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(54) Title: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN CARBON
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(57) **Abrégé/Abstract:**

Isolated nucleic acid molecules, designated SMP nucleic acid molecules, which encode novel SMP proteins from Corynebacterium glutamicum are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing SMP nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated SMP proteins, mutated SMP proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from C. glutamicum based on genetic engineering of SMP genes in this organism.

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JUMBO APPLICATIONS / PATENTS

**THIS SECTION OF THE APPLICATION / PATENT CONTAINS MORE
THAN ONE VOLUME.**

THIS IS VOLUME __1__ OF __3__

NOTE: For additional volumes please contact the Canadian Patent Office.

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***CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING PROTEINS
INVOLVED IN CARBON METABOLISM AND ENERGY PRODUCTION**

Related Applications

5 This application claims priority to prior U.S. Provisional Patent Application
Serial No. 60/141031, filed June 25, 1999, U.S. Provisional Patent Application Serial
No. 60/143208, filed July 9, 1999, and U.S. Provisional Patent Application Serial No.
60/151572, filed August 31, 1999. This application also claims priority to prior German
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10 19931413.6, filed July 8, 1999, German Patent Application No. 19931419.5, filed July
8, 1999, German Patent Application No. 19931420.9, filed July 8, 1999, German Patent
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30 contents of all of the aforementioned application are hereby expressly incorporated
herein by this reference.

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Background of the Invention

Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through the large-scale culture of bacteria developed to produce and secrete large quantities of one or more desired molecules. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as sugar metabolism and oxidative phosphorylation (SMP) proteins.

C. glutamicum is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The SMP nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, *e.g.*, by fermentation processes. Modulation of the expression of the SMP nucleic acids of the invention, or modification of the sequence of the SMP nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a

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microorganism (e.g., to improve the yield or production of one or more fine chemicals from a *Corynebacterium* or *Brevibacterium* species).

The SMP nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the
5 presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain
10 whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The SMP nucleic acid molecules of the invention may also serve as reference
15 points for mapping of the *C. glutamicum* genome, or of genomes of related organisms. Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered *Corynebacterium* or *Brevibacterium* species.

The SMP proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing a function involved in the metabolism of carbon
20 compounds such as sugars or in the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (e.g., *lactofermentum*) (Yoshihama
25 *et al.*, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals. This improved production or efficiency of production of a fine chemical may be due to a
30 direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation.

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There are a number of mechanisms by which the alteration of an SMP protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. The degradation of high-energy carbon molecules such as sugars, and the conversion of compounds such as NADH and FADH₂ to compounds containing high energy phosphate bonds via oxidative phosphorylation results in a number of compounds which themselves may be desirable fine chemicals, such as pyruvate, ATP, NADH, and a number of intermediate sugar compounds. Further, the energy molecules (such as ATP) and the reducing equivalents (such as NADH or NADPH) produced by these metabolic pathways are utilized in the cell to drive reactions which would otherwise be energetically unfavorable. Such unfavorable reactions include many biosynthetic pathways for fine chemicals. By improving the ability of the cell to utilize a particular sugar (*e.g.*, by manipulating the genes encoding enzymes involved in the degradation and conversion of that sugar into energy for the cell), one may increase the amount of energy available to permit unfavorable, yet desired metabolic reactions (*e.g.*, the biosynthesis of a desired fine chemical) to occur.

The mutagenesis of one or more SMP genes of the invention may also result in SMP proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C. glutamicum*. For example, by increasing the efficiency of utilization of one or more sugars (such that the conversion of the sugar to useful energy molecules is improved), or by increasing the efficiency of conversion of reducing equivalents to useful energy molecules (*e.g.*, by improving the efficiency of oxidative phosphorylation, or the activity of the ATP synthase), one can increase the amount of these high-energy compounds available to the cell to drive normally unfavorable metabolic processes. These processes include the construction of cell walls, transcription, translation, and the biosynthesis of compounds necessary for growth and division of the cells (*e.g.*, nucleotides, amino acids, vitamins, lipids, etc.) (Lengeler *et al.* (1999) *Biology of Prokaryotes*, Thieme Verlag: Stuttgart, p. 88-109; 913-918; 875-899). By improving the growth and multiplication of these engineered cells, it is possible to increase both the viability of the cells in large-scale culture, and also to improve their rate of division, such that a relatively larger number of cells can survive in fermentor culture. The yield, production, or efficiency of production may be increased, at least

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due to the presence of a greater number of viable cells, each producing the desired fine chemical. Also, many of the degradation products produced during sugar metabolism are utilized by the cell as precursors or intermediates in the production of other desirable products, such as fine chemicals. So, by increasing the ability of the cell to metabolize
5 sugars, the number of these degradation products available to the cell for other processes should also be increased.

The invention provides novel nucleic acid molecules which encode proteins, referred to herein as SMP proteins, which are capable of, for example, performing a function involved in the metabolism of carbon compounds such as sugars and the
10 generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Nucleic acid molecules encoding an SMP protein are referred to herein as SMP nucleic acid molecules. In a preferred embodiment, the SMP protein participates in the conversion of carbon molecules and degradation products thereof to energy which is utilized by the cell for metabolic processes. Examples of
15 such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an SMP protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of SMP-
20 encoding nucleic acid (*e.g.*, DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth as the odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the
25 isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth as an odd-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5,
30 SEQ ID NO:7....), or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth as an even-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:2, SEQ ID NO:4, SEQ

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ID NO:6, SEQ ID NO:8....). The preferred SMP proteins of the present invention also preferably possess at least one of the SMP activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence
5 which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence having an even-numbered SEQ ID NO: in the Sequence Listing), *e.g.*, sufficiently homologous to an amino acid sequence of the invention such that the protein or portion thereof maintains an SMP activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to perform a function
10 involved in the metabolism of carbon compounds such as sugars or the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%,
15 98%, or 99% or more homologous to an amino acid sequence of the invention (*e.g.*, an entire amino acid sequence selected those having an even-numbered SEQ ID NO in the Sequence Listing). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention (encoded by an open reading frame shown in the corresponding odd-
20 numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....)).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an SMP fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of
25 the amino acid sequences of the invention (*e.g.*, a sequence of one of the even-numbered SEQ ID NOs in the Sequence Listing) and is able to perform a function involved in the metabolism of carbon compounds such as sugars or the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or has one or more of the activities set forth in Table 1, and which also
30 includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

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In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO in the Sequence Listing) A. Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* SMP protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an SMP protein by culturing the host cell in a suitable medium. The SMP protein can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an SMP gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated SMP sequence as a transgene. In another embodiment, an endogenous SMP gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered SMP gene. In another embodiment, an endogenous or introduced SMP gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional SMP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an SMP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the SMP gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the

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sequences set forth in the Sequence Listing as SEQ ID NOs 1 through 782) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated SMP protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated SMP protein or portion thereof is capable of performing a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In another preferred embodiment, the isolated SMP protein or portion thereof is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: in the Sequence Listing) such that the protein or portion thereof maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*.

The invention also provides an isolated preparation of an SMP protein. In preferred embodiments, the SMP protein comprises an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) (encoded by an open reading frame set forth in a corresponding odd-numbered SEQ ID NO: of the Sequence Listing). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In other embodiments, the isolated SMP protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and is able to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or has one or more of the activities set forth in Table 1.

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Alternatively, the isolated SMP protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 5 95%, 96%, 97%, 98,%, or 99% or more homologous to a nucleotide sequence of one of the even-numbered SEQ ID NOs set forth in the Sequence Listing. It is also preferred that the preferred forms of SMP proteins also have one or more of the SMP bioactivities described herein.

The SMP polypeptide, or a biologically active portion thereof, can be operatively 10 linked to a non-SMP polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the SMP protein alone. In other preferred embodiments, this fusion protein performs a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in 15 *Corynebacterium glutamicum*. In particularly preferred embodiments, integration of this fusion protein into a host cell modulates production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which modulate the activity of an SMP protein, either by interacting with the protein itself or a 20 substrate or binding partner of the SMP protein, or by modulating the transcription or translation of an SMP nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an SMP nucleic acid molecule of the invention, such that a fine chemical 25 is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an SMP nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or 30 *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an

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agent which modulates SMP protein activity or SMP nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* carbon metabolism pathways or for the production of energy through processes such as oxidative phosphorylation, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates SMP protein activity can be an agent which stimulates SMP protein activity or SMP nucleic acid expression. Examples of agents which stimulate SMP protein activity or SMP nucleic acid expression include small molecules, active SMP proteins, and nucleic acids encoding SMP proteins that have been introduced into the cell. Examples of agents which inhibit SMP activity or expression include small molecules and antisense SMP nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant SMP gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

Detailed Description of the Invention

The present invention provides SMP nucleic acid and protein molecules which are involved in the metabolism of carbon compounds such as sugars and the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (*e.g.*, where overexpression or optimization of a glycolytic pathway protein has a direct impact on the yield, production, and/or efficiency of production of, *e.g.*, pyruvate from modified *C. glutamicum*), or may have an indirect

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impact which nonetheless results in an increase of yield, production, and/or efficiency of production of the desired compound (*e.g.*, where modulation of proteins involved in oxidative phosphorylation results in alterations in the amount of energy available to perform necessary metabolic processes and other cellular functions, such as nucleic acid and protein biosynthesis and transcription/translation). Aspects of the invention are further explicated below.

I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) Chemicals by Fermentation, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

30 A. Amino Acid Metabolism and Uses

Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-

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recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH: Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins. Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/ L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino acids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others

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described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α -ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain β -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. *Biochemistry* 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own

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production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

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B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although they are readily synthesized by other organisms such as bacteria. These molecules are
10 either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications
15 of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor"
20 includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (e.g., polyunsaturated fatty
25 acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley
30 & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological

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Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

Thiamin (vitamin B₁) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B₂) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B₆' (e.g., pyridoxine, pyridoxamine, pyridoxal-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)- β -alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of β -alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β -alanine and for the condensation to pantothenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of pantothenate, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B₅), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α -ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which in turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B₁₂) and porphyrines belong to a group of chemicals characterized by a tetrapyrrole ring system.

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The biosynthesis of vitamin B₁₂ is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD
5 (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B₆, pantothenate, and
10 biotin. Only Vitamin B₁₂ is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

15 Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a
20 pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA
25 synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

Several publications have described the use of these chemicals for these medical
30 indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of

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enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) *Nucleotides and Related Compounds in Biotechnology* vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: *Progress in Nucleic Acid Research and Molecular Biology*, vol. 42, Academic Press; p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in α , α -1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen
5 foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S. Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) *J. Japan* 172: 97-102). Trehalose is produced by enzymes from
10 many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Sugar and Carbon Molecule Utilization and Oxidative Phosphorylation

Carbon is a critically important element for the formation of all organic
15 compounds, and thus is a nutritional requirement not only for the growth and division of *C. glutamicum*, but also for the overproduction of fine chemicals from this microorganism. Sugars, such as mono-, di-, or polysaccharides, are particularly good carbon sources, and thus standard growth media typically contain one or more of: glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose,
20 sucrose, raffinose, starch, or cellulose (Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes", VCH: Weinheim). Alternatively, more complex forms of sugar may be utilized in the media, such as molasses, or other by-products of sugar refinement. Other compounds aside from the sugars may be used as alternate carbon
25 acids, and organic acids (*e.g.*, acetic acid or lactic acid). For a review of carbon sources and their utilization by microorganisms in culture, see: Ullman's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes", VCH: Weinheim; Stoppok, E. and Buchholz, K. (1996) "Sugar-based raw materials for fermentation applications" in Biotechnology (Rehm, H.J. *et al.*, eds.) vol. 6, VCH: Weinheim, p. 5-29; Rehm, H.J.
30 (1980) *Industrielle Mikrobiologie*, Springer: Berlin; Bartholomew, W.H., and Reiman, H.B. (1979). Economics of Fermentation Processes, in: Peppler, H.J. and Perlman, D., eds. *Microbial Technology* 2nd ed., vol. 2, chapter 18, Academic Press: New York; and

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Kockova-Kratachvilova, A. (1981) Characteristics of Industrial Microorganisms, in: Rehm, H.J. and Reed, G., eds. Handbook of Biotechnology, vol. 1, chapter 1, Verlag Chemie: Weinheim.

After uptake, these energy-rich carbon molecules must be processed such that they are able to be degraded by one of the major sugar metabolic pathways. Such pathways lead directly to useful degradation products, such as ribose-5-phosphate and phosphoenolpyruvate, which may be subsequently converted to pyruvate. Three of the most important pathways in bacteria for sugar metabolism include the Embden-Meyerhoff-Parnas (EMP) pathway (also known as the glycolytic or fructose bisphosphate pathway), the hexosemonophosphate (HMP) pathway (also known as the pentose shunt or pentose phosphate pathway), and the Entner-Doudoroff (ED) pathway (for review, see Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, Wiley: New York, and Stryer, L. (1988) Biochemistry, Chapters 13-19, Freeman: New York, and references therein).

The EMP pathway converts hexose molecules to pyruvate, and in the process produces 2 molecules of ATP and 2 molecules of NADH. Starting with glucose-1-phosphate (which may be either directly taken up from the medium, or alternatively may be generated from glycogen, starch, or cellulose), the glucose molecule is isomerized to fructose-6-phosphate, is phosphorylated, and split into two 3-carbon molecules of glyceraldehyde-3-phosphate. After dehydrogenation, phosphorylation, and successive rearrangements, pyruvate results.

The HMP pathway converts glucose to reducing equivalents, such as NADPH, and produces pentose and tetrose compounds which are necessary as intermediates and precursors in a number of other metabolic pathways. In the HMP pathway, glucose-6-phosphate is converted to ribulose-5-phosphate by two successive dehydrogenase reactions (which also release two NADPH molecules), and a carboxylation step. Ribulose-5-phosphate may also be converted to xyulose-5-phosphate and ribose-5-phosphate; the former can undergo a series of biochemical steps to glucose-6-phosphate, which may enter the EMP pathway, while the latter is commonly utilized as an intermediate in other biosynthetic pathways within the cell.

The ED pathway begins with the compound glucose or gluconate, which is subsequently phosphorylated and dehydrated to form 2-dehydro-3-deoxy-6-P-gluconate.

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Glucuronate and galacturonate may also be converted to 2-dehydro-3-deoxy-6-P-gluconate through more complex biochemical pathways. This product molecule is subsequently cleaved into glyceraldehyde-3-P and pyruvate; glyceraldehyde-3-P may itself also be converted to pyruvate.

5 The EMP and HMP pathways share many features, including intermediates and enzymes. The EMP pathway provides the greatest amount of ATP, but it does not produce ribose-5-phosphate, an important precursor for, *e.g.*, nucleic acid biosynthesis, nor does it produce erythrose-4-phosphate, which is important for amino acid biosynthesis. Microorganisms that are capable of using only the EMP pathway for
10 glucose utilization are thus not able to grow on simple media with glucose as the sole carbon source. They are referred to as fastidious organisms, and their growth requires inputs of complex organic compounds, such as those found in yeast extract.

 In contrast, the HMP pathway produces all of the precursors necessary for both nucleic acid and amino acid biosynthesis, yet yields only half the amount of ATP energy
15 that the EMP pathway does. The HMP pathway also produces NADPH, which may be used for redox reactions in biosynthetic pathways. The HMP pathway does not directly produce pyruvate, however, and thus these microorganisms must also possess this portion of the EMP pathway. It is therefore not surprising that a number of microorganisms, particularly the facultative anaerobes, have evolved such that they
20 possess both of these pathways.

 The ED pathway has thus far has only been found in bacteria. Although this pathway is linked partly to the HMP pathway in the reverse direction for precursor formation, the ED pathway directly forms pyruvate by the aldolase cleavage of 3-ketodeoxy-6-phosphogluconate. The ED pathway can exist on its own and is utilized by
25 the majority of strictly aerobic microorganisms. The net result is similar to that of the HMP pathway, although one mole of ATP can be formed only if the carbon atoms are converted into pyruvate, instead of into precursor molecules.

 The pyruvate molecules produced through any of these pathways can be readily converted into energy via the Krebs cycle (also known as the citric acid cycle, the citrate
30 cycle, or the tricarboxylic acid cycle (TCA cycle)). In this process, pyruvate is first decarboxylated, resulting in the production of one molecule of NADH, 1 molecule of acetyl-CoA, and 1 molecule of CO₂. The acetyl group of acetyl CoA then reacts with

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the 4 carbon unit, oxaloacetate, leading to the formation of citric acid, a 6 carbon organic acid. Dehydration and two additional CO₂ molecules are released. Ultimately, oxaloacetate is regenerated and can serve again as an acetyl acceptor, thus completing the cycle. The electrons released during the oxidation of intermediates in the TCA cycle
5 are transferred to NAD⁺ to yield NADH.

During respiration, the electrons from NADH are transferred to molecular oxygen or other terminal electron acceptors. This process is catalyzed by the respiratory chain, an electron transport system containing both integral membrane proteins and membrane associated proteins. This system serves two basic functions: first, to accept
10 electrons from an electron donor and to transfer them to an electron acceptor, and second, to conserve some of the energy released during electron transfer by the synthesis of ATP. Several types of oxidation-reduction enzymes and electron transport proteins are known to be involved in such processes, including the NADH dehydrogenases, flavin-containing electron carriers, iron sulfur proteins, and cytochromes. The NADH
15 dehydrogenases are located at the cytoplasmic surface of the plasma membrane, and transfer hydrogen atoms from NADH to flavoproteins, in turn accepting electrons from NADH. The flavoproteins are a group of electron carriers possessing a flavin prosthetic group which is alternately reduced and oxidized as it accepts and transfers electrons. Three flavins are known to participate in these reactions: riboflavin, flavin-adenine
20 dinucleotide (FAD) and flavin-mononucleotide (FMN). Iron sulfur proteins contain a cluster of iron and sulfur atoms which are not bonded to a heme group, but which still are able to participate in dehydration and rehydration reactions. Succinate dehydrogenase and aconitase are exemplary iron-sulfur proteins; their iron-sulfur complexes serve to accept and transfer electrons as part of the overall electron-transport
25 chain. The cytochromes are proteins containing an iron porphyrin ring (heme). There are a number of different classes of cytochromes, differing in their reduction potentials. Functionally, these cytochromes form pathways in which electrons may be transferred to other cytochromes having increasingly more positive reduction potentials. A further class of non-protein electron carriers is known: the lipid-soluble quinones (*e.g.*,
30 coenzyme Q). These molecules also serve as hydrogen atom acceptors and electron donors.

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The action of the respiratory chain generates a proton gradient across the cell membrane, resulting in proton motive force. This force is utilized by the cell to synthesize ATP, via the membrane-spanning enzyme, ATP synthase. This enzyme is a multiprotein complex in which the transport of H⁺ molecules through the membrane results in the physical rotation of the intracellular subunits and concomitant phosphorylation of ADP to form ATP (for review, see Fillingame, R.H. and Divall, S. (1999) *Novartis Found. Symp.* 221: 218-229, 229-234).

Non-hexose carbon substrates may also serve as carbon and energy sources for cells. Such substrates may first be converted to hexose sugars in the gluconeogenesis pathway, where glucose is first synthesized by the cell and then is degraded to produce energy. The starting material for this reaction is phosphoenolpyruvate (PEP), which is one of the key intermediates in the glycolytic pathway. PEP may be formed from substrates other than sugars, such as acetic acid, or by decarboxylation of oxaloacetate (itself an intermediate in the TCA cycle). By reversing the glycolytic pathway (utilizing a cascade of enzymes different than those of the original glycolysis pathway), glucose-6-phosphate may be formed. The conversion of pyruvate to glucose requires the utilization of 6 high energy phosphate bonds, whereas glycolysis only produces 2 ATP in the conversion of glucose to pyruvate. However, the complete oxidation of glucose (glycolysis, conversion of pyruvate into acetyl CoA, citric acid cycle, and oxidative phosphorylation) yields between 36-38 ATP, so the net loss of high energy phosphate bonds experienced during gluconeogenesis is offset by the overall greater gain in such high-energy molecules produced by the oxidation of glucose.

III. Elements and Methods of the Invention

The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as SMP nucleic acid and protein molecules, which participate in the conversion of sugars to useful degradation products and energy (*e.g.*, ATP) in *C. glutamicum* or which may participate in the production of useful energy-rich molecules (*e.g.*, ATP) by other processes, such as oxidative phosphorylation. In one embodiment, the SMP molecules participate in the metabolism of carbon compounds such as sugars or the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In a preferred embodiment,

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the activity of the SMP molecules of the present invention to contribute to carbon metabolism or energy production in *C. glutamicum* has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the SMP molecules of the invention are modulated in activity, such that the *C. glutamicum* metabolic and energetic pathways in which the SMP proteins of the invention participate are modulated in yield, production, and/or efficiency of production, which either directly or indirectly modulates the yield, production, and/or efficiency of production of a desired fine chemical by *C. glutamicum*.

The language, "SMP protein" or "SMP polypeptide" includes proteins which are capable of performing a function involved in the metabolism of carbon compounds such as sugars and the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Examples of SMP proteins include those encoded by the SMP genes set forth in Table 1 and by the odd-numbered SEQ ID NOs. The terms "SMP gene" or "SMP nucleic acid sequence" include nucleic acid sequences encoding an SMP protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of SMP genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (*e.g.*, kg product per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (*i.e.*, fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation

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products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The term “degradation product” is art-recognized and includes breakdown products of a compound. Such products may themselves have utility as precursor (starting point) or intermediate molecules necessary for the biosynthesis of other compounds by the cell. The language “metabolism” is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (*e.g.*, the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound.

10 In another embodiment, the SMP molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. There are a number of mechanisms by which the alteration of an SMP protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. The degradation of high-energy carbon molecules such as sugars, and the conversion of compounds such as NADH and FADH₂ to more useful forms via oxidative phosphorylation results in a number of compounds which themselves may be desirable fine chemicals, such as pyruvate, ATP, NADH, and a number of intermediate sugar compounds. Further, the energy molecules (such as ATP) and the reducing equivalents (such as NADH or NADPH) produced by these metabolic pathways are utilized in the cell to drive reactions which would otherwise be energetically unfavorable. Such unfavorable reactions include many biosynthetic pathways for fine chemicals. By improving the ability of the cell to utilize a particular sugar (*e.g.*, by manipulating the genes encoding enzymes involved in the degradation and conversion of that sugar into energy for the cell), one may increase the amount of energy available to permit unfavorable, yet desired metabolic reactions (*e.g.*, the biosynthesis of a desired fine chemical) to occur.

The mutagenesis of one or more SMP genes of the invention may also result in SMP proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C. glutamicum*. For example, by increasing the efficiency of utilization of one or more sugars (such that the conversion of the sugar to useful energy molecules is improved), or by increasing the efficiency of conversion of

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reducing equivalents to useful energy molecules (*e.g.*, by improving the efficiency of oxidative phosphorylation, or the activity of the ATP synthase), one can increase the amount of these high-energy compounds available to the cell to drive normally unfavorable metabolic processes. These processes include the construction of cell walls, transcription, translation, and the biosynthesis of compounds necessary for growth and division of the cells (*e.g.*, nucleotides, amino acids, vitamins, lipids, etc.) (Lengeler *et al.* (1999) *Biology of Prokaryotes*, Thieme Verlag: Stuttgart, p. 88-109; 913-918; 875-899). By improving the growth and multiplication of these engineered cells, it is possible to increase both the viability of the cells in large-scale culture, and also to improve their rate of division, such that a relatively larger number of cells can survive in fermentor culture. The yield, production, or efficiency of production may be increased, at least due to the presence of a greater number of viable cells, each producing the desired fine chemical. Further, a number of the degradation and intermediate compounds produced during sugar metabolism are necessary precursors and intermediates for other biosynthetic pathways throughout the cell. For example, many amino acids are synthesized directly from compounds normally resulting from glycolysis or the TCA cycle (*e.g.*, serine is synthesized from 3-phosphoglycerate, an intermediate in glycolysis). Thus, by increasing the efficiency of conversion of sugars to useful energy molecules, it is also possible to increase the amount of useful degradation products as well.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* SMP DNAs and the predicted amino acid sequences of the *C. glutamicum* SMP proteins are shown in the Sequence Listing as odd-numbered SEQ ID NOs and even-numbered SEQ ID NOs, respectively. Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode proteins having a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of the invention

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(*e.g.*, the sequence of an even-numbered SEQ ID NO of the Sequence Listing). As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, *e.g.*, the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

An SMP protein or a biologically active portion or fragment thereof of the invention can participate in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or can have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections:

A. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode SMP polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of SMP-encoding nucleic acid (*e.g.*, SMP DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the

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genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated SMP nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the
5 nucleic acid is derived (e.g, a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, e.g., a nucleic acid molecule
10 having a nucleotide sequence of an odd-numbered SEQ ID NO of the Sequence Listing, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* SMP DNA can be isolated from a *C. glutamicum* library using all or portion of one of the odd-numbered
15 SEQ ID NO sequences of the Sequence Listing as a hybridization probe and standard hybridization techniques (e.g., as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (e.g., an odd-numbered SEQ ID NO:) can be isolated by
20 the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (e.g., a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (e.g., an odd-numbered SEQ ID NO of the Sequence Listing) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence). For example, mRNA
25 can be isolated from normal endothelial cells (e.g., by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (e.g., Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers
30 for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in the Sequence Listing. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and

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appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an SMP nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*,
5 using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in the Sequence Listing. The nucleic acid sequences of the invention, as set forth in the Sequence Listing, correspond to the *Corynebacterium glutamicum* SMP DNAs of the invention. This DNA comprises
10 sequences encoding SMP proteins (*i.e.*, the "coding region", indicated in each odd-numbered SEQ ID NO: sequence in the Sequence Listing), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in each odd-numbered SEQ ID NO: in the Sequence Listing.. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the sequences in nucleic acid sequences of the
15 Sequence Listing.

For the purposes of this application, it will be understood that each of the nucleic acid and amino acid sequences set forth in the Sequence Listing has an identifying RXA, RXN, or RXS number having the designation "RXA," "RXN," or "RXS" followed by 5 digits (*i.e.*, RXA01626, RXN00043, or RXS0735). Each of the nucleic acid sequences
20 comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, or RXS designation to eliminate confusion. The recitation "one of the odd-numbered sequences of the Sequence Listing", then, refers to any of the nucleic acid sequences in the Sequence Listing, which may also be distinguished by their differing RXA, RXN, or
25 RXS designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is also set forth in the Sequence Listing, as an even-numbered SEQ ID NO: immediately following the corresponding nucleic acid sequence. For example, the coding region for RXA02735 is set forth in SEQ ID NO:1, while the amino acid sequence which it encodes is set forth as SEQ ID NO:2. The
30 sequences of the nucleic acid molecules of the invention are identified by the same RXA, RXN, or RXS designations as the amino acid molecules which they encode, such that they can be readily correlated. For example, the amino acid sequence designated

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RXA00042 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXA00042, and the amino acid sequence designated RXN00043 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXN00043. The correspondence between the RXA, RXN and RXS nucleotide and
5 amino acid sequences of the invention and their assigned SEQ ID NOs is set forth in Table 1.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA designation. For example, SEQ ID NO:11, designated, as indicated on Table 1, as
10 "F RXA01312", is an F-designated gene, as are SEQ ID NOs: 29, 33, and 39 (designated on Table 1 as "F RXA02803", "F RXA02854", and "F RXA01365", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2. In the case of the dapD gene, a sequence
15 for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

20 In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences of the invention is one which is
25 sufficiently complementary to one of the nucleotide sequences shown in the Sequence Listing (*e.g.*, the sequence of an odd-numbered SEQ ID NO:) such that it can hybridize to one of the nucleotide sequences of the invention, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%,
30 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%,

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87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. Ranges and identity values intermediate to the above-recited
5 ranges, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, *e.g.*,
10 hybridizes under stringent conditions, to one of the nucleotide sequences of the invention, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of the sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, for example a fragment which can be used as a probe or primer
15 or a fragment encoding a biologically active portion of an SMP protein. The nucleotide sequences determined from the cloning of the SMP genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning SMP homologues in other cell types and organisms, as well as SMP homologues from other *Corynebacteria* or related species. The probe/primer typically comprises
20 substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the nucleotide sequences of the invention (*e.g.*, a sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing), an anti-sense sequence of
25 one of these sequences, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of the invention can be used in PCR reactions to clone SMP homologues. Probes based on the SMP nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.*
30 the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an SMP protein, such as by measuring a level of an SMP-encoding

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nucleic acid in a sample of cells, *e.g.*, detecting SMP mRNA levels or determining whether a genomic SMP gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently
5 homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO of the Sequence Listing) such that the protein or portion thereof maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. As used
10 herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in a sequence of one of the even-numbered SEQ ID NOs of the Sequence Listing) amino acid residues to an amino acid sequence of the invention such that the
15 protein or portion thereof is able to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Protein members of such sugar metabolic pathways or energy producing systems, as described herein, may play a role in the production and secretion of one or more fine
20 chemicals. Examples of such activities are also described herein. Thus, "the function of an SMP protein" contributes either directly or indirectly to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of SMP protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least
25 about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing).

Portions of proteins encoded by the SMP nucleic acid molecules of the invention
30 are preferably biologically active portions of one of the SMP proteins. As used herein, the term "biologically active portion of an SMP protein" is intended to include a portion, *e.g.*, a domain/motif, of an SMP protein that participates in the metabolism of carbon

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compounds such as sugars, or in energy-generating pathways in *C. glutamicum*, or has an activity as set forth in Table 1. To determine whether an SMP protein or a biologically active portion thereof can participate in the metabolism of carbon compounds or in the production of energy-rich molecules in *C. glutamicum*, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an SMP protein can be prepared by isolating a portion of one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing), expressing the encoded portion of the SMP protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the SMP protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing) (and portions thereof) due to degeneracy of the genetic code and thus encode the same SMP protein as that encoded by the nucleotide sequences of the invention. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in the Sequence Listing (*e.g.*, an even-numbered SEQ ID NO:). In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid of the invention (encoded by an open reading frame shown in an odd-numbered SEQ ID NO: of the Sequence Listing).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (*e.g.*, a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 58% identical to the nucleotide sequence designated RXA00014 (SEQ ID NO:41),

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a nucleotide sequence which is greater than and/or at least % identical to the nucleotide sequence designated RXA00195 (SEQ ID NO:399), and a nucleotide sequence which is greater than and/or at least 42% identical to the nucleotide sequence designated RXA00196 (SEQ ID NO:401). One of ordinary skill in the art would be able to

5 calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the

10 lower threshold so calculated (*e.g.*, at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%,

15 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* SMP nucleotide sequences set forth in the Sequence Listing as odd-numbered SEQ ID NOs, it will be appreciated by those of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of SMP proteins may exist within a population (*e.g.*, the *C.*

20 *glutamicum* population). Such genetic polymorphism in the SMP gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an SMP protein, preferably a *C. glutamicum* SMP protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the

25 SMP gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in SMP that are the result of natural variation and that do not alter the functional activity of SMP proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* SMP DNA of the invention can be isolated based on

30 their homology to the *C. glutamicum* SMP nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in

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another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of of an odd-numbered SEQ ID NO: of the Sequence Listing. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or
5 more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about
10 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by
15 one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a nucleotide sequence of the invention corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*,
20 encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* SMP protein.

In addition to naturally-occurring variants of the SMP sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of the invention, thereby leading to
25 changes in the amino acid sequence of the encoded SMP protein, without altering the functional ability of the SMP protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a nucleotide sequence of the invention. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the SMP proteins (*e.g.*, an
30 even-numbered SEQ ID NO: of the Sequence Listing) without altering the activity of said SMP protein, whereas an "essential" amino acid residue is required for SMP protein activity. Other amino acid residues, however, (*e.g.*, those that are not conserved or only

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semi-conserved in the domain having SMP activity) may not be essential for activity and thus are likely to be amenable to alteration without altering SMP activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding SMP proteins that contain changes in amino acid residues that are not essential for SMP activity. Such SMP proteins differ in amino acid sequence from a sequence of an even-numbered SEQ ID NO: of the Sequence Listing yet retain at least one of the SMP activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of the invention and is capable of participate in the metabolism of carbon compounds such as sugars, or in the biosynthesis of high-energy compounds in *C. glutamicum*, or has one or more activities set forth in Table 1. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to the amino acid sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, more preferably at least about 60-70% homologous to one of these sequences, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of these sequences, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the amino acid sequences of the invention.

To determine the percent homology of two amino acid sequences (*e.g.*, one of the amino acid sequences of the invention and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence (*e.g.*, one of the amino acid sequences the invention) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the amino acid sequence), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

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An isolated nucleic acid molecule encoding an SMP protein homologous to a protein sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of the invention such that

5 one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the nucleotide sequences of the invention by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid

10 substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine,

15 threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an SMP protein is preferably replaced with another amino acid residue from the same

20 side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an SMP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an SMP activity described herein to identify mutants that retain SMP activity. Following mutagenesis of the nucleotide sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing,

25 the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding SMP proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which

30 are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded DNA molecule or

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complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire SMP coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an SMP protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of NO. 3 (RXA01626) comprises nucleotides 1 to 345). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding SMP. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding SMP disclosed herein (*e.g.*, the sequences set forth as odd-numbered SEQ ID NOs in the Sequence Listing), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of SMP mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of SMP mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of SMP mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-

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galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-

5 methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense

10 nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered

15 to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an SMP protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through

20 specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve

25 sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms

30 specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids. Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-

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methylnucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave SMP mRNA transcripts to thereby inhibit translation of SMP mRNA. A ribozyme having specificity for an SMP-encoding nucleic acid can be designed based upon the nucleotide sequence of an SMP cDNA disclosed herein (*i.e.*, SEQ ID NO. 3 (RXA01626)). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an SMP-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, SMP mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

Alternatively, SMP gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an SMP nucleotide sequence (*e.g.*, an SMP promoter and/or enhancers) to form triple helical structures that prevent transcription of an SMP gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

25 B. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an SMP protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of

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autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector.

10 However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as cos-, tac-, trp-, tet-, trp-tet-, lpp-, lac-, lpp-lac-, lacI^q-, T7-, T5-, T3-, gal-, trc-, ara-, SP6-, amy, SPO2, λ -P_R- or λ P_L, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as ADC1, MF α , AC, P-60, CYC1, GAPDH, TEF, rp28, ADH, promoters from plants such as CaMV/35S, SSU, OCS, lib4,

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usp, STLS1, B33, nos or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by those of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors
5 of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, SMP proteins, mutant forms of SMP proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of SMP proteins in prokaryotic or eukaryotic cells. For example, SMP genes
10 can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: *More Gene Manipulations in Fungi*, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic
15 Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: *Applied Molecular Genetics of Fungi*, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* -mediated transformation of *Arabidopsis*
20 *thaliana* leaf and cotyledon explants" *Plant Cell Rep*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

25 Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein but also to the C-terminus or fused within suitable regions in the proteins. Such fusion vectors
30 typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion

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expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

5 Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the SMP protein is cloned into a
10 pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant SMP protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

15 Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315), pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1, λ gt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and
20 Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York IBSN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by
25 host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming *Streptomyces*, while plasmids pUB110, pC194, or pBD214 are suited for transformation
30 of *Bacillus* species. Several plasmids of use in the transfer of genetic information into *Corynebacterium* include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York IBSN 0 444 904018).

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One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another
5 strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

10 In another embodiment, the SMP protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), 2 μ , pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and
15 methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier:
20 New York (IBSN 0 444 904018).

Alternatively, the SMP proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.* (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989)
25 *Virology* 170:31-39).

In another embodiment, the SMP proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New
30 plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHIac+,

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pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York IBSN 0 444 904018). .

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in

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a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to SMP mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an SMP protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to one of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid,

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transposon or other DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, natural competence, chemical-mediated transfer, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an SMP protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by, for example, drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an SMP gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the SMP gene. Preferably, this SMP gene is a *Corynebacterium glutamicum* SMP gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous SMP gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a “knock out” vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous SMP gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous SMP protein). In the homologous recombination vector, the altered portion of the SMP gene is flanked at its 5' and 3' ends by additional nucleic acid of the SMP gene to allow for homologous recombination to occur between the exogenous SMP gene carried by the vector and an endogenous SMP gene in a microorganism. The additional

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flanking SMP nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination
5 vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced SMP gene has homologously recombined with the endogenous SMP gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene.
10 For example, inclusion of an SMP gene on a vector placing it under control of the lac operon permits expression of the SMP gene only in the presence of IPTG. Such regulatory systems are well known in the art.

In another embodiment, an endogenous SMP gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that
15 expression of its protein product does not occur. In another embodiment, an endogenous or introduced SMP gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional SMP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an SMP gene in a microorganism has been altered (*e.g.*, by deletion,
20 truncation, inversion, or point mutation) such that the expression of the SMP gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described SMP gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present invention.

25 A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an SMP protein. Accordingly, the invention further provides methods for producing SMP proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an SMP protein has
30 been introduced, or into which genome has been introduced a gene encoding a wild-type or altered SMP protein) in a suitable medium until SMP protein is produced. In another

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embodiment, the method further comprises isolating SMP proteins from the medium or the host cell.

C. Isolated SMP Proteins

5 Another aspect of the invention pertains to isolated SMP proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes
10 preparations of SMP protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of SMP protein having less than about 30% (by dry weight) of non-SMP protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-SMP protein,
15 still more preferably less than about 10% of non-SMP protein, and most preferably less than about 5% non-SMP protein. When the SMP protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein
20 preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of SMP protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of SMP protein having less than about 30% (by
25 dry weight) of chemical precursors or non-SMP chemicals, more preferably less than about 20% chemical precursors or non-SMP chemicals, still more preferably less than about 10% chemical precursors or non-SMP chemicals, and most preferably less than about 5% chemical precursors or non-SMP chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from
30 the same organism from which the SMP protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* SMP protein in a microorganism such as *C. glutamicum*.

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An isolated SMP protein or a portion thereof of the invention can participate in the metabolism of carbon compounds such as sugars, or in the production of energy compounds (*e.g.*, by oxidative phosphorylation) utilized to drive unfavorable metabolic pathways, or has one or more of the activities set forth in Table 1. In preferred

5 embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) such that the protein or portion thereof maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules by processes such as

10 oxidative phosphorylation in *Corynebacterium glutamicum*. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an SMP protein of the invention has an amino acid sequence set forth as an even-numbered SEQ ID NO: of the Sequence Listing. In yet another preferred embodiment, the SMP protein has an amino acid sequence which is encoded by a

15 nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing). In still another preferred embodiment, the SMP protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least

20 about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of the invention, or a portion thereof. Ranges and identity

25 values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred SMP proteins of the present invention also preferably possess at least one of the SMP activities described

30 herein. For example, a preferred SMP protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention, and

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which can perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or which has one or more of the activities set forth in Table 1.

5 In other embodiments, the SMP protein is substantially homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and retains the functional activity of the protein of one of the amino acid sequences of the invention yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in
10 another embodiment, the SMP protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or
15 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention and which has at least one of the SMP activities described herein. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of
20 identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention.

 Biologically active portions of an SMP protein include peptides comprising
25 amino acid sequences derived from the amino acid sequence of an SMP protein, *e.g.*, an amino acid sequence of an even-numbered SEQ ID NO: of the Sequence Listing or the amino acid sequence of a protein homologous to an SMP protein, which include fewer amino acids than a full length SMP protein or the full length protein which is homologous to an SMP protein, and exhibit at least one activity of an SMP protein.
30 Typically, biologically active portions (peptides, *e.g.*, peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an SMP protein. Moreover, other

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biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an SMP protein include one or more selected domains/motifs or portions thereof having biological activity.

5 SMP proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the SMP protein is expressed in the host cell. The SMP protein can then be isolated from the cells by an appropriate purification scheme using standard
10 protein purification techniques. Alternative to recombinant expression, an SMP protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native SMP protein can be isolated from cells (*e.g.*, endothelial cells), for example using an anti-SMP antibody, which can be produced by standard techniques utilizing an SMP protein or fragment thereof of this invention.

15 The invention also provides SMP chimeric or fusion proteins. As used herein, an SMP "chimeric protein" or "fusion protein" comprises an SMP polypeptide operatively linked to a non-SMP polypeptide. An "SMP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an SMP protein, whereas a "non-SMP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a
20 protein which is not substantially homologous to the SMP protein, *e.g.*, a protein which is different from the SMP protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the SMP polypeptide and the non-SMP polypeptide are fused in-frame to each other. The non-SMP polypeptide can be fused to the N-terminus or C-terminus of
25 the SMP polypeptide. For example, in one embodiment the fusion protein is a GST-SMP fusion protein in which the SMP sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant SMP proteins. In another embodiment, the fusion protein is an SMP protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian
30 host cells), expression and/or secretion of an SMP protein can be increased through use of a heterologous signal sequence.

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Preferably, an SMP chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended
5 termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor
10 primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, Ausubel *et al.*, eds. John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide).
15 An SMP-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the SMP protein.

Homologues of the SMP protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the SMP protein. As used herein, the term "homologue" refers to a variant form of the SMP protein which acts as an agonist or antagonist of the
20 activity of the SMP protein. An agonist of the SMP protein can retain substantially the same, or a subset, of the biological activities of the SMP protein. An antagonist of the SMP protein can inhibit one or more of the activities of the naturally occurring form of the SMP protein, by, for example, competitively binding to a downstream or upstream member of the sugar molecule metabolic cascade or the energy-producing pathway
25 which includes the SMP protein.

In an alternative embodiment, homologues of the SMP protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the SMP protein for SMP protein agonist or antagonist activity. In one embodiment, a variegated library of SMP variants is generated by combinatorial mutagenesis at the nucleic acid
30 level and is encoded by a variegated gene library. A variegated library of SMP variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential SMP

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sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of SMP sequences therein. There are a variety of methods which can be used to produce libraries of potential SMP homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a
5 degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential SMP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3;
10 Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477.

In addition, libraries of fragments of the SMP protein coding can be used to generate a variegated population of SMP fragments for screening and subsequent selection of homologues of an SMP protein. In one embodiment, a library of coding
15 sequence fragments can be generated by treating a double stranded PCR fragment of an SMP coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by
20 treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the SMP protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA
25 libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of SMP homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of
30 vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the

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frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify SMP homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a
5 variegated SMP library, using methods well known in the art.

D. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the
10 following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of SMP protein regions required for function; modulation of an SMP protein activity; modulation of the metabolism of one or more sugars; modulation of high-energy molecule production in a
15 cell (*i.e.*, ATP, NADPH); and modulation of cellular production of a desired compound, such as a fine chemical.

The SMP nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum*
20 or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present.
25 Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to pathogenic species, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli
30 secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and

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spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at least 5,000 deaths since 1990.

5 In one embodiment, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (e.g., the sequences set forth as odd-numbered or even-numbered SEQ ID NOs, respectively, in the Sequence Listing) in a subject, thereby detecting the presence or activity of
10 *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in *C. glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

The nucleic acid and protein molecules of the invention may also serve as
15 markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed
20 with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the
25 invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

The SMP nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic and energy-releasing processes in which
30 the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the

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evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein
5 engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the SMP nucleic acid molecules of the invention may result in the production of SMP proteins having functional differences from the wild-type SMP proteins. These proteins may be improved in efficiency or activity, may be present in
10 greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention provides methods for screening molecules which modulate the activity of an SMP protein, either by interacting with the protein itself or a substrate or binding partner of the SMP protein, or by modulating the transcription or translation of an SMP nucleic acid molecule of the invention. In such methods, a microorganism
15 expressing one or more SMP proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the SMP protein is assessed.

There are a number of mechanisms by which the alteration of an SMP protein of the invention may directly affect the yield, production, and/or efficiency of production
20 of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. The degradation of high-energy carbon molecules such as sugars, and the conversion of compounds such as NADH and FADH₂ to more useful forms via oxidative phosphorylation results in a number of compounds which themselves may be desirable fine chemicals, such as pyruvate, ATP, NADH, and a number of intermediate sugar
25 compounds. Further, the energy molecules (such as ATP) and the reducing equivalents (such as NADH or NADPH) produced by these metabolic pathways are utilized in the cell to drive reactions which would otherwise be energetically unfavorable. Such unfavorable reactions include many biosynthetic pathways for fine chemicals. By improving the ability of the cell to utilize a particular sugar (*e.g.*, by manipulating the
30 genes encoding enzymes involved in the degradation and conversion of that sugar into energy for the cell), one may increase the amount of energy available to permit

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unfavorable, yet desired metabolic reactions (*e.g.*, the biosynthesis of a desired fine chemical) to occur.

Further, modulation of one or more pathways involved in sugar utilization permits optimization of the conversion of the energy contained within the sugar molecule to the production of one or more desired fine chemicals. For example, by reducing the activity of enzymes involved in, for example, gluconeogenesis, more ATP is available to drive desired biochemical reactions (such as fine chemical biosyntheses) in the cell. Also, the overall production of energy molecules from sugars may be modulated to ensure that the cell maximizes its energy production from each sugar molecule. Inefficient sugar utilization can lead to excess CO₂ production and excess energy, which may result in futile metabolic cycles. By improving the metabolism of sugar molecules, the cell should be able to function more efficiently, with a need for fewer carbon molecules. This should result in an improved fine chemical product: sugar molecule ratio (improved carbon yield), and permits a decrease in the amount of sugars that must be added to the medium in large-scale fermentor culture of such engineered *C. glutamicum*.

The mutagenesis of one or more SMP genes of the invention may also result in SMP proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C. glutamicum*. For example, by increasing the efficiency of utilization of one or more sugars (such that the conversion of the sugar to useful energy molecules is improved), or by increasing the efficiency of conversion of reducing equivalents to useful energy molecules (*e.g.*, by improving the efficiency of oxidative phosphorylation, or the activity of the ATP synthase), one can increase the amount of these high-energy compounds available to the cell to drive normally unfavorable metabolic processes. These processes include the construction of cell walls, transcription, translation, and the biosynthesis of compounds necessary for growth and division of the cells (*e.g.*, nucleotides, amino acids, vitamins, lipids, etc.) (Lengeler *et al.* (1999) *Biology of Prokaryotes*, Thieme Verlag: Stuttgart, p. 88-109; 913-918; 875-899). By improving the growth and multiplication of these engineered cells, it is possible to increase both the viability of the cells in large-scale culture, and also to improve their rate of division, such that a relatively larger number of cells can survive in fermentor culture. The yield, production, or efficiency of production may be increased, at least

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due to the presence of a greater number of viable cells, each producing the desired fine chemical.

Further, many of the degradation products produced during sugar metabolism are themselves utilized by the cell as precursors or intermediates for the production of a number of other useful compounds, some of which are fine chemicals. For example, pyruvate is converted into the amino acid alanine, and ribose-5-phosphate is an integral part of, for example, nucleotide molecules. The amount and efficiency of sugar metabolism, then, has a profound effect on the availability of these degradation products in the cell. By increasing the ability of the cell to process sugars, either in terms of efficiency of existing pathways (*e.g.*, by engineering enzymes involved in these pathways such that they are optimized in activity), or by increasing the availability of the enzymes involved in such pathways (*e.g.*, by increasing the number of these enzymes present in the cell), it is possible to also increase the availability of these degradation products in the cell, which should in turn increase the production of many different other desirable compounds in the cell (*e.g.*, fine chemicals).

The aforementioned mutagenesis strategies for SMP proteins to result in increased yields of a fine chemical from *C. glutamicum* are not meant to be limiting; variations on these strategies will be readily apparent to one of ordinary skill in the art. Using such strategies, and incorporating the mechanisms disclosed herein, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated SMP nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any product produced by *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, and the sequence listing cited throughout this application are hereby incorporated by reference.

