A G G C A T C G A T G T A C C T T T C C A C T C C C A G G T A C T G C G	4580
X87822 orf.SEQ	T T C C A G G C A T C G A T G T A C C T T T C C A C T C C C A G G T A C T G C G	4580
FASA pMON70058.SEQ	C G A C G G C G T T C C T G C T T T C G C A G A A A A G C T C G A T G A A C T G	4620
X87822 orf.SEQ	C G A C G G C G T T C C T G C T T T C G C A G A A A A G C T C G A T G A A C T G	4620
FASA pMON70058.SEQ	T T G C C A G A A A C C T T G G A C C T G G A C G C C C T G G T C G G C C G C T	4660
X87822 orf.SEQ	T T G C C A G A A A C C T T G G A C C T G G A C G C C C T G G T C G G C C G C T	4660
FASA pMON70058.SEQ	A C G T G C C G A A C C T G G T G G C G C T G C C A T T C G A G C T G A C C C A	4700
X87822 orf.SEQ	A C G T G C C G A A C C T G G T G G C G C T G C C A T T C G A G C T G A C C C A	4700
FASA pMON70058.SEQ	G G A A T T T G T C G A T A A G G T C A A G C C T T T G G C T C C T T C C G G C	4740
X87822 orf.SEQ	G G A A T T T G T C G A T A A G G T C A A G C C T T T G G C T C C T T C C G G C	4740
FASA pMON70058.SEQ	A A G C T G G A T A A C C T C A A G G T C G A A G A C A C C G A T G A G C A A G	4780
X87822 orf.SEQ	A A G C T G G A T A A C C T C A A G G T C G A A G A C A C C G A T G A G C A A G	4780

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FASA pMON70058.SEQ	C C C T T G C T C G C C T G C T C A T G A T T G A G C T A T T G T C C T G G C A	4820
X87822 orf.SEQ	C C C C T T C T C G C C T G C T C A T G A T T G A G C T A T T G T C C T G G C A	4820
FASA pMON70058.SEQ	G T T C G C A T C A C C T G T G C G C T G G A T T G A A A C C C A G C A G C T G	4860
X87822 orf.SEQ	G T T C G C A T C A C C T G T G C G C T G G A T T G A A A C C C A G C A G C T G	4860
FASA pMON70058.SEQ	C T C T T T G A A G A A G T A G A C C A G A T C A T C G A A G T C G G T C T C G	4900
X87822 orf.SEQ	C T C T T T G A A G A A G T A G A C C A G A T C A T C G A A G T C G G T C T C G	4900
FASA pMON70058.SEQ	C G G C A T C C C C A A C G C T G A C C A A C T T G G C C A A G C G C T C C A T	4940
X87822 orf.SEQ	C T T C A T C C C C A A C G C T G A C C A A C T T G G C C A A G C G C T C C A T	4940
FASA pMON70058.SEQ	G G A T A T C G C C G G C G T G G A C C T C C C G G T C T T C A A C G T C G A A	4980
X87822 orf.SEQ	G G A T A T C G C C G G C G T G G A C C T C C C G G T C T T C A A C G T C G A A	4980
FASA pMON70058.SEQ	C G C G A C C A A G A C C A G G T C A T G C T C C A A G A C G T T C A G G A A G	5020
X87822 orf.SEQ	C G C G A C C A A G A C C A G G T C A T G C T C C A A G A C G T T C A G G A A G	5020
FASA pMON70058.SEQ	C A C C A G C T G C C T C C T T C G A C G T C G A G G A A G G A G A G G C C A C	5060
X87822 orf.SEQ	C A C C A G C T G C C T C C T T C G A C G T C G A G G A A G G A G A G G C C A C	5060
FASA pMON70058.SEQ	C T C T T C G A C C G C A G C G T C T G A A A C C C A G G T G A A T C C G C T	5100
X87822 orf.SEQ	C T C T T C G A C C G C A G C G T C T G A A A C C C A G G T G A A T C C G C T	5100
FASA pMON70058.SEQ	G C G G C G G C C T C G G A T A A T A C C C A G G C C A T C C C A T C G G C T G	5140
X87822 orf.SEQ	G C G G C G G C C T C G G A T A A T A C C C A G G C C A T C C C A T C G G C T G	5140
FASA pMON70058.SEQ	A G C C A C A A A C G G T G G C A G A G G C A C C A G C A C C A T C C G C C G C	5180
X87822 orf.SEQ	A G C C A C A A A C G G T G G C A G A G G C A C C A G C A C C A T C C G C C G C	5180
FASA pMON70058.SEQ	A C C A G C T G G C G G C A C C G C T G C C G C A G A T G C T C C T G A C C T G	5220
X87822 orf.SEQ	A C C A G C T G G C G G C A C C C G T G C C G C A G A T G C T C C T G A C C T G	5220
FASA pMON70058.SEQ	C C A T T T A C C G C A G C A G A A G C C A T C A T G G T T C T G T T C G C T T	5260
X87822 orf.SEQ	C C A T T T A C C G C A G C A G A A G C C A T C A T G G T T C T G T T C G C T T	5260
FASA pMON70058.SEQ	T C C A G A A C A A G A T C C G C C A G G A C C A G A T C A A T G A C T C G G A	5300
X87822 orf.SEQ	T C C A G A A C A A G A T C C G C C A G G A C C A G A T C A A T G A C T C G G A	5300
FASA pMON70058.SEQ	T A C G G T C G A A G A G C T C A C C A A C G G T G T C T C C T C C C G C C G T	5340
X87822 orf.SEQ	T A C G G T C G A A G A G C T C A C C A A C G G T G T C T C C T C C C G C C G T	5340
FASA pMON70058.SEQ	A A C C A A C T G T T G A T G G A T A T G T C C G C A G A A A T C G G C G T G C	5380
X87822 orf.SEQ	A A C C A A C T G T T G A T G G A T A T G T C C G C A G A A A A T C G C G T G C	5380
FASA pMON70058.SEQ	C C G C C A T T G A C G G T G C A G C C G A T G C T G A C G T G G C A A C C T T	5420
X87822 orf.SEQ	C C G C C A T T G A C G G T G C A G C C G A T G C T G A C G T G G C A A C C T T	5420
FASA pMON70058.SEQ	G C G T G A G C G C G T C A A G A C T G C C G C T C C G G G C T A C T C G C C A	5460
X87822 orf.SEQ	G C G T G A G C G C G T C A A G A C T G C C G C T C C G G G C T A C T C G C C A	5460
FASA pMON70058.SEQ	T T C G G C A C C G T C T T G T C T G A G G C T A T T A C C G C T C G T C T G C	5500
X87822 orf.SEQ	T T C G G C A C C G T C T T G T C T G A G G C T A T T A C C G C T C G T C T G C	5500
FASA pMON70058.SEQ	G C C A G C T C A C T G G T G C A G C A G G C G T C A A G C C G G C C T A C A T	5540
X87822 orf.SEQ	G C C A G C T C A C T G G T G C A G C A G G C G T C A A G C C G G C C T A C A T	5540
FASA pMON70058.SEQ	T T C A G A G C G C G T G A C C G G A A C T T G G G G C T T G C C T A T G T C C	5580
X87822 orf.SEQ	T T C A G A G C G C G T G A C C G G A A C T T G G G G G C T G C C T A T G T C C	5580
FASA pMON70058.SEQ	T G G G C A G C C C A C G T T G A G G C T G A A A T C T T G C T C G G C T C C C	5620
X87822 orf.SEQ	T G G G C A G C C C A C G T T G A G G C T G A A A T C T T G C T C G G C T C C C	5620
FASA pMON70058.SEQ	G T G A A G A A G A C T C C G T G C G C G G T G G C T C C T T G T C C A C C G T	5660
X87822 orf.SEQ	G T G A A G A A G A C T C A G T G C G C G G T G G C T C C T T G T C C A C C G T	5660
FASA pMON70058.SEQ	T C C T T C C G C G G C G T C G T C G A A G G C C G A T G T C G A T G C G C T T	5700
X87822 orf.SEQ	T C C T T C C G C G G C G T C G T C G A A G G C C G A T G T C G A T G C G C T T	5700
FASA pMON70058.SEQ	G T C G A T G C C G C G G T T C A G G C C G T A G C C G C A G C A C A C G G C A	5740
X87822 orf.SEQ	G T C G A T G C C G C G G T T C A G G C C G T A G C C G C A G C A C A C G G C A	5740

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FASA pMON70058.SEQ	C C T C G G T A T C C A T G G G T G C T G C G A G T G G C G C G G C G G C G G	5780
X87822 orf.SEQ	C C T C G G T A T C C C A T G G T G C T G C G A G T G G C G C G G C G G C G G	5780
FASA pMON70058.SEQ	T G G A G T C G T C G A C T C C G C A G C C T T G G A T G C T T A C G C A G A T	5820
X87822 orf.SEQ	T G G A G T C G T C G A C T C C G C A G C C T T G G A T G C T T A C G C A G A T	5820
FASA pMON70058.SEQ	A T C G T C A C C G G T G A A A A C G G T G T C C T C G C T A C T G C T G C T C	5860
X87822 orf.SEQ	A T C G T C A C C G G T G A A A A C G G T G T C C T C G C T A C T G C T G C T C	5860
FASA pMON70058.SEQ	G C C A G G T T C T G G C T C A G C T G G G C T T G G T C G A G G A A G C C C C	5900
X87822 orf.SEQ	G C C A G G T T C T G G C T C A G C T G G G C T T G G T C G A G G A A G C C C C	5900
FASA pMON70058.SEQ	T G A G A C C C C T G A G A C C G A T A A C A C C T T G T T C G A G A C C G T C	5940
X87822 orf.SEQ	T G A G A C C C C T G A G A C C G A T A A C A C C T T G T T C G C G A C C G T C	5940
FASA pMON70058.SEQ	G A G G C C G A G C T G G G T T C C G G T T G G G A A A A G A C C G T T A C C C	5980
X87822 orf.SEQ	G A G G C C G A G C T G G G T T C C G G T T G G G A A A A G A C C G T T A C C C	5980
FASA pMON70058.SEQ	C A T C C T T T G A C G C C A A G C G C G C A G T G C T T T T C G A T G A C C G	6020
X87822 orf.SEQ	C A T C C T T T G A C G C C A A G C G C G C A G T G C T T T T C G A T G A C C G	6020
FASA pMON70058.SEQ	C T G G G C G T C T G C T C G C G A A G A T C T C G C C C G C G T G G C A C T C	6060
X87822 orf.SEQ	C T G G G C G T C T G C T C G C G A A G A T C T C G C C C G C G T G G C A C T C	6060
FASA pMON70058.SEQ	G G C G A G A T C G A C T T G C C A G T C A A G C G T T T C C A G G G A A C C G	6100
X87822 orf.SEQ	G G C G A G A T C G A C T T G C C A G T C A A G C G T T T C C A G G G A A C C G	6100
FASA pMON70058.SEQ	G A G A G A C C A T C G C C A A G C A A G C G G A A T G G T G G G C G G A G A A	6140
X87822 orf.SEQ	G A G A G A C C A T C G C C A A G C A A G C G G A A T G G T G G G C G G A G A A	6140
FASA pMON70058.SEQ	C A C C G C T G C T T C C A C T G G T G C G C A C G C G A A G G C A A C C T C T	6180
X87822 orf.SEQ	C A C C G C T G C T T C C A C T G G T G C G C A C G C G A A G G C A A C C G C T	6180
FASA pMON70058.SEQ	G C C G A G A C C C T G C A T G C T A T T G C T G C C G C A G C G C G C G A A G	6220
X87822 orf.SEQ	G C C G A G A C C C T G C A T G C T A T T G C T G C C G C A G C G C G C G A A G	6220
FASA pMON70058.SEQ	A A C T C G A C G G C G A A T T C G C T G G C G A T G T C G C G T T G G T C A C	6260
X87822 orf.SEQ	A A C T C G A C G G C G A A T T C G C T G G C G A T G T C G C G T T G G T C A C	6260
FASA pMON70058.SEQ	C G G T G C A G C C C A G G C T C C A T T G C T A C C G C T C T C G T A G A A	6300
X87822 orf.SEQ	C G G T G C A G C C C A G G C T C C A T T G C T A C C G C T C T C G T A G A A	6300
FASA pMON70058.SEQ	C G C C T G C T G G A A G G C G G C G C G A C C G T C A T C A T G A C T G C G T	6340
X87822 orf.SEQ	C G C C T G C T G G A A G G C G G C G C G A C C G T C A T C A T G A C T G C G T	6340
FASA pMON70058.SEQ	C A C G T G T C A G C C A G T C C C G T A A G G A A T T T G C A C G C A A G C T	6380
X87822 orf.SEQ	C A C G T G T C A G C C A G T C C C G T A A G G A A T T T G C A C G C A A G C T	6380
FASA pMON70058.SEQ	C T A C G C T G C A C A C G C G A T T C C T G G C G C T G C C C T G T G G G T T	6420
X87822 orf.SEQ	C T A C G C T G C A C A C G C G A T T C C T G G C G C T G C C C T G T G G G T T	6420
FASA pMON70058.SEQ	G T T C C T G C G A A C T T G A G C T C C T A C C G C G A T G T T G A T G C T C	6460
X87822 orf.SEQ	G T T C C T G C G A A C T T G C G C T C C T A C C G C G A T G T T G A T G C T C	6460
FASA pMON70058.SEQ	T C A T T G A C T G G A T T G G T A A T G A G C A G C G T G A A T C T G T C G G	6500
X87822 orf.SEQ	T C A T T G A C T G G A T T G G T A A T G A G C A G C G T G C C T C T G T C G G	6500
FASA pMON70058.SEQ	C A A C G A A G T C A A G A T C A C C A A G C C A G C G T T G A C C C C A A C C	6540
X87822 orf.SEQ	C A A C G A A G T C A A G A T C A C C A A G C C A G C G T T G A C C C C A A C C	6540
FASA pMON70058.SEQ	T T G G C C T T C C C A T T C G C G G C A C C T T C C G T G T C C G G T T C T G	6580
X87822 orf.SEQ	T T G G C C T T C C C A T T C G C G G C A C C T T C C G T G T C C G G T T C T G	6580
FASA pMON70058.SEQ	T G G C C G A T G C C G G C C C A C A G G C T G A A A C C A G A C T C G C C T	6620
X87822 orf.SEQ	T G G C C G A T G C C G G C C C A C A G G C T G A A A C C A G A C T C G C C T	6620
FASA pMON70058.SEQ	G C T G C T G T G G T C T G T T G A G C G C A C C A T C G C T G G T C T G T C C	6660
X87822 orf.SEQ	G C T G C T G T G G T C T G T T G A G C G C A C C A T C G C T G G T C T G T C C	6660
FASA pMON70058.SEQ	A A C C T G G C G C A G C A A G G C G T G G A T A C C C G C T G C C A C A T T G	6700
X87822 orf.SEQ	A A C C T G G C G C A G C A A G G C G T G G A T A C C C G C T G C C A C A T T G	6700

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FASA pMON70058.SEQ	T G C T G C C T G G T T C T C C G A A C C G C G G C A T G T T C G G T G G C G A	6740
X87822 orf.SEQ	T G C T G C C T G G T T C T C C G A A C C G C G G C A T G T T C G G T G G C G A	6740
FASA pMON70058.SEQ	C G G C G C T T A C G G C G A A G T C A A G G C A G C C T T G G A C G C T A T T	6780
X87822 orf.SEQ	C G G C G C T T A C G G C G A A G T C A A G G C A G C C T T G G A C G C T A T T	6780
FASA pMON70058.SEQ	T T G G C C A A G T G G T C T G C A G A A G C A G G C T G G C C A G A A G G T G	6820
X87822 orf.SEQ	T T G G C C A A G T G G T C T G C A G A A G C A G G C T G G C C A G A A G G T G	6820
FASA pMON70058.SEQ	T T A C C T T G G C A C A A G C C A A G A T T G G C T G G G T C T C T G G T A C	6860
X87822 orf.SEQ	T T A C C T T G G C A C A A G C C A A G A T T G G C T G G G T C T C T G G T A C	6860
FASA pMON70058.SEQ	C T C C C T G A T G G G C G G C A A C G A C G T T C T G A T T C C G G C A G C G	6900
X87822 orf.SEQ	C T C C C T G A T G G G C G G C A A C G A C G T T C T G A T T C C G G C A G C G	6900
FASA pMON70058.SEQ	G A A G C C G C T G G C A T C C A C G T G T G G G A C C C A G A A G A G A T T T	6940
X87822 orf.SEQ	G A A G C C G C T G G C A T C C A C G T G T G G G A C C C A G A A G A G A T T T	6940
FASA pMON70058.SEQ	C T T C C C A G C T C A T C T C C C T A G C T T C C G A A G A A T C C C G C G C	6980
X87822 orf.SEQ	C T T C C C A G C T C A T C T C C C T A G C T T C C G A A G A A T C C C G C G C	6980
FASA pMON70058.SEQ	G A A G G C A G C C G A G G C T C C A C T A G A G C T G G A T C T G A C C G G T	7020
X87822 orf.SEQ	G A A G G C A G C C G A G G C T C C A C T A G A G C T G G A T C T G A C C G G T	7020
FASA pMON70058.SEQ	G G T C T G G G C T C G T C C A A G A T C T C C A T C T C C G A G C T G G C T G	7060
X87822 orf.SEQ	G G T C T G G G C T C G T C C A A C A T C T C C A T C T C C G A G C T G G C T G	7060
FASA pMON70058.SEQ	C C C A G G C C C G C G A G G A C G C C G A G G C A C A A G C T G C T T C C G G	7100
X87822 orf.SEQ	C C C A G G C C C G C G A G G A C G C C G A G G C A C A A G C T G C T T C C G G	7100
FASA pMON70058.SEQ	T G A T A A T G C A G A C G C A G C T G C G G A A G C T C C T G C A G C C A C G	7140
X87822 orf.SEQ	T G A T A A T G C A G A C G C A G C T G C G G A A G C T C C T G C A G C C A C G	7140
FASA pMON70058.SEQ	A T T C C A G C A C T G C C C T A A T A C C C G T T C A G T A G A G C T G C C T G	7180
X87822 orf.SEQ	A T T C C A G C A C T G C C C T A A T A C C C G T T C A G T A G A G C T G C C T G	7180
FASA pMON70058.SEQ	C A G C G C T A C C G G A A G G T G A A G T G G G C G A C G T A A C C A C G G A	7220
X87822 orf.SEQ	C A G C G C T A C C G G A A G G T G A A G T G G G C G A C G T A A C C A C G G A	7220
FASA pMON70058.SEQ	T C T G G A T G A C A T G G T C G T C A T C G C A G G T G T C G G C G A A G T C	7260
X87822 orf.SEQ	T C T G G A T G A C A T G G T C G T C A T C G C A G G T G T C G G C G A A G T C	7260
FASA pMON70058.SEQ	T C C T C G T G G G G T T C G G G C C G T A C C C G C T T T G A G G C A G A A T	7300
X87822 orf.SEQ	T C C T C G T G G G G T T C G G G C C G T A C C C G C T T T G A G G C A G A A T	7300
FASA pMON70058.SEQ	A T G G C T T G C A G C G C G A T G G C G C T G T G G A C C T G A C C G C C G C	7340
X87822 orf.SEQ	A T G G C T T G C A G C G C G A T G G C G C T G T G G A C C T G A C C G C C G C	7340
FASA pMON70058.SEQ	T G G T G T C T T G G A A T T G G C A T G G A T G A C C G G A C T G A T T T C C	7380
X87822 orf.SEQ	T G G T G T C T T G G A A T T G G C A T G G A T G A C C G G A C T G A T T T C C	7380
FASA pMON70058.SEQ	T G G T C C A A T G A C C C A C G T C C A G C C T G G T A C G A C G A A G A G G	7420
X87822 orf.SEQ	T G G T C C A A T G A C C C A C G T C C A G C C T G G T A C G A C G A A G A G G	7420
FASA pMON70058.SEQ	G C A C C G A A G T C G A T G A A G C A G A T A T C T A C G C T C G C T T C C G	7460
X87822 orf.SEQ	G C A C C G A A G T C G A T G A A G C A G A T A T C T A C G C T C G C T T C C G	7460
FASA pMON70058.SEQ	C G A C G A G G T T G T A G C T C G C T C C G G T A T C C G T A C C T T G A C C	7500
X87822 orf.SEQ	C G A C G A G G T T G T A G C T C G C T C C G G T A T C C G T A C C T T G A C C	7500
FASA pMON70058.SEQ	G A T A A G T A C A A C A T G G T T G A C C A G G G C T C C A T T G A C C T G A	7540
X87822 orf.SEQ	G A T A A G T A C A A C A T G G T T G A C C A G G G C T C C A T T G A C C T G A	7540
FASA pMON70058.SEQ	C T T C T G T G T T C T T G G A C C G C G A T A T C G T C T T C A C C G T T C C	7580
X87822 orf.SEQ	C T T C T G T G T T C T T G G A C C G C G A T A T C G T C T T C A C C G T T C C	7580
FASA pMON70058.SEQ	T A C C G A A C A A G A A G C A C T C G A T A T T G A A G A A G C C G A C C C A	7620
X87822 orf.SEQ	T A C C G A A C A A G A A G C A C T C G A T A T T G A A G A A G C C G A C C C A	7620
FASA pMON70058.SEQ	T C G T T T A C C A A G C T G C G C G A A G T C G A C G G C G A G T G G G A A G	7660
X87822 orf.SEQ	T C G T T T A C C A A G C T G C G C G A A G T C G A C G G C G A G T G G G A A G	7660

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FASA pMON70058.SEQ	T C A C C C G T T T G A A G G G T G C C A C C G C C G C G T G C C A C G C A A	7700
X87822 orf.SEQ	T C A C C C G T T T G A A G G G T G C C A C C G C C G C G T G C C A C G C A A	7700
FASA pMON70058.SEQ	G G C A A C G T T G A C T C G T A C C G T T G C T G G T C A A A T G C C G G A T	7740
X87822 orf.SEQ	G G C A A C G T T G A C T C G T A C C G T T G C T G G T C A A A T G C C G G A T	7740
FASA pMON70058.SEQ	C A C T T C G A T G C T G C C A A G T G G G G C A T T C C A G A C C A C A T G C	7780
X87822 orf.SEQ	C A C T T C G A T G C T G C C A A G T G G G G C A T T C C A G A C C A C A T G C	7780
FASA pMON70058.SEQ	T G G A T G C A C T C G A C C G C A T G G C C G T G T G G A A C C T G G T G A C	7820
X87822 orf.SEQ	T G G A T G C A C T C G A C C G C A T G G C C G T G T G G A A C C T G G T G A C	7820
FASA pMON70058.SEQ	C G C A G T C G A T G C C T T T A C C C A G G C G G G C T T T A G C C C G G C T	7860
X87822 orf.SEQ	C G C A G T C G A T G C C T T T A C C C A G G C G G G C T T T A G C C C G G C T	7860
FASA pMON70058.SEQ	G A G T T G C T G C A G G T T A T T C A C C C A G C G C A G G T T G C T A C C A	7900
X87822 orf.SEQ	G A G T T G C T G C A G G T T A T T C A C C C A G C G C A G G T T G C T A C C A	7900
FASA pMON70058.SEQ	C C C A G G G C A C C G G T A T C G G C G G C A T G G A A T C C C T G C A C A A	7940
X87822 orf.SEQ	C C C A G G G C A C C G G T A T C G G C G G C A T G G A A T C C C T G C A C A A	7940
FASA pMON70058.SEQ	G G T C T T C G T G A C C C G T C T G C T C G G T G A A G A C C G T C C T T C C	7980
X87822 orf.SEQ	G G T C T T C G T G A C C C G T C T G C T C G G T G A A G A C C G T C C T T C C	7980
FASA pMON70058.SEQ	G A C A T C C T G C A G G A A G C A C T G C C T A A C G T T A T T G C A G C G C	8020
X87822 orf.SEQ	G A C A T C C T G C A G G A A G C A C T G C C T A A C G T T A T T G C A G C G C	8020
FASA pMON70058.SEQ	A C A C C A T G C A G T C T T T G G T G G G C G G C T A C G G T T C G A T G A T	8060
X87822 orf.SEQ	A C A C C A T G C A G T C T T T G G T G G G C G G C T A C G G T T C G A T G A T	8060
FASA pMON70058.SEQ	T C A C C C T A T C G G T G C T T G T G C C A C C G C T G C G G T G T C C A T C	8100
X87822 orf.SEQ	T C A C C C T A T C G G T G C T T G T G C C A C C G C T G C G G T G T C C A T C	8100
FASA pMON70058.SEQ	G A A G A A G G C G T G G A C A A G A T T G C C C T G G G C A A G G C C G A C C	8140
X87822 orf.SEQ	G A A G A A G G C G T G G A C A A G A T T G C C C T G G G C A A G G C C G A C C	8140
FASA pMON70058.SEQ	T G G T C G T T G C C G G T G G T A T C G A T G A C G T C C A A G T T G A G T C	8180
X87822 orf.SEQ	T G G T C G T T G C C G G T G G T A T C G A T G A C G T C C A A G T T G A G T C	8180
FASA pMON70058.SEQ	T T T G A C C G G C T T C G G C G A C A T G A A C G C C A C C G C T G A G A C C	8220
X87822 orf.SEQ	T T T G A C C G G C T T C G G C G A C A T G A A C G C C A C C G C T G A G A C C	8220
FASA pMON70058.SEQ	A A G A A G A T G A C C G A T C A G G G C A T T G A T G A C C G C T T C A T C T	8260
X87822 orf.SEQ	A A G A A G A T G A C C G A T C A G G G C A T T G A T G A C C G C T T C A T C T	8260
FASA pMON70058.SEQ	C C C G T G C G A A T G A C C G C C G T C G T G G C G G C T T C C T C G A G G C	8300
X87822 orf.SEQ	C C C G T G C G A A T G A C C G C C G T C G T G G C G G C T T C C T C G A G G C	8300
FASA pMON70058.SEQ	A G A A G G C G G C G G T A C C G T G C T T C T G G T T C G C G G T T C C C T G	8340
X87822 orf.SEQ	A G A A G G C G G C G G T A C C G T G C T T C T G G T T C G C G G T T C C C T G	8340
FASA pMON70058.SEQ	G C T C G T G A G A T G G G T C T G C C G G T C T A C G C G G T C G T T G C G C	8380
X87822 orf.SEQ	G C T C G T G A G A T G G G T C T G C C G G T C T A C G C G G T C G T T G C G C	8380
FASA pMON70058.SEQ	A C G C G G C G T C C T A C G G C G A C G G T G C C C A C A C C T C C A T T C C	8420
X87822 orf.SEQ	A C G A G G C G T C C T A C G G - - - - T G C C C A C A C C T C C A T T C C	8420
FASA pMON70058.SEQ	T G C T C C A G G T T T G G G T G C T T T G G G C G C T G G C C G T G G C C G G	8460
X87822 orf.SEQ	T G C T C C A G G T T T G G G T G C T T T G G G C G C T G G C C G T G G C C G G	8460
FASA pMON70058.SEQ	A A G A A C T C C C G C C T G G C C A A G G G C T T G G C T G G T T T G G G T C	8500
X87822 orf.SEQ	A A G A A C T C C C G C C T G G C C A A G G G C T T G G C T G G T T T G G G T C	8500
FASA pMON70058.SEQ	T G A C T C C A A A T G A C G T C T C G G T A C T G T C C A A G C A C G A C A C	8540
X87822 orf.SEQ	T G A C T C C A A A T G A C G T C T C G G T A C T G T C C A A G C A C G A C A C	8540
FASA pMON70058.SEQ	C T C G A C C A A C G C C A A T G A C C C G A A T G A G T C G G A A C T G C A C	8580
X87822 orf.SEQ	C T C G A C C A A C G C C A A T G A C C C G A A T G A G T C G G A A C T G C A C	8580
FASA pMON70058.SEQ	T C C A T C T T G T G G C C T G C T A T T G G C C G C G A T G T G G A C C A G C	8620
X87822 orf.SEQ	T C C A T C T T G T G G C C T G C T A T T G G C C G C G A T G T G G A C C A G C	8614

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FASA pMON70058.SEQ	C A C T G T T T G T G A T T T C G C A G A A G T C A C T G A C T G G T C A C T C	8660
X87822 orf.SEQ	C A C T G T T T G T G A T T T C G C A G A A G T C A C T G A C T G G T C A C T C	8654
FASA pMON70058.SEQ	C A A G G C T G G T G C C G C G C T G T T C C A G A C C G G C G G T T T G A T T	8700
X87822 orf.SEQ	C A A G G C T G G T G C C G C G C T G T T C C A G A C C G G C G G T T T G A T T	8694
FASA pMON70058.SEQ	G A C G T C T T C C G C A C G G G A C G C A T T C C A G C T A A C C T G T C G C	8740
X87822 orf.SEQ	G A C G T C T T C C G C A C G G G A C G C A T T C C A G C T A A C C T G T C G C	8734
FASA pMON70058.SEQ	T G G A T T G T G T G G A T C C A T T G A T T G A G C C A A A G G C C A C G A A	8780
X87822 orf.SEQ	T G G A T T G T G T G G A T C C A T T G A T T G A G C C A A A G G C C A C G A A	8774
FASA pMON70058.SEQ	C T T G G T C T G G C T A C G C T C C C C A C T A G A T G T G G A A G C A G C C	8820
X87822 orf.SEQ	C T T G G T C T G G C T A C G C T C C C C A C T A G A T G T G G A A G C A G C C	8814
FASA pMON70058.SEQ	A A C C G C C C G G T C A A G G C C G C G G C G C T C A C C T C G C T C G G C T	8860
X87822 orf.SEQ	A A C C G C C C G G T C A A G G C C G C G G C G C T C A C C T C G C T C G G C T	8854
FASA pMON70058.SEQ	T C G G T C A C G T C G G T G C A T T G A T T G T C T A C G C G C A C C C A G G	8900
X87822 orf.SEQ	T C G G T C A C G T C G G T G C A T T G A T T G T C T A C G C G C A C C C A G G	8894
FASA pMON70058.SEQ	T G T C T T C G A G G C T G C C G T T G C C C A G C A G G T T T C G G C C G A G	8940
X87822 orf.SEQ	T G T C T T C G A G G C T G C C G T T G C C C A G C A G G T T T C G G C C G A G	8934
FASA pMON70058.SEQ	G C T G C T G C C G A A T G G C G C G A G A A G G C A A A T G C C C G C C T C G	8980
X87822 orf.SEQ	G C T G C T G C C G A A T G G C G C G A G A A G G C A A A T G C C C G C C T C G	8974
FASA pMON70058.SEQ	C C G C C G G T G C A G C A C G C T T C G A A G C C G G C A T G A T T G G C A A	9020
X87822 orf.SEQ	C C G C C G G T G C A G C A C G C T T C G A A G C C G G C A T G A T T G G C A A	9014
FASA pMON70058.SEQ	G G A A A C C T T G T T C G A G G T C A T C G A C G G C C G C C G C C T G C C T	9060
X87822 orf.SEQ	G G A A A C C T T G T T C G A G G T C A T C G A C G G C C G C C G C C T G C C T	9054
FASA pMON70058.SEQ	G A C G C A G C G G G C A C C G T T G A G A T T G A G A A C T A C G G C C C A G	9100
X87822 orf.SEQ	G A C G C A G C G G G C A C C G T T G A G A T T G A G A A C T A C G G C C C A G	9094
FASA pMON70058.SEQ	T C G C C G C C G A C A A G G C C G C A G A A A T T G C G C T C T T G C T T G A	9140
X87822 orf.SEQ	T C G C C G C C G A C A A G G C C G C A G A A A T T G C G C T C T T G C T T G A	9133
FASA pMON70058.SEQ	C G A C G A C A T C C G T C T T A C C G C C G A A G G C A C T T T C C C T C C G	9180
X87822 orf.SEQ	C G A C G A C A T C C G T C T T A C C G C C G A A G G C A C T T T C C C T C C G	9173
FASA pMON70058.SEQ	G C G A A G T A G	9189
X87822 orf.SEQ	G C G A A G T A G G A C A A A G T A G	9192

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FASA pmon70058.PRO	M S L T P L H T L S N D S T A P A V L F A G Q G S A W Q K A I A D A A A S P H Q	40
FASA X87822.PRO	M S L T P L H T L S N D S T A P A V L F A G Q G S A W Q K A I A D A A A S P H Q	40
FASA pmon70058.PRO	G A Q L R D I L K E V R T T T G P V A R I I A S S C P G V Y E R L E E L A Q T P	80
FASA X87822.PRO	G A Q L R D I L K E V R T T T G P V A R I I A S S C P G V Y E R L E E L A Q T P	80
FASA pmon70058.PRO	A D Q A P V A K E Y D A Y P A Y S I P G I V L G Q I G A I E H L R E L G I D V D	120
FASA X87822.PRO	A D Q A P V A K E Y D A Y P A Y S I P G I V L G Q I G A I E H L <u>A Q</u> L G I D V D	120
FASA pmon70058.PRO	S A Q L A G H S Q G S L G V A A V K D A R Q A L A I A V L M G T A A A V T Q G A	160
FASA X87822.PRO	S A Q L A G H S Q G S L G V A A V K D A R Q A L A I A V L M G T A A A V T Q G A	160
FASA pmon70058.PRO	N D S R S H M L S V R G V P R E M V E E Y L A G D A A I A V V N G R V H F A L S	200
FASA X87822.PRO	N D S R <u>T</u> H M L S V R G V P R E M V E E Y L A G D A A I A V V N G R V H F A L S	200
FASA pmon70058.PRO	G T P E D L A K T E S N L T Q A A E S Y N D A L E E R R I G G S E I N P V F D V	240
FASA X87822.PRO	G T P E D L A K T E S N L T Q A A E S Y N D A L E E R R I G G S E I N P V F D V	240
FASA pmon70058.PRO	L A V A L P F H H A S L Q D A A D L T V D Y A T Q C G L D A E L A R E L A D S I	280
FASA X87822.PRO	L A V A L P F H H A S L Q D A A D L T V D Y A T Q C G L D A E L A R E L A D S I	280
FASA pmon70058.PRO	L V Q P H S W V E T V A G L N S T Y L L S L D R G L S S L T T P L I A G T G K V	320
FASA X87822.PRO	L V Q P H S W V E T V A G L N S T Y L L S L D R G L S S L T T P L I A G T G K V	320
FASA pmon70058.PRO	V V P A A T P A E R D N L A T P G T E L P T A V N Y E K F S P K L I S L P N G K	360
FASA X87822.PRO	V V P A A T P A E R D N L A T P G T E L P T A V N Y E K F S P K L I S L P N G K	360
FASA pmon70058.PRO	S Y T Q T R F S E W T G M S P I I L G G M T P T T M D P G I V A A A A N G G Y W	400
FASA X87822.PRO	S Y T Q T R F S E W T G M S P I I L G G M T P T T M D P G I V A A A A N G G Y W	400
FASA pmon70058.PRO	S E M A G G G Q Y S D E A F T I N K D G M M E L L E P G R T A A F N T M F F D R	440
FASA X87822.PRO	S E M A G G G Q Y S D E A F T I N K D G M M E L L E P G R T A A F N T M F F D R	440
FASA pmon70058.PRO	Y L W N L Q F G V T R I V P K A R A N G A A F T G V T I S A G I P E L D E A K E	480
FASA X87822.PRO	Y L W N L Q F G V T R I <u>C S</u> K A R A N G A A F T G V T I <u>C</u> A G I P E L D E A K E	480
FASA pmon70058.PRO	L L D Q L T S D G F P Y I S F K P G T T K Q I Q D C I A I A A D N P T H R V I I	520
FASA X87822.PRO	L L D Q L T S D G F P Y I S F K P G T T K Q I Q D C <u>V</u> A I A A D N P T H R V I I	520
FASA pmon70058.PRO	Q I E D' G H A G G H S W V D L D E M L L A T Y A S A R E H D N L A I T V G G G	560
FASA X87822.PRO	Q I E D <u>A</u> H A G G H S W V D L D E M L L A T Y A <u>C</u> A R E H D N L A I T V G G G	560
FASA pmon70058.PRO	I H S P D R A S E Y L T G T W S T K Y G L P I M P V D G V F L G T V A M A T K E	600
FASA X87822.PRO	I H S P D R A S E Y L T G T W S T K Y G L P I M P V D G V F L G T V A M A T K E	600
FASA pmon70058.PRO	A T A N D D V K Q L L V D T P G I S P E T N G G W V G R L D A D G G V S S S Q S	640
FASA X87822.PRO	A T A N D D V K Q L L V D T P G I S P E T N G G W V G R L D A D G G V S S S Q S	640
FASA pmon70058.PRO	H L L A D L H E I D N S F A K A S R M I T S I P I E E Y D E R R D E I I A A L D	680
FASA X87822.PRO	H L L A D L H E I D N S F A K A S R M I T S I P I E E Y D E R R D E I I A A L D	680
FASA pmon70058.PRO	K T S K P Y F G D L S E M T Y E D W V A R F A E R A Y P W V D P T W H D R F H D	720
FASA X87822.PRO	K T S K P Y F G D L S E M T Y E D W V A R F A E R A Y P W V D P T W H D R F H D	720
FASA pmon70058.PRO	L L Q R V E A R L N D A D H G D I E T L F P T L D D S E N A P E A V A K L L A A	760
FASA X87822.PRO	L L Q R V E A R L N D A D H G D I E T L F P T L D D S E N A P E A V A K L L A A	760
FASA pmon70058.PRO	Y P N A K T T K V N T R D E A W F P T L I R K H V K P M P W T T A I D G D L K E	800
FASA X87822.PRO	Y P N A K T T K V N T R D E A W F P T L I R K H V K P M P W T T A I D G D L K E	800
FASA pmon70058.PRO	W F A K D T L W Q A Q D P R Y D A D G V R I I P G P V S V A G I T K K N E P V A	840
FASA X87822.PRO	W F A K D T L W Q A Q D P R Y D A D G V R I I P G P V S V A G I T K K N E P V A	840
FASA pmon70058.PRO	N L L G R F E D A T T A A L N D A G V A P V E L Y S R L A S A K N A E E F L R N	880
FASA X87822.PRO	N L L G R F E D A T T A A L N D A G V A P V E L Y S R L A S A K N A E E F L R N	880
FASA pmon70058.PRO	A P T I M W H G H L I A N P A Y E L P E E A F D I V D D G E G F A I R I N S D S	920
FASA X87822.PRO	A P T I M W H G H L I A N P A Y E L P E E A F D I V D D G E G F A I R I N S D S	920
FASA pmon70058.PRO	Y W D N L P E E Q R P F Y V K H V D I P V A L S E A V A T G A S P V V D D A R L	960
FASA X87822.PRO	Y <u>R</u> D N L P E E Q R P F Y V K H V D I P V A L S E A V A T G A S P V V D D A R L	960

