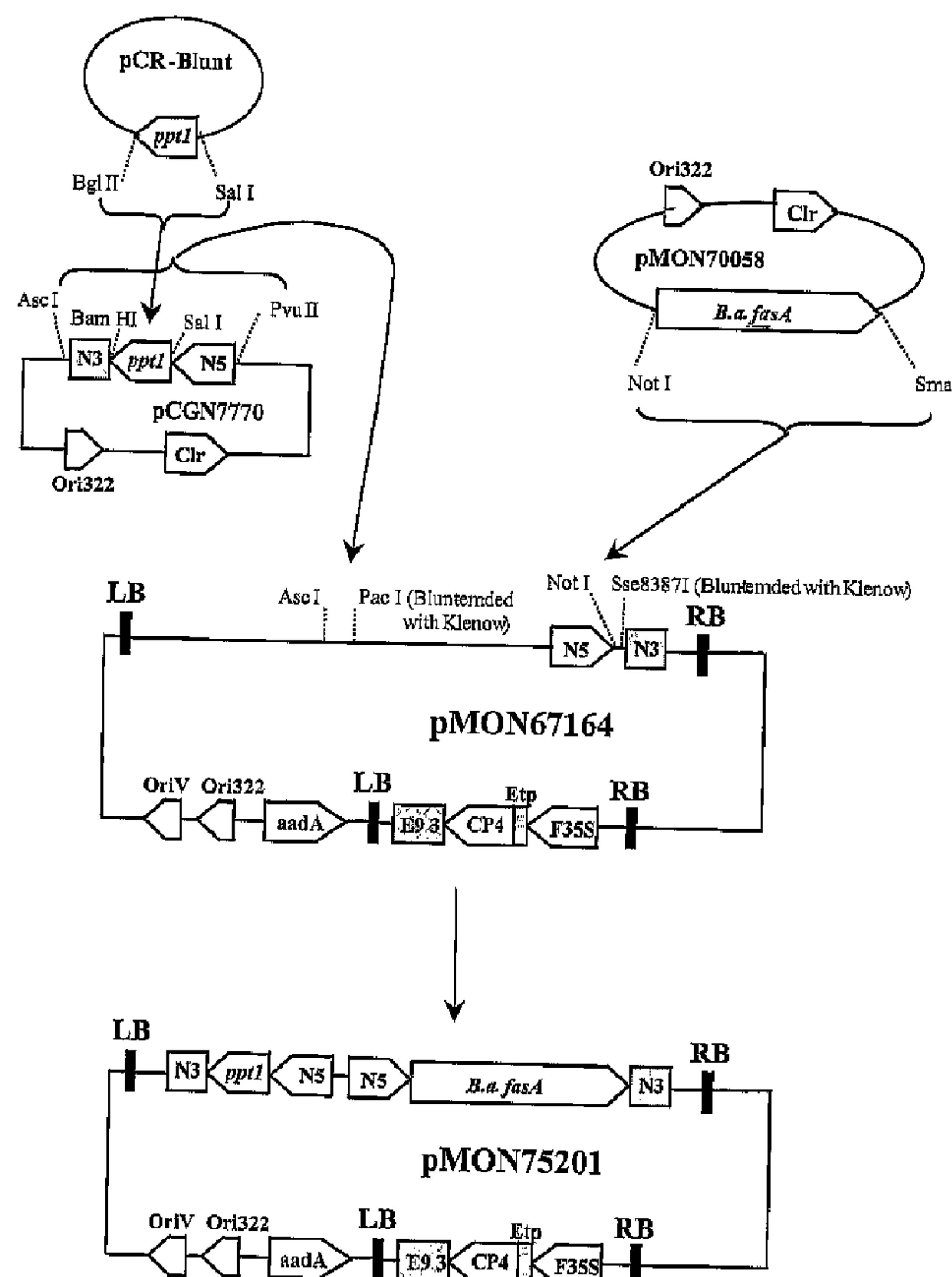




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This present invention provides a method for increasing oil levels in the tissues of Brassica sp. plants by expression of a heterologous multifunctional fatty acid synthase (mfFAS) within the plant. In one embodiment, the present invention provides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



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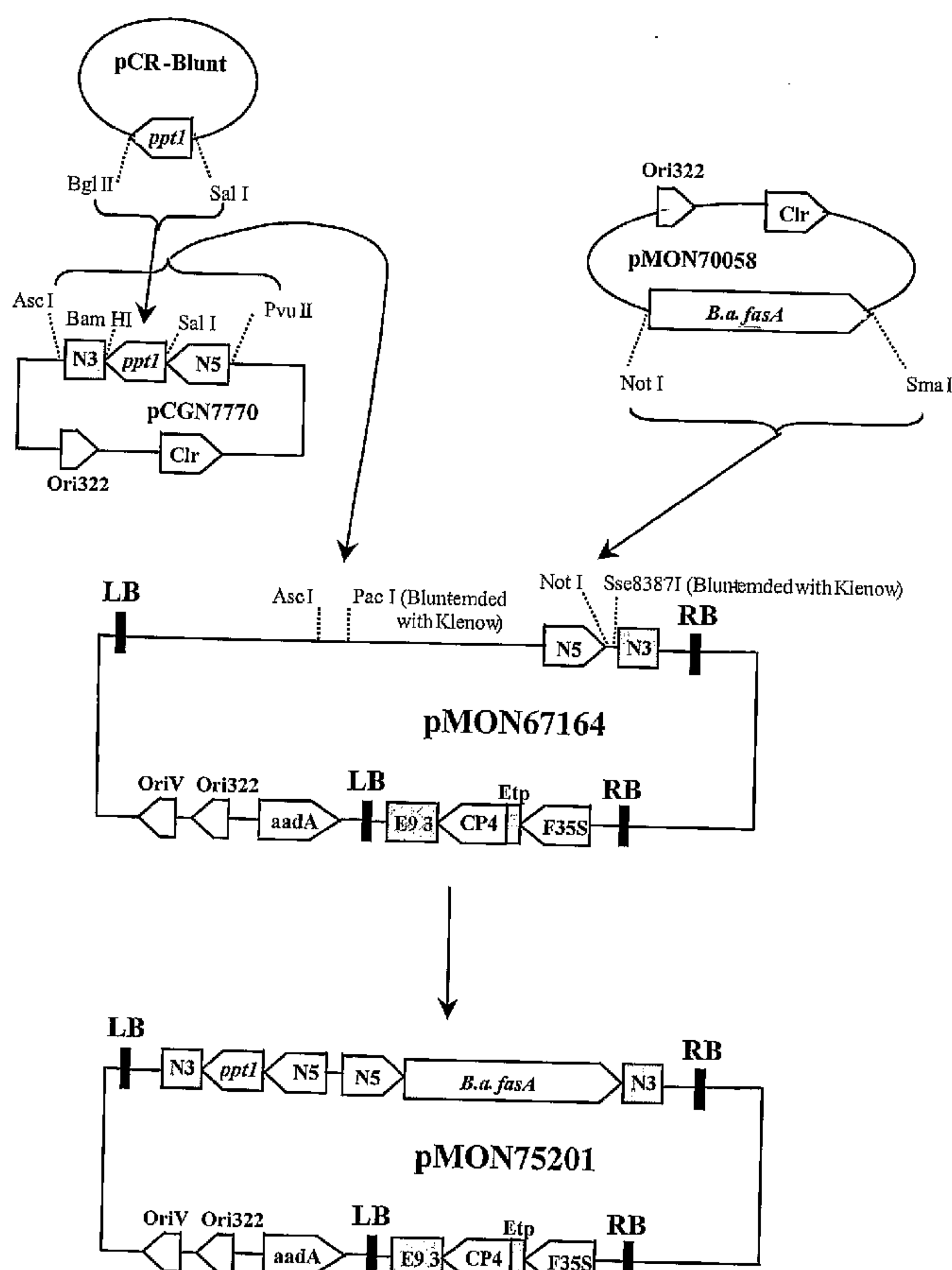
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ELEVATION OF OIL LEVELS IN *BRASSICA* PLANTS

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.

5 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.

10 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.

15 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.

20 DEFINITIONS

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

25 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
30 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.

The term "expression" refers to the transcription of a gene to produce the
5 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.

The term "heterologous" refers to the relationship between 2 or more nucleic acid or
15 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.

The phrase "operably linked" refers to the functional spatial arrangement of 2 or more
25 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.

In the context of the present invention, the terms "plant" or "plants" refer to plants of
30 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. 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 mFAS 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
5 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
10 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
15 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
20 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
25 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).

30 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 µg/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 µg/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 µg/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 Omega™ 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
5 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.)*,
10 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
15 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
20 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
25 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
30 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 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 *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 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 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 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* 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 Lopes *et al.*, *Mol Gen Genet.*, 247:603-613, 1995), L3 oleosin promoter (U.S. Patent 6,433,252), USP promoter and 7S α promoter (U.S. Patent No. 6,825,398), 7S α ' 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).

30 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
5 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
10 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
15 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
20 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
25 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
30 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 hygroscopicus* or the *pat* gene from *Streptomyces viridochromogenes* (U.S. Patent 5,550,318). The enzyme
5 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.

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.

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
25 *et al.*, *Mol. Gen. Genet.*, 204:204, 1986; Marcotte *et al.*, *Nature*, 335:454-457, 1988).

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
5 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
10 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
15 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,
20 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.

25 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.
30 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*
 20 *Rep.*, 7:379, 1988; Battraw and Hall, *Plant Sci.*, 86:191-202, 1992; Christou *et al.*, *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).

25 Assays for gene expression based on the transient expression of cloned nucleic acid 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,
10 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,
15 *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
20 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
25 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
30 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,

5 **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*).

10 **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:

Prehybridization was in a solution of 40% formamide, 5X SSC, 50 mM sodium phosphate, pH 7.0, 5X Denhardt's, 0.1% SDS, 5 mM EDTA, 0.1 µg/ml salmon sperm DNA, and 5% Dextran sulfate for 2 hrs at 42°C and hybridization was in the same solution as described overnight at 42°C. The filters were rinsed briefly in 0.1X SSC, 0.1% SDS at RT and then washed 2 times for 20 min each in 0.1X SSC, 0.1% SDS at 50°C. FasA-containing clones were identified by autoradiography and restriction mapping. Selected cosmid clones were analyzed in more detail and one clone was confirmed to have the full-length *fasA* gene by restriction mapping and comparison with the restriction sites in the published sequence (Stuible *et al.*, *J Bacteriol.*, 178:4787-4793, 1993).

- 40 -

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

5 *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
10 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 /
15 *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
20 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*
25 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
30 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.

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ag 9122

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 <213> Brevibacterium ammoniagenes

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REN-01-032-Util.ST25.txt

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Asp Ala Ala Ala Ser Pro His Gln Gly Ala Gln Leu Arg Asp Ile Leu
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Lys Glu Val Arg Thr Thr Thr Gly Pro Val Ala Arg Ile Ile Ala Ser
50 55 60

Ser Cys Pro Gly Val Tyr Glu Arg Leu Glu Glu Leu Ala Gln Thr Pro
65 70 75 80

Ala Asp Gln Ala Pro Val Ala Lys Glu Tyr Asp Ala Tyr Pro Ala Tyr
85 90 95

Ser Ile Pro Gly Ile Val Leu Gly Gln Ile Gly Ala Ile Glu His Leu
100 105 110

Ala Gln Leu Gly Ile Asp Val Asp Ser Ala Gln Leu Ala Gly His Gln
115 120 125

Gly Ser Leu Gly Val Ala Ala Val Lys Asp Ala Arg Gln Ala Leu Ala
130 135 140

Ile Ala Val Leu Met Gly Thr Ala Ala Ala Val Thr Gln Gly Ala Asn
145 150 155 160

Asp Ser Arg Thr His Met Leu Ser Val Arg Gly Val Pro Arg Glu Met
165 170 175

Val Glu Glu Tyr Leu Ala Gly Asp Ala Ala Ile Ala Val Val Asn Gly
180 185 190

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

Glu Ser Asn Leu Thr Gln Ala Ala Glu Ser Tyr Asn Asp Ala Leu Glu
210 215 220

Glu Arg Arg Ile Gly Gly Ser Glu Ile Asn Pro Val Phe Asp Val Leu
225 230 235 240

Ala Val Ala Leu Pro Phe His His Ala Ser Leu Gln Asp Ala Asp Leu
245 250 255

Thr Val Asp Tyr Ala Thr Gln Cys Gly Leu Asp Ala Glu Leu Ala Arg
260 265 270

Glu Leu Ala Asp Ser Ile Leu Val Gln Pro His Ser Trp Val Glu Thr

REN-01-032-Util.ST25.txt
280 285

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Val Ala Gly Leu Asn Ser Thr Tyr Leu Leu Ser Leu Asp Arg Gly Leu
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305 310 315 320Pro Ala Ala Thr Pro Ala Glu Arg Asp Asn Leu Ala Thr Pro Gly Thr
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370 375 380Pro Gly Ile Val Ala Ala Ala Ala Asn Gly Gly Tyr Trp Ser Glu Met
385 390 395 400Ala Gly Gly Gly Gln Tyr Ser Asp Glu Ala Phe Thr Ile Asn Lys Asp
405 410 415Gly Met Met Glu Leu Leu Glu Pro Gly Arg Thr Ala Ala Phe Asn Thr
420 425 430Met Phe Phe Asp Arg Tyr Leu Trp Asn Leu Gln Phe Gly Val Thr Arg
435 440 445Ile Cys Ser Lys Ala Arg Ala Asn Gly Ala Ala Phe Thr Gly Val Thr
450 455 460Ile Cys Ala Gly Ile Pro Glu Leu Asp Glu Ala Lys Glu Leu Leu Asp
465 470 475 480Gln Leu Thr Ser Asp Gly Phe Pro Tyr Ile Ser Phe Lys Pro Gly Thr
485 490 495Thr Lys Gln Ile Gln Asp Cys Val Ala Ile Ala Ala Asn Pro Thr His
500 505 510Arg Val Ile Ile Gln Ile Glu Asp Ala His Ala Gly Gly His His Ser
515 520 525Trp Val Asp Leu Asp Glu Met Leu Leu Ala Thr Tyr Ala Cys Ala Arg
530 535 540Glu His Asp Asn Leu Ala Ile Thr Val Gly Gly Gly Ile His Ser Pro
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REN-01-032-Util.ST25.txt

545

550

555

560

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Leu Pro Ile Met Pro Val Asp Gly Val Phe Leu Gly Thr Val Ala Met
 580 585 590

Ala Thr Lys Glu Ala Thr Ala Asn Asp Asp Val Lys Gln Leu Leu Val
 595 600 605

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Leu Asp Ala Asp Gly Gly Val Ser Ser Ser Gln His Leu Leu Ala Asp
 625 630 635 640