TABLE 1: GENES IN THE APPLICATION

HMP:

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
1	2	RXS02735	VV0074	14576	15280	6-Phosphoglucolactonase
3	4	RXA01626	GR00452	4270	3926	L-ribulose-phosphate 4-epimerase
5	6	RXA02245	GR00654	13639	14295	RIBULOSE-PHOSPHATE 3-EPIMERASE (EC 5.1.3.1)
7	8	RXA01015	GR00290	346	5	RIBOSE 5-PHOSPHATE ISOMERASE (EC 5.3.1.6)

TCA:

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
9	10	RXN01312	VV0082	20803	18785	SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT (EC 1.3.99.1)
11	12	F RXA01312	GR00380	2690	1614	SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT (EC 1.3.99.1)
13	14	RXN00231	VV0083	15484	14015	SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (EC 1.2.1.16)
15	16	RXA01311	GR00380	1611	865	SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN (EC 1.3.99.1)
17	18	RXA01535	GR00427	1354	2760	FUMARATE HYDRATASE PRECURSOR (EC 4.2.1.2)
19	20	RXA00517	GR00131	1407	2447	MALATE DEHYDROGENASE (EC 1.1.1.37) (EC 1.1.1.82)
21	22	RXA01350	GR00392	1844	2827	MALATE DEHYDROGENASE (EC 1.1.1.37)

EMB-Pathway

<u>Nucleic</u> <u>Acid SEQ</u> <u>ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
23	24	RXA02149	GR00639	17786	18754	GLUCOKINASE (EC 2.7.1.2)
25	26	RXA01814	GR00515	2571	910	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
27	28	RXN02803	VV0086	1	657	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
29	30	F RXA02803	GR00784	2	400	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
31	32	RXN03076	VV0043	1624	35	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
33	34	F RXA02854	GR10002	1588	5	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
35	36	RXA00511	GR00129	1	513	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
37	38	RXN01365	VV0091	1476	103	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
39	40	F RXA01365	GR00397	897	4	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
41	42	RXA00098	GR00014	6525	8144	GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (EC 5.3.1.9)
43	44	RXA01989	GR00578	1	630	GLUCOSE-6-PHOSPHATE ISOMERASE A (GPI A) (EC 5.3.1.9)
45	46	RXA00340	GR00059	1549	2694	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
47	48	RXA02492	GR00720	2201	2917	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
49	50	RXA00381	GR00082	1451	846	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
51	52	RXA02122	GR00636	6511	5813	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
53	54	RXA00206	GR00032	6171	5134	6-PHOSPHOFRUCTOKINASE (EC 2.7.1.11)
55	56	RXA01243	GR00359	2302	3261	1-PHOSPHOFRUCTOKINASE (EC 2.7.1.56)
57	58	RXA01882	GR00538	1165	2154	1-PHOSPHOFRUCTOKINASE (EC 2.7.1.56)
59	60	RXA01702	GR00479	1397	366	FRUCTOSE-BISPHOSPHATE ALDOLASE (EC 4.1.2.13)
61	62	RXA02258	GR00654	26451	27227	TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1)
63	64	RXN01225	VV0064	6382	4943	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12)
65	66	F RXA01225	GR00354	5302	6741	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE HOMOLOG
67	68	RXA02256	GR00654	23934	24935	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12)
69	70	RXA02257	GR00654	25155	26369	PHOSPHOGLYCERATE KINASE (EC 2.7.2.3)
71	72	RXA00235	GR00036	2365	1091	ENOLASE (EC 4.2.1.11)
73	74	RXA01093	GR00306	1552	122	PYRUVATE KINASE (EC 2.7.1.40)
75	76	RXN02675	VV0098	72801	70945	PYRUVATE KINASE (EC 2.7.1.40)
77	78	F RXA02675	GR00754	2	364	PYRUVATE KINASE (EC 2.7.1.40)
79	80	F RXA02695	GR00755	2949	4370	PYRUVATE KINASE (EC 2.7.1.40)
81	82	RXA00682	GR00179	5299	3401	PHOSPHOENOLPYRUVATE SYNTHASE (EC 2.7.9.2)
83	84	RXA00683	GR00179	6440	5349	PHOSPHOENOLPYRUVATE SYNTHASE (EC 2.7.9.2)
85	86	RXN00635	VV0135	22708	20972	PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2.2.2)
87	88	F RXA02807	GR00788	88	552	PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2.2.2)
89	90	F RXA00635	GR00167	3	923	PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2.2.2)
91	92	RXN03044	VV0019	1391	2221	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
93	94	F RXA02852	GR00852	3	281	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
95	96	F RXA00268	GR00041	125	955	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
97	98	RXN03086	VV0049	2243	2650	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
99	100	F RXA02887	GR10022	411	4	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
101	102	RXN03043	VV0019	1	1362	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
103	104	F RXA02897	GR10039	1291	5	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
105	106	RXN03083	VV0047	88	1110	DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8.1.4)
107	108	F RXA02853	GR10001	89	1495	DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8.1.4)
109	110	RXA02259	GR00654	27401	30172	PHOSPHOENOLPYRUVATE CARBOXYLASE (EC 4.1.1.31)
111	112	RXN02326	VV0047	4500	5315	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
113	114	F RXA02326	GR00668	5338	4523	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
115	116	RXN02327	VV0047	3533	4492	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
117	118	F RXA02327	GR00668	6305	5346	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
119	120	RXN02328	VV0047	1842	3437	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
121	122	F RXA02328	GR00668	7783	6401	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
123	124	RXN01048	VV0079	12539	11316	MALIC ENZYME (EC 1.1.1.39)

Table 1 (continued)

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
125	126	F RXA01048	GR00296	3	290	MALIC ENZYME (EC 1.1.1.39)
127	128	F RXA00290	GR00046	4693	5655	MALIC ENZYME (EC 1.1.1.39)
129	130	RXA02694	GR00755	1879	2820	L-LACTATE DEHYDROGENASE (EC 1.1.1.27)
131	132	RXN00296	VV0176	35763	38606	D-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.4)
133	134	F RXA00296	GR00048	3	2837	D-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.4)
135	136	RXA01901	GR00544	4158	5417	L-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.3)
137	138	RXN01952	VV0105	9954	11666	D-LACTATE DEHYDROGENASE (EC 1.1.1.28)
139	140	F RXA01952	GR00562	1	216	D-LACTATE DEHYDROGENASE (EC 1.1.1.28)
141	142	F RXA01955	GR00562	4611	6209	D-LACTATE DEHYDROGENASE (EC 1.1.1.28)
143	144	RXA00293	GR00047	2645	1734	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
145	146	RXN01130	VV0157	6138	5536	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
147	148	F RXA01130	GR00315	2	304	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
149	150	RXN03112	VV0085	509	6	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
151	152	F RXA01133	GR00316	568	1116	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
153	154	RXN00871	VV0127	3127	2240	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
155	156	F RXA00871	GR00239	2344	3207	IOLB PROTEIN
						IOLB PROTEIN: D-FRUCTOSE 1,6-BISPHOSPHATE = GLYCERONE-CC PHOSPHATE + D- GLYCERALDEHYDE 3-PHOSPHATE.
157	158	RXN02829	VV0354	287	559	IOLS PROTEIN
159	160	F RXA02829	GR00816	287	562	IOLS PROTEIN
161	162	RXN01468	VV0019	7474	8298	NAGD PROTEIN
163	164	F RXA01468	GR00422	1250	2074	PUTATIVE N-GLYCERALDEHYDE-2-PHOSPHOTRANSFERASE
165	166	RXA00794	GR00211	3993	2989	GLPX PROTEIN
167	168	RXN02920	VV0213	6135	5224	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
169	170	F RXA02379	GR00690	1390	686	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
171	172	RXN02688	VV0098	59053	58385	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
173	174	RXN03087	VV0052	3216	3428	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
175	176	RXN03186	VV0377	310	519	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
177	178	RXN03187	VV0382	3	281	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
179	180	RXN02591	VV0098	14370	12541	PHOSPHOENOLPYRUVATE CARBOXYKINASE [GTP] (EC 4.1.1.32)
181	182	RXS01260	VV0009	3477	2296	LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED- CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)
183	184	RXS01261	VV0009	3703	3533	LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED- CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)

Glycerol metabolism

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
185	186	RXA02640	GR00749	1400	2926	GLYCEROL KINASE (EC 2.7.1.30)
187	188	RXN01025	VV0143	5483	4488	GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD(P)+) (EC 1.1.1.94)
189	190	F RXA01025	GR00293	939	1853	GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD(P)+) (EC 1.1.1.94)
191	192	RXA01851	GR00525	3515	1830	AEROBIC GLYCEROL-3-PHOSPHATE DEHYDROGENASE (EC 1.1.99.5)
193	194	RXA01242	GR00359	1526	2302	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR
195	196	RXA02288	GR00661	992	147	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR

Table 1 (continued)

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u> <u>NT Stop</u>		<u>Function</u>
197	198	RXN01891	VV0122	24949	24086	GLYCEROL-3-PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
199	200	F RXA01891	GR00541	1736	918	GLYCEROL-3-PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
201	202	RXA02414	GR00703	3808	3062	Uncharacterized protein involved in glycerol metabolism (homolog of Drosophila rhomboid)
203	204	RXN01580	VV0122	22091	22807	Glycerophosphoryl diester phosphodiesterase

Acetate metabolism

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u> <u>NT Stop</u>		<u>Function</u>
205	206	RXA01436	GR00418	2547	1357	ACETATE KINASE (EC 2.7.2.1)
207	208	RXA00686	GR00179	8744	7941	ACETATE OPERON REPRESSOR
209	210	RXA00246	GR00037	4425	3391	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
211	212	RXA01571	GR00438	1360	1959	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
213	214	RXA01572	GR00438	1928	2419	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
215	216	RXA01758	GR00498	3961	2945	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
217	218	RXA02539	GR00726	11676	10159	ALDEHYDE DEHYDROGENASE (EC 1.1.1.1)
219	220	RXN03061	VV0034	108	437	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
221	222	RXN03150	VV0155	10678	10055	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
223	224	RXN01340	VV0033	3	860	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
225	226	RXN01498	VV0008	1598	3160	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
227	228	RXN02674	VV0315	15614	14163	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
229	230	RXN00868	VV0127	2230	320	ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18)
231	232	RXN01143	VV0077	9372	8254	ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18)
233	234	RXN01146	VV0264	243	935	ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18)
235	236	RXN01144	VV0077	8237	7722	ACETOLACTATE SYNTHASE SMALL SUBUNIT (EC 4.1.3.18)

Butanediol, diacetyl and acetoin formation

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u> <u>NT Stop</u>		<u>Function</u>
237	238	RXA02474	GR00715	8082	7309	(S,S)-butane-2,3-diol dehydrogenase (EC 1.1.1.76)
239	240	RXA02453	GR00710	6103	5351	ACETOIN(DIACETYL) REDUCTASE (EC 1.1.1.5)
241	242	RXS01758	VV0112	27383	28399	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)

Table 1 (continued)

HMP-Cycle

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
243	244	RXA02737	GR00763	3312	1771	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (EC 1.1.1.49)
245	246	RXA02738	GR00763	4499	3420	TRANSALDOLASE (EC 2.2.1.2)
247	248	RXA02739	GR00763	6769	4670	TRANSKETOLASE (EC 2.2.1.1)
249	250	RXA00965	GR00270	1232	510	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44)
251	252	RXN00999	VV0106	2817	1366	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44)
253	254	F RXA00999	GR00283	3012	4448	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44)

Nucleotide sugar conversion

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
255	256	RXN02596	VV0098	48784	47582	UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)
257	258	F RXA02596	GR00742	1	489	UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)
259	260	F RXA02642	GR00749	5383	5880	UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)
261	262	RXA02572	GR00737	2	646	UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.22)
263	264	RXA02485	GR00718	2345	3445	UDP-N-ACETYLENOLPYRUVOYLGLUCOSAMINE REDUCTASE (EC 1.1.1.158)
265	266	RXA01216	GR00352	2302	1202	UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23)
267	268	RXA01259	GR00367	987	130	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 2.7.7.9)
269	270	RXA02028	GR00616	573	998	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 2.7.7.9)
271	272	RXA01262	GR00367	8351	7191	GDP-MANNOSE 6-DEHYDROGENASE (EC 1.1.1.132)
273	274	RXA01377	GR00400	3935	5020	MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13)
275	276	RXA02063	GR00626	3301	4527	GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE (EC 2.7.7.27)
277	278	RXN00014	VV0048	8848	9627	GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE (EC 2.7.7.24)
279	280	F RXA00014	GR00002	4448	5227	GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE (EC 2.7.7.24)
281	282	RXA01570	GR00438	427	1281	GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE (EC 2.7.7.24)
283	284	RXA02666	GR00753	7260	6493	D-RIBITOL-5-PHOSPHATE CYTIDYLYLTRANSFERASE (EC 2.7.7.40)
285	286	RXA00825	GR00222	222	1154	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)

Inositol and ribitol metabolism

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
287	288	RXA01887	GR00539	4219	3209	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT		Function
				Start	Stop	
289	290	RXN00013	VV0048	7966	8838	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (EC 3.1.3.25)
291	292	F RXA00013	GR00002	3566	4438	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (EC 3.1.3.25)
293	294	RXA01099	GR00306	6328	5504	INOSITOL MONOPHOSPHATE PHOSPHATASE
295	296	RXN01332	VV0273	579	4	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
297	298	F RXA01332	GR00388	552	4	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
299	300	RXA01632	GR00454	2338	3342	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
301	302	RXA01633	GR00454	3380	4462	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
303	304	RXN01406	VV0278	2999	1977	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
305	306	RXN01630	VV0050	48113	47037	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
307	308	RXN00528	VV0079	23406	22318	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4)
309	310	RXN03057	VV0028	7017	7688	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
311	312	F RXA02902	GR10040	10277	10948	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
313	314	RXA00251	GR00038	931	224	RIBITOL 2-DEHYDROGENASE (EC 1.1.1.56)

Utilization of sugars

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT		Function
				Start	Stop	
315	316	RXN02654	VV0090	12206	13090	GLUCOSE 1-DEHYDROGENASE (EC 1.1.1.47)
317	318	F RXA02654	GR00752	7405	8289	GLUCOSE 1-DEHYDROGENASE II (EC 1.1.1.47)
319	320	RXN01049	VV0079	9633	11114	GLUCONOKINASE (EC 2.7.1.12)
321	322	F RXA01049	GR00296	1502	492	GLUCONOKINASE (EC 2.7.1.12)
323	324	F RXA01050	GR00296	1972	1499	GLUCONOKINASE (EC 2.7.1.12)
325	326	RXA00202	GR00032	1216	275	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR
327	328	RXN00872	VV0127	6557	5604	FRUCTOKINASE (EC 2.7.1.4)
329	330	F RXA00872	GR00240	565	1086	FRUCTOKINASE (EC 2.7.1.4)
331	332	RXN00799	VV0009	58477	56834	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.21) (EC 3.2.1.37)
333	334	F RXA00799	GR00214	1	1584	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.21) (EC 3.2.1.37)
335	336	RXA00032	GR00003	12028	10520	MANNITOL 2-DEHYDROGENASE (EC 1.1.1.67)
337	338	RXA02528	GR00725	6880	7854	FRUCTOSE REPRESSOR
339	340	RXN00316	VV0006	7035	8180	Hypothetical Oxidoreductase (EC 1.1.1.-)
341	342	F RXA00309	GR00053	316	5	GLUCOSE--FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
343	344	RXN00310	VV0006	6616	7050	GLUCOSE--FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
345	346	F RXA00310	GR00053	735	301	GLUCOSE--FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
347	348	RXA00041	GR00007	1246	5	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26)
349	350	RXA02026	GR00615	725	6	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26)
351	352	RXA02061	GR00626	1842	349	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26)

Table 1 (continued)

Nucleic Acid		Amino Acid		Identification Code	Contig.	Function		
SEQ ID NO		SEQ ID NO				NT Start	NT Stop	
353		354	RXN01369	VV0124		595	1776	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8)
355		356	F RXA01369	GR00398		3	503	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8)
357		358	F RXA01373	GR00399		595	1302	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8)
359		360	RXA02611	GR00743		1	1752	1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18)
361		362	RXA02612	GR00743		1793	3985	1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18)
363		364	RXN01884	VV0184		1	1890	GLYCOGEN DEBRANCHING ENZYME (EC 2.4.1.25) (EC 3.2.1.33)
365		366	F RXA01884	GR00539		3	1475	GLYCOGEN DEBRANCHING ENZYME (EC 2.4.1.25) (EC 3.2.1.33)
367		368	RXA01111	GR00306		16981	17427	GLYCOGEN OPERON PROTEIN GLGX (EC 3.2.1.-)
369		370	RXN01550	VV0143		14749	16260	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
371		372	F RXA01550	GR00431		3	1346	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
373		374	RXN02100	VV0318		2	2326	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
375		376	F RXA02100	GR00631		3	920	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
377		378	F RXA02113	GR00633		2	1207	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
379		380	RXA02147	GR00639		15516	16532	ALPHA-AMYLASE (EC 3.2.1.1)
381		382	RXA01478	GR00422		10517	12352	GLUCOAMYLASE G1 AND G2 PRECURSOR (EC 3.2.1.3)
383		384	RXA01888	GR00539		4366	4923	GLUCOSE-RESISTANCE AMYLASE REGULATOR
385		386	RXN01927	VV0127		50623	49244	XYLULOSE KINASE (EC 2.7.1.17)
387		388	F RXA01927	GR00555		3	1118	XYLULOSE KINASE (EC 2.7.1.17)
389		390	RXA02729	GR00762		747	4	RIBOKINASE (EC 2.7.1.15)
391		392	RXA02797	GR00778		1739	2641	RIBOKINASE (EC 2.7.1.15)
393		394	RXA02730	GR00762		1768	731	RIBOSE OPERON REPRESSOR
395		396	RXA02551	GR00729		2193	2552	6-PHOSPHO-BETA-GLUCOSIDASE (EC 3.2.1.86)
397		398	RXA01325	GR00385		5676	5005	DEOXYRIBOSE-PHOSPHATE ALDOLASE (EC 4.1.2.4)
399		400	RXA00195	GR00030		543	1103	1-deoxy-D-xyulose 5-phosphate reductoisomerase (EC 1.1.1.-)
401		402	RXA00196	GR00030		1094	1708	1-deoxy-D-xyulose 5-phosphate reductoisomerase (EC 1.1.1.-)
403		404	RXN01562	VV0191		1230	3137	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE
405		406	F RXA01562	GR00436		2	1039	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE
407		408	F RXA01705	GR00480		971	1573	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE
409		410	RXN00879	VV0099		8763	6646	4-ALPHA-GLUCANOTRANSFERASE (EC 2.4.1.25)
411		412	F RXA00879	GR00242		5927	3828	4-ALPHA-GLUCANOTRANSFERASE (EC 2.4.1.25), amylomaltase
413		414	RXN00043	VV0119		3244	2081	N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25)
415		416	F RXA00043	GR00007		3244	2081	N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25)
417		418	RXN01752	VV0127		35265	33805	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
419		420	F RXA01839	GR00520		1157	510	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
421		422	RXA01859	GR00529		1473	547	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
423		424	RXA00042	GR00007		2037	1279	GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10)
425		426	RXA01482	GR00422		17271	15397	GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (EC 2.6.1.16)
427		428	RXN03179	VV0336		2	667	URONATE ISOMERASE (EC 5.3.1.12)
429		430	F RXA02872	GR10013		675	4	URONATE ISOMERASE, Glucuronate isomerase (EC 5.3.1.12)
431		432	RXN03180	VV0337		672	163	URONATE ISOMERASE (EC 5.3.1.12)
433		434	F RXA02873	GR10014		672	163	URONATE ISOMERASE, Glucuronate isomerase (EC 5.3.1.12)
435		436	RXA02292	GR00662		1611	2285	GALACTOSIDE O-ACETYLTRANSFERASE (EC 2.3.1.18)
437		438	RXA02666	GR00753		7260	6493	D-RIBITOL-5-PHOSPHATE CYTIDYLYLTRANSFERASE (EC 2.7.7.40)
439		440	RXA00202	GR00032		1216	275	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR
441		442	RXA02440	GR00709		5097	4258	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
443	444	RXN01569	VV0009	41086	42444	dTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133)
445	446	F RXA01569	GR00438	2	427	DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133)
447	448	F RXA02055	GR00624	7122	8042	DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133)
449	450	RXA00825	GR00222	222	1154	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)
451	452	RXA02054	GR00624	6103	7119	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)
453	454	RXN00427	VV0112	7004	6219	dTDP-RHAMNOSYL TRANSFERASE RFBF (EC 2.-.-.-)
455	456	F RXA00427	GR00098	1591	2022	DTDP-RHAMNOSYL TRANSFERASE RFBF (EC 2.-.-.-)
457	458	RXA00327	GR00057	10263	9880	PROTEIN ARAJ
459	460	RXA00328	GR00057	11147	10656	PROTEIN ARAJ
461	462	RXA00329	GR00057	12390	11167	PROTEIN ARAJ
463	464	RXN01554	VV0135	28686	26545	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A1 PRECURSOR (EC 3.2.1.39)
465	466	RXN03015	VV0063	289	8	UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.22)
467	468	RXN03056	VV0028	6258	6935	PUTATIVE HEXULOSE-6-PHOSPHATE ISOMERASE (EC 5.-.-.-)
469	470	RXN03030	VV0009	57006	56443	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.21) (EC 3.2.1.37)
471	472	RXN00401	VV0025	12427	11489	5-DEHYDRO-4-DEOXYGLUCARATE DEHYDRATASE (EC 4.2.1.41)
473	474	RXN02125	VV0102	23242	22442	ALDOSE REDUCTASE (EC 1.1.1.21)
475	476	RXN00200	VV0181	1679	5116	arabinosyl transferase subunit B (EC 2.4.2.-)
477	478	RXN01175	VV0017	39688	38303	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)
479	480	RXN01376	VV0091	5610	4750	PUTATIVE GLYCOSYL TRANSFERASE WBIF
481	482	RXN01631	VV0050	47021	46143	PUTATIVE HEXULOSE-6-PHOSPHATE ISOMERASE (EC 5.-.-.-)
483	484	RXN01593	VV0229	13274	12408	NAGD PROTEIN
485	486	RXN00337	VV0197	20369	21418	GALACTOKINASE (EC 2.7.1.6)
487	488	RXS00584	VV0323	5516	6640	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)
489	490	RXS02574				BETA-HEXOSAMINIDASE A PRECURSOR (EC 3.2.1.52)
491	492	RXS03215				GLUCOSE--FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
493	494	F RXA01915	GR00549	1	1008	GLUCOSE--FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
495	496	RXS03224				CYCLOMALTODEXTRINASE (EC 3.2.1.54)
497	498	F RXA00038	GR00006	1417	260	CYCLOMALTODEXTRINASE (EC 3.2.1.54)
499	500	RXC00233				protein involved in sugar metabolism
501	502	RXC00236				Membrane Lipoprotein involved in sugar metabolism
503	504	RXC00271				Exported Protein involved in ribose metabolism
505	506	RXC00338				protein involved in sugar metabolism
507	508	RXC00362				Membrane Spanning Protein involved in metabolism of diols
509	510	RXC00412				Amino Acid ABC Transporter ATP-Binding Protein involved in sugar metabolism
511	512	RXC00526				ABC Transporter ATP-Binding Protein involved in sugar metabolism
513	514	RXC01004				Membrane Spanning Protein involved in sugar metabolism
515	516	RXC01017				Cytosolic Protein involved in sugar metabolism
517	518	RXC01021				Cytosolic Kinase involved in metabolism of sugars and thiamin
519	520	RXC01212				ABC Transporter ATP-Binding Protein involved in sugar metabolism
521	522	RXC01306				Membrane Spanning Protein involved in sugar metabolism
523	524	RXC01366				Cytosolic Protein involved in sugar metabolism
525	526	RXC01372				Cytosolic Protein involved in sugar metabolism

Table 1 (continued)

Nucleic Acid		Amino Acid	Identification Code	Contig.	NT Start		NT Stop		Function
SEQ ID NO		SEQ ID NO							
527		528	RXC01659						protein involved in sugar metabolism
529		530	RXC01663						protein involved in sugar metabolism
531		532	RXC01693						protein involved in sugar metabolism
533		534	RXC01703						Cytosolic Protein involved in sugar metabolism
535		536	RXC02254						Membrane Associated Protein involved in sugar metabolism
537		538	RXC02255						Cytosolic Protein involved in sugar metabolism
539		540	RXC02435						protein involved in sugar metabolism
541		542	F RXA02435	GR00709	825		268		Uncharacterized protein involved in glycerol metabolism (homolog of Drosophila rhomboid)
543		544	RXC03216						protein involved in sugar metabolism

TCA-cycle

Nucleic Acid		Amino Acid	Identification Code	Contig.	NT Start		NT Stop		Function
SEQ ID NO		SEQ ID NO							
545		546	RXA02175	GR00641	10710		9418		CITRATE SYNTHASE (EC 4.1.3.7)
547		548	RXA02621	GR00746	2647		1829		CITRATE LYASE BETA CHAIN (EC 4.1.3.6)
549		550	RXN00519	VV0144	5585		3372		ISOCITRATE DEHYDROGENASE (NADP) (EC 1.1.1.42)
551		552	F RXA00521	GR00133	2		1060		ISOCITRATE DEHYDROGENASE [NADP] (EC 1.1.1.42)
553		554	RXN02209	VV0304	1		1671		ACONITATE HYDRATASE (EC 4.2.1.3)
555		556	F RXA02209	GR00648	3		1661		ACONITATE HYDRATASE (EC 4.2.1.3)
557		558	RXN02213	VV0305	1378		2151		ACONITATE HYDRATASE (EC 4.2.1.3)
559		560	F RXA02213	GR00649	1330		2046		ACONITATE HYDRATASE (EC 4.2.1.3)
561		562	RXA02056	GR00625	3		2870		2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.2)
563		564	RXA01745	GR00495	2		1495		DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
565		566	RXA00782	GR00206	3984		3103		SUCCINYL-COA SYNTHETASE ALPHA CHAIN (EC 6.2.1.5)
567		568	RXA00783	GR00206	5280		4009		SUCCINYL-COA SYNTHETASE BETA CHAIN (EC 6.2.1.5)
569		570	RXN01695	VV0139	11307		12806		L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16)
571		572	F RXA01615	GR00449	8608		9546		L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16)
573		574	F RXA01695	GR00474	4388		4179		L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16)
575		576	RXA00290	GR00046	4693		5655		MALIC ENZYME (EC 1.1.1.39)
577		578	RXN01048	VV0079	12539		11316		MALIC ENZYME (EC 1.1.1.39)
579		580	F RXA01048	GR00296	3		290		MALIC ENZYME (EC 1.1.1.39)
581		582	F RXA00290	GR00046	4693		5655		MALIC ENZYME (EC 1.1.1.39)
583		584	RXN03101	VV0066	2		583		DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
585		586	RXN02046	VV0025	15056		14640		DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
587		588	RXN00389	VV0025	11481		9922		oxoglutarate semialdehyde dehydrogenase (EC 1.2.1.-)

Table 1 (continued)

Glyoxylate bypass

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
589	590	RXN02399	VV0176	19708	18365	ISOCITRATE LYASE (EC 4.1.3.1)
591	592	F RXA02399	GR00699	478	1773	ISOCITRATE LYASE (EC 4.1.3.1)
593	594	RXN02404	VV0176	20259	22475	MALATE SYNTHASE (EC 4.1.3.2)
595	596	F RXA02404	GR00700	3798	1663	MALATE SYNTHASE (EC 4.1.3.2)
597	598	RXA01089	GR00304	3209	3958	GLYOXYLATE-INDUCED PROTEIN
599	600	RXA01886	GR00539	3203	2430	GLYOXYLATE-INDUCED PROTEIN

Methylcitrate-pathway

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
600	602	RXN03117	VV0092	3087	1576	2-methylisocitrate synthase (EC 5.3.3.-)
601	604	F RXA00406	GR00090	978	4	2-methylisocitrate synthase (EC 5.3.3.-)
603	606	F RXA00514	GR00130	1983	1576	2-methylisocitrate synthase (EC 5.3.3.-)
605	608	RXA00512	GR00130	621	4	2-methylcitrate synthase (EC 4.1.3.31)
607	610	RXA00518	GR00131	3069	2773	2-methylcitrate synthase (EC 4.1.3.31)
609	612	RXA01077	GR00300	4647	6017	2-methylisocitrate synthase (EC 5.3.3.-)
611	614	RXN03144	VV0141	2	901	2-methylisocitrate synthase (EC 5.3.3.-)
613	616	F RXA02322	GR00668	415	5	2-methylisocitrate synthase (EC 5.3.3.-)
615	618	RXA02329	GR00669	607	5	2-methylisocitrate synthase (EC 5.3.3.-)
617	620	RXA02332	GR00671	1906	764	2-methylisocitrate synthase (EC 5.3.3.-)
619	622	RXN02333	VV0141	901	1815	2-methylcitrate synthase (EC 4.1.3.31)
621	624	F RXA02333	GR00671	2120	1902	methylisocitrate lyase (EC 4.1.3.30)
623	626	RXA00030	GR00003	9590	9979	methylisocitrate lyase (EC 4.1.3.30) LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5)

Methyl-Malonyl-CoA-Mutases

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
625	628	RXN00148	VV0167	9849	12059	METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT (EC 5.4.99.2)
627	630	F RXA00148	GR00023	2002	5	METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT (EC 5.4.99.2)
629	632	RXA00149	GR00023	3856	2009	METHYLMALONYL-COA MUTASE BETA-SUBUNIT (EC 5.4.99.2)

Table 1 (continued)

Others

Nucleic Acid		Amino Acid	Identification Code	Contig.	NT Start	NT Stop	Function
SEQ ID NO							
631		634	RXN00317	VV0197	26879	27532	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)
635		636	F RXA00317	GR00055	344	6	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)
637		638	RXA02196	GR00645	3956	3264	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)
639		640	RXN02461	VV0124	14236	14643	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)

Redox Chain

Nucleic Acid		Amino Acid	Identification Code	Contig.	NT Start	NT Stop	Function
SEQ ID NO							
641		642	RXN01744	VV0174	2350	812	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-)
643		644	F RXA00055	GR00008	11753	11890	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-)
645		646	F RXA01744	GR00494	2113	812	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-)
647		648	RXA00379	GR00082	212	6	CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCDA
649		650	RXA00385	GR00083	773	435	CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCDA
651		652	RXA01743	GR00494	806	6	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT II (EC 1.10.3.-)
653		654	RXN02480	VV0084	31222	29567	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
655		656	F RXA01919	GR00550	288	4	CYTOCHROME C OXIDASE SUBUNIT I (EC 1.9.3.1)
657		658	F RXA02480	GR00717	1449	601	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
659		660	F RXA02481	GR00717	1945	1334	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
661		662	RXA02140	GR00639	7339	8415	CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1)
663		664	RXA02142	GR00639	9413	10063	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
665		666	RXA02144	GR00639	11025	12248	RIESKE IRON-SULFUR PROTEIN
667		668	RXA02740	GR00763	7613	8542	PROBABLE CYTOCHROME C OXIDASE ASSEMBLY FACTOR
669		670	RXA02743	GR00763	13534	12497	CYTOCHROME AA3 CONTROLLING PROTEIN
671		672	RXA01227	GR00355	1199	1519	FERREDOXIN
673		674	RXA01865	GR00532	436	122	FERREDOXIN
675		676	RXA00680	GR00179	2632	2315	FERREDOXIN VI
677		678	RXA00679	GR00179	2302	1037	FERREDOXIN--NAD(+) REDUCTASE (EC 1.18.1.3)
679		680	RXA00224	GR00032	24965	24015	ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT
681		682	RXA00225	GR00032	25783	24998	ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT
683		684	RXN00606	VV0192	11299	9026	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)
685		686	F RXA00606	GR00160	121	1869	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)
687		688	RXN00595	VV0192	8642	7113	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
689		690	F RXA00608	GR00160	2253	3017	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
691		692	RXA00913	GR00249	3	2120	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)
693		694	RXA00909	GR00247	2552	3406	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)
695		696	RXA00700	GR00182	846	43	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2
697		698	RXN00483	VV0086	44824	46287	NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
699	700	F RXA00483	GR00119	19106	20569	NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3)
701	702	RXA01534	GR00427	1035	547	NADH-DEPENDENT FMN OXYDOREDUCTASE
703	704	RXA00288	GR00046	2646	1636	QUINONE OXIDOREDUCTASE (EC 1.6.5.5)
705	706	RXA02741	GR00763	9585	8620	QUINONE OXIDOREDUCTASE (EC 1.6.5.5)
707	708	RXN02560	VV0101	9922	10788	NADPH-FLAVIN OXIDOREDUCTASE (EC 1.6.99.-)
709	710	F RXA02560	GR00731	6339	7160	NADPH-FLAVIN OXIDOREDUCTASE (EC 1.6.99.-)
711	712	RXA01311	GR00380	1611	865	SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN (EC 1.3.99.1)
713	714	RXN03014	VV0058	1273	368	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
715	716	F RXA00910	GR00248	3	1259	Hydrogenase subunits
717	718	RXN01895	VV0117	955	5	NADH DEHYDROGENASE (EC 1.6.99.3)
719	720	F RXA01895	GR00543	2	817	DEHYDROGENASE
721	722	RXA00703	GR00183	2556	271	FORMATE DEHYDROGENASE ALPHA CHAIN (EC 1.2.1.2)
723	724	RXN00705	VV0005	6111	5197	FDHD PROTEIN
725	726	F RXA00705	GR00184	1291	407	FDHD PROTEIN
727	728	RXN00388	VV0025	2081	3091	CYTOCHROME C BIOGENESIS PROTEIN CCSA
729	730	F RXA00388	GR00085	969	667	essential protein similar to cytochrome c
731	732	F RXA00386	GR00084	514	5	RESC PROTEIN, essential protein similar to cytochrome c biogenesis protein
733	734	RXA00945	GR00259	1876	2847	putative cytochrome oxidase
735	736	RXN02556	VV0101	5602	6759	FLAVOHEMOPROTEIN / DIHYDROPTERIDINE REDUCTASE (EC 1.6.99.7)
737	738	F RXA02556	GR00731	2019	3176	FLAVOHEMOPROTEIN
739	740	RXA01392	GR00408	2297	3373	GLUTATHIONE S-TRANSFERASE (EC 2.5.1.18)
741	742	RXA00800	GR00214	2031	3134	GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (EC 1.2.1.1)
743	744	RXA02143	GR00639	10138	11025	QCRC PROTEIN, menaquinol:cytochrome c oxidoreductase
745	746	RXN03096	VV0058	405	4	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
747	748	RXN02036	VV0176	32683	33063	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3)
749	750	RXN02765	VV0317	3552	2794	Hypothetical Oxidoreductase
751	752	RXN02206	VV0302	1784	849	Hypothetical Oxidoreductase
753	754	RXN02554	VV0101	4633	4010	Hypothetical Oxidoreductase (EC 1.1.1.-)

ATP-Synthase

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
755	756	RXN01204	VV0121	1270	461	ATP SYNTHASE A CHAIN (EC 3.6.1.34)
757	758	F RXA01204	GR00345	394	1155	ATP SYNTHASE A CHAIN (EC 3.6.1.34)
759	760	RXA01201	GR00344	675	2315	ATP SYNTHASE ALPHA CHAIN (EC 3.6.1.34)
761	762	RXN01193	VV0175	5280	3832	ATP SYNTHASE BETA CHAIN (EC 3.6.1.34)
763	764	F RXA01193	GR00343	15	755	ATP SYNTHASE BETA CHAIN (EC 3.6.1.34)
765	766	F RXA01203	GR00344	3355	3993	ATP SYNTHASE BETA CHAIN (EC 3.6.1.34)

Table 1 (continued)

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>		<u>NT Stop</u>		<u>Function</u>
767	768	RXN02821	VV0121	324		85		ATP SYNTHASE C CHAIN (EC 3.6.1.34)
769	770	F RXA02821	GR00802	139		318		ATP SYNTHASE C CHAIN (EC 3.6.1.34)
771	772	RXA01200	GR00344	2		610		ATP SYNTHASE DELTA CHAIN (EC 3.6.1.34)
773	774	RXA01194	GR00343	770		1141		ATP SYNTHASE EPSILON CHAIN (EC 3.6.1.34)
775	776	RXA01202	GR00344	2375		3349		ATP SYNTHASE GAMMA CHAIN (EC 3.6.1.34)
777	778	RXN02434	VV0090	4923		3274		ATP-BINDING PROTEIN

Cytochrome metabolism

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>		<u>NT Stop</u>		<u>Function</u>
779	780	RXN00684	VV0005	29864		28581		CYTOCHROME P450 116 (EC 1.14.-.-)
781	782	RXN00387	VV0025	1150		2004		Hypothetical Cytochrome c Biogenesis Protein

TABLE 2 – Excluded Genes

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvat carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	ftsR		Kimura, E. et al. "Molecular cloning of a novel gene, ftsR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	ftsR1; ftsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkf	transketolase	
AB024708	gltB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenylyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	
AF036932	aroD	3-dehydroquinate dehydratase	
AF038548	pyc	Pyruvate carboxylase	

Table 2 (continued)

	dcfAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF038651			
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamy/phosphate reductase; ornithine acetyltransferase; N- acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1- phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinase synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP- pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," <i>Appl. Environ. Microbiol.</i> , 65(4):1530- 1539 (1999)
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3- dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		

Table 2 (continued)

AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete')	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> ; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol acetyl transferase	
AJ224946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from <i>Corynebacterium glutamicum</i> ," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> : The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the <i>Corynebacterium glutamicum</i> (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87

Table 2 (continued)

E01377	Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937	Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040	Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041	Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307	Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376	Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377	Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484	Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108	Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112	Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93
E05776	Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779	Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110	Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111	Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146	Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825	Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826	Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94

Table 2 (continued)

		Mutated aspartokinase alpha subunit	
E06827			Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membrane protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08649		Aspartase	Kohama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97

Table 2 (continued)

		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
E13655			
L01508	IlvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	IlvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxR	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 56 rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)

Table 2 (continued)

M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of <i>Corynebacterium glutamicum</i> ATCC13032." <i>Gene</i> , 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M89931	aecD; brnQ; yhbW	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbW	Rossol, I. et al. "The <i>Corynebacterium glutamicum</i> aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in <i>Corynebacterium glutamicum</i> ATCC 13032 is directed by the brnQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> : identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthranilate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the <i>Corynebacterium glutamicum</i> ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cglIM; cglIR; cglIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from <i>Corynebacterium glutamicum</i> ATCC 13032 and analysis of its role in intergeneric conjugation with <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The <i>Corynebacterium glutamicum</i> cglIM gene encoding a 5-cytosine in an McrBC-deficient <i>Escherichia coli</i> strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?; gamma glutamyl kinase; similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

Table 2 (continued)

U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thtR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5'-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-biphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i>
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of lambda dacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the <i>Corynebacterium glutamicum</i> lysA gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990)

Table 2 (continued)

X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component 1	Heery, D.M. et al. "Nucleotide sequence of the Corynebacterium glutamicum trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the Corynebacterium glutamicum threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum, and the attP site of lambda dacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a Corynebacterium glutamicum gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the Corynebacterium glutamicum gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the Corynebacterium glutamicum lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)
X66078	copI	PsI protein	Joliff, G. et al. "Cloning and nucleotide sequence of the cspI gene encoding PS1, one of the two major secreted proteins of Corynebacterium glutamicum: The deduced N-terminal region of PS1 is similar to the Mycobacterium antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a Corynebacterium glutamicum IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)

Table 2 (continued)

X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in <i>Corynebacterium glutamicum</i> : enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the <i>Corynebacterium glutamicum</i> icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mtrA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of <i>Corynebacterium glutamicum</i> and <i>Brevibacterium lactofermentum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from <i>Corynebacterium glutamicum</i> and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Norcardia</i> and evidence for the evolutionary origin of the genus <i>Norcardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X81379	dapE	Succinylidiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-56 (1994)

Table 2 (continued)

	16S rDNA	16S ribosomal RNA	
X82061			Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann et al. "Functional analysis of sequences adjacent to dapE of <i>C. glutamicum</i> proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in <i>Corynebacterium glutamicum</i> : enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting 'Arthrobacter aureus C70,' <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

Table 2 (continued)

X90360		Promoter fragment F22	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from C. glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of Corynebacterium glutamicum," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the Corynebacterium glutamicum betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of Corynebacterium glutamicum, encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	lysE; lysG	Lysine exporter protein; Lysine export regulator protein	Vrljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)

Table 2 (continued)

X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicumproline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynephage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)

Table 2 (continued)

Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of <i>Corynebacterium glutamicum</i> glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site Corynebacterium 304L	Moreau, S. et al. "Analysis of the integration functions of φ304L: An integrase module among corynebacteriophages," <i>Virology</i> , 255(1):150-159 (1999)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in <i>Brevibacterium lactofermentum</i> : Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of <i>Brevibacterium lactofermentum</i> encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al "The galE gene encoding the UDP-galactose 4-epimerase of <i>Brevibacterium lactofermentum</i> is coupled transcriptionally to the dmdR gene," <i>Gene</i> , 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of <i>Brevibacterium lactofermentum</i> ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996)
A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.			

TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	ammoniagenes	21054							
Brevibacterium	ammoniagenes	19350							
Brevibacterium	ammoniagenes	19351							
Brevibacterium	ammoniagenes	19352							
Brevibacterium	ammoniagenes	19353							
Brevibacterium	ammoniagenes	19354							
Brevibacterium	ammoniagenes	19355							
Brevibacterium	ammoniagenes	19356							
Brevibacterium	ammoniagenes	21055							
Brevibacterium	ammoniagenes	21077							
Brevibacterium	ammoniagenes	21553							
Brevibacterium	ammoniagenes	21580							
Brevibacterium	ammoniagenes	39101							
Brevibacterium	butanicum	21196							
Brevibacterium	divaricatum	21792	P928						
Brevibacterium	flavum	21474							
Brevibacterium	flavum	21129							
Brevibacterium	flavum	21518							
Brevibacterium	flavum			B11474					
Brevibacterium	flavum			B11472					
Brevibacterium	flavum	21127							
Brevibacterium	flavum	21128							
Brevibacterium	flavum	21427							
Brevibacterium	flavum	21475							
Brevibacterium	flavum	21517							
Brevibacterium	flavum	21528							
Brevibacterium	flavum	21529							
Brevibacterium	flavum			B11477					
Brevibacterium	flavum			B11478					
Brevibacterium	flavum	21127							
Brevibacterium	flavum			B11474					
Brevibacterium	healii	15527							
Brevibacterium	ketoglutamicum	21004							
Brevibacterium	ketoglutamicum	21089							
Brevibacterium	ketosoreductum	21914							
Brevibacterium	lactofermentum				70				
Brevibacterium	lactofermentum				74				
Brevibacterium	lactofermentum				77				
Brevibacterium	lactofermentum	21798							
Brevibacterium	lactofermentum	21799							
Brevibacterium	lactofermentum	21800							
Brevibacterium	lactofermentum	21801							
Brevibacterium	lactofermentum			B11470					
Brevibacterium	lactofermentum			B11471					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							
Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujiokense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							
Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							
Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saimata, Japan.