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FASA pmon70058.PRO	P K A V F D L L A G V A G V G S I S E T G D K I T E L P K V I E G S V S E E N P	1000
FASA X87822.PRO	P K A V F D L L A G V A G V G S I S E T G D K I T E L P K V I E G S V S E E N P	1000
FASA pmon70058.PRO	Y G L V E Y S F T L P S T L L T A H T A V T G A A L G T A N A G T P D A L V G P	1040
FASA X87822.PRO	Y G L V E Y S F T L P S T L L T A H T A V T G A A L G T A N A G T P D A L V G P	1040
FASA pmon70058.PRO	C W P A I Y T A L G T G R L T E E H G E P A G T D F P V I E G L L N A V H L D H	1080
FASA X87822.PRO	C W P A I Y T A L G T G R L T E E H G E P A G T D F P V I E G L L N A V H L D H	1080
FASA pmon70058.PRO	V V D V R V P L H E L A K G E K G E G R R I D V T S R C A S I A E S N S G R I V	1120
FASA X87822.PRO	V V D V R V P L H E L A K G E K G E G <u>G</u> R I D V T S R C A S I A E S N S G R I V	1120
FASA pmon70058.PRO	T V E L E L W D A A T Q E V V A T Q M Q R F A I R G R A T G T S V P V S A P S W	1160
FASA X87822.PRO	T V E L E L W D A A T Q E V V A T Q M Q R F A I R G R A T G T S V P V S A P S W	1160
FASA pmon70058.PRO	G G G K S Q D K I E T T P R S F V D R A I V T A P S D M T P F A L V S G D Y N P	1200
FASA X87822.PRO	G G G K S Q D K I E T T P R S F V D R A I V T A P S D M T P F A L V S G D Y N P	1200
FASA pmon70058.PRO	I H T S T N A A R L V N L D A P L V H G M W L S A T A Q H L A G N H G T V V G W	1240
FASA X87822.PRO	I H T S T N A A R L V N L D A P L V H G M W L S A T A Q H L A G N H G T V V G W	1240
FASA pmon70058.PRO	T Y S M Y G M V Q L N D E V E I T V E R V G R K G I H A A F E V T C R I D G E V	1280
FASA X87822.PRO	T Y S M Y G M V Q L N D E V E I T V E R V G R K G I H A A F E V T C R I D G E V	1280
FASA pmon70058.PRO	V S R G Q A L M A Q P R T A Y V Y P G Q G I Q A E G M G R G D R D A S A A A R E	1320
FASA X87822.PRO	V S R G Q A L M A Q P R T A Y V Y P G Q G I Q A E G M G R G D R D A S A A A R E	1320
FASA pmon70058.PRO	V W R R A D R H T R T A M G F S I R Q I I D D N P T E L V V R G T K F V H P N G	1360
FASA X87822.PRO	V W R R A D R H T R T A <u>L</u> G F S I R Q I I D D N P T E L V V R G T K F V H P N G	1360
FASA pmon70058.PRO	V L H L T Q F T Q V A L A V V A Y A Q T E R L R E A D A L G T N S M Y A G H S L	1400
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Figure 3 (page 2 of 4)

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FASA pmon70058.PRO FASA X87822.PRO	G L V E E A P E T P E T D N T L F E T V E A E L G S G W E K T V T P S F D A K R G L V E E A P E T P E T D N T L F A T V E A E L G S G W E K T V T P S F D A K R	2000 2000
FASA pmon70058.PRO FASA X87822.PRO	A V L F D D R W A S A R E D L A R V A L G E I D L P V K R F Q G T G E T I A K Q A V L F D D R W A S A R E D L A R V A L G E I D L P V K R F Q G T G E T I A K Q	2040 2040
FASA pmon70058.PRO FASA X87822.PRO	A E W W A E N T A A S T G A H A K A T S A E T L H A I A A A A R E E L D G E F A A E W W A E N T A A S T G A H A K A T A A E T L H A I A A A A R E E L D G E F A	2080 2080
FASA pmon70058.PRO FASA X87822.PRO	G D V A L V T G A A P G S I A T A L V E R L L E G G A T V I M T A S R V S Q S R G D V A L V T G A A P G S I A T A L V E R L L E G G A T V I M T A S R V S Q S R	2120 2120
FASA pmon70058.PRO FASA X87822.PRO	K E F A R K L Y A A H A I P G A A L W V V P A N L S S Y R D V D A L I D W I G N K E F A R K L Y A A H A I P G A A L W V V P A N L R S Y R D V D A L I D W I G N	2160 2160
FASA pmon70058.PRO FASA X87822.PRO	E Q R E S V G N E V K I T K P A L T P T L A F P F A A P S V S G S V A D A G P Q E Q R A S V G N E V K I T K P A L T P T L A F P F A A P S V S G S V A D A G P Q	2200 2200
FASA pmon70058.PRO FASA X87822.PRO	A E N Q T R L L L W S V E R T I A G L S N L A Q Q G V D T R C H I V L P G S P N A E N Q T R L L L W S V E R T I A G L S N L A Q Q G V D T R C H I V L P G S P N	2240 2240
FASA pmon70058.PRO FASA X87822.PRO	R G M F G G D G A Y G E V K A A L D A I L A K W S A E A G W P E G V T L A Q A K R G M F G G D G A Y G E V K A A L D A I L A K W S A E A G W P E G V T L A Q A K	2280 2280
FASA pmon70058.PRO FASA X87822.PRO	I G W V S G T S L M G G N D V L I P A A E A A G I H V W D P E E I S S Q L I S L I G W V S G T S L M G G N D V L I P A A E A A G I H V W D P E E I S S Q L I S L	2320 2320
FASA pmon70058.PRO FASA X87822.PRO	A S E E S R A K A A E A P L E L D L T G G L G S S K I S I S E L A A Q A R E D A A S E E S R A K A A E A P L E L D L T G G L G S S N I S I S E L A A Q A R E D A	2360 2360
FASA pmon70058.PRO FASA X87822.PRO	E A Q A A S G D N A D A A A E A P A A T I P A L P N T R S V E L P A A L P E G E E A Q A A S G D N A D A A A E A P A A T I P A L P N T R S V E L P A A L P E G E	2400 2400
FASA pmon70058.PRO FASA X87822.PRO	V G D V T T D L D D M V V I A G V G E V S S W G S G R T R F E A E Y G L Q R D G V G D V T T D L D D M V V I A G V G E V S S W G S G R T R F E A E Y G L Q R D G	2440 2440
FASA pmon70058.PRO FASA X87822.PRO	A V D L T A A G V L E L A W M T G L I S W S N D P R P A W Y D E E G T E V D E A A V D L T A A G V L E L A W M T G L I S W S N D P R P A W Y D E E G T E V D E A	2480 248
FASA pmon70058.PRO FASA X87822.PRO	D I Y A R F R D E V V A R S G I R T L T D K Y N M V D Q G S I D L T S V F L D R D I Y A R F R D E V V A R S G I R T L T D K Y N M V D Q G S I D L T S V F L D R	2520 2520
FASA pmon70058.PRO FASA X87822.PRO	D I V F T V P T E Q E A L D I E E A D P S F T K L R E V D G E W E V T R L K G A D I V F T V P T E Q E A L D I E E A D P S F T K L R E V D G E W E V T R L K G A	2560 2560
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FASA pmon70058.PRO FASA X87822.PRO	A V W N L V T A V D A F T Q A G F S P A E L L Q V I H P A Q V A T T Q G T G I G A V W N L V T A V D A F T Q A G F S P A E L L Q V I H P A Q V A T T Q G T G I G	2640 2640
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FASA pmon70058.PRO FASA X87822.PRO	D D V Q V E S L T G F G D M N A T A E T K K M T D Q G I D D R F I S R A N D R R D D V Q V E S L T G F G D M N A T A E T K K M T D Q G I D D R F I S R A N D R R	2760 2760
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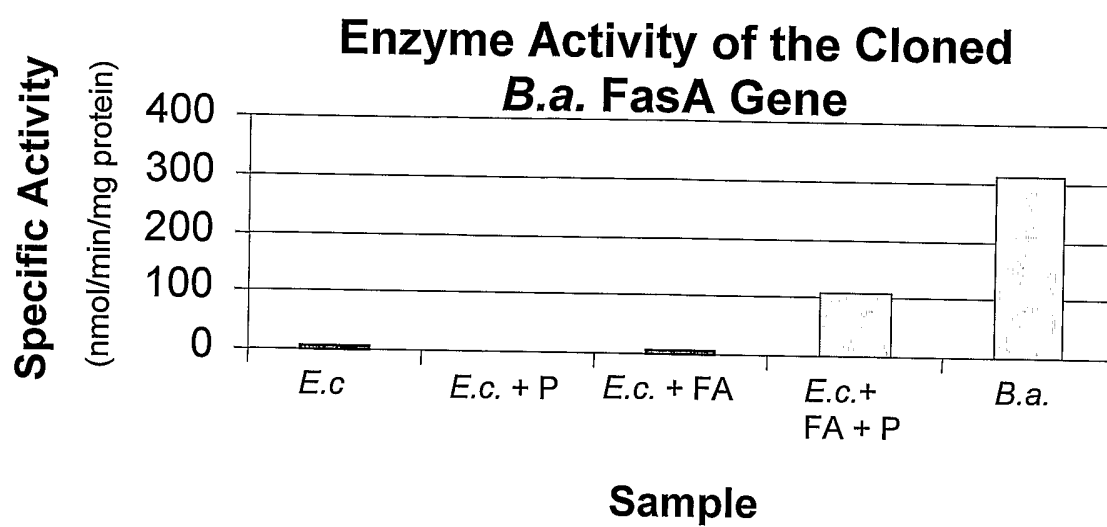
Figure 3 (page 3 of 4)

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FASA X87822.PRO	E A G M I G K E T L F E V I D G R R L P D A A G T V E I E N Y G P V A A D K A A	3038
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FASA X87822.PRO	E L R S C L T T T S V L P P K A L S L R R S R T K .	3064

Boxed Residues Differ from pMON70058

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**Figure 4**

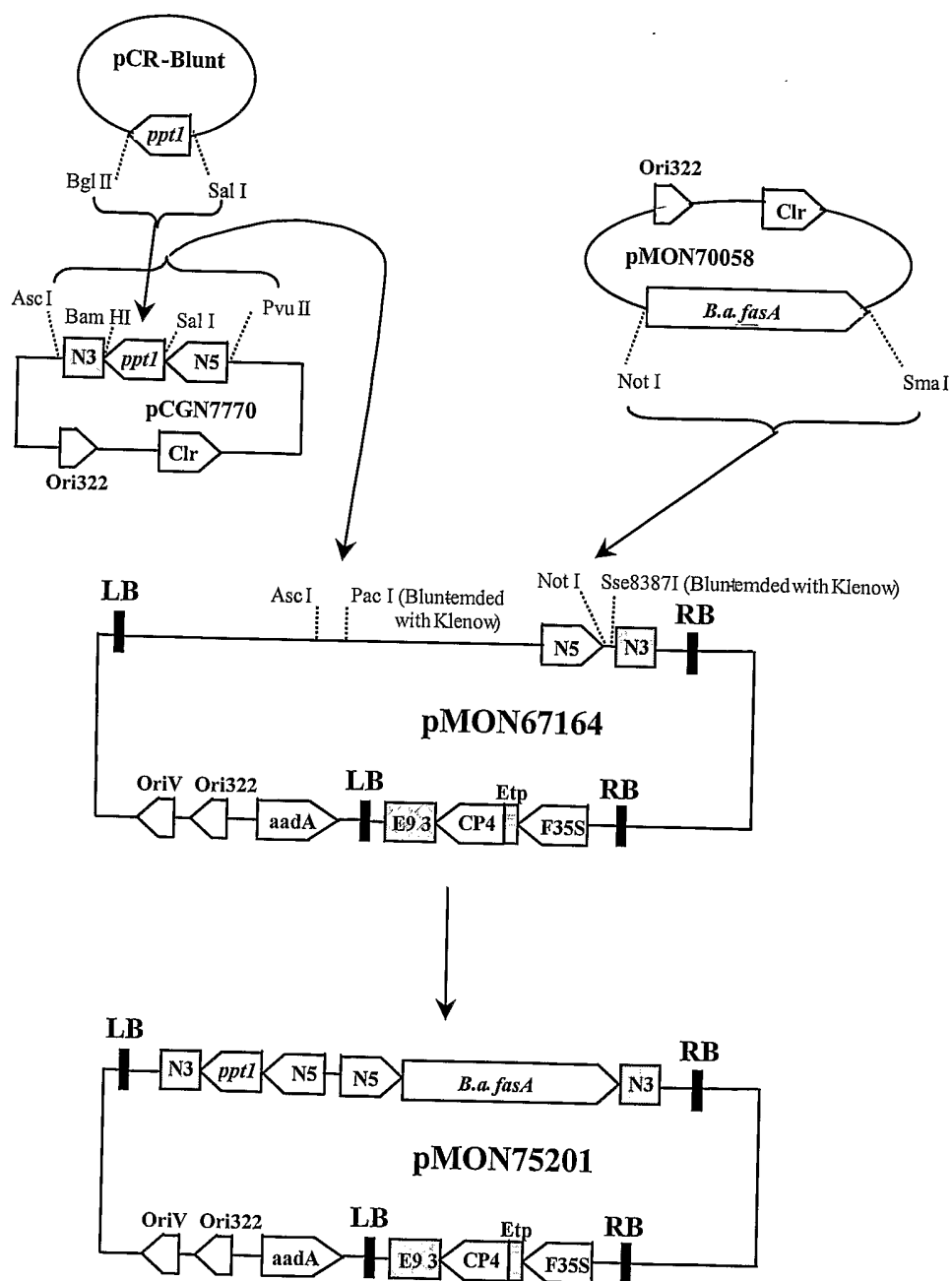


Figure 5

Pedigree	Relative Expression measured by Taqman mfFAS probe* Expt A	Relative Expression measured by Taqman mfFAS probe* Expt B	Relative Expression measured by Taqman PPT probe* Expt A	Relative Expression measured by Taqman PPT probe* Expt B	Western	Oil Increase observed at R2
BN_G1198 ^{a,b}	1	1.34	36.76	61.82	+	
BN_G1299	1.21	1	32.45	89.88	w	
BN_G1220 ^{a,b}	1.64	1.59	36.25	34.06	+	
BN_G1217 ^a	2.6	1.97	48.5	26	+	
BN_G1135	2.93	1.83	22.16	30.06	w	
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BN_G1182	3.32	2.25	58.49	34.54	w	
BN_G1180	3.43	1.95	50.21	32.45	w	
BN_G1091	3.71	4.11	50.91	81.57	w	
BN_G1216	3.94	1.99	1	1	+	+
BN_G1195	7.46	7.67	64.89	85.04	w	
BN_G1193 ^{a,b}	9.25	6.77	65.34	57.28	w	
BN_G1184	10.56	17.15	104.69	364.56	w	
BN_G1183	11.08	19.3	227.54	352.14	w	
BN_G1214 ^{a,b}	12.47	5.24	90.51	77.17	+	
BN_G1239	12.82	3.97	124.5	67.18	+	.
BN_G1194	14.22	6.06	28.44	16.8	w	
BN_G1218	17.88	6.73	254.23	213.78	w	
BN_G1179	21.56	15.89	35.75	60.97	w	
BN_G1139	32.22	7.06	121.10	105.42	w	
BN_G1196	32.45	21.11	53.45	60.55	w	
BN_G1225	53.45	11.47	19.16	24.25	+	
BN_G1223	67.65	7.52	97.68	54.19	+	

Data is normalized to 18S RNA and then relative expression is obtained by comparing the value for each event to an event chosen as the lowest expressor for that experiment.

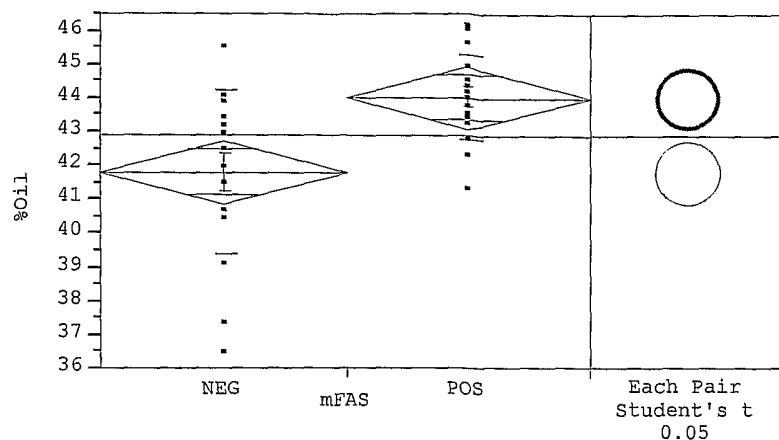
(a) R1 transplant grown in Brawley, CA.

(b) R1 seed planted in Thief River Falls, MN.

The letter w denotes a weak signal and therefore not conclusively positive or negative.

Figure 6

Oneway Analysis of %Oil By mFAS



Oneway Anova

Summary of Fit

Rsquare	0.263684
Adj Rsquare	0.240674
Root Mean Square Error	1.916516
Mean of Response	42.92029
Observations (or Sum Wgts)	34

t-Test

	Difference	t-Test	DF	Prob> t
Estimate	-2.2253	-3.385	32	0.0019
Std Error	0.6574			
Lower 95%	-3.5643			
Upper 95%	-0.8863			
Assuming equal variances				

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
mFAS	1	42.09144	42.0914	11.4596	0.0019
Error	32	117.53706	3.6730		
C. Total	33	159.62850			

Means for Oneway Anova

Level	Number	Mean	Std Error	Lower 95%	Upper 95%
NEG	17	41.8076	0.46482	40.861	42.754
POS	17	44.0329	0.46482	43.086	44.980
Std Error uses a pooled estimate of error variance					

Means and Std Deviations

Level	Number	Mean	Std Dev	Std Err Mean	Lower 95%	Upper 95%
NEG	17	41.8076	2.38814	0.57921	40.580	43.036
POS	17	44.0329	1.28174	0.31087	43.374	44.692

Means Comparisons

Dif=Mean[i]-Mean[j]	POS	NEG
POS	0.0000	2.2253
NEG	-2.2253	0.0000

Alpha=
0.05

Comparisons for each pair using Student's t

t
2.03693

Abs (Dif) -LSD	POS	NEG
POS	-1.3390	0.8863

Figure 7

REN-01-032-Util.ST25.txt
SEQUENCE LISTING

<110> Monsanto Technology, LLC
Savage, Thomas J.
Val, Dale L.
Voelker, Toni A.

<120> Elevation of Oil Levels in Brassica Plants

<130> REN-01-032

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<151> 2002-12-19

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Ser Ile Pro Gly Ile Val Leu Gly Gln Ile Gly Ala Ile Glu His Leu
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Thr Gly Met Ser Pro Ile Ile Leu Gly Gly Met Thr Pro Thr Met Asp
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385 390 400

Ala Gly Gly Gly Gln Tyr Ser Asp Glu Ala Phe Thr Ile Asn Lys Asp
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Thr Lys Gln Ile Gln Asp Cys Val Ala Ile Ala Ala Asn Pro Thr His
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Arg Val Ile Ile Gln Ile Glu Asp Ala His Ala Gly Gly His His Ser
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Page 7

REN-01-032-Ut11.ST25.txt

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595 600 605

Asp Thr Pro Gly Ile Ser Pro Glu Thr Asn Gly Gly Trp Val Gly Arg
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Leu Asp Ala Asp Gly Gly Val Ser Ser Ser Gln His Leu Leu Ala Asp
625 630 635 640

Leu His Glu Ile Asp Asn Ser Phe Ala Lys Ala Ser Arg Met Ile Thr
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Ser Ile Pro Ile Glu Glu Tyr Asp Glu Arg Arg Asp Glu Ile Ile Ala
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Ala Leu Asp Lys Thr Ser Lys Pro Tyr Phe Gly Asp Leu Ser Glu Met
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Thr Tyr Glu Asp Trp Val Ala Arg Phe Ala Glu Arg Ala Tyr Pro Trp
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Pro Thr Leu Asp Asp Ser Glu Asn Ala Pro Glu Ala Val Ala Lys Leu
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785 790 795 800

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Page 8

REN-01-032-Util.ST25.txt

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Ala Lys Asn Ala Glu Glu Phe Leu Arg Asn Ala Pro Thr Ile Met Trp
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His Gly His Leu Ile Ala Asn Pro Ala Glu Leu Pro Glu Glu Ala Phe
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Asp Ile Val Asp Asp Gly Glu Gly Phe Ala Ile Arg Ile Asn Ser Asp
 900 905 910

Ser Tyr Arg Asp Asn Leu Pro Glu Glu Gln Arg Pro Phe Tyr Val Lys
 915 920 925

His Val Asp Ile Pro Val Ala Leu Ser Glu Ala Val Ala Thr Gly Ala
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Ser Pro Val Val Asp Asp Ala Arg Leu Pro Lys Ala Val Phe Asp Leu
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Ile Thr Glu Leu Pro Lys Val Ile Glu Gly Ser Val Ser Glu Glu Asn
 980 985 990

Pro Tyr Gly Leu Val Glu Tyr Ser Phe Thr Leu Pro Ser Thr Leu Leu
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 Page 9

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Page 12

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 Asp Val Asp Ala Leu Ile Asp Trp Ile Gly Asn Glu Gln Arg Ala
 2135 2140 2145
 Ser Val Gly Asn Glu Val Lys Ile Thr Lys Pro Leu Thr Pro Thr
 2150 2155 2160
 Leu Ala Phe Pro Phe Ala Ala Pro Ser Val Ser Gly Ser Val Ala
 2165 2170 2175
 Asp Ala Gly Pro Gln Ala Glu Asn Gln Thr Arg Leu Leu Leu Trp
 2180 2185 2190
 Ser Val Glu Arg Thr Ile Ala Gly Leu Ser Asn Leu Ala Gln Gln
 2195 2200 2205
 Gly Val Asp Thr Arg Cys His Ile Val Leu Pro Gly Ser Pro Asn
 2210 2215 2220
 Arg Gly Met Phe Gly Gly Asp Gly Ala Tyr Gly Glu Val Lys Ala
 2225 2230 2235
 Ala Leu Asp Ala Ile Leu Ala Lys Trp Ser Ala Glu Ala Gly Trp
 2240 2245 2250
 Pro Glu Gly Val Thr Leu Ala Gln Ala Lys Ile Gly Trp Val Ser
 2255 2260 2265
 Gly Thr Ser Leu Met Gly Gly Asn Asp Val Leu Ile Pro Ala Ala
 2270 2275 2280
 Glu Ala Ala Ile His Val Trp Asp Pro Glu Glu Ile Ser Ser Gln
 2285 2290 2295
 Leu Ile Ser Leu Ala Ser Glu Glu Ser Arg Ala Lys Ala Ala Glu
 2300 2305 2310
 Ala Pro Leu Glu Leu Asp Leu Thr Gly Gly Leu Gly Ser Ser Asn
 2315 2320 2325
 Ile Ser Ile Ser Glu Leu Ala Ala Gln Ala Arg Glu Asp Ala Glu
 2330 2335 2340
 Ala Gln Ala Ala Ser Gly Asp Asn Ala Asp Ala Ala Ala Glu Ala
 2345 2350 2355
 Pro Ala Ala Thr Ile Pro Ala Leu Pro Asn Thr Arg Ser Val Glu

2360 REN-01-032-Util.ST25.txt
 2365 2370
 Leu Pro Ala Ala Leu Pro Glu Gly Glu Val Gly Asp Val Thr Thr
 2375 2380 2385
 Asp Leu Asp Asp Met Val Val Ile Ala Gly Val Gly Glu Val Ser
 2390 2395 2400
 Ser Trp Gly Ser Gly Arg Thr Arg Phe Glu Glu Tyr Gly Leu Gln
 2405 2410 2415
 Arg Asp Gly Ala Val Asp Leu Thr Ala Ala Gly Val Leu Glu Leu
 2420 2425 2430
 Ala Trp Met Thr Gly Leu Ile Ser Trp Ser Asn Asp Pro Arg Pro
 2435 2440 2445
 Ala Trp Tyr Asp Glu Glu Gly Thr Glu Val Asp Glu Ala Asp Ile
 2450 2455 2460
 Tyr Ala Arg Phe Arg Asp Glu Val Val Ala Arg Ser Gly Ile Arg
 2465 2470 2475
 Thr Leu Thr Asp Lys Tyr Asn Met Val Asp Gln Gly Ser Ile Asp
 2480 2485 2490
 Leu Thr Ser Val Phe Leu Asp Arg Asp Ile Val Phe Thr Val Pro
 2495 2500 2505
 Thr Glu Gln Glu Ala Leu Asp Ile Glu Glu Ala Asp Pro Ser Phe
 2510 2515 2520
 Thr Lys Leu Arg Glu Val Asp Gly Glu Trp Glu Val Thr Arg Leu
 2525 2530 2535
 Lys Gly Thr Ala Arg Val Pro Arg Lys Ala Thr Leu Thr Arg Thr
 2540 2545 2550
 Val Ala Gly Gln Met Pro Asp His Phe Asp Ala Ala Lys Trp Gly
 2555 2560 2565
 Ile Pro Asp His Met Leu Asp Ala Leu Asp Arg Met Ala Val Trp
 2570 2575 2580
 Asn Leu Val Thr Ala Val Asp Ala Phe Thr Gln Ala Gly Phe Ser
 2585 2590 2595
 Pro Ala Glu Leu Leu Gln Val Ile His Pro Ala Gln Val Ala Thr
 2600 2605 2610
 Thr Gln Gly Thr Gly Ile Gly Gly Met Glu Ser Leu His Lys Val

REN-01-032-Util.ST25.txt

2615 2620 2625

Phe Val Thr Arg Leu Leu Gly Glu Asp Arg Pro Ser Asp Ile Leu
2630 2635 2640

Gln Glu Ala Leu Pro Asn Val Ile Ala Ala His Thr Met Gln Ser
2645 2650 2655

Leu Val Gly Gly Tyr Gly Ser Met Ile Pro Ile Gly Ala Cys Ala
2660 2665 2670

Thr Ala Ala Val Ser Ile Glu Glu Gly Val Asp Lys Ile Ala Leu
2675 2680 2685

Gly Lys Ala Asp Leu Val Val Ala Gly Gly Ile Asp Asp Val Gln
2690 2695 2700

Val Glu Ser Leu Thr Gly Phe Gly Asp Met Asn Ala Thr Ala Glu
2705 2710 2715

Thr Lys Lys Met Thr Asp Gln Gly Ile Asp Asp Arg Phe Ile Ser
2720 2725 2730

Arg Ala Asn Asp Arg Arg Arg Gly Gly Phe Leu Glu Ala Glu Gly
2735 2740 2745

Gly Gly Thr Val Leu Leu Val Arg Gly Ser Leu Ala Arg Glu Met
2750 2755 2760

Gly Leu Pro Val Tyr Ala Val Val Ala His Glu Ala Ser Tyr Gly
2765 2770 2775

Ala His Thr Ser Ile Pro Ala Pro Gly Leu Gly Ala Leu Gly Ala
2780 2785 2790

Gly Arg Gly Arg Lys Asn Ser Arg Leu Ala Lys Gly Leu Ala Gly
2795 2800 2805

Leu Gly Leu Thr Pro Asn Asp Val Ser Val Leu Ser Lys His Asp
2810 2815 2820

Thr Ser Thr Asn Asn Asp Pro Asn Glu Ser Glu Leu His Ser Ile
2825 2830 2835

Leu Trp Pro Ala Ile Gly Arg Asp Val Asp Gln Pro Leu Phe Val
2840 2845 2850

Ile Ser Gln Lys Ser Leu Thr Gly His Ser Lys Ala Gly Ala Ala
2855 2860 2865

Leu Phe Gln Thr Gly Gly Leu Ile Asp Val Phe Arg Thr Gly Arg

REN-01-032-Util.ST25.txt
 2870 2875 2880

Ile Pro Ala Asn Leu Ser Leu Asp Cys Val Asp Pro Leu Ile Glu
 2885 2890 2895

Pro Lys Ala Thr Asn Leu Val Trp Leu Arg Ser Pro Leu Asp Val
 2900 2905 2910

Glu Ala Ala Asn Arg Pro Val Lys Ala Ala Ala Leu Thr Ser Leu
 2915 2920 2925

Gly Phe Gly His Val Gly Ala Leu Ile Val Tyr Ala His Pro Gly
 2930 2935 2940

Val Phe Glu Ala Ala Val Ala Gln Gln Val Ser Glu Ala Ala Ala
 2945 2950 2955

Glu Trp Arg Glu Lys Ala Asn Ala Arg Leu Ala Ala Gly Ala Ala
 2960 2965 2970

Arg Phe Glu Ala Gly Met Ile Gly Lys Glu Thr Leu Phe Glu Val
 2975 2980 2985

Ile Asp Gly Arg Arg Leu Pro Asp Ala Ala Gly Thr Val Glu Ile
 2990 2995 3000

Glu Asn Tyr Gly Pro Val Ala Ala Asp Lys Ala Ala Glu Leu Arg
 3005 3010 3015

Ser Cys Leu Thr Thr Thr Ser Val Leu Pro Pro Lys Ala Leu Ser
 3020 3025 3030

Leu Arg Arg Ser Arg Thr Lys
 3035 3040

<210> 3
 <211> 459
 <212> DNA
 <213> Brevibacterium ammoniagenes

<400> 3
 gtgctcgaca accgtgaagc gatgaccgtg ggtgtggact tgggtccacat ccccggttt 60
 gccgagcaat tgtcgcgccc tggttcgact tttgagcaag tgttttcgcc gttggaacgt 120
 cgtcatgtca aacgcgccgt gacgctgcag cggatgctac gaattcgagc cttgcgggtt 180
 cacggactga gcacctggct gggcgggtggg cggcaaaaga agcgttcac aaggcgtgg 240
 cgcaagcgat ctacgcaagc caccagtgtat tgaaccagac ctggtgaact tcgcagagat 300
 cgaagtcttg cccgaccgct ggggcagggt agcgtgcag cttaaagggt aagttgctgc 360
 aaaacttcag gaatcaatag ggacgtggag ctggcgctga gcatcagcca tgatggcgat 420
 tacgccaccg cgcagtgctt gctgcggtac cagcggtta 459

REN-01-032-util.ST25.txt

<210> 4
 <211> 152
 <212> PRT
 <213> Brevibacterium ammoniagenes

<400> 4

Met Leu Asp Asn Arg Glu Ala Met Thr Val Gly Val Asp Leu Val His
 1 5 10 15

Ile Pro Gly Phe Ala Glu Gln Leu Ser Arg Pro Gly Ser Thr Phe Glu
 20 25 30

Gln Val Phe Ser Pro Leu Glu Arg Arg His Ala Gln Thr Arg Arg Asp
 35 40 45

Ala Ala Ala Asp Ala Thr Asn Ser Ser Leu Ala Gly Ser Arg Thr Glu
 50 55 60

His Leu Ala Gly Arg Trp Ala Ala Lys Glu Ala Phe Ile Lys Ala Trp
 65 70 75 80

Ser Gln Ala Ile Tyr Gly Lys Pro Pro Val Ile Glu Pro Asp Leu Val
 85 90 95

Asn Phe Ala Glu Ile Glu Val Leu Pro Asp Arg Trp Gly Arg Val Ala
 100 105 110

Leu Gln Leu Lys Gly Glu Val Ala Ala Lys Leu Gln Glu Ser Ile Asp
 115 120 125

Val Glu Leu Ala Leu Ser Ile Ser His Asp Gly Asp Tyr Ala Thr Ala
 130 135 140

Gln Cys Leu Leu Arg Tyr Gln Arg
 145 150

<210> 5
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer sequence

<400> 5
 ccagctcaac gatgaagtag

20

<210> 6
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer sequence

REN-01-032-Uti1.ST25.txt

<400> 6
tcgatgatct ggtctacttc 20

<210> 7
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Primer Sequence

<400> 7
gtcgacatgc tcgacaaccg tgaagcg 27

<210> 8
<211> 31
<212> DNA
<213> Artificial

<220>
<223> Primer Sequence

<400> 8
agatcttcac tggtagcttg ccgtagatcg c 31

<210> 9
<211> 37
<212> DNA
<213> Artificial

<220>
<223> Primer Sequence

<400> 9
tctagatgca tagttaacat gtcgttgacc cccttgcc 37

<210> 10
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Primer Sequence

<400> 10
ggtagcgctc atattccttg 20

<210> 11
<211> 40
<212> DNA
<213> Artificial

<220>
<223> Primer Sequence

<400> 11
caaggaatat gacgcgtacc ctcgaggcag aaggcggcgg 40

<210> 12
<211> 37
<212> DNA

REN-01-032-Util.ST25.txt

<213> Artificial

<220>

<223> Primer Sequence

<400> 12

atgcatgtta acatgtctac ttgtcctac ttcgccg

37

<210> 13

<211> 33

<212> DNA

<213> Artificial

<220>

<223> Primer Sequence

<400> 13

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33

<210> 14

<211> 30

<212> DNA

<213> Artificial

<220>

<223> Primer Sequence

<400> 14

agatctatgc attaccgctg gtaccgcagc

30

<210> 15

<211> 2073

<212> PRT

<213> Schizosaccharomyces pombe

<400> 15

Met Val Glu Ala Glu Gln Val His Gln Ser Leu Arg Ser Leu Val Leu
 1 5 10 15

Ser Tyr Ala His Phe Ser Pro Ser Ile Leu Ile Pro Ala Ser Gln Tyr
 20 25 30

Leu Leu Ala Ala Gln Leu Arg Asp Glu Phe Leu Ser Leu His Pro Ala
 35 40 45

Pro Ser Ala Glu Ser Val Glu Lys Glu Gly Ala Glu Leu Glu Phe Glu
 50 55 60

His Glu Leu His Leu Leu Ala Gly Phe Leu Gly Leu Ile Ala Ala Lys
 65 70 75 80

Glu Glu Glu Thr Pro Gly Gln Tyr Thr Gln Leu Leu Arg Ile Ile Thr
 85 90 95

Leu Glu Phe Glu Arg Thr Phe Leu Ala Gly Asn Glu Val His Ala Val
 100 105 110

REN-01-032-util.ST25.txt

Val His Ser Leu Gly Leu Asn Ile Pro Ala Gln Lys Asp Val Val Arg
 115 120 125
 Phe Tyr Tyr His Ser Cys Ala Leu Ile Gly Gln Thr Thr Lys Phe His
 130 135 140
 Gly Ser Ala Leu Leu Asp Glu Ser Ser Val Lys Leu Ala Ala Ile Phe
 145 150 155 160
 Gly Gly Gln Gly Tyr Glu Asp Tyr Phe Asp Glu Leu Ile Glu Leu Tyr
 165 170 175
 Glu Val Tyr Ala Pro Phe Ala Ala Glu Leu Ile Gln Val Leu Ser Lys
 180 185 190
 His Leu Phe Thr Leu Ser Gln Asn Glu Gln Ala Ser Lys Val Tyr Ser
 195 200 205
 Lys Gly Leu Asn Val Leu Asp Trp Leu Ala Gly Glu Arg Pro Glu Arg
 210 215 220
 Asp Tyr Leu Val Ser Ala Pro Val Ser Leu Pro Leu Val Gly Leu Thr
 225 230 235 240
 Gln Leu Val His Phe Ser Val Thr Ala Gln Ile Leu Gly Leu Asn Pro
 245 250 255
 Gly Glu Leu Ala Ser Arg Phe Ser Ala Ala Ser Gly His Ser Gln Gly
 260 265 270
 Ile Val Val Ala Ala Ala Val Ser Ala Ser Thr Asp Ser Ala Ser Phe
 275 280 285
 Met Glu Asn Ala Lys Val Ala Leu Thr Thr Leu Phe Trp Ile Gly Val
 290 295 300
 Arg Ser Gln Gln Thr Phe Pro Thr Thr Thr Leu Pro Pro Ser Val Val
 305 310 315 320
 Ala Asp Ser Leu Ala Ser Ser Glu Gly Asn Pro Thr Pro Met Leu Ala
 325 330 335
 Val Arg Asp Leu Pro Ile Glu Thr Leu Asn Lys His Ile Glu Thr Thr
 340 345 350
 Asn Thr His Leu Pro Glu Asp Arg Lys Val Ser Leu Ser Leu Val Asn
 355 360 365
 Gly Pro Arg Ser Phe Val Val Ser Gly Pro Ala Arg Ser Leu Tyr Gly
 370 375 380