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Ser Ile Pro Ile Glu Glu Tyr Asp Glu Arg Arg Asp Glu Ile Ile Ala
 660 665 670

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Thr Tyr Glu Asp Trp Val Ala Arg Phe Ala Glu Arg Ala Tyr Pro Trp
 690 695 700

Val Asp Pro Thr Trp His Asp Arg Phe His Asp Leu Leu Gln Arg Val
 705 710 715 720

Glu Ala Arg Leu Asn Asp Ala Asp His Gly Asp Ile Glu Thr Leu Phe
 725 730 735

Pro Thr Leu Asp Asp Ser Glu Asn Ala Pro Glu Ala Val Ala Lys Leu
 740 745 750

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 755 760 765

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Thr Thr Ala Ile Asp Gly Asp Leu Lys Glu Trp Phe Ala Lys Asp Thr
 785 790 795 800

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Ile Pro Gly Pro Val Ser Val Ala Gly Ile Thr Lys Lys Asn Glu Pro

REN-01-032-Util.ST25.txt

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825

830

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Asn Asp Ala Gly Val Ala Pro Val Glu Leu Tyr Ser Arg Leu Ala Ser
 850 855 860

Ala Lys Asn Ala Glu Glu Phe Leu Arg Asn Ala Pro Thr Ile Met Trp
 865 870 875 880

His Gly His Leu Ile Ala Asn Pro Ala Glu Leu Pro Glu Glu Ala Phe
 885 890 895

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
 930 935 940

Ser Pro Val Val Asp Asp Ala Arg Leu Pro Lys Ala Val Phe Asp Leu
 945 950 955 960

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

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
 995 1000 1005

Thr Ala His Thr Ala Val Thr Gly Ala Leu Gly Thr Ala Asn Ala
 1010 1015 1020

Gly Thr Pro Asp Ala Leu Val Gly Pro Cys Trp Pro Ala Ile Tyr
 1025 1030 1035

Thr Ala Leu Gly Thr Gly Arg Leu Thr Glu Glu His Gly Glu Pro
 1040 1045 1050

Ala Gly Thr Asp Phe Pro Val Ile Glu Gly Leu Leu Asn Ala Val
 1055 1060 1065

His Leu Asp His Val Val Asp Val Arg Val Pro Leu His Glu Leu
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Ala Lys Gly Glu Lys Gly Glu Gly Gly Arg Ile Asp Val Thr Ser

1085

REN-01-032-Util.ST25.txt
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1100 1105 1110Val Glu Leu Glu Leu Trp Asp Ala Ala Thr Gln Glu Val Val Ala
1115 1120 1125Thr Gln Met Gln Arg Phe Ala Ile Arg Gly Arg Ala Thr Gly Thr
1130 1135 1140Val Pro Val Ser Ala Pro Ser Trp Gly Gly Gly Lys Ser Gln Asp
1145 1150 1155Lys Ile Glu Thr Thr Pro Arg Ser Phe Val Asp Arg Ala Ile Val
1160 1165 1170Thr Ala Pro Ser Asp Met Thr Pro Phe Ala Leu Val Ser Gly Asp
1175 1180 1185Tyr Asn Pro Ile His Thr Ser Thr Asn Ala Ala Arg Leu Val Asn
1190 1195 1200Leu Asp Ala Pro Leu Val His Gly Met Trp Leu Ser Ala Thr Ala
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1220 1225 1230Ser Met Tyr Gly Met Val Gln Leu Asn Asp Glu Val Glu Ile Thr
1235 1240 1245Val Glu Arg Val Gly Arg Lys Gly Ile His Ala Ala Phe Glu Val
1250 1255 1260Thr Cys Arg Ile Asp Gly Glu Val Ser Arg Gly Gln Ala Leu Met
1265 1270 1275Ala Gln Pro Arg Thr Ala Tyr Val Tyr Pro Gly Gln Gly Ile Gln
1280 1285 1290Ala Glu Gly Met Gly Arg Gly Asp Arg Asp Ala Ser Ala Ala Ala
1295 1300 1305Arg Glu Val Trp Arg Arg Ala Asp Arg His Thr Arg Thr Ala Leu
1310 1315 1320Gly Phe Ser Ile Arg Gln Ile Ile Asp Asp Asn Pro Thr Glu Leu
1325 1330 1335Val Val Arg Gly Thr Lys Phe Val His Pro Asn Gly Val Leu His
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REN-01-032-Util.ST25.txt
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1340

Leu Thr Gln Phe Thr Gln Val Ala Leu Ala Val Val Ala Tyr Ala
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Gln Thr Glu Arg Leu Arg Glu Ala Asp Ala Leu Gly Thr Asn Ser
1370 1375 1380

Met Tyr Ala Gly His Ser Leu Gly Glu Tyr Thr Ala Leu Ala Leu
1385 1390 1395

Ala Asn Ile Phe Asp Leu Glu Ala Val Ile Asp Ile Val Tyr Ser
1400 1405 1410

Arg Gly Ser Ala Met Gly Thr Leu Val Glu Arg Asp Glu Asn Gly
1415 1420 1425

Asn Ser Asn Tyr Gly Met Gly Ala Leu Arg Pro Asn Met Ile Gly
1430 1435 1440

Val Pro Ala Asp Gln Val Glu Ala Tyr Ile Ala Gln Thr Ala Glu
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Glu Thr Gly Glu Phe Leu Glu Ile Val Asn Tyr Asn Ile Ala Gly
1460 1465 1470

Gln Gln Tyr Ser Ile Ala Gly Thr Lys Ala Gly Leu Ala Ala Leu
1475 1480 1485

Lys Lys Lys Ala Asn Ser Val Lys Asp Arg Ala Tyr Val Thr Val
1490 1495 1500

Pro Gly Ile Asp Val Pro Phe His Ser Gln Val Leu Arg Asp Gly
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Val Pro Ala Phe Ala Glu Leu Asp Glu Leu Leu Pro Glu Thr Leu
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Asp Leu Asp Ala Leu Val Gly Arg Tyr Val Pro Asn Leu Val Ala
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Leu Pro Phe Glu Leu Thr Gln Glu Phe Val Asp Lys Val Lys Pro
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Leu Ala Pro Ser Gly Lys Leu Asp Asn Leu Lys Val Glu Asp Thr
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Asp Glu Gln Ala Pro Ser Arg Leu Leu Met Ile Glu Leu Leu Ser
1580 1585 1590

Trp Gln Phe Ala Ser Pro Val Arg Trp Ile Glu Thr Gln Gln Leu
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1595 REN-01-032-Util.ST25.txt
1600 1605

Leu Phe Glu Glu Val Asp Gln Ile Ile Glu Val Gly Leu Ala Ser
1610 1615 1620

Ser Pro Thr Leu Thr Asn Leu Ala Lys Arg Ser Met Asp Ile Ala
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Gly Val Asp Leu Pro Val Phe Asn Val Glu Arg Asp Gln Gln Val
1640 1645 1650

Met Leu Gln Asp Val Gln Glu Ala Pro Ala Ala Ser Phe Asp Val
1655 1660 1665

Glu Glu Gly Glu Ala Thr Ser Ser Thr Ala Ala Ser Glu Thr Pro
1670 1675 1680

Gly Glu Ser Ala Ala Ala Ala Ser Asp Asn Thr Gln Ala Ile Pro
1685 1690 1695

Ser Ala Glu Pro Gln Thr Val Ala Glu Ala Pro Ala Pro Ser Ala
1700 1705 1710

Ala Pro Ala Gly Gly Thr Arg Ala Ala Asp Ala Pro Asp Leu Pro
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Phe Thr Ala Ala Glu Ala Ile Met Val Leu Phe Ala Phe Gln Asn
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Lys Ile Arg Gln Asp Gln Ile Asn Asp Ser Asp Thr Val Glu Glu
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Leu Thr Asn Gly Val Ser Ser Arg Arg Asn Gln Leu Leu Met Asp
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Met Ser Ala Glu Asn Val Pro Ala Ile Asp Gly Ala Ala Asp Ala
1775 1780 1785

Asp Val Ala Thr Leu Arg Glu Arg Val Lys Thr Ala Ala Pro Gly
1790 1795 1800

Tyr Ser Pro Phe Gly Thr Val Leu Ser Glu Ala Ile Thr Ala Arg
1805 1810 1815

Leu Arg Gln Leu Thr Gly Ala Ala Gly Val Lys Pro Ala Tyr Ile
1820 1825 1830

Ser Glu Arg Val Thr Gly Thr Trp Gly Leu Pro Met Ser Trp Ala
1835 1840 1845

Ala His Val Glu Ala Glu Ile Leu Leu Gly Ser Arg Glu Glu Asp

REN-01-032-util.ST25.txt

1850 1855 1860

Ser Val Arg Gly Gly Ser Leu Ser Thr Val Pro Ser Ala Ala Ser
1865 1870 1875

Ser Lys Ala Asp Val Asp Ala Leu Val Asp Ala Ala Val Gln Ala
1880 1885 1890

Val Ala Ala Ala His Gly Thr Ser Val Ser His Gly Ala Ser Gly
1895 1900 1905

Ala Gly Gly Gly Gly Val Val Asp Ser Ala Ala Leu Asp Ala Tyr
1910 1915 1920

Ala Asp Ile Val Thr Gly Glu Asn Gly Val Leu Ala Thr Ala Ala
1925 1930 1935

Arg Gln Val Leu Ala Gln Leu Gly Leu Val Glu Glu Ala Pro Glu
1940 1945 1950

Thr Pro Glu Thr Asp Asn Thr Leu Phe Ala Thr Val Glu Ala Glu
1955 1960 1965

Leu Gly Ser Gly Trp Glu Lys Thr Val Thr Pro Ser Phe Asp Ala
1970 1975 1980

Lys Arg Ala Val Leu Phe Asp Asp Arg Trp Ala Ser Ala Arg Glu
1985 1990 1995

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

Arg Phe Gln Gly Thr Gly Glu Thr Ile Ala Lys Gln Ala Glu Trp
2015 2020 2025

Trp Ala Glu Asn Ala Ala Ser Thr Gly Ala His Ala Lys Ala Thr
2030 2035 2040

Ala Ala Glu Thr Leu His Ala Ile Ala Ala Ala Ala Arg Glu Glu
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Leu Asp Gly Glu Phe Ala Gly Asp Val Ala Leu Val Thr Gly Ala
2060 2065 2070

Ala Pro Gly Ser Ile Ala Thr Ala Leu Val Glu Arg Leu Leu Glu
2075 2080 2085

Gly Gly Ala Thr Val Ile Met Thr Ala Ser Arg Val Ser Gln Ser
2090 2095 2100

Arg Lys Glu Phe Ala Arg Lys Leu Tyr Ala Ala His Ala Ile Pro

2105

REN-01-032-Util.ST25.txt
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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
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Ser Val Glu Arg Thr Ile Ala Gly Leu Ser Asn Leu Ala Gln Gln
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Gly Val Asp Thr Arg Cys His Ile Val Leu Pro Gly Ser Pro Asn
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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
Page 14

2360

REN-01-032-Util.ST25.txt
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2375 2380 2385Asp Leu Asp Asp Met Val Val Ile Ala Gly Val Gly Glu Val Ser
2390 2395 2400Ser Trp Gly Ser Gly Arg Thr Arg Phe Glu Glu Tyr Gly Leu Gln
2405 2410 2415Arg Asp Gly Ala Val Asp Leu Thr Ala Ala Gly Val Leu Glu Leu
2420 2425 2430Ala Trp Met Thr Gly Leu Ile Ser Trp Ser Asn Asp Pro Arg Pro
2435 2440 2445Ala Trp Tyr Asp Glu Glu Gly Thr Glu Val Asp Glu Ala Asp Ile
2450 2455 2460Tyr Ala Arg Phe Arg Asp Glu Val Val Ala Arg Ser Gly Ile Arg
2465 2470 2475Thr Leu Thr Asp Lys Tyr Asn Met Val Asp Gln Gly Ser Ile Asp
2480 2485 2490Leu Thr Ser Val Phe Leu Asp Arg Asp Ile Val Phe Thr Val Pro
2495 2500 2505Thr Glu Gln Glu Ala Leu Asp Ile Glu Glu Ala Asp Pro Ser Phe
2510 2515 2520Thr Lys Leu Arg Glu Val Asp Gly Glu Trp Glu Val Thr Arg Leu
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2540 2545 2550Val Ala Gly Gln Met Pro Asp His Phe Asp Ala Ala Lys Trp Gly
2555 2560 2565Ile Pro Asp His Met Leu Asp Ala Leu Asp Arg Met Ala Val Trp
2570 2575 2580Asn Leu Val Thr Ala Val Asp Ala Phe Thr Gln Ala Gly Phe Ser
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2600 2605 2610Thr Gln Gly Thr Gly Ile Gly Gly Met Glu Ser Leu His Lys Val
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2620 2625

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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
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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
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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
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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
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Ile	Ser	Gln	Lys	Ser	Leu	Thr	Gly	His	Ser	Lys	Ala	Gly	Ala	Ala
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REN-01-032-Util.ST25.txt

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 20 25 30

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 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
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Val Glu Leu Ala Leu Ser Ile Ser His Asp Gly Asp Tyr Ala Thr Ala
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REN-01-032-Util.ST25.txt

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REN-01-032-Util.ST25.txt

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<223> Primer Sequence

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<211> 2073

<212> PRT

<213> Schizosaccharomyces pombe

<400> 15

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20 25 30Leu Leu Ala Ala Gln Leu Arg Asp Glu Phe Leu Ser Leu His Pro Ala
35 40 45Pro Ser Ala Glu Ser Val Glu Lys Glu Gly Ala Glu Leu Glu Phe Glu
50 55 60His Glu Leu His Leu Leu Ala Gly Phe Leu Gly Leu Ile Ala Ala Lys
65 70 75 80Glu Glu Glu Thr Pro Gly Gln Tyr Thr Gln Leu Leu Arg Ile Ile Thr
85 90 95Leu 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
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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
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Lys Asp Gly Gln Gly Val Arg Val Ile Val Ala Asp Ser Phe Glu Ser
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Leu Asp Met Gly Ala Lys Phe Glu Ile Phe Asp Arg Asp Ala Lys Ser
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Ile Glu Phe Ala Pro Asn Trp Val Lys Leu Tyr Ser Pro Lys Leu Val
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Lys Asn Lys Leu Gly Arg Val Tyr Val Asp Thr Arg Leu Ser Arg Met
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Leu Gly Leu Pro Pro Leu Trp Val Ala Gly Met Thr Pro Thr Ser Val
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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
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Val Ile Tyr Ile Asn Pro Arg Thr Tyr Ala Trp Gln Ile Pro Leu Ile
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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
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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
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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
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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