Table 4: Alignment Results

ID #	length (NT)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rx00013	996	GB_GSS4:AQ713475	581	AQ713475	HS_5402_B2_A12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=978 Col=24 Row=B, genomic survey sequence.	Homo sapiens	37,148	13-Jul-99
		GB_HTG3:AC007420	130583	AC007420	Drosophila melanogaster chromosome 2 clone BACR07M10 (D630) RPCI-98 07.M.10 map 24A-24D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 83 unordered pieces.	Drosophila melanogaster	34,568	20-Sep-99
		GB_HTG3:AC007420	130583	AC007420	Drosophila melanogaster chromosome 2 clone BACR07M10 (D630) RPCI-98 07.M.10 map 24A-24D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 83 unordered pieces.	Drosophila melanogaster	34,568	20-Sep-99
rx00014	903	GB_BA1:MTCY3A2	25830	Z83867	Mycobacterium tuberculosis H37Rv complete genome; segment 136/162.	Mycobacterium tuberculosis	58,140	17-Jun-98
		GB_BA1:MLCB1779	43254	Z98271	Mycobacterium leprae cosmid B1779.	Mycobacterium leprae	57,589	8-Aug-97
		GB_BA1:SAPURCLUS	9120	X92429	S.alboniger napH, pur7, pur10, pur6, pur4, pur5 and pur3 genes.	Streptomyces anulatus	55,667	28-Feb-96
rx00030	513	GB_EST21:C89713	767	C89713	C89713 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSG229, mRNA sequence.	Dictyostelium discoideum	45,283	20-Apr-98
		GB_EST28:AI497294	484	AI497294	fb63g03.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to SW:AFP4_MYOOC P80961 ANTIFREEZE PROTEIN LS-12. ; mRNA sequence.	Danio rerio	42,991	11-MAR-1999
		GB_EST21:C92167	637	C92167	C92167 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSD179, mRNA sequence.	Dictyostelium discoideum	44,444	12-Jul-99
rx00032	1632	GB_BA2:AF010496	189370	AF010496	Rhodobacter capsulatus strain SB1003, partial genome.	Rhodobacter capsulatus	39,689	12-MAY-1998
		GB_BA2:AF018073	9810	AF018073	Rhodobacter sphaeroides operon regulator (smoC), periplasmic sorbitol-binding protein (smoE), sorbitol/mannitol transport inner membrane protein (smoF), sorbitol/mannitol transport inner membrane protein (smoG), sorbitol/mannitol transport ATP-binding transport protein (smoK), sorbitol dehydrogenase (smoS), mannitol dehydrogenase (mtlK), and periplasmic mannitol-binding protein (smoM) genes, complete cds.	Rhodobacter sphaeroides	48,045	22-OCT-1997
		GB_BA2:AF045245	5930	AF045245	Klebsiella pneumoniae D-arabinitol transporter (dalT), D-arabinitol kinase (dalK), D-arabinitol dehydrogenase (dalD), and repressor (dalR) genes, complete cds.	Klebsiella pneumoniae	38,514	16-Jul-98
rx00041	1342	EM_PAT:E11760	6911	E11760	Base sequence of sucrase gene.	Corynebacterium glutamicum	99,031	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	99,031	07-OCT-1996
		GB_IN1:LMFL5883	31934	AL117384	Leishmania major Friedlin chromosome 23 cosmid L5883, complete sequence.	Leishmania major	43,663	21-OCT-1999
rx00042	882	EM_PAT:E11760	6911	E11760	Base sequence of sucrase gene.	Corynebacterium glutamicum	94,767	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	94,767	07-OCT-1996

Table 4 (continued)

rxa00043	1287	GB_IN1:CEU33051	4899	U33051	Caenorhabditis elegans sur-2 mRNA, complete cds.	40,276	23-Jan-96
		GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	97,591	07-OCT-1996
		EM_PAT:E11760	6911	E11760	Base sequence of sucrose gene.	97,591	08-OCT-1997 (Rel. 52, Created)
rxa00098	1743	GB_PR3:AC005174	39769	AC005174	Homo sapiens clone UWGC:g1564a012 from 7p14-15, complete sequence.	35,879	24-Jun-98
		GB_BA1:MSU88433	1928	U88433	Mycobacterium smegmatis phosphoglucose isomerase gene, complete cds.	62,658	19-Apr-97
rxa00148	2334	GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	37,638	27-Jul-98
		GB_BA1:MTCY10D7	39800	Z79700	Mycobacterium tuberculosis H37Rv complete genome; segment 44/162.	36,784	17-Jun-98
rxa00148	2334	GB_BA1:MTCY277	38300	Z79701	Mycobacterium tuberculosis H37Rv complete genome; segment 65/162.	67,457	17-Jun-98
		GB_BA1:MSGY456	37316	AD000001	Mycobacterium tuberculosis sequence from clone y456.	40,883	03-DEC-1996
rxa00149	1971	GB_BA1:MSGY175	18106	AD000015	Mycobacterium tuberculosis sequence from clone y175.	67,457	10-DEC-1996
		GB_BA1:MSGY456	37316	AD000001	Mycobacterium tuberculosis sequence from clone y456.	35,883	03-DEC-1996
		GB_BA1:MSGY175	18106	AD000015	Mycobacterium tuberculosis sequence from clone y175.	51,001	10-DEC-1996
rxa00195	684	GB_BA1:MTCY277	38300	Z79701	Mycobacterium tuberculosis H37Rv complete genome; segment 65/162.	51,001	17-Jun-98
		GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	35,735	19-Jun-98
rxa00196	738	GB_BA1:MSGB1529CS	36985	L78824	Mycobacterium leprae cosmid B1529 DNA sequence.	57,014	15-Jun-96
		GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	41,892	19-Jun-98
rxa00196	738	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	41,841	19-Jun-98
		GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	36,599	19-Jun-98
rxa00202	1065	GB_RO:RATCBRQ	10752	M55532	Rat carbohydrate binding receptor gene, complete cds.	36,212	27-Apr-93
		GB_EST11:AA253618	313	AA253618	mw95c10.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:678450 5', Mus musculus mRNA sequence.	38,816	13-MAR-1997
		GB_EST26:AI390284	490	AI390284	mw96a03.y1 Soares mouse NML Mus musculus cDNA clone IMAGE:678508 5' Mus musculus similar to TR:O09171 O09171 BETAIN-HOMOCYSTEINE METHYLTRANSFERASE,, mRNA sequence.	42,239	2-Feb-99
rxa00206	1161	GB_EST26:AI390280	467	AI390280	mw95c10.y1 Soares mouse NML Mus musculus cDNA clone IMAGE:678450 5', mRNA sequence.	37,307	2-Feb-99
		GB_BA1:MLCB637	44882	Z99263	Mycobacterium leprae cosmid B637.	58,312	17-Sep-97
		GB_BA1:MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	36,632	23-Jun-99

Table 4 (continued)

	GB_BA1:SC6E10	23990	AL109661	Streptomyces coelicolor cosmid 6E10.	Streptomyces coelicolor A3(2)	38,616	5-Aug-99
rx00224	GB_BA1:BJU32230	1769	U32230	Bradyrhizobium japonicum electron transfer flavoprotein small subunit (etfS) nd large subunit (etfL) genes, complete cds.	Bradyrhizobium japonicum	48,038	25-MAY-1996
	GB_BA1:PDEETFAB	2440	L14864	Paracoccus denitrificans electron transfer flavoprotein alpha and beta subunit genes, complete cds's.	Paracoccus denitrificans	48,351	27-OCT-1993
	GB_HTG3:AC009689	177954	AC009689	Homo sapiens chromosome 4 clone 104_F_7 map 4, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	38,756	28-Aug-99
rx00225	GB_RO:AF060178	2057	AF060178	Mus musculus heparan sulfate 2-sulfotransferase (Hs2st) mRNA, complete cds.	Mus musculus	39,506	18-Jun-98
	GB_GSS11:AQ325043	734	AQ325043	mgxb0020J01r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0020J01r, genomic survey sequence.	Magnaporthe grisea	38,333	8-Jan-99
	GB_EST31:A1676413	551	A1676413	etmEST0167 EtH1 Eimeria tenella cDNA clone etmc074 5', mRNA sequence.	Eimeria tenella	35,542	19-MAY-1999
rx00235	GB_BA1:MTCY10G2	38970	Z92539	Mycobacterium tuberculosis H37Rv complete genome; segment 47/162.	Mycobacterium tuberculosis	65,759	17-Jun-98
	GB_BA2:AF061753	3721	AF061753	Nitrosomonas europaea CTP synthase (pyrG) gene, partial cds; and enolase (eno) gene, complete cds.	Nitrosomonas europaea	58,941	31-Aug-98
	GB_BA2:AF086791	37867	AF086791	Zymomonas mobilis strain ZM4 clone 67E10 carbamoylphosphate synthetase small subunit (carA), carbamoylphosphate synthetase large subunit (carB), transcription elongation factor (greA), enolase (eno), pyruvate dehydrogenase alpha subunit (pdhA), pyruvate dehydrogenase beta subunit (pdhB), ribonuclease H (rnh), homoserine kinase homolog, alcohol dehydrogenase II (adhB), and excinuclease ABC subunit A (uvrA) genes, complete cds; and unknown genes.	Zymomonas mobilis	61,239	4-Nov-98
rx00246	GB_BA2:AF012550	2690	AF012550	Acinetobacter sp. BD413 ComP (comp) gene, complete cds.	Acinetobacter sp. BD413	53,726	27-Sep-99
	GB_PAT:E03856	1506	E03856	gDNA encoding alcohol dehydrogenase.	Bacillus stearothermophilus	51,688	29-Sep-97
	GB_BA1:BACADHT	1688	D90421	B.stearothermophilus adhT gene for alcohol dehydrogenase.	Bacillus stearothermophilus	51,602	7-Feb-99
rx00251	GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	42,875	17-Jun-98
	GB_BA1:MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162.	Mycobacterium tuberculosis	40,380	18-Jun-98
	GB_BA1:MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162.	Mycobacterium tuberculosis	41,789	18-Jun-98
rx00288	GB_BA2:AF050114	1038	AF050114	Pseudomonas sp. W7 alginate lyase gene, complete cds.	Pseudomonas sp. W7	49,898	03-MAR-1999
	GB_GSS3:B16984	469	B16984	344A14.TVC CIT978SKA1 Homo sapiens genomic clone A-344A14, genomic survey sequence.	Homo sapiens	39,355	4-Jun-98
	GB_IN2:AF144549	7887	AF144549	Aedes albopictus ribosomal protein L34 (rpl34) gene, complete cds.	Aedes albopictus	36,509	3-Jun-99
rx00293	GB_EST1:T28483	313	T28483	EST46182 Human Kidney Homo sapiens cDNA 3' end similar to flavin-containing monooxygenase 1 (HT:1956), mRNA sequence.	Homo sapiens	42,997	6-Sep-95

Table 4 (continued)

rxa00296	2967	GB_PR1:HUMFMO1 GB_EST32:AI734238	2134 512	M64082 AI734238	Human flavin-containing monooxygenase (FMO1) mRNA, complete cds. zb73c05.y5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:309224 5' similar to gb:M64082 DIMETHYLANILINE MONOOXYGENASE (HUMAN);, mRNA sequence.	Homo sapiens Homo sapiens	37,915 41,502	8-Nov-94 14-Jun-99
		GB_HTG6:AC011069	168266	AC011069	Drosophila melanogaster chromosome X clone BACR11H20 (D881) RPCI-98 11.H.20 map 12B-12C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 92 unordered pieces.	Drosophila melanogaster	33,890	02-DEC-1999
		GB_EST15:AA531468	414	AA531468	nj63d12.s1 NCI_CGAP_Pr10 Homo sapiens cDNA clone IMAGE:997175, mRNA sequence.	Homo sapiens	40,821	20-Aug-97
		GB_HTG6:AC011069	168266	AC011069	Drosophila melanogaster chromosome X clone BACR11H20 (D881) RPCI-98 11.H.20 map 12B-12C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 92 unordered pieces.	Drosophila melanogaster	30,963	02-DEC-1999
rxa00310	558	GB_VI:VMVY16780 GB_VI:VARCG GB_VI:VWCGAA	186986 186103 185578	Y16780 L22579 X69198	variola minor virus complete genome. Variola major virus (strain Bangladesh-1975) complete genome. Variola virus DNA complete genome.	variola minor virus Variola major virus Variola virus	35,883 34,664 36,000	2-Sep-99 12-Jan-95 13-DEC-1996
rxa00317	777	GB_HTG3:AC009571	159648	AC009571	Homo sapiens chromosome 4 clone 57_A_22 map 4, *** SEQUENCING IN PROGRESS *** , 8 unordered pieces.	Homo sapiens	36,988	29-Sep-99
		GB_HTG3:AC009571	159648	AC009571	Homo sapiens chromosome 4 clone 57_A_22 map 4, *** SEQUENCING IN PROGRESS *** , 8 unordered pieces.	Homo sapiens	36,988	29-Sep-99
rxa00327	507	GB_PR3:AC005697 GB_BA1:LCATPASEB GB_BA1:LCATPASEB	174503 1514 1514	AC005697 X64542 X64542	Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence. L.casei gene for ATPase beta-subunit. L.casei gene for ATPase beta-subunit.	Homo sapiens Lactobacillus casei Lactobacillus casei	36,340 34,664 39,308	09-OCT-1998 11-DEC-1992 11-DEC-1992
rxa00328	615	GB_BA1:STYPUTPE	1887	L01138	Salmonella (S2980) proline permease (putP) gene, 5' end.	Salmonella sp.	39,623	09-MAY-1996
		GB_BA1:STYPUTPF	1887	L01139	Salmonella (S2983) proline permease (putP) gene, 5' end.	Salmonella sp.	39,623	09-MAY-1996
		GB_BA1:STYPUTPI	1889	L01142	Salmonella (S3015) proline permease (putP) gene, 5' end.	Salmonella sp.	42,906	09-MAY-1996
rxa00329	1347	GB_PR3:AC004691	141990	AC004691	Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.	Homo sapiens	38,142	16-MAY-1998
		GB_PR4:AC004916 GB_PR3:AC004691	129014 141990	AC004916 AC004691	Homo sapiens clone DJ0891L14, complete sequence. Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.	Homo sapiens Homo sapiens	38,549 35,865	17-Jul-99 16-MAY-1998
rxa00340	1269	GB_BA1:MTCY427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mycobacterium tuberculosis	38,940	24-Jun-99
		GB_GSS12:AQ412290	238	AQ412290	RPCI-11-195H2.TV RPCI-11 Homo sapiens genomic clone RPCI-11-195H2, genomic survey sequence.	Homo sapiens	36,555	23-MAR-1999
rxa00379	307	GB_PL2:AF112871 GB_HTG1:CEY56A3	2394 224746	AF112871 AL022280	Astasia longa small subunit ribosomal RNA gene, complete sequence. Caenorhabditis elegans chromosome III clone Y56A3, *** SEQUENCING IN PROGRESS *** , in unordered pieces.	Astasia longa Caenorhabditis elegans	36,465 35,179	28-Jun-99 6-Sep-99
		GB_HTG1:CEY56A3	224746	AL022280	Caenorhabditis elegans chromosome III clone Y56A3, *** SEQUENCING IN PROGRESS *** , in unordered pieces.	Caenorhabditis elegans	35,179	6-Sep-99

Table 4 (continued)

	GB_PR2:HS134O19	86897	AL034555	Human DNA sequence from clone 134O19 on chromosome 1p36.11-36.33, complete sequence.	Homo sapiens	40,604	23-Nov-99
rx00381 729	GB_GSS4:AQ730532	416	AQ730532	HS_2149_A1_C06_T7C CIT Approved Human Genomic Sperm Library D	Homo sapiens	35,766	15-Jul-99
				Homo sapiens genomic clone Plate=2149 Col=11 Row=E, genomic survey sequence.			
	GB_EST23:AI120939	561	AI120939	ub74f05.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone IMAGE:1383489 5' similar to gb:J04046 CALMODULIN (HUMAN); gb:M19381	Mus musculus	41,113	2-Sep-98
	GB_EST23:AI120939	561	AI120939	Mouse calmodulin (MOUSE);, mRNA sequence.			
	GB_EST23:AI120939	561	AI120939	ub74f05.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone IMAGE:1383489 5' similar to gb:J04046 CALMODULIN (HUMAN); gb:M19381	Mus musculus	41,113	2-Sep-98
	GB_EST32:AI726450	565	AI726450	Mouse calmodulin (MOUSE);, mRNA sequence.			
rx00385 362	GB_EST32:AI726450	565	AI726450	BNLGH15857 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AF015913) Skb1Hs [Homo sapiens], mRNA sequence.	Gossypium hirsutum	41,152	11-Jun-99
	GB_GSS4:AQ740856	768	AQ740856	HS_2274_A2_A07_T7C CIT Approved Human Genomic Sperm Library D	Homo sapiens	41,360	16-Jul-99
				Homo sapiens genomic clone Plate=2274 Col=14 Row=A, genomic survey sequence.			
	GB_PR1:HSPAIP	1587	X91809	H.sapiens mRNA for GAIP protein.	Homo sapiens	36,792	29-MAR-1996
rx00388 1134	GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	51,852	17-Jun-98
	GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	51,852	03-DEC-1996
	GB_HTG1:AP000471	72466	AP000471	Homo sapiens chromosome 21 clone B2308H15 map 21q22.3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,875	13-Sep-99
rx00427 909	GB_BA1:MSGY126	37164	AD000012	Mycobacterium tuberculosis sequence from clone y126.	Mycobacterium tuberculosis	60,022	10-DEC-1996
	GB_BA1:MTY13D12	37085	Z80343	Mycobacterium tuberculosis H37Rv complete genome; segment 156/162.	Mycobacterium tuberculosis	60,022	17-Jun-98
	GB_HTG1:CEY48C3	270193	Z92855	Caenorhabditis elegans chromosome II clone Y48C3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	28,013	29-MAY-1999
rx00483 1587	GB_PR2:HSAF001550	173882	AF001550	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.	Homo sapiens	38,226	22-Aug-97
	GB_BA1:LLCPJW565	12828	Y12736	Lactococcus lactis cremoris plasmid pJW565 DNA, abiiM, abiiR genes and orfX.	Lactococcus lactis subsp. cremoris	37,492	01-MAR-1999
	GB_HTG2:AC006754	206217	AC006754	Caenorhabditis elegans clone Y40B10, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.	Caenorhabditis elegans	36,648	23-Feb-99
rx00511 615	GB_PR3:HSE127C11	38423	Z74581	Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS.	Homo sapiens	39,831	23-Nov-99
	GB_PR3:HSE127C11	38423	Z74581	Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS.	Homo sapiens	36,409	23-Nov-99
rx00512 718	GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	56,232	17-Jun-98

Table 4 (continued)

	GB_BA1:MSGLTA	1776	X60513	M.smegmatis gltA gene for citrate synthase.	Mycobacterium smegmatis	56,143	20-Sep-91
rxa00517 1164	GB_BA2:ECU73857	128824	U73857	Escherichia coli chromosome minutes 6-8.	Escherichia coli	48,563	14-Jul-99
	GB_HTG2:AC006911	298804	AC006911	Caenorhabditis elegans clone Y94H6x, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Caenorhabditis elegans	37,889	24-Feb-99
	GB_HTG2:AC006911	298804	AC006911	Caenorhabditis elegans clone Y94H6x, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Caenorhabditis elegans	37,889	24-Feb-99
rxa00518 320	GB_EST29:AI602158	481	AI602158	UI-R-AB0-vy-a-01-0-UI.s2 UI-R-AB0 Rattus norvegicus cDNA clone UI-R-AB0- vy-a-01-0-UI 3', mRNA sequence.	Rattus norvegicus	40,833	21-Apr-99
	GB_BA2:ECU73857	128824	U73857	Escherichia coli chromosome minutes 6-8.	Escherichia coli	49,688	14-Jul-99
	GB_BA2:STU51879	8371	U51879	Salmonella typhimurium propionate catabolism operon: RpoN activator protein homolog (prpR), carboxyphosphoenolpyruvate phosphonmutase homolog (prpB), citrate synthase homolog (prpC), prpD and prpE genes, complete cds.	Salmonella typhimurium	50,313	5-Aug-99
rxa00606 2378	GB_BA2:AE000140	12498	AE000140	Escherichia coli K-12 MG1655 section 30 of 400 of the complete genome.	Escherichia coli	49,688	12-Nov-98
	GB_EST32:AU068253	376	AU068253	AU068253 Rice callus Oryza sativa cDNA clone C12658_9A, mRNA sequence.	Oryza sativa	41,333	7-Jun-99
	GB_EST13:AA363046	329	AA363046	EST72922 Ovary II Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	34,347	21-Apr-97
rxa00635 1860	GB_EST32:AU068253	376	AU068253	AU068253 Rice callus Oryza sativa cDNA clone C12658_9A, mRNA sequence.	Oryza sativa	41,899	7-Jun-99
	GB_BA1:PAORF1	1440	X13378	Pseudomonas amylocleramosa DNA for ORF 1.	Pseudomonas amylocleramosa	53,912	14-Jul-95
	GB_BA1:PAORF1	1440	X13378	Pseudomonas amylocleramosa DNA for ORF 1.	Pseudomonas amylocleramosa	54,422	14-Jul-95
rxa00679 1389	GB_PL2:AC010871	80381	AC010871	Arabidopsis thaliana chromosome III BAC T16O11 genomic sequence, complete sequence.	Arabidopsis thaliana	38,244	13-Nov-99
	GB_PL1:AT81KBGEN	81493	X98130	A.thaliana 81kb genomic sequence.	Arabidopsis thaliana	36,091	12-MAR-1997
	GB_PL2:AC010871	80381	AC010871	Arabidopsis thaliana chromosome III BAC T16O11 genomic sequence, complete sequence.	Arabidopsis thaliana	37,135	13-Nov-99
rxa00680 441	GB_PR3:AC004058	38400	AC004058	Homo sapiens chromosome 4 clone B241P19 map 4q25, complete sequence.	Homo sapiens	36,165	30-Sep-98
	GB_PL1:AT81KBGEN	81493	X98130	A.thaliana 81kb genomic sequence.	Arabidopsis thaliana	38,732	12-MAR-1997
	GB_PL1:AB026648	43481	AB026648	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLJ15, complete sequence.	Arabidopsis thaliana	38,732	07-MAY-1999
rxa00682 2022	GB_HTG3:AC010325	197110	AC010325	Homo sapiens chromosome 19 clone CITB-E1_2568A17, *** SEQUENCING IN Homo sapiens PROGRESS *** , 40 unordered pieces.	Homo sapiens	37,976	15-Sep-99
	GB_HTG3:AC010325	197110	AC010325	Homo sapiens chromosome 19 clone CITB-E1_2568A17, *** SEQUENCING IN Homo sapiens PROGRESS *** , 40 unordered pieces.	Homo sapiens	37,976	15-Sep-99
	GB_PR4:AC008179	181745	AC008179	Homo sapiens clone NH0576F01, complete sequence.	Homo sapiens	37,143	28-Sep-99

Table 4 (continued)

rxa00683	1215	GB_BA2:AE000896	10707	AE000896	Methanobacterium thermoautotrophicum from bases 1189349 to 1200055 (section 102 of 148) of the complete genome.	Methanobacterium thermoautotrophicum	38,429	15-Nov-97
		GB_IN1:DMBR7A4	212734	AL109630	Drosophila melanogaster clone BACR7A4.	Drosophila melanogaster	36,454	30-Jul-99
		GB_EST35:AV163010	273	AV163010	AV163010 Mus musculus head C57BL/6J 13-day embryo Mus musculus cDNA clone 3110006J22, mRNA sequence.	Mus musculus	41,758	8-Jul-99
rxa00686	927	GB_HTG2:HSDJ137K2	190223	AL049820	Homo sapiens chromosome 6 clone RP1-137K2 map q25.1-25.3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	38,031	03-DEC-1999
		GB_HTG2:HSDJ137K2	190223	AL049820	Homo sapiens chromosome 6 clone RP1-137K2 map q25.1-25.3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	38,031	03-DEC-1999
		GB_EST12:AA284399	431	AA284399	zs57b04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701551 5', mRNA sequence.	Homo sapiens	39,205	14-Aug-97
rxa00700	927	GB_EST34:AI785570	454	AI785570	uj44d03.x1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1922789 3' similar to gb:Z28407 60S RIBOSOMAL PROTEIN L8 (HUMAN);, mRNA sequence.	Mus musculus	41,943	2-Jul-99
		GB_EST25:AI256147	684	AI256147	uj95e12.x1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1890190 3' similar to gb:Z28407 60S RIBOSOMAL PROTEIN L8 (HUMAN);, mRNA sequence.	Mus musculus	40,791	12-Nov-98
rxa00703	2409	GB_BA1:CARCG12	2079	X14979	C. aurantiacus reaction center genes 1 and 2.	Chloroflexus aurantiacus	37,721	23-Apr-91
		GB_BA1:SC7H2	42655	AL109732	Streptomyces coelicolor cosmid 7H2.	Streptomyces coelicolor A3(2)	56,646	2-Aug-99
		GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	37,369	19-Jun-98
		GB_BA2:REU60056	2520	U60056	Ralstonia eutropha formate dehydrogenase-like protein (cbbBc) gene, complete cds.	Ralstonia eutropha	51,087	16-OCT-1996
rxa00705	1038	GB_GSS15:AQ604477	505	AQ604477	HS_2116_B1_G07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2116 Col=13 Row=N, genomic survey sequence.	Homo sapiens	39,617	10-Jun-99
		GB_EST11:AA224340	443	AA224340	zr14e07.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648804 3', mRNA sequence.	Homo sapiens	35,129	11-MAR-1998
		GB_EST5:N30648	291	N30648	yw77b02.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:258219 3', mRNA sequence.	Homo sapiens	43,986	5-Jan-96
rxa00782	1005	GB_BA1:MTCY10D7	39800	Z79700	Mycobacterium tuberculosis H37Rv complete genome; segment 44/162.	Mycobacterium tuberculosis	63,327	17-Jun-98
		GB_BA1:MLCL373	37304	AL035500	Mycobacterium leprae cosmid L373.	Mycobacterium leprae	62,300	27-Aug-99
		GB_BA2:AF128399	2842	AF128399	Pseudomonas aeruginosa succinyl-CoA synthetase beta subunit (sucC) and succinyl-CoA synthetase alpha subunit (sucD) genes, complete cds.	Pseudomonas aeruginosa	53,698	25-MAR-1999
rxa00783	1395	GB_HTG2:AC008158	118792	AC008158	Homo sapiens chromosome 17 clone hRPK.42_F_20 map 17, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces.	Homo sapiens	35,135	28-Jul-99
		GB_HTG2:AC008158	118792	AC008158	Homo sapiens chromosome 17 clone hRPK.42_F_20 map 17, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces.	Homo sapiens	35,135	28-Jul-99
		GB_PR3:AC005017	137176	AC005017	Homo sapiens BAC clone GS214N13 from 7p14-p15, complete sequence.	Homo sapiens	35,864	8-Aug-98
rxa00794	1128	GB_BA1:MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.	Mycobacterium tuberculosis	40,331	24-Jun-99

Table 4 (continued)

	GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	61,170	27-Aug-99
	GB_PR2:HS151B14	128942	Z82188	Human DNA sequence from clone 151B14 on chromosome 22 Contains SOMATOSTATIN RECEPTOR TYPE 3 (SS3R) gene,pseudogene similar to ribosomal protein L39,RAC2 (RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2 (P21-RAC2)) gene ESTs, STSs, GSSs and CpG islands, complete sequence.	Homo sapiens	37,455	16-Jun-99
rxa00799	1767	GB_PL2:AF016327	616	AF016327	Hordeum vulgare	41,311	01-OCT-1997
		GB_HTG2:HSDJ319M7	128208	AL079341	Homo sapiens	36,845	30-Nov-99
		GB_HTG2:HSDJ319M7	128208	AL079341	Homo sapiens	36,845	30-Nov-99
rxa00800	1227	GB_BA1:MTV022	13025	AL021925	Mycobacterium tuberculosis	63,101	17-Jun-98
		GB_BA1:AB019513	4417	AB019513	Streptomyces coelicolor	41,312	13-Nov-98
		GB_PL1:SCSFAARP	7008	X68020	Saccharomyces cerevisiae	36,288	29-Nov-94
rxa00825	1056	GB_BA1:MTY15C10	33050	Z95436	Mycobacterium tuberculosis	39,980	17-Jun-98
		GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae	39,435	27-Aug-99
		GB_BA2:AF169031	1141	AF169031	Xanthomonas oryzae pv. oryzae	46,232	14-Sep-99
rxa00871				epimerase/dehydratase gene, partial cds.			
rxa00872	1077	GB_IN1:CEF23H12	35564	Z74472	Caenorhabditis elegans	34,502	08-OCT-1999
		GB_HTG2:AC007263	167390	AC007263	Homo sapiens	35,714	24-MAY-1999
		GB_HTG2:AC007263	167390	AC007263	Homo sapiens	35,714	24-MAY-1999
rxa00879	2241	GB_BA1:MTV049	40360	AL022021	Mycobacterium tuberculosis	36,981	19-Jun-98
		GB_PL2:CDU236897	1827	AJ236897	Candida dubliniensis	38,716	1-Sep-99
		GB_PL1:CAACT1A	3206	X16377	Candida albicans	36,610	10-Apr-93
rxa00909	955	GB_BA2:AF010496	189370	AF010496	Rhodobacter capsulatus	51,586	12-MAY-1998
		GB_BA1:RMPHA	7888	X93358	Sinorhizobium meliloti	48,367	12-MAR-1999
		GB_EST16:C23528	317	C23528	Paralichthys olivaceus	41,640	28-Sep-99
rxa00913	2118	GB_HTG2:AC007734	188267	AC007734	Homo sapiens	34,457	5-Jun-99

Table 4 (continued)

	GB_HTG2:AC007734	188267	AC007734	Homo sapiens chromosome 18 clone hRPK.44_O_1 map 18, *** SEQUENCING IN PROGRESS *** , 18 unordered pieces.	Homo sapiens	34,457	5-Jun-99
	GB_EST18:AA709478	406	AA709478	w34a05.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:1224272 5', mRNA sequence.	Mus musculus	42,065	24-DEC-1997
rxa00945	GB_HTG4:AC010351	220710	AC010351	Homo sapiens chromosome 5 clone CITB-H1_2022B6, *** SEQUENCING IN PROGRESS *** , 68 unordered pieces.	Homo sapiens	36,448	31-OCT-1999
	GB_HTG4:AC010351	220710	AC010351	Homo sapiens chromosome 5 clone CITB-H1_2022B6, *** SEQUENCING IN PROGRESS *** , 68 unordered pieces.	Homo sapiens	36,448	31-OCT-1999
	GB_BA1:MTCY05A6	38631	Z96072	Mycobacterium tuberculosis H37Rv complete genome; segment 120/162.	Mycobacterium tuberculosis	36,218	17-Jun-98
rxa00965							
rxa00999	GB_PAT:E13660	1916	E13660	gDNA encoding 6-phosphogluconate dehydrogenase.	Corynebacterium glutamicum	98,349	24-Jun-98
	GB_BA1:MTCY359	36021	Z83859	Mycobacterium tuberculosis H37Rv complete genome; segment 84/162.	Mycobacterium tuberculosis	38,520	17-Jun-98
	GB_BA1:MLCB1788	39228	AL008609	Mycobacterium leprae cosmid B1788.	Mycobacterium leprae	64,355	27-Aug-99
rxa01015	GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	39,860	17-Jun-98
	GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	39,120	17-Jun-98
rxa01025	GB_BA1:SC7A1	32039	AL034447	Streptomyces coelicolor cosmid 7A1.	Streptomyces coelicolor	55,287	15-DEC-1998
	GB_BA1:MSGB1723CS	38477	L78825	Mycobacterium leprae cosmid B1723 DNA sequence.	Mycobacterium leprae	56,847	15-Jun-96
	GB_BA1:MLCB637	44882	Z99263	Mycobacterium leprae cosmid B637.	Mycobacterium leprae	56,676	17-Sep-97
rxa01048	GB_BA2:AF017444	3067	AF017444	Sinorhizobium meliloti NADP-dependent malic enzyme (tme) gene, complete cds.	Sinorhizobium meliloti	53,660	2-Nov-97
	GB_BA1:BSUB0013	218470	Z99116	Bacillus subtilis complete genome (section 13 of 21): from 2395261 to 2613730.	Bacillus subtilis	37,255	26-Nov-97
	GB_VI:HSV2HG52	154746	Z86099	Herpes simplex virus type 2 (strain HG52), complete genome.	human herpesvirus 2	38,081	04-DEC-1998
rxa01049	GB_HTG2:AC002518	131855	AC002518	Homo sapiens chromosome X clone bWXD20, *** SEQUENCING IN PROGRESS *** , 11 unordered pieces.	Homo sapiens	35,647	2-Sep-97
	GB_HTG2:AC002518	131855	AC002518	Homo sapiens chromosome X clone bWXD20, *** SEQUENCING IN PROGRESS *** , 11 unordered pieces.	Homo sapiens	35,647	2-Sep-97
	GB_HTG2:AC002518	131855	AC002518	Homo sapiens chromosome X clone bWXD20, *** SEQUENCING IN PROGRESS *** , 11 unordered pieces.	Homo sapiens	26,180	2-Sep-97
rxa01077	GB_PR3:HSDJ653C5	85237	AL049743	Human DNA sequence from clone 653C5 on chromosome 1p21.3-22.3 Contains CA repeat(D1S435), STSs and GSSs, complete sequence.	Homo sapiens	36,462	23-Nov-99
	GB_BA1:ECU29579	72221	U29579	Escherichia coli K-12 genome; approximately 61 to 62 minutes.	Escherichia coli	41,808	1-Jul-95
	GB_BA1:ECU29579	72221	U29579	Escherichia coli K-12 genome; approximately 61 to 62 minutes.	Escherichia coli	36,130	1-Jul-95
rxa01089	GB_GSS8:AQ044021	387	AQ044021	CIT-HSP-2318C18.TR CIT-HSP Homo sapiens genomic clone 2318C18, genomic survey sequence.	Homo sapiens	36,528	14-Jul-98

Table 4 (continued)

	GB_GSS8:AQ042907	392	AQ042907	CIT-HSP-2318D17.TR CIT-HSP Homo sapiens genomic clone 2318D17, genomic survey sequence.	Homo sapiens	35,969	14-Jul-98
	GB_GSS8:AQ044021	387	AQ044021	CIT-HSP-2318C18.TR CIT-HSP Homo sapiens genomic clone 2318C18, genomic survey sequence.	Homo sapiens	44,545	14-Jul-98
rx01093	GB_BA1:CORPYKI	2795	L27126	Corynebacterium pyruvate kinase gene, complete cds.	Corynebacterium glutamicum	100,000	07-DEC-1994
	GB_BA1:MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162.	Mycobacterium tuberculosis	63,771	17-Jun-98
	GB_BA1:MIU65430	1439	U65430	Mycobacterium intracellulare pyruvate kinase (pykF) gene, complete cds.	Mycobacterium intracellulare	67,061	23-DEC-1996
rx01099	GB_BA2:AF045998	780	AF045998	Corynebacterium glutamicum inositol monophosphate phosphatase (impA) gene, complete cds.	Corynebacterium glutamicum	99,615	19-Feb-98
	GB_BA2:AF051846	738	AF051846	Corynebacterium glutamicum phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase (hisA) gene, complete cds.	Corynebacterium glutamicum	100,000	12-MAR-1998
	GB_GSS1:FR0005503	619	Z89313	F.rubripes GSS sequence, clone 079B16aE8, genomic survey sequence.	Fugu rubripes	37,785	01-MAR-1997
rx01111	GB_PR3:AC004063	177014	AC004063	Homo sapiens chromosome 4 clone B32I8, complete sequence.	Homo sapiens	35,835	10-Jul-98
	GB_PR3:HS1178121	62268	AL109852	Human DNA sequence from clone RP5-1178I21 on chromosome X, complete sequence.	Homo sapiens	37,873	01-DEC-1999
	GB_HTG3:AC009301	163369	AC009301	Homo sapiens clone NH0062F14, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.	Homo sapiens	37,240	13-Aug-99
rx01130	GB_HTG3:AC009444	164587	AC009444	Homo sapiens clone 1_O_3, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.	Homo sapiens	38,416	22-Aug-99
	GB_HTG3:AC009444	164587	AC009444	Homo sapiens clone 1_O_3, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.	Homo sapiens	38,416	22-Aug-99
rx01193	GB_IN1:DMC66A1	34127	AL031227	Drosophila melanogaster cosmid 66A1.	Drosophila melanogaster	38,416	05-OCT-1998
	GB_BA1:CGASO19	1452	X76875	C.glutamicum (ASO 19) ATPase beta-subunit gene.	Corynebacterium glutamicum	99,931	27-OCT-1994
	EM_PAT:E09634	1452	E09634	Brevibacterium flavum UncD gene whose gene product is involved in	Corynebacterium glutamicum	99,242	07-OCT-1997 (Rel. 52, Created)
	GB_BA1:MLU15186	36241	U15186	Mycobacterium leprae cosmid L471.	Mycobacterium leprae	39,153	09-MAR-1995
rx01194	EM_PAT:E09634	1452	E09634	Brevibacterium flavum UncD gene whose gene product is involved in	Corynebacterium glutamicum	100,000	07-OCT-1997 (Rel. 52, Created)
	GB_BA1:CGASO19	1452	X76875	C.glutamicum (ASO 19) ATPase beta-subunit gene.	Corynebacterium glutamicum	100,000	27-OCT-1994
rx01200	GB_VI:HEPCRE4B	414	X60570	Hepatitis C genomic RNA for putative envelope protein (RE4B isolate).	Hepatitis C virus	36,769	5-Apr-92

Table 4 (continued)

rxa01201	1764	GB_BA1:SLATPSYNA	8560	Z22606	S.lividans i protein and ATP synthase genes.	Streptomyces lividans	66,269	01-MAY-1995	100
		GB_BA1:MTCY373	35516	Z73419	Mycobacterium tuberculosis H37Rv complete genome; segment 57/162.	Mycobacterium tuberculosis	65,437	17-Jun-98	
		GB_BA1:MLU15186	36241	U15186	Mycobacterium leprae cosmid L471.	Mycobacterium leprae	39,302	09-MAR-1995	
rxa01202	1098	GB_BA1:SLATPSYNA	8560	Z22606	S.lividans i protein and ATP synthase genes.	Streptomyces lividans	57,087	01-MAY-1995	
		GB_BA1:SLATPSYNA	8560	Z22606	S.lividans i protein and ATP synthase genes.	Streptomyces lividans	38,298	01-MAY-1995	
		GB_BA1:MCSQSSHC	5538	Y09978	M.capsulatus orfx, orfy, orfz, sqs and shc genes.	Methylococcus capsulatus	37,626	26-MAY-1998	
rxa01204	933	GB_PL1:AP000423	154478	AP000423	Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain:Columbia.	Chloroplast Arabidopsis thaliana	38,395	15-Sep-99	
		GB_HTG6:AC009762	164070	AC009762	Homo sapiens clone RP11-114I16, *** SEQUENCING IN PROGRESS *** , 39 unordered pieces.	Homo sapiens	35,459	04-DEC-1999	
		GB_HTG6:AC009762	164070	AC009762	Homo sapiens clone RP11-114I16, *** SEQUENCING IN PROGRESS *** , 39 unordered pieces.	Homo sapiens	36,117	04-DEC-1999	
rxa01216	1124	GB_BA1:MTCY10G2	38970	Z92539	Mycobacterium tuberculosis H37Rv complete genome; segment 47/162.	Mycobacterium tuberculosis	39,064	17-Jun-98	
		GB_BA2:AF017435	4301	AF017435	Methylobacterium extorquens methanol oxidation genes, glmU-like gene, partial cds, and orfL2, orfL1, orfR genes, complete cds.	Methylobacterium extorquens	42,671	10-MAR-1998	PCT/IB00/00943
rxa01225	1563	GB_BA1:CCRFLDBA	4424	M69228	C.crescentus flagellar gene promoter region.	Caulobacter crescentus	41,054	26-Apr-93	
		GB_BA2:AF058302	25306	AF058302	Streptomyces roseofulvus frenolicin biosynthetic gene cluster, complete sequence.	Streptomyces roseofulvus	36,205	2-Jun-98	
		GB_HTG3:AC007301	165741	AC007301	Drosophila melanogaster chromosome 2 clone BACR04B09 (D576) RPCI-98 04.B.9 map 43E12-44F1 strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** , 150 unordered pieces.	Drosophila melanogaster	39,922	17-Aug-99	
		GB_HTG3:AC007301	165741	AC007301	Drosophila melanogaster chromosome 2 clone BACR04B09 (D576) RPCI-98 04.B.9 map 43E12-44F1 strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** , 150 unordered pieces.	Drosophila melanogaster	39,922	17-Aug-99	
rxa01227	444	GB_BA1:SERFDXA	3869	M61119	Saccharopolyspora erythraea ferredoxin (fdxA) gene, complete cds.	Saccharopolyspora erythraea	64,908	13-MAR-1996	
		GB_BA1:MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome; segment 51/162.	Mycobacterium tuberculosis	62,838	17-Jun-98	
		GB_BA1:MSGY348	40056	AD000020	Mycobacterium tuberculosis sequence from clone y348.	Mycobacterium tuberculosis	61,712	10-DEC-1996	
rxa01242	900	GB_PR3:AC005697	174503	AC005697	Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence.	Homo sapiens	35,373	09-OCT-1998	
		GB_HTG3:AC010722	160723	AC010722	Homo sapiens clone NH0122L09, *** SEQUENCING IN PROGRESS *** , 2 unordered pieces.	Homo sapiens	39,863	25-Sep-99	
		GB_HTG3:AC010722	160723	AC010722	Homo sapiens clone NH0122L09, *** SEQUENCING IN PROGRESS *** , 2 unordered pieces.	Homo sapiens	39,863	25-Sep-99	

Table 4 (continued)

rxa01243	1083	GB_GSS10:AQ255057	583	AQ255057	mgxb0008N01r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0008N01r, genomic survey sequence.	Magnaporthe grisea	38,722	23-OCT-1998
rxa01259	981	GB_IN1:CEK05D4	19000	Z92804	Caenorhabditis elegans cosmid K05D4, complete sequence.	Caenorhabditis elegans	35,448	23-Nov-98
		GB_IN1:CEK05D4	19000	Z92804	Caenorhabditis elegans cosmid K05D4, complete sequence.	Caenorhabditis elegans	35,694	23-Nov-98
		GB_BA1:CGLPD	1800	Y16642	Corynebacterium glutamicum lpd gene, complete CDS.	Corynebacterium glutamicum	100,000	1-Feb-99
		GB_HTG4:AC010567	143287	AC010567	Drosophila melanogaster chromosome 3L/69C1 clone RPCI98-11N6, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces.	Drosophila melanogaster	37,178	16-OCT-1999
rxa01262	1284	GB_HTG4:AC010567	143287	AC010567	Drosophila melanogaster chromosome 3L/69C1 clone RPCI98-11N6, ***SEQUENCING IN PROGRESS ***, 70 unordered pieces.	Drosophila melanogaster	37,178	16-OCT-1999
		GB_BA2:AF172324	14263	AF172324	Escherichia coli GalF (galF) gene, partial cds; O-antigen repeat unit transporter Wzx (wzx), WbnA (wbnA), O-antigen polymerase Wzy (wzy), WbnB (wbnB), WbnC (wbnC), WbnD (wbnD), WbnE (wbnE), UDP-Glc-4-epimerase GalE (galE), 6-phosphogluconate dehydrogenase Gnd (gnd), UDP-Glc-6-dehydrogenase Ugd (ugd), and WbnF (wbnF) genes, complete cds; and chain length determinant Wzz (wzz) gene, partial cds.	Escherichia coli	59,719	29-OCT-1999
		GB_BA2:ECU78086	4759	U78086	Escherichia coli hypothetical uridine-5'-diphosphoglucose dehydrogenase (ugd) and O-chain length regulator (wzz) genes, complete cds.	Escherichia coli	59,735	5-Nov-97
		GB_BA1:D90841	20226	D90841	E.coli genomic DNA, Kohara clone #351(45.1-45.5 min.).	Escherichia coli	37,904	21-MAR-1997
rxa01311	870	GB_PR3:AC004103	144368	AC004103	Homo sapiens Xp22 BAC GS-619J3 (Genome Systems Human BAC library) complete sequence.	Homo sapiens	37,340	18-Apr-98
rxa01312	2142	GB_HTG3:AC007383	215529	AC007383	Homo sapiens clone NH0310K15, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Homo sapiens	36,385	25-Sep-99
		GB_HTG3:AC007383	215529	AC007383	Homo sapiens clone NH0310K15, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Homo sapiens	36,385	25-Sep-99
		GB_BA2:AE000487	13889	AE000487	Escherichia coli K-12 MG1655 section 377 of 400 of the complete genome.	Escherichia coli	39,494	12-Nov-98
		GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	46,252	23-Jun-99
rxa01325	795	GB_BA1:U00022	36411	U00022	Mycobacterium leprae cosmid L308.	Mycobacterium leprae	46,368	01-MAR-1994
		GB_HTG4:AC009245	215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 24 unordered pieces.	Homo sapiens	36,016	2-Nov-99
		GB_HTG4:AC009245	215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 24 unordered pieces.	Homo sapiens	36,016	2-Nov-99
		GB_HTG4:AC009245	215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 24 unordered pieces.	Homo sapiens	39,618	2-Nov-99
rxa01332	576	GB_HTG6:AC007186	225851	AC007186	Drosophila melanogaster chromosome 2 clone BACR03D06 (D569) RPCI-98 03.D.6 map 32A-32A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 91 unordered pieces.	Drosophila melanogaster	35,366	07-DEC-1999
rxa01332	576	GB_HTG6:AC007147	202291	AC007147	Drosophila melanogaster chromosome 2 clone BACR19N18 (D572) RPCI-98 19.N.18 map 32A-32A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 22 unordered pieces.	Drosophila melanogaster	35,366	07-DEC-1999

Table 4 (continued)

	GB_HTG3:AC010207	207890	AC010207	Homo sapiens clone RPCI11-375I20, *** SEQUENCING IN PROGRESS *** , 25 Homo sapiens unordered pieces.	34,821	16-Sep-99
rxa01350 1107	GB_BA2:AF109682	990	AF109682	Aquaspirillum arcticum malate dehydrogenase (MDH) gene, complete cds.	58,487	19-OCT-1999
	GB_HTG2:AC006759	103725	AC006759	Caenorhabditis elegans clone Y40G12, *** SEQUENCING IN PROGRESS***, 8 unordered pieces.	37,963	25-Feb-99
	GB_HTG2:AC006759	103725	AC006759	Caenorhabditis elegans clone Y40G12, *** SEQUENCING IN PROGRESS***, 8 unordered pieces.	37,963	25-Feb-99
rxa01365 1497	GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	38,011	17-Jun-98
	GB_BA1:XANXANAB	3410	M83231	Xanthomonas campestris phosphoglucomutase and phosphomannomutase (xanA) and phosphomannose isomerase and GDP-mannose pyrophosphorylase (xanB) genes, complete cds.	47,726	26-Apr-93
rxa01369 1305	GB_GSS10:AQ194038	697	AQ194038	RPCI11-47D24.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-47D24, genomic survey sequence.	36,599	20-Apr-99
	GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	36,940	17-Jun-98
	GB_GSS3:B10037	974	B10037	T27A19-T7 TAMU Arabidopsis thaliana genomic clone T27A19, genomic survey sequence.	35,284	14-MAY-1997
rxa01377 1209	GB_GSS3:B09549	1097	B09549	T21A19-T7.1 TAMU Arabidopsis thaliana genomic clone T21A19, genomic survey sequence.	38,324	14-MAY-1997
	GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	39,778	10-Feb-99
	GB_HTG5:AC007547	262181	AC007547	Homo sapiens clone RP11-252O18, WORKING DRAFT SEQUENCE, 121 unordered pieces.	32,658	16-Nov-99
rxa01392 1200	GB_HTG5:AC007547	262181	AC007547	Homo sapiens clone RP11-252O18, WORKING DRAFT SEQUENCE, 121 unordered pieces.	38,395	16-Nov-99
	GB_BA2:AF072709	8366	AF072709	Streptomyces lividans amplifiable element AUD4; putative transcriptional regulator, putative ferredoxin, putative cytochrome oxidoreductase, and putative oxidoreductase genes, complete unknown genes.	55,221	8-Jul-98
	GB_BA1:CGLYSEG	2374	X96471	C.glutamicum lysE and lysG genes.	100,000	24-Feb-97
rxa01436 1314	GB_PR4:AC005906	185952	AC005906	Homo sapiens 12p13.3 BAC RPCI11-429A20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	36,756	30-Jan-99
	GB_BA1:CGPTAACKA	3657	X89084	C.glutamicum pta gene and ackA gene.	100,000	23-MAR-1999
	GB_BA1:D90861	14839	D90861	E.coli genomic DNA, Kohara clone #405(52.0-52.3 min.).	53,041	29-MAY-1997
rxa01468 948	GB_PAT:E02087	1200	E02087	DNA encoding acetate kinase protein form Escherichia coli.	54,461	29-Sep-97
	GB_GSS1:HPU60627	280	U60627	Helicobacter pylori feoB-like DNA sequence, genomic survey sequence.	39,286	9-Apr-97
	GB_EST31:AI701691	349	AI701691	we81c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347494 3' similar to gb:L19686_rna1 MACROPHAGE MIGRATION INHIBITORY FACTOR (HUMAN);, mRNA sequence.	39,412	3-Jun-99

Table 4 (continued)

	GB_EST15:AA480256	389	AA480256	ne31f04.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:898975 3' similar to gb:L19686_rna1 MACROPHAGE MIGRATION INHIBITORY FACTOR (HUMAN);, mRNA sequence.	Homo sapiens	39,574	14-Aug-97
rx01478	1959	GB_BA1:SCI51	40745	AL109848	Streptomyces coelicolor cosmid I51.	Streptomyces coelicolor A3(2)	16-Aug-99
		GB_BA1:SCE36	12581	AL049763	Streptomyces coelicolor cosmid E36.	Streptomyces coelicolor	05-MAY-1999
		GB_BA1:CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	9-Apr-97
rx01482	1998	GB_BA1:SC6G4	41055	AL031317	Streptomyces coelicolor cosmid 6G4.	Streptomyces coelicolor	20-Aug-98
		GB_BA1:U00020	36947	U00020	Mycobacterium leprae cosmid B229.	Mycobacterium leprae	01-MAR-1994
rx01534		GB_BA1:MTCY77	22255	Z95389	Mycobacterium tuberculosis H37Rv complete genome; segment 146/162.	Mycobacterium tuberculosis	18-Jun-98
rx01535	1530	GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	27-Aug-99
		GB_BA1:MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.	Mycobacterium tuberculosis	24-Jun-99
		GB_BA1:PAU72494	4368	U72494	Pseudomonas aeruginosa fumarase (fumC) and Mn superoxide dismutase (sodA) genes, complete cds.	Pseudomonas aeruginosa	23-OCT-1996
rx01550	1635	GB_BA1:D90907	132419	D90907	Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885.	Synechocystis sp.	7-Feb-99
		GB_IN2:AF073177	9534	AF073177	Drosophila melanogaster glycogen phosphorylase (GlyP) gene, complete cds.	Drosophila melanogaster	1-Jul-99
rx01562		GB_IN2:AF073179	3159	AF073179	Drosophila melanogaster glycogen phosphorylase (Glp1) mRNA, complete cds.	Drosophila melanogaster	27-Apr-99
rx01569	1482	GB_BA1:D78182	7836	D78182	Streptococcus mutans DNA for dTDP-rhamnose synthesis pathway, complete cds.	Streptococcus mutans	5-Feb-99
		GB_BA2:AF079139	4342	AF079139	Streptomyces venezuelae pikCD operon, complete sequence.	Streptomyces venezuelae	28-OCT-1998
		GB_BA2:AF087022	1470	AF087022	Streptomyces venezuelae cytochrome P450 monooxygenase (pick) gene, complete cds.	Streptomyces venezuelae	15-OCT-1998
rx01570	978	GB_BA1:MTCY63	38900	Z96800	Mycobacterium tuberculosis H37Rv complete genome; segment 16/162.	Mycobacterium tuberculosis	17-Jun-98
		GB_BA2:AF097519	4594	AF097519	Klebsiella pneumoniae dTDP-D-glucose 4,6 dehydratase (rmlB), glucose-1-phosphate thymidyl transferase (rmlA), dTDP-4-keto-L-rhamnose reductase (rmlD), dTDP-4-keto-6-deoxy-D-glucose 3,5-epimerase (rmlC), and rhamnosyl transferase (wbbL) genes, complete cds.	Klebsiella pneumoniae	4-Nov-98