REN-01-032-Util.ST25.txt

Leu Asn Leu Ser Leu Arg Lys Glu Lys Ala Asp Gly Gln Asn Gln Ser
 385 390 395 400

Arg Ile Pro His Ser Lys Arg Lys Leu Arg Phe Ile Asn Arg Phe Leu
 405 410 415

Ser Ile Ser Val Pro Phe His Ser Pro Tyr Leu Ala Pro Val Arg Ser
 420 425 430

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

Pro Val Tyr Ser Thr Asp Asp Ala Gly Asp Leu Arg Phe Glu Gln Pro
 450 455 460

Ser Lys Leu Leu Leu Ala Leu Ala Val Met Ile Thr Glu Lys Val Val
 465 470 475 480

His Trp Glu Glu Ala Cys Gly Phe Pro Asp Val Thr His Ile Ile Asp
 485 490 495

Phe Gly Pro Gly Gly Ile Ser Gly Val Gly Ser Leu Thr Arg Ala Asn
 500 505 510

Lys Asp Gly Gln Gly Val Arg Val Ile Val Ala Asp Ser Phe Glu Ser
 515 520 525

Leu Asp Met Gly Ala Lys Phe Glu Ile Phe Asp Arg Asp Ala Lys Ser
 530 535 540

Ile Glu Phe Ala Pro Asn Trp Val Lys Leu Tyr Ser Pro Lys Leu Val
 545 550 555 560

Lys Asn Lys Leu Gly Arg Val Tyr Val Asp Thr Arg Leu Ser Arg Met
 565 570 575

Leu Gly Leu Pro Pro Leu Trp Val Ala Gly Met Thr Pro Thr Ser Val
 580 585 590

Pro Trp Gln Phe Cys Ser Ala Ile Ala Lys Ala Gly Phe Thr Tyr Glu
 595 600 605

Leu Ala Gly Gly Gly Tyr Phe Asp Pro Lys Met Met Arg Glu Ala Ile
 610 615 620

His Lys Leu Ser Leu Asn Ile Pro Pro Gly Ala Gly Ile Cys Val Asn
 625 630 635 640

Val Ile Tyr Ile Asn Pro Arg Thr Tyr Ala Trp Gln Ile Pro Leu Ile
 645 650 655

REN-01-032-Util.ST25.txt

Arg Asp Met Val Ala Glu Gly Tyr Pro Ile Arg Gly Val Thr Ile Ala
660 665 670

Ala Gly Ile Pro Ser Leu Glu Val Ala Asn Glu Leu Ile Ser Thr Leu
675 680 685

Gly Val Gln Tyr Leu Cys Leu Lys Pro Gly Ser Val Glu Ala Val Asn
690 695 700

Ala Val Ile Ser Ile Ala Lys Ala Asn Pro Thr Phe Pro Ile Val Leu
705 710 715 720

Gln Trp Thr Gly Gly Arg Ala Gly Gly His His Ser Phe Glu Asp Phe
725 730 735

His Ser Pro Ile Leu Leu Thr Tyr Ser Ala Ile Arg Arg Cys Asp Asn
740 745 750

Ile Val Leu Ile Ala Gly Ser Gly Phe Gly Gly Ala Asp Asp Thr Glu
755 760 765

Pro Tyr Leu Thr Gly Glu Trp Ser Ala Ala Phe Lys Leu Pro Pro Met
770 775 780

Pro Phe Asp Gly Ile Leu Phe Gly Ser Arg Leu Met Val Ala Lys Glu
785 790 795 800

Ala His Thr Ser Leu Ala Ala Lys Glu Ala Ile Val Ala Ala Lys Gly
805 810 815

Val Asp Asp Ser Glu Trp Glu Lys Thr Tyr Asp Gly Pro Thr Gly Gly
820 825 830

Ile Val Thr Val Leu Ser Glu Leu Gly Glu Pro Ile His Lys Leu Ala
835 840 845

Thr Arg Gly Ile Met Phe Trp Lys Glu Leu Asp Asp Thr Ile Phe Ser
850 855 860

Leu Pro Arg Pro Lys Arg Leu Pro Ala Leu Leu Ala Lys Lys Gln Tyr
865 870 875 880

Ile Ile Lys Arg Leu Asn Asp Asp Phe Gln Lys Val Tyr Phe Pro Ala
885 890 895

His Ile Val Glu Gln Val Ser Pro Glu Lys Phe Lys Phe Glu Ala Val
900 905 910

Asp Ser Val Glu Asp Met Thr Tyr Ala Glu Leu Leu Tyr Arg Ala Ile
915 920 925

REN-01-032-Util.ST25.txt

Asp Leu Met Tyr Val Thr Lys Glu Lys Arg Trp Ile Asp Val Thr Leu
 930 935 940

Arg Thr Phe Thr Gly Lys Leu Met Arg Arg Ile Glu Glu Arg Phe Thr
 945 950 955 960

Gln Asp Val Gly Lys Thr Thr Leu Ile Glu Asn Phe Glu Asp Leu Asn
 965 970 975

Asp Pro Tyr Pro Val Ala Ala Arg Phe Leu Asp Ala Tyr Pro Glu Ala
 980 985 990

Ser Thr Gln Asp Leu Asn Thr Gln Asp Ala Gln Phe Phe Tyr Ser Leu
 995 1000 1005

Cys Ser Asn Pro Phe Gln Lys Pro Val Pro Phe Ile Pro Ala Ile
 1010 1015 1020

Asp Asp Thr Phe Glu Phe Tyr Phe Lys Lys Asp Ser Leu Trp Gln
 1025 1030 1035

Ser Glu Asp Leu Ala Ala Val Val Gly Glu Asp Val Gly Arg Val
 1040 1045 1050

Ala Ile Leu Gln Gly Pro Met Ala Ala Lys His Ser Thr Lys Val
 1055 1060 1065

Asn Glu Pro Ala Lys Glu Leu Leu Asp Gly Ile Asn Glu Thr His
 1070 1075 1080

Ile Gln His Phe Ile Lys Lys Phe Tyr Ala Gly Asp Glu Lys Lys
 1085 1090 1095

Ile Pro Ile Val Glu Tyr Phe Gly Gly Val Pro Pro Val Asn Val
 1100 1105 1110

Ser His Lys Ser Leu Glu Ser Val Ser Val Thr Glu Glu Ala Gly
 1115 1120 1125

Ser Lys Val Tyr Lys Leu Pro Glu Ile Gly Ser Asn Ser Ala Leu
 1130 1135 1140

Pro Ser Lys Lys Leu Trp Phe Glu Leu Leu Ala Gly Pro Glu Tyr
 1145 1150 1155

Thr Trp Phe Arg Ala Ile Phe Thr Thr Gln Arg Val Ala Lys Gly
 1160 1165 1170

Trp Lys Leu Glu His Asn Pro Val Arg Arg Ile Phe Ala Pro Arg
 1175 1180 1185

REN-01-032-Util.ST25.txt

Tyr	Gly	Gln	Arg	Ala	Val	Val	Lys	Gly	Lys	Asp	Asn	Asp	Thr	Val
	1190					1195					1200			
Val	Glu	Leu	Tyr	Glu	Thr	Gln	Ser	Gly	Asn	Tyr	Val	Leu	Ala	Ala
	1205					1210					1215			
Arg	Leu	Ser	Tyr	Asp	Gly	Glu	Thr	Ile	Val	Val	Ser	Met	Phe	Glu
	1220					1225					1230			
Asn	Arg	Asn	Ala	Leu	Lys	Lys	Glu	Val	His	Leu	Asp	Phe	Leu	Phe
	1235					1240					1245			
Lys	Tyr	Glu	Pro	Ser	Ala	Gly	Tyr	Ser	Pro	Val	Ser	Glu	Ile	Leu
	1250					1255					1260			
Asp	Gly	Arg	Asn	Asp	Arg	Ile	Lys	His	Phe	Tyr	Trp	Ala	Leu	Trp
	1265					1270					1275			
Phe	Gly	Glu	Glu	Pro	Tyr	Pro	Glu	Asn	Ala	Ser	Ile	Thr	Asp	Thr
	1280					1285					1290			
Phe	Thr	Gly	Pro	Glu	Val	Thr	Val	Thr	Gly	Asn	Met	Ile	Glu	Asp
	1295					1300					1305			
Phe	Cys	Arg	Thr	Val	Gly	Asn	His	Asn	Glu	Ala	Tyr	Thr	Lys	Arg
	1310					1315					1320			
Ala	Ile	Arg	Lys	Arg	Met	Ala	Pro	Met	Asp	Phe	Ala	Ile	Val	Val
	1325					1330					1335			
Gly	Trp	Gln	Ala	Ile	Thr	Lys	Ala	Ile	Phe	Pro	Lys	Ala	Ile	Asp
	1340					1345					1350			
Gly	Asp	Leu	Leu	Arg	Leu	Val	His	Leu	Ser	Asn	Ser	Phe	Arg	Met
	1355					1360					1365			
Val	Gly	Ser	His	Ser	Leu	Met	Glu	Gly	Asp	Lys	Val	Thr	Thr	Ser
	1370					1375					1380			
Ala	Ser	Ile	Ile	Ala	Ile	Leu	Asn	Asn	Asp	Ser	Gly	Lys	Thr	Val
	1385					1390					1395			
Thr	Val	Lys	Gly	Thr	Val	Tyr	Arg	Asp	Gly	Lys	Glu	Val	Ile	Glu
	1400					1405					1410			
Val	Ile	Ser	Arg	Phe	Leu	Tyr	Arg	Gly	Thr	Phe	Thr	Asp	Phe	Glu
	1415					1420					1425			
Asn	Thr	Phe	Glu	His	Thr	Gln	Glu	Thr	Pro	Met	Gln	Leu	Thr	Leu
	1430					1435					1440			

REN-01-032-Util.ST25.txt

Ala Thr	Pro Lys Asp Val	Ala Val Leu Gln Ser	Lys Ser Trp Phe
1445		1450	1455
Gln Leu	Leu Asp Pro Ser	Gln Asp Leu Ser Gly	Ser Ile Leu Thr
1460		1465	1470
Phe Arg	Leu Asn Ser Tyr	Val Arg Phe Lys Asp	Gln Lys Val Lys
1475		1480	1485
Ser Ser	Val Glu Thr Lys	Gly Ile Val Leu Ser	Glu Leu Pro Ser
1490		1495	1500
Lys Ala	Ile Ile Gln Val	Ala Ser Val Asp Phe	Gln Ser Val Asp
1505		1510	1515
Cys His	Gly Asn Pro Val	Ile Glu Phe Leu Lys	Arg Asn Gly Lys
1520		1525	1530
Pro Ile	Glu Gln Pro Val	Glu Phe Glu Asn Gly	Gly Tyr Ser Val
1535		1540	1545
Ile Gln	Val Met Asp Glu	Gly Tyr Ser Pro Val	Phe Val Thr Pro
1550		1555	1560
Pro Thr	Asn Ser Pro Tyr	Ala Glu Val Ser Gly	Asp Tyr Asn Pro
1565		1570	1575
Ile His	Val Ser Pro Thr	Phe Ala Ala Phe Val	Glu Leu Pro Gly
1580		1585	1590
Thr His	Gly Ile Thr His	Gly Met Tyr Thr Ser	Ala Ala Ala Arg
1595		1600	1605
Arg Phe	Val Glu Thr Tyr	Ala Ala Gln Asn Val	Pro Glu Arg Val
1610		1615	1620
Lys His	Tyr Glu Val Thr	Phe Val Asn Met Val	Leu Pro Asn Thr
1625		1630	1635
Glu Leu	Ile Thr Lys Leu	Ser His Thr Gly Met	Ile Asn Gly Arg
1640		1645	1650
Lys Ile	Ile Lys Val Glu	Val Leu Asn Gln Glu	Thr Ser Glu Pro
1655		1660	1665
Val Leu	Val Gly Thr Ala	Glu Val Glu Gln Pro	Val Ser Ala Tyr
1670		1675	1680
Val Phe	Thr Gly Gln Gly	Ser Gln Glu Gln Gly	Met Gly Met Asp
1685		1690	1695

REN-01-032-Util.ST25.txt

Leu Tyr Ala Ser Ser Pro Val Ala Arg Lys Ile Trp Asp Ser Ala
1700 1705 1710

Asp Lys His Phe Leu Thr Asn Tyr Gly Phe Ser Ile Ile Asp Ile
1715 1720 1725

Val Lys His Asn Pro His Ser Ile Thr Ile His Phe Gly Gly Ser
1730 1735 1740

Lys Gly Lys Lys Ile Arg Asp Asn Tyr Met Ala Met Ala Tyr Glu
1745 1750 1755

Lys Leu Met Glu Asp Gly Thr Ser Lys Val Val Pro Val Phe Glu
1760 1765 1770

Thr Ile Thr Lys Asp Ser Thr Ser Phe Ser Phe Thr His Pro Ser
1775 1780 1785

Gly Leu Leu Ser Ala Thr Gln Phe Thr Gln Pro Ala Leu Thr Leu
1790 1795 1800

Met Glu Lys Ser Ala Phe Glu Asp Met Arg Ser Lys Gly Leu Val
1805 1810 1815

Gln Asn Asp Cys Ala Phe Ala Gly His Ser Leu Gly Glu Tyr Ser
1820 1825 1830

Ala Leu Ser Ala Met Gly Asp Val Leu Ser Ile Glu Ala Leu Val
1835 1840 1845

Asp Leu Val Phe Leu Arg Gly Leu Thr Met Gln Asn Ala Val His
1850 1855 1860

Arg Asp Glu Leu Gly Arg Ser Asp Tyr Gly Met Val Ala Ala Asn
1865 1870 1875

Pro Ser Arg Val Ser Ala Ser Phe Thr Asp Ala Ala Leu Arg Phe
1880 1885 1890

Ile Val Asp His Ile Gly Gln Gln Thr Asn Leu Leu Leu Glu Ile
1895 1900 1905

Val Asn Tyr Asn Val Glu Asn Gln Gln Tyr Val Val Ser Gly Asn
1910 1915 1920

Leu Leu Ser Leu Ser Thr Leu Gly His Val Leu Asn Phe Leu Lys
1925 1930 1935

Val Gln Lys Ile Asp Phe Glu Lys Leu Lys Glu Thr Leu Thr Ile
1940 1945 1950

REN-01-032-Util.ST25.txt
 Glu Gln Leu Lys Glu Gln Leu Thr Asp Ile Val Glu Ala Cys His
 1955 1960 1965

Ala Lys Thr Leu Glu Gln Gln Lys Lys Thr Gly Arg Ile Glu Leu
 1970 1975 1980

Glu Arg Gly Tyr Ala Thr Ile Pro Leu Lys Ile Asp Val Pro Phe
 1985 1990 1995

His Ser Ser Phe Leu Arg Gly Gly Val Arg Met Phe Arg Glu Tyr
 2000 2005 2010

Leu Val Lys Lys Ile Phe Pro His Gln Ile Asn Val Ala Lys Leu
 2015 2020 2025

Arg Gly Lys Tyr Ile Pro Asn Leu Thr Ala Lys Pro Phe Glu Ile
 2030 2035 2040

Ser Lys Glu Tyr Phe Gln Asn Val Tyr Asp Leu Thr Gly Ser Gln
 2045 2050 2055

Arg Ile Lys Lys Ile Leu Gln Asn Trp Asp Glu Tyr Glu Ser Ser
 2060 2065 2070

<210> 16
 <211> 6232
 <212> DNA
 <213> Schizosaccharomyces pombe

<400> 16
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 gttaaacctg agtgttccca cgcgatagta aaggatcaag ttaactagaa ccaacaacta 180
 aagcaggtgt tggagttttg ttaaaccatt tgaataatga gaccagaagt tgagcaggag 240
 cttgctcata ctttattatt ggagttgctt gcataccagt ttgcatctcc tgtccggttg 300
 attgagacgc aagatgtaat tctttctcct ccagtatcgg ctgaacgtat cgtcgaaatt 360
 ggacctagtc ctaccttagc tggatatggc aagcgtacct tgaaattgaa atatgagaac 420
 atggatgccg ctttaagtat taatcgtgaa gttctttgct actctaaaga tgctcgtgaa 480
 atctattaca actttgagga cgaggttgct gatgaacctg ccgaagcccc agcttcaacc 540
 agctccactc caaagggtga aactgctgct gctgccgctc ccgctgccac gccagcccct 600
 gccccagcac aaacatcagc cccagctgct gctttacctg acgagcctcc caaagctctt 660
 gaggtacttc atactcttgt tgcccaaaag ttgaagaaaa gcatcgagga agtctcccct 720
 caaaaatcta tcaaagattt ggttggcggt aagtccactt tgcaaaacga aattcttggt 780
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REN-01-032-Utl1.ST25.txt

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REN-01-032-Uti1.ST25.txt

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REN-01-032-Uti1.ST25.txt

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<211> 1842

<212> PRT

<213> Schizosaccharomyces pombe

<400> 17

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Asp Val Ile Leu Ser Pro Pro Val Ser Ala Glu Arg Ile Val Glu Ile
35 40 45

Gly Pro Ser Pro Thr Leu Ala Gly Met Ala Lys Arg Thr Leu Lys Leu
50 55 60

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

REN-01-032-Uti1.ST25.txt

Cys Tyr Ser Lys Asp Ala Arg Glu Ile Tyr Tyr Asn Phe Glu Asp Glu
85 90 95

Val Ala Asp Glu Pro Ala Glu Ala Pro Ala Ser Thr Ser Ser Thr Pro
100 105 110

Lys Val Glu Thr Ala Ala Ala Ala Ala Pro Ala Ala Thr Pro Ala Pro
115 120 125

Ala Pro Ala Gln Thr Ser Ala Pro Ala Ala Ala Leu Pro Asp Glu Pro
130 135 140

Pro Lys Ala Leu Glu Val Leu His Thr Leu Val Ala Gln Lys Leu Lys
145 150 155 160

Lys Ser Ile Glu Glu Val Ser Pro Gln Lys Ser Ile Lys Asp Leu Val
165 170 175

Gly Gly Lys Ser Thr Leu Gln Asn Glu Ile Leu Gly Asp Leu Gln Lys
180 185 190

Glu Phe Gly Ala Thr Pro Glu Lys Pro Glu Glu Val Pro Leu Asp Glu
195 200 205

Leu Gly Ala Ile Met Gln Ser Ser Phe Asn Gly Ser Leu Gly Lys Gln
210 215 220

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

Phe Asn Asn Ser Ala Val Arg Gly Tyr Leu Gly Asn Arg Tyr Gly Leu
245 250 255

Gly Pro Gly Arg Leu Glu Ser Val Leu Leu Leu Ala Leu Thr Met Glu
260 265 270

Pro Ala Ser Arg Leu Gly Ser Glu Ala Asp Ala Lys Ala Trp Leu Asp
275 280 285

Ser Val Ala Gln Lys Tyr Ala Ala Arg Asn Gly Val Thr Leu Ser Ser
290 295 300

Pro Thr Ala Glu Gly Gly Ser Ser Ser Gly Ser Ala Ala Val Ile Asp
305 310 315 320

Glu Glu Thr Phe Lys Lys Leu Thr Lys Asn Asn Thr Met Leu Val Thr
325 330 335

Gln Gln Leu Glu Leu Phe Ala Arg Tyr Leu Asn Lys Asp Leu Arg Ala
340 345 350

REN-01-032-Util.ST25.txt

Gly Gln Lys Ala Gln Val Ala Glu Lys Val Ile Ser Asp Thr Leu Arg
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Ala Gln Leu Asp Leu Trp Asn Glu Glu His Gly Glu Phe Tyr Ala Ser
 370 375 380

Gly Ile Ala Pro Ile Phe Ser Pro Leu Lys Ala Arg Val Tyr Asp Ser
 385 390 395 400

Asp Trp Asn Trp Ala Arg Gln Asp Ala Leu Lys Met Phe Phe Asp Ile
 405 410 415

Ile Phe Gly Arg Leu Arg His Val Asp Thr Glu Ile Val Ala Arg Cys
 420 425 430

Ile Ser Val Met Asn Arg Ser Asn Pro Thr Leu Leu Glu Phe Met Gln
 435 440 445

Tyr His Ile Asp His Cys Pro Ala Glu Lys Gly Glu Thr Tyr Gln Leu
 450 455 460

Ala Lys Thr Leu Gly Gln Gln Leu Ile Asp Asn Cys Lys Ser Val Ile
 465 470 475 480

Asp Ala Pro Pro Val Phe Lys Asn Val Asn His Pro Thr Ala Pro Ser
 485 490 495

Thr Thr Ile Asp Glu Arg Gly Asn Leu Asn Tyr Glu Glu Ile Pro Arg
 500 505 510

Pro Gly Val Arg Lys Leu Thr His Tyr Val Thr Glu Met Ala Lys Gly
 515 520 525

Gly Lys Leu Pro Thr Glu Ser Lys Asn Lys Ala Lys Val Gln Asn Asp
 530 535 540

Leu Ala Arg Ile Tyr Arg Ile Ile Lys Ser Gln Asn Lys Met Ser Arg
 545 550 555 560

Ser Ser Lys Leu Gln Ile Lys Gln Leu Tyr Gly Gln Val Leu His Ala
 565 570 575

Leu Ser Leu Pro Leu Pro Ser Ser Asn Asp Glu Gln Thr Pro Val Lys
 580 585 590

Glu Thr Ile Pro Phe Leu His Ile Arg Lys Lys Ser Val Asp Gly Asn
 595 600 605

Trp Glu Phe Asn Lys Ser Leu Thr Gly Thr Tyr Leu Asp Val Leu Glu
 610 615 620

REN-01-032-util.ST25.txt

Ser Gly Ala Lys Asn Gly Ile Thr Tyr Gln Asp Lys Tyr Ala Leu Val
 625 630 635 640

Thr Gly Ala Gly Ala Gly Ser Ile Gly Ala Gln Ile Val Glu Gly Leu
 645 650 655

Leu Ala Gly Gly Ala Lys Val Val Val Thr Thr Ser Arg Phe Ser Arg
 660 665 670

Lys Val Thr Glu Phe Tyr Gln Ser Leu Tyr Thr Arg His Gly Ser Arg
 675 680 685

Gly Ser Cys Leu Ile Val Val Pro Phe Asn Gln Gly Ser Lys Thr Asp
 690 695 700

Val Glu Ala Leu Ile Asp Tyr Ile Tyr Asp Glu Lys Lys Gly Leu Gly
 705 710 715 720

Trp Asn Leu Asp Tyr Ile Val Pro Phe Ala Ala Ile Pro Glu Asn Gly
 725 730 735

Arg Glu Ile Asp Gly Ile Asp Ser Arg Ser Glu Phe Ala His Arg Ile
 740 745 750

Met Leu Thr Asn Ile Leu Arg Leu Leu Gly Ala Val Lys Ser Gln Lys
 755 760 765

Ala Ser Arg Gly Met Asp Thr Arg Pro Ala Gln Val Ile Leu Pro Leu
 770 775 780

Ser Pro Asn His Gly Thr Phe Gly Asn Asp Gly Leu Tyr Ser Glu Ser
 785 790 795 800

Lys Leu Gly Leu Glu Thr Leu Phe Asn Arg Trp Tyr Ser Glu Ser Trp
 805 810 815

Ala Asn Tyr Leu Thr Ile Cys Gly Ala Val Ile Gly Trp Thr Arg Gly
 820 825 830

Thr Gly Leu Met Ala Pro Asn Asn Ile Val Ser Gln Gly Ile Glu Lys
 835 840 845

Tyr Gly Val Arg Thr Phe Ser Gln Ser Glu Met Ala Phe Asn Ile Leu
 850 855 860

Gly Leu Met Ser Gln Lys Val Val Asp Leu Cys Gln Ser Glu Pro Ile
 865 870 875 880

Tyr Ala Asn Leu Asn Gly Gly Leu Glu Leu Leu Pro Asp Leu Lys Asp
 885 890 895

REN-01-032-Uti1.ST25.txt

Leu Ser Thr Arg Leu Arg Thr Glu Leu Leu Glu Thr Ala Glu Ile Arg
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 Arg Ala Val Ala Ala Glu Thr Ala Phe Asp His Ser Ile Thr Asn Gly
 915 920 925
 Pro Asp Ser Glu Ala Val Phe Gln Lys Thr Ala Ile Gln Pro Arg Ala
 930 935 940
 Asn Leu Lys Phe Asn Phe Pro Lys Leu Lys Pro Tyr Glu Ala Leu Ser
 945 950 955 960
 His Leu Ser Asp Leu Arg Gly Met Val Asp Leu Glu Lys Val Pro Val
 965 970 975
 Val Thr Gly Phe Ser Glu Val Gly Pro Trp Gly Asn Ser Arg Thr Arg
 980 985 990
 Trp Asp Met Glu Cys Tyr Gly Glu Phe Ser Leu Glu Gly Cys Val Glu
 995 1000 1005
 Ile Ala Trp Ile Met Gly Leu Ile Lys Asn Phe Asn Gly Lys Gly
 1010 1015 1020
 Lys Asp Gly Lys Pro Tyr Ser Gly Trp Val Asp Thr Lys Thr Gly
 1025 1030 1035
 Glu Pro Val Asp Asp Lys Asp Val Lys Ala Lys Tyr Glu Lys Tyr
 1040 1045 1050
 Ile Leu Glu His Cys Gly Ile Arg Ile Ile Glu Ala Glu Leu Phe
 1055 1060 1065
 His Gly Tyr Asn Pro Glu Lys Lys Glu Leu Leu Gln Glu Val Val
 1070 1075 1080
 Ile Asp His Asp Leu Glu Pro Phe Glu Ala Ser Lys Glu Ala Ala
 1085 1090 1095
 His Glu Phe Lys Leu Arg His Gly Asp Gln Val Glu Ile Phe Glu
 1100 1105 1110
 Ile Pro Asp Ser Thr Glu Trp Ser Val Arg Phe Lys Arg Gly Thr
 1115 1120 1125
 Ser Met Leu Ile Pro Lys Ala Leu Arg Phe Asp Arg Phe Val Ala
 1130 1135 1140
 Gly Gln Ile Pro Leu Gly Trp Asp Pro Lys Arg Tyr Gly Ile Pro
 1145 1150 1155

REN-01-032-util.ST25.txt

Asp Asp Ile Ile Ser Gln Val Asp Pro Thr Thr Leu Tyr Val Leu
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 Val Ser Thr Val Glu Ala Leu Val Ala Ser Gly Ile Thr Asp Pro
 1175 1180 1185
 Tyr Glu Cys Tyr Lys Tyr Ile His Val Ser Glu Leu Gly Asn Thr
 1190 1195 1200
 Val Gly Ser Gly Ile Gly Gly Met Ser Ala Leu Arg Gly Met Tyr
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 Lys Asp Arg Trp Thr Asp Lys Pro Val Gln Lys Asp Ile Leu Gln
 1220 1225 1230
 Glu Ser Phe Ile Asn Thr Ala Asn Ala Trp Ile Asn Met Leu Leu
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 1250 1255 1260
 Thr Ala Val Glu Ser Val Asp Ala Ala Val Asp Leu Ile Thr Ser
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 Gly Lys Ala Arg Ile Cys Ile Ser Gly Gly Tyr Asp Asp Phe Ser
 1280 1285 1290
 Glu Glu Gly Ser Tyr Glu Phe Ala Asn Met Gly Ala Thr Ser Asn
 1295 1300 1305
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 Arg Pro Ala Thr Ser Thr Arg Asp Gly Phe Met Glu Ser Gln Gly
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 Ala Gly Val Gln Ile Ile Met Gln Ala Lys Leu Ala Ile Glu Met
 1340 1345 1350
 Gly Val Pro Ile His Gly Ile Val Gly Tyr Val Ser Thr Ala Met
 1355 1360 1365
 Asp Lys Gln Gly Arg Ser Val Pro Ala Pro Gly Gln Gly Ile Leu
 1370 1375 1380
 Thr Gly Ala Arg Glu Ile Ala Thr Lys Thr Pro Leu Pro Ile Val
 1385 1390 1395
 Asp Leu Lys Phe Arg Ser Arg Gln Leu Gln Arg Arg Arg Ser Gln
 1400 1405 1410

REN-01-032-Uti1.ST25.txt

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 Tyr Arg Ile Glu Arg Ile Asn Val Ile Lys Glu Glu Val Val Arg
 1445 1450 1455
 Gln Glu Lys Glu Ala Leu Asn Thr Phe Gly Asn Glu Phe Trp Lys
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 Arg Asp Pro Thr Ile Ala Pro Ile Arg Gly Ala Leu Ala Val Trp
 1475 1480 1485
 Gly Leu Thr Ile Asp Asp Leu Gly Val Ala Ser Phe His Gly Thr
 1490 1495 1500
 Ser Thr Lys Ala Asn Glu Lys Asn Glu Cys Asp Val Ile Asp Ser
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 Gln Leu Thr His Leu Gly Arg Ser Lys Gly Asn Ala Val Tyr Gly
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 Val Phe Gln Lys Tyr Leu Thr Gly His Ser Lys Gly Gly Ala Gly
 1535 1540 1545
 Ala Trp Met Leu Asn Gly Ala Leu Gln Ile Leu Arg Ser Gly Phe
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 Val Pro Gly Asn Arg Asn Ala Asp Asn Ile Asp Glu Tyr Leu Ala
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 Arg Phe Asp Arg Val Met Phe Pro Ser Glu Gly Ile Gln Thr Asp
 1580 1585 1590
 Gly Ile Lys Ala Ala Ser Val Thr Ala Phe Gly Phe Gly Gln Val
 1595 1600 1605
 Gly Gly Gln Val Ile Val Ile His Pro Asp Tyr Ile Tyr Gly Val
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 Ile Asp Glu Ala Thr Tyr Asn Ala Tyr Lys Ala Lys Thr Ala Ala
 1625 1630 1635
 Arg Tyr Lys Ala Ser Tyr Arg Tyr Thr His Asp Ala Leu Val Tyr
 1640 1645 1650
 Asn Asn Leu Val Arg Ala Lys Asp Ser Pro Pro Tyr Thr Lys Glu
 1655 1660 1665

REN-01-032-util.ST25.txt

Gln Glu Lys Ala Val Tyr Leu Asn Pro Leu Ala Arg Ala Ser Lys
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Ser Lys Ala Gly Thr Trp Thr Phe Pro Ala Thr Leu Pro Ala Glu
1685 1690 1695

Ser Asp Ile Ser Lys Thr Asn Glu Thr Thr Arg Thr Leu Gln Ser
1700 1705 1710

Leu Thr Thr Ser Leu Thr Asn Ser Asn Glu Asn Val Gly Val Asp
1715 1720 1725

Val Glu Leu Val Ser Ala Ile Ser Ile Asp Asn Glu Thr Phe Ile
1730 1735 1740

Glu Arg Asn Phe Thr Asp Thr Glu Arg Lys Tyr Cys Phe Ala Ala
1745 1750 1755

Pro Asn Pro Gln Ala Ser Phe Ala Gly Arg Trp Ser Ala Lys Glu
1760 1765 1770

Ala Val Phe Lys Ser Leu Gly Ile Ser Gly Lys Gly Ala Ala Ala
1775 1780 1785

Pro Leu Lys Asp Ile Glu Ile Ile Ser Ser Glu Ser Gly Ala Pro
1790 1795 1800

Glu Val Val Leu His Gly Glu Ala Ala Lys Ala Ala Thr Thr Ala
1805 1810 1815

Gly Val Lys Ser Val Ser Val Ser Ile Ser His Asp Asp Asn Gln
1820 1825 1830

Ser Val Ser Val Ala Leu Ala His Lys
1835 1840

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<400> 18

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Leu Gln Glu Gln Phe Asn Lys Ile Leu Pro Glu Pro Thr Glu Gly Phe
35 40 45

REN-01-032-Uti1.ST25.txt

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 Asp Gln Val Leu Asn Leu Cys Leu Thr Glu Phe Glu Asn Cys Tyr Leu
 85 90 95
 Glu Gly Asn Asp Ile His Ala Leu Ala Ala Lys Leu Leu Gln Glu Asn
 100 105 110
 Asp Thr Thr Leu Val Lys Thr Lys Glu Leu Ile Lys Asn Tyr Ile Thr
 115 120 125
 Ala Arg Ile Met Ala Lys Arg Pro Phe Asp Lys Lys Ser Asn Ser Ala
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 Leu Phe Arg Ala Val Gly Glu Gly Asn Ala Gln Leu Val Ala Ile Phe
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 Gly Gly Gln Gly Asn Thr Asp Asp Tyr Phe Glu Glu Leu Arg Asp Leu
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 Tyr Gln Thr Tyr His Val Leu Val Gly Asp Leu Ile Lys Phe Ser Ala
 180 185 190
 Glu Thr Leu Ser Glu Leu Ile Arg Thr Thr Leu Asp Ala Glu Lys Val
 195 200 205
 Phe Thr Gln Gly Leu Asn Ile Leu Glu Trp Leu Glu Asn Pro Ser Asn
 210 215 220
 Thr Pro Asp Lys Asp Tyr Leu Leu Ser Ile Pro Ile Ser Cys Pro Leu
 225 230 235 240
 Ile Gly Val Ile Gln Leu Ala His Tyr Val Val Thr Ala Lys Leu Leu
 245 250 255
 Gly Phe Thr Pro Gly Glu Leu Arg Ser Tyr Leu Lys Gly Ala Thr Gly
 260 265 270
 His Ser Gln Gly Leu Val Thr Ala Val Ala Ile Ala Glu Thr Asp Ser
 275 280 285
 Trp Glu Ser Phe Phe Val Ser Val Arg Lys Ala Ile Thr Val Leu Phe
 290 295 300
 Phe Ile Gly Val Arg Cys Tyr Glu Ala Tyr Pro Asn Thr Ser Leu Pro
 305 310 315 320

REN-01-032-Util.ST25.txt

Pro Ser Ile Leu Glu Asp Ser Leu Glu Asn Asn Glu Gly Val Pro Ser
 325 330 335
 Pro Met Leu Ser Ile Ser Asn Leu Thr Gln Glu Gln Val Gln Asp Tyr
 340 345 350
 Val Asn Lys Thr Asn Ser His Leu Pro Ala Gly Lys Gln Val Glu Ile
 355 360 365
 Ser Leu Val Asn Gly Ala Lys Asn Leu Val Val Ser Gly Pro Pro Gln
 370 375 380
 Ser Leu Tyr Gly Leu Asn Leu Thr Leu Arg Lys Ala Lys Ala Pro Ser
 385 390 395 400
 Gly Leu Asp Gln Ser Arg Ile Pro Phe Ser Glu Arg Lys Leu Lys Phe
 405 410 415
 Ser Asn Arg Phe Leu Pro Val Ala Ser Pro Phe His Ser His Leu Leu
 420 425 430
 Val Pro Ala Ser Asp Leu Ile Asn Lys Asp Leu Val Lys Asn Asn Val
 435 440 445
 Ser Phe Asn Ala Lys Asp Ile Gln Ile Pro Val Tyr Asp Thr Phe Asp
 450 455 460
 Gly Ser Asp Leu Arg Val Leu Ser Gly Ser Ile Ser Glu Arg Ile Val
 465 470 475 480
 Asp Cys Ile Ile Arg Leu Pro Val Lys Trp Glu Thr Thr Thr Gln Phe
 485 490 495
 Lys Ala Thr His Ile Leu Asp Phe Gly Pro Gly Gly Ala Ser Gly Leu
 500 505 510
 Gly Val Leu Thr His Arg Asn Lys Asp Gly Thr Gly Val Arg Val Ile
 515 520 525
 Val Ala Gly Thr Leu Asp Ile Asn Pro Asp Asp Asp Tyr Gly Phe Lys
 530 535 540
 Gln Glu Ile Phe Asp Val Thr Ser Asn Gly Leu Lys Lys Asn Pro Asn
 545 550 555 560
 Trp Leu Glu Glu Tyr His Pro Lys Leu Ile Lys Asn Lys Ser Gly Lys
 565 570 575
 Ile Phe Val Glu Thr Lys Phe Ser Lys Leu Ile Gly Arg Pro Pro Leu
 580 585 590