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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
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Asp	Gly	Arg	Asn	Asp	Arg	Ile	Lys	His	Phe	Tyr	Trp	Ala	Leu	Trp
1265						1270					1275			
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1295						1300					1305			
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1310						1315					1320			
Ala	Ile	Arg	Lys	Arg	Met	Ala	Pro	Met	Asp	Phe	Ala	Ile	Val	Val
1325						1330					1335			
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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
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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
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Gln Leu	Leu Asp Pro Ser	Gln Asp Leu Ser Gly Ser	Ile Leu Thr
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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
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 Asp Lys His Phe Leu Thr Asn Tyr Gly Phe Ser Ile Ile Asp Ile
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 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
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 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
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 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
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 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
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REN-01-032-Uti1.ST25.txt

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 <213> Schizosaccharomyces pombe

<400> 17

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

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

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-Util.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 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
 355 360 365

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-Util.ST25.txt

Leu Ser Thr Arg Leu Arg Thr Glu Leu Leu Glu Thr Ala Glu Ile Arg
 900 905 910

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
 1160 1165 1170
 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
 1205 1210 1215
 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
 1235 1240 1245
 Leu Ser Ala Ser Gly Pro Ile Lys Thr Pro Val Gly Ala Cys Ala
 1250 1255 1260
 Thr Ala Val Glu Ser Val Asp Ala Ala Val Asp Leu Ile Thr Ser
 1265 1270 1275
 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
 Ala Ala Lys Glu Thr Glu Arg Gly Arg Thr Pro Gln Glu Met Ser
 1310 1315 1320
 Arg Pro Ala Thr Ser Thr Arg Asp Gly Phe Met Glu Ser Gln Gly
 1325 1330 1335
 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-Util.ST25.txt

Ile Gly Glu Trp Ala Glu Arg Glu Tyr Leu Tyr Leu Glu Glu Glu
 1415 1420 1425
 Leu Asp Ala Met Lys Val Gln Asn Pro Asp Leu Asp Leu Glu Ala
 1430 1435 1440
 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
 1460 1465 1470
 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
 1505 1510 1515
 Gln Leu Thr His Leu Gly Arg Ser Lys Gly Asn Ala Val Tyr Gly
 1520 1525 1530
 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
 1550 1555 1560
 Val Pro Gly Asn Arg Asn Ala Asp Asn Ile Asp Glu Tyr Leu Ala
 1565 1570 1575
 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
 1610 1615 1620
 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-Utl1.ST25.txt

Gln Glu Lys Ala Val Tyr Leu Asn Pro Leu Ala Arg Ala Ser Lys
 1670 1675 1680

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

<210> 18
 <211> 2051
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 18

Met Asp Ala Tyr Ser Thr Arg Pro Leu Thr Leu Ser His Gly Ser Leu
 1 5 10 15

Glu His Val Leu Leu Val Pro Thr Ala Ser Phe Phe Ile Ala Ser Gln
 20 25 30

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

Ala Ala Asp Asp Glu Pro Thr Thr Pro Ala Glu Leu Val Gly Lys Phe
 50 55 60

Leu Gly Tyr Val Ser Ser Leu Val Glu Pro Ser Lys Val Gly Gln Phe
 65 70 75 80

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
 130 135 140

Leu Phe Arg Ala Val Gly Glu Gly Asn Ala Gln Leu Val Ala Ile Phe
 145 150 155 160

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

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

Leu Val Pro Gly Met Thr Pro Cys Thr Val Ser Pro Asp Phe Val Ala
595 600 605

Ala Thr Thr Asn Ala Gly Tyr Thr Ile Glu Leu Ala Gly Gly Gly Tyr
610 615 620

Phe Ser Ala Ala Gly Met Thr Ala Ala Ile Asp Ser Val Val Ser Gln
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-Util.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 1450 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-Util.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

<400> 19

Met Lys Pro Glu Val Glu Gln Glu Leu Ala His Ile Leu Leu Thr Glu
 1 5 10 15

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 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
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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
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Lys Phe Met Glu Tyr His Ile Ser Asn Thr Asp Glu Thr Lys Gly Glu
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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
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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
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Thr Thr Gln Leu Ala Gly Met Asp Val Glu Asp Ala Leu Asp Lys Asp
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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
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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
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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
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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
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Ser Gln Lys Glu Met Ala Phe Asn Leu Leu Gly Leu Leu Thr Pro Glu
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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
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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
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Phe Ala Glu Val Gly Pro Trp Gly Ser Ala Arg Thr Arg Trp Glu
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Met Glu Ala Phe Gly Glu Phe Ser Leu Glu Gly Cys Val Glu Met
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Ala Trp Ile Met Gly Phe Ile Ser Tyr His Asn Gly Asn Leu Lys
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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
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Val Val Glu Ala Phe Ile Ala Ser Gly Ile Thr Asp Pro Tyr Glu
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Met Tyr Lys Tyr Val His Val Ser Glu Val Gly Asn Cys Ser Gly
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Ser Gly Met Gly Gly Val Ser Ala Leu Arg Gly Met Phe Lys Asp
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Arg Phe Lys Asp Glu Pro Val Gln Asn Asp Ile Leu Gln Glu Ser
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Phe Ile Asn Thr Met Ser Ala Trp Val Asn Met Leu Leu Ile Ser
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Ser Ser Gly Pro Ile Lys Thr Pro Val Gly Ala Cys Ala Thr Ser
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Val Glu Ser Val Asp Ile Gly Val Glu Thr Ile Leu Ser Gly Lys
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Ala Arg Ile Cys Ile Val Gly Gly Tyr Asp Asp Phe Gln Glu Glu
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Gly Ser Phe Glu Phe Gly Asn Met Lys Ala Thr Ser Asn Thr Leu
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Glu Glu Phe Glu His Gly Arg Thr Pro Ala Glu Met Ser Arg Pro
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Ala Thr Thr Thr Arg Asn Gly Phe Met Glu Ala Gln Gly Ala Gly
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Ile Gln Ile Ile Met Gln Ala Asp Leu Ala Leu Lys Met Gly Val
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REN-01-032-Util.ST25.txt
Pro Ile Tyr Gly Ile Val Ala Met Ala Ala Thr Ala Thr Asp Lys
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Ile Gly Arg Ser Val Pro Ala Pro Gly Lys Gly Ile Leu Thr Thr
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Ala Arg Glu His His Ser Ser Val Lys Tyr Ala Ser Pro Asn Leu
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Asn Met Lys Tyr Arg Lys Arg Gln Leu Val Thr Arg Glu Ala Gln
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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
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Ala Gln Gln Gln Trp Gly Asn Asp Phe Tyr Lys Arg Asp Pro Arg
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Ile Ala Pro Leu Arg Gly Ala Leu Ala Thr Tyr Gly Leu Thr Ile
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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

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 <212> PRT
 <213> Candida albicans

REN-01-032-Util.ST25.txt

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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

260

265

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

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

Ser Leu Arg Asn Met Tyr Gly Asp Phe Leu Arg Arg Val Glu Glu Arg
930 935 940

Phe Thr Ser Ser Ala Gly Thr Val Ser Leu Leu Gln Asn Phe Asn Gln
945 950 955 960

Leu Asn Glu Pro Glu Gln Phe Thr Ala Asp Phe Phe Glu Lys Phe Pro
965 970 975

Gln Ala Gly Lys Gln Leu Ile Ser Glu Glu Asp Cys Asp Tyr Phe Leu
980 985 990

Met Leu Ala Ala Arg Pro Gly Gln Lys Pro Val Pro Phe Val Pro Val
995 1000 1005

Leu Asp Glu Arg Phe Glu Phe Phe Phe Lys Lys Asp Ser Leu Trp
1010 1015 1020

Gln Ser Glu Asp Leu Glu Ser Val Val Asp Glu Asp Val Gln Arg
1025 1030 1035

Thr Cys Ile Leu His Gly Pro Val Ala Ser Gln Tyr Thr Ser Lys
1040 1045 1050

Val Asp Glu Pro Ile Gly Asp Ile Leu Asn Ser Ile His Glu Gly
1055 1060 1065

His Ile Ala Arg Leu Ile Lys Glu Glu Tyr Ala Gly Asp Glu Ser
Page 57

1070 REN-01-032-Util.ST25.txt 1080
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 Lys Ile Pro Val Val Glu Tyr Phe Gly Gly Lys Lys Pro Ala Ser
 1085 1090 1095
 Val Ser Ala Thr Ser Val Asn Ile Ile Asp Gly Asn Gln Val Val
 1100 1105 1110
 Tyr Glu Ile Asp Ser Glu Leu Pro Asn Lys Gln Glu Trp Leu Asp
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 Thr Asp Arg Ile Val Gln Gly Ser Lys His Val Ser Asn Pro Leu
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 His Asp Ile Leu Thr Pro Ala Lys His Ser Lys Val Thr Ile Asp
 1160 1165 1170
 Lys Lys Thr Lys Lys Leu Thr Ala Phe Glu Asn Ile Lys Gly Asp
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 Gln Leu Ser Leu Ile Glu His Arg Thr Ala Asp Thr Asn Pro Val
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 Ala Leu Pro Phe Leu Tyr Lys Tyr Asn Pro Ala Asp Gly Phe Ala
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 Pro Ile Leu Glu Ile Met Glu Asp Arg Asn Glu Arg Ile Lys Glu
 1235 1240 1245
 Phe Tyr Trp Lys Leu Trp Phe Gly Ser Ser Val Pro Tyr Ser Asn
 1250 1255 1260
 Asp Ile Asn Val Glu Lys Ala Ile Leu Gly Asp Glu Ile Thr Ile
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 Ser Ser Gln Thr Ile Ser Glu Phe Thr His Ala Ile Gly Asn Lys
 1280 1285 1290
 Cys Asp Ala Phe Val Asp Arg Pro Gly Lys Ala Thr Leu Ala Pro
 1295 1300 1305
 Met Asp Phe Ala Ile Val Ile Gly Trp Lys Ala Ile Ile Lys Ala
 1310 1315 1320
 Ile Phe Pro Lys Ser Val Asp Gly Asp Leu Leu Lys Leu Val His
 Page 58

1325 REN-01-032-Util.ST25.txt
 1330 1335
 Leu Ser Asn Gly Tyr Lys Met Ile Thr Gly Ala Ala Pro Leu Lys
 1340 1345 1350
 Lys Gly Asp Val Val Ser Thr Lys Ala Glu Ile Lys Ala Val Leu
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 Arg Glu Gly Lys Pro Val Met Glu Val Thr Ser Gln Phe Leu Tyr
 1385 1390 1395
 Arg Gly Glu Tyr Asn Asp Tyr Cys Asn Thr Phe Gln Lys Val Thr
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 Glu Thr Pro Val Gln Val Ala Phe Lys Ser Ala Lys Asp Leu Ala
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 Val Leu Arg Ser Lys Glu Trp Phe His Leu Glu Lys Asp Val Gln
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 Thr Ile Thr His Gly Met Tyr Ser Ser Ala Ser Ile Arg Ala Leu
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REN-01-032-Util.ST25.txt
1585 1590

1580

Phe Lys Cys Asp Phe Val Gly Met Val Leu Pro Asn Asp Thr Leu
1595 1600 1605Gln Thr Thr Met Glu His Val Gly Met Ile Asn Gly Arg Lys Ile
1610 1615 1620Ile Lys Val Glu Thr Arg Asn Val Glu Thr Glu Leu Pro Val Leu
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1715 1720 1725Gly Glu Asp Gly Ala Leu Lys Ser Glu Lys Ile Phe Lys Asp Ile
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1745 1750 1755Leu Ser Ala Thr Gln Phe Thr Gln Pro Ala Leu Thr Leu Met Glu
1760 1765 1770Lys Ala Ala Tyr Glu Asp Ile Lys Ser Lys Gly Leu Ile Pro Ser
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1790 1795 1800Ser Ser Leu Ala Asn Val Met Pro Ile Glu Ser Leu Val Asp Val
1805 1810 1815Val Phe Tyr Arg Gly Met Thr Met Gln Val Ala Val Pro Arg Asp
1820 1825 1830Glu Leu Gly Arg Ser Asn Tyr Gly Met Val Ala Val Asn Pro Ser
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REN-01-032-Util.ST25.txt
1840 1845

1835

Arg Val Ser Ala Thr Phe Asp Asp Ser Ala Leu Arg Phe Val Val
1850 1855 1860

Asp Glu Val Ala Asn Lys Thr Lys Trp Leu Leu Glu Ile Val Asn
1865 1870 1875

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
1910 1915 1920

Val Lys Glu His Leu Tyr Glu Ile Val Asp Glu Val Ala Ala Lys
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

Leu Met Ser Gly Val Lys Pro Phe Gln Arg Phe Leu Cys Lys Lys
1970 1975 1980

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1985 1990 1995

Ile Pro Asn Leu Thr Ala Lys Pro Phe Glu Leu Thr Lys Glu Tyr
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tatatttttc aaagtttttt ttattctttt actgtttatt caactaactt gtttttattt 180
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REN-01-032-Uti1.ST25.txt

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gattcagtta	gaaaatttga	acaatatgtg	tatgaaatgg	ccaagggtgg	tgctatgacc	1800
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caagcttcca	aagatagcaa	attggaattg	caaagagttt	acgaagattt	attgaagggtg	1920
gttgaaagtt	ccaaggaaat	cgaaaccgaa	caattgacta	aagatatttt	acaagctgct	1980
acagttccaa	caaccccaac	agaggaagta	gacgatcctt	gtactccttc	ttcggatgat	2040
gaaattgctt	ctttaccaga	taagacttct	atcattcaac	ctgtctcgtc	tactattcca	2100
tctcaaacta	ttccattttt	gcacattcag	aaaaagacca	aagacgggtg	ggaatacaat	2160
aagaaattat	cttctcttta	cttggaatgga	ttggaatcag	ctgccattaa	tggtttaact	2220
ttcaaagaca	agtatgtctt	agttactgggt	gctgggtgctg	gctctattgg	tgccgaaatt	2280

REN-01-032-Uti1.ST25.txt

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attgttggtc cgttcaacca aggttctaaa caagatgttg atgcattggt tcaatacatt 2460
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gaagaagggt cttatgaatt cgccaatatg aatgctactt ctaattctat tgaagagttc 4260
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REN-01-032-Uti1.ST25.txt

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 tctgttccag caccaggtaa aggtattttg accactgcca gagaacatca tggcaacttg 4500
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 gccaaagaag aatttgggtga cgaattttct atgcatgagt tcttgaaaga gagaactgaa 4680
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 aatgaatctg ccacaatcaa caatatgatg aaacacttgg gtagatccga aggtaaccga 4920
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 atgttgaatg gtgccattca aattcttgag tctggtcttg ttccaggtaa cagaaatgcg 5040
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 caacaaataa aa 6072