Table 4 (continued)

	GB_BA2:NGOCPSPS	8905	L09189	Neisseria meningitidis dTDP-D-glucose 4,6-dehydratase (rfbB), glucose-1-phosphate thymidyl transferase (rfbA) and rfbC genes, complete cds and UPD-glucose-4-epimerase (galE) pseudogene.	Neisseria meningitidis	58,384	30-Jul-96
rx01571 723	GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	57,500	7-Aug-98
	GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	35,655	7-Aug-98
rx01572 615	GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	57,843	7-Aug-98
	GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	38,119	7-Aug-98
rx01606 2799	GB_VI:CFU72240	4783	U72240	Choristoneura fumiferana nuclear polyhedrosis virus ETM protein homolog, 79 kDa protein homolog, 15 kDa protein homolog and GTA protein homolog genes, complete cds.	Choristoneura fumiferana nucleopolyhedrovirus	37,115	29-Jan-99
	GB_GSS10:AQ213248	408	AQ213248	HS_3249_B1_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3249 Col=3 Row=B, genomic survey sequence.	Homo sapiens	34,559	18-Sep-98
	GB_GSS8:AQ070145	285	AQ070145	HS_3027_B1_H02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=3 Row=P, genomic survey sequence.	Homo sapiens	40,351	5-Aug-98
rx01626 468	GB_PR4:AF152510	2490	AF152510	Homo sapiens protocadherin gamma A3 short form protein (PCDH-gamma-A3) variable region sequence, complete cds.	Homo sapiens	34,298	14-Jul-99
	GB_PR4:AF152323	4605	AF152323	Homo sapiens protocadherin gamma A3 (PCDH-gamma-A3) mRNA, complete cds.	Homo sapiens	34,298	22-Jul-99
rx01632 1128	GB_PR4:AF152509	2712	AF152509	Homo sapiens PCDH-gamma-A3 gene, aberrantly spliced, mRNA sequence.	Homo sapiens	34,298	14-Jul-99
	GB_HTG4:AC006590	127171	AC006590	Drosophila melanogaster chromosome 2 clone BACR13N02 (D543) RPCI-98 13.N.2 map 36E-36E strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Drosophila melanogaster	33,812	19-OCT-1999
	GB_HTG4:AC006590	127171	AC006590	Drosophila melanogaster chromosome 2 clone BACR13N02 (D543) RPCI-98 13.N.2 map 36E-36E strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Drosophila melanogaster	33,812	19-OCT-1999
rx01633 1206	GB_GSS8:B99182	415	B99182	CIT-HSP-2280113.TR CIT-HSP Homo sapiens genomic clone 2280113, genomic survey sequence.	Homo sapiens	36,111	26-Jun-98
	GB_BA1:BSUB0009	208780	Z99112	Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200.	Bacillus subtilis	36,591	26-Nov-97
	GB_BA1:BSUB0009	208780	Z99112	Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200.	Bacillus subtilis	34,941	26-Nov-97
	GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR48I10 (D505) RPCI-98 48.I.10 map 49E6-49F8 strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 17 unordered pieces.	Drosophila melanogaster	37,037	2-Aug-99

Table 4 (continued)

rxa01695	1623	GB_BA1:CGA224946	2408	AJ224946	Corynebacterium glutamicum DNA for L-Malate:quinone oxidoreductase.	Corynebacterium glutamicum	100,000	11-Aug-98
		GB_BA1:MTCY24A1	20270	Z95207	Mycobacterium tuberculosis H37Rv complete genome; segment 124/162.	Mycobacterium tuberculosis	38,626	17-Jun-98
		GB_IN1:DMU15974	2994	U15974	Drosophila melanogaster kinesin-like protein (klp68d) mRNA, complete cds.	Drosophila melanogaster	36,783	18-Jul-95
rxa01702	1155	GB_BA1:CGFDA	3371	X17313	Corynebacterium glutamicum fda gene for fructose-bisphosphate aldolase (EC 4.1.2.13).	Corynebacterium glutamicum	99,913	12-Sep-93
		GB_BA1:MTY13E10	35019	Z95324	Mycobacterium tuberculosis H37Rv complete genome; segment 18/162.	Mycobacterium tuberculosis	38,786	17-Jun-98
		GB_BA1:MLCB4	36310	AL023514	Mycobacterium leprae cosmid B4.	Mycobacterium leprae	38,238	27-Aug-99
rxa01743	901	GB_IN2:CELC27H5	35840	U14635	Caenorhabditis elegans cosmid C27H5.	Caenorhabditis elegans	35,334	13-Jul-95
		GB_EST24:AI167112	579	AI167112	xylem.est.878 Poplar xylem Lambda ZAPII library Populus balsamifera subsp. trichocarpa cDNA 5', mRNA sequence.	Populus balsamifera subsp. trichocarpa	39,222	03-DEC-1998
		GB_GSS9:AQ102635	347	AQ102635	HS_3048_B1_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=15 Row=L, genomic survey sequence.	Homo sapiens	40,653	27-Aug-98
rxa01744	1662	GB_BA1:MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162.	Mycobacterium tuberculosis	36,650	17-Jun-98
		GB_GSS1:AF009226	665	AF009226	Mycobacterium tuberculosis cytochrome D oxidase subunit I (appC) gene, partial sequence, genomic survey sequence.	Mycobacterium tuberculosis	63,438	31-Jul-97
		GB_BA1:SCD78	36224	AL034355	Streptomyces coelicolor cosmid D78.	Streptomyces coelicolor	53,088	26-Nov-98
rxa01745	836	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	62,081	17-Jun-98
		GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	61,364	22-Aug-97
		GB_BA2:AE000175	15067	AE000175	Escherichia coli K-12 MG1655 section 65 of 400 of the complete genome.	Escherichia coli	52,323	12-Nov-98
rxa01758	1140	GB_PR3:HS57G9	113872	Z95116	Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.	Homo sapiens	39,209	23-Nov-99
		GB_PL2:YSCH9666	39057	U10397	Saccharomyces cerevisiae chromosome VIII cosmid 9666.	Saccharomyces cerevisiae	40,021	5-Sep-97
		GB_PL2:YSCH9986	41664	U00027	Saccharomyces cerevisiae chromosome VIII cosmid 9986.	Saccharomyces cerevisiae	34,375	29-Aug-97
rxa01814	1785	GB_BA1:ABCCELB	2058	L24077	Acetobacter xylinum phosphoglucomutase (celB) gene, complete cds.	Acetobacter xylinus	62,173	21-Sep-94
		GB_BA1:MTCY22D7	31859	Z83866	Mycobacterium tuberculosis H37Rv complete genome; segment 133/162.	Mycobacterium tuberculosis	39,749	17-Jun-98
		GB_BA1:MTCY22D7	31859	Z83866	Mycobacterium tuberculosis H37Rv complete genome; segment 133/162.	Mycobacterium tuberculosis	40,034	17-Jun-98
rxa01851	1809	GB_GSS9:AQ142579	529	AQ142579	HS_2222_B1_H03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=5 Row=P, genomic survey sequence.	Homo sapiens	38,068	24-Sep-98
		GB_IN2:AC005889	108924	AC005889	Drosophila melanogaster, chromosome 2L, region 30A3- 30A6, P1 clones DS06958 and DS03097, complete sequence.	Drosophila melanogaster	36,557	30-OCT-1998
		GB_GSS1:AG008814	637	AG008814	Homo sapiens genomic DNA, 21q region, clone: B137B7BB68, genomic survey sequence.	Homo sapiens	35,316	7-Feb-99

Table 4 (continued)

rx01859	1050	GB_BA2:AF183408	63626	AF183408	Microcystis aeruginosa DNA polymerase III beta subunit (dnaN) gene, partial cds; microcystin synthetase gene cluster, complete sequence; Uma1 (uma1), Uma2 (uma2), Uma3 (uma3), Uma4 (uma4), and Uma5 (uma5) genes, complete cds; and Uma6 (uma6) gene, partial cds.	Microcystis aeruginosa	36,364	03-OCT-1999
		GB_HTG5:AC008031	158889	AC008031	Trypanosoma brucei chromosome II clone RPCI93-25N14, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.	Trypanosoma brucei	35,334	15-Nov-99
		GB_BA2:AF183408	63626	AF183408	Microcystis aeruginosa DNA polymerase III beta subunit (dnaN) gene, partial cds; microcystin synthetase gene cluster, complete sequence; Uma1 (uma1), Uma2 (uma2), Uma3 (uma3), Uma4 (uma4), and Uma5 (uma5) genes, complete cds; and Uma6 (uma6) gene, partial cds.	Microcystis aeruginosa	36,529	03-OCT-1999
rx01865	438	GB_BA1:SERFDXA	3869	M61119	Saccharopolyspora erythraea ferredoxin (fdxA) gene, complete cds.	Saccharopolyspora erythraea	59,862	13-MAR-1996
		GB_BA1:MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome; segment 51/162.	Mycobacterium tuberculosis	61,949	17-Jun-98
		GB_BA1:MSGY348	40056	AD000020	Mycobacterium tuberculosis sequence from clone y348.	Mycobacterium tuberculosis	59,908	10-DEC-1996
rx01882	1113	GB_PR1:HUMADRA2C	1491	J03853	Human kidney alpha-2-adrenergic receptor mRNA, complete cds.	Homo sapiens	36,899	27-Apr-93
		GB_PR4:HSU72648	4850	U72648	Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.	Homo sapiens	36,899	23-Nov-98
		GB_GSS3:B42200	387	B42200	HS-1055-B1-A03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 777 Col=5 Row=B, genomic survey sequence.	Homo sapiens	34,805	18-OCT-1997
rx01884	1913	GB_BA1:MTCY48	35377	Z74020	Mycobacterium tuberculosis H37Rv complete genome; segment 69/162.	Mycobacterium tuberculosis	37,892	17-Jun-98
		GB_BA1:SCO001206	9184	AJ001206	Streptomyces coelicolor A3(2), glycogen metabolism cluster II.	Streptomyces coelicolor	40,413	29-MAR-1999
rx01886	897	GB_BA1:D90908	122349	D90908	Synechocystis sp. PCC6803 complete genome, 10/27, 1188886-1311234.	Synechocystis sp.	47,792	7-Feb-99
		GB_GSS9:AQ116291	572	AQ116291	RPCI11-49P6.TK.1 RPCI-11 Homo sapiens genomic clone RPCI-11-49P6, genomic survey sequence.	Homo sapiens	43,231	20-Apr-99
		GB_BA2:AE001721	17632	AE001721	Thermotoga maritima section 33 of 136 of the complete genome.	Thermotoga maritima	39,306	2-Jun-99
		GB_EST16:AA567090	596	AA567090	GM01044.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM01044 5prime, mRNA sequence.	Drosophila melanogaster	42,807	28-Nov-98
rx01887	1134	GB_HTG6:AC008147	303147	AC008147	Homo sapiens clone RP3-405J10, *** SEQUENCING IN PROGRESS ***, 102 unordered pieces.	Homo sapiens	36,417	03-DEC-1999
		GB_HTG6:AC008147	303147	AC008147	Homo sapiens clone RP3-405J10, *** SEQUENCING IN PROGRESS ***, 102 unordered pieces.	Homo sapiens	37,667	03-DEC-1999
		GB_BA2:ALW243431	26953	AJ243431	Acinetobacter lwoffii wcz, wza, weeA, weeB, weeC, wzx, wzy, weeD, weeE, weeF, weeG, weeH, weel, weeJ, week, galU, ugd, pgI, galE, pgm (partial) and mip (partial) genes (emulsan biosynthetic gene cluster), strain RAG-1.	Acinetobacter lwoffii	39,640	01-OCT-1999
rx01888	658	GB_HTG2:AC008197	125235	AC008197	Drosophila melanogaster chromosome 3 clone BACR02L12 (D753) RPCI-98 02.L.12 map 94B-94C strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 113 unordered pieces.	Drosophila melanogaster	32,969	2-Aug-99

Table 4 (continued)

GB_HTG2:AC008197		125235	AC008197	Drosophila melanogaster chromosome 3 clone BACR02L12 (D753) RPCI-98 02.L.12 map 94B-94C strain y; cn bw sp, *** SEQUENCING IN PROGRESS	Drosophila melanogaster	32,969	2-Aug-99
GB_EST36:AI881527		598	AI881527	***, 113 unordered pieces.			
GB_VI:HIV232971		621	AJ232971	606070C09.y1 606 - Ear tissue cDNA library from Schmidt lab Zea mays cDNA, Zea mays mRNA sequence.		43,617	21-Jul-99
rxa01891 887	GB_PL1:AFCHSE	6158	Y09542	A.fumigatus chsE gene.	Human immunodeficiency virus type 1 subtype C nef gene, patient MP83.	40,040	05-MAR-1999
	GB_PR3:AF064858	193387	AF064858	Homo sapiens chromosome 21q22.3 BAC 28F9, complete sequence.	Aspergillus fumigatus	37,844	1-Apr-97
	GB_BA1:CGL238250	1593	AJ238250	Corynebacterium glutamicum ndh gene.	Homo sapiens	37,136	2-Jun-98
	GB_BA2:AF038423	1376	AF038423	Mycobacterium smegmatis NADH dehydrogenase (ndh) gene, complete cds.	Corynebacterium glutamicum	100,000	24-Apr-99
rxa01901 1383	GB_BA1:MTCY359	36021	Z83859	Mycobacterium tuberculosis H37Rv complete genome; segment 84/162.	Mycobacterium tuberculosis	40,058	17-Jun-98
	GB_BA1:MSGB38COS	37114	L01095	M. leprae genomic DNA sequence, cosmid B38 bfr gene, complete cds.	Mycobacterium leprae	59,551	6-Sep-94
	GB_BA1:SCE63	37200	AL035640	Streptomyces coelicolor cosmid E63.	Streptomyces coelicolor	39,468	17-MAR-1999
	GB_PR3:AF093117	147216	AF093117	Homo sapiens chromosome 7qtelo BAC E3, complete sequence.	Homo sapiens	39,291	02-OCT-1998
rxa01927 1503	GB_BA1:CGPAN	2164	X96580	C.glutamicum panB, panC & xyIB genes.	Corynebacterium glutamicum	38,384	11-MAY-1999
	GB_BA1:ASXYLA	1905	X59466	Arthrobacter Sp. N.R.R.L. B3728 xyIA gene for D-xylose(D-glucose) isomerase.	Arthrobacter sp.	56,283	04-MAY-1992
	GB_HTG3:AC009500	176060	AC009500	Homo sapiens clone NH0511A20, *** SEQUENCING IN PROGRESS *** , 6 unordered pieces.	Homo sapiens	37,593	24-Aug-99
	GB_BA2:AE000739	13335	AE000739	Aquifex aeolicus section 71 of 109 of the complete genome.	Aquifex aeolicus	36,309	25-MAR-1998
rxa01989 630	GB_EST28:AI519629	612	AI519629	LD39282.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD39282 5prime, mRNA sequence.	Drosophila melanogaster	41,941	16-MAR-1999
	GB_EST21:AA949396	767	AA949396	LD28277.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD28277 5prime, mRNA sequence.	Drosophila melanogaster	39,855	25-Nov-98
	GB_BA1:BSPGIA	1822	X16639	Bacillus stearothermophilus pgIA gene for phosphoglucoisomerase isoenzyme A (EC 5.3.1.9).	Bacillus stearothermophilus	66,292	20-Apr-95
	GB_BA1:BSUB0017	217420	Z99120	Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.	Bacillus subtilis	37,255	26-Nov-97
rxa02026 720	GB_BA2:AF132127	8452	AF132127	Streptococcus mutans sorbitol phosphoenolpyruvate:sugar phosphotransferase operon, complete sequence and unknown gene.	Streptococcus mutans	63,607	28-Sep-99
	GB_BA1:SXSCRBA	3161	X67744	S.xylosus scrB and scrR genes.	Staphylococcus xylosus	67,778	28-Nov-96
	GB_BA1:BSUB0020	212150	Z99123	Bacillus subtilis complete genome (section 20 of 21): from 3798401 to 4010550.	Bacillus subtilis	35,574	26-Nov-97
	GB_BA1:BSGENR	97015	X73124	B.subtilis genomic region (325 to 333).	Bacillus subtilis	51,826	2-Nov-93
rxa02028 526	GB_BA1:MTCI237	27030	Z94752	Mycobacterium tuberculosis H37Rv complete genome; segment 46/162.	Mycobacterium tuberculosis	54,476	17-Jun-98

Table 4 (continued)

	GB_PL2:SCE9537	66030	U18778	Saccharomyces cerevisiae chromosome V cosmid 9537, 9581, 9495, 9867, and lambda clone 5898.	Saccharomyces cerevisiae	36,100	1-Aug-97
	GB_GSS13:AQ501177	767	AQ501177	V26G9 mTn-3xHA/lacZ Insertion Library Saccharomyces cerevisiae genomic 5', genomic survey sequence.	Saccharomyces cerevisiae	32,039	29-Apr-99
rx02054	GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	61,896	27-Aug-99
	GB_BA1:MTY13E12	43401	Z95390	Mycobacterium tuberculosis H37Rv complete genome; segment 147/162.	Mycobacterium tuberculosis	59,964	17-Jun-98
rx02056	GB_BA1:MTU43540	3453	U43540	Mycobacterium tuberculosis rfbA, rhamnose biosynthesis protein (rfbA), and rmlC genes, complete cds.	Mycobacterium tuberculosis	59,659	14-Aug-97
	GB_PAT:E14601	4394	E14601	Brevibacterium lactofermentum gene for alpha-ketoglutaric acid dehydrogenase.	Corynebacterium glutamicum	98,928	28-Jul-99
	GB_BA1:D84102	4394	D84102	Corynebacterium glutamicum DNA for 2-oxoglutarate dehydrogenase, complete cds.	Corynebacterium glutamicum	98,928	6-Feb-99
	GB_BA1:MTV006	22440	AL021006	Mycobacterium tuberculosis H37Rv complete genome; segment 54/162.	Mycobacterium tuberculosis	39,265	18-Jun-98
rx02061	GB_HTG7:AC005883	211682	AC005883	Homo sapiens chromosome 17 clone RP11-958E11 map 17, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	37,453	08-DEC-1999
	GB_PL2:ATAC003033	84254	AC003033	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence.	Arabidopsis thaliana	37,711	19-DEC-1997
	GB_PL2:ATAC002334	75050	AC002334	Arabidopsis thaliana chromosome II BAC F25I18 genomic sequence, complete sequence.	Arabidopsis thaliana	37,711	04-MAR-1998
rx02063	GB_BA1:SCGLGC	1518	X89733	S.coelicolor DNA for glgC gene.	Streptomyces coelicolor	56,972	12-Jul-99
	GB_GSS4:AQ687350	786	AQ687350	nbxb0074H11r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0074H11r, genomic survey sequence.	Oryza sativa	40,696	1-Jul-99
	GB_EST38:AW028530	444	AW028530	wv27f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2530795 3' similar to WP:T03G11.6 CE04874 ;, mRNA sequence.	Homo sapiens	36,795	27-OCT-1999
rx02100	GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	Mycobacterium tuberculosis	40,156	10-DEC-1996
	GB_BA1:MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162.	Mycobacterium tuberculosis	55,218	17-Jun-98
	GB_BA1:SCO001205	9589	AJ001205	Streptomyces coelicolor A3(2) glycogen metabolism clusterl.	Streptomyces coelicolor	38,475	29-MAR-1999
rx02122	GB_BA1:D90858	13548	D90858	E.coli genomic DNA, Kohara clone #401(51.3-51.6 min.).	Escherichia coli	38,586	29-MAY-1997
	GB_EST37:A1948595	469	A1948595	wq07d12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2470583 3', mRNA sequence.	Homo sapiens	37,259	6-Sep-99
rx02140	GB_HTG3:AC010387	220665	AC010387	Homo sapiens chromosome 5 clone CITB-H1_2074D8, *** SEQUENCING IN PROGRESS ***, 77 unordered pieces.	Homo sapiens	38,868	15-Sep-99
	GB_BA1:MSGB1551CS	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	51,399	15-Jun-96
	GB_BA1:MSGB1554CS	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	51,399	15-Jun-96
	GB_RO:AF093099	2482	AF093099	Mus musculus transcription factor TBLYM (Tblym) mRNA, complete cds.	Mus musculus	36,683	01-OCT-1999
rx02142	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	57,292	17-Jun-98

Table 4 (continued)

	GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	35,058	24-MAR-1999
	GB_BA1:AB016787	5550	AB016787	Pseudomonas putida genes for cytochrome o ubiquinol oxidase A-E and 2 ORFs, complete cds.	Pseudomonas putida	47,403	5-Aug-99
rx02143	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	57,317	17-Jun-98
	GB_BA1:MSG B1551CS	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	38,159	15-Jun-96
	GB_BA1:MSG B1554CS	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	38,159	15-Jun-96
rx02144	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	55,530	17-Jun-98
	GB_HTG3:AC011500_0	300851	AC011500	Homo sapiens chromosome 19 clone C1T978SKB_60E11, *** SEQUENCING IN PROGRESS ***, 246 unordered pieces.	Homo sapiens	39,659	18-Feb-00
	GB_HTG3:AC011500_0	300851	AC011500	Homo sapiens chromosome 19 clone C1T978SKB_60E11, *** SEQUENCING IN PROGRESS ***, 246 unordered pieces.	Homo sapiens	39,659	18-Feb-00
rx02147	GB_EST28:AI492095	485	AI492095	tg07a01.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108040 3', mRNA sequence.	Homo sapiens	39,798	30-MAR-1999
	GB_EST10:AA157467	376	AA157467	zo50e01.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590328 5', mRNA sequence.	Homo sapiens	36,436	11-DEC-1996
	GB_EST10:AA157467	376	AA157467	zo50e01.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590328 5', mRNA sequence.	Homo sapiens	36,436	11-DEC-1996
rx02149	GB_PR3:HSBK277P6	61698	AL117347	Human DNA sequence from clone 277P6 on chromosome 1q25.3-31.2, complete sequence.	Homo sapiens	36,872	23-Nov-99
	GB_BA2:EMB065R075	360	AF116423	Rhizobium etli mutant MB045 RosR-transcriptionally regulated sequence.	Rhizobium etli	43,175	06-DEC-1999
	GB_EST34:AI789323	574	AI789323	uk53g05.y1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1972760 5' similar to WP:K11H12.8 CE12160 :, mRNA sequence.	Mus musculus	39,715	2-Jul-99
rx02175	GB_BA1:CGGLTG	3013	X66112	C.glutamicum glt gene for citrate synthase and ORF.	Corynebacterium glutamicum	100,000	17-Feb-95
	GB_BA1:MTCY31	37630	Z73101	Mycobacterium tuberculosis H37Rv complete genome; segment 41/162.	Mycobacterium tuberculosis	64,331	17-Jun-98
	GB_BA1:MLCB57	38029	Z99494	Mycobacterium leprae cosmid B57.	Mycobacterium leprae	62,491	10-Feb-99
rx02196	GB_RO:RATDAPRP	2819	M76426	Rattus norvegicus dipeptidyl aminopeptidase-related protein (dpp6) mRNA, complete cds.	Rattus norvegicus	38,791	31-MAY-1995
	GB_GSS8:AQ012162	763	AQ012162	127PB037070197 Cosmid library of chromosome II Rhodobacter sphaeroides genomic clone 127PB037070197, genomic survey sequence.	Rhodobacter sphaeroides	40,044	4-Jun-98
	GB_RO:RATDAPRP	2819	M76426	Rattus norvegicus dipeptidyl aminopeptidase-related protein (dpp6) mRNA, complete cds.	Rattus norvegicus	37,312	31-MAY-1995
rx02209	GB_BA1:AB025424	2995	AB025424	Corynebacterium glutamicum gene for aconitase, partial cds.	Corynebacterium glutamicum	99,173	3-Apr-99
	GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.	Mycobacterium avium	40,219	26-MAR-1998

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Table 4 (continued)

rx02213 874	GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	38,253	17-Jun-98
	GB_BA1:AB025424	2995	AB025424	Corynebacterium glutamicum gene for aconitase, partial cds.	Corynebacterium glutamicum	99,096	3-Apr-99
	GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	34,937	17-Jun-98
	GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.	Mycobacterium avium tuberculosis	36,885	26-MAR-1998
rx02245 780	GB_BA2:RCU23145	5960	U23145	Rhodobacter capsulatus Calvin cycle carbon dioxide fixation operon: fructose-1,6-/sedoheptulose-1,7-bisphosphate aldolase (cbbA) gene, partial cds, Form II ribulose-1,5-bisphosphate carboxylase/oxygenase (cbbM) gene, complete cds, and Calvin cycle operon: pentose-5-phosphate-3-epimerase (cbbE), phosphoglycolate phosphatase (cbbZ), and cbbY genes, complete cds.	Rhodobacter capsulatus	48,701	28-OCT-1997
	GB_BA1:ECU82664	139818	U82664	Escherichia coli minutes 9 to 11 genomic sequence.	Escherichia coli	39,119	11-Jan-97
rx02256 1125	GB_HTG2:AC007922	158858	AC007922	Homo sapiens chromosome 18 clone HRPK.178_F_10 map 18, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces.	Homo sapiens	33,118	26-Jun-99
	GB_BA1:CGGAPPGK	3804	X59403	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase.	Corynebacterium glutamicum	99,289	05-OCT-1992
	GB_BA1:SCC54	30753	AL035591	Streptomyces coelicolor cosmid C54.	Streptomyces coelicolor	36,951	11-Jun-99
	GB_BA1:MTCY493	40790	Z95844	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162.	Mycobacterium tuberculosis	64,196	19-Jun-98
rx02257 1338	GB_BA1:CGGAPPGK	3804	X59403	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase.	Corynebacterium glutamicum	98,873	05-OCT-1992
	GB_BA1:MTCY493	40790	Z95844	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162.	Mycobacterium glutamicum	61,273	19-Jun-98
	GB_BA2:MAU82749	2530	U82749	Mycobacterium avium glyceraldehyde-3-phosphate dehydrogenase homolog (gapdh) gene, complete cds; and phosphoglycerate kinase gene, partial cds.	Mycobacterium avium tuberculosis	61,772	6-Jan-98
	GB_BA1:CGGAPPGK	3804	X59403	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase.	Corynebacterium glutamicum	99,667	05-OCT-1992
rx02258 900	GB_BA1:CORPEPC	4885	M25819	C.glutamicum phosphoenolpyruvate carboxylase gene, complete cds.	Corynebacterium glutamicum	100,000	15-DEC-1995
	GB_PAT:A09073	4885	A09073	C.glutamicum ppg gene for phosphoenol pyruvate carboxylase.	Corynebacterium glutamicum	100,000	25-Aug-93
	GB_BA1:CORPEPC	4885	M25819	C.glutamicum phosphoenolpyruvate carboxylase gene, complete cds.	Corynebacterium glutamicum	100,000	15-DEC-1995
	GB_PAT:A09073	4885	A09073	C.glutamicum ppg gene for phosphoenol pyruvate carboxylase.	Corynebacterium glutamicum	100,000	25-Aug-93
rx02259 2895	GB_BA1:CGPPC	3292	X14234	Corynebacterium glutamicum phosphoenolpyruvate carboxylase gene (EC 4.1.1.31).	Corynebacterium glutamicum	99,827	12-Sep-93

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Table 4 (continued)

rxa02288	969	GB_PR3:HSDJ94E24	243145	AL050317	Human DNA sequence from clone RP1-94E24 on chromosome 20q12, complete sequence.	Homo sapiens	36,039	03-DEC-1999	111
		GB_HTG3:AC010091	159526	AC010091	Homo sapiens clone NH0295A01, *** SEQUENCING IN PROGRESS *** , 4 unordered pieces.	Homo sapiens	35,331	11-Sep-99	
		GB_HTG3:AC010091	159526	AC010091	Homo sapiens clone NH0295A01, *** SEQUENCING IN PROGRESS *** , 4 unordered pieces.	Homo sapiens	35,331	11-Sep-99	
rxa02292	798	GB_BA2:AF125164	26443	AF125164	Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.	Bacteroides fragilis	39,747	01-DEC-1999	
		GB_GSS5:AQ744695	827	AQ744695	HS_5505_A2_C06_RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1081 Col=12 Row=E, genomic survey sequence.	Homo sapiens	39,185	16-Jul-99	111
		GB_EST14:AA381925	309	AA381925	EST95058 Activated T-cells Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	35,922	21-Apr-97	
rxa02322	511	GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	57,677	17-Jun-98	
		GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	37,143	17-Jun-98	
rxa02326	939	GB_BA1:CGPYC	3728	Y09548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	100,000	08-MAY-1998	111
		GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Corynebacterium glutamicum	100,000	24-DEC-1997	
		GB_BA1:MTCY349	43523	Z83018	Mycobacterium tuberculosis H37Rv complete genome; segment 131/162.	Mycobacterium tuberculosis	37,363	17-Jun-98	
rxa02327	1083	GB_BA1:CGPYC	3728	Y09548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	99,259	08-MAY-1998	
		GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Corynebacterium glutamicum	99,259	24-DEC-1997	111
		GB_BA1:MTCY349	43523	Z83018	Mycobacterium tuberculosis H37Rv complete genome; segment 131/162.	Mycobacterium tuberculosis	41,317	17-Jun-98	
rxa02328	1719	GB_BA1:CGPYC	3728	Y09548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	100,000	08-MAY-1998	
		GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Corynebacterium glutamicum	100,000	24-DEC-1997	
rxa02332	1266	GB_PL2:AF097728	3916	AF097728	Aspergillus terreus pyruvate carboxylase (Pyc) mRNA, complete cds.	Aspergillus terreus	52,248	29-OCT-1998	PCT/IB00/00943
		GB_BA1:MSGLTA	1776	X60513	M.smegmatis gltA gene for citrate synthase.	Mycobacterium smegmatis	58,460	20-Sep-91	
		GB_BA2:ABU85944	1334	U85944	Antarctic bacterium DS2-3R citrate synthase (cisy) gene, complete cds.	Antarctic bacterium DS2-3R	57,154	23-Sep-97	
rxa02333	1038	GB_BA2:AE000175	15067	AE000175	Escherichia coli K-12 MG1655 section 65 of 400 of the complete genome.	Escherichia coli	38,164	12-Nov-98	
		GB_BA1:MSGLTA	1776	X60513	M.smegmatis gltA gene for citrate synthase.	Mycobacterium smegmatis	58,929	20-Sep-91	PCT/IB00/00943
		GB_PR4:HUAC002299	171681	AC002299	Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 ~complete genomic sequence, complete sequence.	Homo sapiens	33,070	23-Nov-99	

Table 4 (continued)

	GB_HTG2:AC007889	127840	AC007889	Drosophila melanogaster chromosome 3 clone BACR48E12 (D695) RPCI-98 48.E.12 map 87A-87B strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 86 unordered pieces.	Drosophila melanogaster	34,897	2-Aug-99
rx02399 1467	GB_BA1:CGACEA	2427	X75504	C.glutamicum aceA gene and thiX genes (partial).	Corynebacterium glutamicum	100,000	9-Sep-94
	GB_BA1:CORACEA	1905	L28760	Corynebacterium glutamicum isocitrate lyase (aceA) gene.	Corynebacterium glutamicum	100,000	10-Feb-95
rx02404 2340	GB_PAT:I13693	2135	I13693	Sequence 3 from patent US 5439822.	Unknown.	99,795	26-Sep-95
	GB_BA1:CGACEB	3024	X78491	C.glutamicum (ATCC 13032) aceB gene.	Corynebacterium glutamicum	99,914	13-Jan-95
	GB_BA1:CORACEB	2725	L27123	Corynebacterium glutamicum malate synthase (aceB) gene, complete cds.	Corynebacterium glutamicum	99,786	8-Jun-95
	GB_BA1:PFFC2	5588	Y11998	P.fluorescens FC2.1, FC2.2, FC2.3c, FC2.4 and FC2.5c open reading frames.	Pseudomonas fluorescens	63,539	11-Jul-97
rx02414 870	GB_PR4:AC007102	176258	AC007102	Homo sapiens chromosome 4 clone C0162P16 map 4p16, complete sequence.	Homo sapiens	35,069	2-Jun-99
	GB_HTG3:AC011214	183414	AC011214	Homo sapiens clone 5_C_3, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	36,885	03-OCT-1999
	GB_HTG3:AC011214	183414	AC011214	Homo sapiens clone 5_C_3, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	36,885	03-OCT-1999
rx02435 681	GB_BA2:AF101055	7457	AF101055	Clostridium acetobutylicum atp operon, complete sequence.	Clostridium acetobutylicum	39,605	03-MAR-1999
	GB_OM:RABPKA	4441	J03247	Rabbit phosphorylase kinase (alpha subunit) mRNA, complete cds.	Oryctolagus cuniculus	36,061	27-Apr-93
	GB_OM:RABPLASISM	4458	M64656	Oryctolagus cuniculus phosphorylase kinase alpha subunit mRNA, complete cds.	Oryctolagus cuniculus	36,000	22-Jun-98
rx02440 963	GB_EST14:AA417723	374	AA417723	zv01b12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746207 3' similar to contains Alu repetitive element;contains element L1 repetitive element ;, mRNA sequence.	Homo sapiens	38,770	16-OCT-1997
	GB_EST11:AA215428	303	AA215428	zr95a07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683412 3' similar to contains Alu repetitive element;, mRNA sequence.	Homo sapiens	39,934	13-Aug-97
	GB_BA1:MTCY77	22255	Z95389	Mycobacterium tuberculosis H37Rv complete genome; segment 146/162.	Mycobacterium tuberculosis	38,889	18-Jun-98
rx02453 876	GB_EST14:AA426336	375	AA426336	zv53g02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757394 3', mRNA sequence.	Homo sapiens	38,043	16-OCT-1997
	GB_BA1:STMAACC8	1353	M55426	S.fradiae aminoglycoside acetyltransferase (aacC8) gene, complete cds.	Streptomyces fradiae	37,097	05-MAY-1993
	GB_PR3:AC004500	77538	AC004500	Homo sapiens chromosome 5, P1 clone 1076B9 (LBNL H14), complete sequence.	Homo sapiens	33,256	30-MAR-1998
rx02474 897	GB_BA1:AB009078	2686	AB009078	Brevibacterium saccharolyticum gene for L-2,3-butanediol dehydrogenase, complete cds.	Brevibacterium saccharolyticum	96,990	13-Feb-99
	GB_OM:BTU71200	877	U71200	Bos taurus acetoin reductase mRNA, complete cds.	Bos taurus	51,659	8-Oct-97
	GB_EST2:F12685	287	F12685	HSC3DA031 normalized infant brain cDNA Homo sapiens cDNA clone c-3da03, mRNA sequence	Homo sapiens	41,509	14-Mar-95
rx02480 1779	GB_BA1:MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	Mycobacterium tuberculosis	36,737	23-Jun-99

Table 4 (continued)

rxa02485	GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	35,511	24-MAR-1999
	GB_BA1:AP000060	347800	AP000060	Aeropyrum pernix genomic DNA, section 3/7.	Aeropyrum pernix	48,014	22-Jun-99
rx02492	GB_BA1:STMPGM	921	M83661	Streptomyces coelicolor phosphoglycerate mutase (PGM) gene, complete cds.	Streptomyces coelicolor	65,672	26-Apr-93
	GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	61,436	17-Jun-98
rx02528	GB_BA1:U00018	42991	U00018	Mycobacterium leprae cosmid B2168.	Mycobacterium leprae	37,893	01-MAR-1994
	GB_PR2:HS161N10	56075	AL008707	Human DNA sequence from PAC 161N10 on chromosome Xq25. Contains EST.	Homo sapiens	37,051	23-Nov-99
rx02539	GB_HTG2:AC008235	136017	AC008235	Drosophila melanogaster chromosome 3 clone BACR15B19 (D995) RPCI-98 15.B.19 map 94F-95A strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** , 125 unordered pieces.	Drosophila melanogaster	36,822	2-Aug-99
	GB_HTG2:AC008235	136017	AC008235	Drosophila melanogaster chromosome 3 clone BACR15B19 (D995) RPCI-98 15.B.19 map 94F-95A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 125 unordered pieces.	Drosophila melanogaster	36,822	2-Aug-99
rx02551	GB_BA2:RSU17129	17425	U17129	Rhodococcus erythropolis ThcA (thcA) gene, complete cds; and unknown genes.	Rhodococcus erythropolis	66,117	16-Jul-99
	GB_BA1:MTV038	16094	AL021933	Mycobacterium tuberculosis H37Rv complete genome; segment 24/162.	Mycobacterium tuberculosis	65,174	17-Jun-98
rx02551	GB_BA2:AF068264	3152	AF068264	Pseudomonas aeruginosa quinoprotein ethanol dehydrogenase (exaA)gene, partial cds; cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrroloquinoline quinone synthesis A (pqqA) genes, complete cds; and pyrroloquinoline quinone synthesis B (pqqB) gene, partial cds.	Pseudomonas aeruginosa	65,448	18-MAR-1999
	GB_BA1:BACHYPTP	17057	D29985	Bacillus subtilis wapA and orf genes for wall-associated protein and hypothetical proteins.	Bacillus subtilis	53,602	7-Feb-99
rx02556	GB_BA1:BACHUTWAP	28954	D31856	Bacillus subtilis genome containing the hut and wapA loci.	Bacillus subtilis	53,602	7-Feb-99
	GB_BA1:BSGBGLUC	4290	Z34526	B.subtilis (Marburg 168) genes for beta-glucoside permease and beta-glucosidase.	Bacillus subtilis	53,602	3-Jul-95
rx02560	GB_HTG3:AC008128	335761	AC008128	Homo sapiens, *** SEQUENCING IN PROGRESS *** , 106 unordered pieces.	Homo sapiens	34,022	22-Aug-99
	GB_HTG3:AC008128	335761	AC008128	Homo sapiens, *** SEQUENCING IN PROGRESS *** , 106 unordered pieces.	Homo sapiens	34,022	22-Aug-99
rx02560	GB_PL2:AC005292	99053	AC005292	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence.	Arabidopsis thaliana	33,858	16-Apr-99
	GB_IN1:CEF07A11	35692	Z66511	Caenorhabditis elegans cosmid F07A11, complete sequence.	Caenorhabditis elegans	36,420	2-Sep-99
rx02560	GB_EST32:AI731605	566	AI731605	BNLGH10201 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AC004684) hypothetical protein [Arabidopsis thaliana], mRNA sequence.	Gossypium hirsutum	38,095	11-Jun-99
	GB_IN1:CEF07A11	35692	Z66511	Caenorhabditis elegans cosmid F07A11, complete sequence.	Caenorhabditis elegans	33,707	2-Sep-99

Table 4 (continued)

rx02572 668	GB_BA1:MTCY63	38900	Z96800	Mycobacterium tuberculosis H37Rv complete genome; segment 16/162.	Mycobacterium tuberculosis	61,677	17-Jun-98
	GB_BA1:MTCY63	38900	Z96800	Mycobacterium tuberculosis H37Rv complete genome; segment 16/162.	Mycobacterium tuberculosis	37,170	17-Jun-98
	GB_HTG1:HS24H01	46989	AL121632	Homo sapiens chromosome 21 clone LLNLc116H0124 map 21q21, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	19,820	29-Sep-99
rx02596 1326	GB_BA1:MTV026	23740	AL022076	Mycobacterium tuberculosis H37Rv complete genome; segment 157/162.	Mycobacterium tuberculosis	36,957	24-Jun-99
	GB_BA2:AF026540	1778	AF026540	Mycobacterium tuberculosis UDP-galactopyranose mutase (glf) gene, complete cds.	Mycobacterium tuberculosis	67,627	30-OCT-1998
	GB_BA2:MTU96128	1200	U96128	Mycobacterium tuberculosis UDP-galactopyranose mutase (glf) gene, complete cds.	Mycobacterium tuberculosis	70,417	25-MAR-1998
rx02611 1775	GB_BA1:MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162.	Mycobacterium tuberculosis	38,532	17-Jun-98
	GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	Mycobacterium tuberculosis	60,575	10-DEC-1996
	GB_BA1:U00014	36470	U00014	Mycobacterium leprae cosmid B1549.	Mycobacterium leprae	57,486	29-Sep-94
rx02612 2316	GB_BA1:MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162.	Mycobacterium tuberculosis	38,018	17-Jun-98
	GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	Mycobacterium tuberculosis	58,510	10-DEC-1996
	GB_BA1:STMGLGEN	2557	L11647	Streptomyces aureofaciens glycogen branching enzyme (glgB) gene, complete cds.	Streptomyces aureofaciens	57,193	25-MAY-1995
rx02621 942	GB_BA1:CGL133719	1839	AJ133719	Corynebacterium glutamicum yjcc gene, amtR gene and citE gene, partial.	Corynebacterium glutamicum	36,858	12-Aug-99
	GB_IN1:CEM106	39973	Z46935	Caenorhabditis elegans cosmid M106, complete sequence.	Caenorhabditis elegans	37,608	2-Sep-99
	GB_EST29:AI547662	377	AI547662	UI-R-C3-sz-h-03-0-UI.s1 UI-R-C3 Rattus norvegicus cDNA clone UI-R-C3-sz-h-03-0-UI 3', mRNA sequence.	Rattus norvegicus	50,667	3-Jul-99
rx02640 1650	GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	39,187	24-Jun-99
	GB_BA1:PAU49666	4495	U49666	Pseudomonas aeruginosa (orfX), glycerol dffusion facilitator (glpF), glycerol kinase (glpK), and Glp repressor (glpR) genes, complete cds, and (orfK) gene, partial cds.	Pseudomonas aeruginosa	59,273	18-MAY-1997
	GB_BA1:AB015974	1641	AB015974	Pseudomonas tolaasii glpK gene for glycerol kinase, complete cds.	Pseudomonas tolaasii	58,339	28-Aug-99
rx02654 1008	GB_EST6:N65787	512	N65787	20827 Lambda-PRL2 Arabidopsis thaliana cDNA clone 232B7T7, mRNA sequence.	Arabidopsis thaliana	39,637	5-Jan-98
	GB_PL2:T17H3	65839	AC005916	Arabidopsis thaliana chromosome 1 BAC T17H3 sequence, complete sequence.	Arabidopsis thaliana	33,735	5-Aug-99
	GB_RO:MMU58105	88871	U58105	Mus musculus Btk locus, alpha-D-galactosidase A (Ags), ribosomal protein (L44L), and Bruton's tyrosine kinase (Btk) genes, complete cds.	Mus musculus	35,431	13-Feb-97
rx02666 891	GB_PR3:AC004643	43411	AC004643	Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.	Homo sapiens	38,851	01-MAY-1998

Table 4 (continued)

				Homo sapiens		41,599	01-MAY-1998
				Corynebacterium glutamicum		40,413	1-Jul-98
				Paracoccus denitrificans		40,735	20-MAY-1993
				Mycobacterium tuberculosis		36,471	17-Jun-98
				Myxococcus xanthus		38,477	27-Jan-94
				Bacillus caldolyticus		57,371	26-Apr-93
				Bacillus stearothermophilus		57,277	26-Apr-93
				Bacillus stearothermophilus		57,277	29-Jul-93
				Danio rerio		50,746	27-Jun-97
				Danio rerio		36,364	27-Jun-97
				Homo sapiens		37,059	29-DEC-1998
				Danio rerio		42,149	27-Jun-97
				Homo sapiens		37,655	15-Nov-99
				Corynebacterium glutamicum		99,580	24-Jun-98
				Mycobacterium tuberculosis		38,363	19-Jun-98
				Streptomyces coelicolor		39,444	27-Jul-98
				Corynebacterium glutamicum		98,226	24-Jun-98
				Streptomyces coelicolor		60,399	12-Jul-99
				Streptomyces coelicolor		36,426	27-Jul-98
				Corynebacterium glutamicum		99,640	20-Feb-99

Table 4 (continued)

rxa02829	373	GB_HTG1:HSU9G8	48735	AL008714	Homo sapiens chromosome X clone LL0XNC01-9G8, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	41,595	23-Nov-99
		GB_HTG1:HSU9G8	48735	AL008714	Homo sapiens chromosome X clone LL0XNC01-9G8, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	41,595	23-Nov-99
		GB_PR3:HSU85B5	39550	Z69724	Human DNA sequence from cosmid U85B5, between markers DXS366 and DXS87 on chromosome X.	Homo sapiens	41,595	23-Nov-99
rx03216	1141	GB_HTG3:AC008184	151720	AC008184	Drosophila melanogaster chromosome 2 clone BACR04D05 (D540) RPCI-98 04.D.5 map 36E5-36F2 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.	Drosophila melanogaster	39,600	2-Aug-99
		GB_EST15:AA477537	411	AA477537	zu36g12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740134 5' similar to contains Alu repetitive element;contains element HGR repetitive element ;, mRNA sequence.	Homo sapiens	37,260	9-Nov-97
		GB_EST26:AI330662	412	AI330662	fa91d08.y1 zebrafish fin day1 regeneration Danio rerio cDNA 5', mRNA sequence.	Danio rerio	37,805	28-DEC-1998
rx03215	1038	GB_BA1:SC3F9	19830	AL023862	Streptomyces coelicolor cosmid 3F9.	Streptomyces coelicolor A3(2)	48,657	10-Feb-99
		GB_BA1:SLLINC	36270	X79146	S.lincolnensis (78-11) Lincomycin production genes.	Streptomyces lincolnensis	39,430	15-MAY-1996
		GB_HTG5:AC009660	204320	AC009660	Homo sapiens chromosome 15 clone RP11-424J10 map 15, *** SEQUENCING IN PROGRESS ***, 41 unordered pieces.	Homo sapiens	35,151	04-DEC-1999
rx03224	1288	GB_PR3:AC004076	41322	AC004076	Homo sapiens chromosome 19, cosmid R30217, complete sequence.	Homo sapiens	37,788	29-Jan-98
		GB_PL2:SPAC926	23193	AL110469	S.pombe chromosome I cosmid c926.	Schizosaccharomyces pombe	38,474	2-Sep-99
		GB_BA2:AE001081	11473	AE001081	Archaeoglobus fulgidus section 26 of 172 of the complete genome.	Archaeoglobus fulgidus	35,871	15-DEC-1997

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

5 A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose,
10 2.46 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 10 ml/l KH_2PO_4 solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l $(\text{NH}_4)_2\text{SO}_4$, 1 g/l NaCl, 2 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 0.2 g/l CaCl_2 , 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l $\text{FeSO}_4 \times \text{H}_2\text{O}$, 10 mg/l $\text{ZnSO}_4 \times 7 \text{H}_2\text{O}$, 3 mg/l $\text{MnCl}_2 \times 4 \text{H}_2\text{O}$, 30 mg/l H_3BO_3 , 20 mg/l $\text{CoCl}_2 \times 6 \text{H}_2\text{O}$, 1 mg/l $\text{NiCl}_2 \times 6 \text{H}_2\text{O}$, 3 mg/l $\text{Na}_2\text{MoO}_4 \times 2 \text{H}_2\text{O}$, 500 mg/l complexing agent
15 (EDTA or critic acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting
20 protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca.18 h at 37°C. The DNA was purified by
25 extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20
30 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30

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min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

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Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (*see e.g.*, Sambrook, J. *et al.* (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

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Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (*see e.g.*, Fleischman, R.D. *et al.* (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

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Example 4: *In vivo* Mutagenesis

In vivo mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (*e.g.* *Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain

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the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (*e.g.*, mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as *e.g.*, pHM1519 or pBL1) which replicate autonomously (for review see, *e.g.*, Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli* and *C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see *e.g.*, Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597, Martin J.F. *et al.* (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159:306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described *e.g.* in Schäfer, A *et al.*

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(1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an Mcr-deficient
5 *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be
10 overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other *Corynebacterium* or *Brevibacterium* species may be accomplished by well-known
15 methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as
20 homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) *From Genes to Clones – Introduction to Gene Technology*. VCH:
25 Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity
30 to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.*

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(1988) Current Protocols in Molecular Biology, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Procaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be

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advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or
5 ammonia salts, such as NH_4Cl or $(\text{NH}_4)_2\text{SO}_4$, NH_4OH , nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt,
10 molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic
15 acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A
20 Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if
25 necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to
30 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It

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is also possible to maintain a constant culture pH through the addition of NaOH or NH₄OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes.