REN-01-032-util.ST25.txt

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 Ala Thr Thr Asn Ala Gly Tyr Thr Ile Glu Leu Ala Gly Gly Gly Tyr
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 625 630 635 640
 Ile Glu Lys Gly Ser Thr Phe Gly Ile Asn Leu Ile Tyr Val Asn Pro
 645 650 655
 Phe Met Leu Gln Trp Gly Ile Pro Leu Ile Lys Glu Leu Arg Ser Lys
 660 665 670
 Gly Tyr Pro Ile Gln Phe Leu Thr Ile Gly Ala Gly Val Pro Ser Leu
 675 680 685
 Glu Val Ala Ser Glu Tyr Ile Glu Thr Leu Gly Leu Lys Tyr Leu Gly
 690 695 700
 Leu Lys Pro Gly Ser Ile Asp Ala Ile Ser Gln Val Ile Asn Ile Ala
 705 710 715 720
 Lys Ala His Pro Asn Phe Pro Ile Ala Leu Gln Trp Thr Gly Gly Arg
 725 730 735
 Gly Gly Gly His His Ser Phe Glu Asp Ala His Thr Pro Met Leu Gln
 740 745 750
 Met Tyr Ser Lys Ile Arg Arg His Pro Asn Ile Met Leu Ile Phe Gly
 755 760 765
 Ser Gly Phe Gly Ser Ala Asp Asp Thr Tyr Pro Tyr Leu Thr Gly Glu
 770 775 780
 Trp Ser Thr Lys Phe Asp Tyr Pro Pro Met Pro Phe Asp Gly Phe Leu
 785 790 795 800
 Phe Gly Ser Arg Val Met Ile Ala Lys Glu Val Lys Thr Ser Pro Asp
 805 810 815
 Ala Lys Lys Cys Ile Ala Ala Cys Thr Gly Val Pro Asp Asp Lys Trp
 820 825 830
 Glu Gln Thr Tyr Lys Lys Pro Thr Gly Gly Ile Val Thr Val Arg Ser
 835 840 845
 Glu Met Gly Glu Pro Ile His Lys Ile Ala Thr Arg Gly Val Met Leu
 850 855 860

REN-01-032-Uti1.ST25.txt

Trp Lys Glu Phe Asp Glu Thr Ile Phe Asn Leu Pro Lys Asn Lys Leu
865 870 875 880

Val Pro Thr Leu Glu Ala Lys Arg Asp Tyr Ile Ile Ser Arg Leu Asn
885 890 895

Ala Asp Phe Gln Lys Pro Trp Phe Ala Thr Val Asn Gly Gln Ala Arg
900 905 910

Asp Leu Ala Thr Met Thr Tyr Glu Glu Val Ala Lys Arg Leu Val Glu
915 920 925

Leu Met Phe Ile Arg Ser Thr Asn Ser Trp Phe Asp Val Thr Trp Arg
930 935 940

Thr Phe Thr Gly Asp Phe Leu Arg Arg Val Glu Glu Arg Phe Thr Lys
945 950 955 960

Ser Lys Thr Leu Ser Leu Ile Gln Ser Tyr Ser Leu Leu Asp Lys Pro
965 970 975

Asp Glu Ala Ile Glu Lys Val Phe Asn Ala Tyr Pro Ala Ala Arg Glu
980 985 990

Gln Phe Leu Asn Ala Gln Asp Ile Asp His Phe Leu Ser Met Cys Gln
995 1000 1005

Asn Pro Met Gln Lys Pro Val Pro Phe Val Pro Val Leu Asp Arg
1010 1015 1020

Arg Phe Glu Ile Phe Phe Lys Lys Asp Ser Leu Trp Gln Ser Glu
1025 1030 1035

His Leu Glu Ala Val Val Asp Gln Asp Val Gln Arg Thr Cys Ile
1040 1045 1050

Leu His Gly Pro Val Ala Ala Gln Phe Thr Lys Val Ile Asp Glu
1055 1060 1065

Pro Ile Lys Ser Ile Met Asp Gly Ile His Asp Gly His Ile Lys
1070 1075 1080

Lys Leu Leu His Gln Tyr Tyr Gly Asp Asp Glu Ser Lys Ile Pro
1085 1090 1095

Ala Val Glu Tyr Phe Gly Gly Glu Ser Pro Val Asp Val Gln Ser
1100 1105 1110

Gln Val Asp Ser Ser Ser Val Ser Glu Asp Ser Ala Val Phe Lys
1115 1120 1125

REN-01-032-Util.ST25.txt

Ala Thr Ser Ser Thr Asp Glu Glu Ser Trp Phe Lys Ala Leu Ala
 1130 1135 1140
 Gly Ser Glu Ile Asn Trp Arg His Ala Ser Phe Leu Cys Ser Phe
 1145 1150 1155
 Ile Thr Gln Asp Lys Met Phe Val Ser Asn Pro Ile Arg Lys Val
 1160 1165 1170
 Phe Lys Pro Ser Gln Gly Met Val Val Glu Ile Ser Asn Gly Asn
 1175 1180 1185
 Thr Ser Ser Lys Thr Val Val Thr Leu Ser Glu Pro Val Gln Gly
 1190 1195 1200
 Glu Leu Lys Pro Thr Val Ile Leu Lys Leu Leu Lys Glu Asn Ile
 1205 1210 1215
 Ile Gln Met Glu Met Ile Glu Asn Arg Thr Met Asp Gly Lys Pro
 1220 1225 1230
 Val Ser Leu Pro Leu Leu Tyr Asn Phe Asn Pro Asp Asn Gly Phe
 1235 1240 1245
 Ala Pro Ile Ser Glu Val Met Glu Asp Arg Asn Gln Arg Ile Lys
 1250 1255 1260
 Glu Met Tyr Trp Lys Leu Trp Ile Asp Glu Pro Phe Asn Leu Asp
 1265 1270 1275
 Phe Asp Pro Arg Asp Val Ile Lys Gly Lys Asp Phe Glu Ile Thr
 1280 1285 1290
 Ala Lys Glu Val Tyr Asp Phe Thr His Ala Val Gly Asn Asn Cys
 1295 1300 1305
 Glu Asp Phe Val Ser Arg Pro Asp Arg Thr Met Leu Ala Pro Met
 1310 1315 1320
 Asp Phe Ala Ile Val Val Gly Trp Arg Ala Ile Ile Lys Ala Ile
 1325 1330 1335
 Phe Pro Asn Thr Val Asp Gly Asp Leu Leu Lys Leu Val His Leu
 1340 1345 1350
 Ser Asn Gly Tyr Lys Met Ile Pro Gly Ala Lys Pro Leu Gln Val
 1355 1360 1365
 Gly Asp Val Val Ser Thr Thr Ala Val Ile Glu Ser Val Val Asn
 1370 1375 1380

REN-01-032-Util.ST25.txt

Gln Pro Thr Gly Lys Ile Val Asp Val Val Gly Thr Leu Ser Arg
 1385 1390 1395
 Asn Gly Lys Pro Val Met Glu Val Thr Ser Ser Phe Phe Tyr Arg
 1400 1405 1410
 Gly Asn Tyr Thr Asp Phe Glu Asn Thr Phe Gln Lys Thr Val Glu
 1415 1420 1425
 Pro Val Tyr Gln Met His Ile Lys Thr Ser Lys Asp Ile Ala Val
 1430 1435 1440
 Leu Arg Ser Lys Glu Trp Phe Gln Leu Asp Asp Glu Asp Phe Asp
 1445 1455
 Leu Leu Asn Lys Thr Leu Thr Phe Glu Thr Glu Thr Glu Val Thr
 1460 1465 1470
 Phe Lys Asn Ala Asn Ile Phe Ser Ser Val Lys Cys Phe Gly Pro
 1475 1480 1485
 Ile Lys Val Glu Leu Pro Thr Lys Glu Thr Val Glu Ile Gly Ile
 1490 1495 1500
 Val Asp Tyr Glu Ala Gly Ala Ser His Gly Asn Pro Val Val Asp
 1505 1510 1515
 Phe Leu Lys Arg Asn Gly Ser Thr Leu Glu Gln Lys Val Asn Leu
 1520 1525 1530
 Glu Asn Pro Ile Pro Ile Ala Val Leu Asp Ser Tyr Thr Pro Ser
 1535 1540 1545
 Thr Asn Glu Pro Tyr Ala Arg Val Ser Gly Asp Leu Asn Pro Ile
 1550 1555 1560
 His Val Ser Arg His Phe Ala Ser Tyr Ala Asn Leu Pro Gly Thr
 1565 1570 1575
 Ile Thr His Gly Met Phe Ser Ser Ala Ser Val Arg Ala Leu Ile
 1580 1585 1590
 Glu Asn Trp Ala Ala Asp Ser Val Ser Ser Arg Val Arg Gly Tyr
 1595 1600 1605
 Thr Cys Gln Phe Val Asp Met Val Leu Pro Asn Thr Ala Leu Lys
 1610 1615 1620
 Thr Ser Ile Gln His Val Gly Met Ile Asn Gly Arg Lys Leu Ile
 1625 1630 1635

REN-01-032-Uti1.ST25.txt

Lys Phe Glu Thr Arg Asn Glu Asp Asp Val Val Val Leu Thr Gly
 1640 1645 1650
 Glu Ala Glu Ile Glu Gln Pro Val Thr Thr Phe Val Phe Thr Gly
 1655 1660 1665
 Gln Gly Ser Gln Glu Gln Gly Met Gly Met Asp Leu Tyr Lys Thr
 1670 1675 1680
 Ser Lys Ala Ala Gln Asp Val Trp Asn Arg Ala Asp Asn His Phe
 1685 1690 1695
 Lys Asp Thr Tyr Gly Phe Ser Ile Leu Asp Ile Val Ile Asn Asn
 1700 1705 1710
 Pro Val Asn Leu Thr Ile His Phe Gly Gly Glu Lys Gly Lys Arg
 1715 1720 1725
 Ile Arg Glu Asn Tyr Ser Ala Met Ile Phe Glu Thr Ile Val Asp
 1730 1735 1740
 Gly Lys Leu Lys Thr Glu Lys Ile Phe Lys Glu Ile Asn Glu His
 1745 1750 1755
 Ser Thr Ser Tyr Thr Phe Arg Ser Glu Lys Gly Leu Leu Ser Ala
 1760 1765 1770
 Thr Gln Phe Thr Gln Pro Ala Leu Thr Leu Met Glu Lys Ala Ala
 1775 1780 1785
 Phe Glu Asp Leu Lys Ser Lys Gly Leu Ile Pro Ala Asp Ala Thr
 1790 1795 1800
 Phe Ala Gly His Ser Leu Gly Glu Tyr Ala Ala Leu Ala Ser Leu
 1805 1810 1815
 Ala Asp Val Met Ser Ile Glu Ser Leu Val Glu Val Val Phe Tyr
 1820 1825 1830
 Arg Gly Met Thr Met Gln Val Ala Val Pro Arg Asp Glu Leu Gly
 1835 1840 1845
 Arg Ser Asn Tyr Gly Met Ile Ala Ile Asn Pro Gly Arg Val Ala
 1850 1855 1860
 Ala Ser Phe Ser Gln Glu Ala Leu Gln Tyr Val Val Glu Arg Val
 1865 1870 1875
 Gly Lys Arg Thr Gly Trp Leu Val Glu Ile Val Asn Tyr Asn Val
 1880 1885 1890

REN-01-032-Util.ST25.txt

Glu Asn Gln Gln Tyr Val Ala Ala Gly Asp Leu Arg Ala Leu Asp
1895 1900 1905

Thr Val Thr Asn Val Leu Asn Phe Ile Lys Leu Gln Lys Ile Asp
1910 1915 1920

Ile Ile Glu Leu Gln Lys Ser Leu Ser Leu Glu Glu Val Glu Gly
1925 1930 1935

His Leu Phe Glu Ile Ile Asp Glu Ala Ser Lys Lys Ser Ala Val
1940 1945 1950

Lys Pro Arg Pro Leu Lys Leu Glu Arg Gly Phe Ala Cys Ile Pro
1955 1960 1965

Leu Val Gly Ile Ser Val Pro Phe His Ser Thr Tyr Leu Met Asn
1970 1975 1980

Gly Val Lys Pro Phe Lys Ser Phe Leu Lys Lys Asn Ile Ile Lys
1985 1990 1995

Glu Asn Val Lys Val Ala Arg Leu Ala Gly Lys Tyr Ile Pro Asn
2000 2005 2010

Leu Thr Ala Lys Pro Phe Gln Val Thr Lys Glu Tyr Phe Gln Asp
2015 2020 2025

Val Tyr Asp Leu Thr Gly Ser Glu Pro Ile Lys Glu Ile Ile Asp
2030 2035 2040

Asn Trp Glu Lys Tyr Glu Gln Ser
2045 2050

<210> 19

<211> 1887

<212> PRT

<213> Saccharomyces cerevisiae

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Met Lys Pro Glu Val Glu Gln Glu Leu Ala His Ile Leu Leu Thr Glu
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Leu Leu Ala Tyr Gln Phe Ala Ser Pro Val Arg Trp Ile Glu Thr Gln
20 25 30

Asp Val Phe Leu Lys Asp Phe Asn Thr Glu Arg Val Val Glu Ile Gly
35 40 45

Pro Ser Pro Thr Leu Ala Gly Met Ala Gln Arg Thr Leu Lys Asn Lys
50 55 60

REN-01-032-Util.ST25.txt

Tyr Glu Ser Tyr Asp Ala Ala Leu Ser Leu His Arg Glu Ile Leu Cys
 65 70 75 80

Tyr Ser Lys Asp Ala Lys Glu Ile Tyr Tyr Thr Pro Asp Pro Ser Glu
 85 90 95

Leu Ala Ala Lys Glu Glu Pro Ala Lys Glu Glu Ala Pro Ala Pro Thr
 100 105 110

Pro Ala Ala Ser Ala Pro Ala Pro Ala Ala Ala Ala Pro Ala Pro Val
 115 120 125

Ala Ala Ala Ala Pro Ala Ala Ala Ala Glu Ile Ala Asp Glu Pro
 130 135 140

Val Lys Ala Ser Leu Leu Leu His Val Leu Val Ala His Lys Leu Lys
 145 150 155 160

Lys Ser Leu Asp Ser Ile Pro Met Ser Lys Thr Ile Lys Asp Leu Val
 165 170 175

Gly Gly Lys Ser Thr Val Gln Asn Glu Ile Leu Gly Asp Leu Gly Lys
 180 185 190

Glu Phe Gly Thr Thr Pro Glu Lys Pro Glu Glu Thr Pro Leu Glu Glu
 195 200 205

Leu Ala Glu Thr Phe Gln Asp Thr Phe Ser Gly Ala Leu Gly Lys Gln
 210 215 220

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

Phe Thr Ile Thr Val Ala Arg Lys Tyr Leu Gln Thr Arg Trp Gly Leu
 245 250 255

Pro Ser Gly Arg Gln Asp Gly Val Leu Leu Val Ala Leu Ser Asn Glu
 260 265 270

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

Ser Met Ala Gln Lys Tyr Ala Ser Ile Val Gly Val Asp Leu Ser Ser
 290 295 300

Ala Ala Ser Ala Ser Gly Ala Ala Gly Ala Gly Ala Ala Ala Gly Ala
 305 310 315 320

Ala Met Ile Asp Ala Gly Ala Leu Glu Glu Ile Thr Lys Asp His Lys
 325 330 335

REN-01-032-Util.ST25.txt

Val Leu Ala Arg Gln Gln Leu Gln Val Leu Ala Arg Tyr Leu Lys Met
 340 345 350

Asp Leu Asp Asn Gly Glu Arg Lys Phe Leu Lys Glu Lys Asp Thr Val
 355 360 365

Ala Glu Leu Gln Ala Gln Leu Asp Tyr Leu Asn Ala Glu Leu Gly Glu
 370 375 380

Phe Phe Val Asn Gly Val Ala Thr Ser Phe Ser Arg Lys Lys Ala Arg
 385 390 395 400

Thr Phe Asp Ser Ser Trp Asn Trp Ala Lys Gln Ser Leu Leu Ser Leu
 405 410 415

Tyr Phe Glu Ile Ile His Gly Val Leu Lys Asn Val Asp Arg Glu Val
 420 425 430

Val Ser Glu Ala Ile Asn Ile Met Asn Arg Ser Asn Asp Ala Leu Ile
 435 440 445

Lys Phe Met Glu Tyr His Ile Ser Asn Thr Asp Glu Thr Lys Gly Glu
 450 455 460

Asn Tyr Gln Leu Val Lys Thr Leu Gly Glu Gln Leu Ile Glu Asn Cys
 465 470 475 480

Lys Gln Val Leu Asp Val Asp Pro Val Tyr Lys Asp Val Ala Lys Pro
 485 490 495

Thr Gly Pro Lys Thr Ala Ile Asp Lys Asn Gly Asn Ile Thr Tyr Ser
 500 505 510

Glu Glu Pro Arg Glu Lys Val Arg Lys Leu Ser Gln Tyr Val Gln Glu
 515 520 525

Met Ala Leu Gly Gly Pro Ile Thr Lys Glu Ser Gln Pro Thr Ile Glu
 530 535 540

Glu Asp Leu Thr Arg Val Tyr Lys Ala Ile Ser Ala Gln Ala Asp Lys
 545 550 555 560

Gln Asp Ile Ser Ser Ser Thr Arg Val Glu Phe Glu Lys Leu Tyr Ser
 565 570 575

Asp Leu Met Lys Phe Leu Glu Ser Ser Lys Glu Ile Asp Pro Ser Gln
 580 585 590

Thr Thr Gln Leu Ala Gly Met Asp Val Glu Asp Ala Leu Asp Lys Asp
 595 600 605

REN-01-032-Util.ST25.txt

Ser Thr Lys Glu Val Ala Ser Leu Pro Asn Lys Ser Thr Ile Ser Lys
610 615 620

Thr Val Ser Ser Thr Ile Pro Arg Glu Thr Ile Pro Phe Leu His Leu
625 630 635 640

Arg Lys Lys Thr Pro Ala Gly Asp Trp Lys Tyr Asp Arg Gln Leu Ser
645 650 655

Ser Leu Phe Leu Asp Gly Leu Glu Lys Ala Ala Phe Asn Gly Val Thr
660 665 670

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

Gly Ala Glu Val Leu Gln Gly Leu Leu Gln Gly Gly Ala Lys Val Val
690 695 700

Val Thr Thr Ser Arg Phe Ser Lys Gln Val Thr Asp Tyr Tyr Gln Ser
705 710 715 720

Ile Tyr Ala Lys Tyr Gly Ala Lys Gly Ser Thr Leu Ile Val Val Pro
725 730 735

Phe Asn Gln Gly Ser Lys Gln Asp Val Glu Ala Leu Ile Glu Phe Ile
740 745 750

Tyr Asp Thr Glu Lys Asn Gly Gly Leu Gly Trp Asp Leu Asp Ala Ile
755 760 765

Ile Pro Phe Ala Ala Ile Pro Glu Gln Gly Ile Glu Leu Glu His Ile
770 775 780

Asp Ser Lys Ser Glu Phe Ala His Arg Ile Met Leu Thr Asn Ile Leu
785 790 795 800

Arg Met Met Gly Cys Val Lys Lys Gln Lys Ser Ala Arg Gly Ile Glu
805 810 815

Thr Arg Pro Ala Gln Val Ile Leu Pro Met Ser Pro Asn His Gly Thr
820 825 830

Phe Gly Gly Asp Gly Met Tyr Ser Glu Ser Lys Leu Ser Leu Glu Thr
835 840 845

Leu Phe Asn Arg Trp His Ser Glu Ser Trp Ala Asn Gln Leu Thr Val
850 855 860

Cys Gly Ala Ile Ile Gly Trp Thr Arg Gly Thr Gly Leu Met Ser Ala
865 870 875 880

REN-01-032-Util.ST25.txt

Asn Asn Ile Ile Ala Glu Gly Ile Glu Lys Met Gly Val Arg Thr Phe
 885 890 895

Ser Gln Lys Glu Met Ala Phe Asn Leu Leu Gly Leu Leu Thr Pro Glu
 900 905 910

Val Val Glu Leu Cys Gln Lys Ser Pro Val Met Ala Asp Leu Asn Gly
 915 920 925

Gly Leu Gln Phe Val Pro Glu Leu Lys Glu Phe Thr Ala Lys Leu Arg
 930 935 940

Lys Glu Leu Val Glu Thr Ser Glu Val Arg Lys Ala Val Ser Ile Glu
 945 950 955 960

Thr Ala Leu Glu His Lys Val Val Asn Gly Asn Ser Ala Asp Ala Ala
 965 970 975

Tyr Ala Gln Val Glu Ile Gln Pro Arg Ala Asn Ile Gln Leu Asp Phe
 980 985 990

Pro Glu Leu Lys Pro Tyr Lys Gln Val Lys Gln Ile Ala Pro Ala Glu
 995 1000 1005

Leu Glu Gly Leu Leu Asp Leu Glu Arg Val Ile Val Val Thr Gly
 1010 1015 1020

Phe Ala Glu Val Gly Pro Trp Gly Ser Ala Arg Thr Arg Trp Glu
 1025 1030 1035

Met Glu Ala Phe Gly Glu Phe Ser Leu Glu Gly Cys Val Glu Met
 1040 1045 1050

Ala Trp Ile Met Gly Phe Ile Ser Tyr His Asn Gly Asn Leu Lys
 1055 1060 1065

Gly Arg Pro Tyr Thr Gly Trp Val Asp Ser Lys Thr Lys Glu Pro
 1070 1075 1080

Val Asp Asp Lys Asp Val Lys Ala Lys Tyr Glu Thr Ser Ile Leu
 1085 1090 1095

Glu His Ser Gly Ile Arg Leu Ile Glu Pro Glu Leu Phe Asn Gly
 1100 1105 1110

Tyr Asn Pro Glu Lys Lys Glu Met Ile Gln Glu Val Ile Val Glu
 1115 1120 1125

Glu Asp Leu Glu Pro Phe Glu Ala Ser Lys Glu Thr Ala Glu Gln
 1130 1135 1140

REN-01-032-Util.ST25.txt

Phe Lys His Gln His Gly Asp Lys Val Asp Ile Phe Glu Ile Pro
 1145 1150 1155

Glu Thr Gly Glu Tyr Ser Val Lys Leu Leu Lys Gly Ala Thr Leu
 1160 1165 1170

Tyr Ile Pro Lys Ala Leu Arg Phe Asp Arg Leu Val Ala Gly Gln
 1175 1180 1185

Ile Pro Thr Gly Trp Asn Ala Lys Thr Tyr Gly Ile Ser Asp Asp
 1190 1195 1200

Ile Ile Ser Gln Val Asp Pro Ile Thr Leu Phe Val Leu Val Ser
 1205 1210 1215

Val Val Glu Ala Phe Ile Ala Ser Gly Ile Thr Asp Pro Tyr Glu
 1220 1225 1230

Met Tyr Lys Tyr Val His Val Ser Glu Val Gly Asn Cys Ser Gly
 1235 1240 1245

Ser Gly Met Gly Gly Val Ser Ala Leu Arg Gly Met Phe Lys Asp
 1250 1255 1260

Arg Phe Lys Asp Glu Pro Val Gln Asn Asp Ile Leu Gln Glu Ser
 1265 1270 1275

Phe Ile Asn Thr Met Ser Ala Trp Val Asn Met Leu Leu Ile Ser
 1280 1285 1290

Ser Ser Gly Pro Ile Lys Thr Pro Val Gly Ala Cys Ala Thr Ser
 1295 1300 1305

Val Glu Ser Val Asp Ile Gly Val Glu Thr Ile Leu Ser Gly Lys
 1310 1315 1320

Ala Arg Ile Cys Ile Val Gly Gly Tyr Asp Asp Phe Gln Glu Glu
 1325 1330 1335

Gly Ser Phe Glu Phe Gly Asn Met Lys Ala Thr Ser Asn Thr Leu
 1340 1345 1350

Glu Glu Phe Glu His Gly Arg Thr Pro Ala Glu Met Ser Arg Pro
 1355 1360 1365

Ala Thr Thr Thr Arg Asn Gly Phe Met Glu Ala Gln Gly Ala Gly
 1370 1375 1380

Ile Gln Ile Ile Met Gln Ala Asp Leu Ala Leu Lys Met Gly Val
 1385 1390 1395

REN-01-032-Util.ST25.txt
Pro Ile Tyr Gly Ile Val Ala Met Ala Ala Thr Ala Thr Asp Lys
1400 1405 1410

Ile Gly Arg Ser Val Pro Ala Pro Gly Lys Gly Ile Leu Thr Thr
1415 1420 1425

Ala Arg Glu His His Ser Ser Val Lys Tyr Ala Ser Pro Asn Leu
1430 1435 1440

Asn Met Lys Tyr Arg Lys Arg Gln Leu Val Thr Arg Glu Ala Gln
1445 1450 1455

Ile Lys Asp Trp Val Glu Asn Glu Leu Glu Ala Leu Lys Leu Glu
1460 1465 1470

Ala Glu Glu Ile Pro Ser Glu Asp Gln Asn Glu Phe Leu Leu Glu
1475 1480 1485

Arg Thr Arg Glu Ile His Asn Glu Ala Glu Ser Gln Leu Arg Ala
1490 1495 1500

Ala Gln Gln Gln Trp Gly Asn Asp Phe Tyr Lys Arg Asp Pro Arg
1505 1510 1515

Ile Ala Pro Leu Arg Gly Ala Leu Ala Thr Tyr Gly Leu Thr Ile
1520 1525 1530

Asp Asp Leu Gly Val Ala Ser Phe His Gly Thr Ser Thr Lys Ala
1535 1540 1545

Asn Asp Lys Asn Glu Ser Ala Thr Ile Asn Glu Met Met Lys His
1550 1555 1560

Leu Gly Arg Ser Glu Gly Asn Pro Val Ile Gly Val Phe Gln Lys
1565 1570 1575

Phe Leu Thr Gly His Pro Lys Gly Ala Ala Gly Ala Trp Met Met
1580 1585 1590

Asn Gly Ala Leu Gln Ile Leu Asn Ser Gly Ile Ile Pro Gly Asn
1595 1600 1605

Arg Asn Ala Asp Asn Val Asp Lys Ile Leu Glu Gln Phe Glu Tyr
1610 1615 1620

Val Leu Tyr Pro Ser Lys Thr Leu Lys Thr Asp Gly Val Arg Ala
1625 1630 1635

Val Ser Ile Thr Ser Phe Gly Phe Gly Gln Lys Gly Gly Gln Ala
1640 1645 1650

REN-01-032-Util.ST25.txt

Ile Val Val His Pro Asp Tyr Leu Tyr Gly Ala Ile Thr Glu Asp
1655 1660 1665

Arg Tyr Asn Glu Tyr Val Ala Lys Val Ser Ala Arg Glu Lys Ser
1670 1675 1680

Ala Tyr Lys Phe Phe His Asn Gly Met Ile Tyr Asn Lys Leu Phe
1685 1690 1695

Val Ser Lys Glu His Ala Pro Tyr Thr Asp Glu Leu Glu Glu Asp
1700 1705 1710

Val Tyr Leu Asp Pro Leu Ala Arg Val Ser Lys Asp Lys Lys Ser
1715 1720 1725

Gly Ser Leu Thr Phe Asn Ser Lys Asn Ile Gln Ser Lys Asp Ser
1730 1735 1740

Tyr Ile Asn Ala Asn Thr Ile Glu Thr Ala Lys Met Ile Glu Asn
1745 1750 1755

Met Thr Lys Glu Lys Val Ser Asn Gly Gly Val Gly Val Asp Val
1760 1765 1770

Glu Leu Ile Thr Ser Ile Asn Val Glu Asn Asp Thr Phe Ile Glu
1775 1780 1785

Arg Asn Phe Thr Pro Gln Glu Ile Glu Tyr Cys Ser Ala Gln Pro
1790 1795 1800

Ser Val Gln Ser Ser Phe Ala Gly Thr Trp Ser Ala Lys Glu Ala
1805 1810 1815

Val Phe Lys Ser Leu Gly Val Lys Ser Leu Gly Gly Gly Ala Ala
1820 1825 1830

Leu Lys Asp Ile Glu Ile Val Arg Val Asn Lys Asn Ala Pro Ala
1835 1840 1845

Val Glu Leu His Gly Asn Ala Lys Lys Ala Ala Glu Glu Ala Gly
1850 1855 1860

Val Thr Asp Val Lys Val Ser Ile Ser His Asp Asp Leu Gln Ala
1865 1870 1875

Val Ala Val Ala Val Ser Thr Lys Lys
1880 1885

<210> 20
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 <213> Candida albicans

REN-01-032-Uti1.ST25.txt

<400> 20

Met Ser Thr His Arg Pro Phe Gln Leu Thr His Gly Ser Ile Glu His
 1 5 10 15

Thr Leu Leu Val Pro Asn Asp Leu Phe Phe Asn Tyr Ser Gln Leu Lys
 20 25 30

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

Asp Asp Glu Pro Ser Ser Pro Ala Glu Leu Tyr Gly Lys Phe Ile Gly
 50 55 60

Phe Ile Ser Asn Ala Gln Phe Pro Gln Ile Val Glu Leu Ser Leu Lys
 65 70 75 80

Asp Phe Glu Ser Arg Phe Leu Asp Asn Asn Asn Asp Asn Ile His Ser
 85 90 95

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

Lys Val Lys Glu Asn Ile Val Lys Asn Tyr Tyr Lys Ala Val Lys Ser
 115 120 125

Ile Asn Lys Val Glu Ser Asn Leu Leu Tyr His Cys Lys His Asp Ala
 130 135 140

Lys Leu Val Ala Ile Phe Gly Gly Gln Gly Asn Thr Asp Asp Tyr Phe
 145 150 155 160

Glu Glu Leu Arg Glu Leu Tyr Thr Leu Tyr Gln Gly Leu Ile Glu Asp
 165 170 175

Leu Leu Val Ser Ile Ala Glu Lys Leu Asn Gln Leu His Pro Ser Phe
 180 185 190

Asp Lys Ile Tyr Thr Gln Gly Leu Asn Ile Leu Ser Trp Leu Lys His
 195 200 205

Pro Glu Thr Thr Pro Asp Gln Asp Tyr Leu Leu Ser Val Pro Val Ser
 210 215 220

Cys Pro Val Ile Cys Val Ile Gln Leu Cys His Tyr Thr Ile Thr Cys
 225 230 235 240

Lys Val Leu Gly Leu Thr Pro Gly Glu Phe Arg Asn Ser Leu Lys Trp
 245 250 255

Ser Thr Gly His Ser Gln Gly Leu Val Thr Ala Val Thr Ile Ala Ala

REN-01-032-Util.ST25.txt
265

260

270

Ser Asp Ser Trp Asp Ser Phe Leu Lys Asn Ser Leu Thr Ala Val Ser
275 280 285

Leu Leu Leu Phe Ile Gly Ser Arg Cys Leu Ser Thr Tyr Pro Arg Thr
290 295 300

Ser Leu Pro Pro Thr Met Leu Gln Asp Ser Leu Asp Asn Gly Glu Gly
305 310 315 320

Arg Pro Ser Pro Met Leu Ser Val Arg Asp Leu Ser Ile Lys Gln Val
325 330 335

Glu Lys Phe Ile Glu Gln Thr Asn Ser His Leu Pro Arg Glu Lys His
340 345 350

Ile Ala Ile Ser Leu Ile Asn Gly Ala Arg Asn Leu Val Leu Ser Gly
355 360 365

Pro Pro Glu Ser Leu Tyr Gly Phe Asn Leu Asn Leu Arg Asn Gln Lys
370 375 380

Ala Pro Met Gly Leu Asp Gln Ser Arg Val Pro Phe Ser Glu Arg Lys
385 390 395 400

Leu Lys Cys Ser Asn Arg Phe Leu Pro Ile Phe Ala Pro Phe His Ser
405 410 415

His Leu Leu Ala Asp Ala Thr Glu Leu Ile Leu Asp Asp Val Lys Glu
420 425 430

His Gly Leu Ser Phe Glu Gly Leu Lys Ile Pro Val Tyr Asp Thr Phe
435 440 445

Asp Gly Ser Asp Phe Gln Ala Leu Lys Glu Pro Ile Ile Asp Arg Val
450 455 460

Val Lys Leu Ile Thr Glu Leu Pro Val His Trp Glu Glu Ala Thr Asn
465 470 475 480

His Lys Ala Thr His Ile Leu Asp Phe Gly Pro Gly Gly Val Ser Gly
485 490 495

Leu Gly Val Leu Thr His Arg Asn Lys Glu Gly Thr Gly Ala Arg Ile
500 505 510

Ile Leu Ala Gly Thr Leu Asp Ser Asn Pro Ile Asp Asp Glu Tyr Gly
515 520 525

Phe Lys His Glu Ile Phe Gln Thr Ser Ala Asp Lys Ala Ile Lys Trp
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530 REN-01-032-Util.ST25.txt
535 540

Ala Pro Asp Trp Leu Lys Glu Leu Arg Pro Thr Leu Val Lys Asn Ser
545 550 555 560

Glu Gly Lys Ile Tyr Val Lys Thr Lys Phe Ser Gln Leu Leu Gly Arg
565 570 575

Ala Pro Leu Met Val Ala Gly Met Thr Pro Thr Thr Val Asn Thr Asp
580 585 590

Ile Val Ser Ala Ser Leu Asn Ala Gly Tyr His Ile Glu Leu Ala Gly
595 600 605

Gly Gly Tyr Phe Ser Pro Val Met Met Thr Arg Ala Ile Asp Asp Ile
610 615 620

Val Ser Arg Ile Lys Pro Gly Tyr Gly Leu Gly Ile Asn Leu Ile Tyr
625 630 635 640

Val Asn Pro Phe Met Leu Gln Trp Gly Ile Pro Leu Ile Lys Asp Leu
645 650 655

Arg Glu Lys Gly Tyr Pro Ile Gln Ser Leu Thr Ile Gly Ala Gly Val
660 665 670

Pro Ser Ile Glu Val Ala Thr Glu Tyr Ile Glu Asp Leu Gly Leu Thr
675 680 685

His Leu Gly Leu Lys Pro Gly Ser Val Asp Ala Ile Ser Gln Val Ile
690 695 700

Ala Ile Ala Lys Ala His Pro Thr Phe Pro Ile Val Leu Gln Trp Thr
705 710 715 720

Gly Gly Arg Gly Gly Gly His His Ser Phe Glu Asp Phe His Gln Pro
725 730 735

Ile Ile Gln Met Tyr Ser Lys Ile Arg Arg Cys Ser Asn Ile Val Leu
740 745 750

Val Ala Gly Ser Gly Phe Gly Ser Asp Glu Asp Thr Tyr Pro Tyr Leu
755 760 765

Ser Gly Tyr Trp Ser Glu Lys Phe Asn Tyr Pro Pro Met Pro Phe Asp
770 775 780

Gly Val Leu Phe Gly Ser Arg Val Met Thr Ser Lys Glu Ser His Thr
785 790 795 800

Ser Leu Ala Ala Lys Lys Leu Ile Val Glu Cys Lys Gly Val Pro Asp
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805

810

815

Gln Gln Trp Glu Gln Thr Tyr Lys Lys Pro Thr Gly Gly Ile Ile Thr
 820 825 830

Val Arg Ser Glu Met Gly Glu Pro Ile His Lys Ile Ala Thr Arg Gly
 835 840 845

Val Met Phe Trp Lys Glu Leu Asp Asp Thr Ile Phe Asn Leu Pro Lys
 850 855 860

Asn Lys Leu Leu Asp Ala Leu Asn Lys Lys Arg Asp His Ile Ile Lys
 865 870 875 880

Lys Leu Asn Asn Asp Phe Gln Lys Pro Trp Phe Gly Lys Asn Ala Asn
 885 890 895

Gly Val Cys Asp Leu Gln Glu Met Thr Tyr Lys Glu Val Ala Asn Arg
 900 905 910

Leu Val Glu Leu Met Tyr Val Lys Lys Ser His Arg Trp Ile Asp Val
 915 920 925

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 Page 57

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Thr Ile Thr His Gly Met Tyr Ser Ser Ala Ser Ile Arg Ala Leu
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1835

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1850 1855 1860

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Tyr Asn Val Glu Asn Gln Gln Tyr Val Ala Ala Gly Asp Leu Arg
1880 1885 1890