<210> 22
 <211> 1885
 <212> PRT
 <213> Candida albicans

<400> 22

REN-01-032-Util.ST25.txt

Met Lys Pro Glu Ile Glu Gln Glu Leu Ser His Thr Leu Leu Thr Glu
 1 5 10 15
 Leu Leu Ala Tyr Gln Phe Ala Ser Pro Val Arg Trp Ile Glu Thr Gln
 20 25 30
 Asp Val Phe Leu Lys Gln His Asn Thr Glu Arg Ile Ile Glu Ile Gly
 35 40 45
 Pro Ser Pro Thr Leu Ala Gly Met Ala Asn Arg Thr Ile Lys Ala Lys
 50 55 60
 Tyr Glu Ser Tyr Asp Ala Ala Leu Ser Leu Gln Arg Gln Val Leu Cys
 65 70 75 80
 Tyr Ser Lys Asp Ala Lys Glu Ile Tyr Tyr Lys Pro Asp Pro Ala Asp
 85 90 95
 Leu Ala Pro Lys Glu Thr Pro Lys Gln Glu Glu Ser Thr Pro Ser Ala
 100 105 110
 Pro Ala Ala Ala Thr Pro Thr Pro Ala Ala Ala Ala Ala Pro Thr Pro
 115 120 125
 Ala Pro Ala Pro Ala Ser Ala Gly Pro Val Glu Ser Ile Pro Asp Glu
 130 135 140
 Pro Val Lys Ala Asn Leu Leu Ile His Val Leu Val Ala Gln Lys Leu
 145 150 155 160
 Lys Lys Pro Leu Asp Ala Val Pro Met Thr Lys Ala Ile Lys Asp Leu
 165 170 175
 Val Asn Gly Lys Ser Thr Val Gln Asn Glu Ile Leu Gly Asp Leu Gly
 180 185 190
 Lys Glu Phe Gly Ser Thr Pro Glu Lys Pro Glu Asp Thr Pro Leu Glu
 195 200 205
 Glu Leu Ala Glu Gln Phe Gln Asp Ser Phe Ser Gly Gln Leu Gly Lys
 210 215 220
 Thr Ser Thr Ser Leu Ile Gly Arg Leu Met Ser Ser Lys Met Pro Gly
 225 230 235 240
 Gly Phe Ser Ile Thr Thr Ala Arg Lys Tyr Leu Glu Ser Arg Phe Gly
 245 250 255
 Leu Gly Ala Gly Arg Gln Asp Ser Val Leu Leu Met Ala Leu Thr Asn
 260 265 270

REN-01-032-Uti1.ST25.txt

Glu Pro Ala Asn Arg Leu Gly Ser Glu Ala Asp Ala Lys Thr Phe Phe
 275 280 285
 Asp Gly Ile Ala Gln Lys Tyr Ala Ser Ser Ala Gly Ile Ser Leu Ser
 290 295 300
 Ser Gly Ala Gly Ser Gly Ala Gly Ala Ala Asn Ser Gly Gly Ala Val
 305 310 315 320
 Val Asp Ser Ala Ala Leu Asp Ala Leu Thr Ala Glu Asn Lys Lys Leu
 325 330 335
 Ala Lys Gln Gln Leu Glu Val Leu Ala Arg Tyr Leu Gln Ser Arg Leu
 340 345 350
 Lys Gln Gly Ser Leu Lys Ser Phe Ile Lys Glu Lys Glu Ala Ser Ala
 355 360 365
 Val Leu Gln Lys Glu Leu Asp Leu Trp Glu Ala Glu His Gly Glu Phe
 370 375 380
 Tyr Ala Lys Gly Ile Gln Pro Thr Phe Ser Ala Leu Lys Ser Arg Thr
 385 390 395 400
 Tyr Asp Ser Tyr Trp Asn Trp Ala Arg Gln Asp Val Leu Ser Met Tyr
 405 410 415
 Phe Asp Ile Ile Phe Gly Lys Leu Thr Ser Val Asp Arg Glu Thr Ile
 420 425 430
 Asn Gln Cys Ile Gln Ile Met Asn Arg Ala Asn Pro Thr Leu Ile Lys
 435 440 445
 Phe Met Gln Tyr His Ile Asp His Cys Pro Glu Tyr Lys Gly Glu Thr
 450 455 460
 Tyr Lys Leu Ala Lys Arg Leu Gly Gln Gln Leu Ile Asp Asn Cys Lys
 465 470 475 480
 Gln Val Leu Thr Glu Asp Pro Val Tyr Lys Asp Val Ser Arg Ile Thr
 485 490 495
 Gly Pro Lys Thr Lys Val Ser Ala Lys Gly Asn Ile Glu Tyr Glu Glu
 500 505 510
 Thr Gln Lys Asp Ser Val Arg Lys Phe Glu Gln Tyr Val Tyr Glu Met
 515 520 525
 Ala Gln Gly Gly Ala Met Thr Lys Val Ser Gln Pro Thr Ile Gln Glu
 530 535 540

REN-01-032-Util.ST25.txt

Asp Leu Ala Arg Val Tyr Lys Ala Ile Ser Lys Gln Ala Ser Lys Asp
 545 550 555 560
 Ser Lys Leu Glu Leu Gln Arg Val Tyr Glu Asp Leu Leu Lys Val Val
 565 570 575
 Glu Ser Ser Lys Glu Ile Glu Thr Glu Gln Leu Thr Lys Asp Ile Leu
 580 585 590
 Gln Ala Ala Thr Val Pro Thr Thr Pro Thr Glu Glu Val Asp Asp Pro
 595 600 605
 Cys Thr Pro Ser Ser Asp Asp Glu Ile Ala Ser Leu Pro Asp Lys Thr
 610 615 620
 Ser Ile Ile Gln Pro Val Ser Ser Thr Ile Pro Ser Gln Thr Ile Pro
 625 630 635 640
 Phe Leu His Ile Gln Lys Lys Thr Lys Asp Gly Trp Glu Tyr Asn Lys
 645 650 655
 Lys Leu Ser Ser Leu Tyr Leu Asp Gly Leu Glu Ser Ala Ala Ile Asn
 660 665 670
 Gly Leu Thr Phe Lys Asp Lys Tyr Val Leu Val Thr Gly Ala Gly Ala
 675 680 685
 Gly Ser Ile Gly Ala Glu Ile Leu Gln Gly Leu Ile Ser Gly Gly Ala
 690 695 700
 Lys Val Ile Val Thr Thr Ser Arg Phe Ser Lys Lys Val Thr Glu Tyr
 705 710 715 720
 Tyr Gln Asn Met Tyr Ala Arg Tyr Gly Ala Ala Gly Ser Thr Leu Ile
 725 730 735
 Val Val Pro Phe Asn Gln Gly Ser Lys Gln Asp Val Asp Ala Leu Val
 740 745 750
 Gln Tyr Ile Tyr Asp Glu Pro Lys Lys Gly Gly Leu Gly Trp Asp Leu
 755 760 765
 Asp Ala Ile Ile Pro Phe Ala Ala Ile Pro Glu Asn Gly Asn Gly Leu
 770 775 780
 Asp Asn Ile Asp Ser Lys Ser Glu Phe Ala His Arg Ile Met Leu Thr
 785 790 795 800
 Asn Leu Leu Arg Leu Leu Gly Ala Val Lys Ser Lys Lys Pro Thr Asp
 805 810 815

REN-01-032-Uti1.ST25.txt

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

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

Leu Phe Asn Arg Trp Tyr Ser Glu Asp Trp Gly Ser Lys Leu Thr Val
 850 855 860

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

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

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

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

Gly Leu Gln Phe Ile Asp Asn Leu Lys Asp Phe Thr Ser Lys Leu Arg
 930 935 940

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

Ser Ala Ile Glu Gln Lys Val Val Asn Gly Asp Asn Val Asp Ala Asn
 965 970 975

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

Pro Thr Leu Lys Ser Tyr Asp Glu Ile Lys Gln Ile Ala Pro Glu Leu
 995 1000 1005

Glu Gly Met Leu Asp Leu Glu Asn Val Val Val Val Thr Gly Phe
 1010 1015 1020

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

Glu Ala Tyr Gly Glu Phe Ser Leu Glu Gly Ala Ile Glu Met Ala
 1040 1045 1050

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

Lys Pro Tyr Ser Gly Trp Val Asp Ala Lys Thr Gln Thr Pro Ile
 1070 1075 1080

REN-01-032-Util.ST25.txt

Asp Glu Lys Asp Ile Lys Ser Lys Tyr Glu Glu Glu Ile Leu Glu
 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 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

REN-01-032-Util.ST25.txt
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

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
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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

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

REN-01-032-Util.ST25.txt
1030 1035

1025

Pro Glu Leu Leu Ser Pro Val Lys Asp Gly Thr Ala Ile Val Thr
1040 1045 1050Val Asp Trp Asn Pro Glu Arg Val Ala Asp His Thr Gly Val Thr
1055 1060 1065Ala Thr Phe Arg Glu Pro Leu Ala Pro Ser Leu Ala Thr Val Pro
1070 1075 1080Asp Ala Leu Val Gly Ala Cys Trp Pro Ala Val Phe Ser Ala Ile
1085 1090 1095Gly Ser Ala Val Thr Glu Ala Gly Val Leu Val Val Glu Gly Leu
1100 1105 1110Leu Asn Leu Leu His Leu Asp His Ala Val Cys Val Val Gly Lys
1115 1120 1125Leu Pro Thr Val Pro Ala Gln Leu Thr Val Thr Ala Thr Val Ser
1130 1135 1140Leu Ala Ile Asp Thr Asp Met Gly Arg Val Val Pro Val Ser Val
1145 1150 1155Thr Ile Arg Asp Thr Thr Gly Ala Asp Gly Ala Val Leu Ala Thr
1160 1165 1170Leu Glu Glu Arg Phe Val Ile Leu Gly Arg Thr Gly Thr Ala Glu
1175 1180 1185Leu Thr Gly Pro Val Arg Ala Gly Gly Ala Ile Ser Glu Asn Ala
1190 1195 1200Thr Asp Thr Pro Arg Arg Arg Arg Arg Asp Val Thr Leu Thr Ala
1205 1210 1215Pro Ile Asp Met Arg Pro Phe Ala Val Val Ser Gly Asp His Asn
1220 1225 1230Pro Ile His Thr Asp Arg Thr Ala Ala Leu Leu Ala Gly Leu Glu
1235 1240 1245Ser Pro Ile Val His Gly Met Trp Leu Ser Ala Ala Ala Gln His
1250 1255 1260Val 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

REN-01-032-Util.ST25.txt
1285 1290

1280

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
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1790 REN-01-032-Util.ST25.txt 1800
 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
 Page 91

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
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2300

REN-01-032-Util.ST25.txt
2305 2310Arg Val Ser Leu Ala His Ala Leu Ile Gly Trp Thr Arg Gly Thr
2315 2320 2325Gly Leu Met Gly His Asn Asp Val Ile Val Ser Ala Val Glu Glu
2330 2335 2340Ala Gly Val Thr Thr Tyr Ser Thr Asp Glu Met Ala Ala Met Leu
2345 2350 2355Leu Asp Leu Cys Asn Ala Glu Ser Lys Val Ala Ala Ala Gly Thr
2360 2365 2370Pro Ile Thr Val Asp Leu Thr Gly Gly Leu Gly Glu Val Asp Leu
2375 2380 2385Asp Met Ala Glu Leu Ala Ala Lys Ala Arg Glu Asp His Ala Ala
2390 2395 2400Gln Ala Ala Glu Asp Glu Ala Thr Glu Ala Ser Glu Val Ala Gly
2405 2410 2415Thr Ile Ala Ala Leu Pro Ser Pro Pro Arg Gly Tyr Thr Pro Ala
2420 2425 2430Ser Pro His Trp Asp Asp Leu Asp Val Asp Pro Ala Asp Leu Val
2435 2440 2445Val Ile Val Gly Gly Ala Glu Ile Gly Pro Tyr Gly Ser Ser Arg
2450 2455 2460Thr Arg Phe Glu Met Glu Val Ala Gly Glu Leu Ser Ala Ala Gly
2465 2470 2475Val Leu Glu Leu Val Trp Thr Thr Gly Leu Ile Arg Trp Glu Asp
2480 2485 2490Asp Pro Gln Pro Gly Trp Tyr Asp Thr Glu Ser Gly Glu Leu Val
2495 2500 2505Asp Glu Ser Glu Leu Val Glu Arg Tyr His Asp Thr Val Val Gln
2510 2515 2520Arg Cys Gly Ile Arg Glu Phe Val Asp Asp Gly Thr Ile Asp Pro
2525 2530 2535Asp 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

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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

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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
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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

Gly 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

Val 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 Glu 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-Utl1.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-Utl1.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
 1010 1015 1020
 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

REN-01-032-Util.ST25.txt

Leu Gln Thr Ala Leu Leu Ala Glu Arg Ser Asp Thr Leu Arg Leu
 1055 1060 1065
 Pro Thr Arg Val Arg His Leu Arg Ile Asp Pro Asn Lys His Leu
 1070 1075 1080
 Glu His Val Val Glu Lys Asp Gly Ile Gln Val Ile Glu Leu Arg
 1085 1090 1095
 Asn Asp His Ser Thr Asn Gly Cys Ile Ala Gly Gly Val Glu Cys
 1100 1105 1110
 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
 1130 1135 1140
 His Asn Cys Leu Ser Gly His Lys Lys Thr Ser Thr Ile Leu Lys
 1145 1150 1155
 Asp Tyr Ser Ala Val Ile Lys Gln Gln Leu Tyr Thr Gly Phe Ser
 1160 1165 1170
 Lys Trp Gln Ser Ala Gly Leu Leu Lys Lys Leu Lys Asn Gly Ala
 1175 1180 1185
 Gln Ile Val Lys Ala Leu Ala Val Leu Lys Ala Ser Gln Ser Asp
 1190 1195 1200
 Val Val Leu Asp Asp Thr Val Thr Arg Phe Thr His Asp Gly Lys
 1205 1210 1215
 Cys Thr Val Leu His His Ile Ala Asp Met Phe Lys Ile Glu Asp
 1220 1225 1230
 Cys Glu Asp Phe Glu Asp Arg Val Ala Ala Lys Leu Lys Ser Val
 1235 1240 1245
 Arg Gly Ile Phe Glu Leu Asp Arg Leu Trp Ala Gly Ala Val Leu
 1250 1255 1260
 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
 1295 1300 1305