For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD₆₀₀ of 0.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2,5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

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Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be

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found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) Enzymes. Longmans: London; Fersht, (1985) Enzyme Structure and Mechanism. Freeman: New York; Walsh, (1979) Enzymatic Reaction Mechanisms. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) Fundamentals of Enzymology. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) The Enzymes, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) Enzymkinetik, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) Methods of Enzymatic Analysis, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in Biomembranes, Molecular Structure and Function, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical chromatography such as high performance liquid chromatography (see, for example,

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Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to determine the overall efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum*

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cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on
5 a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule
10 to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. Biochemical
15 Engineering Fundamentals, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994)
20 *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotekhnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley and Sons; Fallon, A. *et al.*
25 (1987) Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17.

Example 11: Analysis of the Gene Sequences of the Invention

The comparison of sequences and determination of percent homology between
30 two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA*

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90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to SMP nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to SMP protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM. described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins.* John Wiley and Sons: New York). The gene sequences of the invention

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were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a
5 combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the
10 length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP
15 (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment homology percentages set forth in Table 4 under the heading “% homology (GAP)” are listed in the European numerical format, wherein a ‘,’ represents a decimal point. For
20 example, a value of “40,345” in this column represents “40.345%”.

Example 12: Construction and Operation of DNA Microarrays

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are
25 well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose,
30 nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label

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may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the
5 expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice
10 and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide
15 synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the
20 synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be
25 labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998),
30 *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as

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described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (*e.g.*, in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (*e.g.*, during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18:

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1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and
5 include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (*e.g.*, ^{35}S -methionine, ^{35}S -cysteine, ^{14}C -labelled amino acids, ^{15}N -amino acids, $^{15}\text{NO}_3$ or $^{15}\text{NH}_4^+$ or ^{13}C -labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly,
10 fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount
15 of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other
20 standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, *e.g.*, Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

25 The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (*e.g.*, different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications,
30 such as to compare the behavior of various organisms in a given (*e.g.*, metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

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Equivalents

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of
5 the invention described herein. Such equivalents are intended to be encompassed by the following claims.

SEQUENCE LISTING

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 40 45 50

 gtt gat gcg gct gac ctt gcc tgg gat cgc att cat gtg ttc ttc ggc 307
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Asp Cys Ile Val Phe His Val Glu Ala Thr Glu Gly His Val Glu Leu
      90              95              100

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		40					45					50				
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Thr	Val	Asn	Asp	Pro	Gly	Ser	Leu	Gly	Ile	Val	Leu	Gly	Gly	Ser	Gly	
	55					60					65					
aac	ggc	gag	cag	atc	gcc	gcc	aac	aag	gtc	aag	ggt	gca	cgt	tgt	gca	355
Asn	Gly	Glu	Gln	Ile	Ala	Ala	Asn	Lys	Val	Lys	Gly	Ala	Arg	Cys	Ala	
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gcg	aac	ctc	atc	ggc	atc	ggc	ggc	cgc	atg	cac	tca	gag				442
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Ala	Ile	Ala	Glu	His	Leu	Lys	Ala	His	Gly	His	Glu	Val	Ile	Asp	Cys
			20					25					30		

Gly	Ala	His	Thr	Tyr	Asp	Ala	Glu	Asp	Asp	Tyr	Pro	Ala	Phe	Cys	Ile
		35					40					45			

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

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

Gly	Ala	Arg	Cys	Ala	Leu	Ala	Trp	Ser	Val	Glu	Thr	Ala	Arg	Leu	Ala
				85					90					95	

Arg	Glu	His	Asn	Asn	Ala	Asn	Leu	Ile	Gly	Ile	Gly	Gly	Arg	Met	His
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Ser Glu

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<211> 2142

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

WO 01/00844

PCT/IB00/00943

<222> (101)..(2119)

<223> RXN01312

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 Met Ser Thr His Ser
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gaa acc acc cgc cca gag ttc atc cac cca gtc tca gtc ctc cca gag 163
 Glu Thr Thr Arg Pro Glu Phe Ile His Pro Val Ser Val Leu Pro Glu
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gtc tca gct ggt acg gtc ctt gac gct gca gag cca gca ggc gtt ccc 211
 Val Ser Ala Gly Thr Val Leu Asp Ala Ala Glu Pro Ala Gly Val Pro
 25 30 35

acc aaa gat atg tgg gaa tac caa aaa gac cac atg aac ctg gtc tcc 259
 Thr Lys Asp Met Trp Glu Tyr Gln Lys Asp His Met Asn Leu Val Ser
 40 45 50

cca ctg aac cga cgc aag ttc cgt gtc ctc gtc gtt ggc acc ggc ctg 307
 Pro Leu Asn Arg Arg Lys Phe Arg Val Leu Val Val Gly Thr Gly Leu
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tcc ggt ggt gct gca gca gca gcc ctc ggc gaa ctc gga tac gac gtc 355
 Ser Gly Gly Ala Ala Ala Ala Leu Gly Glu Leu Gly Tyr Asp Val
 70 75 80 85

aag gcg ttc acc tac cac gac gca cct cgc cgt gcg cac tcc att gct 403
 Lys Ala Phe Thr Tyr His Asp Ala Pro Arg Arg Ala His Ser Ile Ala
 90 95 100

gca cag ggt ggc gtt aac tcc gcc cgc ggc aag aag gta gac aac gac 451
 Ala Gln Gly Gly Val Asn Ser Ala Arg Gly Lys Lys Val Asp Asn Asp
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ggc gca tac cgc cac gtc aag gac acc gtc aag ggc ggc gac tac cgt 499
 Gly Ala Tyr Arg His Val Lys Asp Thr Val Lys Gly Gly Asp Tyr Arg
 120 125 130

ggt cgc gag tcc gac tgc tgg cgt ctc gcc gtc gag tcc gtc cgc gtc 547
 Gly Arg Glu Ser Asp Cys Trp Arg Leu Ala Val Glu Ser Val Arg Val
 135 140 145

atc gac cac atg aac gcc atc ggt gca cca ttc gcc cgc gaa tac ggt 595
 Ile Asp His Met Asn Ala Ile Gly Ala Pro Phe Ala Arg Glu Tyr Gly
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ggc gcc ttg gca acc cgt tcc ttc ggt ggt gtg cag gtc tcc cgt acc 643
 Gly Ala Leu Ala Thr Arg Ser Phe Gly Gly Val Gln Val Ser Arg Thr
 170 175 180

tac tac acc cgt gga caa acc gga cag cag ctg cag ttc tcc acc gca 691
 Tyr Tyr Thr Arg Gly Gln Thr Gly Gln Gln Leu Gln Phe Ser Thr Ala
 185 190 195

tcc gca cta cag cgc cag atc cac ctc ggc tcc gta gaa atc ttc acc 739
 Ser Ala Leu Gln Arg Gln Ile His Leu Gly Ser Val Glu Ile Phe Thr
 200 205 210

cat aac gaa atg gtt gac gtc att gtc acc gaa cgt aac ggt gaa aag	787
His Asn Glu Met Val Asp Val Ile Val Thr Glu Arg Asn Gly Glu Lys	
215 220 225	
cgc tgc gaa ggc ctg atc atg cgc aac ctg atc acc ggc gag ctc acc	835
Arg Cys Glu Gly Leu Ile Met Arg Asn Leu Ile Thr Gly Glu Leu Thr	
230 235 240 245	
gca cac acc ggc cat gcc gtt atc ctg gca acc ggt ggc tac ggc aac	883
Ala His Thr Gly His Ala Val Ile Leu Ala Thr Gly Gly Tyr Gly Asn	
250 255 260	
gtg tac cac atg tcc acc ctg gcc aag aac tcc aac gcc tcg gcc atc	931
Val Tyr His Met Ser Thr Leu Ala Lys Asn Ser Asn Ala Ser Ala Ile	
265 270 275	
atg cgt gca tac gaa gcc ggc gca tac ttc gcg tcc cca tcg ttc atc	979
Met Arg Ala Tyr Glu Ala Gly Ala Tyr Phe Ala Ser Pro Ser Phe Ile	
280 285 290	
cag ttc cac cca acc ggc ctg cct gtg aac tcc acc tgg cag tcc aag	1027
Gln Phe His Pro Thr Gly Leu Pro Val Asn Ser Thr Trp Gln Ser Lys	
295 300 305	
acc att ctg atg tcc gag tcg ctg cgt aac gac ggc cgc atc tgg tcc	1075
Thr Ile Leu Met Ser Glu Ser Leu Arg Asn Asp Gly Arg Ile Trp Ser	
310 315 320 325	
cct aag gaa ccg aac gat aac cgc gat cca aac acc atc cct gag gat	1123
Pro Lys Glu Pro Asn Asp Asn Arg Asp Pro Asn Thr Ile Pro Glu Asp	
330 335 340	
gag cgc gac tac ttc ctg gag cgc cgc tac cca gca ttc ggt aac ctc	1171
Glu Arg Asp Tyr Phe Leu Glu Arg Arg Tyr Pro Ala Phe Gly Asn Leu	
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gtc cca cgt gac gtt gct tcc cgt gcg atc tcc cag cag atc aat gct	1219
Val Pro Arg Asp Val Ala Ser Arg Ala Ile Ser Gln Gln Ile Asn Ala	
360 365 370	
ggt ctc ggt gtt gga cct ctg aac aac gct gca tac ctg gac ttc cgc	1267
Gly Leu Gly Val Gly Pro Leu Asn Asn Ala Ala Tyr Leu Asp Phe Arg	
375 380 385	
gac gcc acc gag cgc ctc gga cag gac acc atc cgc gag cgt tac tcc	1315
Asp Ala Thr Glu Arg Leu Gly Gln Asp Thr Ile Arg Glu Arg Tyr Ser	
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aac ctc ttc acc atg tac gaa gag gca att ggc gag gac cca tac tcc	1363
Asn Leu Phe Thr Met Tyr Glu Glu Ala Ile Gly Glu Asp Pro Tyr Ser	
410 415 420	
agc cca atg cgt att gca ccg acc tgc cac ttc acc atg ggt ggc ctc	1411
Ser Pro Met Arg Ile Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu	
425 430 435	
tgg act gac ttc aac gaa atg acg tca ctc cca ggt ctg ttc tgc gca	1459
Trp Thr Asp Phe Asn Glu Met Thr Ser Leu Pro Gly Leu Phe Cys Ala	
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Ser Leu Leu Ser Ala Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr	
470 475 480 485	
atc cct aac tac ctc ggc cca ttg ctt ggc tcc gag cgt ctg tca gag	1603
Ile Pro Asn Tyr Leu Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu	
490 495 500	
gat gca cca gaa gca cag gca gcg att gcg cgt gca cag gct cgc att	1651
Asp Ala Pro Glu Ala Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile	
505 510 515	
gac cgc ctc atg ggc aac cgc cca gag tgg gtc ggt gac aac gtt cac	1699
Asp Arg Leu Met Gly Asn Arg Pro Glu Trp Val Gly Asp Asn Val His	
520 525 530	
gga cct gag tac tac cac cgc cag ctt ggc gat atc ctg tac ttc tcc	1747
Gly Pro Glu Tyr Tyr His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser	
535 540 545	
tgt ggc gtt tcc cga aac gta gaa gac ctc cag gat ggc atc aac aag	1795
Cys Gly Val Ser Arg Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys	
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atc cgt gcc ctc cgc gat gac ttc tgg aag aac atg cgc atc acc ggc	1843
Ile Arg Ala Leu Arg Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly	
570 575 580	
agc acc gat gag atg aac cag gtt ctc gaa tac gca gca cgc gta gcc	1891
Ser Thr Asp Glu Met Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala	
585 590 595	
gac tac atc gac ctc ggc gaa ctc atg tgt gtc gac gcc ctc gac cgc	1939
Asp Tyr Ile Asp Leu Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg	
600 605 610	
gac gag tcc tgt ggc gct cac ttc cgc gac gac cac ctc tcc gaa gat	1987
Asp Glu Ser Cys Gly Ala His Phe Arg Asp Asp His Leu Ser Glu Asp	
615 620 625	
ggc gaa gca caa cgt gac gac caa aac tgg tgc ttc gtc tcc gca tgg	2035
Gly Glu Ala Gln Arg Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp	
630 635 640 645	
gaa cca ggc gag aat gga acc ttc gtc tgc cac gca gaa cca ctg ttc	2083
Glu Pro Gly Glu Asn Gly Thr Phe Val Cys His Ala Glu Pro Leu Phe	
650 655 660	
ttc gaa tct gtc cca ctg cag aca agg aac tac aag taatgaaact	2129
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PCT/IB00/00943

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Pro Ala Gly Val Pro Thr Lys Asp Met Trp Glu Tyr Gln Lys Asp His
          35           40           45

Met Asn Leu Val Ser Pro Leu Asn Arg Arg Lys Phe Arg Val Leu Val
 50           55           60

Val Gly Thr Gly Leu Ser Gly Gly Ala Ala Ala Ala Leu Gly Glu
 65           70           75           80

Leu Gly Tyr Asp Val Lys Ala Phe Thr Tyr His Asp Ala Pro Arg Arg
          85           90           95

Ala His Ser Ile Ala Ala Gln Gly Gly Val Asn Ser Ala Arg Gly Lys
          100          105          110

Lys Val Asp Asn Asp Gly Ala Tyr Arg His Val Lys Asp Thr Val Lys
          115          120          125

Gly Gly Asp Tyr Arg Gly Arg Glu Ser Asp Cys Trp Arg Leu Ala Val
          130          135          140

Glu Ser Val Arg Val Ile Asp His Met Asn Ala Ile Gly Ala Pro Phe
          145          150          155          160

Ala Arg Glu Tyr Gly Gly Ala Leu Ala Thr Arg Ser Phe Gly Gly Val
          165          170          175

Gln Val Ser Arg Thr Tyr Tyr Thr Arg Gly Gln Thr Gly Gln Gln Leu
          180          185          190

Gln Phe Ser Thr Ala Ser Ala Leu Gln Arg Gln Ile His Leu Gly Ser
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Val Glu Ile Phe Thr His Asn Glu Met Val Asp Val Ile Val Thr Glu
          210          215          220

Arg Asn Gly Glu Lys Arg Cys Glu Gly Leu Ile Met Arg Asn Leu Ile
          225          230          235          240

Thr Gly Glu Leu Thr Ala His Thr Gly His Ala Val Ile Leu Ala Thr
          245          250          255

Gly Gly Tyr Gly Asn Val Tyr His Met Ser Thr Leu Ala Lys Asn Ser
          260          265          270

Asn Ala Ser Ala Ile Met Arg Ala Tyr Glu Ala Gly Ala Tyr Phe Ala
          275          280          285

Ser Pro Ser Phe Ile Gln Phe His Pro Thr Gly Leu Pro Val Asn Ser
          290          295          300

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Gly	Arg	Ile	Trp	Ser	Pro	Lys	Glu	Pro	Asn	Asp	Asn	Arg	Asp	Pro	Asn	
				325					330					335		
Thr	Ile	Pro	Glu	Asp	Glu	Arg	Asp	Tyr	Phe	Leu	Glu	Arg	Arg	Tyr	Pro	
			340					345						350		
Ala	Phe	Gly	Asn	Leu	Val	Pro	Arg	Asp	Val	Ala	Ser	Arg	Ala	Ile	Ser	
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Gln	Gln	Ile	Asn	Ala	Gly	Leu	Gly	Val	Gly	Pro	Leu	Asn	Asn	Ala	Ala	
	370					375					380					
Tyr	Leu	Asp	Phe	Arg	Asp	Ala	Thr	Glu	Arg	Leu	Gly	Gln	Asp	Thr	Ile	
385					390					395					400	
Arg	Glu	Arg	Tyr	Ser	Asn	Leu	Phe	Thr	Met	Tyr	Glu	Glu	Ala	Ile	Gly	
				405					410					415		
Glu	Asp	Pro	Tyr	Ser	Ser	Pro	Met	Arg	Ile	Ala	Pro	Thr	Cys	His	Phe	
			420					425					430			
Thr	Met	Gly	Gly	Leu	Trp	Thr	Asp	Phe	Asn	Glu	Met	Thr	Ser	Leu	Pro	
		435					440					445				
Gly	Leu	Phe	Cys	Ala	Gly	Glu	Ala	Ser	Trp	Thr	Tyr	His	Gly	Ala	Asn	
	450					455					460					
Arg	Leu	Gly	Ala	Asn	Ser	Leu	Leu	Ser	Ala	Ser	Val	Asp	Gly	Trp	Phe	
465					470					475					480	
Thr	Leu	Pro	Phe	Thr	Ile	Pro	Asn	Tyr	Leu	Gly	Pro	Leu	Leu	Gly	Ser	
				485					490					495		
Glu	Arg	Leu	Ser	Glu	Asp	Ala	Pro	Glu	Ala	Gln	Ala	Ala	Ile	Ala	Arg	
			500					505					510			
Ala	Gln	Ala	Arg	Ile	Asp	Arg	Leu	Met	Gly	Asn	Arg	Pro	Glu	Trp	Val	
		515					520					525				
Gly	Asp	Asn	Val	His	Gly	Pro	Glu	Tyr	Tyr	His	Arg	Gln	Leu	Gly	Asp	
	530					535					540					
Ile	Leu	Tyr	Phe	Ser	Cys	Gly	Val	Ser	Arg	Asn	Val	Glu	Asp	Leu	Gln	
545					550					555					560	
Asp	Gly	Ile	Asn	Lys	Ile	Arg	Ala	Leu	Arg	Asp	Asp	Phe	Trp	Lys	Asn	
				565					570					575		
Met	Arg	Ile	Thr	Gly	Ser	Thr	Asp	Glu	Met	Asn	Gln	Val	Leu	Glu	Tyr	
			580					585					590			
Ala	Ala	Arg	Val	Ala	Asp	Tyr	Ile	Asp	Leu	Gly	Glu	Leu	Met	Cys	Val	
		595					600					605				
Asp	Ala	Leu	Asp	Arg	Asp	Glu	Ser	Cys	Gly	Ala	His	Phe	Arg	Asp	Asp	
	610					615					620					
His	Leu	Ser	Glu	Asp	Gly	Glu	Ala	Gln	Arg	Asp	Asp	Gln	Asn	Trp	Cys	

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PCT/IB00/00943

625		630		635		640
Phe Val Ser Ala Trp	Glu Pro Gly Glu Asn	Gly Thr Phe Val	Cys His			
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Ala Glu Pro Leu Phe	Phe Glu Ser Val	Pro Leu Gln Thr	Arg Asn Tyr			
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Lys

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gat aac cgc gat cca aac acc atc cct gag gat gag cgc gac tac ttc	96
Asp Asn Arg Asp Pro Asn Thr Ile Pro Glu Asp Glu Arg Asp Tyr Phe	
20 25 30	
ctg gag cgc cgc tac cca gca ttc ggt aac ctc gtc cca cgt gac gtt	144
Leu Glu Arg Arg Tyr Pro Ala Phe Gly Asn Leu Val Pro Arg Asp Val	
35 40 45	
gct tcc cgt gcg atc tcc cag cag atc aat gct ggt ctc ggt gtt gga	192
Ala Ser Arg Ala Ile Ser Gln Gln Ile Asn Ala Gly Leu Gly Val Gly	
50 55 60	
cct ctg aac aac gct gca tac ctg gac ttc cgc gac gcc acc gag cgc	240
Pro Leu Asn Asn Ala Ala Tyr Leu Asp Phe Arg Asp Ala Thr Glu Arg	
65 70 75 80	
ctc gga cag gac acc atc cgc gag cgt tac tcc aac ctc ttc acc atg	288
Leu Gly Gln Asp Thr Ile Arg Glu Arg Tyr Ser Asn Leu Phe Thr Met	
85 90 95	
tac gaa gag gca att ggc gag gac cca tac tcc agc cca atg cgt att	336
Tyr Glu Glu Ala Ile Gly Glu Asp Pro Tyr Ser Ser Pro Met Arg Ile	
100 105 110	
gca ccg acc tgc cac ttc acc atg ggt ggc ctc tgg act gac ttc aac	384
Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu Trp Thr Asp Phe Asn	
115 120 125	
gaa atg acg tca ctc cca ggt ctg ttc tgc gca ggc gaa gca tcc tgg	432
Glu Met Thr Ser Leu Pro Gly Leu Phe Cys Ala Gly Glu Ala Ser Trp	
130 135 140	
acc tac cac ggt gca aac cgt ctg ggc gca aac tcc ctg ctc tcc gct	480
Thr Tyr His Gly Ala Asn Arg Leu Gly Ala Asn Ser Leu Leu Ser Ala	

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tcc gtc gat ggc tgg ttc acc ctg cca ttc acc atc cct aac tac ctc				528
Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu	165	170	175	
ggc cca ttg ctt ggc tcc gag cgt ctg tca gag gat gca cca gaa gca				576
Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala	180	185	190	
cag gca gcg att gcg cgt gca cag gct cgc att gac cgc ctc atg ggc				624
Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile Asp Arg Leu Met Gly	195	200	205	
aac cgc cca gag tgg gtc ggt gac aac gtt cac gga cct gag tac tac				672
Asn Arg Pro Glu Trp Val Gly Asp Asn Val His Gly Pro Glu Tyr Tyr	210	215	220	
cac cgc cag ctt ggc gat atc ctg tac ttc tcc tgt ggc gtt tcc cga				720
His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser Cys Gly Val Ser Arg	225	230	235	240
aac gta gaa gac ctc cag gat ggc atc aac aag atc cgt gcc ctc cgc				768
Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys Ile Arg Ala Leu Arg	245	250	255	
gat gac ttc tgg aag aac atg cgc atc acc ggc agc acc gat gag atg				816
Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly Ser Thr Asp Glu Met	260	265	270	
aac cag gtt ctc gaa tac gca gca cgc gta gcc gac tac atc gac ctc				864
Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu	275	280	285	
ggc gaa ctc atg tgt gtc gac gcc ctc gac cgc gac gag tcc tgt ggc				912
Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly	290	295	300	
gct cac ttc cgc gac gac cac ctc tcc gaa gat ggc gaa gca caa cgt				960
Ala His Phe Arg Asp Asp His Leu Ser Glu Asp Gly Glu Ala Gln Arg	305	310	315	320
gac gac caa aac tgg tgc ttc gtc tcc gca tgg gaa cca ggc gag aat				1008
Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp Glu Pro Gly Glu Asn	325	330	335	
gga acc ttc gtc tgc cac gca gaa cca ctg ttc ttc gaa tct gtc cca				1056
Gly Thr Phe Val Cys His Ala Glu Pro Leu Phe Phe Glu Ser Val Pro	340	345	350	
ctg cag aca agg aac tac aag taatgaaact tacacttgag atc				1100
Leu Gln Thr Arg Asn Tyr Lys	355			

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<211> 359

<212> PRT

<213> Corynebacterium glutamicum

<400> 12

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PCT/IB00/00943

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Asp	Asn	Arg	Asp	Pro	Asn	Thr	Ile	Pro	Glu	Asp	Glu	Arg	Asp	Tyr	Phe	20	25	30	
Leu	Glu	Arg	Arg	Tyr	Pro	Ala	Phe	Gly	Asn	Leu	Val	Pro	Arg	Asp	Val	35	40	45	
Ala	Ser	Arg	Ala	Ile	Ser	Gln	Gln	Ile	Asn	Ala	Gly	Leu	Gly	Val	Gly	50	55	60	
Pro	Leu	Asn	Asn	Ala	Ala	Tyr	Leu	Asp	Phe	Arg	Asp	Ala	Thr	Glu	Arg	65	70	75	80
Leu	Gly	Gln	Asp	Thr	Ile	Arg	Glu	Arg	Tyr	Ser	Asn	Leu	Phe	Thr	Met	85	90	95	
Tyr	Glu	Glu	Ala	Ile	Gly	Glu	Asp	Pro	Tyr	Ser	Ser	Pro	Met	Arg	Ile	100	105	110	
Ala	Pro	Thr	Cys	His	Phe	Thr	Met	Gly	Gly	Leu	Trp	Thr	Asp	Phe	Asn	115	120	125	
Glu	Met	Thr	Ser	Leu	Pro	Gly	Leu	Phe	Cys	Ala	Gly	Glu	Ala	Ser	Trp	130	135	140	
Thr	Tyr	His	Gly	Ala	Asn	Arg	Leu	Gly	Ala	Asn	Ser	Leu	Leu	Ser	Ala	145	150	155	160
Ser	Val	Asp	Gly	Trp	Phe	Thr	Leu	Pro	Phe	Thr	Ile	Pro	Asn	Tyr	Leu	165	170	175	
Gly	Pro	Leu	Leu	Gly	Ser	Glu	Arg	Leu	Ser	Glu	Asp	Ala	Pro	Glu	Ala	180	185	190	
Gln	Ala	Ala	Ile	Ala	Arg	Ala	Gln	Ala	Arg	Ile	Asp	Arg	Leu	Met	Gly	195	200	205	
Asn	Arg	Pro	Glu	Trp	Val	Gly	Asp	Asn	Val	His	Gly	Pro	Glu	Tyr	Tyr	210	215	220	
His	Arg	Gln	Leu	Gly	Asp	Ile	Leu	Tyr	Phe	Ser	Cys	Gly	Val	Ser	Arg	225	230	235	240
Asn	Val	Glu	Asp	Leu	Gln	Asp	Gly	Ile	Asn	Lys	Ile	Arg	Ala	Leu	Arg	245	250	255	
Asp	Asp	Phe	Trp	Lys	Asn	Met	Arg	Ile	Thr	Gly	Ser	Thr	Asp	Glu	Met	260	265	270	
Asn	Gln	Val	Leu	Glu	Tyr	Ala	Ala	Arg	Val	Ala	Asp	Tyr	Ile	Asp	Leu	275	280	285	
Gly	Glu	Leu	Met	Cys	Val	Asp	Ala	Leu	Asp	Arg	Asp	Glu	Ser	Cys	Gly	290	295	300	
Ala	His	Phe	Arg	Asp	Asp	His	Leu	Ser	Glu	Asp	Gly	Glu	Ala	Gln	Arg	305	310	315	320
Asp	Asp	Gln	Asn	Trp	Cys	Phe	Val	Ser	Ala	Trp	Glu	Pro	Gly	Glu	Asn				

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PCT/IB00/00943

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Gly Thr Phe Val Cys His Ala Glu Pro Leu Phe Phe Glu Ser Val Pro					
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Leu Gln Thr Arg Asn Tyr Lys					
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 <223> RXN00231

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 Met Thr Ile Asn Val
 1 5
 ttc gaa cta ctt gtc aaa agt ccc acg ggt cta ctg att ggt gat tcc 163
 Phe Glu Leu Leu Val Lys Ser Pro Thr Gly Leu Leu Ile Gly Asp Ser
 10 15 20
 tgg gtg gaa gca tcc gac ggc ggt act ttc gat gtg gaa aac cca gcg 211
 Trp Val Glu Ala Ser Asp Gly Gly Thr Phe Asp Val Glu Asn Pro Ala
 25 30 35
 acg ggt gaa aca atc gca acg ctc gcg tct gct act tcc gag gat gca 259
 Thr Gly Glu Thr Ile Ala Thr Leu Ala Ser Ala Thr Ser Glu Asp Ala
 40 45 50
 ctg gct gct ctt gat gct gca tgc gct gtt cag gcc gag tgg gct agg 307
 Leu Ala Ala Leu Asp Ala Ala Cys Ala Val Gln Ala Glu Trp Ala Arg
 55 60 65
 atg cca gcg cgc gag cgt tct aat att tta cgc cgc ggt ttt gag ctc 355
 Met Pro Ala Arg Glu Arg Ser Asn Ile Leu Arg Arg Gly Phe Glu Leu
 70 75 80 85
 gta gca gaa cgt gca gaa gag ttc gcc acc ctc atg acc ttg gaa atg 403
 Val Ala Glu Arg Ala Glu Glu Phe Ala Thr Leu Met Thr Leu Glu Met
 90 95 100
 ggc aag cct ttg gct gaa gct cgc ggc gaa gtc acc tac ggc aac gaa 451
 Gly Lys Pro Leu Ala Glu Ala Arg Gly Glu Val Thr Tyr Gly Asn Glu
 105 110 115
 ttc ctg cgc tgg ttc tct gag gaa gca gtt cgt ctg tat ggc cgt tac 499
 Phe Leu Arg Trp Phe Ser Glu Glu Ala Val Arg Leu Tyr Gly Arg Tyr
 120 125 130
 gga acc aca cca gaa ggc aac ttg cgg atg ctg acc gcc ctc aag cca 547
 Gly Thr Thr Pro Glu Gly Asn Leu Arg Met Leu Thr Ala Leu Lys Pro
 135 140 145

gtt ggc ccg tgc ctc ctg atc acc cca tgg aac ttc cca cta gca atg	595
Val Gly Pro Cys Leu Leu Ile Thr Pro Trp Asn Phe Pro Leu Ala Met	
150 155 160 165	
gct acc cgc aag gtc gca cct gcg atc gct gca ggt tgt gtc atg gtg	643
Ala Thr Arg Lys Val Ala Pro Ala Ile Ala Ala Gly Cys Val Met Val	
170 175 180	
ctc aag cca gct cga ctt acc ccg ctg acc tcc cag tat ttt gct cag	691
Leu Lys Pro Ala Arg Leu Thr Pro Leu Thr Ser Gln Tyr Phe Ala Gln	
185 190 195	
acc atg ctt gat gcc ggt ctt cca gca ggt gtc ctc aat gtg gtc tcc	739
Thr Met Leu Asp Ala Gly Leu Pro Ala Gly Val Leu Asn Val Val Ser	
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ggt gct tcc gcc tct gcg att tcc aac ccg att atg gaa gac gat cgc	787
Gly Ala Ser Ala Ser Ala Ile Ser Asn Pro Ile Met Glu Asp Asp Arg	
215 220 225	
ctt cgt aaa gtc tcc ttc acc ggc tcc acc cca gtt ggc cag cag ctg	835
Leu Arg Lys Val Ser Phe Thr Gly Ser Thr Pro Val Gly Gln Gln Leu	
230 235 240 245	
ctc aaa aag gct gcc gat aaa gtt ctg cgc acc tcc atg gaa ctt ggt	883
Leu Lys Lys Ala Ala Asp Lys Val Leu Arg Thr Ser Met Glu Leu Gly	
250 255 260	
ggc aac gca cct ttc att gtc ttc gag gac gcc gac cta gat ctc gcg	931
Gly Asn Ala Pro Phe Ile Val Phe Glu Asp Ala Asp Leu Asp Leu Ala	
265 270 275	
atc gaa ggt gcc atg ggt gcc aaa atg cgc aac atc ggc gaa gct tgc	979
Ile Glu Gly Ala Met Gly Ala Lys Met Arg Asn Ile Gly Glu Ala Cys	
280 285 290	
acc gca gcc aac cgt ttc tta gtc cac gaa tcc gtc gcc gat gaa ttc	1027
Thr Ala Ala Asn Arg Phe Leu Val His Glu Ser Val Ala Asp Glu Phe	
295 300 305	
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Gly Arg Arg Phe Ala Ala Arg Leu Glu Glu Gln Val Leu Gly Asn Gly	
310 315 320 325	
ctc gac gaa ggc gtc acc gtg ggc ccc ctg gtt gag gaa aaa gca cga	1123
Leu Asp Glu Gly Val Thr Val Gly Pro Leu Val Glu Glu Lys Ala Arg	
330 335 340	
gac agc gtt gca tcg ctt gtc gac gcc gcc gtc gcc gaa ggt gcc acc	1171
Asp Ser Val Ala Ser Leu Val Asp Ala Ala Val Ala Glu Gly Ala Thr	
345 350 355	
gtc ctc acc ggc ggc aag gcc ggc aca ggt gca ggc tac ttc tac gaa	1219
Val Leu Thr Gly Gly Lys Ala Gly Thr Gly Ala Gly Tyr Phe Tyr Glu	
360 365 370	
cca acg gtg ctc acg gga gtt tca aca gat gcg gct atc ctg aac gaa	1267
Pro Thr Val Leu Thr Gly Val Ser Thr Asp Ala Ala Ile Leu Asn Glu	
375 380 385	

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gag atc ttc ggt ccc gtc gca ccg atc gtc acc ttc caa acc gag gaa 1315
 Glu Ile Phe Gly Pro Val Ala Pro Ile Val Thr Phe Gln Thr Glu Glu
 390 395 400 405

 gaa gcc ctg cgt cta gcc aac tcc acc gaa tac gga ctg gcc tcc tat 1363
 Glu Ala Leu Arg Leu Ala Asn Ser Thr Glu Tyr Gly Leu Ala Ser Tyr
 410 415 420

 gtg ttc acc cag gac acc tca cgt att ttc cgc gtc tcc gat ggt ctc 1411
 Val Phe Thr Gln Asp Thr Ser Arg Ile Phe Arg Val Ser Asp Gly Leu
 425 430 435

 gag ttc ggc cta gtg ggc gtc aat tcc ggt gtc atc tct aac gct gct 1459
 Glu Phe Gly Leu Val Gly Val Asn Ser Gly Val Ile Ser Asn Ala Ala
 440 445 450

 gca cct ttt ggt ggc gta aaa caa tcc gga atg ggc cgc gaa ggt ggt 1507
 Ala Pro Phe Gly Gly Val Lys Gln Ser Gly Met Gly Arg Glu Gly Gly
 455 460 465

 ctc gaa gga atc gag gag tac acc tcc gtg cag tac atc ggt atc cgg 1555
 Leu Glu Gly Ile Glu Glu Tyr Thr Ser Val Gln Tyr Ile Gly Ile Arg
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 Asp Pro Tyr Ala Gly
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 Val Glu Asn Pro Ala Thr Gly Glu Thr Ile Ala Thr Leu Ala Ser Ala
 35 40 45

 Thr Ser Glu Asp Ala Leu Ala Ala Leu Asp Ala Ala Cys Ala Val Gln
 50 55 60

 Ala Glu Trp Ala Arg Met Pro Ala Arg Glu Arg Ser Asn Ile Leu Arg
 65 70 75 80

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

 Met Thr Leu Glu Met Gly Lys Pro Leu Ala Glu Ala Arg Gly Glu Val
 100 105 110

 Thr Tyr Gly Asn Glu Phe Leu Arg Trp Phe Ser Glu Glu Ala Val Arg
 115 120 125

 Leu Tyr Gly Arg Tyr Gly Thr Thr Pro Glu Gly Asn Leu Arg Met Leu
 130 135 140

Thr	Ala	Leu	Lys	Pro	Val	Gly	Pro	Cys	Leu	Leu	Ile	Thr	Pro	Trp	Asn	145	150	155	160
Phe	Pro	Leu	Ala	Met	Ala	Thr	Arg	Lys	Val	Ala	Pro	Ala	Ile	Ala	Ala	165	170	175	
Gly	Cys	Val	Met	Val	Leu	Lys	Pro	Ala	Arg	Leu	Thr	Pro	Leu	Thr	Ser	180	185	190	
Gln	Tyr	Phe	Ala	Gln	Thr	Met	Leu	Asp	Ala	Gly	Leu	Pro	Ala	Gly	Val	195	200	205	
Leu	Asn	Val	Val	Ser	Gly	Ala	Ser	Ala	Ser	Ala	Ile	Ser	Asn	Pro	Ile	210	215	220	
Met	Glu	Asp	Asp	Arg	Leu	Arg	Lys	Val	Ser	Phe	Thr	Gly	Ser	Thr	Pro	225	230	235	240
Val	Gly	Gln	Gln	Leu	Leu	Lys	Lys	Ala	Ala	Asp	Lys	Val	Leu	Arg	Thr	245	250	255	
Ser	Met	Glu	Leu	Gly	Gly	Asn	Ala	Pro	Phe	Ile	Val	Phe	Glu	Asp	Ala	260	265	270	
Asp	Leu	Asp	Leu	Ala	Ile	Glu	Gly	Ala	Met	Gly	Ala	Lys	Met	Arg	Asn	275	280	285	
Ile	Gly	Glu	Ala	Cys	Thr	Ala	Ala	Asn	Arg	Phe	Leu	Val	His	Glu	Ser	290	295	300	
Val	Ala	Asp	Glu	Phe	Gly	Arg	Arg	Phe	Ala	Ala	Arg	Leu	Glu	Glu	Gln	305	310	315	320
Val	Leu	Gly	Asn	Gly	Leu	Asp	Glu	Gly	Val	Thr	Val	Gly	Pro	Leu	Val	325	330	335	
Glu	Glu	Lys	Ala	Arg	Asp	Ser	Val	Ala	Ser	Leu	Val	Asp	Ala	Ala	Val	340	345	350	
Ala	Glu	Gly	Ala	Thr	Val	Leu	Thr	Gly	Gly	Lys	Ala	Gly	Thr	Gly	Ala	355	360	365	
Gly	Tyr	Phe	Tyr	Glu	Pro	Thr	Val	Leu	Thr	Gly	Val	Ser	Thr	Asp	Ala	370	375	380	
Ala	Ile	Leu	Asn	Glu	Glu	Ile	Phe	Gly	Pro	Val	Ala	Pro	Ile	Val	Thr	385	390	395	400
Phe	Gln	Thr	Glu	Glu	Glu	Ala	Leu	Arg	Leu	Ala	Asn	Ser	Thr	Glu	Tyr	405	410	415	
Gly	Leu	Ala	Ser	Tyr	Val	Phe	Thr	Gln	Asp	Thr	Ser	Arg	Ile	Phe	Arg	420	425	430	
Val	Ser	Asp	Gly	Leu	Glu	Phe	Gly	Leu	Val	Gly	Val	Asn	Ser	Gly	Val	435	440	445	
Ile	Ser	Asn	Ala	Ala	Ala	Pro	Phe	Gly	Gly	Val	Lys	Gln	Ser	Gly	Met	450	455	460	

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Gly Arg Glu Gly Gly Leu Glu Gly Ile Glu Glu Tyr Thr Ser Val Gln
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Tyr Ile Gly Ile Arg Asp Pro Tyr Ala Gly
 485 490

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 <223> RXA01311

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tcttcgaatc tgtcccactg cagacaagga actacaagta atg aaa ctt aca ctt 115
 Met Lys Leu Thr Leu
 1 5

gag atc tgg cgt caa gca ggc cca act gcg gaa ggc aag ttc gaa acc 163
 Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu Gly Lys Phe Glu Thr
 10 15 20

gtc cag gtt gac gac gcc gtc gcg cag atg tcc atc ctg gag ctg ctt 211
 Val Gln Val Asp Asp Ala Val Ala Gln Met Ser Ile Leu Glu Leu Leu
 25 30 35

gac cac gta aac aac aag ttc atc gaa gaa ggc aaa gaa cca ttc gcg 259
 Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly Lys Glu Pro Phe Ala
 40 45 50

ttc gcc tct gac tgc cgc gaa ggc att tgt ggt acc tgt ggt ctc ctc 307
 Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly Thr Cys Gly Leu Leu
 55 60 65

gtg aac ggt cgc cct cac ggc gcc gac cag aac aag cct gcc tgt gcg 355
 Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn Lys Pro Ala Cys Ala
 70 75 80 85

cag cgc ctg gtc agc tac aag gaa ggc gac acc ctc aag atc gaa cca 403
 Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr Leu Lys Ile Glu Pro
 90 95 100

ctg cgt tcc gcc gca tac cca gtg atc aag gac atg gtc gtc gac cgc 451
 Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp Met Val Val Asp Arg
 105 110 115

tcc gca ctg gac cgt gtc atg gaa cag ggt ggc tac gtg acc atc aac 499
 Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly Tyr Val Thr Ile Asn
 120 125 130

gca ggt acc gca cct gac gct gat acc ctc cac gtc aac cac gaa acc 547
 Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His Val Asn His Glu Thr
 135 140 145

gca gaa ctc gca ctt gac cac gca gcc tgc atc ggc tgt ggc gca tgt 595

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Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile Gly Cys Gly Ala Cys
 150 155 160 165

gtt gct gcc tgc cct aac ggc gca gca cac ctg ttc acc ggc gca aag 643
 Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu Phe Thr Gly Ala Lys
 170 175 180

ctt gtt cac ctc tcc ctc ctc cca ctg ggt aag gaa gag cgc gga ctg 691
 Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys Glu Glu Arg Gly Leu
 185 190 195

cgt gca cgt aag atg gtt gat gaa atg gaa acc aac ttc gga cac tgc 739
 Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr Asn Phe Gly His Cys
 200 205 210

tcc ctc tac ggc gag tgc gca gat gtc tgc ccc gca ggc atc cca ctg 787
 Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro Ala Gly Ile Pro Leu
 215 220 225

acc gct gtg gca gct gtc acc aag gaa cgt gcg cgt gca gct ttc cga 835
 Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala Arg Ala Ala Phe Arg
 230 235 240 245

ggc aaa gac gac tagtcctttaa tccaagtaag tac 870
 Gly Lys Asp Asp

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Gly Lys Phe Glu Thr Val Gln Val Asp Asp Ala Val Ala Gln Met Ser
 20 25 30

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

Lys Glu Pro Phe Ala Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly
 50 55 60

Thr Cys Gly Leu Leu Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn
 65 70 75 80

Lys Pro Ala Cys Ala Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr
 85 90 95

Leu Lys Ile Glu Pro Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp
 100 105 110

Met Val Val Asp Arg Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly
 115 120 125

Tyr Val Thr Ile Asn Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His
 130 135 140

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Val Asn His Glu Thr Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile
 145 150 155 160

Gly Cys Gly Ala Cys Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu
 165 170 175

Phe Thr Gly Ala Lys Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys
 180 185 190

Glu Glu Arg Gly Leu Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr
 195 200 205

Asn Phe Gly His Cys Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro
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Ala Gly Ile Pro Leu Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala
 225 230 235 240

Arg Ala Ala Phe Arg Gly Lys Asp Asp
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 Met Thr Glu Gln Glu
 1 5

ttc cgt att gag cac gac acc atg ggt gaa gtg aag gtt cca gca aag 163
 Phe Arg Ile Glu His Asp Thr Met Gly Glu Val Lys Val Pro Ala Lys
 10 15 20

gct ctg tgg cag gca cag acc cag cgc gct gtt gag aac ttc cct atc 211
 Ala Leu Trp Gln Ala Gln Thr Gln Arg Ala Val Glu Asn Phe Pro Ile
 25 30 35

tct ggt cgt ggt ctg gaa tcc gca cag atc cgc gca atg ggt ctg ctg 259
 Ser Gly Arg Gly Leu Glu Ser Ala Gln Ile Arg Ala Met Gly Leu Leu
 40 45 50

aag gca gct tgt gcg cag gta aac aag gac tcc ggt gcg ctg gat gca 307
 Lys Ala Ala Cys Ala Gln Val Asn Lys Asp Ser Gly Ala Leu Asp Ala
 55 60 65

gag aag gca gat gcc atc att gca gct ggt aag gag atc gcg tcc ggt 355
 Glu Lys Ala Asp Ala Ile Ile Ala Ala Gly Lys Glu Ile Ala Ser Gly
 70 75 80 85

aag cat gac gct gag ttc cca att gat gtg ttc cag act ggt tcc ggt 403
 Lys His Asp Ala Glu Phe Pro Ile Asp Val Phe Gln Thr Gly Ser Gly

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act	tcc	tcc	aac	atg	aac	acc	aat	gag	gtt	atc	gct	tcc	atc	gcg	aag	451
Thr	Ser	Ser	Asn	Met	Asn	Thr	Asn	Glu	Val	Ile	Ala	Ser	Ile	Ala	Lys	
			105					110					115			
gct	aac	ggc	gtt	gag	gtt	cac	cca	aat	gac	cac	gtc	aac	atg	ggc	cag	499
Ala	Asn	Gly	Val	Glu	Val	His	Pro	Asn	Asp	His	Val	Asn	Met	Gly	Gln	
		120					125					130				
tcc	tcc	aat	gac	acc	ttc	cct	act	gca	act	cac	gtt	gct	gca	acc	gaa	547
Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Ala	Thr	His	Val	Ala	Ala	Thr	Glu	
	135					140					145					
gct	gct	gtc	aat	gac	ctc	atc	cca	ggc	ctg	aag	gtt	ctg	cac	gag	tct	595
Ala	Ala	Val	Asn	Asp	Leu	Ile	Pro	Gly	Leu	Lys	Val	Leu	His	Glu	Ser	
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ttg	gcg	aag	aag	gct	aac	gag	tgg	tct	gag	gtt	gtt	aag	tcc	ggc	cgc	643
Leu	Ala	Lys	Lys	Ala	Asn	Glu	Trp	Ser	Glu	Val	Val	Lys	Ser	Gly	Arg	
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acc	cac	ctg	atg	gac	gct	gtt	cca	gta	acc	ctg	ggc	cag	gag	ttc	ggc	691
Thr	His	Leu	Met	Asp	Ala	Val	Pro	Val	Thr	Leu	Gly	Gln	Glu	Phe	Gly	
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ggc	tac	gct	cgc	cag	atc	cag	ctc	ggc	atc	gag	cgc	gtt	gag	gct	act	739
Gly	Tyr	Ala	Arg	Gln	Ile	Gln	Leu	Gly	Ile	Glu	Arg	Val	Glu	Ala	Thr	
	200						205					210				
ctt	cct	cgc	ctt	ggc	gag	ctg	gct	att	ggc	ggc	acc	gct	gct	ggc	acc	787
Leu	Pro	Arg	Leu	Gly	Glu	Leu	Ala	Ile	Gly	Gly	Thr	Ala	Ala	Gly	Thr	
	215					220					225					
ggc	atc	aac	acc	tcc	gct	gat	ttc	ggc	ggc	aag	gtt	gtt	gct	gaa	ctg	835
Gly	Ile	Asn	Thr	Ser	Ala	Asp	Phe	Gly	Gly	Lys	Val	Val	Ala	Glu	Leu	
230					235					240					245	
atc	aac	ttg	acc	gac	gtc	aag	gag	ctc	aag	gaa	gct	gag	aac	cac	ttc	883
Ile	Asn	Leu	Thr	Asp	Val	Lys	Glu	Leu	Lys	Glu	Ala	Glu	Asn	His	Phe	
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gag	gct	cag	gct	gca	cgc	gac	gct	ctt	gtt	gag	ttc	tcc	ggc	gca	atg	931
Glu	Ala	Gln	Ala	Ala	Arg	Asp	Ala	Leu	Val	Glu	Phe	Ser	Gly	Ala	Met	
			265					270					275			
cgc	gtt	atc	gct	gtc	tcc	ttg	tac	aag	atc	gct	aac	gat	atc	cgc	ctc	979
Arg	Val	Ile	Ala	Val	Ser	Leu	Tyr	Lys	Ile	Ala	Asn	Asp	Ile	Arg	Leu	
		280					285					290				
atg	ggc	tcc	ggc	cca	ctg	acc	ggc	ctt	ggc	gag	atc	cgt	ctc	cca	gac	1027
Met	Gly	Ser	Gly	Pro	Leu	Thr	Gly	Leu	Gly	Glu	Ile	Arg	Leu	Pro	Asp	
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Leu	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Leu	
310					315					320					325	
tgt	gag	acc	gct	acc	cag	gtt	tcc	gct	cag	gtt	atc	ggc	aat	gac	gca	1123
Cys	Glu	Thr	Ala	Thr	Gln	Val	Ser	Ala	Gln	Val	Ile	Gly	Asn	Asp	Ala	
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atc cca gtg atg gct cgc aac gtg ctt gag tcc gct cgc ctg ctg gct 1219
 Ile Pro Val Met Ala Arg Asn Val Leu Glu Ser Ala Arg Leu Leu Ala
 360 365 370

aac act tcc cgc gtg ttc gca acc cgt ctc gtt gat ggc att gag cca 1267
 Asn Thr Ser Arg Val Phe Ala Thr Arg Leu Val Asp Gly Ile Glu Pro
 375 380 385

aac gag gca cac atg aag gag ctc gct gag tct tca cct tcc atc gtt 1315
 Asn Glu Ala His Met Lys Glu Leu Ala Glu Ser Ser Pro Ser Ile Val
 390 395 400 405

acc cca ctg aac tct gca atc ggc tac gaa gct gct gca aag gtg gct 1363
 Thr Pro Leu Asn Ser Ala Ile Gly Tyr Glu Ala Ala Ala Lys Val Ala
 410 415 420

aag act gct ttg gct gag ggc aag acc atc cgc cag act gtc atc gat 1411
 Lys Thr Ala Leu Ala Glu Gly Lys Thr Ile Arg Gln Thr Val Ile Asp
 425 430 435

ttg ggc ttg gtt gat ggc gag aag ctc acc gag gaa gag ctg gac aag 1459
 Leu Gly Leu Val Asp Gly Glu Lys Leu Thr Glu Glu Glu Leu Asp Lys
 440 445 450

cgc ctc gac gtt ctt gct atg gct cac acc gag cgc gag aac aag ttc 1507
 Arg Leu Asp Val Leu Ala Met Ala His Thr Glu Arg Glu Asn Lys Phe
 455 460 465

taaaactaga acccgataaa taa 1530

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

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Ala	Ser	Ile	Ala	Lys	Ala	Asn	Gly	Val	Glu	Val	His	Pro	Asn	Asp	His		
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Val	Asn	Met	Gly	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Ala	Thr	His		
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Val	Ala	Ala	Thr	Glu	Ala	Ala	Val	Asn	Asp	Leu	Ile	Pro	Gly	Leu	Lys		
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Val	Lys	Ser	Gly	Arg	Thr	His	Leu	Met	Asp	Ala	Val	Pro	Val	Thr	Leu		
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Arg	Val	Glu	Ala	Thr	Leu	Pro	Arg	Leu	Gly	Glu	Leu	Ala	Ile	Gly	Gly		
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Thr	Ala	Ala	Gly	Thr	Gly	Ile	Asn	Thr	Ser	Ala	Asp	Phe	Gly	Gly	Lys		
	225				230					235					240		
Val	Val	Ala	Glu	Leu	Ile	Asn	Leu	Thr	Asp	Val	Lys	Glu	Leu	Lys	Glu		
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Ala	Glu	Asn	His	Phe	Glu	Ala	Gln	Ala	Ala	Arg	Asp	Ala	Leu	Val	Glu		
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Phe	Ser	Gly	Ala	Met	Arg	Val	Ile	Ala	Val	Ser	Leu	Tyr	Lys	Ile	Ala		
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Ile	Arg	Leu	Pro	Asp	Leu	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys		
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Glu	Leu	Asn	Val	Phe	Ile	Pro	Val	Met	Ala	Arg	Asn	Val	Leu	Glu	Ser		
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Ala	Arg	Leu	Leu	Ala	Asn	Thr	Ser	Arg	Val	Phe	Ala	Thr	Arg	Leu	Val		
	370						375				380						
Asp	Gly	Ile	Glu	Pro	Asn	Glu	Ala	His	Met	Lys	Glu	Leu	Ala	Glu	Ser		
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Ser	Pro	Ser	Ile	Val	Thr	Pro	Leu	Asn	Ser	Ala	Ile	Gly	Tyr	Glu	Ala		
				405					410					415			
Ala	Ala	Lys	Val	Ala	Lys	Thr	Ala	Leu	Ala	Glu	Gly	Lys	Thr	Ile	Arg		
			420					425					430				