Ala Leu Asp Thr Leu Thr Asn Val Leu Asn Val Leu Lys Ile Asn
1895 1900 1905

Lys Ile Asp Ile Val Lys Leu Gln Glu Gln Met Ser Ile Glu Lys
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1925 1930 1935

Ser Leu Ala Lys Pro Gln Pro Ile Asp Leu Glu Arg Gly Phe Ala
1940 1945 1950

Val Ile Pro Leu Lys Gly Ile Ser Val Pro Phe His Ser Ser Tyr
1955 1960 1965

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REN-01-032-Uti1.ST25.txt

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REN-01-032-Util.ST25.txt

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REN-01-032-Util.ST25.txt

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REN-01-032-Util.ST25.txt

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REN-01-032-Util.ST25.txt

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 1085 1090 1095
 His Ser Gly Ile Arg Leu Ile Glu Pro Glu Leu Phe Asn Gly Tyr
 1100 1105 1110
 Asp Pro Lys Lys Lys Gln Met Ile Gln Glu Ile Val Val Gln His
 1115 1120 1125
 Asp Leu Glu Pro Phe Glu Cys Ser Lys Glu Thr Ala Glu Gln Tyr
 1130 1135 1140
 Lys His Glu His Gly Glu Lys Cys Glu Ile Phe Glu Ile Glu Glu
 1145 1150 1155
 Ser Gly Glu Tyr Thr Val Arg Ile Leu Lys Gly Ala Thr Leu Tyr
 1160 1165 1170
 Val Pro Lys Ala Leu Arg Phe Asp Arg Leu Val Ala Gly Gln Ile
 1175 1180 1185
 Pro Thr Gly Trp Asp Ala Arg Thr Tyr Gly Ile Pro Glu Asp Thr
 1190 1195 1200
 Ile Ser Gln Val Asp Pro Ile Thr Leu Tyr Val Leu Val Ala Thr
 1205 1210 1215
 Val Glu Ala Leu Leu Ser Ala Gly Ile Thr Asp Pro Tyr Glu Phe
 1220 1225 1230
 Tyr Lys Tyr Val His Val Ser Glu Val Gly Asn Cys Ser Gly Ser
 1235 1240 1245
 Gly Met Gly Gly Val Ser Ala Leu Arg Gly Met Phe Lys Asp Arg
 1250 1255 1260
 Tyr Ala Asp Lys Pro Val Gln Asn Asp Ile Leu Gln Glu Ser Phe
 1265 1270 1275
 Ile Asn Thr Met Ser Ala Trp Val Asn Met Leu Leu Leu Ser Ser
 1280 1285 1290
 Ser Gly Pro Ile Lys Thr Pro Val Gly Ala Cys Ala Thr Ala Val
 1295 1300 1305
 Glu Ser Val Asp Ile Gly Ile Glu Thr Ile Leu Ser Gly Lys Ala
 1310 1315 1320
 Lys Val Val Leu Val Gly Gly Tyr Asp Asp Phe Gln Glu Glu Gly
 1325 1330 1335

REN-01-032-Util.ST25.txt

Ser Tyr Glu Phe Ala Asn Met Asn Ala Thr Ser Asn Ser Ile Glu
 1340 1345 1350
 Glu Phe Lys His Gly Arg Thr Pro Lys Glu Met Ser Arg Pro Thr
 1355 1360 1365
 Thr Thr Thr Arg Asn Gly Phe Met Glu Ala Gln Gly Ser Gly Ile
 1370 1375 1380
 Gln Val Ile Met Thr Ala Asp Leu Ala Leu Lys Met Gly Val Pro
 1385 1390 1395
 Ile His Ala Val Leu Ala Met Thr Ala Thr Ala Thr Asp Lys Ile
 1400 1405 1410
 Gly Arg Ser Val Pro Ala Pro Gly Lys Gly Ile Leu Thr Thr Ala
 1415 1420 1425
 Arg Glu His His Gly Asn Leu Lys Tyr Pro Ser Pro Leu Leu Asn
 1430 1435 1440
 Ile Lys Tyr Arg Lys Arg Gln Leu Asn Lys Arg Leu Glu Gln Ile
 1445 1450 1455
 Lys Ser Trp Glu Glu Thr Glu Leu Ser Tyr Leu Gln Glu Glu Ala
 1460 1465 1470
 Glu Leu Ala Lys Glu Glu Phe Gly Asp Glu Phe Ser Met His Glu
 1475 1480 1485
 Phe Leu Lys Glu Arg Thr Glu Glu Val Tyr Arg Glu Ser Lys Arg
 1490 1495 1500
 Gln Val Ser Asp Ala Lys Lys Gln Trp Gly Asn Ser Phe Tyr Lys
 1505 1510 1515
 Ser Asp Pro Arg Ile Ala Pro Leu Arg Gly Ala Leu Ala Ala Phe
 1520 1525 1530
 Asn Leu Thr Ile Asp Asp Ile Gly Val Ala Ser Phe His Gly Thr
 1535 1540 1545
 Ser Thr Val Ala Asn Asp Lys Asn Glu Ser Ala Thr Ile Asn Asn
 1550 1555 1560
 Met Met Lys His Leu Gly Arg Ser Glu Gly Asn Pro Val Phe Gly
 1565 1570 1575
 Val Phe Gln Lys Tyr Leu Thr Gly His Pro Lys Gly Ala Ala Gly
 1580 1585 1590

REN-01-032-Util.ST25.txt

Ala	Trp	Met	Leu	Asn	Gly	Ala	Ile	Gln	Ile	Leu	Glu	Ser	Gly	Leu
1595						1600					1605			
Val	Pro	Gly	Asn	Arg	Asn	Ala	Asp	Asn	Val	Asp	Lys	Leu	Leu	Glu
1610						1615					1620			
Gln	Tyr	Glu	Tyr	Val	Leu	Tyr	Pro	Ser	Arg	Ser	Ile	Gln	Thr	Asp
1625						1630					1635			
Gly	Ile	Lys	Ala	Val	Ser	Val	Thr	Ser	Phe	Gly	Phe	Gly	Gln	Lys
1640						1645					1650			
Gly	Ala	Gln	Ala	Val	Val	Val	His	Pro	Asp	Tyr	Leu	Phe	Ala	Val
1655						1660					1665			
Leu	Asp	Arg	Ser	Thr	Tyr	Glu	Glu	Tyr	Ala	Thr	Lys	Val	Ser	Ala
1670						1675					1680			
Arg	Asn	Lys	Lys	Thr	Tyr	Arg	Tyr	Met	His	Asn	Ala	Ile	Thr	Arg
1685						1690					1695			
Asn	Thr	Met	Phe	Val	Ala	Lys	Asp	Lys	Ala	Pro	Tyr	Ser	Asp	Glu
1700						1705					1710			
Leu	Glu	Gln	Pro	Val	Tyr	Leu	Asp	Pro	Leu	Ala	Arg	Val	Glu	Glu
1715						1720					1725			
Asn	Lys	Lys	Lys	Leu	Val	Phe	Ser	Asp	Lys	Thr	Ile	Gln	Ser	Asn
1730						1735					1740			
Gln	Ser	Tyr	Val	Gly	Glu	Val	Ala	Gln	Lys	Thr	Ala	Lys	Ala	Leu
1745						1750					1755			
Ser	Thr	Leu	Asn	Lys	Ser	Ser	Lys	Gly	Val	Gly	Val	Asp	Val	Glu
1760						1765					1770			
Leu	Leu	Ser	Ala	Ile	Asn	Ile	Asp	Asn	Glu	Thr	Phe	Ile	Glu	Arg
1775						1780					1785			
Asn	Phe	Thr	Gly	Asn	Glu	Val	Glu	Tyr	Cys	Leu	Asn	Thr	Ala	His
1790						1795					1800			
Pro	Gln	Ala	Ser	Phe	Thr	Gly	Thr	Trp	Ser	Ala	Lys	Glu	Ala	Val
1805						1810					1815			
Phe	Lys	Ala	Leu	Gly	Val	Glu	Ser	Lys	Gly	Ala	Gly	Ala	Ser	Leu
1820						1825					1830			
Ile	Asp	Ile	Glu	Ile	Thr	Arg	Asp	Val	Asn	Gly	Ala	Pro	Lys	Val
1835						1840					1845			

REN-01-032-Uti1.ST25.txt

Ile Leu His Gly Glu Ala Lys Lys Ala Ala Ala Lys Ala Gly Val
 1850 1855 1860

Lys Asn Val Asn Ile Ser Ile Ser His Asp Asp Phe Gln Ala Thr
 1865 1870 1875

Ala Val Ala Leu Ser Glu Phe
 1880 1885

<210> 23
 <211> 3069
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 23

Met Thr Ile His Glu His Asp Arg Val Ser Ala Asp Arg Gly Gly Asp
 1 5 10 15

Ser Pro His Thr Thr His Ala Leu Val Asp Arg Leu Met Ala Gly Glu
 20 25 30

Pro Tyr Ala Val Ala Phe Gly Gly Gln Gly Ser Ala Trp Leu Glu Thr
 35 40 45

Leu Glu Glu Leu Val Ser Ala Thr Gly Ile Glu Thr Glu Leu Ala Thr
 50 55 60

Leu Val Gly Glu Ala Glu Leu Leu Leu Asp Pro Val Thr Asp Glu Leu
 65 70 75 80

Ile Val Val Arg Pro Ile Gly Phe Glu Pro Leu Gln Trp Val Arg Ala
 85 90 95

Leu Ala Ala Glu Asp Pro Val Pro Ser Asp Lys His Leu Thr Ser Ala
 100 105 110

Ala Val Ser Val Pro Gly Val Leu Leu Thr Gln Ile Ala Ala Thr Arg
 115 120 125

Ala Leu Ala Arg Gln Gly Met Asp Leu Val Ala Thr Pro Pro Val Ala
 130 135 140

Met Ala Gly His Ser Gln Gly Val Leu Ala Val Glu Ala Leu Lys Ala
 145 150 155 160

Gly Gly Ala Arg Asp Val Glu Leu Phe Ala Leu Ala Gln Leu Ile Gly
 165 170 175

Ala Ala Gly Thr Leu Val Ala Arg Arg Arg Gly Ile Ser Val Leu Gly
 180 185 190

REN-01-032-Util.ST25.txt

Asp Arg Pro Pro Met Val Ser Val Thr Asn Ala Asp Pro Glu Arg Ile
 195 200 205
 Gly Arg Leu Leu Asp Glu Phe Ala Gln Asp Val Arg Thr Val Leu Pro
 210 215 220
 Pro Val Leu Ser Ile Arg Asn Gly Arg Arg Ala Val Val Ile Thr Gly
 225 230 235 240
 Thr Pro Glu Gln Leu Ser Arg Phe Glu Leu Tyr Cys Arg Gln Ile Ser
 245 250 255
 Glu Lys Glu Glu Ala Asp Arg Lys Asn Lys Val Arg Gly Gly Asp Val
 260 265 270
 Phe Ser Pro Val Phe Glu Pro Val Gln Val Glu Val Gly Phe His Thr
 275 280 285
 Pro Arg Leu Ser Asp Gly Ile Asp Ile Val Ala Gly Trp Ala Glu Lys
 290 295 300
 Ala Gly Leu Asp Val Ala Leu Ala Arg Glu Leu Ala Asp Ala Ile Leu
 305 310 315 320
 Ile Arg Lys Val Asp Trp Val Asp Glu Ile Thr Arg Val His Ala Ala
 325 330 335
 Gly Ala Arg Trp Ile Leu Asp Leu Gly Pro Gly Asp Ile Leu Thr Arg
 340 345 350
 Leu Thr Ala Pro Val Ile Arg Gly Leu Gly Ile Gly Ile Val Pro Ala
 355 360 365
 Ala Thr Arg Gly Gly Gln Arg Asn Leu Phe Thr Val Gly Ala Thr Pro
 370 375 380
 Glu Val Ala Arg Ala Trp Ser Ser Tyr Ala Pro Thr Val Val Arg Leu
 385 390 395 400
 Pro Asp Gly Arg Val Lys Leu Ser Thr Lys Phe Thr Arg Leu Thr Gly
 405 410 415
 Arg Ser Pro Ile Leu Leu Ala Gly Met Thr Pro Thr Thr Val Asp Ala
 420 425 430
 Lys Ile Val Ala Ala Ala Ala Asn Ala Gly His Trp Ala Glu Leu Ala
 435 440 445
 Gly Gly Gly Gln Val Thr Glu Glu Ile Phe Gly Asn Arg Ile Glu Gln
 450 455 460

REN-01-032-Util.ST25.txt

Met Ala Gly Leu Leu Glu Pro Gly Arg Thr Tyr Gln Phe Asn Ala Leu
 465 470 475 480

Phe Leu Asp Pro Tyr Leu Trp Lys Leu Gln Val Gly Gly Lys Arg Leu
 485 490 495

Val Gln Lys Ala Arg Gln Ser Gly Ala Ala Ile Asp Gly Val Val Ile
 500 505 510

Ser Ala Gly Ile Pro Asp Leu Asp Glu Ala Val Glu Leu Ile Asp Glu
 515 520 525

Leu Gly Asp Ile Gly Ile Ser His Val Val Phe Lys Pro Gly Thr Ile
 530 535 540

Glu Gln Ile Arg Ser Val Ile Arg Ile Ala Thr Glu Val Pro Thr Lys
 545 550 555 560

Pro Val Ile Met His Val Glu Gly Gly Arg Ala Gly Gly His His Ser
 565 570 575

Trp Glu Asp Leu Asp Asp Leu Leu Leu Ala Thr Tyr Ser Glu Leu Arg
 580 585 590

Ser Arg Ala Asn Ile Thr Val Cys Val Gly Gly Gly Ile Gly Thr Pro
 595 600 605

Arg Arg Ala Ala Glu Tyr Leu Ser Gly Arg Trp Ala Gln Ala Tyr Gly
 610 615 620

Phe Pro Leu Met Pro Ile Asp Gly Ile Leu Val Gly Thr Ala Ala Met
 625 630 635 640

Ala Thr Lys Glu Ser Thr Thr Ser Pro Ser Val Lys Arg Met Leu Val
 645 650 655

Asp Thr Gln Gly Thr Asp Gln Trp Ile Ser Ala Gly Lys Ala Gln Gly
 660 665 670

Gly Met Ala Ser Ser Arg Ser Gln Leu Gly Ala Asp Ile His Glu Ile
 675 680 685

Asp Asn Ser Ala Ser Arg Cys Gly Arg Leu Leu Asp Glu Val Ala Gly
 690 695 700

Asp Ala Glu Ala Val Ala Glu Arg Arg Asp Glu Ile Ile Ala Ala Met
 705 710 715 720

Ala Lys Thr Ala Lys Pro Tyr Phe Gly Asp Val Ala Asp Met Thr Tyr
 725 730 735

REN-01-032-Util.ST25.txt

Leu Gln Trp Leu Arg Arg Tyr Val Glu Leu Ala Ile Gly Glu Gly Asn
 740 745 750

Ser Thr Ala Asp Thr Ala Ser Val Gly Ser Pro Trp Leu Ala Asp Thr
 755 760 765

Trp Arg Asp Arg Phe Glu Gln Met Leu Gln Arg Ala Glu Ala Arg Leu
 770 775 780

His Pro Gln Asp Phe Gly Pro Ile Gln Thr Leu Phe Thr Asp Ala Gly
 785 790 795 800

Leu Leu Asp Asn Pro Gln Gln Ala Ile Ala Ala Leu Leu Ala Arg Tyr
 805 810 815

Pro Asp Ala Glu Thr Val Gln Leu His Pro Ala Asp Val Pro Phe Phe
 820 825 830

Val Thr Leu Cys Lys Thr Leu Gly Lys Pro Val Asn Phe Val Pro Val
 835 840 845

Ile Asp Gln Asp Val Arg Arg Trp Trp Arg Ser Asp Ser Leu Trp Gln
 850 855 860

Ala His Asp Ala Arg Tyr Asp Ala Asp Ala Val Cys Ile Ile Pro Gly
 865 870 875 880

Thr Ala Ser Val Ala Gly Ile Thr Arg Met Asp Glu Pro Val Gly Glu
 885 890 895

Leu Leu Asp Arg Phe Glu Gln Ala Ala Ile Asp Glu Val Leu Gly Ala
 900 905 910

Gly Val Glu Pro Lys Asp Val Ala Ser Arg Arg Leu Gly Arg Ala Asp
 915 920 925

Val Ala Gly Pro Leu Ala Val Val Leu Asp Ala Pro Asp Val Arg Trp
 930 935 940

Ala Gly Arg Thr Val Thr Asn Pro Val His Arg Ile Ala Asp Pro Ala
 945 950 955 960

Glu Trp Gln Val His Asp Gly Pro Glu Asn Pro Arg Ala Thr His Ser
 965 970 975

Ser Thr Gly Ala Arg Leu Gln Thr His Gly Asp Asp Val Ala Leu Ser
 980 985 990

Val Pro Val Ser Gly Thr Trp Val Asp Ile Arg Phe Thr Leu Pro Ala
 995 1000 1005

REN-01-032-Util.ST25.txt

Asn Thr Val Asp Gly Gly Thr Pro Val Ile Ala Thr Glu Asp Ala
1010 1015 1020

Thr Ser Ala Met Arg Thr Val Leu Ala Ile Ala Ala Gly Val Asp
1025 1030 1035

Ser Pro Glu Phe Leu Pro Ala Val Ala Asn Gly Thr Ala Thr Leu
1040 1045 1050

Thr Val Asp Trp His Pro Glu Arg Val Ala Asp His Thr Gly Val
1055 1060 1065

Thr Ala Thr Phe Gly Glu Pro Leu Ala Pro Ser Leu Thr Asn Val
1070 1075 1080

Pro Asp Ala Leu Val Gly Pro Cys Trp Pro Ala Val Phe Ala Ala
1085 1090 1095

Ile Gly Ser Ala Val Thr Asp Thr Gly Glu Pro Val Val Glu Gly
1100 1105 1110

Leu Leu Ser Leu Val His Leu Asp His Ala Ala Arg Val Val Gly
1115 1120 1125

Gln Leu Pro Thr Val Pro Ala Gln Leu Thr Val Thr Ala Thr Ala
1130 1135 1140

Ala Asn Ala Thr Asp Thr Asp Met Gly Arg Val Val Pro Val Ser
1145 1150 1155

Val Val Val Thr Gly Ala Asp Gly Ala Val Ile Ala Thr Leu Glu
1160 1165 1170

Glu Arg Phe Ala Ile Leu Gly Arg Thr Gly Ser Ala Glu Leu Ala
1175 1180 1185

Asp Pro Ala Arg Ala Gly Gly Ala Val Ser Ala Asn Ala Thr Asp
1190 1195 1200

Thr Pro Arg Arg Arg Arg Arg Asp Val Thr Ile Thr Ala Pro Val
1205 1210 1215

Asp Met Arg Pro Phe Ala Val Val Ser Gly Asp His Asn Pro Ile
1220 1225 1230

His Thr Asp Arg Ala Ala Ala Leu Leu Ala Gly Leu Glu Ser Pro
1235 1240 1245

Ile Val His Gly Met Trp Leu Ser Ala Ala Ala Gln His Ala Val
1250 1255 1260

REN-01-032-Util.ST25.txt

Thr Ala Thr Asp Gly Gln Ala Arg Pro Pro Ala Arg Leu Val Gly
1265 1270 1275

Trp Thr Ala Arg Phe Leu Gly Met Val Arg Pro Gly Asp Glu Val
1280 1285 1290

Asp Phe Arg Val Glu Arg Val Gly Ile Asp Gln Gly Ala Glu Ile
1295 1300 1305

Val Asp Val Ala Ala Arg Val Gly Ser Asp Leu Val Met Ser Ala
1310 1315 1320

Ser Ala Arg Leu Ala Ala Pro Lys Thr Val Tyr Ala Phe Pro Gly
1325 1330 1335

Gln Gly Ile Gln His Lys Gly Met Gly Met Glu Val Arg Ala Arg
1340 1345 1350

Ser Lys Ala Ala Arg Lys Val Trp Asp Thr Ala Asp Lys Phe Thr
1355 1360 1365

Arg Asp Thr Leu Gly Phe Ser Val Leu His Val Val Arg Asp Asn
1370 1375 1380

Pro Thr Ser Ile Ile Ala Ser Gly Val His Tyr His His Pro Asp
1385 1390 1395

Gly Val Leu Tyr Leu Thr Gln Phe Thr Gln Val Ala Met Ala Thr
1400 1405 1410

Val Ala Ala Ala Gln Val Ala Glu Met Arg Glu Gln Gly Ala Phe
1415 1420 1425

Val Glu Gly Ala Ile Ala Cys Gly His Ser Val Gly Glu Tyr Thr
1430 1435 1440

Ala Leu Ala Cys Val Thr Gly Ile Tyr Gln Leu Glu Ala Leu Leu
1445 1450 1455

Glu Met Val Phe His Arg Gly Ser Lys Met His Asp Ile Val Pro
1460 1465 1470

Arg Asp Glu Leu Gly Arg Ser Asn Tyr Arg Leu Ala Ala Ile Arg
1475 1480 1485

Pro Ser Gln Ile Asp Leu Asp Asp Ala Asp Val Pro Ala Phe Val
1490 1495 1500

Ala Gly Ile Ala Glu Ser Thr Gly Glu Phe Leu Glu Ile Val Asn
1505 1510 1515

REN-01-032-Util.ST25.txt

Phe Asn Leu Arg Gly Ser Gln Tyr Ala Ile Ala Gly Thr Val Arg
 1520 1525 1530

Gly Leu Glu Ala Leu Glu Ala Glu Val Glu Arg Arg Arg Glu Leu
 1535 1540 1545

Thr Gly Gly Arg Arg Ser Phe Ile Leu Val Pro Gly Ile Asp Val
 1550 1555 1560

Pro Phe His Ser Arg Val Leu Arg Val Gly Val Ala Glu Phe Arg
 1565 1570 1575

Arg Ser Leu Asp Arg Val Met Pro Arg Asp Ala Asp Pro Asp Leu
 1580 1585 1590

Ile Ile Gly Arg Tyr Ile Pro Asn Leu Val Pro Arg Leu Phe Thr
 1595 1600 1605

Leu Asp Arg Asp Phe Ile Gln Glu Ile Arg Asp Leu Val Pro Ala
 1610 1615 1620

Glu Pro Leu Asp Glu Ile Leu Ala Asp Tyr Asp Thr Trp Leu Arg
 1625 1630 1635

Glu Arg Pro Arg Glu Met Ala Arg Thr Val Phe Ile Glu Leu Leu
 1640 1645 1650

Ala Trp Gln Phe Ala Ser Pro Val Arg Trp Ile Glu Thr Gln Asp
 1655 1660 1665

Leu Leu Phe Ile Glu Glu Ala Ala Gly Gly Leu Gly Val Glu Arg
 1670 1675 1680

Phe Val Glu Ile Gly Val Lys Ser Ser Pro Thr Val Ala Gly Leu
 1685 1690 1695

Ala Thr Asn Thr Leu Lys Leu Pro Glu Tyr Ala His Ser Thr Val
 1700 1705 1710

Glu Val Leu Asn Ala Glu Arg Asp Ala Ala Val Leu Phe Ala Thr
 1715 1720 1725

Asp Thr Asp Pro Glu Pro Glu Pro Glu Glu Asp Glu Pro Val Ala
 1730 1735 1740

Glu Ser Pro Ala Pro Asp Val Val Ser Glu Ala Ala Pro Val Ala
 1745 1750 1755

Pro Ala Ala Ser Ser Ala Gly Pro Arg Pro Asp Asp Leu Val Phe
 1760 1765 1770

REN-01-032-util.ST25.txt
 Asp Ala Ala Asp Ala Thr Leu Ala Leu Ile Ala Leu Ser Ala Lys
 1775 1780 1785

Met Arg Ile Asp Gln Ile Glu Glu Leu Asp Ser Ile Glu Ser Ile
 1790 1795 1800

Thr Asp Gly Ala Ser Ser Arg Arg Asn Gln Leu Leu Val Asp Leu
 1805 1810 1815

Gly Ser Glu Leu Asn Leu Gly Ala Ile Asp Gly Ala Ala Glu Ser
 1820 1825 1830

Asp Leu Ala Gly Leu Arg Ser Gln Val Thr Lys Leu Ala Arg Thr
 1835 1840 1845

Tyr Lys Pro Tyr Gly Pro Val Leu Ser Asp Ala Ile Asn Asp Gln
 1850 1855 1860

Leu Arg Thr Val Leu Gly Pro Ser Gly Lys Arg Pro Gly Ala Ile
 1865 1870 1875

Ala Glu Arg Val Lys Lys Thr Trp Glu Leu Gly Glu Gly Trp Ala
 1880 1885 1890

Lys His Val Thr Val Glu Val Ala Leu Gly Thr Arg Glu Gly Ser
 1895 1900 1905

Ser Val Arg Gly Gly Ala Met Gly His Leu His Glu Gly Ala Leu
 1910 1915 1920

Ala Asp Ala Ala Ser Val Asp Lys Val Ile Asp Ala Ala Val Ala
 1925 1930 1935

Ser Val Ala Ala Arg Gln Gly Val Ser Val Ala Leu Pro Ser Ala
 1940 1945 1950

Gly Ser Gly Gly Gly Ala Thr Ile Asp Ala Ala Ala Leu Ser Glu
 1955 1960 1965

Phe Thr Asp Gln Ile Thr Gly Arg Glu Gly Val Leu Ala Ser Ala
 1970 1975 1980

Ala Arg Leu Val Leu Gly Gln Leu Gly Leu Asp Asp Pro Val Asn
 1985 1990 1995

Ala Leu Pro Ala Ala Pro Asp Ser Glu Leu Ile Asp Leu Val Thr
 2000 2005 2010

Ala Glu Leu Gly Ala Asp Trp Pro Arg Leu Val Ala Pro Val Phe
 2015 2020 2025

REN-01-032-Util.ST25.txt
 Asp Pro Lys Lys Ala Val Val Phe Asp Asp Arg Trp Ala Ser Ala
 2030 2035 2040
 Arg Glu Asp Leu Val Lys Leu Trp Leu Thr Asp Glu Gly Asp Ile
 2045 2050 2055
 Asp Ala Asp Trp Pro Arg Leu Ala Glu Arg Phe Glu Gly Ala Gly
 2060 2065 2070
 His Val Val Ala Thr Gln Ala Thr Trp Trp Gln Gly Lys Ser Leu
 2075 2080 2085
 Ala Ala Gly Arg Gln Ile His Ala Ser Leu Tyr Gly Arg Ile Ala
 2090 2100
 Ala Gly Ala Glu Asn Pro Glu Pro Gly Arg Tyr Gly Gly Glu Val
 2105 2110 2115
 Ala Val Val Thr Gly Ala Ser Lys Gly Ser Ile Ala Ala Ser Val
 2120 2125 2130
 Val Ala Arg Leu Leu Asp Gly Gly Ala Thr Val Ile Ala Thr Thr
 2135 2140 2145
 Ser Lys Leu Asp Glu Glu Arg Leu Ala Phe Tyr Arg Thr Leu Tyr
 2150 2155 2160
 Arg Asp His Ala Arg Tyr Gly Ala Ala Leu Trp Leu Val Ala Ala
 2165 2170 2175
 Asn Met Ala Ser Tyr Ser Asp Val Asp Ala Leu Val Glu Trp Ile
 2180 2185 2190
 Gly Thr Glu Gln Thr Glu Ser Leu Gly Pro Gln Ser Ile His Ile
 2195 2200 2205
 Lys Asp Ala Gln Thr Pro Thr Leu Leu Phe Pro Phe Ala Ala Pro
 2210 2215 2220
 Arg Val Val Gly Asp Leu Ser Glu Ala Gly Ser Arg Ala Glu Met
 2225 2230 2235
 Glu Met Lys Val Leu Leu Trp Ala Val Gln Arg Leu Ile Gly Gly
 2240 2245 2250
 Leu Ser Thr Ile Gly Ala Glu Arg Asp Ile Ala Ser Arg Leu His
 2255 2260 2265
 Val Val Leu Pro Gly Ser Pro Asn Arg Gly Met Phe Gly Gly Asp
 2270 2275 2280

REN-01-032-util.ST25.txt

Gly	Ala	Tyr	Gly	Glu	Ala	Lys	Ser	Ala	Leu	Asp	Ala	Val	Val	Ser
2285						2290					2295			
Arg	Trp	His	Ala	Glu	Ser	Ser	Trp	Ala	Ala	Arg	Val	Ser	Leu	Ala
2300						2305					2310			
His	Ala	Leu	Ile	Gly	Trp	Thr	Arg	Gly	Thr	Gly	Leu	Met	Gly	His
2315						2320					2325			
Asn	Asp	Ala	Ile	Val	Ala	Ala	Val	Glu	Glu	Ala	Gly	Val	Thr	Thr
2330						2335					2340			
Tyr	Ser	Thr	Asp	Glu	Met	Ala	Ala	Leu	Leu	Leu	Asp	Leu	Cys	Asp
2345						2350					2355			
Ala	Glu	Ser	Lys	Val	Ala	Ala	Ala	Arg	Ser	Pro	Ile	Lys	Ala	Asp
2360						2365					2370			
Leu	Thr	Gly	Gly	Leu	Ala	Glu	Ala	Asn	Leu	Asp	Met	Ala	Glu	Leu
2375						2380					2385			
Ala	Ala	Lys	Ala	Arg	Glu	Gln	Met	Ser	Ala	Ala	Ala	Ala	Val	Asp
2390						2395					2400			
Glu	Asp	Ala	Glu	Ala	Pro	Gly	Ala	Ile	Ala	Ala	Leu	Pro	Ser	Pro
2405						2410					2415			
Pro	Arg	Gly	Phe	Thr	Pro	Ala	Pro	Pro	Pro	Gln	Trp	Asp	Asp	Leu
2420						2425					2430			
Asp	Val	Asp	Pro	Ala	Asp	Leu	Val	Val	Ile	Val	Gly	Gly	Ala	Glu
2435						2440					2445			
Ile	Gly	Pro	Tyr	Gly	Ser	Ser	Arg	Thr	Arg	Phe	Glu	Met	Glu	Val
2450						2455					2460			
Glu	Asn	Glu	Leu	Ser	Ala	Ala	Gly	Val	Leu	Glu	Leu	Ala	Trp	Thr
2465						2470					2475			
Thr	Gly	Leu	Ile	Arg	Trp	Glu	Asp	Asp	Pro	Gln	Pro	Gly	Trp	Tyr
2480						2485					2490			
Asp	Thr	Glu	Ser	Gly	Glu	Met	Val	Asp	Glu	Ser	Glu	Leu	Val	Gln
2495						2500					2505			
Arg	Tyr	His	Asp	Ala	Val	Val	Gln	Arg	Val	Gly	Ile	Arg	Glu	Phe
2510						2515					2520			
Val	Asp	Asp	Gly	Ala	Ile	Asp	Pro	Asp	His	Ala	Ser	Pro	Leu	Leu
2525						2530					2535			

REN-01-032-Util.ST25.txt

Val	Ser	Val	Phe	Leu	Glu	Lys	Asp	Phe	Ala	Phe	Val	Val	Ser	Ser
2540						2545					2550			
Glu	Ala	Asp	Ala	Arg	Ala	Phe	Val	Glu	Phe	Asp	Pro	Glu	His	Thr
2555						2560					2565			
Val	Ile	Arg	Pro	Val	Pro	Asp	Ser	Thr	Asp	Trp	Gln	Val	Ile	Arg
2570						2575					2580			
Lys	Ala	Gly	Thr	Glu	Ile	Arg	Val	Pro	Arg	Lys	Thr	Lys	Leu	Ser
2585						2590					2595			
Arg	Val	Val	Gly	Gly	Gln	Ile	Pro	Thr	Gly	Phe	Asp	Pro	Thr	Val
2600						2605					2610			
Trp	Gly	Ile	Ser	Ala	Asp	Met	Ala	Gly	Ser	Ile	Asp	Arg	Leu	Ala
2615						2620					2625			
Val	Trp	Asn	Met	Val	Ala	Thr	Val	Asp	Ala	Phe	Leu	Ser	Ser	Gly
2630						2635					2640			
Phe	Ser	Pro	Ala	Glu	Val	Met	Arg	Tyr	Val	His	Pro	Ser	Leu	Val
2645						2650					2655			
Ala	Asn	Thr	Gln	Gly	Thr	Gly	Met	Gly	Gly	Gly	Thr	Ser	Met	Gln
2660						2665					2670			
Thr	Met	Tyr	His	Gly	Asn	Leu	Leu	Gly	Arg	Asn	Lys	Pro	Asn	Asp
2675						2680					2685			
Ile	Phe	Gln	Glu	Val	Leu	Pro	Asn	Ile	Ile	Ala	Ala	His	Val	Val
2690						2695					2700			
Gln	Ser	Tyr	Val	Gly	Ser	Tyr	Gly	Ala	Met	Ile	His	Pro	Val	Ala
2705						2710					2715			
Ala	Cys	Ala	Thr	Ala	Ala	Val	Ser	Val	Glu	Glu	Gly	Val	Asp	Lys
2720						2725					2730			
Ile	Arg	Leu	Gly	Lys	Ala	Gln	Leu	Val	Val	Ala	Gly	Gly	Leu	Asp
2735						2740					2745			
Asp	Leu	Thr	Leu	Glu	Gly	Ile	Ile	Gly	Phe	Gly	Asp	Met	Ala	Ala
2750						2755					2760			
Thr	Ala	Asp	Thr	Ser	Met	Met	Cys	Gly	Arg	Gly	Ile	His	Asp	Ser
2765						2770					2775			
Lys	Phe	Ser	Arg	Pro	Asn	Asp	Arg	Arg	Arg	Leu	Gly	Phe	Val	Glu
2780						2785					2790			

REN-01-032-Util.ST25.txt
 Ala Gln Gly Gly Gly Thr Ile Leu Leu Ala Arg Gly Asp Leu Ala
 2795 2800 2805
 Leu Arg Met Gly Leu Pro Val Leu Ala Val Val Ala Phe Ala Gln
 2810 2815 2820
 Ser Phe Gly Asp Gly Val His Thr Ser Ile Pro Ala Pro Gly Leu
 2825 2830 2835
 Gly Ala Leu Gly Ala Gly Arg Gly Gly Lys Asp Ser Pro Leu Ala
 2840 2845 2850
 Arg Ala Leu Ala Lys Leu Gly Val Ala Ala Asp Asp Val Ala Val
 2855 2860 2865
 Ile Ser Lys His Asp Thr Ser Thr Leu Ala Asn Asp Pro Asn Glu
 2870 2875 2880
 Thr Glu Leu His Glu Arg Leu Ala Asp Ala Leu Gly Arg Ser Glu
 2885 2890 2895
 Gly Ala Pro Leu Phe Val Val Ser Gln Lys Ser Leu Thr Gly His
 2900 2905 2910
 Ala Lys Gly Gly Ala Ala Val Phe Gln Met Met Gly Leu Cys Gln
 2915 2920 2925
 Ile Leu Arg Asp Gly Val Ile Pro Pro Asn Arg Ser Leu Asp Cys
 2930 2935 2940
 Val Asp Asp Glu Leu Ala Gly Ser Ala His Phe Val Trp Val Arg
 2945 2950 2955
 Asp Thr Leu Arg Leu Gly Gly Lys Phe Pro Leu Lys Ala Gly Met
 2960 2965 2970
 Leu Thr Ser Leu Gly Phe Gly His Val Ser Gly Leu Val Ala Leu
 2975 2980 2985
 Val His Pro Gln Ala Phe Ile Ala Ser Leu Asp Pro Ala Gln Arg
 2990 2995 3000
 Ala Asp Tyr Gln Arg Arg Ala Asp Ala Arg Leu Leu Ala Gly Gln
 3005 3010 3015
 Arg Arg Leu Ala Ser Ala Ile Ala Gly Gly Ala Pro Met Tyr Gln
 3020 3025 3030
 Arg Pro Gly Asp Arg Arg Phe Asp His His Ala Pro Glu Arg Pro
 3035 3040 3045

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Gln Glu Ala Ser Met Leu Leu Asn Pro Ala Ala Arg Leu Gly Asp
 3050 3055 3060