REN-01-032-Utl1.ST25.txt

Leu Leu Glu Thr Asp Tyr Thr Cys Ile Gly Ala Asn Val Asp His
 1310 1315 1320
 Leu Asp Glu Ser Thr Leu Glu Ile Ile Gly Gly Lys Lys Gln Lys
 1325 1330 1335
 Ile Asp Leu Glu Asn Asn Phe Thr Gly His Gly Glu Val Lys Asn
 1340 1345 1350
 Leu Asp Tyr Val Leu Leu Asp Lys Val Ile Ser Lys Lys Ala Asp
 1355 1360 1365
 Pro Ile Ala Phe Ile Glu Ala Cys Lys His Leu Ile Arg Glu Thr
 1370 1375 1380
 Gly Phe Leu Leu Val Val Glu Val Thr Ser Gln Tyr Glu Ile Ala
 1385 1390 1395
 Leu Ala Ile Glu Gly Leu Leu Gly Asn Glu Met Val Gly Asp Ala
 1400 1405 1410
 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
 1445 1450 1455
 Ile Pro Arg Asp Pro Val Phe Ile Asp Val Asp Asp Val Lys Glu
 1460 1465 1470
 Phe Asn Trp Ile Glu Pro Leu Gln Lys Val Ser Glu Glu Arg Leu
 1475 1480 1485
 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
 1505 1510 1515
 Asn Leu Lys Ile Asn Arg Phe Arg Ser Ala Phe Asp Met Ser Ala
 1520 1525 1530
 Asn Lys Glu Ile Arg Asp Gly Pro Pro Val Trp Asn Ile Gly Asp
 1535 1540 1545
 Glu Glu Thr Lys Lys Ile Val Glu Leu Asp Leu His Ala Asn Asp
 1550 1555 1560

REN-01-032-Util.ST25.txt

Tyr Met Asp Gly Gln Trp Gly Ser Met Arg His Ile Val Val Lys
 1565 1570 1575
 Asp Glu Asp Val His Val Tyr Lys Asp Cys Glu His Ala Phe Ile
 1580 1585 1590
 Asn Thr Leu Thr Arg Gly Asp Val Ser Ser Leu Thr Trp Phe Glu
 1595 1600 1605
 Ser Pro Asn Gln Tyr Phe Asp Ser Met Val Lys Ser Lys Ala Thr
 1610 1615 1620
 Gln Glu Leu Cys Ser Val Tyr Tyr Ala Pro Ile Asn Phe Arg Asp
 1625 1630 1635
 Ile Met Leu Ala Tyr Gly Arg Leu Pro Pro Asp Ala Ile Pro Gly
 1640 1645 1650
 Asn Phe Ala Asp Arg Glu Cys Leu Leu Gly Met Glu Phe Ser Gly
 1655 1660 1665
 Arg Leu Lys Asp Gly Thr Arg Leu Met Gly Ile Leu Pro Ala Gln
 1670 1675 1680
 Ala Leu Ala Thr Thr Val Met Val Asp Arg Asp Tyr Ala Trp Glu
 1685 1690 1695
 Val Pro Arg Asp Trp Thr Leu Ala Glu Ala Ser Thr Val Pro Val
 1700 1705 1710
 Val Tyr Thr Thr Ala Tyr Tyr Ala Leu Val Arg Arg Gly Leu Met
 1715 1720 1725
 Lys Lys Gly Asp Lys Ile Leu Ile His Gly Gly Ala Gly Gly Val
 1730 1735 1740
 Gly Gln Ala Ala Ile Ala Ile Ala Leu Ala Ala Gly Cys Glu Val
 1745 1750 1755
 Phe Thr Thr Val Gly Ser Ala Glu Lys Arg Glu Phe Leu Lys Asn
 1760 1765 1770
 Leu Phe Pro Gln Leu Gln Glu His His Phe Ala Asn Ser Arg Ser
 1775 1780 1785
 Ala Asp Phe Glu Leu His Ile Arg Gln His Thr Lys Gly Arg Gly
 1790 1795 1800
 Val Asn Ile Val Leu Asn Ser Leu Ala Asn Glu Met Leu Gln Ala
 1805 1810 1815

REN-01-032-Util.ST25.txt

Ser Leu Arg Cys Leu Ala Arg His Gly Arg Phe Leu Glu Ile Gly
 1820 1825 1830
 Lys Val Asp Leu Ser Gln Asn Ser Ser Leu Gly Met Ala Lys Leu
 1835 1840 1845
 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
 Pro Ile Gly Gly Ile Phe His Leu Ala Met Val Leu Arg Asp Cys
 2030 2035 2040
 Leu Phe Glu Asn Gln Asn Val Gln Asn Phe Lys Asp Ala Ala Glu
 2045 2050 2055
 Ala Lys Tyr Tyr Gly Thr Ile Asn Leu Asp Tyr Ala Ser Arg Glu
 2060 2065 2070

REN-01-032-Util.ST25.txt

His Cys Asp Lys Asn Ile Leu Lys Trp Phe Val Val Phe Ser Ser
 2075 2080 2085
 Ile Thr Ser Gly Arg Gly Asn Ala Gly Gln Thr Asn Tyr Gly Trp
 2090 2100
 Ser Asn Ser Cys Met Glu Arg Met Ile Asp Gln Arg Arg Ala Asp
 2105 2110 2115
 Gly Phe Pro Gly Ile Ala Ile Gln Trp Gly Ala Ile Gly Asp Val
 2120 2125 2130
 Gly Val Ile Leu Glu Asn Met Gly Asp Asn Asn Thr Val Val Gly
 2135 2140 2145
 Gly Thr Leu Pro Gln Arg Met Pro Ser Cys Leu Ser Ser Leu Asp
 2150 2155 2160
 Asn Phe Leu Ser Trp Asn His Pro Ile Val Ser Ser Phe Ile Lys
 2165 2170 2175
 Ala Glu Leu Gly Ser Lys Lys Asn Val Gly Gly Gly Asp Leu Met
 2180 2185 2190
 Ala Thr Ile Ala His Ile Leu Gly Val Asn Asp Ile Ser Gln Leu
 2195 2200 2205
 Asn Ala Asp Ala Asn Leu Ser Asp Leu Gly Leu Asp Ser Leu Met
 2210 2215 2220
 Gly Val Glu Ile Lys Gln Ala Leu Glu Arg Asp His Asp Ile Val
 2225 2230 2235
 Leu Ser Met Lys Glu Ile Arg Thr Leu Thr Leu Asn Lys Leu Gln
 2240 2245 2250
 Gln Leu Ala Asp Gln Gly Gly Thr Gly Arg Thr Ala Leu Gln Val
 2255 2260 2265
 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

REN-01-032-Util.ST25.txt

Ser Ile Glu Gly Ile Ala Thr Pro Leu Lys Lys Val Met Asn Lys
 2330 2335 2340
 Cys Glu Phe Pro Ala Tyr Cys Phe Gln Ser Thr Lys Asn Val Pro
 2345 2350 2355
 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
 2405 2410 2415
 Ser His Leu Tyr Met Gln Thr Tyr Arg Asn Val Tyr Arg Met Ala
 2420 2425 2430
 Phe Gly Val Thr Gly Asp Ser Leu Val Asn Asn Pro Leu Phe Glu
 2435 2440 2445
 Ser Glu Ile Met Cys Ala Met Thr Leu Arg Phe Ala Asn Val Asp
 2450 2455 2460
 Tyr Lys Lys Phe Arg Phe Glu Leu Leu Gln Gln Pro Gly Phe Lys
 2465 2470 2475
 Ala Arg Val Gln Lys Val Val Asp Gln Val Met Leu Thr Gly Leu
 2480 2485 2490
 Phe Lys Ser Pro Glu Thr Val Ala Phe Ala Cys Glu Ala Met His
 2495 2500 2505
 Ser Lys Phe Leu Met Ala Asp Lys Tyr Lys Pro Arg Arg Asn Phe
 2510 2515 2520
 Gly Gly His Ile Thr Leu Ile Arg Ala Glu Gln Gly Ala Ala Arg
 2525 2530 2535
 Glu Glu Asp Val Gly Glu Asp Tyr Gly Val Ala Ala Val Ser Glu
 2540 2545 2550
 Asp Cys Glu Val Leu Lys Val Lys Gly Asp His Asp Thr Phe Val
 2555 2560 2565
 Gln Gly Lys Ser Ser Ser Val Thr Val Glu His Ile Asn Arg Ile
 2570 2575 2580

REN-01-032-Uti1.ST25.txt

Ile Leu Gln
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<211> 8936
<212> DNA
<213> Rattus norvegicus

<400> 26
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tgctgctgga agtcagctat gaagctattg tggacggagg tatcaacccg gcctcactcc 180
gaggaacaaa cactggtgtc tgggtgggtg tgagtgggtc cgaggcgctg gaggccctga 240
gcagagatcc tgagactctt ctgggctaca gcatgggtggg ctgccagaga gcaatgatgg 300
ccaaccggct ctctttcttc ttcgacttca aaggaccag cattgccctg gacacagcct 360
gctcctctag cctactggca ctacagaatg cctatcaggc tatccgcagt ggggagtgcc 420
ctgctgccat tgtgggcggg atcaacctgc tgctaaagcc taacacctct gtgcagttca 480
tgaagctagg catgctcagc cccgatggca cctgcagatc ctttgatgat tcagggaacg 540
ggatttgccg tgctgaggct gtcgtggcag ttctgctgac taagaagtcc ttggctcggc 600
gagtctatgc cactattctg aatgccggga cgaacacaga tggctgcaag gagcaaggcg 660
tgacattccc ctctggagaa gccaggaac aactcatccg ttctctgtat cagccgggcg 720
gtgtggcccc cgagtctctt gaatatattg aagcccatgg cacgggcacc aagggtggggg 780
acccccagga actgaacggc attactcggg ccctgtgtgc tttccgccag agccctttgt 840
taattggctc caccaaattc aacatgggac accctgagcc tgccctcggg cttgcagccc 900
tgaccaaggt gctgttatcc ctagaaaatg gggtttgggc cccaacctg catttccaca 960
acccaaccc tgaaatccca gcacttcttg atgggcggct gcagggtggc gataggcccc 1020
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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-Util.ST25.txt

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<400> 27

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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
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REN-01-032-Util.ST25.txt

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 130 135 140
 Gly Asn Gly Tyr Cys Arg Ala Glu Ala Val Val Ala Val Leu Leu Thr
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 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
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 Ala Pro Glu Ser Leu Glu Tyr Ile Glu Ala His Gly Thr Gly Thr Lys
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 Val Gly Asp Pro Gln Glu Leu Asn Gly Ile Thr Arg Ser Leu Cys Ala
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 Phe Arg Gln Ser Pro Leu Leu Ile Gly Ser Thr Lys Ser Asn Met Gly
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 His Pro Glu Pro Ala Ser Gly Leu Ala Ala Leu Thr Lys Val Leu Leu
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 Ser Leu Glu Asn Gly Val Trp Ala Pro Asn Leu His Phe His Asn Pro
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 Asn Pro Glu Ile Pro Ala Leu Leu Asp Gly Arg Leu Gln Val Val Asp
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 Arg Pro Leu Pro Val Arg Gly Gly Ile Val Gly Ile Asn Ser Phe Gly
 305 310 315 320
 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
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 Ser Gly Arg Thr Met Glu Ala Val Gln Gly Leu Leu Glu Gln Gly Arg
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REN-01-032-util.ST25.txt

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405 410 415

Pro Leu Trp Phe Ile Cys Ser Gly Met Gly Thr Gln Trp Arg Gly Met
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Gly Leu Ser Leu Met Arg Leu Asp Ser Phe Arg Glu Ser Ile Leu Arg
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Ser Asp Glu Ala Leu Lys Pro Leu Gly Val Lys Val Ser Asp Leu Leu
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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
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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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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-Uti1.ST25.txt

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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
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805 810 815

Tyr Leu Tyr Leu Val Trp Lys Thr Leu Ala Arg Ser Leu Ser Leu Ser
820 825 830

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835 840 845

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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

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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
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Leu Lys Met Thr Val Pro Gly Leu Glu Asp Leu Pro Gln His Gly
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Leu Pro Arg Leu Leu Ala Ala Ala Cys Gln Leu Gln Leu Asn Gly
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Ala Leu Lys Ala Cys Ile Asp Thr Ala Leu Glu Asn Leu Ser Thr
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Leu Lys Met Lys Val Val Glu Val Leu Ala Gly Glu Gly His Leu
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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

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Cys Gln Pro Gln Glu Thr Cys Asn Leu Pro Arg Leu Val Gln Val Cys
 340 345 350

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
 405 410 415

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
 435 440 445

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
 545 550 555 560

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

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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

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Ser Gly Lys Ile Ser Leu Leu Glu Asn Asp Ala Leu Lys Asn Phe His
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Asn Gln Leu Ala Asp Phe Gln Ser Gln Ala Asn Val Thr Ala Lys Ser
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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

Asn Gly Leu His Ala Ser Val Ala Pro Arg Arg Gln Gln Glu Arg
 1025 1030 1035

Ile Ser Pro Thr Leu Glu Lys Phe Ser Phe Val Pro Tyr Ile Glu
 1040 1045 1050

Ser Asp Cys Leu Ser Ser Ser Thr Gln Leu His Ala Tyr Leu Glu
 1055 1060 1065

His Cys Lys Gly Leu Ile Gln Lys Leu Gln Ala Lys Met Ala Leu
 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
 1100 1105 1110

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
 1145 1150 1155

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
 1370 1375 1380

Leu Gly Met Val Asn Cys Leu Arg Leu Glu Ala Glu Gly His Arg
 1385 1390 1395

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Ile	Arg	Cys	Val	Phe	Val	Ser	Asn	Leu	Ser	Pro	Ser	Ser	Thr	Val
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Pro	Ala	Thr	Ser	Leu	Ser	Ser	Leu	Glu	Met	Gln	Lys	Ile	Ile	Glu
1415						1420					1425			
Arg	Asp	Leu	Val	Met	Asn	Val	Tyr	Arg	Asp	Gly	Lys	Trp	Gly	Ser
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			

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Ser	Arg	Asn	Thr	Thr	Phe	Glu	Gln	His	Ile	Leu	Arg	Val	Thr	Asn
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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			
Ala	Leu	Gly	Ile	Gln	Val	Leu	Val	Ser	Thr	Ser	Asp	Val	Gly	Thr
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			

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Met Ile Glu Asn Gln Thr Pro Glu Leu Phe Trp Glu Val Asn Lys
1910 1915 1920

Pro Lys Tyr Ser Gly Thr Leu His Leu Asp Trp Val Thr Arg Lys
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