Gln Thr Val Ile Asp Leu Gly Leu Val Asp Gly Glu Lys Leu Thr Glu
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Glu Glu Leu Asp Lys Arg Leu Asp Val Leu Ala Met Ala His Thr Glu
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Arg Glu Asn Lys Phe
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<211> 1164

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1141)

<223> RXA00517

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Met Pro Glu Val Thr
1 5

gtc aac gcc caa caa ctc act gtt ctc tgc aca gac atc ctc acc aaa 163
Val Asn Ala Gln Gln Leu Thr Val Leu Cys Thr Asp Ile Leu Thr Lys
10 15 20

act gga gta cct gca gca gac gcc cat ctt gtc ggt gat agt ttg gtg 211
Thr Gly Val Pro Ala Ala Asp Ala His Leu Val Gly Asp Ser Leu Val
25 30 35

cag gct gat ctt tgg ggt cac ccc tcc cac ggt gtg ctt cga ctg cct 259
Gln Ala Asp Leu Trp Gly His Pro Ser His Gly Val Leu Arg Leu Pro
40 45 50

tgg tat gtg cgc aga ctc cac agt ggc gcg atg act aca cat gca cac 307
Trp Tyr Val Arg Arg Leu His Ser Gly Ala Met Thr Thr His Ala His
55 60 65

gtg gag gtt ctc aat gat ttg ggt gcc gtg ttg gcg ttg gat gga cac 355
Val Glu Val Leu Asn Asp Leu Gly Ala Val Leu Ala Leu Asp Gly His
70 75 80 85

aat gga atc ggc caa gtt tta gct gat cat gct cgt aaa gaa gca gtg 403
Asn Gly Ile Gly Gln Val Leu Ala Asp His Ala Arg Lys Glu Ala Val
90 95 100

act agg gca atg atg ttc ggc atc ggt gcg gtg tcg gtg cgc aac tcc 451
Thr Arg Ala Met Met Phe Gly Ile Gly Ala Val Ser Val Arg Asn Ser
105 110 115

aat cat ttt gga act gcc atg tac tac acc cgg aaa gcg gca gcg caa 499
Asn His Phe Gly Thr Ala Met Tyr Tyr Thr Arg Lys Ala Ala Ala Gln
120 125 130

gga tgt gtt tcc att ctc acc acc aat gca tct ccg gcg atg gcg ccc 547

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Trp	Gly	Gly	Arg	Glu	Lys	Arg	Ile	Gly	Thr	Asn	Pro	Trp	Ser	Ile	Ala	
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Ala	Pro	Phe	Gly	Glu	Thr	Ala	Thr	Val	Val	Asp	Ile	Ala	Asn	Thr	Ala	
				170					175					180		
gtt	gcg	cgc	gga	aag	atc	tac	cac	gca	cga	cag	aca	aac	atg	ccc	att	691
Val	Ala	Arg	Gly	Lys	Ile	Tyr	His	Ala	Arg	Gln	Thr	Asn	Met	Pro	Ile	
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cct	gag	act	tgg	gcg	atc	acg	agt	gag	ggc	gca	ccc	acc	acg	gat	cct	739
Pro	Glu	Thr	Trp	Ala	Ile	Thr	Ser	Glu	Gly	Ala	Pro	Thr	Thr	Asp	Pro	
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gct	gag	gca	atc	aac	ggt	gtc	gtc	ctt	ccc	atg	gct	ggg	cac	aaa	ggt	787
Ala	Glu	Ala	Ile	Asn	Gly	Val	Val	Leu	Pro	Met	Ala	Gly	His	Lys	Gly	
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tat	gcg	att	agc	ttc	atg	atg	gat	gtg	ctt	tct	gga	gtt	ctc	act	ggt	835
Tyr	Ala	Ile	Ser	Phe	Met	Met	Asp	Val	Leu	Ser	Gly	Val	Leu	Thr	Gly	
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tcc	cag	cac	agc	acc	aag	gta	cat	ggt	ccg	tat	gat	ccc	act	ccc	cca	883
Ser	Gln	His	Ser	Thr	Lys	Val	His	Gly	Pro	Tyr	Asp	Pro	Thr	Pro	Pro	
				250					255					260		
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Gly	Gly	Ala	Gly	His	Leu	Phe	Ile	Ala	Leu	Asp	Val	Ala	Ala	Phe	Arg	
			265					270					275			
gat	cca	caa	gat	ttc	gat	gac	gca	ctc	agc	gat	ctg	gtt	ggg	gaa	gtt	979
Asp	Pro	Gln	Asp	Phe	Asp	Asp	Ala	Leu	Ser	Asp	Leu	Val	Gly	Glu	Val	
		280					285					290				
aaa	tcc	act	ccg	aaa	gca	caa	aac	acc	gag	gag	att	ttc	tac	ccc	ggt	1027
Lys	Ser	Thr	Pro	Lys	Ala	Gln	Asn	Thr	Glu	Glu	Ile	Phe	Tyr	Pro	Gly	
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gaa	tcg	gaa	gac	cgt	gcg	cat	cgg	aaa	aac	tct	gcg	cac	ggt	att	tca	1075
Glu	Ser	Glu	Asp	Arg	Ala	His	Arg	Lys	Asn	Ser	Ala	His	Gly	Ile	Ser	
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ttg	cct	gaa	aaa	acg	tgg	atg	gaa	ctg	caa	gaa	ctg	gca	atc	gag	aac	1123
Leu	Pro	Glu	Lys	Thr	Trp	Met	Glu	Leu	Gln	Glu	Leu	Ala	Ile	Glu	Asn	
				330					335					340		
cat	gtt	gta	act	cac	cgt	tgatctgcgc	gttaaacctg	gcc								1164
His	Val	Val	Thr	His	Arg											
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<211> 347

<212> PRT

<213> Corynebacterium glutamicum

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<400> 20

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			20					25					30		
Gly	Asp	Ser	Leu	Val	Gln	Ala	Asp	Leu	Trp	Gly	His	Pro	Ser	His	Gly
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Val	Leu	Arg	Leu	Pro	Trp	Tyr	Val	Arg	Arg	Leu	His	Ser	Gly	Ala	Met
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Thr	Thr	His	Ala	His	Val	Glu	Val	Leu	Asn	Asp	Leu	Gly	Ala	Val	Leu
65					70					75					80
Ala	Leu	Asp	Gly	His	Asn	Gly	Ile	Gly	Gln	Val	Leu	Ala	Asp	His	Ala
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Arg	Lys	Glu	Ala	Val	Thr	Arg	Ala	Met	Met	Phe	Gly	Ile	Gly	Ala	Val
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Ser	Val	Arg	Asn	Ser	Asn	His	Phe	Gly	Thr	Ala	Met	Tyr	Tyr	Thr	Arg
		115					120					125			
Lys	Ala	Ala	Ala	Gln	Gly	Cys	Val	Ser	Ile	Leu	Thr	Thr	Asn	Ala	Ser
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Pro	Ala	Met	Ala	Pro	Trp	Gly	Gly	Arg	Glu	Lys	Arg	Ile	Gly	Thr	Asn
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Pro	Trp	Ser	Ile	Ala	Ala	Pro	Phe	Gly	Glu	Thr	Ala	Thr	Val	Val	Asp
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Ile	Ala	Asn	Thr	Ala	Val	Ala	Arg	Gly	Lys	Ile	Tyr	His	Ala	Arg	Gln
			180					185					190		
Thr	Asn	Met	Pro	Ile	Pro	Glu	Thr	Trp	Ala	Ile	Thr	Ser	Glu	Gly	Ala
		195					200					205			
Pro	Thr	Thr	Asp	Pro	Ala	Glu	Ala	Ile	Asn	Gly	Val	Val	Leu	Pro	Met
	210					215					220				
Ala	Gly	His	Lys	Gly	Tyr	Ala	Ile	Ser	Phe	Met	Met	Asp	Val	Leu	Ser
225					230					235					240
Gly	Val	Leu	Thr	Gly	Ser	Gln	His	Ser	Thr	Lys	Val	His	Gly	Pro	Tyr
				245					250					255	
Asp	Pro	Thr	Pro	Pro	Gly	Gly	Ala	Gly	His	Leu	Phe	Ile	Ala	Leu	Asp
			260					265					270		
Val	Ala	Ala	Phe	Arg	Asp	Pro	Gln	Asp	Phe	Asp	Asp	Ala	Leu	Ser	Asp
		275					280					285			
Leu	Val	Gly	Glu	Val	Lys	Ser	Thr	Pro	Lys	Ala	Gln	Asn	Thr	Glu	Glu
	290					295					300				
Ile	Phe	Tyr	Pro	Gly	Glu	Ser	Glu	Asp	Arg	Ala	His	Arg	Lys	Asn	Ser
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Ala His Gly Ile Ser Leu Pro Glu Lys Thr Trp Met Glu Leu Gln Glu
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Leu Ala Ile Glu Asn His Val Val Thr His Arg
 340 345

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 <213> Corynebacterium glutamicum

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 <223> RXA01350

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 Met Asn Ser Pro Gln
 1 5

aac gtc tcc acc aag aag gtc acc gtc acc ggc gca gct ggt caa atc 163
 Asn Val Ser Thr Lys Lys Val Thr Val Thr Gly Ala Ala Gly Gln Ile
 10 15 20

tct tat tca ctg ttg tgg cgc atc gcc aac ggt gaa gta ttc ggc acc 211
 Ser Tyr Ser Leu Leu Trp Arg Ile Ala Asn Gly Glu Val Phe Gly Thr
 25 30 35

gac acc cct gta gaa ctg aaa ctt ctg gag atc cct cag gct ctt ggc 259
 Asp Thr Pro Val Glu Leu Lys Leu Leu Glu Ile Pro Gln Ala Leu Gly
 40 45 50

ggg gca gag ggt gtg gct atg gaa ctt ctg gat tct gcc ttc ccc ctc 307
 Gly Ala Glu Gly Val Ala Met Glu Leu Leu Asp Ser Ala Phe Pro Leu
 55 60 65

ctg cga aac atc acc atc acc gcg gat gcc aat gag gca ttc gac ggc 355
 Leu Arg Asn Ile Thr Ile Thr Ala Asp Ala Asn Glu Ala Phe Asp Gly
 70 75 80 85

gct aat gcg gcg ttt ttg gtc ggt gcg aag cct cgc gga aaa ggc gaa 403
 Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro Arg Gly Lys Gly Glu
 90 95 100

gag cgc gca gat ttg ctg gct aac aac ggc aag att ttc gga cct caa 451
 Glu Arg Ala Asp Leu Leu Ala Asn Asn Gly Lys Ile Phe Gly Pro Gln
 105 110 115

ggt aaa gct atc aat gac aac gcc gca gat gac att cgt gtc cta gtt 499
 Gly Lys Ala Ile Asn Asp Asn Ala Ala Asp Asp Ile Arg Val Leu Val
 120 125 130

gtt gga aac cca gcg aac acc aac gcg ttg att gct tca gct gcg gcc 547
 Val Gly Asn Pro Ala Asn Thr Asn Ala Leu Ile Ala Ser Ala Ala Ala
 135 140 145

cca gat gtt cca gca tcc cgc ttc aac gca atg atg cgc ctt gat cac 595

WO 01/00844

PCT/IB00/00943

Pro Asp Val Pro Ala Ser Arg Phe Asn Ala Met Met Arg Leu Asp His
 150 155 160 165

aac cgt gcg atc tcc cag ctg gcc acc aag ctt ggc cgt gga tct gcg 643
 Asn Arg Ala Ile Ser Gln Leu Ala Thr Lys Leu Gly Arg Gly Ser Ala
 170 175 180

gaa ttt aac aac att gtg gtc tgg gga aat cac tcc gca acc cag ttc 691
 Glu Phe Asn Asn Ile Val Val Trp Gly Asn His Ser Ala Thr Gln Phe
 185 190 195

cca gac atc acc tac gca acc gtt ggt gga gaa aag gtc act gac ctg 739
 Pro Asp Ile Thr Tyr Ala Thr Val Gly Gly Glu Lys Val Thr Asp Leu
 200 205 210

gtt gat cac gat tgg tat gtg gag gag ttc att cct cgc gtg gct aac 787
 Val Asp His Asp Trp Tyr Val Glu Glu Phe Ile Pro Arg Val Ala Asn
 215 220 225

cgt ggc gct gaa atc att gag gtc cgt gga aag tct tct gca gct tct 835
 Arg Gly Ala Glu Ile Ile Glu Val Arg Gly Lys Ser Ser Ala Ala Ser
 230 235 240 245

gca gca tcc tct gcg att gat cac atg cgc gat tgg gta cag ggc acc 883
 Ala Ala Ser Ser Ala Ile Asp His Met Arg Asp Trp Val Gln Gly Thr
 250 255 260

gag gcg tgg tcc tct gcg gca att cct tcc acc ggt gca tac ggc att 931
 Glu Ala Trp Ser Ser Ala Ala Ile Pro Ser Thr Gly Ala Tyr Gly Ile
 265 270 275

cct gag ggc att ttt gtc ggt ctg cca acc gta tcc cgc aac ggt gag 979
 Pro Glu Gly Ile Phe Val Gly Leu Pro Thr Val Ser Arg Asn Gly Glu
 280 285 290

tgg gaa atc gtt gaa ggc ctg gag att tcc gat ttc cag cgc gcc cgc 1027
 Trp Glu Ile Val Glu Gly Leu Glu Ile Ser Asp Phe Gln Arg Ala Arg
 295 300 305

atc gac gcg aat gct cag gaa ttg cag gcc gag cgc gag gca gtg cgc 1075
 Ile Asp Ala Asn Ala Gln Glu Leu Gln Ala Glu Arg Glu Ala Val Arg
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gac ttg ctc taatctttaa cgcatgactt cgc 1107
 Asp Leu Leu

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<212> PRT

<213> Corynebacterium glutamicum

<400> 22

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PCT/IB00/00943

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Glu	Ala	Phe	Asp	Gly	Ala	Asn	Ala	Ala	Phe	Leu	Val	Gly	Ala	Lys	Pro
				85					90					95	
Arg	Gly	Lys	Gly	Glu	Glu	Arg	Ala	Asp	Leu	Leu	Ala	Asn	Asn	Gly	Lys
			100					105					110		
Ile	Phe	Gly	Pro	Gln	Gly	Lys	Ala	Ile	Asn	Asp	Asn	Ala	Ala	Asp	Asp
		115					120					125			
Ile	Arg	Val	Leu	Val	Val	Gly	Asn	Pro	Ala	Asn	Thr	Asn	Ala	Leu	Ile
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	145					150					155				160
Met	Arg	Leu	Asp	His	Asn	Arg	Ala	Ile	Ser	Gln	Leu	Ala	Thr	Lys	Leu
				165					170					175	
Gly	Arg	Gly	Ser	Ala	Glu	Phe	Asn	Asn	Ile	Val	Val	Trp	Gly	Asn	His
			180					185					190		
Ser	Ala	Thr	Gln	Phe	Pro	Asp	Ile	Thr	Tyr	Ala	Thr	Val	Gly	Gly	Glu
		195					200					205			
Lys	Val	Thr	Asp	Leu	Val	Asp	His	Asp	Trp	Tyr	Val	Glu	Glu	Phe	Ile
	210					215					220				
Pro	Arg	Val	Ala	Asn	Arg	Gly	Ala	Glu	Ile	Ile	Glu	Val	Arg	Gly	Lys
	225					230					235				240
Ser	Ser	Ala	Ala	Ser	Ala	Ala	Ser	Ser	Ala	Ile	Asp	His	Met	Arg	Asp
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Trp	Val	Gln	Gly	Thr	Glu	Ala	Trp	Ser	Ser	Ala	Ala	Ile	Pro	Ser	Thr
			260					265					270		
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		275					280					285			
Ser	Arg	Asn	Gly	Glu	Trp	Glu	Ile	Val	Glu	Gly	Leu	Glu	Ile	Ser	Asp
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Phe	Gln	Arg	Ala	Arg	Ile	Asp	Ala	Asn	Ala	Gln	Glu	Leu	Gln	Ala	Glu
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<223> RXA02149

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Ala	Ser	Phe	Ala	Val	Gly	Phe	Asp	Ile	Gly	Gly	Thr	Asn	Met	Arg	Ala	
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ggg	ctt	gtc	gac	gaa	tcc	ggg	cgc	atc	gtg	acc	agt	ttg	tcg	gcg	ccg	211
Gly	Leu	Val	Asp	Glu	Ser	Gly	Arg	Ile	Val	Thr	Ser	Leu	Ser	Ala	Pro	
			25					30					35			

tcg	ccg	cgc	acg	acg	cag	gca	atg	gaa	cag	ggg	att	ttt	gat	cta	gtc	259
Ser	Pro	Arg	Thr	Thr	Gln	Ala	Met	Glu	Gln	Gly	Ile	Phe	Asp	Leu	Val	
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gaa	cag	ctc	aag	gcc	gaa	tac	ccg	gtt	ggg	gct	gtg	gga	ctt	gcc	gtc	307
Glu	Gln	Leu	Lys	Ala	Glu	Tyr	Pro	Val	Gly	Ala	Val	Gly	Leu	Ala	Val	
	55					60					65					

gcg	gga	ttt	ttg	gat	cct	gag	tgc	gag	gtt	gtt	cga	ttt	gcc	ccg	cac	355
Ala	Gly	Phe	Leu	Asp	Pro	Glu	Cys	Glu	Val	Val	Arg	Phe	Ala	Pro	His	
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Leu	Pro	Trp	Arg	Asp	Glu	Pro	Val	Arg	Glu	Lys	Leu	Glu	Asn	Leu	Leu	
				90				95						100		

ggc	ctg	cct	gtt	cgt	ttg	gaa	cat	gat	gcc	aac	tca	gca	gcg	tgg	ggg	451
Gly	Leu	Pro	Val	Arg	Leu	Glu	His	Asp	Ala	Asn	Ser	Ala	Ala	Trp	Gly	
			105					110					115			

gag	cat	cgt	ttt	ggg	gca	gct	caa	ggc	gct	gac	aac	tgg	gtt	ttg	ttg	499
Glu	His	Arg	Phe	Gly	Ala	Ala	Gln	Gly	Ala	Asp	Asn	Trp	Val	Leu	Leu	
		120					125					130				

gca	ctc	ggc	act	gga	att	ggg	gca	gcg	ctg	att	gaa	aaa	ggc	gaa	att	547
Ala	Leu	Gly	Thr	Gly	Ile	Gly	Ala	Ala	Leu	Ile	Glu	Lys	Gly	Glu	Ile	
	135					140					145					

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Tyr	Arg	Gly	Ala	Tyr	Gly	Thr	Ala	Pro	Glu	Phe	Gly	His	Leu	Arg	Val	
150					155					160					165	

gtt	cgt	ggc	gga	cgc	gca	tgt	gcg	tgt	ggc	aaa	gaa	ggc	tgc	ctg	gag	643
Val	Arg	Gly	Gly	Arg	Ala	Cys	Ala	Cys	Gly	Lys	Glu	Gly	Cys	Leu	Glu	
			170						175					180		

cgt	tac	tgt	tcc	ggg	act	gcc	ttg	gtt	tac	act	gcg	cgt	gaa	ttg	gct	691
Arg	Tyr	Cys	Ser	Gly	Thr	Ala	Leu	Val	Tyr	Thr	Ala	Arg	Glu	Leu	Ala	
			185					190					195			

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Ser His Gly Ser Phe Arg Asn Ser Gly Leu Phe Asp Lys Ile Lys Ala
      200                205                210

gat ccg aat tcc atc aat gga aaa acg atc act gcg gca gcg cgc caa 787
Asp Pro Asn Ser Ile Asn Gly Lys Thr Ile Thr Ala Ala Ala Arg Gln
      215                220                225

gaa gac cca ctt gct ctc gcc gtt ctg gaa gat ttc agc gag tgg ctg 835
Glu Asp Pro Leu Ala Leu Ala Val Leu Glu Asp Phe Ser Glu Trp Leu
230                235                240                245

ggc gaa act ttg gcg atc att gct gat gtc ctt gac cca ggc atg atc 883
Gly Glu Thr Leu Ala Ile Ile Ala Asp Val Leu Asp Pro Gly Met Ile
      250                255                260

atc att ggt ggc gga ctg tcc aat gct gcc gac ctt tat ttg gat cgc 931
Ile Ile Gly Gly Gly Leu Ser Asn Ala Ala Asp Leu Tyr Leu Asp Arg
      265                270                275

tcg gtc aac cac tat tcc acc cgc atc gtc ggc gca gga tat cgc cct 979
Ser Val Asn His Tyr Ser Thr Arg Ile Val Gly Ala Gly Tyr Arg Pro
      280                285                290

ttg gca cgc gtt gcc aca gct cag ttg ggt gcg gat gct ggc atg atc 1027
Leu Ala Arg Val Ala Thr Ala Gln Leu Gly Ala Asp Ala Gly Met Ile
      295                300                305

ggt gtc gct gat cta gct cga cgc tct gta gtg gaa gcc aac 1069
Gly Val Ala Asp Leu Ala Arg Arg Ser Val Val Glu Ala Asn
310                315                320

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Ser Leu Ser Ala Pro Ser Pro Arg Thr Thr Gln Ala Met Glu Gln Gly
      35                40                45

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

Val Gly Leu Ala Val Ala Gly Phe Leu Asp Pro Glu Cys Glu Val Val
      65                70                75                80

Arg Phe Ala Pro His Leu Pro Trp Arg Asp Glu Pro Val Arg Glu Lys
      85                90                95

Leu Glu Asn Leu Leu Gly Leu Pro Val Arg Leu Glu His Asp Ala Asn
100                105                110

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Ser Ala Ala Trp Gly Glu His Arg Phe Gly Ala Ala Gln Gly Ala Asp
 115 120 125
 Asn Trp Val Leu Leu Ala Leu Gly Thr Gly Ile Gly Ala Ala Leu Ile
 130 135 140
 Glu Lys Gly Glu Ile Tyr Arg Gly Ala Tyr Gly Thr Ala Pro Glu Phe
 145 150 155 160
 Gly His Leu Arg Val Val Arg Gly Gly Arg Ala Cys Ala Cys Gly Lys
 165 170 175
 Glu Gly Cys Leu Glu Arg Tyr Cys Ser Gly Thr Ala Leu Val Tyr Thr
 180 185 190
 Ala Arg Glu Leu Ala Ser His Gly Ser Phe Arg Asn Ser Gly Leu Phe
 195 200 205
 Asp Lys Ile Lys Ala Asp Pro Asn Ser Ile Asn Gly Lys Thr Ile Thr
 210 215 220
 Ala Ala Ala Arg Gln Glu Asp Pro Leu Ala Leu Ala Val Leu Glu Asp
 225 230 235 240
 Phe Ser Glu Trp Leu Gly Glu Thr Leu Ala Ile Ile Ala Asp Val Leu
 245 250 255
 Asp Pro Gly Met Ile Ile Ile Gly Gly Gly Leu Ser Asn Ala Ala Asp
 260 265 270
 Leu Tyr Leu Asp Arg Ser Val Asn His Tyr Ser Thr Arg Ile Val Gly
 275 280 285
 Ala Gly Tyr Arg Pro Leu Ala Arg Val Ala Thr Ala Gln Leu Gly Ala
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 Asp Ala Gly Met Ile Gly Val Ala Asp Leu Ala Arg Arg Ser Val Val
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 Glu Ala Asn

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <223> RXA01814

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 Met Ala His Glu Arg
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gcc ggg caa ctc gcc caa cca gaa gat ctc atc gat gtt gcg gaa ctg	163
Ala Gly Gln Leu Ala Gln Pro Glu Asp Leu Ile Asp Val Ala Glu Leu	
10 15 20	
gtc acc gca tat ttc acc cgc aag ccg gac gtg aac aac cct gat cag	211
Val Thr Ala Tyr Phe Thr Arg Lys Pro Asp Val Asn Asn Pro Asp Gln	
25 30 35	
cag gtc gct ttc ggc acc tcc gga cac cgt ggc ttc gcg ctg gac agc	259
Gln Val Ala Phe Gly Thr Ser Gly His Arg Gly Phe Ala Leu Asp Ser	
40 45 50	
gct ttc aac gag gac cac atc ctg gca acc acc cag gcg atc gtc gac	307
Ala Phe Asn Glu Asp His Ile Leu Ala Thr Thr Gln Ala Ile Val Asp	
55 60 65	
tac cgc aac cag cag cca aaa aac tgg gtc ggc ccg ctg ttt atc ggc	355
Tyr Arg Asn Gln Gln Pro Lys Asn Trp Val Gly Pro Leu Phe Ile Gly	
70 75 80 85	
cgc gat acg cac gcg ctg tcc gaa cca gcg atg atc agc gcg ctt gag	403
Arg Asp Thr His Ala Leu Ser Glu Pro Ala Met Ile Ser Ala Leu Glu	
90 95 100	
gtc ctc att gcc aac gac gtc gaa gtg ctt gtc gac gcc gac ggc cgc	451
Val Leu Ile Ala Asn Asp Val Glu Val Leu Val Asp Ala Asp Gly Arg	
105 110 115	
tac acc ccg acg ccc gca gtg tcc cac gcg atc cta cga cac aac gat	499
Tyr Thr Pro Thr Pro Ala Val Ser His Ala Ile Leu Arg His Asn Asp	
120 125 130	
ggc atc atc ctt ggc acc gca gga ccc tcc cgc ccc tac gcc gac ggc	547
Gly Ile Ile Leu Gly Thr Ala Gly Pro Ser Arg Pro Tyr Ala Asp Gly	
135 140 145	
atc gtg atc acc cca tcc cac aac cct cct cgt gat ggc gga ttc aaa	595
Ile Val Ile Thr Pro Ser His Asn Pro Pro Arg Asp Gly Gly Phe Lys	
150 155 160 165	
tac aac cca gcc aac ggt ggc cct gca gat acc gac gcc acc gac tgg	643
Tyr Asn Pro Ala Asn Gly Gly Pro Ala Asp Thr Asp Ala Thr Asp Trp	
170 175 180	
atc gcc aac cgc gcc aac gat att ctg cgc ggc gac ctt gca gac gtg	691
Ile Ala Asn Arg Ala Asn Asp Ile Leu Arg Gly Asp Leu Ala Asp Val	
185 190 195	
aag cga gtt cca gtt tcc ggt gtc ctc gac gag cgc acc act gcc tac	739
Lys Arg Val Pro Val Ser Gly Val Leu Asp Glu Arg Thr Thr Ala Tyr	
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gac ttc aag ggc att tac atc gct gac ctg cca aac gtg gtc aac atc	787
Asp Phe Lys Gly Ile Tyr Ile Ala Asp Leu Pro Asn Val Val Asn Ile	
215 220 225	
gat gcc atc cgc gaa gct ggt gtt cga atc ggc gca gac cca atg ggt	835
Asp Ala Ile Arg Glu Ala Gly Val Arg Ile Gly Ala Asp Pro Met Gly	
230 235 240 245	
ggc gca tcc gtg gat tac tgg ggt gcc atc gca gaa acc cat ggc ctc	883

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Gly	Ala	Ser	Val	Asp	Tyr	Trp	Gly	Ala	Ile	Ala	Glu	Thr	His	Gly	Leu	
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aac	ctc	acc	gtg	gtc	aac	cca	cac	ggt	gat	tcc	acc	ttc	cgc	ttc	atg	931
Asn	Leu	Thr	Val	Val	Asn	Pro	His	Val	Asp	Ser	Thr	Phe	Arg	Phe	Met	
			265					270					275			
aca	ttg	gac	acc	gac	ggc	aag	atc	cgc	atg	gac	tgc	tcc	agc	cca	cac	979
Thr	Leu	Asp	Thr	Asp	Gly	Lys	Ile	Arg	Met	Asp	Cys	Ser	Ser	Pro	His	
			280				285					290				
gca	atg	gca	tcg	ctg	att	gac	aac	cga	gac	aag	ttc	gat	gtg	gca	acc	1027
Ala	Met	Ala	Ser	Leu	Ile	Asp	Asn	Arg	Asp	Lys	Phe	Asp	Val	Ala	Thr	
	295					300					305					
ggc	aac	gac	gcc	gac	gcc	gac	cgc	cac	ggc	atc	gtc	acc	cca	gac	gct	1075
Gly	Asn	Asp	Ala	Asp	Ala	Asp	Arg	His	Gly	Ile	Val	Thr	Pro	Asp	Ala	
310					315					320					325	
ggc	ttg	atg	aac	ccc	aac	cac	tac	ctc	gca	gta	gca	att	gag	tac	ctc	1123
Gly	Leu	Met	Asn	Pro	Asn	His	Tyr	Leu	Ala	Val	Ala	Ile	Glu	Tyr	Leu	
				330					335					340		
ttt	gct	cac	cgc	cca	ggt	tgg	tcc	gca	gat	acc	gca	gtg	ggc	aaa	acc	1171
Phe	Ala	His	Arg	Pro	Gly	Trp	Ser	Ala	Asp	Thr	Ala	Val	Gly	Lys	Thr	
			345					350					355			
ctg	gtc	agc	tcc	tcc	atg	atc	gac	cgc	ggt	gtg	gcg	cag	ctt	ggc	cgc	1219
Leu	Val	Ser	Ser	Ser	Met	Ile	Asp	Arg	Val	Val	Ala	Gln	Leu	Gly	Arg	
			360				365					370				
acc	ctc	ggt	gag	ggt	cca	gtc	gga	ttc	aag	tgg	ttt	gtc	cca	ggt	ttg	1267
Thr	Leu	Val	Glu	Val	Pro	Val	Gly	Phe	Lys	Trp	Phe	Val	Pro	Gly	Leu	
	375					380					385					
atc	tcc	ggc	gaa	atc	gga	ttc	ggt	ggt	gaa	gaa	tcc	gca	ggt	gca	tcc	1315
Ile	Ser	Gly	Glu	Ile	Gly	Phe	Gly	Gly	Glu	Glu	Ser	Ala	Gly	Ala	Ser	
390					395				400						405	
ttc	ctc	cgc	atg	gac	ggc	acc	acc	tgg	tcc	acc	gac	aag	gac	ggc	ctc	1363
Phe	Leu	Arg	Met	Asp	Gly	Thr	Thr	Trp	Ser	Thr	Asp	Lys	Asp	Gly	Leu	
				410				415						420		
atc	ctt	gac	ctc	ctg	gca	gct	gag	atc	att	gca	gta	acc	ggc	aag	acc	1411
Ile	Leu	Asp	Leu	Leu	Ala	Ala	Glu	Ile	Ile	Ala	Val	Thr	Gly	Lys	Thr	
			425				430						435			
cca	tca	cag	cgc	tac	gca	gaa	ctc	gcc	gaa	gaa	ttc	ggt	gca	cct	gcc	1459
Pro	Ser	Gln	Arg	Tyr	Ala	Glu	Leu	Ala	Glu	Glu	Phe	Gly	Ala	Pro	Ala	
			440				445					450				
tac	gcc	cgc	acc	gat	gca	gaa	gcc	aac	cga	gaa	caa	aag	gcc	atc	ctg	1507
Tyr	Ala	Arg	Thr	Asp	Ala	Glu	Ala	Asn	Arg	Glu	Gln	Lys	Ala	Ile	Leu	
	455					460					465					
aag	gca	ctg	tcc	cca	gaa	cag	gtc	acc	gcc	acc	gaa	cta	gcc	ggc	gaa	1555
Lys	Ala	Leu	Ser	Pro	Glu	Gln	Val	Thr	Ala	Thr	Glu	Leu	Ala	Gly	Glu	
470					475				480						485	
gca	atc	acc	gct	aag	ctc	acc	gaa	gct	ccc	ggc	aat	ggc	gca	gcc	atc	1603
Ala	Ile	Thr	Ala	Lys	Leu	Thr	Glu	Ala	Pro	Gly	Asn	Gly	Ala	Ala	Ile	

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	490		495		500	
	gga gga cta aaa gtg acc acc gaa aac gcc tgg ttc gca gca cgc cca					1651
	Gly Gly Leu Lys Val Thr Thr Glu Asn Ala Trp Phe Ala Ala Arg Pro					
	505		510		515	
	tcc ggc acc gaa gac aag tac aag atc tac gca gaa tcc ttc aag ggc					1699
	Ser Gly Thr Glu Asp Lys Tyr Lys Ile Tyr Ala Glu Ser Phe Lys Gly					
	520		525		530	
	gaa gag cac ctc gcc cag gtt cag aag gaa gcc caa gcg ttg gtc agc					1747
	Glu Glu His Leu Ala Gln Val Gln Lys Glu Ala Gln Ala Leu Val Ser					
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	gaa gta ctc gga cag taaaactgcg gacttgctga caa					1785
	Glu Val Leu Gly Gln					
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<212> PRT

<213> Corynebacterium glutamicum

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Asn	Asn	Pro	Asp	Gln	Gln	Val	Ala	Phe	Gly	Thr	Ser	Gly	His	Arg	Gly
		35					40					45			
Phe	Ala	Leu	Asp	Ser	Ala	Phe	Asn	Glu	Asp	His	Ile	Leu	Ala	Thr	Thr
	50					55					60				
Gln	Ala	Ile	Val	Asp	Tyr	Arg	Asn	Gln	Gln	Pro	Lys	Asn	Trp	Val	Gly
	65				70					75					80
Pro	Leu	Phe	Ile	Gly	Arg	Asp	Thr	His	Ala	Leu	Ser	Glu	Pro	Ala	Met
				85					90					95	
Ile	Ser	Ala	Leu	Glu	Val	Leu	Ile	Ala	Asn	Asp	Val	Glu	Val	Leu	Val
			100					105					110		
Asp	Ala	Asp	Gly	Arg	Tyr	Thr	Pro	Thr	Pro	Ala	Val	Ser	His	Ala	Ile
	115						120					125			
Leu	Arg	His	Asn	Asp	Gly	Ile	Ile	Leu	Gly	Thr	Ala	Gly	Pro	Ser	Arg
	130					135					140				
Pro	Tyr	Ala	Asp	Gly	Ile	Val	Ile	Thr	Pro	Ser	His	Asn	Pro	Pro	Arg
	145				150					155					160
Asp	Gly	Gly	Phe	Lys	Tyr	Asn	Pro	Ala	Asn	Gly	Gly	Pro	Ala	Asp	Thr
				165					170					175	
Asp	Ala	Thr	Asp	Trp	Ile	Ala	Asn	Arg	Ala	Asn	Asp	Ile	Leu	Arg	Gly
			180					185					190		

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Asp	Leu	Ala	Asp	Val	Lys	Arg	Val	Pro	Val	Ser	Gly	Val	Leu	Asp	Glu
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Arg	Thr	Thr	Ala	Tyr	Asp	Phe	Lys	Gly	Ile	Tyr	Ile	Ala	Asp	Leu	Pro
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Asn	Val	Val	Asn	Ile	Asp	Ala	Ile	Arg	Glu	Ala	Gly	Val	Arg	Ile	Gly
225					230					235					240
Ala	Asp	Pro	Met	Gly	Gly	Ala	Ser	Val	Asp	Tyr	Trp	Gly	Ala	Ile	Ala
				245					250					255	
Glu	Thr	His	Gly	Leu	Asn	Leu	Thr	Val	Val	Asn	Pro	His	Val	Asp	Ser
			260					265					270		
Thr	Phe	Arg	Phe	Met	Thr	Leu	Asp	Thr	Asp	Gly	Lys	Ile	Arg	Met	Asp
		275					280					285			
Cys	Ser	Ser	Pro	His	Ala	Met	Ala	Ser	Leu	Ile	Asp	Asn	Arg	Asp	Lys
	290					295					300				
Phe	Asp	Val	Ala	Thr	Gly	Asn	Asp	Ala	Asp	Ala	Asp	Arg	His	Gly	Ile
305					310					315					320
Val	Thr	Pro	Asp	Ala	Gly	Leu	Met	Asn	Pro	Asn	His	Tyr	Leu	Ala	Val
				325					330					335	
Ala	Ile	Glu	Tyr	Leu	Phe	Ala	His	Arg	Pro	Gly	Trp	Ser	Ala	Asp	Thr
			340					345					350		
Ala	Val	Gly	Lys	Thr	Leu	Val	Ser	Ser	Ser	Met	Ile	Asp	Arg	Val	Val
		355					360					365			
Ala	Gln	Leu	Gly	Arg	Thr	Leu	Val	Glu	Val	Pro	Val	Gly	Phe	Lys	Trp
	370					375					380				
Phe	Val	Pro	Gly	Leu	Ile	Ser	Gly	Glu	Ile	Gly	Phe	Gly	Gly	Glu	Glu
385					390					395					400
Ser	Ala	Gly	Ala	Ser	Phe	Leu	Arg	Met	Asp	Gly	Thr	Thr	Trp	Ser	Thr
				405					410					415	
Asp	Lys	Asp	Gly	Leu	Ile	Leu	Asp	Leu	Leu	Ala	Ala	Glu	Ile	Ile	Ala
			420				425						430		
Val	Thr	Gly	Lys	Thr	Pro	Ser	Gln	Arg	Tyr	Ala	Glu	Leu	Ala	Glu	Glu
		435					440					445			
Phe	Gly	Ala	Pro	Ala	Tyr	Ala	Arg	Thr	Asp	Ala	Glu	Ala	Asn	Arg	Glu
	450					455					460				
Gln	Lys	Ala	Ile	Leu	Lys	Ala	Leu	Ser	Pro	Glu	Gln	Val	Thr	Ala	Thr
465					470					475					480
Glu	Leu	Ala	Gly	Glu	Ala	Ile	Thr	Ala	Lys	Leu	Thr	Glu	Ala	Pro	Gly
			485						490					495	
Asn	Gly	Ala	Ala	Ile	Gly	Gly	Leu	Lys	Val	Thr	Thr	Glu	Asn	Ala	Trp
			500					505					510		
Phe	Ala	Ala	Arg	Pro	Ser	Gly	Thr	Glu	Asp	Lys	Tyr	Lys	Ile	Tyr	Ala

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 <222> (1)..(657)
 <223> RXN02803

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cag ggt gtt gat gtc att cgt gtt ggt gtc atc cca acc cca gct gtt	96
Gln Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val	
20 25 30	
gca ttc ctc acc gat gat tat ggc gct gac atg ggc gtg atg att tct	144
Ala Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser	
35 40 45	
gca tcc cac aac cca atg ccg gac aac gga atc aag ttc ttt tct gca	192
Ala Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala	
50 55 60	
ggt gga cac aag ctt cca gac cat gtg gaa gac gag att gag cgt gtt	240
Gly Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val	
65 70 75 80	
atg gac agc ttg cca gca gaa ggc cca aca ggg cat gga gtt ggc cgt	288
Met Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg	
85 90 95	
gtc atc gaa gaa gca acc gat gca cag gac cgt tac cta gag cac ctg	336
Val Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu	
100 105 110	
aag gaa gct gtt cct acg tca ctt gaa ggc atc aag att gtt gtg gat	384
Lys Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp	
115 120 125	
gca gcc aat ggt gcg gca agt gtt gta gct cca acg gct tat gag gct	432
Ala Ala Asn Gly Ala Ala Ser Val Val Ala Pro Thr Ala Tyr Glu Ala	
130 135 140	
gcg ggt gca act gta att gct att cat aac aag cca gac tca tac aac	480
Ala Gly Ala Thr Val Ile Ala Ile His Asn Lys Pro Asp Ser Tyr Asn	
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Ala	Phe	Leu	Thr	Asp	Asp	Tyr	Gly	Ala	Asp	Met	Gly	Val	Met	Ile	Ser
		35					40					45			
Ala	Ser	His	Asn	Pro	Met	Pro	Asp	Asn	Gly	Ile	Lys	Phe	Phe	Ser	Ala
	50					55					60				
Gly	Gly	His	Lys	Leu	Pro	Asp	His	Val	Glu	Asp	Glu	Ile	Glu	Arg	Val
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Met	Asp	Ser	Leu	Pro	Ala	Glu	Gly	Pro	Thr	Gly	His	Gly	Val	Gly	Arg
				85					90					95	
Val	Ile	Glu	Glu	Ala	Thr	Asp	Ala	Gln	Asp	Arg	Tyr	Leu	Glu	His	Leu
			100					105					110		
Lys	Glu	Ala	Val	Pro	Thr	Ser	Leu	Glu	Gly	Ile	Lys	Ile	Val	Val	Asp
		115					120					125			
Ala	Ala	Asn	Gly	Ala	Ala	Ser	Val	Val	Ala	Pro	Thr	Ala	Tyr	Glu	Ala
		130				135					140				
Ala	Gly	Ala	Thr	Val	Ile	Ala	Ile	His	Asn	Lys	Pro	Asp	Ser	Tyr	Asn
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Ile	Asn	Met	Asp	Cys	Gly	Ser	Thr	His	Ile	Asp	Gln	Ala	Gln	Pro	Pro
				165					170					175	
Val	Leu	Lys	His	Gly	Ala	Asp	Leu	Gly	Leu	Ala	His	Asp	Gly	Asp	Ala
			180					185					190		
Asp	Arg	Cys	Leu	Ala	Val	Asn	Lys	Asp	Ala	Asn	Leu	Val	Asp	Gly	Asp

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195	200	205
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<223> FRXA02803		
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ggt gtt gat gtc att cgt gtt ggt gtc atc cca acc cca gct gtt gca		96
Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val Ala		
20 25 30		
ttc ctc acc gat gat tat ggc gct gac atg ggc gtg atg att tct gca		144
Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser Ala		
35 40 45		
tcc cac aac cca atg ccg gac aac gga atc aag ttc ttt tct gca ggt		192
Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala Gly		
50 55 60		
gga cac aag ctt cca gac cat gtg gaa gac gag att gag cgt gtt atg		240
Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val Met		
65 70 75 80		
gac agc ttg cca gca gaa ggc cca aca ggg cat gga gtt ggc cgt gtc		288
Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg Val		
85 90 95		
atc gaa gaa gca acc gat gca cag gac cgc tac cta gag cac ctg aag		336
Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu Lys		
100 105 110		
gaa gct gtt cct acg tca ctt gaa ggc atc aag att gtt gtg gat gca		384
Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp Ala		
115 120 125		
gcc aat ggt gcg gca		399
Ala Asn Gly Ala Ala		
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<210> 30
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 <212> PRT
 <213> Corynebacterium glutamicum

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 Ser Gly Glu Met Leu Ala Ala Ala Leu Ser Ala Gly Met Ala Ser Gln

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Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser Ala	35	40	45
Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala Gly	50	55	60
Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val Met	65	70	75
Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg Val	85	90	95
Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu Lys	100	105	110
Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp Ala	115	120	125
Ala Asn Gly Ala Ala	130		

<210> 31
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 <212> DNA
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<220>
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 <222> (101)..(1690)
 <223> RXN03076

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 Met Asp Glu Ser Arg
 1 5
 cag ctt agt ttc ggc aca gca ggg ttg cgt gca cca gtt ggc ccg gcg 163
 Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala Pro Val Gly Pro Ala
 10 15 20
 cgc cat cag atg aat gtt ttg cag gta acc aga act aca gca ggt gtt 211
 Arg His Gln Met Asn Val Leu Gln Val Thr Arg Thr Thr Ala Gly Val
 25 30 35
 gct agt tgg ttg gca gaa cgt gcg gca cta aat cca gtg ccg cat ttg 259
 Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn Pro Val Pro His Leu
 40 45 50
 gtt cct gag gat gaa aca gga atc ggc agg gcg ttg tat ccc caa gat 307
 Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala Leu Tyr Pro Gln Asp
 55 60 65
 ggt ccg ttg cgg gtc gtt gtg ggg tat gac gct cgc tat ggt tcg cat 355