Gly Glu Ala Tyr Ile Gly
 3065

<210> 24
 <211> 3076
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 24

Met Thr Ile His Glu His Asp Gln Val Ser Ala Asp Arg Asn Gly Asn
 1 5 10 15

Ser Leu His Gly Ser Arg Ala Leu Ala Asp Arg Leu Lys Ala Gly Glu
 20 25 30

Pro Tyr Val Val Ala Phe Gly Gly Gln Gly Ser Ala Trp Leu Glu Thr
 35 40 45

Leu Glu Glu Leu Val Ser Ser Ala Gly Leu Glu Ala Asp Leu Ala Thr
 50 55 60

Leu Val Cys Glu Val Glu Leu Leu Leu Glu Pro Val Ala Lys Glu Leu
 65 70 75 80

Val Val Val Arg Pro Ile Gly Phe Glu Pro Leu Gln Trp Val Arg Ala
 85 90 95

Leu Leu Ala Glu Asp Leu Val Pro Ser Asp Lys His Leu Thr Ser Ala
 100 105 110

Ala Val Ser Val Pro Gly Val Leu Leu Thr Gln Ile Ala Val Gly Arg
 115 120 125

Ala Leu Ala Arg Gln Gly Met Asp Leu Ile Ala Thr Pro Pro Val Gly
 130 135 140

Ile Val Gly His Ser Gln Gly Val Leu Ala Val Glu Ala Leu Lys Ala
 145 150 155 160

Gly Gly Ala Arg Asp Ala Glu Leu Leu Ala Met Ala Gln Leu Ile Gly
 165 170 175

Ala Ala Gly Thr Leu Val Ala Arg Arg Arg Gly Ile Ser Val Leu Gly
 180 185 190

Asp Arg Pro Pro Met Val Ser Val Thr Asn Ala Asp Pro Glu Arg Ile
 195 200 205

Arg Arg Leu Leu Asp Glu Phe Ala Gln Asp Val Arg Thr Val Leu Pro
 Page 84

210 REN-01-032-Util.ST25.txt
 215 220
 Pro Val Leu Ser Ile Arg Asn Gly Trp Arg Ser Val Val Ile Thr Gly
 225 230 235 240
 Thr Pro Glu Gln Leu Ser Arg Phe Glu Arg Tyr Cys Arg Gln Ile Ser
 245 250 255
 Asp Lys Glu Glu Glu Asp Arg Arg Lys Lys Ile Arg Gly Gly Asp Ile
 260 265 270
 Phe Ala Pro Val Phe Asp Pro Val Gln Val Glu Ile Gly Phe His Thr
 275 280 285
 Pro His Leu Ala Asp Gly Ile Gly Ile Val Gly Gly Trp Ala Glu Lys
 290 295 300
 Val Gly Leu Asp Val Thr Leu Ala Arg Glu Leu Thr Glu Ala Ile Leu
 305 310 315 320
 Val Arg Gly Val Asp Trp Val Arg Glu Ile Thr Arg Val His Gly Ala
 325 330 335
 Gly Val Arg Trp Ile Ile Asp Leu Gly Pro Gly Asp Ile Leu Thr Arg
 340 345 350
 Leu Thr Ala Pro Val Ile Arg Gly Leu Gly Val Gly Ile Val Pro Val
 355 360 365
 Ala Asn Arg Gly Gly Gln Arg Thr Leu Phe Thr Val Gly Ala Val Pro
 370 375 380
 Glu Val Val Arg Ala Trp Leu Ser Tyr Ala Pro Thr Val Val Gln Leu
 385 390 395 400
 Pro Asp Gly Arg Ile Lys Leu Ser Thr Lys Phe Thr Arg Leu Thr Gly
 405 410 415
 Arg Ser Pro Ile Leu Leu Ala Gly Met Thr Pro Thr Thr Val Asp Ala
 420 425 430
 Asn Ile Val Ala Ala Ala Ala Asn Ala Gly His Trp Ala Glu Leu Ala
 435 440 445
 Gly Gly Gly Gln Val Thr Glu Glu Ile Phe Ala Asn Arg Val Glu Gln
 450 455 460
 Leu Ser Gly Leu Leu Glu Pro Gly Arg Thr Tyr Gln Phe Asn Ala Leu
 465 470 475 480
 Phe Leu Asp Pro Tyr Leu Trp Lys Leu Gln Val Gly Gly Lys Arg Leu

REN-01-032-Util.ST25.txt

485

490

495

Val Gln Lys Ala Arg Gln Ser Gly Ala Ala Ile Asp Gly Val Val Ile
 500 505 510

Ser Gly Gly Ile Leu Asp Leu Glu Asp Ala Val Glu Leu Ile Glu Glu
 515 520 525

Leu Gly Gly Ile Gly Ile Ser Tyr Val Val Phe Lys Pro Gly Thr Ile
 530 535 540

Glu Gln Ile Arg Ser Val Ile Arg Ile Ala Thr Glu Met Ser Thr Lys
 545 550 555 560

Pro Val Ile Met His Val Glu Gly Gly Arg Ala Gly Gly His His Ser
 565 570 575

Trp Glu Asp Leu Asp Asp Leu Leu Leu Ala Thr Tyr Ser Glu Leu Arg
 580 585 590

Ser His Ala Asn Ile Thr Val Cys Val Gly Gly Gly Ile Gly Thr Pro
 595 600 605

Glu Lys Ala Ala Glu Tyr Leu Ser Gly Arg Trp Ala Gln Ala Tyr Gly
 610 615 620

Phe Pro Leu Met Pro Ile Asp Gly Ile Leu Val Gly Thr Ala Ala Met
 625 630 635 640

Ala Thr Lys Glu Ala Thr Thr Ser Pro Ser Val Lys Arg Met Leu Val
 645 650 655

Glu Thr Gln Gly Thr Asp Gln Trp Ile Gly Ser Gly Lys Ala Gln Gly
 660 665 670

Gly Met Ala Ser Ser Arg Ser Gln Leu Gly Ala Asp Ile His Glu Ile
 675 680 685

Asp Asn Ala Ala Ser Arg Cys Gly Arg Leu Leu Asp Glu Val Ala Gly
 690 695 700

Asp Ala Glu Ala Val Ala Glu Arg Arg Asp Glu Ile Ile Ala Ala Met
 705 710 715 720

Ala Asn Thr Ala Lys Pro Tyr Phe Gly Asp Val Ser Glu Met Thr Tyr
 725 730 735

Leu Gln Trp Leu Gln Arg Tyr Val Glu Leu Thr Ile Gly Glu Gly Asn
 740 745 750

Ser Thr Ala Asp Thr Ala Ser Pro Gly Ser Pro Trp Leu Ala Asp Thr
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REN-01-032-Util.ST25.txt
760 765

755

Trp Arg Asp Arg Phe Gln Lys Met Leu Gln Arg Ala Glu Ser Arg Leu
770 775 780

His Pro Ser Asp Phe Gly Leu Ile Lys Thr Ile Phe Thr Asp Pro Val
785 790 795 800

Leu Leu Glu Lys Pro Asn Gln Ala Ile Ala Ala Leu Leu Lys Tyr Tyr
805 810 815

Pro Asp Ala Glu Thr Val Gln Leu His Pro Ala Asp Ala Pro Phe Phe
820 825 830

Val Met Leu Cys Gln Met Leu Gly Lys Pro Val Asn Phe Val Pro Val
835 840 845

Ile Asp Lys Asp Val Arg Arg Trp Trp Arg Ser Asp Ser Leu Trp Gln
850 855 860

Ala His Asp Ala Arg Tyr Asp Ala Asp Gln Val Cys Ile Ile Pro Gly
865 870 875 880

Ile Ala Ala Val Ala Gly Ile Thr Gln Met Asp Glu Pro Val Gly Glu
885 890 895

Leu Leu Asp Arg Phe Glu Gln Ala Ala Ile Asp Glu Val Leu Ala Gly
900 905 910

Gly Ala Glu Pro Val Val Val Met Ser Arg Arg Leu Gly Arg Ala Asp
915 920 925

Val Ala Gly Pro Leu Ala Val Val Leu Asp Ala Pro Asp Val Leu Trp
930 935 940

Ala Gly Arg Ile Ala Thr Asn Pro Val His Arg Ile Ala Asp Pro Asn
945 950 955 960

Glu Trp Gln Val Asn Gly Asn Leu Ser Ala Thr His Ser Ser Thr Gly
965 970 975

Ala Gln Leu Gln Val Lys Ser Glu Asp Gln Gln Val Val Leu Ser Val
980 985 990

Pro Val Ser Asn Gly Trp Ile Asp Ile Pro Phe Thr Leu Pro Thr Asn
995 1000 1005

Thr Val Asp Gly Gly Ala Leu Leu Val Ser Thr Glu Asp Ala Thr
1010 1015 1020

Ser Ala Met Arg Ala Val Leu Ala Ile Val Ala Gly Val Asp Gly
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1025 REN-01-032-util.ST25.txt
 1030 1035
 Pro Glu Leu Leu Ser Pro Val Lys Asp Gly Thr Ala Ile Val Thr
 1040 1045 1050
 Val Asp Trp Asn Pro Glu Arg Val Ala Asp His Thr Gly Val Thr
 1055 1060 1065
 Ala Thr Phe Arg Glu Pro Leu Ala Pro Ser Leu Ala Thr Val Pro
 1070 1075 1080
 Asp Ala Leu Val Gly Ala Cys Trp Pro Ala Val Phe Ser Ala Ile
 1085 1090 1095
 Gly Ser Ala Val Thr Glu Ala Gly Val Leu Val Val Glu Gly Leu
 1100 1105 1110
 Leu Asn Leu Leu His Leu Asp His Ala Val Cys Val Val Gly Lys
 1115 1120 1125
 Leu Pro Thr Val Pro Ala Gln Leu Thr Val Thr Ala Thr Val Ser
 1130 1135 1140
 Leu Ala Ile Asp Thr Asp Met Gly Arg Val Val Pro Val Ser Val
 1145 1150 1155
 Thr Ile Arg Asp Thr Thr Gly Ala Asp Gly Ala Val Leu Ala Thr
 1160 1165 1170
 Leu Glu Glu Arg Phe Val Ile Leu Gly Arg Thr Gly Thr Ala Glu
 1175 1180 1185
 Leu Thr Gly Pro Val Arg Ala Gly Gly Ala Ile Ser Glu Asn Ala
 1190 1195 1200
 Thr Asp Thr Pro Arg Arg Arg Arg Arg Asp Val Thr Leu Thr Ala
 1205 1210 1215
 Pro Ile Asp Met Arg Pro Phe Ala Val Val Ser Gly Asp His Asn
 1220 1225 1230
 Pro Ile His Thr Asp Arg Thr Ala Ala Leu Leu Ala Gly Leu Glu
 1235 1240 1245
 Ser Pro Ile Val His Gly Met Trp Leu Ser Ala Ala Ala Gln His
 1250 1255 1260
 Val Val Met Ala Thr Asp Gly Gln Ala Arg Pro Ala Ala Arg Leu
 1265 1270 1275
 Ile Gly Trp Thr Ala Arg Phe Leu Gly Met Ala His Pro Gly Asp

1280 REN-01-032-Util.ST25.txt
 1285 1290
 Lys Val Asp Phe Arg Val Asp Arg Ile Gly Ile Asp Gln Gly Ala
 1295 1300 1305
 Glu Ile Leu Glu Val Ser Ala Arg Ile Ser Ser Gly Leu Val Met
 1310 1315 1320
 Ser Ala Thr Ala Arg Leu Ala Ala Pro Lys Thr Val Tyr Ala Phe
 1325 1330 1335
 Pro Gly Gln Gly Ile Gln His Lys Gly Met Gly Met Asp Val Arg
 1340 1345 1350
 Ala Arg Ser Lys Ala Ala Arg Arg Val Trp Asp Asp Ala Asp Lys
 1355 1360 1365
 Phe Thr Arg Ser Gly Leu Gly Phe Ser Val Leu His Val Val Arg
 1370 1375 1380
 Asp Asn Pro Thr Asn Ile Thr Ala Asn Gly Val His Tyr His His
 1385 1390 1395
 Pro Asp Gly Val Leu Tyr Leu Thr Gln Phe Thr Gln Val Ala Met
 1400 1405 1410
 Ala Thr Val Ala Val Ala Gln Val Ala Glu Met Arg Glu Gln Gly
 1415 1420 1425
 Ala Phe Val Glu Gly Ala Ile Ala Cys Gly His Ser Val Gly Glu
 1430 1435 1440
 Tyr Thr Ala Leu Ala Cys Val Met Gly Val Tyr Glu Leu Glu Ala
 1445 1450 1455
 Leu Leu Glu Thr Val Phe His Arg Gly Ser Lys Met His Asp Ile
 1460 1465 1470
 Val Leu Arg Asp Glu Leu Gly Arg Ser Asn Tyr Arg Leu Ala Ala
 1475 1480 1485
 Ile Arg Pro Ser Gln Ile Gly Leu Pro Asp Asp Glu Val Pro Ala
 1490 1495 1500
 Phe Val Arg Gly Ile Ala Glu Ser Thr Gly Glu Phe Leu Glu Ile
 1505 1510 1515
 Val Asn Phe Asn Leu Arg Gly Ser Gln Tyr Ala Ile Ala Gly Thr
 1520 1525 1530
 Val His Gly Leu Glu Ala Leu Glu Ala Glu Val Glu Arg Arg Arg

REN-01-032-Util.ST25.txt
1535 1540 1545

Glu Leu Thr Gly Gly Arg Arg Ser Phe Ile Leu Val Pro Gly Ile
1550 1555 1560

Asp Val Pro Phe His Ser Arg Val Leu Arg Val Gly Val Ala Glu
1565 1570 1575

Phe Arg Arg Ser Leu Asp Arg Val Leu Pro Gln Asp Gln Asp Pro
1580 1585 1590

Asp Trp Ile Ile Gly Arg Tyr Ile Pro Asn Leu Val Pro Arg Pro
1595 1600 1605

Phe Thr Leu Ala Arg Asp Phe Ile Gln Glu Ile Arg Asp Leu Val
1610 1615 1620

Pro Ala Glu Pro Leu Asp Asp Ile Leu Ala Asp Tyr Asp Thr Trp
1625 1630 1635

Arg Arg Glu Arg Pro Ser Glu Met Ala Arg Arg Val Leu Ile Glu
1640 1645 1650

Leu Leu Ala Trp Gln Phe Ala Ser Pro Val Arg Trp Ile Glu Thr
1655 1660 1665

Gln Asp Leu Leu Phe Thr Glu Glu Ala Ala Gly Gly Leu Gly Val
1670 1675 1680

Glu Arg Phe Val Glu Ile Gly Val Lys Ser Ala Pro Thr Val Ala
1685 1690 1695

Gly Leu Ala Thr Asp Thr Leu Lys Leu Pro Glu Tyr Ser His Asn
1700 1705 1710

Thr Val Glu Val Leu Asn Val Glu Arg Asp Ala Ala Val Leu Phe
1715 1720 1725

Ala Thr Asp Thr Asp Pro Glu Leu Glu Pro Glu Pro Glu Asn Val
1730 1735 1740

Ser Asp Ala Ser Ala Ala Leu Pro Ala Glu Ser Ala Leu Ala Leu
1745 1750 1755

Gly Thr Val Ala Pro Ala Pro Val Val Pro Ser Gly Pro Arg Pro
1760 1765 1770

Glu Asp Ile Ser Phe Gly Ala Ala Asp Ala Thr Leu Ala Leu Ile
1775 1780 1785

Ala Leu Ser Ala Lys Met Arg Leu Asp Gln Ile Glu Glu Met Asp

1790 REN-01-032-Util.ST25.txt
 1795 1800
 Ser Ile Glu Ser Ile Thr Asp Gly Ala Ser Ser Arg Arg Asn Gln
 1805 1810 1815
 Leu Leu Val Asp Leu Gly Ser Glu Leu Ser Leu Gly Ala Ile Asp
 1820 1825 1830
 Gly Val Ala Glu Ala Asp Leu Ala Gly Leu Arg Ser Gln Val Thr
 1835 1840 1845
 Lys Leu Ala Arg Thr Tyr Lys Pro Tyr Gly Pro Val Leu Ser Glu
 1850 1855 1860
 Leu Ile Asn Asp Gln Leu Arg Ser Ala Leu Gly Pro Ser Gly Lys
 1865 1870 1875
 Arg Pro Gly Val Ile Ala Glu Arg Val Lys Lys Ile Trp Glu Leu
 1880 1885 1890
 Gly Asp Gly Trp Val Lys His Val Thr Val Glu Ile Ala Leu Gly
 1895 1900 1905
 Thr Arg Glu Gly Thr Ser Val Arg Gly Gly Pro Leu Gly Asn Leu
 1910 1915 1920
 Asn Glu Gly Ala Leu Ala Asp Val Asp Ser Val Asp Lys Ala Val
 1925 1930 1935
 Asp Ala Ala Val Ala Ser Val Ala Ala Arg His Gly Val Val Val
 1940 1945 1950
 Ala Leu Pro Ser Ala Gly Ser Gly Gly Ser Ala Thr Val Asp Val
 1955 1960 1965
 Ala Ala Leu Ser Glu Phe Thr Asp Gln Ile Thr Gly His Asp Gly
 1970 1975 1980
 Val Leu Ala Ser Ala Ala Arg Leu Val Leu Gly Gln Leu Gly Leu
 1985 1990 1995
 Asp Gly Pro Val Thr Ala Ala Pro Ala Thr Thr Asp Thr Gly Leu
 2000 2005 2010
 Ile Asp Leu Val Thr Ala Glu Leu Ser Thr Asp Trp Pro Arg Leu
 2015 2020 2025
 Val Ala Pro Val Phe Asp Val Lys Lys Ala Val Val Phe Asp Asp
 2030 2035 2040
 Arg Trp Ala Ser Ala Arg Glu Asp Leu Val Arg Leu Trp Leu Asn

2045 REN-01-032-util.ST25.txt
 2050 2055
 Asp Glu Gly Glu Ile Glu Ala Gln Trp Ser His Leu Ser Glu Arg
 2060 2065 2070
 Phe Glu Gly Ala Gly His Val Val Ala Thr Gln Ala Thr Trp Trp
 2075 2080 2085
 Gln Gly Lys Ser Leu Ala Ala Gly Arg Gln Ile His Ala Ser Leu
 2090 2095 2100
 Tyr Gly Arg Ile Ala Ala Gly Ala Gln Asn Pro Asp Arg Gly Leu
 2105 2110 2115
 Tyr Ser Ser Glu Ile Ala Val Val Thr Gly Ala Ser Lys Gly Ser
 2120 2125 2130
 Ile Ala Ala Ser Val Ala Ala Arg Leu Leu Asp Gly Gly Ala Thr
 2135 2140 2145
 Val Ile Ala Thr Thr Ser Lys Leu Asp Glu Glu Arg Ile Thr Phe
 2150 2155 2160
 Tyr Arg Ala Leu Tyr Arg Asp His Ala Arg Tyr Gly Ala Ala Leu
 2165 2170 2175
 Trp Val Val Ala Ala Asn Met Ala Ser Tyr Ser Asp Ile Asp Ala
 2180 2185 2190
 Leu Val Glu Trp Ile Gly Asn Glu Gln Thr Glu Ser Leu Gly Pro
 2195 2200 2205
 Gln Ser Ile His Ile Lys Asp Ala Gln Thr Pro Thr Leu Leu Phe
 2210 2215 2220
 Pro Phe Ala Ala Pro Arg Val Ile Gly Asp Leu Ser Glu Ala Gly
 2225 2230 2235
 Ala Arg Ser Glu Ile Glu Met Lys Val Leu Leu Trp Ala Val Gln
 2240 2245 2250
 Arg Leu Ile Val Gly Leu Ser Lys Ile Gly Thr Glu Arg Asp Val
 2255 2260 2265
 Ala Ser Arg Leu His Val Val Leu Pro Gly Ser Pro Asn Arg Gly
 2270 2275 2280
 Met Phe Gly Gly Asp Gly Ala Tyr Gly Glu Ala Lys Ser Ala Leu
 2285 2290 2295
 Asp Ala Val Val Ser Arg Trp His Ala Glu Ser Ser Trp Ala Ala

2300 REN-01-032-Util.ST25.txt
 2305 2310
 Arg Val Ser Leu Ala His Ala Leu Ile Gly Trp Thr Arg Gly Thr
 2315 2320 2325
 Gly Leu Met Gly His Asn Asp Val Ile Val Ser Ala Val Glu Glu
 2330 2335 2340
 Ala Gly Val Thr Thr Tyr Ser Thr Asp Glu Met Ala Ala Met Leu
 2345 2350 2355
 Leu Asp Leu Cys Asn Ala Glu Ser Lys Val Ala Ala Ala Gly Thr
 2360 2365 2370
 Pro Ile Thr Val Asp Leu Thr Gly Gly Leu Gly Glu Val Asp Leu
 2375 2380 2385
 Asp Met Ala Glu Leu Ala Ala Lys Ala Arg Glu Asp His Ala Ala
 2390 2395 2400
 Gln Ala Ala Glu Asp Glu Ala Thr Glu Ala Ser Glu Val Ala Gly
 2405 2410 2415
 Thr Ile Ala Ala Leu Pro Ser Pro Pro Arg Gly Tyr Thr Pro Ala
 2420 2425 2430
 Ser Pro His Trp Asp Asp Leu Asp Val Asp Pro Ala Asp Leu Val
 2435 2440 2445
 Val Ile Val Gly Gly Ala Glu Ile Gly Pro Tyr Gly Ser Ser Arg
 2450 2455 2460
 Thr Arg Phe Glu Met Glu Val Ala Gly Glu Leu Ser Ala Ala Gly
 2465 2470 2475
 Val Leu Glu Leu Val Trp Thr Thr Gly Leu Ile Arg Trp Glu Asp
 2480 2485 2490
 Asp Pro Gln Pro Gly Trp Tyr Asp Thr Glu Ser Gly Glu Leu Val
 2495 2500 2505
 Asp Glu Ser Glu Leu Val Glu Arg Tyr His Asp Thr Val Val Gln
 2510 2515 2520
 Arg Cys Gly Ile Arg Glu Phe Val Asp Asp Gly Thr Ile Asp Pro
 2525 2530 2535
 Asp His Ala Tyr Pro Leu Leu Val Ser Val Phe Leu Asp Lys Asp
 2540 2545 2550
 Phe Ala Phe Val Val Ser Ser Glu Ala Asp Ala Arg Ala Phe Val

2555 REN-01-032-Util.ST25.txt 2560 2565
 Glu Phe Asp Pro Glu His Thr Val Ile Arg Pro Val Pro Asp Ser
 2570 2575 2580
 Ser Asp Trp Gln Val Ile Arg Lys Ala Gly Thr Glu Ile Arg Val
 2585 2590 2595
 Pro Arg Lys Met Lys Leu Ser Arg Val Val Gly Gly Gln Ile Pro
 2600 2605 2610
 Thr Gly Phe Asp Pro Thr Val Trp Gly Ile Ser Pro Asp Met Val
 2615 2620 2625
 Ser Ser Ile Asp Arg Val Ala Val Trp Ser Ile Val Ala Thr Val
 2630 2635 2640
 Asp Ala Phe Leu Ser Ala Gly Phe Thr Pro Ala Glu Val Met Arg
 2645 2650 2655
 Tyr Val His Pro Ser Leu Val Ala Asn Thr Met Gly Thr Gly Met
 2660 2665 2670
 Gly Gly Gly Thr Ser Ile Gln Arg Leu Tyr His Ser Ser Leu Leu
 2675 2680 2685
 Gly Arg Asn Lys Pro Asn Asp Ile Phe Gln Glu Ile Leu Pro Asn
 2690 2695 2700
 Ile Val Ala Ala His Val Val Gln Ser Tyr Ile Gly Ser Tyr Gly
 2705 2710 2715
 Ser Met Ile His Pro Val Ala Ala Cys Ala Thr Ala Ala Val Ser
 2720 2725 2730
 Val Glu Glu Gly Val Asp Lys Ile Arg Leu Gly Lys Ala Glu Leu
 2735 2740 2745
 Val Val Ala Gly Gly Ile Asp Asp Leu Thr Leu Glu Gly Ile Ile
 2750 2755 2760
 Gly Phe Gly Asp Met Ala Ala Thr Ala Asp Thr Ala Met Met Arg
 2765 2770 2775
 Gly Arg Gly Ile His Asp Ser Lys Phe Ser Arg Pro Asn Asp Arg
 2780 2785 2790
 Arg Arg Leu Gly Phe Val Glu Ala Gln Gly Gly Gly Thr Ile Leu
 2795 2800 2805
 Leu Ala Arg Gly Asp Leu Ala Leu Lys Met Gly Leu Pro Val Phe

2810 REN-01-032-Util.ST25.txt
 2815 2820
 Ala Val Val Ala Phe Ala Gln Ser Phe Gly Asp Gly Val His Thr
 2825 2830 2835
 Ser Ile Pro Ala Pro Gly Leu Gly Ala Leu Gly Ala Gly Arg Gly
 2840 2845 2850
 Gly Lys Asp Ser Pro Leu Val Gln Ser Leu Ala Lys Leu Gly Val
 2855 2860 2865
 Ser Ala Asp Asp Ile Ala Val Ile Ser Lys His Asp Thr Ser Thr
 2870 2875 2880
 Leu Ala Asn Asp Pro Asn Glu Thr Glu Leu His Glu Arg Leu Ala
 2885 2890 2895
 Asp Ala Met Gly Arg Ser Ala Gly Ala Pro Leu Phe Val Val Ser
 2900 2905 2910
 Gln Lys Ser Leu Thr Gly His Ala Lys Gly Gly Ala Ala Val Phe
 2915 2920 2925
 Gln Met Met Gly Leu Cys Gln Met Leu Arg Asp Gly Val Ile Pro
 2930 2935 2940
 Pro Asn Arg Ser Leu Asp Cys Val Asp Glu Glu Leu Ala Gly Ala
 2945 2950 2955
 Ala His Phe Val Trp Leu Arg Asp Thr Leu Arg Leu Gly Glu Lys
 2960 2965 2970
 Phe Pro Leu Lys Ala Gly Met Leu Thr Ser Leu Gly Phe Gly His
 2975 2980 2985
 Val Ser Gly Leu Val Ala Leu Val His Pro Gln Ala Phe Ile Ala
 2990 2995 3000
 Ala Leu Asp Pro Gly Gln Arg Asp Asp Tyr Gln Arg Arg Ala Asn
 3005 3010 3015
 Val Arg Leu Leu Ala Gly Gln Arg Arg Leu Ala Ser Ala Ile Ala
 3020 3025 3030
 Gly Gly Ala Pro Met Tyr Glu Arg Pro Pro Asp Arg Arg Phe Asp
 3035 3040 3045
 His His Val Pro Glu Lys Leu Gln Glu Ala Ala Met Leu Leu Asn
 3050 3055 3060
 Pro Ala Ala Arg Leu Gly Asp Gly Asp Ala Tyr Ile Gly

3065

REN-01-032-Util.ST25.txt
3070 3075

<210> 25
 <211> 2586
 <212> PRT
 <213> Caenorhabditis elegans

<400> 25

Met Asp Pro Thr Gln Trp Trp Gln Lys Gln Asp Asp Ile Val Ile Ser
 1 5 10 15

Gly Val Ser Gly Arg Phe Pro Arg Cys Asp Asn Val Lys Met Phe Gly
 20 25 30

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

Trp Thr Pro Gly Phe Cys Asp Leu Pro Lys Arg His Gly Lys Leu Lys
 50 55 60

Val Leu Asn Lys Phe Asp Ala Gly Phe Phe Gln Val Thr Pro Lys Gln
 65 70 75 80

Ala Asn Phe Met Asp Pro Gln Val Arg Leu Leu Leu Glu Ala Ser Trp
 85 90 95

Glu Ala Met Val Asp Ala Gly Ile Asn Pro Thr Asp Leu Arg Gly Ser
 100 105 110

Lys Thr Gly Val Phe Val Gly Cys Ser Ala Ser Glu Thr Ser Gly Met
 115 120 125

Leu Thr Gln Asp Pro Asp Thr Val Thr Gly Tyr Thr Leu Thr Gly Cys
 130 135 140

Val Arg Ser Met Phe Ser Asn Arg Ile Ser Tyr Thr Phe Asp Leu Gln
 145 150 155 160

Gly Pro Ser Phe Ser Val Asp Thr Ala Cys Ser Ser Ser Leu Leu Ala
 165 170 175

Leu Gln Leu Ala Val Asp Ser Ile Arg Gln Gly Gln Cys Asp Ala Ala
 180 185 190

Ile Val Ala Gly Ala His Leu Thr Leu Thr Pro Thr Ala Ala Leu Gln
 195 200 205

Phe Leu Arg Leu Gly Met Leu Thr Asp Lys Gly Ser Cys Arg Ser Phe
 210 215 220

Asp Glu Ser Gly Asp Gly Tyr Cys Arg Thr Glu Gly Val Ala Ala Ile
 225 230 235 240

REN-01-032-Uti1.ST25.txt

Phe Ile Gln Arg Lys₂₄₅ Lys Lys Ala Gln Arg₂₅₀ Leu Tyr Ala Thr Val₂₅₅ Val
 His Ala Lys Ser₂₆₀ Asn Thr Asp Gly His₂₆₅ Lys Glu His Gly Ile₂₇₀ Thr Phe
 Pro Ser Gly₂₇₅ Glu Arg Gln Ala Gln₂₈₀ Leu Leu Gln Glu Val₂₈₅ Tyr Ser Glu
 Ala Gly₂₉₀ Ile Asp Pro Asn Ser₂₉₅ Val Tyr Tyr Val Glu₃₀₀ Ala His Gly Thr
 Gly₃₀₅ Thr Lys Val Gly Asp₃₁₀ Pro Gln Glu Ala Asn₃₁₅ Ala Ile Cys Glu Val₃₂₀
 Phe Cys Ser Lys Arg₃₂₅ Thr Asp Ser Leu Leu₃₃₀ Ile Gly Ser Val Lys₃₃₅ Ser
 Asn Met Gly His₃₄₀ Ala Glu Pro Ala Ser₃₄₅ Gly Val Cys Ser Leu₃₅₀ Thr Lys
 Ile Leu Leu₃₅₅ Ser Ile Glu Arg Gln₃₆₀ Leu Ile Pro Pro Asn₃₆₅ Leu His Tyr
 Asn Thr₃₇₀ Pro Asn Gln Tyr Ile₃₇₅ Pro Gly Leu Thr Asp₃₈₀ Gly Arg Leu Lys
 Val₃₈₅ Val Thr Glu Pro Thr₃₉₀ Ala Leu Pro Gly Gly₃₉₅ Leu Ile Gly Ile Asn₄₀₀
 Ser Phe Gly Phe Gly₄₀₅ Gly Ser Asn Thr His₄₁₀ Val Ile Leu Lys Ala₄₁₅ Ala
 Asp His Ile Ala₄₂₀ Pro Pro Ile Thr Pro₄₂₅ His Pro Phe Thr Lys₄₃₀ Leu Val
 Thr Tyr Cys₄₃₅ Gly Arg Thr Gln Glu₄₄₀ Ala Val Glu Asn Ile₄₄₅ Phe Thr Glu
 Ile Glu₄₅₀ Ser Asn Lys Asp Asp₄₅₅ Leu Tyr Leu Gln Ala₄₆₀ Leu Leu Ala Asn
 Gln Ala Asn Met Pro Ala₄₇₀ Asn Leu Leu Pro Phe₄₇₅ Arg Gly Tyr Met Leu₄₈₀
 Leu Asp Arg Glu Asn₄₈₅ Asn Val Glu Thr Leu₄₉₀ Lys Ser Ile Thr Lys₄₉₅ Val
 Pro Ile Thr Glu₅₀₀ Ala Arg Pro Ile Tyr₅₀₅ Phe Ile Tyr Ser Gly₅₁₀ Met Gly

REN-01-032-Uti1.ST25.txt

Ser Gln Trp Pro Gly Met Ala Ile Lys Leu Met Lys Ile Pro Met Phe
 515 520 525
 Asp Asp Ser Leu Arg Ala Ser Ser Lys Thr Leu Glu Glu Phe Gly Leu
 530 535 540
 Asp Val Tyr Gly Met Leu Cys Asn Pro Asp Pro Glu Gln Tyr Ser Asn
 545 550 555 560
 Asn Thr Met Asn Cys Met Leu Ala Ile Thr Ala Ile Gln Ile Ala Leu
 565 570 575
 Thr Asp Val Leu Thr Ala Leu Gly Val Ser Pro Asp Gly Ile Ile Gly
 580 585 590
 His Ser Thr Gly Glu Met Gly Cys Gly Tyr Ala Asp Gly Gly Ile Thr
 595 600 605
 Arg Glu Gln Thr Met Arg Leu Ala Tyr His Arg Gly Thr Thr Ile Met
 610 615 620
 Lys His Thr Glu Ile Lys Gly Ala Met Ala Ala Val Gly Leu Thr Trp
 625 630 635 640
 Glu Gln Val Lys Glu Gln Ala Pro Pro Gly Val Val Ala Ala Cys His
 645 650 655
 Asn Gly Ala Asp Ser Val Thr Ile Ser Gly Asp Ala Glu Gly Val Ala
 660 665 670
 Thr Phe Cys Ala Gln Leu Lys Glu Lys Asp Ile Phe Ala Lys Val Val
 675 680 685
 Asp Thr Ser Gly Ile Pro Phe His Ser Pro Ala Met Leu Ala Val Gln
 690 695 700
 Asp Glu Met Ile Glu Cys Met Arg Thr Ala Val Pro Glu Pro Lys Pro
 705 710 715 720
 Arg Ser Ser Lys Trp Ile Ser Thr Ser Ile Pro Glu Asp Asp Trp Glu
 725 730 735
 Ser Asp Leu Ala Ala Thr Cys Ser Ala Glu Tyr His Val His Asn Ala
 740 745 750
 Cys Ser Pro Val Leu Phe Tyr Glu Ala Ile Gln Lys Ile Pro Ala Asn
 755 760 765
 Ala Val Thr Ile Glu Met Ala Pro His Ser Leu Met Gln Ala Ile Leu
 770 775 780

REN-01-032-Util.ST25.txt

Arg Arg Ser Leu Gln Lys Thr Val Thr Asn Val Gly Leu Met Asn Arg
 785 790 795 800
 Pro Lys Ser Glu Asn Asp Asp Glu Leu Glu Ser Phe Leu Gly Ser Leu
 805 810 815
 Gly Lys Ile Tyr Gln Ala Gly Val Asn Ile Gln Ile Thr Glu Leu Tyr
 820 825 830
 Pro Gly Gly Gln Tyr Lys Gly Val Val Pro Lys Gly Thr Pro Met Ile
 835 840 845
 Gly Pro Met Trp Lys Trp Asp His Thr Gln Asp Trp Leu Thr Ile Asp
 850 855 860
 Gly Arg Gln Val Leu Ala Gly Gly Ser Gly Ser Val Ala Ser Ser Ala
 865 870 875 880
 Thr Tyr Asn Ile Asp Pro Phe Ala Thr Asp Ser Lys Glu Thr Tyr Leu
 885 890 895
 Leu Asp His Val Ile Asp Gly Arg Val Leu Tyr Pro Phe Thr Gly His
 900 905 910
 Met Val Leu Ala Trp Arg Thr Leu Cys Lys Leu Lys Gly Leu Asp Tyr
 915 920 925
 Thr Lys Thr Pro Val Val Phe Glu Asn Ile Asn Val Phe Ser Ala Thr
 930 935 940
 Ile Leu Thr Lys Pro Ile Lys Leu Asp Val Val Leu Ser Pro Gly Asn
 945 950 955 960
 Gly Tyr Phe Glu Ile Ile Ser Asp Asp Gln Val Ala Ala Ser Gly Arg
 965 970 975
 Ile Tyr Ile Pro Glu Asp Asn Gln Pro Phe Tyr Tyr Gly Lys Leu Glu
 980 985 990
 Asp Ile Arg Thr Ser Glu Ile Ala Asp Arg Ile Glu Leu Asp Thr Glu
 995 1000 1005
 Asp Ala Tyr Lys Glu Phe Leu Leu Arg Gly Tyr Glu Tyr Gly Gln
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 Ala Phe Arg Gly Ile Tyr Lys Thr Cys Asn Ser Gly Glu Arg Gly
 1025 1030 1035
 Phe Leu Tyr Trp Thr Gly Asn Trp Val Thr Phe Leu Asp Ser Leu
 1040 1045 1050