Leu Gln Gln Ile Ser Ser Cys Leu Glu Val Leu Asp Met Phe Leu
2015 2020 2025

Asn Gln Pro His Pro Val Met Ser Ser Phe Val Leu Ala Glu Lys
2030 2035 2040

Val Ser Val Lys Ser Glu Gly Gly Ser Gln Arg Asp Leu Val Glu
2045 2050 2055

Ala Val Ala His Ile Leu Gly Val Arg Asp Val Ser Ser Leu Asn
2060 2065 2070

Ala Glu Ser Ser Leu Ala Asp Leu Gly Leu Asp Ser Leu Met Gly
2075 2080 2085

Val Glu Val Arg Gln Thr Leu Glu Arg Asp Tyr Asp Ile Val Met
2090 2095 2100

Thr Met Arg Glu Ile Arg Leu Leu Thr Ile Asn Lys Leu Arg Glu
2105 2110 2115

Leu Ser Ser Lys Thr Gly Thr Ala Glu Glu Leu Lys Pro Ser Gln
2120 2125 2130

Val Leu Lys Thr Gly Pro Gly Glu Pro Pro Lys Leu Asp Leu Asn
2135 2140 2145

Asn Leu Leu Val Asn Pro Glu Gly Pro Thr Ile Thr Arg Leu Asn
2150 2155 2160

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Glu	Val	Gln	Ser	Thr	Glu	Arg	Pro	Leu	Phe	Leu	Val	His	Pro	Ile
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2180						2185					2190			
Met	Pro	Cys	Tyr	Gly	Leu	Gln	Cys	Thr	Lys	Ala	Ala	Pro	Leu	Asp
2195						2200					2205			
Ser	Ile	Gln	Ser	Leu	Ala	Ser	Tyr	Tyr	Ile	Asp	Cys	Met	Lys	Gln
2210						2215					2220			
Ile	Gln	Pro	Glu	Gly	Pro	Tyr	Arg	Ile	Ala	Gly	Tyr	Ser	Phe	Gly
2225						2230					2235			
Ala	Cys	Val	Ala	Phe	Glu	Met	Cys	Ser	Gln	Leu	Gln	Ala	Gln	Gln
2240						2245					2250			
Asn	Ala	Ser	His	Ala	Leu	Asn	Ser	Leu	Phe	Leu	Phe	Asp	Gly	Ser
2255						2260					2265			
His	Ser	Phe	Val	Ala	Ala	Tyr	Thr	Gln	Cys	Phe	Ser	Phe	Ser	Leu
2270						2275					2280			
Phe	Gln	Ser	Tyr	Arg	Ala	Lys	Leu	Thr	Gln	Gly	Asn	Glu	Ala	Ala
2285						2290					2295			
Leu	Glu	Thr	Glu	Ala	Leu	Cys	Ala	Phe	Val	Gln	Gln	Phe	Thr	Gly
2300						2305					2310			
Ile	Glu	Tyr	Asn	Lys	Leu	Leu	Glu	Ile	Leu	Leu	Pro	Leu	Glu	Asp
2315						2320					2325			
Leu	Glu	Ala	Arg	Val	Asn	Ala	Ala	Ala	Asp	Leu	Ile	Thr	Gln	Ile
2330						2335					2340			
His	Lys	Asn	Ile	Asn	Arg	Glu	Ala	Leu	Ser	Phe	Ala	Ala	Ala	Ser
2345						2350					2355			
Phe	Tyr	His	Lys	Leu	Lys	Ala	Ala	Asp	Lys	Tyr	Ile	Pro	Glu	Ser
2360						2365					2370			
Lys	Tyr	His	Gly	Asn	Val	Thr	Leu	Met	Arg	Ala	Lys	Thr	His	Asn
2375						2380					2385			
Glu	Tyr	Glu	Glu	Gly	Leu	Gly	Gly	Asp	Tyr	Arg	Leu	Ser	Glu	Val
2390						2395					2400			
Cys	Asp	Gly	Lys	Val	Ser	Val	His	Ile	Ile	Glu	Gly	Asp	His	Arg
2405						2410					2415			

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Thr	Leu	Leu	Glu	Gly	Asp	Gly	Val	Glu	Ser	Ile	Ile	Gly	Ile	Ile
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	2435					2440					2445		

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 <212> DNA
 <213> Mycobacterium bovis

<400> 30

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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-Util.ST25.txt

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<400> 31

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Arg Gly Asp Pro Gly Ala Gly Pro Ser Arg His Gly Pro Arg Gly His
35 40 45

Pro Ala Gly Arg His Gly Gly His Ser Gln Gly Val Leu Ala Val Glu
50 55 60

Ala Leu Lys Ala Gly Gly Ala Arg Asp Val Glu Leu Phe Ala Leu Ala
65 70 75 80

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

Pro Ser Trp Ala Ile Ala Pro Met Val Ser Val Thr Asn Ala Asp Pro
100 105 110

Glu Arg Ile Gly Arg Leu Leu Asp Glu Phe Ala Gln Asp Val Arg Thr
115 120 125

Val Leu Pro Pro Val Leu Ser Ile Arg Asn Gly Arg Arg Ala Val Val
130 135 140

Ile Thr Gly Thr Pro Glu Gln Leu Ser Arg Phe Glu Leu Tyr Cys Arg
145 150 155 160

REN-01-032-Uti1.ST25.txt

Gln Ile Ser Glu Lys Glu Glu Ala Asp Arg Lys Asn Lys Val Arg Gly
165 170 175

Gly Asp Val Phe Ser Pro Val Phe Glu Pro Val Gln Val Glu Val Gly
180 185 190

Phe His Thr Pro Arg Leu Ser Asp Gly Ile Asp Ile Val Ala Gly Trp
195 200 205

Ala Glu Lys Ala Gly Leu Asp Val Ala Leu Ala Arg Glu Leu Ala Asp
210 215 220

Ala Ile Leu Ile Arg Lys Val Asp Trp Val Asp Glu Ile Thr Arg Val
225 230 235 240

His Arg Ala Gly Ala Arg Trp Ile Leu Asp Leu Gly Pro Gly Asp Ile
245 250 255

Leu Thr Arg Leu Thr Ala Pro Val Ile Arg Gly Leu Gly Ile Gly Ile
260 265 270

Val Pro Ala Arg Thr Arg Gly Gly Gln Arg Asn Leu Phe Thr Val Gly
275 280 285

Ala Thr Pro Glu Val Ala Arg Ala Trp Ser Ser Tyr Ala Pro Thr Val
290 295 300

Val Arg Leu Pro Asp Gly Arg Val Lys Leu Ser Thr Lys Phe Thr Arg
305 310 315 320

Leu Thr Arg Arg Ser Pro Ile Leu Leu Ala Gly Met Thr Pro Thr Thr
325 330 335

Val Asp Ala Lys Ile Val Ala Ala Ala Asn Gly Arg His Trp Ala
340 345 350

Glu Leu Ala Ala Arg Gly Arg Ser Pro Lys Arg Ser Ser Val Thr Ala
355 360 365

Ser Asn Lys Trp Pro Ala Cys Ser Ser Arg Ala Ala Pro Ile Ser Ser
370 375 380

Thr Arg Cys Ser Ser Ile Pro Thr Cys Glu Ala Ser Gly Gly Arg Gln
385 390 395 400

Ala Val Gly Ala Glu Gly Pro Pro Val Arg Arg Arg Asp Arg Arg Arg
405 410 415

Gly Asp Gln Arg Arg His Pro Arg Pro Arg Arg Gly Arg Arg Ala Asp
420 425 430

REN-01-032-Util.ST25.txt

Arg Arg Thr Gly Arg His Arg His Gln Pro Arg Arg Val Gln Thr Arg
435 440 445

Asp His Arg Ala Asp Pro Leu Gly Asp Ser His Arg His Arg Gly Ala
450 455 460

His Gln Ala Gly Asp His Ala Arg Arg Gly Pro Gly Ala Pro Ala Gly
465 470 475 480

Thr Ile Pro Gly Arg Ile Ser His Leu Leu Leu Ala Thr Tyr Ser Ala
485 490 495

Asp Arg Ala Pro Arg Gln His His Val Cys Val Gly Gly Gly His Leu
500 505 510

Gly Thr Pro Lys Lys Gly Cys Gly Tyr Leu Ser Gly Pro Gly Arg Ser
515 520 525

Val Arg Leu Pro Ile Asp Ala Asp Arg Arg Ile Leu Val Gly Thr Ala
530 535 540

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

Leu Val Asp Thr Gln Gly Thr Asp Gln Trp Ile Ser Ala Gly Lys Ala
565 570 575

Gln Gly Arg Met Pro Pro Ala Glu Ser Ala Arg Cys Arg His Pro Arg
580 585 590

Asp Arg His Ser Ala Ser Val Arg Arg Cys Ser Thr Arg Trp Pro Val
595 600 605

Thr Arg Arg Arg Ser Arg Ser Val Ala Trp Pro Arg Pro Pro Ser Pro
610 615 620

Thr Cys Arg Arg Arg Arg His Asp Leu Pro Ala Val Ala Ala Gly Ala
625 630 635 640

Thr Ser Asn Trp Pro Ser Gly Lys Ala Thr Arg Pro Pro Thr Pro Pro
645 650 655

Arg Trp Ala Ala Arg Gly Trp Pro Thr Leu Ala Gly Pro Leu Arg Ala
660 665 670

Asp Ala Ala Ala Cys Arg Ser Pro Val Ala Pro Thr Gly Phe Arg Pro
675 680 685

Asp Pro Asp Ala Ile His Arg Cys Trp Pro Ala Gly Gln Ser Ala Ala
690 695 700

REN-01-032-Uti1.ST25.txt

Ala Ile Ala Ala Leu Val Ala Arg Tyr Pro Asp Ala Glu Thr Val Gln
705 710 715 720

Leu His Pro Ala Asp Val Pro Phe Phe Val Thr Leu Cys Lys Thr Leu
725 730 735

Gly Lys Pro Val Asn Phe Val Pro Ala Ile Asp Leu Val Val Arg Ala
740 745 750

Gly Gly Ala Ala Thr Arg Cys Gly Arg Pro Thr Thr Pro Ala Thr Thr
755 760 765

Pro Met Arg Cys Ala Ser Phe Arg Ala Arg Val Gly Ser Arg Ile Thr
770 775 780

Arg Met Asp Glu Pro Val Gly Glu Leu Leu Asp Ala Phe Glu Gln Ala
785 790 795 800

Ala Ile Asp Glu Val Leu Gly Ala Gly Val Glu Pro Lys Asp Val Ala
805 810 815

Ser Gly Arg Leu Gly Arg Ala Asp Val Ala Gly Pro Leu Ala Val Val
820 825 830

Leu Asp Ala Pro Asp Val Arg Trp Ala Gly Arg Thr Val Thr Asn Pro
835 840 845

Val His Arg Ile Arg Asp Pro Ala Glu Trp Gln Val His Asp Gly Pro
850 855 860

Glu Asn Pro Arg Ala Ala His Ser Ser Thr Gly Ala Arg Leu Gln Thr
865 870 875 880

His Gly Asp Asp Val Ala Leu Ser Val Ala Arg Leu Gly His Leu Gly
885 890 895

Arg His Pro Ile His Val Ala Gly Gln His Arg Arg Trp Arg His Pro
900 905 910

Gly Asp Arg His Arg Gly Arg His His Ala Met Arg Thr Val Leu Arg
915 920 925

Ser Pro Pro Val Ser Thr Ala Arg Ser Ser Cys Cys Gly Gly Gln Arg
930 935 940

Asp Gly His Phe Asp Gly Gly Leu Ala Pro Arg Ala Cys Cys Arg Pro
945 950 955 960

His Arg His Arg His Val Arg Cys Ala Leu Ala Pro Ser Leu Thr Asn
965 970 975

REN-01-032-Uti1.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

REN-01-032-Uti1.ST25.txt

Met Gly Met Glu Val Arg Ala Ala Pro Arg Arg Pro Ala Arg Cys
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 Gly Thr Pro Arg Thr Ser Ser Pro Ala Thr Pro Trp Ala Ser Arg
 1250 1255 1260
 Tyr Cys Thr Trp Ser Ala Thr Thr Arg Pro Ala Ser Ser Pro Ala
 1265 1270 1275
 Val Cys Thr Thr Thr Thr Asp Gly Val Leu Tyr Leu Thr Gln Phe
 1280 1285 1290
 Thr Gln Val Ala Met Ala Thr Val Ala Ala Gly Gln Val Ala Glu
 1295 1300 1305
 Met Arg Glu Gln Gly Ala Phe Val Glu Gly Ala Ile Ala Cys Gly
 1310 1315 1320
 His Ser Val Gly Glu Tyr Thr Ala Leu Ala Cys Val Thr Gly Ile
 1325 1330 1335
 Tyr Gln Leu Glu Ala Leu Leu Glu Met Val Phe His Arg Gly Ser
 1340 1345 1350
 Lys Met His Asp Ile Val Pro Arg Asp Glu Leu Gly Arg Ser Asn
 1355 1360 1365
 Tyr Arg Leu Ser Ala Ile Arg Pro Ser Gln Ile Asp Leu Asp Asp
 1370 1375 1380
 Ala Asp Val Pro Ala Phe Val Ala Gly Ile Ala Glu Ser Thr Gly
 1385 1390 1395
 Glu Phe Leu Glu Ile Glu Asn Phe Asn Leu Gly Gly Ser Gln Tyr
 1400 1405 1410
 Ala Ile Ala Gly Thr Val Arg Gly Leu Glu Ala Leu Glu Ala Glu
 1415 1420 1425
 Val Glu Arg Arg Arg Glu Leu Thr Gly Gly Arg Arg Ser Phe Ile
 1430 1435 1440
 Leu Val Pro Gly Ile Asp Val Pro Phe His Ser Arg Val Leu Arg
 1445 1450 1455
 Val Gly Val Ala Glu Phe Arg Arg Ser Leu Asp Arg Val Met Arg
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 Pro Thr Arg Thr Arg Pro Asp His Arg Ala Leu His Ser Gln Pro
 1475 1480 1485

REN-01-032-Util.ST25.txt

Gly Ala Ala Glu Val Gln Pro Trp Thr Ala Thr Ser Ser Arg Lys
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 Ser Gly Ile Trp Cys Pro Ala Glu Pro Leu Asp Glu Ile Leu Ala
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 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
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 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
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 Lys Pro Pro Pro Ser Arg Arg Pro Leu Arg Arg Arg Ala Arg Val
 1640 1645 1650
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 Ser Ile Glu Ser Ile Thr Asp Gly Ala Ser Ser Arg Arg Asn Gln
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 1700 1705 1710
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 Gln Thr Gly Ala His Leu Gln Arg Tyr Gly Pro Val Leu Ser Asp
 1730 1735 1740

REN-01-032-Util.ST25.txt

Ala Ile Asn Asp His Val Arg Thr Val Leu Gly Pro Ser Gly Lys
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 Arg Pro Gly Ala Ile Ala Glu Arg Val Lys Lys Thr Trp Glu Leu
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 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
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 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