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Thr	Phe	Ala	Ala	Thr 90	Thr	Ala	Glu	Val	Phe 95	Ala	Gly	Ala	Gly	Phe	Glu	
gtg	acg	ttg	ctc	ccc	acg	cct	agc	cct	acg	ccg	ttg	att	ccg	tgg	ttg	451
Val	Thr	Leu	Leu 105	Pro	Thr	Pro	Ser	Pro 110	Thr	Pro	Leu	Ile	Pro 115	Trp	Leu	
gtg	aac	aag	cat	ggg	ttg	gat	gcg	ggc	gtt	cag	atc	acg	gct	tcg	cat	499
Val	Asn	Lys 120	His	Gly	Leu	Asp	Ala 125	Gly	Val	Gln	Ile	Thr 130	Ala	Ser	His	
aat	ggt	gcg	gcg	gac	aat	ggc	tac	aag	gtg	ttt	ttg	tct	aat	ggt	cgc	547
Asn	Gly 135	Ala	Ala	Asp	Asn	Gly 140	Tyr	Lys	Val	Phe	Leu 145	Ser	Asn	Gly	Arg	
cag	ctt	tat	tct	gaa	ctg	gag	cct	gag	ctt	gag	gcg	cat	atc	aat	gct	595
Gln	Leu	Tyr	Ser	Glu	Leu 155	Glu	Pro	Glu	Leu	Glu	Ala	His	Ile	Asn	Ala 165	
gtg	gaa	gat	ccg	att	cg	gtt	cct	cg	gtg	acg	gtg	cgc	ccc	act	gct	643
Val	Glu	Asp	Pro	Ile 170	Arg	Val	Pro	Arg	Val 175	Thr	Val	Arg	Pro	Thr	Ala 180	
gat	cag	ctg	cgt	cga	tat	gtt	gat	gag	atg	gtg	tcg	ttg	gtg	act	cct	691
Asp	Gln	Leu	Arg 185	Arg	Tyr	Val	Asp	Glu 190	Met	Val	Ser	Leu	Val 195	Thr	Pro	
gat	cag	gct	gat	ttg	ttg	cg	gtg	aat	tct	gag	cg	ggc	aat	ctt	cgc	739
Asp	Gln	Ala 200	Asp	Leu	Leu	Arg	Val 205	Asn	Ser	Glu	Arg	Gly 210	Asn	Leu	Arg	
gtg	gtg	tat	acc	gct	ctg	cat	ggt	gtg	ggt	ggc	cgc	gcg	atg	gcc	aat	787
Val	Val 215	Tyr	Thr	Ala	Leu	His 220	Gly	Val	Gly	Gly	Arg 225	Ala	Met	Ala	Asn	
gct	ttc	caa	ttt	gct	ggt	ttt	ccc	cat	act	cat	ggc	gtg	aag	gct	cag	835
Ala	Phe	Gln	Phe	Ala	Gly 235	Phe	Pro	His	Thr	His 240	Gly	Val	Lys	Ala	Gln 245	
cag	tat	cct	gat	ccc	acc	ttc	ccc	act	gtg	gcg	ttc	ccc	aat	ccg	gaa	883
Gln	Tyr	Pro	Asp	Pro 250	Thr	Phe	Pro	Thr	Val 255	Ala	Phe	Pro	Asn	Pro 260	Glu	
gag	cct	tct	gcg	att	gag	ttg	ttg	ttg	gaa	cgc	gca	aag	gaa	aag	aac	931
Glu	Pro	Ser	Ala 265	Ile	Glu	Leu	Leu 270	Leu	Glu	Arg	Ala	Lys	Glu 275	Lys	Asn	
gct	gac	att	ttg	ttt	gcg	ctt	gat	cct	gat	gcc	gat	cgt	tgt	gct	gtg	979
Ala	Asp	Ile 280	Leu	Phe	Ala	Leu	Asp 285	Pro	Asp	Ala	Asp	Arg 290	Cys	Ala	Val	
ggt	att	cgt	acc	gct	gat	ggc	ggc	cac	cga	atg	ctc	tct	ggc	gat	gag	1027
Gly	Ile 295	Arg	Thr	Ala	Asp	Gly 300	Gly	His	Arg	Met	Leu 305	Ser	Gly	Asp	Glu	
gtg	ggc	aca	ctt	ttg	gct	act	cgt	ttg	gtt	ccg	gag	tat	tcc	ggt	gaa	1075
Val	Gly	Thr	Leu	Leu	Ala	Thr	Arg	Leu	Val	Pro	Glu	Tyr	Ser	Gly	Glu	

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310	315	320	325	
ggc cca cgt ccc gtg gtt gcc acc acg gtg gtg tct tcg cag ctt ctg				1123
Gly Pro Arg Pro Val Val Ala Thr Thr Val Val Ser Ser Gln Leu Leu				
	330	335	340	
ggt atc atc gcc gag gat aaa ggg tgg gat tat tcc gag aca ctg acg				1171
Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr Ser Glu Thr Leu Thr				
	345	350	355	
gga ttc aaa aat ctg tcg agg gct gcc gat ggt ctc gac gga ccg ctt				1219
Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly Leu Asp Gly Pro Leu				
	360	365	370	
gct ttc gct tat gag gaa gct gtg ggc acc tgc ccg gtt cca gat gtc				1267
Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys Pro Val Pro Asp Val				
	375	380	385	
gtg ccg gat aag gac ggc atc tct aca gcg ttg ttc atg gcg tcg tgg				1315
Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu Phe Met Ala Ser Trp				
	390	395	400	405
gct gcc gaa ctg aag gct cag ggc gca agc ctg cag caa aaa ctc aat				1363
Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu Gln Gln Lys Leu Asn				
	410	415	420	
gag ttg tat cgc cga tat ggg tat ttt gcg tcc tcg caa att gct gtg				1411
Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser Ser Gln Ile Ala Val				
	425	430	435	
cgc acg agc agt cca cgc gag tta gtt gat cac tgg att gcg cat cct				1459
Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His Trp Ile Ala His Pro				
	440	445	450	
cag caa gaa ctc att gga gtg tct gtc acc cca cat att ctt cct gaa				1507
Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro His Ile Leu Pro Glu				
	455	460	465	
aaa cag ggc att gct ttg cat ggc cag gtg ggg cat gtg cat atc cgt				1555
Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly His Val His Ile Arg				
	470	475	480	485
gct att ggt cga gtc tct gga act gag gcg aaa gcc aag ctc tat ttg				1603
Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys Ala Lys Leu Tyr Leu				
	490	495	500	
gaa gtt ggt cag gcc agc tcc cat gat gaa gca gct cag ttg ttg cat				1651
Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala Ala Gln Leu Leu His				
	505	510	515	
cag ctg gag gat gaa gtc caa agc tgg ttg agc aag ctt tagtttcctg				1700
Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser Lys Leu				
	520	525	530	
gctgctcccg gtt				1713

<210> 32

<211> 530

<212> PRT

<213> Corynebacterium glutamicum

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<400> 32

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Pro	Val	Gly	Pro	Ala	Arg	His	Gln	Met	Asn	Val	Leu	Gln	Val	Thr	Arg
			20					25					30		
Thr	Thr	Ala	Gly	Val	Ala	Ser	Trp	Leu	Ala	Glu	Arg	Ala	Ala	Leu	Asn
		35					40					45			
Pro	Val	Pro	His	Leu	Val	Pro	Glu	Asp	Glu	Thr	Gly	Ile	Gly	Arg	Ala
	50					55					60				
Leu	Tyr	Pro	Gln	Asp	Gly	Pro	Leu	Arg	Val	Val	Val	Gly	Tyr	Asp	Ala
65					70					75					80
Arg	Tyr	Gly	Ser	His	Thr	Phe	Ala	Ala	Thr	Thr	Ala	Glu	Val	Phe	Ala
				85					90					95	
Gly	Ala	Gly	Phe	Glu	Val	Thr	Leu	Leu	Pro	Thr	Pro	Ser	Pro	Thr	Pro
			100					105					110		
Leu	Ile	Pro	Trp	Leu	Val	Asn	Lys	His	Gly	Leu	Asp	Ala	Gly	Val	Gln
		115					120					125			
Ile	Thr	Ala	Ser	His	Asn	Gly	Ala	Ala	Asp	Asn	Gly	Tyr	Lys	Val	Phe
	130					135					140				
Leu	Ser	Asn	Gly	Arg	Gln	Leu	Tyr	Ser	Glu	Leu	Glu	Pro	Glu	Leu	Glu
145					150					155					160
Ala	His	Ile	Asn	Ala	Val	Glu	Asp	Pro	Ile	Arg	Val	Pro	Arg	Val	Thr
			165						170					175	
Val	Arg	Pro	Thr	Ala	Asp	Gln	Leu	Arg	Arg	Tyr	Val	Asp	Glu	Met	Val
			180					185					190		
Ser	Leu	Val	Thr	Pro	Asp	Gln	Ala	Asp	Leu	Leu	Arg	Val	Asn	Ser	Glu
	195						200					205			
Arg	Gly	Asn	Leu	Arg	Val	Val	Tyr	Thr	Ala	Leu	His	Gly	Val	Gly	Gly
	210					215					220				
Arg	Ala	Met	Ala	Asn	Ala	Phe	Gln	Phe	Ala	Gly	Phe	Pro	His	Thr	His
225					230					235					240
Gly	Val	Lys	Ala	Gln	Gln	Tyr	Pro	Asp	Pro	Thr	Phe	Pro	Thr	Val	Ala
				245					250					255	
Phe	Pro	Asn	Pro	Glu	Glu	Pro	Ser	Ala	Ile	Glu	Leu	Leu	Leu	Glu	Arg
			260					265					270		
Ala	Lys	Glu	Lys	Asn	Ala	Asp	Ile	Leu	Phe	Ala	Leu	Asp	Pro	Asp	Ala
		275					280					285			
Asp	Arg	Cys	Ala	Val	Gly	Ile	Arg	Thr	Ala	Asp	Gly	Gly	His	Arg	Met
	290					295					300				
Leu	Ser	Gly	Asp	Glu	Val	Gly	Thr	Leu	Leu	Ala	Thr	Arg	Leu	Val	Pro
305					310					315					320

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

<210> 33
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <223> FRXA02854

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 Met Asp Glu Ser Arg
 1 5

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cag ctt agt ttc ggc aca gca ggg ttg cgt gca cca gtt ggc ccg gcg	163
Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala Pro Val Gly Pro Ala	
10 15 20	
cgc cat cag atg aat gtt ttg cag gta acc aga act aca gca ggt gtt	211
Arg His Gln Met Asn Val Leu Gln Val Thr Arg Thr Thr Ala Gly Val	
25 30 35	
gct agt tgg ttg gca gaa cgt gcg gca cta aat cca gtg ccg cat ttg	259
Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn Pro Val Pro His Leu	
40 45 50	
gtt cct gag gat gaa aca gga atc ggc agg gcg ttg tat ccc caa gat	307
Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala Leu Tyr Pro Gln Asp	
55 60 65	
ggc ccg ttg cgg gtc gtt gtg ggg tat gac gct cgc tat ggt tcg cat	355
Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala Arg Tyr Gly Ser His	
70 75 80 85	
act ttt gct gca acc act gcg gag gtg ttc gcg ggt gct ggt ttt gag	403
Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala Gly Ala Gly Phe Glu	
90 95 100	
gtg acg ttg ctc ccc acg cct agc cct acg ccg ttg att ccg tgg ttg	451
Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro Leu Ile Pro Trp Leu	
105 110 115	
gtg aac aag cat ggg ttg gat gcg ggc gtt cag atc acg gct tcg cat	499
Val Asn Lys His Gly Leu Asp Ala Gly Val Gln Ile Thr Ala Ser His	
120 125 130	
aat ggt gcg gcg gac aat ggc tac aag gtg ttt ttg tct aat ggt cgc	547
Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe Leu Ser Asn Gly Arg	
135 140 145	
cag ctt tat tct gaa ctg gag cct gag ctt gag gcg cat atc aat gct	595
Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu Ala His Ile Asn Ala	
150 155 160 165	
gtg gaa gat ccg att cgg gtt cct cgg gtg acg gtg cgc ccc act gct	643
Val Glu Asp Pro Ile Arg Val Pro Arg Val Thr Val Arg Pro Thr Ala	
170 175 180	
gat cag ctg cgt cga tat gtt gat gag atg gtg tcg ttg gtg act cct	691
Asp Gln Leu Arg Arg Tyr Val Asp Glu Met Val Ser Leu Val Thr Pro	
185 190 195	
gat cag gct gat ttg ttg cgg gtg aat tct gag cgg ggc aat ctt cgc	739
Asp Gln Ala Asp Leu Leu Arg Val Asn Ser Glu Arg Gly Asn Leu Arg	
200 205 210	
gtg gtg tat acc gct ctg cat ggt gtg ggt ggc cgc gcg atg gcc aat	787
Val Val Tyr Thr Ala Leu His Gly Val Gly Gly Arg Ala Met Ala Asn	
215 220 225	
gct ttc caa ttt gct ggt ttt ccc cat act cat ggc gtg aag gct cag	835
Ala Phe Gln Phe Ala Gly Phe Pro His Thr His Gly Val Lys Ala Gln	
230 235 240 245	
cag tat cct gat ccc acc ttc ccc act gtg gcg ttc ccc aat ccg gaa	883

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Gln	Tyr	Pro	Asp	Pro	Thr	Phe	Pro	Thr	Val	Ala	Phe	Pro	Asn	Pro	Glu	
				250					255					260		
gag	cct	tct	gcg	att	gag	ttg	ttg	ttg	gaa	cgc	gca	aag	gaa	aag	aac	931
Glu	Pro	Ser	Ala	Ile	Glu	Leu	Leu	Leu	Glu	Arg	Ala	Lys	Glu	Lys	Asn	
			265					270					275			
gct	gac	att	ttg	ttt	gcg	ctt	gat	cct	gat	gcc	gat	cgt	tgt	gct	gtg	979
Ala	Asp	Ile	Leu	Phe	Ala	Leu	Asp	Pro	Asp	Ala	Asp	Arg	Cys	Ala	Val	
		280					285					290				
ggt	att	cgt	acc	gct	gat	ggc	ggc	cac	cga	atg	ctc	tct	ggc	gat	gag	1027
Gly	Ile	Arg	Thr	Ala	Asp	Gly	Gly	His	Arg	Met	Leu	Ser	Gly	Asp	Glu	
	295					300					305					
gtg	ggc	aca	ctt	ttg	gct	act	cgt	ttg	gtt	ccg	gag	tat	tcc	ggt	gaa	1075
Val	Gly	Thr	Leu	Leu	Ala	Thr	Arg	Leu	Val	Pro	Glu	Tyr	Ser	Gly	Glu	
310					315					320					325	
ggc	cca	cgt	ccc	gtg	gtt	gcc	acc	acg	gtg	gtg	tct	tcg	cag	ctt	ctg	1123
Gly	Pro	Arg	Pro	Val	Val	Ala	Thr	Thr	Val	Val	Ser	Ser	Gln	Leu	Leu	
				330					335					340		
ggt	atc	atc	gcc	gag	gat	aaa	ggg	tgg	gat	tat	tcc	gag	aca	ctg	acg	1171
Gly	Ile	Ile	Ala	Glu	Asp	Lys	Gly	Trp	Asp	Tyr	Ser	Glu	Thr	Leu	Thr	
			345					350					355			
gga	ttc	aaa	aat	ctg	tcg	agg	gct	gcc	gat	ggt	ctc	gac	gga	ccg	ctt	1219
Gly	Phe	Lys	Asn	Leu	Ser	Arg	Ala	Ala	Asp	Gly	Leu	Asp	Gly	Pro	Leu	
		360					365					370				
gct	ttc	gct	tat	gag	gaa	gct	gtg	ggc	acc	tgc	ccg	gtt	cca	gat	gtc	1267
Ala	Phe	Ala	Tyr	Glu	Glu	Ala	Val	Gly	Thr	Cys	Pro	Val	Pro	Asp	Val	
	375					380					385					
gtg	ccg	gat	aag	gac	ggc	atc	tct	aca	gcg	ttg	ttc	atg	gcg	tcg	tgg	1315
Val	Pro	Asp	Lys	Asp	Gly	Ile	Ser	Thr	Ala	Leu	Phe	Met	Ala	Ser	Trp	
390					395					400					405	
gct	gcc	gaa	ctg	aag	gct	cag	ggc	gca	agc	ctg	cag	caa	aaa	ctc	aat	1363
Ala	Ala	Glu	Leu	Lys	Ala	Gln	Gly	Ala	Ser	Leu	Gln	Gln	Lys	Leu	Asn	
				410				415						420		
gag	ttg	tat	cgc	cga	tat	ggg	tat	ttt	gcg	tcc	tcg	caa	att	gct	gtg	1411
Glu	Leu	Tyr	Arg	Arg	Tyr	Gly	Tyr	Phe	Ala	Ser	Ser	Gln	Ile	Ala	Val	
			425				430						435			
cgc	acg	agc	agt	cca	cgc	gag	tta	gtt	gat	cac	tgg	att	gcg	cat	cct	1459
Arg	Thr	Ser	Ser	Pro	Arg	Glu	Leu	Val	Asp	His	Trp	Ile	Ala	His	Pro	
		440					445					450				
cag	caa	gaa	ctc	att	gga	gtg	tct	gtc	acc	cca	cat	att	ctt	cct	gaa	1507
Gln	Gln	Glu	Leu	Ile	Gly	Val	Ser	Val	Thr	Pro	His	Ile	Leu	Pro	Glu	
	455					460					465					
aaa	cag	ggc	att	gct	ttg	cat	ggc	cag	gtg	ggg	cat	gtg	cat	atc	cgt	1555
Lys	Gln	Gly	Ile	Ala	Leu	His	Gly	Gln	Val	Gly	His	Val	His	Ile	Arg	
470					475					480					485	
gct	att	ggt	cga	gtc	tct	gga	act	gag	gcg	aaa	gcc	aag	ctc	tat	ttg	1603
Ala	Ile	Gly	Arg	Val	Ser	Gly	Thr	Glu	Ala	Lys	Ala	Lys	Leu	Tyr	Leu	

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490	495	500	
gaa gtt ggt cag gcc agc tcc cat gat	gaa gca gct cag ttg ttg cat		1651
Glu Val Gly Gln Ala Ser Ser His Asp	Glu Ala Ala Gln Leu Leu His		
505	510	515	

cag ctg gag gat gaa gtc caa agc tgg ttg agc		1684
Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser		
520	525	

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 <211> 528
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 34
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 Thr Thr Ala Gly Val Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn
 35 40 45
 Pro Val Pro His Leu Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala
 50 55 60
 Leu Tyr Pro Gln Asp Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala
 65 70 75 80
 Arg Tyr Gly Ser His Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala
 85 90 95
 Gly Ala Gly Phe Glu Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro
 100 105 110
 Leu Ile Pro Trp Leu Val Asn Lys His Gly Leu Asp Ala Gly Val Gln
 115 120 125
 Ile Thr Ala Ser His Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe
 130 135 140
 Leu Ser Asn Gly Arg Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu
 145 150 155 160
 Ala His Ile Asn Ala Val Glu Asp Pro Ile Arg Val Pro Arg Val Thr
 165 170 175
 Val Arg Pro Thr Ala Asp Gln Leu Arg Arg Tyr Val Asp Glu Met Val
 180 185 190
 Ser Leu Val Thr Pro Asp Gln Ala Asp Leu Leu Arg Val Asn Ser Glu
 195 200 205
 Arg Gly Asn Leu Arg Val Val Tyr Thr Ala Leu His Gly Val Gly Gly
 210 215 220
 Arg Ala Met Ala Asn Ala Phe Gln Phe Ala Gly Phe Pro His Thr His
 225 230 235 240

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Gly Val Lys Ala Gln Gln Tyr Pro Asp Pro Thr Phe Pro Thr Val Ala
 245 250 255
 Phe Pro Asn Pro Glu Glu Pro Ser Ala Ile Glu Leu Leu Leu Glu Arg
 260 265 270
 Ala Lys Glu Lys Asn Ala Asp Ile Leu Phe Ala Leu Asp Pro Asp Ala
 275 280 285
 Asp Arg Cys Ala Val Gly Ile Arg Thr Ala Asp Gly Gly His Arg Met
 290 295 300
 Leu Ser Gly Asp Glu Val Gly Thr Leu Leu Ala Thr Arg Leu Val Pro
 305 310 315 320
 Glu Tyr Ser Gly Glu Gly Pro Arg Pro Val Val Ala Thr Thr Val Val
 325 330 335
 Ser Ser Gln Leu Leu Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr
 340 345 350
 Ser Glu Thr Leu Thr Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly
 355 360 365
 Leu Asp Gly Pro Leu Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys
 370 375 380
 Pro Val Pro Asp Val Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu
 385 390 395 400
 Phe Met Ala Ser Trp Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu
 405 410 415
 Gln Gln Lys Leu Asn Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser
 420 425 430
 Ser Gln Ile Ala Val Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His
 435 440 445
 Trp Ile Ala His Pro Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro
 450 455 460
 His Ile Leu Pro Glu Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly
 465 470 475 480
 His Val His Ile Arg Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys
 485 490 495
 Ala Lys Leu Tyr Leu Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala
 500 505 510
 Ala Gln Leu Leu His Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser
 515 520 525

<210> 35

<211> 536

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PCT/IB00/00943

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

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<223> RXA00511

<400> 35

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1				5				10						15		

ttg	aag	att	gct	atg	gat	gaa	gcc	gga	att	aca	ctg	cgt	acc	acc	aag	96
Leu	Lys	Ile	Ala	Met	Asp	Glu	Ala	Gly	Ile	Thr	Leu	Arg	Thr	Thr	Lys	
			20					25					30			

gta	gga	gac	cgc	tac	gtg	ctg	gaa	gac	ctc	aat	gca	ggt	gga	ttc	agc	144
Val	Gly	Asp	Arg	Tyr	Val	Leu	Glu	Asp	Leu	Asn	Ala	Gly	Gly	Phe	Ser	
		35					40					45				

ctg	ggc	ggc	gag	caa	tct	ggc	cac	att	gtt	ctt	cca	gat	cat	ggc	acc	192
Leu	Gly	Gly	Glu	Gln	Ser	Gly	His	Ile	Val	Leu	Pro	Asp	His	Gly	Thr	
	50					55					60					

act	ggc	gat	gga	act	ttg	act	ggt	ctt	tcc	atc	atg	gcg	cgc	atg	gct	240
Thr	Gly	Asp	Gly	Thr	Leu	Thr	Gly	Leu	Ser	Ile	Met	Ala	Arg	Met	Ala	
65					70					75					80	

gaa	acc	gga	aag	tcc	ttg	ggc	gag	ttg	gca	caa	gct	atg	acg	gtg	ctg	288
Glu	Thr	Gly	Lys	Ser	Leu	Gly	Glu	Leu	Ala	Gln	Ala	Met	Thr	Val	Leu	
				85					90					95		

cca	cag	gtt	ctg	atc	aat	gtg	cca	gtt	tcc	gat	aag	tcc	acc	atc	gtg	336
Pro	Gln	Val	Leu	Ile	Asn	Val	Pro	Val	Ser	Asp	Lys	Ser	Thr	Ile	Val	
			100					105					110			

agc	cac	cca	agc	gtt	gtg	gct	gcg	atc	gcg	gaa	gca	gaa	gct	gag	ttg	384
Ser	His	Pro	Ser	Val	Val	Ala	Ala	Ile	Ala	Glu	Ala	Glu	Ala	Glu	Leu	
		115				120						125				

ggc	gcc	acc	ggt	cgc	gtt	ctt	ctt	cgt	gct	tct	ggc	acc	gaa	gag	ctt	432
Gly	Ala	Thr	Gly	Arg	Val	Leu	Leu	Arg	Ala	Ser	Gly	Thr	Glu	Glu	Leu	
	130					135					140					

ttc	cgc	gtg	atg	gtt	gag	gct	gga	gac	aag	gaa	caa	gct	cgt	cgt	atc	480
Phe	Arg	Val	Met	Val	Glu	Ala	Gly	Asp	Lys	Glu	Gln	Ala	Arg	Arg	Ile	
145					150					155					160	

gcg	gga	cgt	ctt	gct	gca	gtg	gtt	gca	gaa	gtc	taattcactt	cagtcacagc	533
Ala	Gly	Arg	Leu	Ala	Ala	Val	Val	Ala	Glu	Val			
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gca																536

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<211> 171

<212> PRT

<213> Corynebacterium glutamicum

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<400> 36

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Leu Lys Ile Ala Met Asp Glu Ala Gly Ile Thr Leu Arg Thr Thr Lys
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Val Gly Asp Arg Tyr Val Leu Glu Asp Leu Asn Ala Gly Gly Phe Ser
 35 40 45

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

Thr Gly Asp Gly Thr Leu Thr Gly Leu Ser Ile Met Ala Arg Met Ala
 65 70 75 80

Glu Thr Gly Lys Ser Leu Gly Glu Leu Ala Gln Ala Met Thr Val Leu
 85 90 95

Pro Gln Val Leu Ile Asn Val Pro Val Ser Asp Lys Ser Thr Ile Val
 100 105 110

Ser His Pro Ser Val Val Ala Ala Ile Ala Glu Ala Glu Ala Glu Leu
 115 120 125

Gly Ala Thr Gly Arg Val Leu Leu Arg Ala Ser Gly Thr Glu Glu Leu
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Phe Arg Val Met Val Glu Ala Gly Asp Lys Glu Gln Ala Arg Arg Ile
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Ala Gly Arg Leu Ala Ala Val Val Ala Glu Val
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<210> 37

<211> 1497

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1474)

<223> RXN01365

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 Met Arg Thr Arg Glu
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tct gtc aca gct gta att aag gcg tat gac gtc cgt ggt gtt gtt ggt 163
 Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val Arg Gly Val Val Gly
 10 15 20

gtc gat att gat gct gat ttc att tct gag act ggc gct gcc ttt ggt 211
 Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr Gly Ala Ala Phe Gly
 25 30 35

cgg ctc atg cgt agt gag ggt gaa acc acc gtt gct att ggc cat gac 259

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Arg	Leu	Met	Arg	Ser	Glu	Gly	Glu	Thr	Thr	Val	Ala	Ile	Gly	His	Asp	
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atg	cgt	gat	tcc	tcc	cct	gaa	ttg	gcc	aag	gcg	ttt	gcc	gat	ggc	gtg	307
Met	Arg	Asp	Ser	Ser	Pro	Glu	Leu	Ala	Lys	Ala	Phe	Ala	Asp	Gly	Val	
	55					60					65					
act	gca	cag	ggg	ttg	gat	gtt	gtt	cat	ttg	gga	ctg	act	tct	act	gat	355
Thr	Ala	Gln	Gly	Leu	Asp	Val	Val	His	Leu	Gly	Leu	Thr	Ser	Thr	Asp	
	70				75					80					85	
gag	ctg	tac	ttt	gcg	tcc	gga	acc	ttg	aag	tgt	gct	ggg	gcg	atg	ttt	403
Glu	Leu	Tyr	Phe	Ala	Ser	Gly	Thr	Leu	Lys	Cys	Ala	Gly	Ala	Met	Phe	
				90					95					100		
act	gcg	tcg	cat	aac	ccc	gct	gag	tac	aac	ggc	atc	aag	ttg	tgt	cgt	451
Thr	Ala	Ser	His	Asn	Pro	Ala	Glu	Tyr	Asn	Gly	Ile	Lys	Leu	Cys	Arg	
			105					110					115			
gcg	ggg	gct	cgt	ccg	gtc	ggg	cag	gat	tct	ggg	ttg	gcc	aac	atc	att	499
Ala	Gly	Ala	Arg	Pro	Val	Gly	Gln	Asp	Ser	Gly	Leu	Ala	Asn	Ile	Ile	
		120					125					130				
gat	gat	ctg	gtt	gag	ggg	gtt	cca	gcg	ttt	gat	ggg	gag	tca	ggg	tcg	547
Asp	Asp	Leu	Val	Glu	Gly	Val	Pro	Ala	Phe	Asp	Gly	Glu	Ser	Gly	Ser	
	135					140					145					
gtt	tct	gag	cag	gat	ttg	ctg	agc	gca	tat	gcc	gag	tac	ctc	aat	gag	595
Val	Ser	Glu	Gln	Asp	Leu	Leu	Ser	Ala	Tyr	Ala	Glu	Tyr	Leu	Asn	Glu	
	150				155					160					165	
ctt	gtt	gat	ctg	aag	aac	atc	cgc	ccg	atg	aag	gtt	gct	gtg	gat	gcg	643
Leu	Val	Asp	Leu	Lys	Asn	Ile	Arg	Pro	Met	Lys	Val	Ala	Val	Asp	Ala	
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gca	aac	ggc	atg	ggg	ggg	ttc	act	gtc	cct	gag	gta	ttc	aag	ggg	ctg	691
Ala	Asn	Gly	Met	Gly	Gly	Phe	Thr	Val	Pro	Glu	Val	Phe	Lys	Gly	Leu	
			185					190					195			
cca	ctt	gat	gtt	gcg	cca	ctg	tat	ttt	gag	ctt	gac	ggc	aat	ttc	ccc	739
Pro	Leu	Asp	Val	Ala	Pro	Leu	Tyr	Phe	Glu	Leu	Asp	Gly	Asn	Phe	Pro	
		200					205					210				
aac	cat	gag	gcc	aac	cct	ctg	gag	cct	gcc	aac	ctg	gtt	gat	ttg	cag	787
Asn	His	Glu	Ala	Asn	Pro	Leu	Glu	Pro	Ala	Asn	Leu	Val	Asp	Leu	Gln	
	215					220					225					
aag	ttt	acc	gta	gag	acc	gga	tct	gat	atc	ggg	ttg	gcg	ttc	gac	ggc	835
Lys	Phe	Thr	Val	Glu	Thr	Gly	Ser	Asp	Ile	Gly	Leu	Ala	Phe	Asp	Gly	
	230				235					240					245	
gat	gcg	gat	cgt	tgc	ttc	gtg	gtc	gat	gag	aag	ggc	cag	cca	gtc	agc	883
Asp	Ala	Asp	Arg	Cys	Phe	Val	Val	Asp	Glu	Lys	Gly	Gln	Pro	Val	Ser	
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cct	tcg	gcg	atc	tgt	gcg	atc	gta	gcg	gag	cgt	tac	ttg	gag	aag	ctt	931
Pro	Ser	Ala	Ile	Cys	Ala	Ile	Val	Ala	Glu	Arg	Tyr	Leu	Glu	Lys	Leu	
			265					270					275			
ccg	ggg	tcc	acc	atc	atc	cac	aac	ctg	att	acc	tct	aag	gct	gtg	cct	979
Pro	Gly	Ser	Thr	Ile	Ile	His	Asn	Leu	Ile	Thr	Ser	Lys	Ala	Val	Pro	

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Glu	Val	Ile	Ala	Glu	Asn	Gly	Gly	Thr	Ala	Val	Arg	Thr	Arg	Val	Gly				
295						300						305							
cac	tcc	ttc	atc	aag	gcg	aag	atg	gca	gag	acc	ggt	gcg	gcc	ttt	ggt	1075			
His	Ser	Phe	Ile	Lys	Ala	Lys	Met	Ala	Glu	Thr	Gly	Ala	Ala	Phe	Gly				
310						315						320						325	
ggc	gag	cac	tct	gcg	cac	tac	tac	ttc	act	gag	ttc	ttc	aat	gcg	gac	1123			
Gly	Glu	His	Ser	Ala	His	Tyr	Tyr	Phe	Thr	Glu	Phe	Phe	Asn	Ala	Asp				
330						335						340							
tcc	ggc	att	ttg	gct	gcg	atg	cac	gtg	ctg	gct	gcg	ctg	gga	agc	cag	1171			
Ser	Gly	Ile	Leu	Ala	Ala	Met	His	Val	Leu	Ala	Ala	Leu	Gly	Ser	Gln				
345						350						355							
gac	cag	cca	ctc	agt	gag	atg	atg	gct	agg	tat	aac	cgg	tac	gtt	gct	1219			
Asp	Gln	Pro	Leu	Ser	Glu	Met	Met	Ala	Arg	Tyr	Asn	Arg	Tyr	Val	Ala				
360						365						370							
tca	ggc	gag	ttg	aac	tcc	cgt	ttg	gct	aat	gca	gag	gcg	cag	caa	gag	1267			
Ser	Gly	Glu	Leu	Asn	Ser	Arg	Leu	Ala	Asn	Ala	Glu	Ala	Gln	Gln	Glu				
375						380						385							
cgc	acc	cag	gct	gtg	ctc	gat	gcg	ttc	gct	gat	cgc	acc	gag	tcc	gtg	1315			
Arg	Thr	Gln	Ala	Val	Leu	Asp	Ala	Phe	Ala	Asp	Arg	Thr	Glu	Ser	Val				
390						395						400						405	
gac	acc	ctt	gac	ggc	gtg	act	gtg	gaa	ctc	aag	gac	acc	tcc	gcg	tgg	1363			
Asp	Thr	Leu	Asp	Gly	Val	Thr	Val	Glu	Leu	Lys	Asp	Thr	Ser	Ala	Trp				
410						415						420							
ttc	aac	gtg	cgt	gcg	tcc	aac	acc	gag	ccg	ctg	ctt	cgc	ctc	aat	gtt	1411			
Phe	Asn	Val	Arg	Ala	Ser	Asn	Thr	Glu	Pro	Leu	Leu	Arg	Leu	Asn	Val				
425						430						435							
gaa	gct	gca	tcg	aag	gaa	gaa	gtc	gat	gcg	ttg	gta	gcg	gag	att	cta	1459			
Glu	Ala	Ala	Ser	Lys	Glu	Glu	Val	Asp	Ala	Leu	Val	Ala	Glu	Ile	Leu				
440						445						450							
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<212> PRT

<213> Corynebacterium glutamicum

<400> 38

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Gly	Ala	Ala	Phe	Gly	Arg	Leu	Met	Arg	Ser	Glu	Gly	Glu	Thr	Thr	Val
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Ala	Ile	Gly	His	Asp	Met	Arg	Asp	Ser	Ser	Pro	Glu	Leu	Ala	Lys	Ala			
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Phe	Ala	Asp	Gly	Val	Thr	Ala	Gln	Gly	Leu	Asp	Val	Val	His	Leu	Gly			
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Leu	Thr	Ser	Thr	Asp	Glu	Leu	Tyr	Phe	Ala	Ser	Gly	Thr	Leu	Lys	Cys			
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Ala	Gly	Ala	Met	Phe	Thr	Ala	Ser	His	Asn	Pro	Ala	Glu	Tyr	Asn	Gly			
			100					105					110					
Ile	Lys	Leu	Cys	Arg	Ala	Gly	Ala	Arg	Pro	Val	Gly	Gln	Asp	Ser	Gly			
		115					120					125						
Leu	Ala	Asn	Ile	Ile	Asp	Asp	Leu	Val	Glu	Gly	Val	Pro	Ala	Phe	Asp			
	130					135					140							
Gly	Glu	Ser	Gly	Ser	Val	Ser	Glu	Gln	Asp	Leu	Leu	Ser	Ala	Tyr	Ala			
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				165					170					175				
Val	Ala	Val	Asp	Ala	Ala	Asn	Gly	Met	Gly	Gly	Phe	Thr	Val	Pro	Glu			
			180					185					190					
Val	Phe	Lys	Gly	Leu	Pro	Leu	Asp	Val	Ala	Pro	Leu	Tyr	Phe	Glu	Leu			
		195					200					205						
Asp	Gly	Asn	Phe	Pro	Asn	His	Glu	Ala	Asn	Pro	Leu	Glu	Pro	Ala	Asn			
	210					215					220							
Leu	Val	Asp	Leu	Gln	Lys	Phe	Thr	Val	Glu	Thr	Gly	Ser	Asp	Ile	Gly			
	225				230					235					240			
Leu	Ala	Phe	Asp	Gly	Asp	Ala	Asp	Arg	Cys	Phe	Val	Val	Asp	Glu	Lys			
				245					250					255				
Gly	Gln	Pro	Val	Ser	Pro	Ser	Ala	Ile	Cys	Ala	Ile	Val	Ala	Glu	Arg			
			260					265					270					
Tyr	Leu	Glu	Lys	Leu	Pro	Gly	Ser	Thr	Ile	Ile	His	Asn	Leu	Ile	Thr			
		275					280					285						
Ser	Lys	Ala	Val	Pro	Glu	Val	Ile	Ala	Glu	Asn	Gly	Gly	Thr	Ala	Val			
	290					295					300							
Arg	Thr	Arg	Val	Gly	His	Ser	Phe	Ile	Lys	Ala	Lys	Met	Ala	Glu	Thr			
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Gly	Ala	Ala	Phe	Gly	Gly	Glu	His	Ser	Ala	His	Tyr	Tyr	Phe	Thr	Glu			
				325					330					335				
Phe	Phe	Asn	Ala	Asp	Ser	Gly	Ile	Leu	Ala	Ala	Met	His	Val	Leu	Ala			
			340					345					350					
Ala	Leu	Gly	Ser	Gln	Asp	Gln	Pro	Leu	Ser	Glu	Met	Met	Ala	Arg	Tyr			
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Asn Arg Tyr Val Ala Ser Gly Glu Leu Asn Ser Arg Leu Ala Asn Ala
 370 375 380
 Glu Ala Gln Gln Glu Arg Thr Gln Ala Val Leu Asp Ala Phe Ala Asp
 385 390 395 400
 Arg Thr Glu Ser Val Asp Thr Leu Asp Gly Val Thr Val Glu Leu Lys
 405 410 415
 Asp Thr Ser Ala Trp Phe Asn Val Arg Ala Ser Asn Thr Glu Pro Leu
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 <222> (101)..(994)
 <223> FRXA01365

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 Met Arg Thr Arg Glu
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 tct gtc aca gct gta att aag gcg tat gac gtc cgt ggt gtt gtt ggt 163
 Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val Arg Gly Val Val Gly
 10 15 20
 gtc gat att gat gct gat ttc att tct gag act ggc gct gcc ttt ggt 211
 Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr Gly Ala Ala Phe Gly
 25 30 35
 cgg ctc atg cgt agt gag ggt gaa acc acc gtt gct att ggc cat gac 259
 Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val Ala Ile Gly His Asp
 40 45 50
 atg cgt gat tcc tcc cct gaa ttg gcc aag gcg ttt gcc gat ggc gtg 307
 Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala Phe Ala Asp Gly Val
 55 60 65
 act gca cag ggt ttg gat gtt gtt cat ttg gga ctg act tct act gat 355
 Thr Ala Gln Gly Leu Asp Val Val His Leu Gly Leu Thr Ser Thr Asp
 70 75 80 85
 gag ctg tac ttt gcg tcc gga acc ttg aag tgt gct ggt gcg atg ttt 403
 Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys Ala Gly Ala Met Phe
 90 95 100
 act gcg tcg cat aac ccc gct gag tac aac ggc atc aag ttg tgt cgt 451

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Ala	Gly	Ala	Arg	Pro	Val	Gly	Gln	Asp	Ser	Gly	Leu	Ala	Asn	Ile	Ile		
			120				125					130					
gat	gat	ctg	gtt	gag	ggt	gtt	cca	gcg	ttt	gat	ggt	gag	tca	ggt	tcg	547	
Asp	Asp	Leu	Val	Glu	Gly	Val	Pro	Ala	Phe	Asp	Gly	Glu	Ser	Gly	Ser		
			135			140					145						
gtt	tct	gag	cag	gat	ttg	ctg	agc	gca	tat	gcc	gag	tac	ctc	aat	gag	595	
Val	Ser	Glu	Gln	Asp	Leu	Leu	Ser	Ala	Tyr	Ala	Glu	Tyr	Leu	Asn	Glu		
					155					160					165		
ctt	gtt	gat	ctg	aag	aac	atc	cgc	ccg	atg	aag	gtt	gct	gtg	gat	gcg	643	
Leu	Val	Asp	Leu	Lys	Asn	Ile	Arg	Pro	Met	Lys	Val	Ala	Val	Asp	Ala		
				170					175					180			
gca	aac	ggc	atg	ggt	ggg	ttc	act	gtc	cct	gag	gta	ttc	aag	ggt	ctg	691	
Ala	Asn	Gly	Met	Gly	Gly	Phe	Thr	Val	Pro	Glu	Val	Phe	Lys	Gly	Leu		
			185					190					195				
cca	ctt	gat	gtt	gcg	cca	ctg	tat	ttt	gag	ctt	gac	ggc	aat	ttc	ccc	739	
Pro	Leu	Asp	Val	Ala	Pro	Leu	Tyr	Phe	Glu	Leu	Asp	Gly	Asn	Phe	Pro		
			200				205					210					
aac	cat	gag	gcc	aat	cct	ctg	gag	cct	gcc	aac	ctg	gtt	gat	ttg	cag	787	
Asn	His	Glu	Ala	Asn	Pro	Leu	Glu	Pro	Ala	Asn	Leu	Val	Asp	Leu	Gln		
			215			220					225						
aag	ttt	acc	gta	gag	acc	gga	tct	gat	atc	ggt	ttg	gcg	ttc	gac	ggc	835	
Lys	Phe	Thr	Val	Glu	Thr	Gly	Ser	Asp	Ile	Gly	Leu	Ala	Phe	Asp	Gly		
					235					240					245		
gat	gcg	gat	cgt	tgc	ttc	gtg	gtc	gat	gag	aag	ggc	cag	cca	gtc	agc	883	
Asp	Ala	Asp	Arg	Cys	Phe	Val	Val	Asp	Glu	Lys	Gly	Gln	Pro	Val	Ser		
				250				255						260			
cct	tcg	gcg	atc	tgt	gcg	atc	gta	gcg	gag	cgt	tac	ttg	gag	aag	ctt	931	
Pro	Ser	Ala	Ile	Cys	Ala	Ile	Val	Ala	Glu	Arg	Tyr	Leu	Glu	Lys	Leu		
			265					270					275				
ccg	ggt	tcc	acc	atc	atc	cac	aac	ctg	att	acc	tct	aag	gct	gtg	cct	979	
Pro	Gly	Ser	Thr	Ile	Ile	His	Asn	Leu	Ile	Thr	Ser	Lys	Ala	Val	Pro		
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Glu	Val	Ile	Ala	Glu													
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<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 40

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Arg Gly Val Val Gly Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr
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 Gly Ala Ala Phe Gly Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val
 35 40 45
 Ala Ile Gly His Asp Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala
 50 55 60
 Phe Ala Asp Gly Val Thr Ala Gln Gly Leu Asp Val Val His Leu Gly
 65 70 75 80
 Leu Thr Ser Thr Asp Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys
 85 90 95
 Ala Gly Ala Met Phe Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly
 100 105 110
 Ile Lys Leu Cys Arg Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly
 115 120 125
 Leu Ala Asn Ile Ile Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp
 130 135 140
 Gly Glu Ser Gly Ser Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala
 145 150 155 160
 Glu Tyr Leu Asn Glu Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys
 165 170 175
 Val Ala Val Asp Ala Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu
 180 185 190
 Val Phe Lys Gly Leu Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu
 195 200 205
 Asp Gly Asn Phe Pro Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn
 210 215 220
 Leu Val Asp Leu Gln Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly
 225 230 235 240
 Leu Ala Phe Asp Gly Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys
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 Gly Gln Pro Val Ser Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg
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 275 280 285
 Ser Lys Ala Val Pro Glu Val Ile Ala Glu
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<210> 41

<211> 1743

<212> DNA

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<220>

WO 01/00844

PCT/IB00/00943

<221> CDS

<222> (101)..(1720)

<223> RXA00098

<400> 41

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				Met	Ala	Asp	Ile	Ser	
				1				5	

acc	acc	cag	gtt	tgg	caa	gac	ctg	acc	gat	cat	tac	tca	aac	ttc	cag	163
Thr	Thr	Gln	Val	Trp	Gln	Asp	Leu	Thr	Asp	His	Tyr	Ser	Asn	Phe	Gln	
			10					15						20		

gca	acc	act	ctg	cgt	gaa	ctt	ttc	aag	gaa	gaa	aac	cgc	gcc	gag	aag	211
Ala	Thr	Thr	Leu	Arg	Glu	Leu	Phe	Lys	Glu	Glu	Asn	Arg	Ala	Glu	Lys	
			25					30					35			

tac	acc	ttc	tcc	gcg	gct	ggc	ctc	cac	gtc	gac	ctg	tcg	aag	aat	ctg	259
Tyr	Thr	Phe	Ser	Ala	Ala	Gly	Leu	His	Val	Asp	Leu	Ser	Lys	Asn	Leu	
		40				45					50					

ctt	gac	gac	gcc	acc	ctc	acc	aag	ctc	ctt	gca	ctg	acc	gaa	gaa	tct	307
Leu	Asp	Asp	Ala	Thr	Leu	Thr	Lys	Leu	Leu	Ala	Leu	Thr	Glu	Glu	Ser	
	55					60					65					

ggc	ctt	cgc	gaa	cgc	att	gac	gcg	atg	ttt	gcc	ggt	gaa	cac	ctc	aac	355
Gly	Leu	Arg	Glu	Arg	Ile	Asp	Ala	Met	Phe	Ala	Gly	Glu	His	Leu	Asn	
70					75					80					85	

aac	acc	gaa	gac	cgc	gct	gtc	ctc	cac	acc	gcg	ctg	cgc	ctt	cct	gcc	403
Asn	Thr	Glu	Asp	Arg	Ala	Val	Leu	His	Thr	Ala	Leu	Arg	Leu	Pro	Ala	
				90					95					100		

gaa	gct	gat	ctg	tca	gta	gat	ggc	caa	gat	gtt	gct	gct	gat	gtc	cac	451
Glu	Ala	Asp	Leu	Ser	Val	Asp	Gly	Gln	Asp	Val	Ala	Ala	Asp	Val	His	
			105					110					115			

gaa	gtt	ttg	gga	cgc	atg	cgt	gac	ttc	gct	act	gcg	ctg	cgc	tca	ggc	499
Glu	Val	Leu	Gly	Arg	Met	Arg	Asp	Phe	Ala	Thr	Ala	Leu	Arg	Ser	Gly	
		120					125					130				

aac	tgg	ttg	gga	cac	acc	ggc	cac	acg	atc	aag	aag	atc	gtc	aac	att	547
Asn	Trp	Leu	Gly	His	Thr	Gly	His	Thr	Ile	Lys	Lys	Ile	Val	Asn	Ile	
	135					140					145					

ggt	atc	ggt	ggc	tct	gac	ctc	gga	cca	gcc	atg	gct	acg	aag	gct	ctg	595
Gly	Ile	Gly	Gly	Ser	Asp	Leu	Gly	Pro	Ala	Met	Ala	Thr	Lys	Ala	Leu	
150					155					160					165	

cgt	gca	tac	gcg	acc	gct	ggt	atc	tca	gca	gaa	ttc	gtc	tcc	aac	gtc	643
Arg	Ala	Tyr	Ala	Thr	Ala	Gly	Ile	Ser	Ala	Glu	Phe	Val	Ser	Asn	Val	
				170					175					180		

gac	cca	gca	gac	ctc	gtt	tct	gtg	ttg	gaa	gac	ctc	gat	gca	gaa	tcc	691
Asp	Pro	Ala	Asp	Leu	Val	Ser	Val	Leu	Glu	Asp	Leu	Asp	Ala	Glu	Ser	
			185					190					195			

aca	ttg	ttc	gtg	atc	gct	tcg	aaa	act	ttc	acc	acc	cag	gag	acg	ctg	739
Thr	Leu	Phe	Val	Ile	Ala	Ser	Lys	Thr	Phe	Thr	Thr	Gln	Glu	Thr	Leu	