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Leu Gln Thr Ala Leu Leu Ala Glu Arg Ser Asp Thr Leu Arg Leu
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 Pro Thr Arg Val Arg His Leu Arg Ile Asp Pro Asn Lys His Leu
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 Glu His Val Val Glu Lys Asp Gly Ile Gln Val Ile Glu Leu Arg
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 Asn Asp His Ser Thr Asn Gly Cys Ile Ala Gly Gly Val Glu Cys
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 Cys Asp Leu Asn Ala His Ser Val Ala Arg Arg Ile Gln Val Ser
 1115 1120 1125
 Gly Gln Leu Tyr His Glu Lys Ile Phe Phe Val Pro His Phe Asp
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 His Asn Cys Leu Ser Gly His Lys Lys Thr Ser Thr Ile Leu Lys
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 Asp Tyr Ser Ala Val Ile Lys Gln Gln Leu Tyr Thr Gly Phe Ser
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 Cys Thr Val Leu His His Ile Ala Asp Met Phe Lys Ile Glu Asp
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 Cys Glu Asp Phe Glu Asp Arg Val Ala Ala Lys Leu Lys Ser Val
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 Arg Gly Ile Phe Glu Leu Asp Arg Leu Trp Ala Gly Ala Val Leu
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 Asn Asp Arg Ile Val Lys Ser Leu Gln Asp Ile Cys Ile Glu Asn
 1265 1270 1275
 Ser Ala Gly His His Ala Thr Met Ala Ala Val Asp Leu Val Ser
 1280 1285 1290
 Thr Asp Gln Ile Arg His Cys Ile Glu Ala Asn Ser Ser His Pro
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Leu Leu Glu Thr Asp Tyr Thr Cys Ile Gly Ala Asn Val Asp His
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 1370 1375 1380
 Gly Phe Leu Leu Val Val Glu Val Thr Ser Gln Tyr Glu Ile Ala
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 Ser Arg Lys Tyr Asn Gln Phe Phe Thr His Glu Gln Leu Leu Asp
 1415 1420 1425
 Met Phe Lys Ser Thr Gly Phe Leu Ile Cys Asn Phe Gln Ser Asp
 1430 1435 1440
 Pro Ala Leu Met Thr Thr Thr Tyr Ala Val Arg Arg Val Ser Pro
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 Ile Pro Arg Asp Pro Val Phe Ile Asp Val Asp Asp Val Lys Glu
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 Phe Asn Trp Ile Glu Pro Leu Gln Lys Val Ser Glu Glu Arg Leu
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 Asn Glu Pro Asp Ser Lys Thr Ile Trp Leu Val Ser Asn Lys Cys
 1490 1495 1500
 Arg Asn Asn Gly Ile Val Gly Leu Gly Leu Cys Phe Val Glu Glu
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 1535 1540 1545
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Tyr Met Asp Gly Gln Trp Gly Ser Met Arg His Ile Val Val Lys
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 Arg Leu Lys Asp Gly Thr Arg Leu Met Gly Ile Leu Pro Ala Gln
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 Val Tyr Thr Thr Ala Tyr Tyr Ala Leu Val Arg Arg Gly Leu Met
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 Phe Thr Thr Val Gly Ser Ala Glu Lys Arg Glu Phe Leu Lys Asn
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 1775 1780 1785
 Ala Asp Phe Glu Leu His Ile Arg Gln His Thr Lys Gly Arg Gly
 1790 1795 1800
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 1805 1810 1815

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 Lys Val Asp Leu Ser Gln Asn Ser Ser Leu Gly Met Ala Lys Leu
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 Leu Asp Asn Val Ser Val His Gly Ile Leu Leu Asp Ser Ile Met
 1850 1855 1860
 Asp Pro Thr Val Gly Asp Leu Asp Glu Trp Lys Glu Ile Ala Arg
 1865 1870 1875
 Leu Leu Glu Gln Gly Ile Lys Ser Gly Val Val Lys Pro Leu His
 1880 1885 1890
 Ser His Ser Phe Pro Ala Asp Lys Ala Glu Glu Ala Phe Arg Phe
 1895 1900 1905
 Met Ser Ala Gly Lys His Ile Gly Lys Val Ile Met Glu Ile Arg
 1910 1915 1920
 Pro Asp Glu Gly Thr Lys Val Cys Pro Pro Ser Lys Ile Ser Val
 1925 1930 1935
 Arg Ala Ile Cys Arg Thr Leu Cys His Pro Gln His Thr Tyr Leu
 1940 1945 1950
 Ile Thr Gly Gly Leu Gly Gly Phe Gly Leu Glu Leu Ala Gln Trp
 1955 1960 1965
 Leu Ile Asn Arg Gly Ala Arg Lys Leu Val Leu Thr Ser Arg Thr
 1970 1975 1980
 Gly Ile Arg Thr Gly Tyr Gln Ala Arg Cys Val His Phe Trp Arg
 1985 1990 1995
 Arg Thr Gly Val Ser Val Leu Val Ser Thr Leu Asn Ile Ala Lys
 2000 2005 2010
 Lys Ser Asp Ala Val Glu Leu Ile Asn Gln Cys Thr Ala Met Gly
 2015 2020 2025
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 Gln Leu Ala Asp Gln Gly Gly Thr Gly Arg Thr Ala Leu Gln Val
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 Asn Glu Leu Glu Met Lys Lys Asp Gly Glu Arg Asp Ala Glu Leu
 2270 2275 2280
 Asn Thr Ala Glu Met Leu Glu Gln Gln Met Asn Gln Leu Phe Lys
 2285 2290 2295
 Met Arg Val Asp Val Asn Asp Leu Asp Pro Gln Asp Ile Ile Val
 2300 2305 2310
 Lys Ala Asn Lys Val Glu Glu Gly Pro Ile Thr Phe Phe Val His
 2315 2320 2325

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 Gln Thr Ser Ile Glu Asp Val Ala Lys Cys Tyr Ile Arg Glu Met
 2360 2365 2370
 Lys Lys Ile Gln Pro Ser Gly Pro Tyr Arg Leu Val Gly Tyr Ser
 2375 2380 2385
 Tyr Gly Ala Cys Ile Gly Phe Glu Met Ala Asn Met Leu Gln Glu
 2390 2395 2400
 Ser Asp Gly Arg Asp Ala Val Glu Arg Leu Ile Leu Leu Asp Gly
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 Ser His Leu Tyr Met Gln Thr Tyr Arg Asn Val Tyr Arg Met Ala
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 2450 2455 2460
 Tyr Lys Lys Phe Arg Phe Glu Leu Leu Gln Gln Pro Gly Phe Lys
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 Phe Lys Ser Pro Glu Thr Val Ala Phe Ala Cys Glu Ala Met His
 2495 2500 2505
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<212> DNA
<213> Rattus norvegicus

<400> 26
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REN-01-032-util.ST25.txt

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<400> 27

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 20 25 30

Val Trp Val Gly Val Ser Gly Ser Glu Ala Ser Glu Ala Leu Ser Arg
 35 40 45

Asp Pro Glu Thr Leu Leu Gly Tyr Ser Met Val Gly Cys Gln Arg Ala
 50 55 60

Met Met Ala Asn Arg Leu Ser Phe Phe Phe Asp Phe Lys Gly Pro Ser
 65 70 75 80

Ile Ala Leu Asp Thr Ala Cys Ser Ser Ser Leu Leu Ala Leu Gln Asn
 85 90 95

REN-01-032-Util.ST25.txt

Ala Tyr Gln Ala Ile Arg Ser Gly Glu Cys Pro Ala Ala Ile Val Gly
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 Gly Ile Asn Leu Leu Leu Lys Pro Asn Thr Ser Val Gln Phe Met Lys
 115 120 125
 Leu Gly Met Leu Ser Pro Asp Gly Thr Cys Arg Ser Phe Asp Asp Ser
 130 135 140
 Gly Asn Gly Tyr Cys Arg Ala Glu Ala Val Val Ala Val Leu Leu Thr
 145 150 155 160
 Lys Lys Ser Leu Ala Arg Arg Val Tyr Ala Thr Ile Leu Asn Ala Gly
 165 170 175
 Thr Asn Thr Asp Gly Cys Lys Glu Gln Gly Val Thr Phe Pro Ser Gly
 180 185 190
 Glu Ala Gln Glu Gln Leu Ile Arg Ser Leu Tyr Gln Pro Gly Gly Val
 195 200 205
 Ala Pro Glu Ser Leu Glu Tyr Ile Glu Ala His Gly Thr Gly Thr Lys
 210 215 220
 Val Gly Asp Pro Gln Glu Leu Asn Gly Ile Thr Arg Ser Leu Cys Ala
 225 230 235 240
 Phe Arg Gln Ser Pro Leu Leu Ile Gly Ser Thr Lys Ser Asn Met Gly
 245 250 255
 His Pro Glu Pro Ala Ser Gly Leu Ala Ala Leu Thr Lys Val Leu Leu
 260 265 270
 Ser Leu Glu Asn Gly Val Trp Ala Pro Asn Leu His Phe His Asn Pro
 275 280 285
 Asn Pro Glu Ile Pro Ala Leu Leu Asp Gly Arg Leu Gln Val Val Asp
 290 295 300
 Arg Pro Leu Pro Val Arg Gly Gly Ile Val Gly Ile Asn Ser Phe Gly
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 Phe Gly Gly Ala Asn Val His Val Ile Leu Gln Pro Asn Thr Gln Gln
 325 330 335
 Ala Pro Ala Pro Ala Pro His Ala Ala Leu Pro His Leu Leu His Ala
 340 345 350
 Ser Gly Arg Thr Met Glu Ala Val Gln Gly Leu Leu Glu Gln Gly Arg
 355 360 365

REN-01-032-Util.ST25.txt

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 Ala Thr Pro Thr Ala Ala Met Pro Phe Arg Gly Tyr Thr Val Leu Gly
 385 390 395 400
 Val Glu Gly His Val Gln Glu Val Gln Gln Val Pro Ala Ser Gln Arg
 405 410 415
 Pro Leu Trp Phe Ile Cys Ser Gly Met Gly Thr Gln Trp Arg Gly Met
 420 425 430
 Gly Leu Ser Leu Met Arg Leu Asp Ser Phe Arg Glu Ser Ile Leu Arg
 435 440 445
 Ser Asp Glu Ala Leu Lys Pro Leu Gly Val Lys Val Ser Asp Leu Leu
 450 455 460
 Leu Ser Thr Asp Glu His Thr Phe Asp Asp Ile Val His Ser Phe Val
 465 470 475 480
 Ser Leu Thr Ala Ile Gln Ile Ala Leu Ile Asp Leu Leu Thr Ser Met
 485 490 495
 Gly Leu Lys Pro Asp Gly Ile Ile Gly His Ser Leu Gly Glu Val Ala
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 Cys Gly Tyr Ala Asp Gly Cys Leu Ser Gln Arg Glu Ala Val Leu Ala
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 Ala Tyr Trp Arg Gly Gln Cys Ile Lys Asp Ala Asn Leu Pro Ala Gly
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 Ser Met Ala Ala Val Gly Leu Ser Trp Glu Glu Cys Lys Gln Arg Cys
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 Pro Pro Gly Val Val Pro Ala Cys His Asn Ser Glu Asp Thr Val Thr
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 Ile Ser Gly Pro Gln Ala Ala Val Asn Glu Phe Val Glu Gln Leu Lys
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 Gln Glu Gly Val Phe Ala Lys Glu Val Arg Thr Gly Gly Leu Ala Phe
 595 600 605
 His Ser Tyr Phe Met Glu Gly Ile Ala Pro Thr Leu Leu Gln Ala Leu
 610 615 620
 Lys Lys Val Ile Arg Glu Pro Arg Pro Arg Ser Ala Arg Trp Leu Ser
 625 630 635 640

REN-01-032-Util.ST25.txt

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 Ser Ala Glu Tyr Asn Val Asn Asn Leu Val Ser Pro Val Leu Phe Gln
 660 665 670
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 675 680 685
 Pro His Ala Leu Leu Gln Ala Val Leu Lys Arg Gly Val Lys Pro Ser
 690 695 700
 Cys Thr Ile Ile Pro Leu Met Lys Arg Asp His Lys Asp Asn Leu Glu
 705 710 715 720
 Phe Phe Leu Thr Asn Leu Gly Lys Val His Leu Thr Gly Ile Asp Ile
 725 730 735
 Asn Pro Asn Ala Leu Phe Pro Pro Val Glu Phe Pro Val Pro Arg Gly
 740 745 750
 Thr Pro Leu Ile Ser Pro His Ile Lys Trp Asp His Ser Gln Thr Trp
 755 760 765
 Asp Ile Pro Val Ala Glu Asp Phe Pro Asn Gly Ser Ser Ser Ser Ser
 770 775 780
 Ala Thr Val Tyr Asn Ile Asp Ala Ser Ser Glu Ser Pro Asp His Tyr
 785 790 795 800
 Leu Val Asp His Cys Ile Asp Gly Arg Val Leu Phe Pro Gly Thr Gly
 805 810 815
 Tyr Leu Tyr Leu Val Trp Lys Thr Leu Ala Arg Ser Leu Ser Leu Ser
 820 825 830
 Leu Glu Glu Thr Pro Val Val Phe Glu Asn Val Thr Phe His Gln Ala
 835 840 845
 Thr Ile Leu Pro Arg Thr Gly Thr Val Pro Leu Glu Val Arg Leu Leu
 850 855 860
 Glu Ala Ser His Ala Phe Glu Val Ser Asp Ser Gly Asn Leu Ile Val
 865 870 875 880
 Ser Gly Lys Val Tyr Gln Trp Glu Asp Pro Asp Ser Lys Leu Phe Asp
 885 890 895
 His Pro Glu Val Pro Ile Pro Ala Glu Ser Glu Ser Val Ser Arg Leu
 900 905 910

REN-01-032-Uti1.ST25.txt

Thr Gln Gly Glu Val Tyr Lys Glu Leu Arg Leu Arg Gly Tyr Asp Tyr
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Gly Pro His Phe Gln Gly Val Tyr Glu Ala Thr Leu Glu Gly Glu Gln
 930 935 940

Gly Lys Leu Leu Trp Lys Asp Asn Trp Val Thr Phe Met Asp Thr Met
 945 950 955 960

Leu Gln Ile Ser Ile Leu Gly Phe Ser Lys Gln Ser Leu Gln Leu Pro
 965 970 975

Thr Arg Val Thr Ala Ile Tyr Ile Asp Pro Ala Thr His Leu Gln Lys
 980 985 990

Val Tyr Met Leu Glu Gly Asp Thr Gln Val Ala Asp Val Thr Thr Ser
 995 1000 1005

Arg Cys Leu Gly Val Thr Val Ser Gly Gly Val Tyr Ile Ser Arg
 1010 1015 1020

Leu Gln Thr Thr Ala Thr Ser Arg Arg Gln Gln Glu Gln Leu Val
 1025 1030 1035

Pro Thr Leu Glu Lys Phe Val Phe Thr Pro His Val Glu Pro Glu
 1040 1045 1050

Cys Leu Ser Glu Ser Ala Ile Leu Gln Lys Glu Leu Gln Leu Cys
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Lys Gly Leu Ala Lys Ala Leu Gln Thr Lys Ala Thr Gln Gln Gly
 1070 1075 1080

Leu Lys Met Thr Val Pro Gly Leu Glu Asp Leu Pro Gln His Gly
 1085 1090 1095

Leu Pro Arg Leu Leu Ala Ala Ala Cys Gln Leu Gln Leu Asn Gly
 1100 1105 1110

Asn Leu Gln Leu Glu Leu Gly Glu Val Leu Ala Arg Glu Arg Leu
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Leu Leu Pro Glu Asp Pro Leu Ile Ser Gly Leu Leu Asn Ser Gln
 1130 1135 1140

Ala Leu Lys Ala Cys Ile Asp Thr Ala Leu Glu Asn Leu Ser Thr
 1145 1150 1155

Leu Lys Met Lys Val Val Glu Val Leu Ala Gly Glu Gly His Leu
 1160 1165 1170

REN-01-032-Util.ST25.txt

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 Leu Glu Tyr Thr Ala Thr Asp Arg His Pro Gln Ala Leu Lys Asp
 1190 1195 1200
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 1205 1210 1215
 Asp Pro Ser Gly Pro Ala Pro Thr Asn Leu Gly Ala Leu Asp Leu
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 Val Val Cys Asn Cys Ala Leu Ala Thr Leu Gly Asp Pro Ala Leu
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 Ala Leu Asp Asn Met Val Ala Ala Leu Lys Asp Gly Gly Phe Leu
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 Gln Glu Glu Trp Glu Ser Leu Phe Ser Arg Lys Ala Leu His Leu
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 Val Gly Leu Lys Lys Ser Phe Tyr Gly Thr Ala Leu Phe Leu Cys
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 Lys Val Leu Glu Ser Asp Leu Val Met Asn Val Tyr Arg Asp Gly
 1415 1420 1425

REN-01-032-util.ST25.txt

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 Glu Glu Gln Thr Ala His Ala Phe Val Asn Val Leu Thr Arg Gly
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 Gln Pro Pro Ser Ser Ser Gly Ala Gln Leu Cys Thr Val Tyr Tyr
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 Ala Ser Leu Asn Phe Arg Asp Ile Met Leu Ala Thr Gly Lys Leu
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 Ser Pro Asp Ala Ile Pro Gly Lys Trp Ala Ser Arg Asp Cys Met
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 Leu Gly Met Glu Phe Ser Gly Arg Asp Lys Cys Gly Arg Arg Val
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 Ser Pro Asp Phe Leu Trp Asp Val Pro Ser Ser Trp Thr Leu Glu
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 Glu Ala Ala Ser Val Pro Val Val Tyr Thr Thr Ala Tyr Tyr Ser
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 Leu Val Val Arg Gly Arg Ile Gln His Gly Glu Thr Val Leu Ile
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 His Ser Gly Ser Gly Gly Val Gly Gln Ala Ala Ile Ser Ile Ala
 1595 1600 1605
 Leu Ser Leu Gly Cys Arg Val Phe Thr Thr Val Gly Ser Ala Glu
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 Lys Arg Ala Tyr Leu Gln Ala Arg Phe Pro Gln Leu Asp Asp Thr
 1625 1630 1635
 Ser Phe Ala Asn Ser Arg Asp Thr Ser Phe Glu Gln His Val Leu
 1640 1645 1650
 Leu His Thr Gly Gly Lys Gly Val Asp Leu Val Leu Asn Ser Leu
 1655 1660 1665
 Ala Glu Glu Lys Leu Gln Ala Ser Val Arg Cys Leu Ala Gln His
 1670 1675 1680

REN-01-032-Util.ST25.txt

Gly Arg Phe Leu Glu Ile Gly Lys Phe Asp Leu Ser Asn Asn His
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 Pro Leu Gly Met Ala Ile Phe Leu Lys Asn Val Thr Phe His Gly
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 Ile Leu Leu Asp Ala Leu Phe Glu Gly Ala Asn Asp Ser Trp Arg
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 Glu Val Ala Glu Leu Leu Lys Ala Gly Ile Arg Asp Gly Val Val
 1730 1735 1740
 Lys Pro Leu Lys Cys Thr Val Phe Pro Lys Ala Gln Val Glu Asp
 1745 1750 1755
 Ala Phe Arg Tyr Met Ala Gln Gly Lys His Ile Gly Lys Val Leu
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 Val Gln Val Arg Glu Glu Glu Pro Glu Ala Met Leu Pro Gly Ala
 1775 1780 1785
 Gln Pro Thr Leu Ile Ser Ala Ile Ser Lys Thr Phe Cys Pro Glu
 1790 1795 1800
 His Lys Ser Tyr Ile Ile Thr Gly Gly Leu Gly Gly Phe Gly Leu
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 Glu Leu Ala Arg Trp Leu Val Leu Arg Gly Ala Gln Arg Leu Val
 1820 1825 1830
 Leu Thr Ser Arg Ser Gly Ile Arg Thr Gly Tyr Gln Ala Lys His
 1835 1840 1845
 Val Arg Glu Trp Arg Arg Gln Gly Ile His Val Leu Val Ser Thr
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 1865 1870 1875
 Ala Thr Lys Leu Gly Pro Val Gly Gly Val Phe Asn Leu Ala Met
 1880 1885 1890
 Val Leu Arg Asp Ala Met Leu Glu Asn Gln Thr Pro Glu Leu Phe
 1895 1900 1905
 Gln Asp Val Asn Lys Pro Lys Tyr Asn Gly Thr Leu Asn Leu Asp
 1910 1915 1920
 Arg Ala Thr Arg Glu Ala Cys Pro Glu Leu Asp Tyr Phe Val Ala
 1925 1930 1935

REN-01-032-Uti1.ST25.txt

Phe Ser Ser Val Ser Cys Gly Arg Gly Asn Ala Gly Gln Ser Asn
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 1970 1975 1980
 Gly Asp Val Gly Ile Ile Leu Glu Ala Met Gly Thr Asn Asp Thr
 1985 1990 1995
 Val Val Gly Gly Thr Leu Pro Gln Arg Ile Ser Ser Cys Met Glu
 2000 2005 2010
 Val Leu Asp Leu Phe Leu Asn Gln Pro His Ala Val Leu Ser Ser
 2015 2020 2025
 Phe Val Leu Ala Glu Lys Lys Ala Val Ala His Gly Asp Gly Glu
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 Arg Asp Leu Ala Gly Ile Asn Leu Asp Ser Ser Leu Ala Asp Leu
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 2180 2185 2190

REN-01-032-Uti1.ST25.txt

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 2285 2290 2295
 Glu His Ser Lys Val Leu Glu Ala Leu Leu Pro Leu Lys Ser Leu
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 Gln Ser Leu Asp Arg Arg Asp Leu Ser Phe Ala Ala Val Ser Phe
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REN-01-032-Uti1.ST25.txt