REN-01-032-Util.ST25.txt

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
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 2060 2065 2070
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 2075 2080 2085
 His Ile Lys Asp Ala Gln Thr Pro Thr Leu Leu Phe Arg Ser Arg
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 2105 2110 2115
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 2195 2200 2205
 Gln Arg Cys His Arg Gly Arg Arg Arg Arg Gly Arg Gly His His
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 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

REN-01-032-Uti1.ST25.txt

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 Arg Thr Pro Arg Pro Leu Ala Pro Ser Pro Arg Cys Arg Arg Arg
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 Pro Gly Phe Thr Pro Ala Pro Pro Pro Gln Trp Asp Asp Leu Asp
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 2315 2320 2325
 Gly Pro Tyr Gly Ser Ser Arg Thr Arg Phe Glu Met Glu Val Glu
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 Asn Glu Leu Ser Ala Ala Gly Val Leu Glu Leu Ala Trp Thr Thr
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 Asp Gly Ala Ile Asp Pro Asp His Ala Ser Pro Leu Leu Val Ser
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 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
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 Tyr His Gly Asn Leu Leu Gly Arg Asn Lys Pro Asn Asp Ile Phe
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 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
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Ser Ser Arg
 2795

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 <213> Bacillus subtilis

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 gctcaccgca ccctgctggg agatgtgctc gttcgctcag tcataagcag gcagtatcag 180
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 100 105 110

Pro Ile Ser Leu Glu Ile Ala Lys Arg Phe Phe Ser Lys Thr Glu Tyr
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Ser Asp Leu Leu Ala Lys Asp Lys Asp Glu Gln Thr Asp Tyr Phe Tyr
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Gln Val Ser Ile Glu Leu Pro Asp Ser His Ser Pro Cys Tyr Ile Lys
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 35 40 45

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Glu Asn Ile Leu Phe Arg Lys Asn Glu Tyr Gly Lys Pro Phe Val Asp
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Phe Asp Ile His Phe Asn Ile Ser His Ser Asp Glu Trp Val Val Cys
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Trp Leu Gln Ser Lys Ala Gln Asn Ser Gln Val Ser Ser Phe Phe Glu
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Leu Trp Thr Ile Lys Glu Ser Tyr Ile Lys Ala Ile Gly Lys Gly Met
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Tyr Ile Pro Ile Asn Ser Phe Trp Ile Asp Lys Asn Gln Thr Gln Thr
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Val Ile Tyr Lys Gln Asn Lys Lys Glu Pro Val Thr Ile Tyr Glu Pro
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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
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Gln His Ala Gly Arg Lys Arg Lys Thr Glu His Leu Ala Gly Arg Ile
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Thr Gly Leu Asn Phe Gln Glu Leu Lys Phe Asp Lys Gly Ser Phe Gly
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Lys Pro Phe Leu Asp Asn Asn Arg Phe Leu Pro Phe Ser Met Thr Ile
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Leu Trp Ser Leu Lys Glu Ser Tyr Thr Lys Phe Thr Gly Thr Gly Leu
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 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
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 50 55 60

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 65 70 75 80

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 85 90 95

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21

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WHAT IS CLAIMED IS:

1. 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 wherein the multifunctional fatty acid synthase has an amino acid sequence comprising the protein of SEQ ID NO: 2; and
 - b. regenerating a plant from the plant cell,
 wherein the increased oil content is relative to a wild type plant lacking the nucleic acid molecule.
2. The method of claim 1, further comprising introducing a second nucleic acid molecule encoding a phosphopantetheine:protein transferase enzyme into the plant cell.
3. The method of claim 1 or 2, wherein the first nucleic acid molecule is isolated from *Brevibacterium ammoniagenes* (ATCC 6871).
4. The method of claim 2, 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.
5. The method of claim 1 or 2, wherein the multifunctional fatty acid synthase produces increased oil levels in a seed of the plant.
6. The method of claim 2, wherein the first nucleic acid molecule encoding a multifunctional fatty acid synthase and 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.
7. The method of claim 6, 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.

8. The method of claim 6, wherein the promoter provides expression of the multifunctional fatty acid synthase and the phosphopantetheine:protein transferase enzyme within plant seeds.

9. The method of claim 1 or 2, wherein the multifunctional fatty acid synthase is located in the cytosol of the plant cell.

10. 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 wherein said multifunctional fatty acid synthase comprises the amino acid sequence of SEQ ID NO: 2; and

b) extracting oil from the seeds.

11. A *Brassica* sp. plant cell comprising a heterologous nucleic acid molecule encoding a multifunctional fatty acid synthase comprising the amino acid sequence of SEQ ID NO: 2.

12. The plant cell of claim 11, wherein the multifunctional fatty acid synthase increases oil levels in the seed of a plant that has been transformed with said nucleic acid molecule relative to a wild type plant lacking said heterologous nucleic acid molecule.

13. The plant cell of claim 11 or 12, wherein the multifunctional fatty acid synthase is located in the cytosol of the plant cell.

14. The plant cell of claim 11, 12 or 13, wherein the multifunctional fatty acid synthase is from *Brevibacterium ammoniagenes* (ATCC 5871).
15. The plant cell of any one of claims 11 to 14, further comprising a second heterologous nucleic acid molecule encoding a phosphopantetheine:protein transferase enzyme.
16. The plant cell of claim 15, wherein the nucleic acid molecule encoding a phosphopantetheine:protein transferase enzyme comprises SEQ ID NOs: 4, 33, 35, 37, 39, 41 or 43.
17. The plant cell of any one of claims 11 to 16, that further comprises a promoter that is operably linked to the nucleic acid encoding a multifunctional fatty acid synthase or when present, the second nucleic acid encoding a phosphopantetheine:protein transferase enzyme, wherein the promoter is functional in a plant cell.
18. The plant cell of claim 17, wherein the promoter provides expression of the multifunctional fatty acid synthase or the phosphopantetheine:protein transferase enzyme within plant seeds.
19. The plant cell 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.

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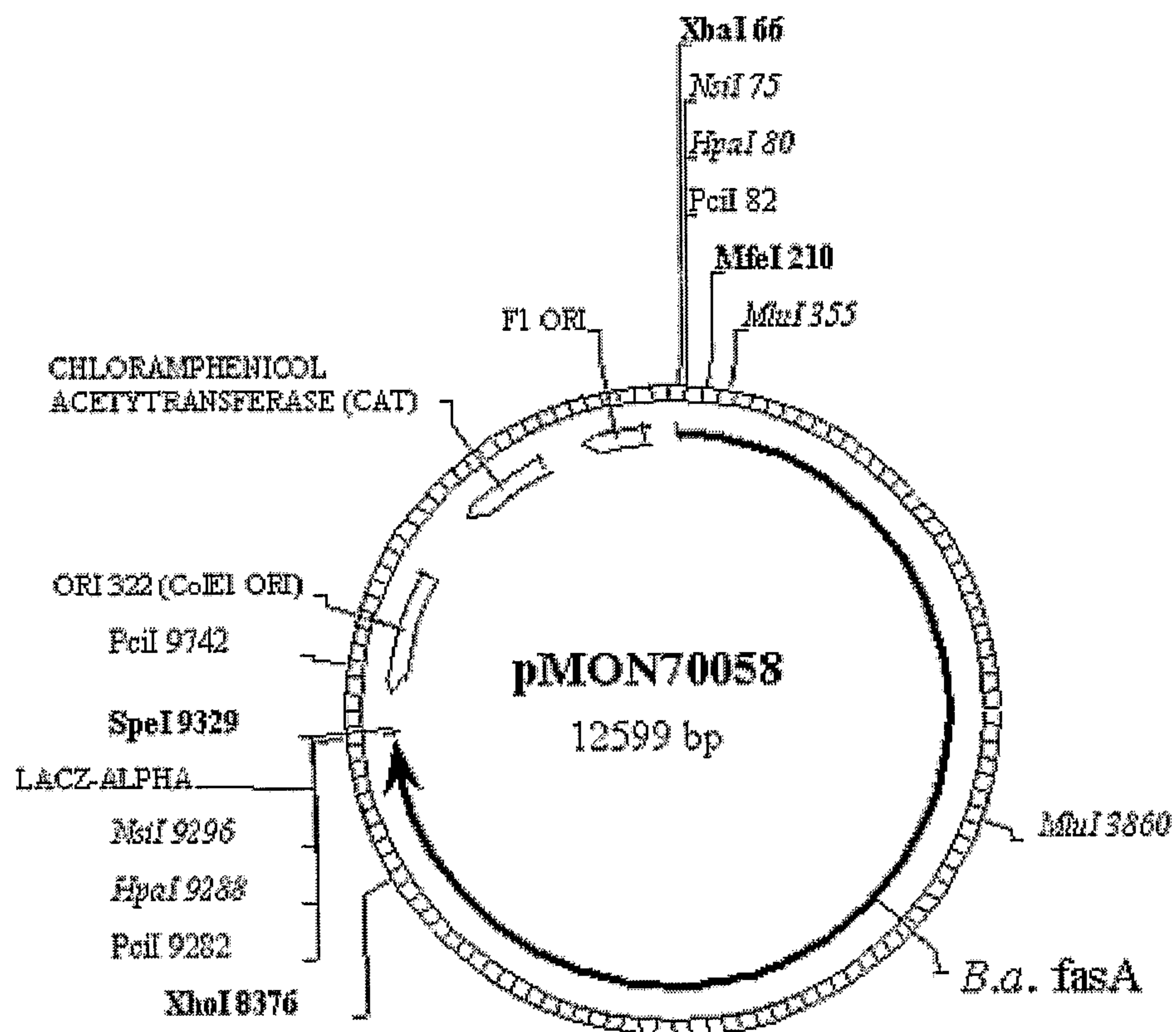


Figure 1

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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 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 ₂ 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 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 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

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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 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

Boxed Residues Differ from pMON70058

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 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 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 A T C 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 G C 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 C 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 C 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 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 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 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 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 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 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

Boxed Residues Differ from pMON70058

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 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 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 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 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 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

Boxed Residues Differ from pMON70058

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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 A Q 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 T 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 C S K A R A N G A A F T G V T I C 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 V 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 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 A H A G G H H S W V D L D E M L L A T Y A C 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 R 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 G 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 L 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
FASA X87822.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
FASA pmon70058.PRO	G E Y T A L A S L A N I F D L E A V I D I V Y S R G S A M G T L V E R D E N G N	1440
FASA X87822.PRO	G E Y T A L A S L A N I F D L E A V I D I V Y S R G S A M G T L V E R D E N G N	1440
FASA pmon70058.PRO	S N Y G M G A L R P N M I G V P A D Q V E A Y I A Q T A E E T G E F L E I V N Y	1480
FASA X87822.PRO	S N Y G M G A L R P N M I G V P A D Q V E A Y I A Q T A E E T G E F L E I V N Y	1480
FASA pmon70058.PRO	N I A G Q Q Y S I A G T K A G L A A L K K K A N S V K D R A Y V T V P G I D V P	1520
FASA X87822.PRO	N I A G Q Q Y S I A G T K A G L A A L K K K A N S V K D R A Y V T V P G I D V P	1520
FASA pmon70058.PRO	F H S Q V L R D G V P A F A E K L D E L L P E T L D L D A L V G R Y V P N L V A	1560
FASA X87822.PRO	F H S Q V L R D G V P A F A E K L D E L L P E T L D L D A L V G R Y V P N L V A	1560
FASA pmon70058.PRO	L P F E L T Q E F V D K V K P L A P S G K L D N L K V E D T D E Q A L A R L L M	1600
FASA X87822.PRO	L P F E L T Q E F V D K V K P L A P S G K L D N L K V E D T D E Q A P S R L L M	1600
FASA pmon70058.PRO	I E L L S W Q F A S P V R W I E T Q Q L L F E E V D Q I I E V G L A A S P T L T	1640
FASA X87822.PRO	I E L L S W Q F A S P V R W I E T Q Q L L F E E V D Q I I E V G L A S S P T L T	1640
FASA pmon70058.PRO	N L A K R S M D I A G V D L P V F N V E R D Q D Q V M L Q D V Q E A P A A S F D	1680
FASA X87822.PRO	N L A K R S M D I A G V D L P V F N V E R D Q D Q V M L Q D V Q E A P A A S F D	1680
FASA pmon70058.PRO	V E E G E A T S S T A A S E T P G E S A A A A S D N T Q A I P S A E P Q T V A E	1720
FASA X87822.PRO	V E E G E A T S S T A A S E T P G E S A A A A S D N T Q A I P S A E P Q T V A E	1720
FASA pmon70058.PRO	A P A P S A A P A G G T A A A D A P D L P F T A A E A I M V L F A F Q N K I R Q	1760
FASA X87822.PRO	A P A P S A A P A G G T R A A D A P D L P F T A A E A I M V L F A F Q N K I R Q	1760
FASA pmon70058.PRO	D Q I N D S D T V E E L T N G V S S R R N Q L L M D M S A E I G V P A I D G A A	1800
FASA X87822.PRO	D Q I N D S D T V E E L T N G V S S R R N Q L L M D M S A E N R V P A I D G A A	1800
FASA pmon70058.PRO	D A D V A T L R E R V K T A A P G Y S P F G T V L S E A I T A R L R Q L T G A A	1840
FASA X87822.PRO	D A D V A T L R E R V K T A A P G Y S P F G T V L S E A I T A R L R Q L T G A A	1840
FASA pmon70058.PRO	G V K P A Y I S E R V T G T W G L P M S W A A H V E A E I L L G S R E E D S V R	1880
FASA X87822.PRO	G V K P A Y I S E R V T G T W G L P M S W A A H V E A E I L L G S R E E D S V R	1880
FASA pmon70058.PRO	G G S L S T V P S A A S S K A D V D A L V D A A V Q A V A A A H G T S V S M G A	1920
FASA X87822.PRO	G G S L S T V P S A A S S K A D V D A L V D A A V Q A V A A A H G T S V S H G A	1920

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FASA pmon70058.PRO	A S G A G G G G V V D S A A L D A Y A D I V T G E N G V L A T A A R Q V L A Q L	1960
FASA X87822.PRO	A S G A G G G G V V D S A A L D A Y A D I V T G E N G V L A T A A R Q V L A Q L	1960
FASA pmon70058.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	2000
FASA X87822.PRO	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
FASA pmon70058.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	2040
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	2040
FASA pmon70058.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	2080
FASA X87822.PRO	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
FASA pmon70058.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	2120
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	2120
FASA pmon70058.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	2160
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 R S Y R D V D A L I D W I G N	2160
FASA pmon70058.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	2200
FASA X87822.PRO	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
FASA pmon70058.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	2240
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	2240
FASA pmon70058.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	2280
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	2280
FASA pmon70058.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	2320
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	2320
FASA pmon70058.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	2360
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 N I S I S E L A A Q A R E D A	2360
FASA pmon70058.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	2400
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	2400
FASA pmon70058.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	2440
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	2440
FASA pmon70058.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	2480
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	248
FASA pmon70058.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	2520
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	2520
FASA pmon70058.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	2560
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	2560
FASA pmon70058.PRO	T A R V P R K A T L T R T V A G Q M P D H F D A A K W G I P D H M L D A L D R M	2600
FASA X87822.PRO	T A R V P R K A T L T R T V A G Q M P D H F D A A K W G I P D H M L D A L D R M	2600
FASA pmon70058.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	2640
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	2640
FASA pmon70058.PRO	G M E S L H K V F V T R L L G E D R P S D I L Q E A L P N V I A A H T M Q S L V	2680
FASA X87822.PRO	G M E S L H K V F V T R L L G E D R P S D I L Q E A L P N V I A A H T M Q S L V	2680
FASA pmon70058.PRO	G G Y G S M I H P I G A C A T A A V S I E E G V D K I A L G K A D L V V A G G I	2720
FASA X87822.PRO	G G Y G S M I H P I G A C A T A A V S I E E G V D K I A L G K A D L V V A G G I	2720
FASA pmon70058.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	2760
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	2760
FASA pmon70058.PRO	R G G F L E A E G G G T V L L V R G S L A R E M G L P V Y A V V A H A A S Y G D	2800
FASA X87822.PRO	R G G F L E A E G G G T V L L V R G S L A R E M G L P V Y A V V A H E A S Y G -	2799
FASA pmon70058.PRO	G A H T S I P A P G L G A L G A G R G R K N S R L A K G L A G L G L T P N D V S	2840
FASA X87822.PRO	- A H T S I P A P G L G A L G A G R G R K N S R L A K G L A G L G L T P N D V S	2838
FASA pmon70058.PRO	V L S K H D T S T N A N D P N E S E L H S I L W P A I G R D V D Q P L F V I S Q	2880
FASA X87822.PRO	V L S K H D T S T N A N D P N E S E L H S I L W P A I G R D V D Q P L F V I S Q	2878

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FASA pmon70058.PRO	K S L T G H S K A G A A L F Q T G G L I D V F R T G R I P A N L S L D C V D P L	2920	
FASA X87822.PRO	K S L T G H S K A G A A L F Q T G G L I D V F R T G R I P A N L S L D C V D P L	2918	
FASA pmon70058.PRO	I E P K A T N L V W L R S P L D V E A A N R P V K A A A L T S L G F G H V G A L	2960	
FASA X87822.PRO	I E P K A T N L V W L R S P L D V E A A N R P V K A A A L T S L G F G H V G A L	2958	
FASA pmon70058.PRO	I V Y A H P G V F E A A V A Q Q V S A E A A A E W R E K A N A R L A A G A A R F	3000	
FASA X87822.PRO	I V Y A H P G V F E A A V A Q Q V S A E A A A E W R E K A N A R L A A G A A R F	2998	
FASA pmon70058.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	3040	
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	
FASA pmon70058.PRO	E I A L L L D D D I R L T A E G T F P P A K	3063	
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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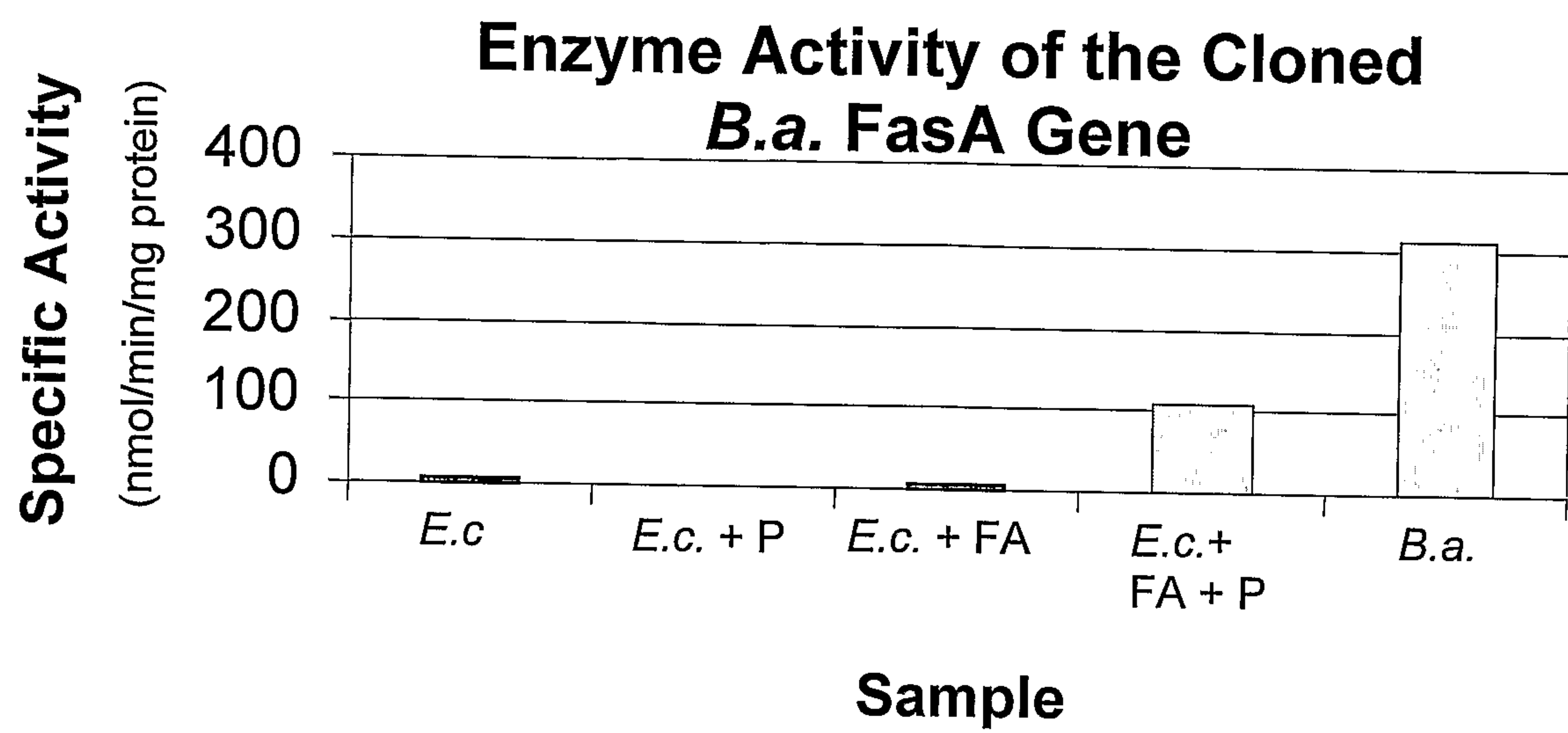


Figure 4

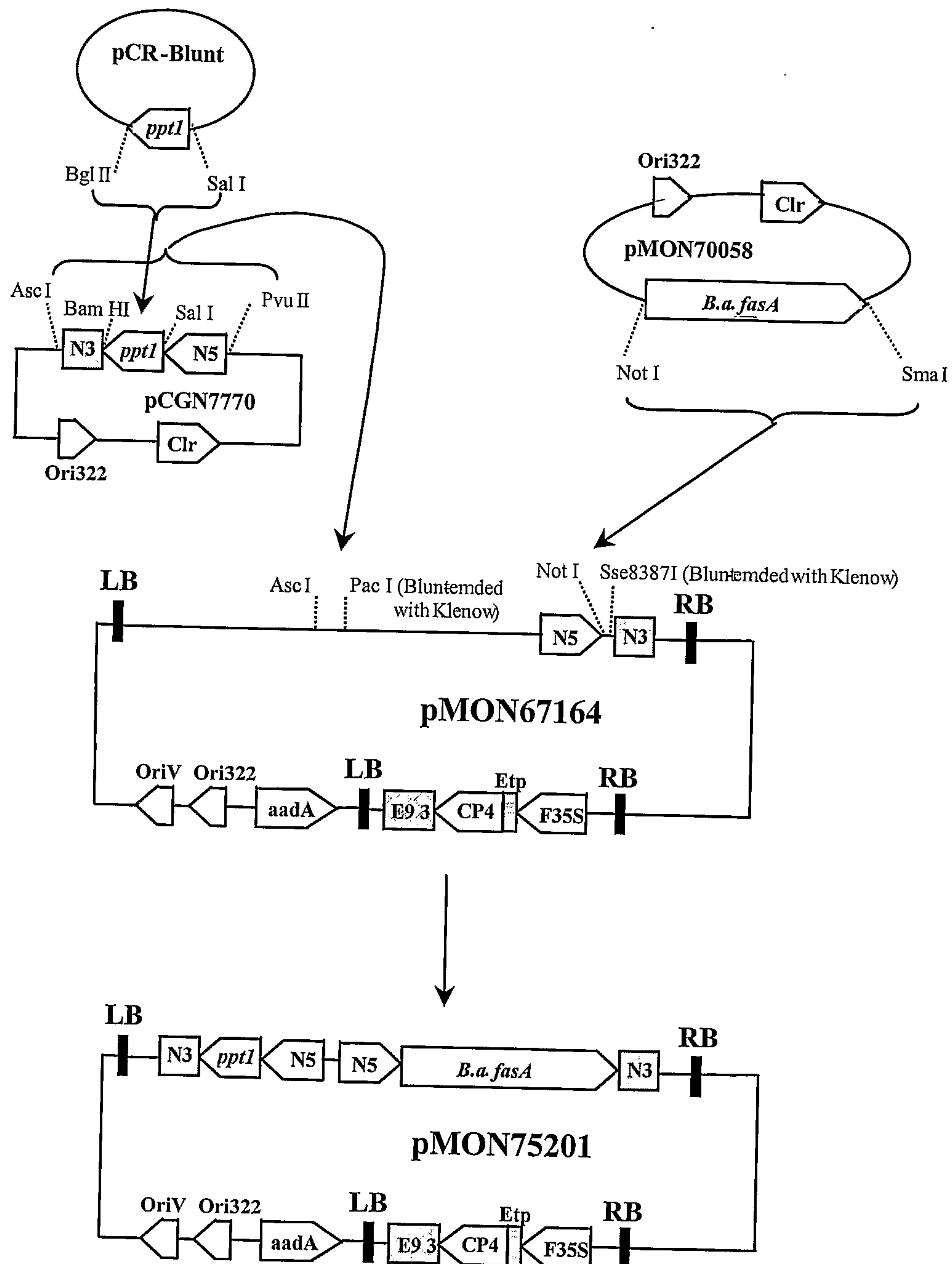


Figure 5

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	
BN_G1185	3.23	1.20	30.27	43.11	w	
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.

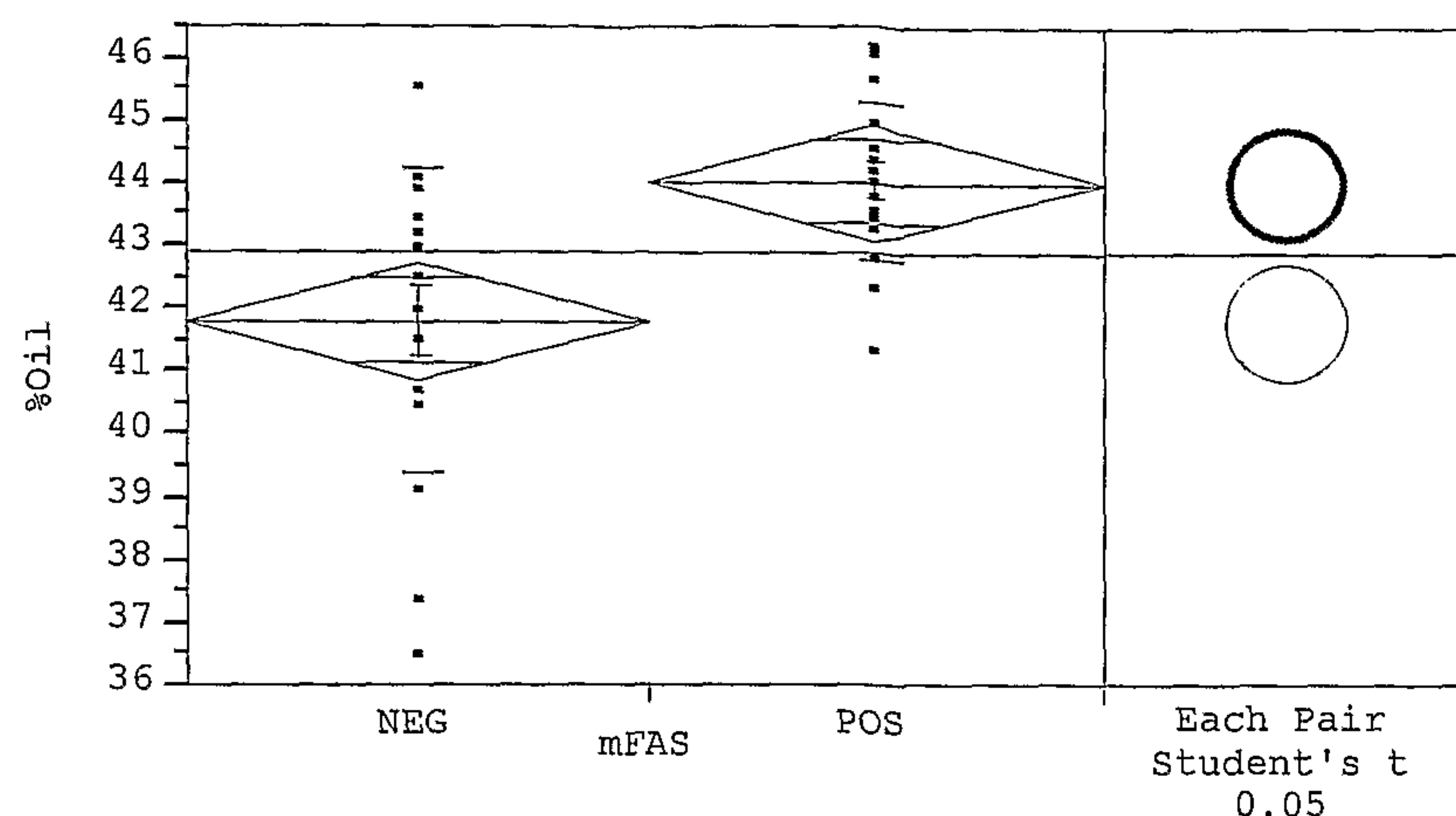
(b) R1 seed planted in Thief River Falls, MN.

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

Figure 6

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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