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REN-01-032-Util.ST25.txt

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REN-01-032-Uti1.ST25.txt

```

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REN-01-032-Uti1.ST25.txt

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REN-01-032-Uti1.ST25.txt

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 <211> 2447
 <212> PRT
 <213> Gallus gallus

<400> 29

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Leu Asp Gly Gly Ile Asn Pro Thr Ala Leu Arg Gly Thr Asp Thr Gly
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Val Trp Val Gly Ala Ser Gly Ser Glu Ala Ala Glu Ala Leu Ser Gln
35 40 45

Asp Pro Glu Glu Leu Leu Gly Tyr Ser Met Thr Gly Cys Gln Arg Ala
50 55 60

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Met Leu Ala Asn Arg Ile Ser Tyr Phe Tyr Asp Phe Thr Gly Pro Ser
 65 70 75 80

Leu Thr Ile Asp Thr Ala Cys Ser Ser Ser Leu Met Ala Leu Glu Asn
 85 90 95

Ala Tyr Lys Ala Ile Arg His Gly Gln Cys Ser Ala Ala Leu Val Gly
 100 105 110

Gly Val Asn Ile Leu Leu Lys Pro Asn Thr Ser Val Gln Phe Met Lys
 115 120 125

Leu Gly Met Leu Ser Pro Asp Gly Ala Cys Lys Ala Phe Asp Val Ser
 130 135 140

Gly Asn Gly Tyr Cys Arg Ser Glu Ala Val Val Val Val Leu Leu Thr
 145 150 155 160

Lys Lys Ser Met Ala Lys Arg Val Tyr Ala Thr Ile Val Asn Ala Gly
 165 170 175

Ser Asn Thr Asp Gly Phe Lys Glu Gln Gly Val Thr Phe Pro Ser Gly
 180 185 190

Glu Met Gln Gln Gln Leu Val Gly Ser Leu Tyr Arg Glu Cys Gly Ile
 195 200 205

Lys Pro Gly Asp Val Glu Tyr Val Glu Ala His Gly Thr Gly Thr Lys
 210 215 220

Val Gly Asp Pro Gln Glu Val Asn Gly Ile Val Asn Val Phe Cys Gln
 225 230 235 240

Cys Glu Arg Glu Pro Leu Leu Ile Gly Ser Thr Lys Ser Asn Met Gly
 245 250 255

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

Ser Leu Glu His Gly Leu Trp Ala Pro Asn Leu His Phe Asn Asp Pro
 275 280 285

Asn Pro Asp Ile Pro Ala Leu His Asp Gly Ser Leu Lys Val Val Cys
 290 295 300

Lys Pro Thr Pro Val Lys Gly Gly Leu Val Ser Ile Asn Ser Phe Gly
 305 310 315 320

Phe Gly Gly Ser Asn Ala His Val Ile Leu Arg Pro Asn Glu Lys Lys
 325 330 335

REN-01-032-Util.ST25.txt

Cys Gln Pro Gln Glu Thr Cys Asn Leu Pro Arg Leu Val Gln Val Cys
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 Gly Arg Thr Gln Glu Ala Val Glu Ile Leu Ile Glu Glu Ser Arg Lys
 355 360 365
 His Gly Gly Cys Ser Pro Phe Leu Ser Leu Leu Ser Asp Ile Ser Ala
 370 375 380
 Val Pro Val Ser Ser Met Pro Tyr Arg Gly Tyr Thr Leu Val Gly Thr
 385 390 395 400
 Glu Ser Asp Ile Thr Glu Ile Gln Gln Val Gln Ala Ser Gly Arg Pro
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 Leu Trp Tyr Ile Cys Ser Gly Met Gly Thr Gln Trp Lys Gly Met Gly
 420 425 430
 Leu Ser Leu Met Lys Leu Asp Leu Phe Arg Gln Ser Ile Leu Arg Ser
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 Asp Glu Ala Leu Lys Ser Thr Gly Leu Lys Val Ser Asp Leu Leu Leu
 450 455 460
 Asn Ala Asp Glu Asn Thr Phe Asp Asp Thr Val His Ala Phe Val Gly
 465 470 475 480
 Leu Ala Ala Ile Gln Ile Ala Gln Ile Asp Val Leu Lys Ala Ala Gly
 485 490 495
 Leu Gln Pro Asp Gly Ile Leu Gly His Ser Val Gly Glu Leu Ala Cys
 500 505 510
 Gly Tyr Ala Asp Asn Ser Leu Ser His Glu Glu Ala Val Leu Ala Ala
 515 520 525
 Tyr Trp Arg Gly Arg Cys Val Lys Glu Ala Lys Leu Pro Pro Gly Gly
 530 535 540
 Met Ala Ala Val Gly Leu Thr Trp Glu Glu Cys Lys Gln Arg Cys Pro
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 Pro Asn Val Val Pro Ala Cys His Asn Ser Glu Asp Thr Val Thr Val
 565 570 575
 Ser Gly Pro Leu Asp Ser Val Ser Glu Phe Val Thr Lys Leu Lys Lys
 580 585 590
 Asp Gly Val Phe Ala Lys Glu Val Arg Ser Ala Gly Val Ala Phe His
 595 600 605

REN-01-032-util.ST25.txt

Ser Tyr Tyr Met Ala Ser Ile Ala Pro Ala Leu Leu Ser Ala Leu Lys
 610 615 620

Lys Val Ile Pro His Pro Lys Pro Arg Ser Ala Arg Trp Ile Ser Thr
 625 630 635 640

Ser Ile Pro Glu Ser Gln Trp Gln Ser Asp Leu Ala Arg Asn Ser Ser
 645 650 655

Ala Glu Tyr His Val Asn Asn Leu Val Asn Pro Val Leu Phe His Glu
 660 665 670

Gly Leu Lys His Ile Pro Glu Asn Ala Val Val Val Glu Ile Ala Pro
 675 680 685

His Ala Leu Leu Gln Ala Ile Leu Arg Arg Thr Leu Lys Pro Thr Cys
 690 695 700

Thr Ile Leu Pro Leu Met Lys Lys Asp His Lys Asn Asn Leu Glu Phe
 705 710 715 720

Phe Leu Thr Gln Thr Gly Lys Ile His Leu Thr Gly Ile Asn Val Leu
 725 730 735

Gly Asn Asn Leu Phe Pro Pro Val Glu Tyr Pro Val Pro Val Gly Thr
 740 745 750

Pro Leu Ile Ser Pro Tyr Ile Lys Trp Asp His Ser Gln Asp Trp Asp
 755 760 765

Val Pro Lys Ala Glu Asp Phe Pro Ser Gly Ser Lys Gly Ser Ala Ser
 770 775 780

Ala Ser Val Tyr Asn Ile Asp Val Ser Pro Asp Ser Pro Asp His Tyr
 785 790 795 800

Leu Val Gly His Cys Ile Asp Gly Arg Val Leu Tyr Pro Ala Thr Gly
 805 810 815

Tyr Leu Val Leu Ala Trp Arg Thr Leu Ala Arg Ser Leu Gly Met Val
 820 825 830

Met Glu Gln Thr Ala Val Met Phe Glu Glu Val Thr Ile His Gln Ala
 835 840 845

Thr Ile Leu Pro Lys Lys Gly Ser Thr Gln Leu Glu Val Arg Ile Met
 850 855 860

Pro Ala Ser His Ser Phe Glu Val Ser Gly Asn Gly Asn Leu Ala Val
 865 870 875 880

REN-01-032-Util.ST25.txt

Ser Gly Lys Ile Ser Leu Leu Glu Asn Asp Ala Leu Lys Asn Phe His
 885 890 895
 Asn Gln Leu Ala Asp Phe Gln Ser Gln Ala Asn Val Thr Ala Lys Ser
 900 905 910
 Gly Leu Leu Met Glu Asp Val Tyr Gln Glu Leu His Leu Arg Gly Tyr
 915 920 925
 Asn Tyr Gly Pro Thr Phe Gln Gly Val Leu Glu Cys Asn Ser Glu Gly
 930 935 940
 Ser Ala Gly Lys Ile Leu Trp Asn Gly Asn Trp Val Thr Phe Leu Asp
 945 950 955 960
 Thr Leu Leu His Leu Ile Val Leu Ala Glu Thr Gly Arg Ser Leu Arg
 965 970 975
 Leu Pro Thr Arg Ile Arg Ser Val Tyr Ile Asp Pro Val Leu His Gln
 980 985 990
 Glu Gln Val Tyr Gln Tyr Gln Asp Asn Val Glu Ala Phe Asp Val Val
 995 1000 1005
 Val Asp Arg Cys Leu Asp Ser Leu Lys Ala Gly Gly Val Gln Ile
 1010 1015 1020
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 1040 1045 1050
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 1070 1075 1080
 His Gly Val Lys Leu Val Ile His Gly Leu Glu Thr Asn Gly Ala
 1085 1090 1095
 Ala Ala Gly Ser Pro Pro Thr Gln Lys Gly Leu Gln His Ile Leu
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 Thr Glu Ile Cys His Leu Glu Leu Asn Gly Asn Leu His Ser Glu
 1115 1120 1125
 Leu Glu Gln Ile Val Thr Gln Glu Lys Met His Leu Gln Asp Asp
 1130 1135 1140

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Pro Leu Leu Asn Gly Leu Leu Asp Ser Ser Glu Leu Lys Thr Cys
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Leu Asp Val Ala Lys Glu Asn Thr Thr Ser His Arg Met Lys Ile
 1160 1165 1170

Val Glu Ala Leu Ala Gly Ser Gly Arg Leu Phe Ser Arg Val Gln
 1175 1180 1185

Ser Ile Leu Asn Thr Gln Pro Leu Leu Gln Leu Asp Tyr Ile Ala
 1190 1195 1200

Thr Asp Cys Thr Pro Glu Thr Leu Ser Asn Asp Glu Thr Glu Leu
 1205 1210 1215

His Asp Ala Gly Ile Ser Phe Ser Gln Trp Asp Pro Ser Ser Leu
 1220 1225 1230

Pro Ser Gly Asn Leu Thr Asn Ala Asp Leu Ala Val Cys Asn Cys
 1235 1240 1245

Ser Thr Ser Val Leu Gly Asn Thr Ala Glu Ile Ile Ser Asn Leu
 1250 1255 1260

Ala Ala Ala Val Lys Glu Gly Gly Phe Val Leu Leu His Thr Leu
 1265 1270 1275

Leu Lys Glu Glu Thr Leu Gly Glu Ile Val Ser Phe Leu Thr Ser
 1280 1285 1290

Pro Asp Leu Gln Gln Glu His Ser Phe Leu Ser Gln Ala Gln Trp
 1295 1300 1305

Glu Glu Leu Phe Ser Lys Ala Ser Leu Asn Leu Val Ala Met Lys
 1310 1315 1320

Arg Ser Phe Phe Gly Ser Val Ile Phe Leu Cys Arg Arg Gln Ser
 1325 1330 1335

Pro Ala Lys Ala Pro Ile Leu Leu Pro Val Asp Asp Thr His Tyr
 1340 1345 1350

Lys Trp Val Asp Ser Leu Lys Glu Ile Leu Ala Asp Ser Ser Glu
 1355 1360 1365

Gln Pro Leu Trp Leu Thr Ala Thr Asn Cys Gly Asn Ser Gly Ile
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Leu Gly Met Val Asn Cys Leu Arg Leu Glu Ala Glu Gly His Arg
 1385 1390 1395

REN-01-032-Util.ST25.txt

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1415			1420		1425	
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1430			1435		1440	
Phe Arg	His Leu	Pro Leu	Gln	Gln Ala Gln Pro	Gln	Glu Leu Thr
1445			1450		1455	
Glu Tyr	Ala Tyr	Val Asn	Val	Leu Thr Arg Gly	Asp	Leu Ser Ser
1460			1465		1470	
Leu Arg	Trp Ile	Val Ser	Pro	Leu Arg His Phe	Gln	Thr Thr Asn
1475			1480		1485	
Pro Asn	Val Gln	Leu Cys	Lys	Val Tyr Tyr Ala	Ser	Leu Asn Phe
1490			1495		1500	
Arg Asp	Ile Met	Leu Ala	Thr	Gly Lys Leu Ser	Pro	Asp Ala Ile
1505			1510		1515	
Pro Gly	Asn Trp	Thr Leu	Gln	Gln Cys Met Leu	Gly	Met Glu Phe
1520			1525		1530	
Ser Gly	Arg Asp	Leu Ala	Gly	Arg Arg Val Met	Gly	Leu Leu Pro
1535			1540		1545	
Ala Lys	Gly Leu	Ala Thr	Val	Val Asp Cys Asp	Lys	Arg Phe Leu
1550			1555		1560	
Trp Glu	Val Pro	Glu Asn	Trp	Thr Leu Glu Glu	Ala	Ala Ser Val
1565			1570		1575	
Pro Val	Val Tyr	Ala Thr	Ala	Tyr Tyr Ala Leu	Val	Val Arg Gly
1580			1585		1590	
Gly Met	Lys Lys	Gly Glu	Ser	Val Leu Ile His	Ser	Gly Ser Gly
1595			1600		1605	
Gly Val	Gly Ala	Ser Ser	His	Cys His Arg Leu	Glu	His Gly Leu
1610			1615		1620	
Ala Arg	Val Phe	Ala Thr	Val	Gly Ser Ala Glu	Lys	Arg Glu Tyr
1625			1630		1635	
Leu Gln	Ala Arg	Phe Pro	Gln	Leu Asp Ala Asn	Ser	Phe Ala Ser
1640			1645		1650	

REN-01-032-Util.ST25.txt

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1670						1675					1680			
Leu	Gln	Ala	Ser	Leu	Arg	Cys	Leu	Ala	Gln	His	Gly	Arg	Phe	Leu
1685						1690					1695			
Glu	Ile	Gly	Lys	Phe	Asp	Leu	Ser	Asn	Asn	Ser	Gln	Leu	Gly	Met
1700						1705					1710			
Ala	Leu	Phe	Leu	Lys	Asn	Val	Ala	Phe	His	Gly	Ile	Leu	Leu	Asp
1715						1720					1725			
Ser	Ile	Phe	Glu	Glu	Gly	Asn	Gln	Glu	Trp	Glu	Val	Val	Ser	Glu
1730						1735					1740			
Leu	Leu	Thr	Lys	Gly	Ile	Lys	Asp	Gly	Val	Val	Lys	Pro	Leu	Arg
1745						1750					1755			
Thr	Thr	Val	Phe	Gly	Lys	Glu	Glu	Val	Glu	Ala	Ala	Phe	Arg	Phe
1760						1765					1770			
Met	Ala	Gln	Gly	Lys	His	Ile	Gly	Lys	Val	Met	Ile	Lys	Ile	Gln
1775						1780					1785			
Glu	Glu	Glu	Lys	Gln	Tyr	Pro	Leu	Arg	Ser	Glu	Pro	Val	Lys	Leu
1790						1795					1800			
Ser	Ala	Ile	Ser	Arg	Thr	Ser	Cys	Pro	Pro	Thr	Lys	Ser	Tyr	Ile
1805						1810					1815			
Ile	Thr	Gly	Gly	Leu	Gly	Gly	Phe	Gly	Leu	Glu	Leu	Ala	Gln	Trp
1820						1825					1830			
Leu	Ile	Glu	Arg	Gly	Ala	Gln	Lys	Leu	Val	Leu	Thr	Ser	Arg	Ser
1835						1840					1845			
Gly	Ile	Arg	Thr	Gly	Tyr	Gln	Ala	Lys	Cys	Val	Arg	Glu	Trp	Lys
1850						1855					1860			
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1865						1870					1875			
Leu	Glu	Gly	Thr	Gln	Leu	Leu	Ile	Glu	Glu	Ala	Leu	Lys	Leu	Gly
1880						1885					1890			
Pro	Val	Gly	Gly	Ile	Phe	Asn	Leu	Ala	Val	Val	Leu	Lys	Asp	Ala
1895						1900					1905			

REN-01-032-Util.ST25.txt
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1925 1930 1935
Lys Cys Pro Asp Leu Asp Tyr Phe Val Val Phe Ser Ser Val Ser
1940 1945 1950
Cys Gly Arg Gly Asn Ala Gly Gln Ser Asn Tyr Gly Phe Ala Asn
1955 1960 1965
Ser Ala Met Glu Arg Ile Cys Glu Gln Arg His His Asp Gly Leu
1970 1975 1980
Pro Gly Leu Ala Val Gln Trp Gly Ala Ile Gly Asp Val Gly Ile
1985 1990 1995
Leu Lys Ala Met Gly Asn Arg Glu Val Val Ile Gly Gly Thr Val
2000 2005 2010
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2075 2080 2085
Val Glu Val Arg Gln Thr Leu Glu Arg Asp Tyr Asp Ile Val Met
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Phe Gln Ser Tyr Arg Ala Lys Leu Thr Gln Gly Asn Glu Ala Ala
2285 2290 2295

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2345 2350 2355

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Arg Gly Asp Pro Gly Ala Gly Pro Ser Arg His Gly Pro Arg Gly His
35          40          45

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Pro Ala Gly Arg His Gly Gly His Ser Gln Gly Val Leu Ala Val Glu
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Ala Leu Lys Ala Gly Gly Ala Arg Asp Val Glu Leu Phe Ala Leu Ala
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Gln Leu Ile Gly Ala Ala Gly Thr Leu Val Ala Arg Arg Arg Glu Phe
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Pro Ser Trp Ala Ile Ala Pro Met Val Ser Val Thr Asn Ala Asp Pro
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Glu Arg Ile Gly Arg Leu Leu Asp Glu Phe Ala Gln Asp Val Arg Thr
115         120         125

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Val Leu Pro Pro Val Leu Ser Ile Arg Asn Gly Arg Arg Ala Val Val
130         135         140

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Ile Thr Gly Thr Pro Glu Gln Leu Ser Arg Phe Glu Leu Tyr Cys Arg
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 195 200 205
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 His Arg Ala Gly Ala Arg Trp Ile Leu Asp Leu Gly Pro Gly Asp Ile
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 325 330 335
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REN-01-032-Util.ST25.txt

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Gly Thr Pro Lys Lys Gly Cys Gly Tyr Leu Ser Gly Pro Gly Arg Ser
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Val Arg Leu Pro Ile Asp Ala Asp Arg Arg Ile Leu Val Gly Thr Ala
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Gln Gly Arg Met Pro Pro Ala Glu Ser Ala Arg Cys Arg His Pro Arg
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Asp Arg His Ser Ala Ser Val Arg Arg Cys Ser Thr Arg Trp Pro Val
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 610 615 620

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Asp Pro Asp Ala Ile His Arg Cys Trp Pro Ala Gly Gln Ser Ala Ala
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 755 760 765
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 770 775 780
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 785 790 795 800
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 915 920 925
 Ser Pro Pro Val Ser Thr Ala Arg Ser Ser Cys Cys Gly Gly Gln Arg
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 His Arg His Arg His Val Arg Cys Ala Leu Ala Pro Ser Leu Thr Asn
 965 970 975

REN-01-032-util.ST25.txt

Val Pro Thr Arg Leu Val Gly Pro Cys Trp Pro Ala Val Phe Ala Ala
 980 985 990
 Ile Gly Ser Ala Val Thr Asp Thr Gly Glu Pro Val Val Glu Gly Leu
 995 1000 1005
 Leu Ser Leu Val His Leu Asp Thr Arg Pro Arg Val Val Gly Gln
 1010 1015 1020
 Leu Pro Thr Val Pro Ala Gln Leu Thr Val Thr Gln Arg Leu Pro
 1025 1030 1035
 Thr Gln Pro Ile Arg Thr Trp Ala Ala Ser Cys Arg Ser Arg Ser
 1040 1045 1050
 Ser Phe Thr Ala Trp Arg Arg Asp Arg His Ser Arg Gly Ala Ile
 1055 1060 1065
 Arg Asp Pro Gly Ser His Arg Phe Ala Glu Leu Asp Arg Arg Glu
 1070 1075 1080
 Pro Val Ala Arg Cys Arg Glu Arg His Arg His Pro Ala Arg Arg
 1085 1090 1095
 Arg Arg Asp Val Thr Ile Thr Ala Pro Val Asp Met Arg Pro Phe
 1100 1105 1110
 Ala Val Val Ser Gly Asp His Asn Pro Ile His Thr Asp Arg Ala
 1115 1120 1125
 Ala Ala Ala Cys Arg Pro Gly Val Ala Asp Arg Ala Arg His Val
 1130 1135 1140
 Ala Val Gly Arg Gly Ala Thr Arg Gly Asp Arg His Arg Arg Ala
 1145 1150 1155
 Gly Pro Pro Pro Ala Arg Leu Val Gly Trp Thr Ala Arg Phe Leu
 1160 1165 1170
 Gly Met Val Ala Pro Ala Thr Arg Trp Thr Ser Gly Arg Ala Arg
 1175 1180 1185
 Arg Ile Asp Gln Gly Ala Glu Ile Val Asp Val Ala Ala Arg Val
 1190 1195 1200
 Gly Ser Asp Leu Val Met Ser Ala Ser Ala Arg Leu Ala Ala Pro
 1205 1210 1215
 Lys Thr Val Tyr Ala Phe Pro Gly Gln Gly Ile Gln His Lys Gly
 1220 1225 1230

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Met Gly 1235	Met Glu Val Arg	Ala 1240	Ala Pro Arg Arg Pro 1245	Ala Arg Cys
Gly Thr 1250	Pro Arg Thr Ser	Ser 1255	Pro Ala Thr Pro Trp 1260	Ala Ser Arg
Tyr Cys 1265	Thr Trp Ser Ala	Thr 1270	Thr Arg Pro Ala Ser 1275	Ser Pro Ala
Val Cys 1280	Thr Thr Thr Thr	Asp 1285	Gly Val Leu Tyr Leu 1290	Thr Gln Phe
Thr Gln 1295	Val Ala Met Ala	Thr 1300	Val Ala Ala Gly Gln 1305	Val Ala Glu
Met Arg 1310	Glu Gln Gly Ala	Phe 1315	Val Glu Gly Ala Ile 1320	Ala Cys Gly
His Ser 1325	Val Gly Glu Tyr	Thr 1330	Ala Leu Ala Cys Val 1335	Thr Gly Ile
Tyr Gln 1340	Leu Glu Ala Leu	Leu 1345	Glu Met Val Phe His 1350	Arg Gly Ser
Lys Met 1355	His Asp Ile Val	Pro 1360	Arg Asp Glu Leu Gly 1365	Arg Ser Asn
Tyr Arg 1370	Leu Ser Ala Ile	Arg 1375	Pro Ser Gln Ile Asp 1380	Leu Asp Asp
Ala Asp 1385	Val Pro Ala Phe	Val 1390	Ala Gly Ile Ala Glu 1395	Ser Thr Gly
Glu Phe 1400	Leu Glu Ile Glu	Asn 1405	Phe Asn Leu Gly Gly 1410	Ser Gln Tyr
Ala Ile 1415	Ala Gly Thr Val	Arg 1420	Gly Leu Glu Ala Leu 1425	Glu Ala Glu
Val Glu 1430	Arg Arg Arg Glu	Leu 1435	Thr Gly Gly Arg Arg 1440	Ser Phe Ile
Leu Val 1445	Pro Gly Ile Asp	Val 1450	Pro Phe His Ser Arg 1455	Val Leu Arg
Val Gly 1460	Val Ala Glu Phe	Arg 1465	Arg Ser Leu Asp Arg 1470	Val Met Arg
Pro Thr 1475	Arg Thr Arg Pro	Asp 1480	His Arg Ala Leu His 1485	Ser Gln Pro

REN-01-032-Util.ST25.txt

Gly Ala Ala Glu Val Gln Pro Trp Thr Ala Thr Ser Ser Arg Lys
 1490 1495 1500
 Ser Gly Ile Trp Cys Pro Ala Glu Pro Leu Asp Glu Ile Leu Ala
 1505 1510 1515
 Asp Tyr Asp Thr Trp Leu Arg Asp Asp Arg Arg Asp Gly Ala His
 1520 1525 1530
 Gly Val His Arg Ala Ala Gly Met Ala Ile Arg Gln Pro Gly Ala
 1535 1540 1545
 Leu Asp Arg Asp Ala Gly Ser Ala Val His Arg Gly Gly Ala Gly
 1550 1555 1560
 Gly Leu Gly Val Glu Arg Phe Val Glu Ile Gly Val Lys Ser Ser
 1565 1570 1575
 Pro Thr Val Ala Gly Ser Cys His Gln His Pro Gln Thr Ala Arg
 1580 1585 1590
 Ile Arg Pro Gln His Ser Glu Val Leu Asn Ala Glu Arg Asp Ala
 1595 1600 1605
 Arg Cys Cys Ser Pro Pro Thr Pro Thr Arg Ser Arg Ser Arg Arg
 1610 1615 1620
 Lys Thr Ser Arg Ser Arg Asn Arg Pro Arg Arg Thr Ser Ser Arg
 1625 1630 1635
 Lys Pro Pro Pro Ser Arg Arg Pro Leu Arg Arg Arg Ala Arg Val
 1640 1645 1650
 Pro Thr Ile Trp Phe Ser Thr Pro Pro Met Pro Arg Cys Val Ile
 1655 1660 1665
 Ala Leu Ser Ala Lys Met Arg Ile Asp Gln Ile Glu Glu Leu Asp
 1670 1675 1680
 Ser Ile Glu Ser Ile Thr Asp Gly Ala Ser Ser Arg Arg Asn Gln
 1685 1690 1695
 Leu Leu Val Asp Leu Gly Ser Glu Leu Asn Leu Gly Ala Ile Glu
 1700 1705 1710
 Arg Arg Arg Arg Ile Gly Pro Gly Arg Ser Ala Leu Thr Gly Asp
 1715 1720 1725
 Gln Thr Gly Ala His Leu Gln Arg Tyr Gly Pro Val Leu Ser Asp
 1730 1735 1740

REN-01-032-Uti1.ST25.txt

Ala Ile Asn Asp His Val Arg Thr Val Leu Gly Pro Ser Gly Lys
 1745 1750 1755
 Arg Pro Gly Ala Ile Ala Glu Arg Val Lys Lys Thr Trp Glu Leu
 1760 1765 1770
 Gly Glu Ala Gly Pro Ser Met Ser Pro Ser Arg Ser Arg Trp Ala
 1775 1780 1785
 Pro Ala Arg Ala Ala Ala Phe Ala Ala Ala Pro Trp Ala Thr Cys
 1790 1795 1800
 Thr Arg Ala Arg Trp Pro Met Pro Pro Pro Ser Thr Arg Ser Ser
 1805 1810 1815
 Thr Arg Arg Ser His Arg Trp Pro Arg Pro Gly Arg Phe Gly Ser
 1820 1825 1830
 Ala Ala Ser Ala Gly Ser Gly Gly Ala Thr Ile Asp Ala Ala Ala
 1835 1840 1845
 Leu Ser Glu Phe Thr Asp Gln Ile Thr Gly Arg Glu Gly Val Leu
 1850 1855 1860
 Pro Pro Arg Pro Ala Trp Cys Trp Gly Ser Trp Asp Trp Thr Thr
 1865 1870 1875
 Pro Ser Thr Val Ala Gly Arg Pro Asp Ser Glu Leu Ile Asp Leu
 1880 1885 1890
 Val Thr Ala Glu Leu Gly Arg Thr Gly Arg Gly Trp Trp His Arg
 1895 1900 1905
 Cys Ser Thr Pro Arg Arg Pro Ser Tyr Ser Thr Thr Ala Gly Gln
 1910 1915 1920
 Arg Pro Arg Gly Pro Gly Glu Ala Val Ala Asp Arg Arg Lys Asp
 1925 1930 1935
 Arg Arg Arg His Arg Arg Arg Leu Ala Ala Leu Ala Glu Arg Phe
 1940 1945 1950
 Glu Gly Ala Ala Thr Ser Trp Arg Pro Arg Leu Pro Gly Gly Lys
 1955 1960 1965
 Val Ser Arg Ser Arg Gly Pro Ala Asp Pro Cys Ile Ala Val Arg
 1970 1975 1980
 Pro His Ala Ala Gly Ala Glu Asn Pro Glu Pro Arg Val Arg Arg
 1985 1990 1995

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Arg Ser Cys Arg Gly Asp Arg Arg Phe Glu Gly Phe Asp Arg Arg
 2000 2005 2010
 Val Gly Gly Gly Ser Ala Ala Arg Arg Gly Ala Thr Val Ile Ala
 2015 2020 2025
 Thr Thr Ser Lys Leu Asp Glu Glu Arg Leu Arg Phe Tyr Arg Thr
 2030 2035 2040
 Leu Tyr Arg Asp His Ala Arg Tyr Gly Ala Ala Leu Trp Leu Val
 2045 2050 2055
 Ala Ala Asn Met Ala Ser Tyr Ser Asp Val Asp Ala Leu Val Glu
 2060 2065 2070
 Trp Ile Gly Thr Glu Gln Thr Glu Ser Leu Gly Pro Gln Ser Ile
 2075 2080 2085
 His Ile Lys Asp Ala Gln Thr Pro Thr Leu Leu Phe Arg Ser Arg
 2090 2095 2100
 Arg Thr Arg Val Gly Thr Val Gly Gly Arg Phe Ala Arg Arg Asp
 2105 2110 2115
 Gly Asp Glu Ser Ala Ala Val Ala Val Gln Arg Leu Ile Gly Gly
 2120 2125 2130
 Leu Ser Thr Ile Gly Ala Glu Arg Asp Met Pro Ser Arg Leu Glu
 2135 2140 2145
 Arg Gly Ala Ala Arg Leu Ala Gln Pro Trp His Val Arg Arg Arg
 2150 2155 2160
 Arg Ala Leu Arg Arg Ser Gln Val Arg Ala Gly Cys Arg Gly Asp
 2165 2170 2175
 Ala Leu Ala Arg Arg Val Val Leu Gly Gly Thr Gly Gln Pro Gly
 2180 2185 2190
 Ala Arg Ala His Arg Leu Asp Pro Arg His Arg Ala Asp Gly Pro
 2195 2200 2205
 Gln Arg Cys His Arg Gly Arg Arg Arg Arg Gly Arg Gly His His
 2210 2215 2220
 Leu Leu Asp Arg Arg Asp Gly Ala Ala Ala Ala Arg Pro Val Ser
 2225 2230 2235
 Cys Gly Ile Gln Gly Gly Cys Gly Arg Ser Pro Ile Lys Ala Asp
 2240 2245 2250

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Leu Thr Gly Gly Leu Pro Arg Pro Thr Ser Thr Trp Pro Ser Trp
 2255 2260 2265
 Arg Pro Arg Arg Ala Ser Arg Cys Arg Gln Arg Arg Pro Ser Thr
 2270 2275 2280
 Arg Thr Pro Arg Pro Leu Ala Pro Ser Pro Arg Cys Arg Arg Arg
 2285 2290 2295
 Pro Gly Phe Thr Pro Ala Pro Pro Pro Gln Trp Asp Asp Leu Asp
 2300 2310
 Val Asp Pro Ala Asp Leu Val Val Ile Val Gly Gly Arg Glu Ile
 2315 2320 2325
 Gly Pro Tyr Gly Ser Ser Arg Thr Arg Phe Glu Met Glu Val Glu
 2330 2335 2340
 Asn Glu Leu Ser Ala Ala Gly Val Leu Glu Leu Ala Trp Thr Thr
 2345 2350 2355
 Gly Leu Ile Ala Gly Arg Arg Pro Ala Thr Arg Leu Val Arg His
 2360 2365 2370
 Arg Ile Arg Arg Asn Gly Arg Arg Ile Arg Val Gly Ala Ala Leu
 2375 2380 2385
 His Asp Ala Val Val Gln Arg Val Gly Ile Arg Glu Phe Val Asp
 2390 2395 2400
 Asp Gly Ala Ile Asp Pro Asp His Ala Ser Pro Leu Leu Val Ser
 2405 2410 2415
 Val Phe Leu Glu Lys Asp Phe Ala Phe Val Val Ser Ser Glu Ala
 2420 2425 2430
 Asp Ala Arg Ala Phe Val Glu Phe Asp Pro Glu His Thr Val Ile
 2435 2440 2445
 Arg Pro Val Pro Asp Ser Thr Asp Trp Gln Val Ile Arg Lys Ala
 2450 2455 2460
 Gly Thr Glu Ile Arg Val Pro Arg Lys Thr Lys Leu Ser Arg Val
 2465 2470 2475
 Val Gly Gly Gln Ile Pro Thr Gly Phe Asp Pro Thr Val Trp Gly
 2480 2485 2490
 Ile Ser Ala Asp Met Ala Gly Ser Ile Asp Arg Leu Ala Val Trp
 2495 2500 2505

REN-01-032-Util.ST25.txt

Asn Met Trp Arg Thr Val Asp Arg Phe Leu Ser Ser Gly Phe Ser
 2510 2515 2520
 Pro Ala Glu Val Met Arg Tyr Val His Pro Ser Leu Val Ala Asn
 2525 2530 2535
 Thr Gln Gly Thr Gly Met Gly Gly Gly Thr Ser Met Gln Thr Met
 2540 2545 2550
 Tyr His Gly Asn Leu Leu Gly Arg Asn Lys Pro Asn Asp Ile Phe
 2555 2560 2565
 Gln Glu Val Leu Pro Ile Ser Phe Ala Ala His Val Val Gln Ser
 2570 2575 2580
 Tyr Val Gly Ser Tyr Gly Ala Met Ile His Pro Val Ala Ala Cys
 2585 2590 2595
 Ala Thr Ala Ala Val Ser Val Glu Glu Gly Val Asp Lys Ile Arg
 2600 2605 2610
 Leu Gly Arg Leu Asn Trp Trp Ser Ala Ala Val Asp Asp Leu Thr
 2615 2620 2625
 Leu Glu Gly Ile Ile Gly Phe Gly Asp Met Ala Ala Thr Ala Asp
 2630 2635 2640
 Thr Ser Met Met Arg Gly Arg Gly Ile His Asp Ser Lys Phe Ser
 2645 2650 2655
 Arg Pro Asn Asp Arg Arg Arg Leu Ala Ser Ser Lys Pro Lys Ala
 2660 2665 2670
 Ala Gly Arg Ser Cys Trp Ala Arg Gly Pro Gly Ala Ala Asp Gly
 2675 2680 2685
 Ala Ala Gly Ala Gly Gly Gly Gly Phe Ala Gln Ser Phe Gly Asp
 2690 2695 2700
 Gly Val His Thr Ser Ile Arg Pro Gly Pro Gly Arg Ala Gly Gly
 2705 2710 2715
 Gly Ala Arg Arg Gln Gly Phe Ser Cys Gly Gly Arg Trp Pro Ser
 2720 2725 2730
 Cys Val Ala Ala Asp Asp Val Ala Val Ile Ser Lys His Asp Thr
 2735 2740 2745
 Ser Thr Leu Ala Asn Asp Pro Asn Glu Thr Glu Leu His Glu Arg
 2750 2755 2760

REN-01-032-Util.ST25.txt

Leu Ala Asp Ala Leu Gly Arg Ser Glu Gly Ala Pro Leu Phe Val
 2765 2770 2775

Val Ser Gln Lys Ser Leu Thr Gly Gln Pro Arg Ala Ala Arg Arg
 2780 2785 2790

Ser Ser Arg
 2795

<210> 32
 <211> 675
 <212> DNA
 <213> Bacillus subtilis

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 atgactttca tatcacctga aaaacgggag aaatgccgga gattttatca taaagaagat 120
 gctcaccgca ccctgctggg agatgtgctc gttcgctcag tcataagcag gcagtatcag 180
 ttggacaaat ccgatatccg ctttagcacg caggaatacg ggaagccgtg catccctgat 240
 cttcccgacg ctcatattcaa cttttctcac tccggccgct gggtcattgg tgcgtttgat 300
 tcacagccga tcggcataga tatcgaaaaa acgaaaccga tcagccttga gatcgccaag 360
 cgcttctttt caaaaacaga gtacagcgac cttttagcaa aagacaagga cgagcagaca 420
 gactatTTTT atcatctatg gtcaatgaaa gaaagcttta tcaaacagga aggcaaaggc 480
 ttatcgcttc cgcttgattc cttttcagtg cgcttgcac aggacggaca agtatccatt 540
 gagcttccgg acagccattc cccatgctat atcaaaacgt atgaggtcga tcccggtac 600
 aaaatggctg tatgcgccgc acaccctgat ttccccgagg atatcacaat ggtctcgtac 660
 gaagagcttt tataa 675

<210> 33
 <211> 224
 <212> PRT
 <213> Bacillus subtilis

<400> 33

Met Lys Ile Tyr Gly Ile Tyr Met Asp Arg Pro Leu Ser Gln Glu Glu
 1 5 10 15

Asn Glu Arg Phe Met Thr Phe Ile Ser Pro Glu Lys Arg Glu Lys Cys
 20 25 30

Arg Arg Phe Tyr His Lys Glu Asp Ala His Arg Thr Leu Leu Gly Asp
 35 40 45

Val Leu Val Arg Ser Val Ile Ser Arg Gln Tyr Gln Leu Asp Lys Ser
 50 55 60

REN-01-032-Util.ST25.txt

Asp Ile Arg Phe Ser Thr Gln Glu Tyr Gly Lys Pro Cys Ile Pro Asp
65 70 75 80

Leu Pro Asp Ala His Phe Asn Ile Ser His Ser Gly Arg Trp Val Ile
85 90 95

Gly Ala Phe Asp Ser Gln Pro Ile Gly Ile Asp Ile Glu Lys Thr Lys
100 105 110

Pro Ile Ser Leu Glu Ile Ala Lys Arg Phe Phe Ser Lys Thr Glu Tyr
115 120 125

Ser Asp Leu Leu Ala Lys Asp Lys Asp Glu Gln Thr Asp Tyr Phe Tyr
130 135 140

His Leu Trp Ser Met Lys Glu Ser Phe Ile Lys Gln Glu Gly Lys Gly
145 150 155 160

Leu Ser Leu Pro Leu Asp Ser Phe Ser Val Arg Leu His Gln Asp Gly
165 170 175

Gln Val Ser Ile Glu Leu Pro Asp Ser His Ser Pro Cys Tyr Ile Lys
180 185 190

Thr Tyr Glu Val Asp Pro Gly Tyr Lys Met Ala Val Cys Ala Ala His
195 200 205

Pro Asp Phe Pro Glu Asp Ile Thr Met Val Ser Tyr Glu Glu Leu Leu
210 215 220

<210> 34
<211> 714
<212> DNA
<213> Brevibacillus brevis

<400> 34
atgatagaaa tgttatttgt aaaggttcca aacgaaatcg atagggcatgt gtttaacttc 60
ttgtcatcaa atgtgagtaa ggaaaaacag caggcgtttg ttcgatacgt taatgtgaaa 120
gatgcttatac gttctctttt aggggaattg cttattagaa aatatttgat acaagtatta 180
aacattccta atgaaaacat tctatttagg aaaaatgaat atggaaaacc ttttgttgat 240
ttcgatattc attttaatat ttccactct gatgaatggg ttgtatgtgc aatttcaaat 300
catcctgttg gaattgatat cgagcgtatt tcggagatag acattaaaat agcagaacaa 360
ttttttcatg aaaatgaata tatatggttg cagtctaaag cccaaaatag tcaagtttct 420
tctttttttg agctttggac tattaagaa agttatataa aagctattgg taaaggatatg 480
tacataccga ttaattcatt ttggattgat aagaatcaaa cacaaactgt aatttacaaa 540
cagaataaaa aagaacctgt tactatttat gaaccagagt tgtttgaggg ctacaagtgt 600
tcttgttggt ctttgttttc ttctgtaacg aacttgtcta ttactaaatt gcaagtgcaa 660

REN-01-032-Util.ST25.txt

gagttatgta atttgtttct agattctaca ttttctgaaa ataataactt ttag

714

<210> 35
 <211> 237
 <212> PRT
 <213> Brevibacillus brevis

<400> 35

Met Ile Glu Met Leu Phe Val Lys Val Pro Asn Glu Ile Asp Arg His
 1 5 10 15

Val Phe Asn Phe Leu Ser Ser Asn Val Ser Lys Glu Lys Gln Gln Ala
 20 25 30

Phe Val Arg Tyr Val Asn Val Lys Asp Ala Tyr Arg Ser Leu Leu Gly
 35 40 45

Glu Leu Leu Ile Arg Lys Tyr Leu Ile Gln Val Leu Asn Ile Pro Asn
 50 55 60

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

Phe Asp Ile His Phe Asn Ile Ser His Ser Asp Glu Trp Val Val Cys
 85 90 95

Ala Ile Ser Asn His Pro Val Gly Ile Asp Ile Glu Arg Ile Ser Glu
 100 105 110

Ile Asp Ile Lys Ile Ala Glu Gln Phe Phe His Glu Asn Glu Tyr Ile
 115 120 125

Trp Leu Gln Ser Lys Ala Gln Asn Ser Gln Val Ser Ser Phe Phe Glu
 130 135 140

Leu Trp Thr Ile Lys Glu Ser Tyr Ile Lys Ala Ile Gly Lys Gly Met
 145 150 155 160

Tyr Ile Pro Ile Asn Ser Phe Trp Ile Asp Lys Asn Gln Thr Gln Thr
 165 170 175

Val Ile Tyr Lys Gln Asn Lys Lys Glu Pro Val Thr Ile Tyr Glu Pro
 180 185 190

Glu Leu Phe Glu Gly Tyr Lys Cys Ser Cys Cys Ser Leu Phe Ser Ser
 195 200 205

Val Thr Asn Leu Ser Ile Thr Lys Leu Gln Val Gln Glu Leu Cys Asn
 210 215 220

Leu Phe Leu Asp Ser Thr Phe Ser Glu Asn Asn Asn Phe
 225 230 235

REN-01-032-Uti1.ST25.txt

<210> 36
 <211> 648
 <212> DNA
 <213> Escherichia coli

<400> 36
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 ggacatacgc tgcattttgt tgagttcgat ccggcgaatt tttgtgagca ggatttactc 120
 tggctgccgc actacgcaca actgcaacac gctggacgta aacgtaaaac agagcattta 180
 gccggacgga tcgctgctgt ttatgctttg cgggaatatg gctataaatg tgtgcccgca 240
 atcggcgagc tacgccaacc tgtctggcct gcggaggtat acggcagtat tagccactgt 300
 gggactacgg cattagccgt ggtatctcgt caaccgattg gcattgatat agaagaaatt 360
 ttttctgtac aaaccgcaag agaattgaca gacaacatta ttacaccagc ggaacacgag 420
 cgactcgag actgcggttt agccttttct ctggcgctga cactggcatt ttccgcaaaa 480
 gagagcgcat ttaaggcaag tgagatcaa actgatgcag gttttctgga ctatcagata 540
 attagctgga ataaacagca ggtcatcatt catcgtgaga atgagatggt tgctgtgcac 600
 tggcagataa aagaaaagat agtcataacg ctgtgccaac acgattaa 648

<210> 37
 <211> 215
 <212> PRT
 <213> Escherichia coli

<400> 37

Met Ser Ser Val Ser Asn Met Val Asp Met Lys Thr Thr His Thr Ser
 1 5 10 15

Leu Pro Phe Ala Gly His Thr Leu His Phe Val Glu Phe Asp Pro Ala
 20 25 30

Asn Phe Cys Glu Gln Asp Leu Leu Trp Leu Pro His Tyr Ala Gln Leu
 35 40 45

Gln His Ala Gly Arg Lys Arg Lys Thr Glu His Leu Ala Gly Arg Ile
 50 55 60

Ala Ala Val Tyr Ala Leu Arg Glu Tyr Gly Tyr Lys Cys Val Pro Ala
 65 70 75 80

Ile Gly Glu Leu Arg Gln Pro Val Trp Pro Ala Glu Val Tyr Gly Ser
 85 90 95

Ile Ser His Cys Gly Thr Thr Ala Leu Ala Val Val Ser Arg Gln Pro
 100 105 110

Ile Gly Ile Asp Ile Glu Glu Ile Phe Ser Val Gln Thr Ala Arg Glu
 115 120 125

REN-01-032-Uti1.ST25.txt

Leu Thr Asp Asn Ile Ile Thr Pro Ala Glu His Glu Arg Leu Ala Asp
 130 135 140

Cys Gly Leu Ala Phe Ser Leu Ala Leu Thr Leu Ala Phe Ser Ala Lys
 145 150 155 160

Glu Ser Ala Phe Lys Ala Ser Glu Ile Gln Thr Asp Ala Gly Phe Leu
 165 170 175

Asp Tyr Gln Ile Ile Ser Trp Asn Lys Gln Gln Val Ile Ile His Arg
 180 185 190

Glu Asn Glu Met Phe Ala Val His Trp Gln Ile Lys Glu Lys Ile Val
 195 200 205

Ile Thr Leu Cys Gln His Asp
 210 215

<210> 38
 <211> 741
 <212> DNA
 <213> Streptomyces verticillus

<400> 38
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 gacgaccggt tgagcctcct cttccccgag gaggccgccc acgtcgcccc cgccgtcccc 120
 aagcgctgc acgagttcgc caccgtccgg gtgtgcgccc gcgccgccct cggccgggtg 180
 ggcctccccgc ccggtccgct gctgcccggc cgacggggcg cgccgagctg gccggacggg 240
 gtggtgggga gcatgacgca ctgtcagggc ttccggggcg ccgcggtcgc ccggggccgcc 300
 gacgccggt cgctcgggat agacgccgag ccgaacgggc cgctcccgga cggcgtcctc 360
 gccatggtct cgctgccgtc cgagcgcgag tggctcgccg gactggcggc ccgccggccg 420
 gacgtgcact gggaccggct gctgttcagc gccaaggaga gcgtcttcaa ggcgtggtac 480
 ccgctgaccg gcctggagct ggacttcgac gaggccgagc tggccgtcga tccggacgcc 540
 gggacgttca cggcccggct gctggtgccg ggaccggtgg tcggcgggccg tcggctggac 600
 gggttcgagg ggcgctgggc ggcgggagc ggcctcgtcgc tcacggccat cgccgtcgcg 660
 gcgccggccg gtaccgcgga ggaatcggcg gaaggggccc ggaaggaagc gactgcggac 720
 gaccggaccg ccgtcccgtg a 741

<210> 39
 <211> 246
 <212> PRT
 <213> Streptomyces verticillus

<400> 39

Met Ile Ala Ala Leu Leu Pro Ser Trp Ala Val Thr Glu His Ala Phe
 1 5 10 15

REN-01-032-Util.ST25.txt

Thr Asp Ala Pro Asp Asp Pro Val Ser Leu Leu Phe Pro Glu Glu Ala
 20 25 30
 Ala His Val Ala Arg Ala Val Pro Lys Arg Leu His Glu Phe Ala Thr
 35 40 45
 Val Arg Val Cys Ala Arg Ala Ala Leu Gly Arg Leu Gly Leu Pro Pro
 50 55 60
 Gly Pro Leu Leu Pro Gly Arg Arg Gly Ala Pro Ser Trp Pro Asp Gly
 65 70 75 80
 Val Val Gly Ser Met Thr His Cys Gln Gly Phe Arg Gly Ala Ala Val
 85 90 95
 Ala Arg Ala Ala Asp Ala Ala Ser Leu Gly Ile Asp Ala Glu Pro Asn
 100 105 110
 Gly Pro Leu Pro Asp Gly Val Leu Ala Met Val Ser Leu Pro Ser Glu
 115 120 125
 Arg Glu Trp Leu Ala Gly Leu Ala Ala Arg Arg Pro Asp Val His Trp
 130 135 140
 Asp Arg Leu Leu Phe Ser Ala Lys Glu Ser Val Phe Lys Ala Trp Tyr
 145 150 155 160
 Pro Leu Thr Gly Leu Glu Leu Asp Phe Asp Glu Ala Glu Leu Ala Val
 165 170 175
 Asp Pro Asp Ala Gly Thr Phe Thr Ala Arg Leu Leu Val Pro Gly Pro
 180 185 190
 Val Val Gly Gly Arg Arg Leu Asp Gly Phe Glu Gly Arg Trp Ala Ala
 195 200 205
 Gly Glu Gly Leu Val Val Thr Ala Ile Ala Val Ala Ala Pro Ala Gly
 210 215 220
 Thr Ala Glu Glu Ser Ala Glu Gly Ala Gly Lys Glu Ala Thr Ala Asp
 225 230 235 240
 Asp Arg Thr Ala Val Pro
 245

<210> 40
 <211> 819
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 40

REN-01-032-Util.ST25.txt

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gcagggtatat tcgttggtga aattcaagag gatatactcg cggatgagtt tacgttcgag      120
gcattaatga gaactttgcc attggcgtct caagccagaa tcctcaataa aaaatcgttt      180
cacgatagat gttcaaatct atgcagccag ctgctgcagt tgtttggctg ctctatagta      240
acgggcttaa attttcaaga gctgaaatth gacaagggca gcttcggtaa gccattctta      300
gacaacaatc gttttcttcc atttagcatg accatcggtg aacaatatgt agctatgttc      360
ctcgtaaaat gtgtaagtac agatgaatac caggatgtcg gaattgatat cgcttctccg      420
tgcaattatg gcgggagggg agagttggag ctattttaaag aagtttttag tgaaagagaa      480
tttaacggtt tactgaaagc gtctgatcca tgcacaatat ttacttactt atggtccttg      540
aaggagtcgt atacaaaatt tactggaact ggccttaaca cagacttgtc actaatagat      600
tttggcgcta tcagcttttt tccggctgag ggagcttcta tgtgcataac tctggatgaa      660
gttccattga ttttccattc tcaatgggtc aataacgaaa ttgtcactat ctgtatgccaa      720
aagtccatca gtgataaaat caacacgaac agaccaaata tatataatat cagcttatct      780
acgttgattg attatttcat cgaaaatgat ggtttataa      819

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<210> 41
 <211> 272
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 41

Met Val Lys Thr Thr Glu Val Val Ser Glu Val Ser Lys Val Ala Gly
 1 5 10 15

Val Arg Pro Trp Ala Gly Ile Phe Val Val Glu Ile Gln Glu Asp Ile
 20 25 30

Leu Ala Asp Glu Phe Thr Phe Glu Ala Leu Met Arg Thr Leu Pro Leu
 35 40 45

Ala Ser Gln Ala Arg Ile Leu Asn Lys Lys Ser Phe His Asp Arg Cys
 50 55 60

Ser Asn Leu Cys Ser Gln Leu Leu Gln Leu Phe Gly Cys Ser Ile Val
 65 70 75 80

Thr Gly Leu Asn Phe Gln Glu Leu Lys Phe Asp Lys Gly Ser Phe Gly
 85 90 95

Lys Pro Phe Leu Asp Asn Asn Arg Phe Leu Pro Phe Ser Met Thr Ile
 100 105 110

Gly Glu Gln Tyr Val Ala Met Phe Leu Val Lys Cys Val Ser Thr Asp
 115 120 125

REN-01-032-Util.ST25.txt

Glu Tyr Gln Asp Val Gly Ile Asp Ile Ala Ser Pro Cys Asn Tyr Gly
 130 135 140

Gly Arg Glu Glu Leu Glu Leu Phe Lys Glu Val Phe Ser Glu Arg Glu
 145 150 155 160

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

Leu Trp Ser Leu Lys Glu Ser Tyr Thr Lys Phe Thr Gly Thr Gly Leu
 180 185 190

Asn Thr Asp Leu Ser Leu Ile Asp Phe Gly Ala Ile Ser Phe Phe Pro
 195 200 205

Ala Glu Gly Ala Ser Met Cys Ile Thr Leu Asp Glu Val Pro Leu Ile
 210 215 220

Phe His Ser Gln Trp Phe Asn Asn Glu Ile Val Thr Ile Cys Met Pro
 225 230 235 240

Lys Ser Ile Ser Asp Lys Ile Asn Thr Asn Arg Pro Lys Leu Tyr Asn
 245 250 255

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 35 40 45

Ala Val Glu Leu Leu Thr Glu Ala Val Asn Leu Leu Val Leu Gln Val
 50 55 60

Phe Arg Lys Asp Asp Tyr Ala Val Lys Tyr Ala Val Glu Pro Leu Leu
 65 70 75 80

Asp Gly Asp Gly Pro Leu Gly Asp Leu Ser Val Arg Leu Lys Leu Ile
 85 90 95

Tyr Gly Leu Gly Val Ile Asn Arg Gln Glu Tyr Glu Asp Ala Glu Leu
 100 105 110

Leu Met Ala Leu Arg Glu Glu Leu Asn His Asp Gly Asn Glu Tyr Ala
 115 120 125

Phe Thr Asp Asp Glu Ile Leu Gly Pro Phe Gly Glu Leu His Cys Val
 130 135 140

Ala Ala Leu Pro Pro Pro Gln Phe Glu Pro Ala Asp Ser Ser Leu
 145 150 155 160

Tyr Ala Met Gln Ile Gln Arg Tyr Gln Gln Ala Val Arg Ser Thr Met
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Val Leu Ser Leu Thr Glu Leu Ile Ser Lys Ile Ser Leu Lys Lys Ala
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Phe Gln Lys
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Arg Ile Asn Ser Asp Ser Tyr Trp Asp Asn Leu Pro Glu Glu Gln Arg
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20