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200	205	210	
tcc aac gct cgt gca gct cgt gct tgg ctg gta gag aag ctc ggt gaa Ser Asn Ala Arg Ala Ala Arg Ala Trp Leu Val Glu Lys Leu Gly Glu 215 220 225			787
gag gct gtc gcg aag cac ttc gtc gca gtg tcc acc aat gct gaa aag Glu Ala Val Ala Lys His Phe Val Ala Val Ser Thr Asn Ala Glu Lys 230 235 240 245			835
gtc gca gag ttc ggt atc gac acg gac aac atg ttc ggc ttc tgg gac Val Ala Glu Phe Gly Ile Asp Thr Asp Asn Met Phe Gly Phe Trp Asp 250 255 260			883
tgg gtc gga ggt cgt tac tcc gtg gac tcc gca gtt ggt ctt tcc ctc Trp Val Gly Gly Arg Tyr Ser Val Asp Ser Ala Val Gly Leu Ser Leu 265 270 275			931
atg gca gtg atc ggc cct cgc gac ttc atg cgt ttc ctc ggt gga ttc Met Ala Val Ile Gly Pro Arg Asp Phe Met Arg Phe Leu Gly Gly Phe 280 285 290			979
cac gcg atg gat gaa cac ttc cgc acc acc aag ttc gaa gag aac gtt His Ala Met Asp Glu His Phe Arg Thr Thr Lys Phe Glu Glu Asn Val 295 300 305			1027
cca atc ttg atg gct ctg ctc ggt gtc tgg tac tcc gat ttc tat ggt Pro Ile Leu Met Ala Leu Leu Gly Val Trp Tyr Ser Asp Phe Tyr Gly 310 315 320 325			1075
gca gaa acc cac gct gtc cta cct tat tcc gag gat ctc agc cgt ttt Ala Glu Thr His Ala Val Leu Pro Tyr Ser Glu Asp Leu Ser Arg Phe 330 335 340			1123
gct gct tac ctc cag cag ctg acc atg gaa tca aat ggc aag tca gtc Ala Ala Tyr Leu Gln Gln Leu Thr Met Glu Ser Asn Gly Lys Ser Val 345 350 355			1171
cac cgc gac ggc tcc cct gtt tcc act ggc act ggc gaa att tac tgg His Arg Asp Gly Ser Pro Val Ser Thr Gly Thr Gly Glu Ile Tyr Trp 360 365 370			1219
ggt gag cct ggc aca aat ggc cag cac gct ttc ttc cag ctg atc cac Gly Glu Pro Gly Thr Asn Gly Gln His Ala Phe Phe Gln Leu Ile His 375 380 385			1267
cag ggc act cgc ctt gtt cca gct gat ttc att ggt ttc gct cgt cca Gln Gly Thr Arg Leu Val Pro Ala Asp Phe Ile Gly Phe Ala Arg Pro 390 395 400 405			1315
aag cag gat ctt cct gcc ggt gag cgc acc atg cat gac ctt ttg atg Lys Gln Asp Leu Pro Ala Gly Glu Arg Thr Met His Asp Leu Leu Met 410 415 420			1363
agc aac ttc ttc gca cag acc aag gtt ttg gct ttc ggt aag aac gct Ser Asn Phe Phe Ala Gln Thr Lys Val Leu Ala Phe Gly Lys Asn Ala 425 430 435			1411
gaa gag atc gct gcg gaa ggt gtc gca cct gag ctg gtc aac cac aag Glu Glu Ile Ala Ala Glu Gly Val Ala Pro Glu Leu Val Asn His Lys 440 445 450			1459

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gtc atg cca ggt aat cgc cca acc acc acc att ttg gcg gag gaa ctt 1507
Val Met Pro Gly Asn Arg Pro Thr Thr Thr Ile Leu Ala Glu Glu Leu
    455                460                465

acc cct tct att ctc ggt gcg ttg atc gct ttg tac gaa cac atc gtg 1555
Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Ile Val
    470                475                480                485

atg gtt cag ggc gtg att tgg gac atc aac tcc ttc gac caa tgg ggt 1603
Met Val Gln Gly Val Ile Trp Asp Ile Asn Ser Phe Asp Gln Trp Gly
                490                495                500

gtt gaa ctg ggc aaa cag cag gca aat gac ctc gct ccg gct gtc tct 1651
Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu Ala Pro Ala Val Ser
                505                510                515

ggt gaa gag gat gtt gac tcg gga gat tct tcc act gat tca ctg att 1699
Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser Thr Asp Ser Leu Ile
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aag tgg tac cgc gca aat agg tagtcgcttg cttatagggt cag 1743
Lys Trp Tyr Arg Ala Asn Arg
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 <213> Corynebacterium glutamicum

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Asn Arg Ala Glu Lys Tyr Thr Phe Ser Ala Ala Gly Leu His Val Asp
    35                40                45

Leu Ser Lys Asn Leu Leu Asp Asp Ala Thr Leu Thr Lys Leu Leu Ala
    50                55                60

Leu Thr Glu Glu Ser Gly Leu Arg Glu Arg Ile Asp Ala Met Phe Ala
    65                70                75                80

Gly Glu His Leu Asn Asn Thr Glu Asp Arg Ala Val Leu His Thr Ala
    85                90                95

Leu Arg Leu Pro Ala Glu Ala Asp Leu Ser Val Asp Gly Gln Asp Val
    100                105                110

Ala Ala Asp Val His Glu Val Leu Gly Arg Met Arg Asp Phe Ala Thr
    115                120                125

Ala Leu Arg Ser Gly Asn Trp Leu Gly His Thr Gly His Thr Ile Lys
    130                135                140

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

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Ala	Thr	Lys	Ala	Leu	Arg	Ala	Tyr	Ala	Thr	Ala	Gly	Ile	Ser	Ala	Glu
				165					170					175	
Phe	Val	Ser	Asn	Val	Asp	Pro	Ala	Asp	Leu	Val	Ser	Val	Leu	Glu	Asp
			180					185					190		
Leu	Asp	Ala	Glu	Ser	Thr	Leu	Phe	Val	Ile	Ala	Ser	Lys	Thr	Phe	Thr
		195					200					205			
Thr	Gln	Glu	Thr	Leu	Ser	Asn	Ala	Arg	Ala	Ala	Arg	Ala	Trp	Leu	Val
	210					215					220				
Glu	Lys	Leu	Gly	Glu	Glu	Ala	Val	Ala	Lys	His	Phe	Val	Ala	Val	Ser
225					230					235					240
Thr	Asn	Ala	Glu	Lys	Val	Ala	Glu	Phe	Gly	Ile	Asp	Thr	Asp	Asn	Met
				245					250					255	
Phe	Gly	Phe	Trp	Asp	Trp	Val	Gly	Gly	Arg	Tyr	Ser	Val	Asp	Ser	Ala
			260					265					270		
Val	Gly	Leu	Ser	Leu	Met	Ala	Val	Ile	Gly	Pro	Arg	Asp	Phe	Met	Arg
		275					280					285			
Phe	Leu	Gly	Gly	Phe	His	Ala	Met	Asp	Glu	His	Phe	Arg	Thr	Thr	Lys
	290					295					300				
Phe	Glu	Glu	Asn	Val	Pro	Ile	Leu	Met	Ala	Leu	Leu	Gly	Val	Trp	Tyr
305					310					315					320
Ser	Asp	Phe	Tyr	Gly	Ala	Glu	Thr	His	Ala	Val	Leu	Pro	Tyr	Ser	Glu
				325					330					335	
Asp	Leu	Ser	Arg	Phe	Ala	Ala	Tyr	Leu	Gln	Gln	Leu	Thr	Met	Glu	Ser
			340					345					350		
Asn	Gly	Lys	Ser	Val	His	Arg	Asp	Gly	Ser	Pro	Val	Ser	Thr	Gly	Thr
		355					360					365			
Gly	Glu	Ile	Tyr	Trp	Gly	Glu	Pro	Gly	Thr	Asn	Gly	Gln	His	Ala	Phe
	370					375					380				
Phe	Gln	Leu	Ile	His	Gln	Gly	Thr	Arg	Leu	Val	Pro	Ala	Asp	Phe	Ile
385					390					395					400
Gly	Phe	Ala	Arg	Pro	Lys	Gln	Asp	Leu	Pro	Ala	Gly	Glu	Arg	Thr	Met
				405				410						415	
His	Asp	Leu	Leu	Met	Ser	Asn	Phe	Phe	Ala	Gln	Thr	Lys	Val	Leu	Ala
			420					425					430		
Phe	Gly	Lys	Asn	Ala	Glu	Glu	Ile	Ala	Ala	Glu	Gly	Val	Ala	Pro	Glu
		435					440					445			
Leu	Val	Asn	His	Lys	Val	Met	Pro	Gly	Asn	Arg	Pro	Thr	Thr	Thr	Ile
	450					455					460				
Leu	Ala	Glu	Glu	Leu	Thr	Pro	Ser	Ile	Leu	Gly	Ala	Leu	Ile	Ala	Leu
465					470					475					480

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Tyr Glu His Ile Val Met Val Gln Gly Val Ile Trp Asp Ile Asn Ser
 485 490 495

Phe Asp Gln Trp Gly Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu
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Ala Pro Ala Val Ser Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser
 515 520 525

Thr Asp Ser Leu Ile Lys Trp Tyr Arg Ala Asn Arg
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 <223> RXA01989

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 Val Lys Ser Ile His Lys Thr Ile His Glu Gly Thr Gly Ala Gly Ser
 1 5 10 15

gac ttc tta ggc tgg gtt gat tta cca gtt gat tac gac aaa gaa gaa 96
 Asp Phe Leu Gly Trp Val Asp Leu Pro Val Asp Tyr Asp Lys Glu Glu
 20 25 30

ttt tca aga att gtt gaa gca tca aaa cgc att aaa gaa aat tct gat 144
 Phe Ser Arg Ile Val Glu Ala Ser Lys Arg Ile Lys Glu Asn Ser Asp
 35 40 45

gtt tta gta gtc atc ggt att ggt ggt tct tac tta ggt gca cgt gca 192
 Val Leu Val Val Ile Gly Ile Gly Gly Ser Tyr Leu Gly Ala Arg Ala
 50 55 60

gca atc gaa atg tta acg tca tca ttt aga aac agc aat gaa tac cct 240
 Ala Ile Glu Met Leu Thr Ser Ser Phe Arg Asn Ser Asn Glu Tyr Pro
 65 70 75 80

gaa att gta ttt gtt ggt aat cac tta tca tca aca tat acg aaa gag 288
 Glu Ile Val Phe Val Gly Asn His Leu Ser Ser Thr Tyr Thr Lys Glu
 85 90 95

tta gtt gat tat tta gca gac aaa gat ttc tct gta aac gtt att tct 336
 Leu Val Asp Tyr Leu Ala Asp Lys Asp Phe Ser Val Asn Val Ile Ser
 100 105 110

aaa tct ggt aca act aca gaa cca gca gtt gca ttt aga ttg ttc aaa 384
 Lys Ser Gly Thr Thr Thr Glu Pro Ala Val Ala Phe Arg Leu Phe Lys
 115 120 125

caa tta gtt gaa gaa aga tac ggt aaa gaa gaa gca caa aaa cgt ata 432
 Gln Leu Val Glu Glu Arg Tyr Gly Lys Glu Glu Ala Gln Lys Arg Ile
 130 135 140

ttt gca aca acg gat aaa gaa aaa ggt gct tta aaa cag ttg gct aca 480

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PCT/IB00/00943

Phe Ala Thr Thr Asp Lys Glu Lys Gly Ala Leu Lys Gln Leu Ala Thr
 145 150 155 160
 aac gaa ggt tat gaa acg ttt atc gta cct gat gat gta ggt gga aga 528
 Asn Glu Gly Tyr Glu Thr Phe Ile Val Pro Asp Asp Val Gly Gly Arg
 165 170 175
 tat tct gtt tta aca gca gta gga tta tta cca att gca aca gct gga 576
 Tyr Ser Val Leu Thr Ala Val Gly Leu Leu Pro Ile Ala Thr Ala Gly
 180 185 190
 att aac atc gaa gct atg atg att ggt gct gca aaa gca cgt gaa gaa 624
 Ile Asn Ile Glu Ala Met Met Ile Gly Ala Ala Lys Ala Arg Glu Glu
 195 200 205
 tta tct 630
 Leu Ser
 210

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 <213> Corynebacterium glutamicum

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 20 25 30
 Phe Ser Arg Ile Val Glu Ala Ser Lys Arg Ile Lys Glu Asn Ser Asp
 35 40 45
 Val Leu Val Val Ile Gly Ile Gly Gly Ser Tyr Leu Gly Ala Arg Ala
 50 55 60
 Ala Ile Glu Met Leu Thr Ser Ser Phe Arg Asn Ser Asn Glu Tyr Pro
 65 70 75 80
 Glu Ile Val Phe Val Gly Asn His Leu Ser Ser Thr Tyr Thr Lys Glu
 85 90 95
 Leu Val Asp Tyr Leu Ala Asp Lys Asp Phe Ser Val Asn Val Ile Ser
 100 105 110
 Lys Ser Gly Thr Thr Thr Glu Pro Ala Val Ala Phe Arg Leu Phe Lys
 115 120 125
 Gln Leu Val Glu Glu Arg Tyr Gly Lys Glu Glu Ala Gln Lys Arg Ile
 130 135 140
 Phe Ala Thr Thr Asp Lys Glu Lys Gly Ala Leu Lys Gln Leu Ala Thr
 145 150 155 160
 Asn Glu Gly Tyr Glu Thr Phe Ile Val Pro Asp Asp Val Gly Gly Arg
 165 170 175
 Tyr Ser Val Leu Thr Ala Val Gly Leu Leu Pro Ile Ala Thr Ala Gly
 180 185 190

Ile Asn Ile Glu Ala Met Met Ile Gly Ala Ala Lys Ala Arg Glu Glu
 195 200 205

Leu Ser
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 Val Lys Leu Val Ile
 1 5

gag gcc gac ggc ggc tcc cgc gga aac ccc ggc gtc gcc ggc tcc ggc 163
 Glu Ala Asp Gly Gly Ser Arg Gly Asn Pro Gly Val Ala Gly Ser Gly
 10 15 20

acc gtg gtg tac tcc gac aac aaa gca gaa gtt ctc aaa gaa atc gcc 211
 Thr Val Val Tyr Ser Asp Asn Lys Ala Glu Val Leu Lys Glu Ile Ala
 25 30 35

tat gtt gtc gga aca aaa gcc acc aac aac gtc gcc gaa tac cgc gga 259
 Tyr Val Val Gly Thr Lys Ala Thr Asn Asn Val Ala Glu Tyr Arg Gly
 40 45 50

cta ctc gaa ggc ctc aaa gca gcc cgc gag ctc ggc gct acc tcc gtg 307
 Leu Leu Glu Gly Leu Lys Ala Ala Arg Glu Leu Gly Ala Thr Ser Val
 55 60 65

gat gtc tac atg gac tcc aaa ctt gtc gtt gaa caa atg tcc ggc cgg 355
 Asp Val Tyr Met Asp Ser Lys Leu Val Val Glu Gln Met Ser Gly Arg
 70 75 80 85

tgg aaa atc aaa cac ccc gac atg aaa gtt cta gcg atc gaa gcc aag 403
 Trp Lys Ile Lys His Pro Asp Met Lys Val Leu Ala Ile Glu Ala Lys
 90 95 100

gag att gct tcc gaa atc ggg tcc gtt tct tat acg tgg att ccg cgt 451
 Glu Ile Ala Ser Glu Ile Gly Ser Val Ser Tyr Thr Trp Ile Pro Arg
 105 110 115

gag aaa aac aaa cga gct gac gca ttg tcc aac gtg gcg atg gat gct 499
 Glu Lys Asn Lys Arg Ala Asp Ala Leu Ser Asn Val Ala Met Asp Ala
 120 125 130

gca gcg gca ggt aag ccg gta ggt gtt gta ggg gat tct gct tct gta 547
 Ala Ala Ala Gly Lys Pro Val Gly Val Val Gly Asp Ser Ala Ser Val
 135 140 145

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PCT/IB00/00943

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Ser Ser Ala Ser Ser Val Ala Gly Ser Glu Lys Glu Asp Leu Asn Cys	
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acc gaa acc aaa ccc acc aac tgg aac ggc gca acc aca gat ccc act	643
Thr Glu Thr Lys Pro Thr Asn Trp Asn Gly Ala Thr Thr Asp Pro Thr	
170 175 180	
cgt ttc ttg ttg ctt cgc cac ggc caa act gct atg tca gtg gca cgc	691
Arg Phe Leu Leu Leu Arg His Gly Gln Thr Ala Met Ser Val Ala Arg	
185 190 195	
ctt tac tcc ggt agg tcc aac cca gag ctg tct gaa ctt ggt gaa aaa	739
Leu Tyr Ser Gly Arg Ser Asn Pro Glu Leu Ser Glu Leu Gly Glu Lys	
200 205 210	
caa gca gca gcg gca gca cga cga ctc gct caa acc ggt ggc atc gac	787
Gln Ala Ala Ala Ala Ala Arg Arg Leu Ala Gln Thr Gly Gly Ile Asp	
215 220 225	
gct att gtg agt tct ccg ctc acc cgc acg atg caa acc gca gaa gca	835
Ala Ile Val Ser Ser Pro Leu Thr Arg Thr Met Gln Thr Ala Glu Ala	
230 235 240 245	
gca gcg gcc gca ctg gga atg aaa gta cgt gtt atc gat gat ctc atc	883
Ala Ala Ala Ala Leu Gly Met Lys Val Arg Val Ile Asp Asp Leu Ile	
250 255 260	
gaa act gac ttt gga ctg tgg gat gga aaa tca ttt tca gaa gcc cac	931
Glu Thr Asp Phe Gly Leu Trp Asp Gly Lys Ser Phe Ser Glu Ala His	
265 270 275	
gaa caa gat cca gaa ctg cac acc aag tgg ctc act gac tca tct gta	979
Glu Gln Asp Pro Glu Leu His Thr Lys Trp Leu Thr Asp Ser Ser Val	
280 285 290	
gcc cca ccc ggt ggt gag tcc ctg cag acg gtt aat cga cgt gtg aaa	1027
Ala Pro Pro Gly Gly Glu Ser Leu Gln Thr Val Asn Arg Arg Val Lys	
295 300 305	
aag gct cgt gaa agc ctc caa cgc gaa tac ggt gca gcg aat gtt ttg	1075
Lys Ala Arg Glu Ser Leu Gln Arg Glu Tyr Gly Ala Ala Asn Val Leu	
310 315 320 325	
gtg gtc agc cac gtc acc cca atc aaa gcc atc atg agg caa gca ttg	1123
Val Val Ser His Val Thr Pro Ile Lys Ala Ile Met Arg Gln Ala Leu	
330 335 340	
gac gca ggc cca tcc ttc ttt cag aag gca cac ctt gac ttg gcg tcg	1171
Asp Ala Gly Pro Ser Phe Phe Gln Lys Ala His Leu Asp Leu Ala Ser	
345 350 355	
ctg tcg atc gca gag ttt tac gaa gac ggc cca acc tgc gta aga ctg	1219
Leu Ser Ile Ala Glu Phe Tyr Glu Asp Gly Pro Thr Cys Val Arg Leu	
360 365 370	
ttc aac gac acc tca cac ctg gaa gcg tgacgacagt ctgacggaag	1266
Phe Asn Asp Thr Ser His Leu Glu Ala	
375 380	
ctc	1269

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 <213> Corynebacterium glutamicum

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 Leu Lys Glu Ile Ala Tyr Val Val Gly Thr Lys Ala Thr Asn Asn Val
 35 40 45
 Ala Glu Tyr Arg Gly Leu Leu Glu Gly Leu Lys Ala Ala Arg Glu Leu
 50 55 60
 Gly Ala Thr Ser Val Asp Val Tyr Met Asp Ser Lys Leu Val Val Glu
 65 70 75 80
 Gln Met Ser Gly Arg Trp Lys Ile Lys His Pro Asp Met Lys Val Leu
 85 90 95
 Ala Ile Glu Ala Lys Glu Ile Ala Ser Glu Ile Gly Ser Val Ser Tyr
 100 105 110
 Thr Trp Ile Pro Arg Glu Lys Asn Lys Arg Ala Asp Ala Leu Ser Asn
 115 120 125
 Val Ala Met Asp Ala Ala Ala Ala Gly Lys Pro Val Gly Val Val Gly
 130 135 140
 Asp Ser Ala Ser Val Ser Ser Ala Ser Ser Val Ala Gly Ser Glu Lys
 145 150 155 160
 Glu Asp Leu Asn Cys Thr Glu Thr Lys Pro Thr Asn Trp Asn Gly Ala
 165 170 175
 Thr Thr Asp Pro Thr Arg Phe Leu Leu Leu Arg His Gly Gln Thr Ala
 180 185 190
 Met Ser Val Ala Arg Leu Tyr Ser Gly Arg Ser Asn Pro Glu Leu Ser
 195 200 205
 Glu Leu Gly Glu Lys Gln Ala Ala Ala Ala Ala Arg Arg Leu Ala Gln
 210 215 220
 Thr Gly Gly Ile Asp Ala Ile Val Ser Ser Pro Leu Thr Arg Thr Met
 225 230 235 240
 Gln Thr Ala Glu Ala Ala Ala Ala Ala Leu Gly Met Lys Val Arg Val
 245 250 255
 Ile Asp Asp Leu Ile Glu Thr Asp Phe Gly Leu Trp Asp Gly Lys Ser
 260 265 270
 Phe Ser Glu Ala His Glu Gln Asp Pro Glu Leu His Thr Lys Trp Leu
 275 280 285

Thr Asp Ser Ser Val Ala Pro Pro Gly Gly Glu Ser Leu Gln Thr Val
 290 295 300
 Asn Arg Arg Val Lys Lys Ala Arg Glu Ser Leu Gln Arg Glu Tyr Gly
 305 310 315 320
 Ala Ala Asn Val Leu Val Val Ser His Val Thr Pro Ile Lys Ala Ile
 325 330 335
 Met Arg Gln Ala Leu Asp Ala Gly Pro Ser Phe Phe Gln Lys Ala His
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 370 375 380

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 <223> RXA02492

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 Met Thr Asn Gly Lys
 1 5
 ttg att ctt ctt cgt cac ggt cag agc gaa tgg aac gca tcc aac cag 163
 Leu Ile Leu Leu Arg His Gly Gln Ser Glu Trp Asn Ala Ser Asn Gln
 10 15 20
 ttc act gga tgg gtc gac gtc aat ctg acc gaa cag ggt gag gct gag 211
 Phe Thr Gly Trp Val Asp Val Asn Leu Thr Glu Gln Gly Glu Ala Glu
 25 30 35
 gcc aaa ggc gtc ctc cca ggc gtt gta tac acc tcc ttg ctg cgt cgc 259
 Ala Lys Gly Val Leu Pro Gly Val Val Tyr Thr Ser Leu Leu Arg Arg
 40 45 50
 gcg atc cgc act gca aac atc gca ctg aac gct gca gac cgc cac tgg 307
 Ala Ile Arg Thr Ala Asn Ile Ala Leu Asn Ala Ala Asp Arg His Trp
 55 60 65
 atc cca gtg atc cgc gac tgg cgc ctc aac gag cgt cac tac ggc gca 355
 Ile Pro Val Ile Arg Asp Trp Arg Leu Asn Glu Arg His Tyr Gly Ala
 70 75 80 85
 ctg cag ggc ctt gac aag gct gca acc aag gaa aaa tac ggc gac gac 403
 Leu Gln Gly Leu Asp Lys Ala Ala Thr Lys Glu Lys Tyr Gly Asp Asp
 90 95 100

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cag ttc atg gaa tgg cgc cgc tcc tac gac acc cca cca cca gag ctc 451
 Gln Phe Met Glu Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Glu Leu
 105 110 115

gcg gat gac gca gag tac tcc cag gca aat gac cct cgt tac gcg gac 499
 Ala Asp Asp Ala Glu Tyr Ser Gln Ala Asn Asp Pro Arg Tyr Ala Asp
 120 125 130

ctc gac gta gtt cca cgc acc gaa tgc ctc aag gac gtt gtg gtt cgt 547
 Leu Asp Val Val Pro Arg Thr Glu Cys Leu Lys Asp Val Val Val Arg
 135 140 145

ttt gtt cct tac ttc gag gaa gaa atc ctg cca cgc gca aag aag ggc 595
 Phe Val Pro Tyr Phe Glu Glu Glu Ile Leu Pro Arg Ala Lys Lys Gly
 150 155 160 165

gaa acc gtc ctc atc gca gca cac ggc aac tcc ctg cgt gcg ctg gtt 643
 Glu Thr Val Leu Ile Ala Ala His Gly Asn Ser Leu Arg Ala Leu Val
 170 175 180

aag cac ctt gac ggc atc tcc gat gct gat atc gca gag ctc aac atc 691
 Lys His Leu Asp Gly Ile Ser Asp Ala Asp Ile Ala Glu Leu Asn Ile
 185 190 195

cca acc ggc atc cca ctg gtc tac gaa atc gcc gaa gac ggt tcc gta 739
 Pro Thr Gly Ile Pro Leu Val Tyr Glu Ile Ala Glu Asp Gly Ser Val
 200 205 210

gta aac cca ggc ggc acc tac ctc gat cct gag gca gca gca gcc ggc 787
 Val Asn Pro Gly Gly Thr Tyr Leu Asp Pro Glu Ala Ala Ala Ala Gly
 215 220 225

gca gca gca gta gca aac cag ggt aat aag tagctatttg taggtgagca 837
 Ala Ala Ala Val Ala Asn Gln Gly Asn Lys
 230 235

ctc 840

<210> 48

<211> 239

<212> PRT

<213> Corynebacterium glutamicum

<400> 48

Met Thr Asn Gly Lys Leu Ile Leu Leu Arg His Gly Gln Ser Glu Trp
 1 5 10 15

Asn Ala Ser Asn Gln Phe Thr Gly Trp Val Asp Val Asn Leu Thr Glu
 20 25 30

Gln Gly Glu Ala Glu Ala Lys Gly Val Leu Pro Gly Val Val Tyr Thr
 35 40 45

Ser Leu Leu Arg Arg Ala Ile Arg Thr Ala Asn Ile Ala Leu Asn Ala
 50 55 60

Ala Asp Arg His Trp Ile Pro Val Ile Arg Asp Trp Arg Leu Asn Glu
 65 70 75 80

Arg His Tyr Gly Ala Leu Gln Gly Leu Asp Lys Ala Ala Thr Lys Glu

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85								90				95			
Lys	Tyr	Gly	Asp	Asp	Gln	Phe	Met	Glu	Trp	Arg	Arg	Ser	Tyr	Asp	Thr
			100					105					110		
Pro	Pro	Pro	Glu	Leu	Ala	Asp	Asp	Ala	Glu	Tyr	Ser	Gln	Ala	Asn	Asp
		115					120					125			
Pro	Arg	Tyr	Ala	Asp	Leu	Asp	Val	Val	Pro	Arg	Thr	Glu	Cys	Leu	Lys
	130					135					140				
Asp	Val	Val	Val	Arg	Phe	Val	Pro	Tyr	Phe	Glu	Glu	Glu	Ile	Leu	Pro
145					150					155					160
Arg	Ala	Lys	Lys	Gly	Glu	Thr	Val	Leu	Ile	Ala	Ala	His	Gly	Asn	Ser
				165					170					175	
Leu	Arg	Ala	Leu	Val	Lys	His	Leu	Asp	Gly	Ile	Ser	Asp	Ala	Asp	Ile
			180					185					190		
Ala	Glu	Leu	Asn	Ile	Pro	Thr	Gly	Ile	Pro	Leu	Val	Tyr	Glu	Ile	Ala
		195					200					205			
Glu	Asp	Gly	Ser	Val	Val	Asn	Pro	Gly	Gly	Thr	Tyr	Leu	Asp	Pro	Glu
	210					215					220				
Ala	Ala	Ala	Ala	Gly	Ala	Ala	Ala	Val	Ala	Asn	Gln	Gly	Asn	Lys	
225					230					235					

<210> 49

<211> 729

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> RXA00381

<400> 49

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tcaagcccgc	cgcacgtgca	gcagcagaag	cgaaggcatc	atg	acg	caa	acc	att		115
				Met	Thr	Gln	Thr	Ile		
				1				5		

gtc	cat	cta	gtt	cgc	cac	ggc	gaa	gtc	cac	aac	cca	gag	aaa	atc	ctg	163
Val	His	Leu	Val	Arg	His	Gly	Glu	Val	His	Asn	Pro	Glu	Lys	Ile	Leu	
			10					15						20		

tac	gga	cgc	atg	ccc	gga	tac	agg	ttg	tct	tcc	cgt	gga	cgc	agc	caa	211
Tyr	Gly	Arg	Met	Pro	Gly	Tyr	Arg	Leu	Ser	Ser	Arg	Gly	Arg	Ser	Gln	
			25					30					35			

gcc	gcc	cgc	act	gca	gct	tct	ttt	gaa	ggc	cac	gat	gtc	acc	tac	att	259
Ala	Ala	Arg	Thr	Ala	Ala	Ser	Phe	Glu	Gly	His	Asp	Val	Thr	Tyr	Ile	
		40					45					50				

gcg	gcc	tcc	cca	ttg	cag	cgt	gtg	cag	gaa	acc	tcc	gaa	ccg	ttc	atc	307
Ala	Ala	Ser	Pro	Leu	Gln	Arg	Val	Gln	Glu	Thr	Ser	Glu	Pro	Phe	Ile	

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55	60	65	
aag gtc aca ggc cta gaa ctg atc acc gac gag gat ctt ctg gaa gca			355
Lys Val Thr Gly Leu Glu Leu Ile Thr Asp Glu Asp Leu Leu Glu Ala			
70	75	80	85
ggc aac cgt ttc gaa ggc ctg cgc acc aaa ggt tgg cgt tcc cag ttg			403
Gly Asn Arg Phe Glu Gly Leu Arg Thr Lys Gly Trp Arg Ser Gln Leu			
	90	95	100
tgg aac ccc gtg cgt tgg cct ttg atg tac aac ccc acg ctt ccc agc			451
Trp Asn Pro Val Arg Trp Pro Leu Met Tyr Asn Pro Thr Leu Pro Ser			
	105	110	115
tgg ggc gaa cac tac acc gac att ttg gaa aga atg atg gcg gct gtg			499
Trp Gly Glu His Tyr Thr Asp Ile Leu Glu Arg Met Met Ala Ala Val			
	120	125	130
gaa cga gct cgg gtg gca gcg gaa gga cac gaa gca atc ctg gtg acc			547
Glu Arg Ala Arg Val Ala Ala Glu Gly His Glu Ala Ile Leu Val Thr			
	135	140	145
cac cag ttg ccg atc gtg tgc gtg caa cgc cac gcc cgc gga caa agc			595
His Gln Leu Pro Ile Val Cys Val Gln Arg His Ala Arg Gly Gln Ser			
	150	155	160
ctg tcc cat aac cca gcg acc agg caa tgc gac ctc gcc tca gtg aca			643
Leu Ser His Asn Pro Ala Thr Arg Gln Cys Asp Leu Ala Ser Val Thr			
	170	175	180
tcc ttg gtg ttc caa gac gat caa att gtc ggc gtg cat tac aac gaa			691
Ser Leu Val Phe Gln Asp Asp Gln Ile Val Gly Val His Tyr Asn Glu			
	185	190	195
cca gct cag gag att tgatcactcg tgcgtttgac caa			729
Pro Ala Gln Glu Ile			
	200		

<210> 50

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 50

Met Thr Gln Thr Ile Val His Leu Val Arg His Gly Glu Val His Asn
1 5 10 15

Pro Glu Lys Ile Leu Tyr Gly Arg Met Pro Gly Tyr Arg Leu Ser Ser
20 25 30

Arg Gly Arg Ser Gln Ala Ala Arg Thr Ala Ala Ser Phe Glu Gly His
35 40 45

Asp Val Thr Tyr Ile Ala Ala Ser Pro Leu Gln Arg Val Gln Glu Thr
50 55 60

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

Asp Leu Leu Glu Ala Gly Asn Arg Phe Glu Gly Leu Arg Thr Lys Gly

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				85						90					95				
Trp	Arg	Ser	Gln	Leu	Trp	Asn	Pro	Val	Arg	Trp	Pro	Leu	Met	Tyr	Asn				
			100					105					110						
Pro	Thr	Leu	Pro	Ser	Trp	Gly	Glu	His	Tyr	Thr	Asp	Ile	Leu	Glu	Arg				
		115					120					125							
Met	Met	Ala	Ala	Val	Glu	Arg	Ala	Arg	Val	Ala	Ala	Glu	Gly	His	Glu				
		130				135					140								
Ala	Ile	Leu	Val	Thr	His	Gln	Leu	Pro	Ile	Val	Cys	Val	Gln	Arg	His				
145					150					155					160				
Ala	Arg	Gly	Gln	Ser	Leu	Ser	His	Asn	Pro	Ala	Thr	Arg	Gln	Cys	Asp				
				165					170					175					
Leu	Ala	Ser	Val	Thr	Ser	Leu	Val	Phe	Gln	Asp	Asp	Gln	Ile	Val	Gly				
			180					185					190						
Val	His	Tyr	Asn	Glu	Pro	Ala	Gln	Glu	Ile										
		195					200												

<210> 51

<211> 822

<212> DNA

<213> Corynebacterium glutamicum .

<220>

<221> CDS

<222> (101)..(799)

<223> RXA02122

<400> 51

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ccttttttta	agtgggcggt	caggaatttt	tcgcacaggt	atg	ctg	cat	gtc	atg		115
				Met	Leu	His	Val	Met		
				1				5		

aag	ccg	ggt	tca	cac	gca	gct	gcc	gaa	aag	act	caa	tcc	act	gtg	ggt		163
Lys	Pro	Gly	Ser	His	Ala	Ala	Ala	Glu	Lys	Thr	Gln	Ser	Thr	Val	Val		
			10					15						20			

tta	ctc	att	cgg	cat	ggg	caa	acc	cca	aca	act	ggt	cag	ggt	ctg	cct		211
Leu	Leu	Ile	Arg	His	Gly	Gln	Thr	Pro	Thr	Thr	Gly	Gln	Val	Leu	Pro		
			25				30						35				

ggt	cag	acg	ccg	ggt	tta	cac	ctg	tct	gat	aag	ggt	gaa	gag	cag	gcg		259
Gly	Gln	Thr	Pro	Gly	Leu	His	Leu	Ser	Asp	Lys	Gly	Glu	Glu	Gln	Ala		
		40					45					50					

cgg	gag	gtg	gca	cag	cgt	ctg	gcg	gag	gtg	ccg	att	acc	gct	gtg	tat		307
Arg	Glu	Val	Ala	Gln	Arg	Leu	Ala	Glu	Val	Pro	Ile	Thr	Ala	Val	Tyr		
		55				60					65						

tca	tcg	ccg	atg	gag	cgt	gcg	cag	gaa	aca	gca	gca	ccg	acg	gtc	agc		355
Ser	Ser	Pro	Met	Glu	Arg	Ala	Gln	Glu	Thr	Ala	Ala	Pro	Thr	Val	Ser		
70					75				80						85		

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gct cat ggc ctc gag ttg acg gtg gaa cct ggg ctt att gaa tgc gat 403
 Ala His Gly Leu Glu Leu Thr Val Glu Pro Gly Leu Ile Glu Cys Asp
 90 95 100

ttc ggc gag tgg acg ggc cgg aaa cta act gag ctc aat gcc cta gag 451
 Phe Gly Glu Trp Thr Gly Arg Lys Leu Thr Glu Leu Asn Ala Leu Glu
 105 110 115

gag tgg aaa gcg gtg cag aag aca ccg tct acc ttc agg ttt cca ggt 499
 Glu Trp Lys Ala Val Gln Lys Thr Pro Ser Thr Phe Arg Phe Pro Gly
 120 125 130

ggt gag agt ttc gtg gaa atg cag gat cgg atg gtg gag gct atc ggc 547
 Gly Glu Ser Phe Val Glu Met Gln Asp Arg Met Val Glu Ala Ile Gly
 135 140 145

aac att gcg cag cag cat ccg gga gaa atc gtt gct gcg ttt agt cat 595
 Asn Ile Ala Gln Gln His Pro Gly Glu Ile Val Ala Ala Phe Ser His
 150 155 160 165

gcc gac acg atc aag gct gcg gtg gct cat ttt gta ggc act cca ctg 643
 Ala Asp Thr Ile Lys Ala Ala Val Ala His Phe Val Gly Thr Pro Leu
 170 175 180

gat tct ttt cag cgc att ttc atc gac acg gcg tca att tcc gca gtg 691
 Asp Ser Phe Gln Arg Ile Phe Ile Asp Thr Ala Ser Ile Ser Ala Val
 185 190 195

gaa ttt acc ggg aaa tct tca ggc gtc tcc tcc cat atg ctg ctg aca 739
 Glu Phe Thr Gly Lys Ser Ser Gly Val Ser Ser His Met Leu Leu Thr
 200 205 210

aat tcc aga aca gga tcg ttg gga tac ctt cga gac aaa ctt ccg aaa 787
 Asn Ser Arg Thr Gly Ser Leu Gly Tyr Leu Arg Asp Lys Leu Pro Lys
 215 220 225

gct ccg caa cca tgatcacctc accatttgag cgc 822
 Ala Pro Gln Pro
 230

<210> 52
 <211> 233
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 52
 Met Leu His Val Met Lys Pro Gly Ser His Ala Ala Ala Glu Lys Thr
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Gln Ser Thr Val Val Leu Leu Ile Arg His Gly Gln Thr Pro Thr Thr
 20 25 30

Gly Gln Val Leu Pro Gly Gln Thr Pro Gly Leu His Leu Ser Asp Lys
 35 40 45

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

Ile Thr Ala Val Tyr Ser Ser Pro Met Glu Arg Ala Gln Glu Thr Ala
 65 70 75 80

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cag ctg tat gac gat gaa gat att gac cga atc ctc ctt cga ggc ggc	307
Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile Leu Leu Arg Gly Gly	
55 60 65	
acc att ttg ggc act ggt cgc ctc cat ccg gac aag ttt aag gcc gga	355
Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp Lys Phe Lys Ala Gly	
70 75 80 85	
att gat cag att aag gcc aac tta gaa gac gcc ggc atc gat gcc ctt	403
Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala Gly Ile Asp Ala Leu	
90 95 100	
atc cca atc ggt ggc gaa gga acc ctg aag ggt gcc aag tgg ctg tct	451
Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp Leu Ser	
105 110 115	
gat aac ggt atc cct gtt gtc ggt gtc cca aag acc att gac aat gac	499
Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys Thr Ile Asp Asn Asp	
120 125 130	
gtg aat ggc act gac ttc acc ttc ggt ttc gat act gct gtg gca gtg	547
Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp Thr Ala Val Ala Val	
135 140 145	
gct acc gac gct gtt gac cgc ctg cac acc acc gct gaa tct cac aac	595
Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr Ala Glu Ser His Asn	
150 155 160 165	
cgt gtg atg atc gtg gag gtc atg ggc cgc cac gtg ggt tgg att gct	643
Arg Val Met Ile Val Glu Val Met Gly Arg His Val Gly Trp Ile Ala	
170 175 180	
ctg cac gca ggt atg gcc ggc ggt gct cac tac acc gtt att cca gaa	691
Leu His Ala Gly Met Ala Gly Gly Ala His Tyr Thr Val Ile Pro Glu	
185 190 195	
gta cct ttc gat att gca gag atc tgc aag gcg atg gaa cgt cgc ttc	739
Val Pro Phe Asp Ile Ala Glu Ile Cys Lys Ala Met Glu Arg Arg Phe	
200 205 210	
cag atg ggc gag aag tac ggc att atc gtc gtt gcg gaa ggt gcg ttg	787
Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val Ala Glu Gly Ala Leu	
215 220 225	
cca cgc gaa ggc acc atg gag ctt cgt gaa ggc cac att gac cag ttc	835
Pro Arg Glu Gly Thr Met Glu Leu Arg Glu Gly His Ile Asp Gln Phe	
230 235 240 245	
ggt cac aag acc ttc acg gga att gga cag cag atc gct gat gag atc	883
Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln Ile Ala Asp Glu Ile	
250 255 260	
cac gtg cgc ctc ggc cac gat gtt cgt acg acc gtt ctt ggc cac att	931
His Val Arg Leu Gly His Asp Val Arg Thr Thr Val Leu Gly His Ile	
265 270 275	
caa cgt ggt gga acc cca act gct ttc gac cgt gtt ctg gcc act cgt	979
Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg Val Leu Ala Thr Arg	
280 285 290	
tat ggt gtt cgt gca gct cgt gcg tgc cat gag gga agc ttt gac aag	1027

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Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu Gly Ser Phe Asp Lys
 295 300 305
 gtt gtt gct ttg aag ggt gag agc att gag atg atc acc ttt gaa gaa 1075
 Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met Ile Thr Phe Glu Glu 325
 310 315 320
 gca gtc gga acc ttg aag gaa gtt cca ttc gaa cgc tgg gtt act gcc 1123
 Ala Val Gly Thr Leu Lys Glu Val Pro Phe Glu Arg Trp Val Thr Ala 340
 330 335
 cag gca atg ttt gga tagtttttcg ggctttttatc aac 1161
 Gln Ala Met Phe Gly 345

<210> 54
 <211> 346
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 54
 Met Glu Asp Met Arg Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro
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 Gly Leu Asn Ala Val Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu
 20 25 30
 Phe Gly Ser Thr Val Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu
 35 40 45
 Gly Asp Arg Arg Val Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile
 50 55 60
 Leu Leu Arg Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp
 65 70 75 80
 Lys Phe Lys Ala Gly Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala
 85 90 95
 Gly Ile Asp Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly
 100 105 110
 Ala Lys Trp Leu Ser Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys
 115 120 125
 Thr Ile Asp Asn Asp Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp
 130 135 140
 Thr Ala Val Ala Val Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr
 145 150 155 160
 Ala Glu Ser His Asn Arg Val Met Ile Val Glu Val Met Gly Arg His
 165 170 175
 Val Gly Trp Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr
 180 185 190
 Thr Val Ile Pro Glu Val Pro Phe Asp Ile Ala Glu Ile Cys Lys Ala
 195 200 205

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Met Glu Arg Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val
 210 215 220

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

His Ile Asp Gln Phe Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln
 245 250 255

Ile Ala Asp Glu Ile His Val Arg Leu Gly His Asp Val Arg Thr Thr
 260 265 270

Val Leu Gly His Ile Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg
 275 280 285

Val Leu Ala Thr Arg Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu
 290 295 300

Gly Ser Phe Asp Lys Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met
 305 310 315 320

Ile Thr Phe Glu Glu Ala Val Gly Thr Leu Lys Glu Val Pro Phe Glu
 325 330 335

Arg Trp Val Thr Ala Gln Ala Met Phe Gly
 340 345

<210> 55
 <211> 1083
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1060)
 <223> RXA01243

<400> 55
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agcagttgcg agaacgcgat gtagaagttg tgattgcaga atg att ctt aca gtc 115
 Met Ile Leu Thr Val
 1 5

act gca agt ccg tat ctg ttg agc acc aat gag ctt gac ggc acc atc 163
 Thr Ala Ser Pro Tyr Leu Leu Ser Thr Asn Glu Leu Asp Gly Thr Ile
 10 15 20

gaa att ggc gaa gca aac aaa atc cgg cag gtt tcc act gtt gcc ggt 211
 Glu Ile Gly Glu Ala Asn Lys Ile Arg Gln Val Ser Thr Val Ala Gly
 25 30 35

ggg ttt ggc acc ggt gtg gct gcc acc ttg ttt tat ggc ggc aat gaa 259
 Gly Phe Gly Thr Gly Val Ala Ala Thr Leu Phe Tyr Gly Gly Asn Glu
 40 45 50

act ttt gca gtt ttt ccc gct cca gaa atc tct cat tac atg cgc ctg 307
 Thr Phe Ala Val Phe Pro Ala Pro Glu Ile Ser His Tyr Met Arg Leu
 55 60 65

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gtg	acg	ttt	gct	ggg	ttg	cct	cat	gaa	att	att	ccg	gtg	gca	ggt	ccc	355
Val	Thr	Phe	Ala	Gly	Leu	Pro	His	Glu	Ile	Ile	Pro	Val	Ala	Gly	Pro	
70					75					80					85	
atc	ccc	atg	cat	ttg	acc	atg	cgt	gat	gca	gag	ggc	aat	gag	act	aag	403
Ile	Pro	Met	His	Leu	Thr	Met	Arg	Asp	Ala	Glu	Gly	Asn	Glu	Thr	Lys	
				90					95					100		
ttc	aaa	gac	tcc	ccc	atg	cct	ttg	gat	gtg	tcc	cag	ttg	gca	att	ctt	451
Phe	Lys	Asp	Ser	Pro	Met	Pro	Leu	Asp	Val	Ser	Gln	Leu	Ala	Ile	Leu	
			105					110					115			
cgt	gat	cta	gtg	gtg	cgt	cga	gcc	gaa	gat	gcc	gcg	tgg	gtg	ttg	ttg	499
Arg	Asp	Leu	Val	Val	Arg	Arg	Ala	Glu	Asp	Ala	Ala	Trp	Val	Leu	Leu	
		120					125					130				
ggt	ggc	aat	ttg	ccg	tct	atc	gcg	cct	gct	gcg	tgg	ttt	gtg	gat	gtg	547
Gly	Gly	Asn	Leu	Pro	Ser	Ile	Ala	Pro	Ala	Ala	Trp	Phe	Val	Asp	Val	
	135					140					145					
gtg	aga	tca	ctt	cgc	ttg	tac	cac	cct	cat	gtg	aag	gta	gct	atc	gca	595
Val	Arg	Ser	Leu	Arg	Leu	Tyr	His	Pro	His	Val	Lys	Val	Ala	Ile	Ala	
150					155					160					165	
gca	act	ggt	gct	gcg	ttg	cgt	gcg	gtt	att	cga	cag	ctt	gca	gct	acg	643
Ala	Thr	Gly	Ala	Ala	Leu	Arg	Ala	Val	Ile	Arg	Gln	Leu	Ala	Ala	Thr	
				170					175						180	
tcc	ccg	gat	gcg	ctg	att	gtg	gct	gcg	gaa	gaa	atc	gaa	att	gcc	act	691
Ser	Pro	Asp	Ala	Leu	Ile	Val	Ala	Ala	Glu	Glu	Ile	Glu	Ile	Ala	Thr	
			185					190					195			
gga	tta	gaa	ccc	aaa	acc	ttg	aga	ggt	cca	tgg	gta	gag	gga	gat	ctc	739
Gly	Leu	Glu	Pro	Lys	Thr	Leu	Arg	Gly	Pro	Trp	Val	Glu	Gly	Asp	Leu	
		200					205					210				
tcc	ccg	act	gtg	gcg	gca	gcg	cgc	gct	tta	att	gat	agc	ggt	gtc	acc	787
Ser	Pro	Thr	Val	Ala	Ala	Ala	Arg	Ala	Leu	Ile	Asp	Ser	Gly	Val	Thr	
	215					220					225					
gag	gtg	ttg	gtt	acc	aac	aag	cgg	acg	gaa	tct	ttg	tat	gtt	tcc	gag	835
Glu	Val	Leu	Val	Thr	Asn	Lys	Arg	Thr	Glu	Ser	Leu	Tyr	Val	Ser	Glu	
230					235					240					245	
tct	gaa	tca	ctg	tta	gcc	agc	tac	gac	agc	acc	cct	ggt	aag	cag	ggc	883
Ser	Glu	Ser	Leu	Leu	Ala	Ser	Tyr	Asp	Ser	Thr	Pro	Gly	Lys	Gln	Gly	
				250				255						260		
gtg	aat	tgg	cgg	gaa	tct	ttt	act	gca	gga	ttc	ttg	gca	gca	tcc	aat	931
Val	Asn	Trp	Arg	Glu	Ser	Phe	Thr	Ala	Gly	Phe	Leu	Ala	Ala	Ser	Asn	
			265					270					275			
gat	gga	aaa	tcc	act	gag	gac	agc	gtg	atc	aac	gcg	gtt	gct	tac	gcc	979
Asp	Gly	Lys	Ser	Thr	Glu	Asp	Ser	Val	Ile	Asn	Ala	Val	Ala	Tyr	Ala	
		280					285					290				
aac	gct	gaa	ggc	agt	gag	tgg	gac	aac	tac	att	ccc	aca	ccc	gat	aag	1027
Asn	Ala	Glu	Gly	Ser	Glu	Trp	Asp	Asn	Tyr	Ile	Pro	Thr	Pro	Asp	Lys	
	295					300					305					
ctt	cgg	gcg	gag	cac	gtg	gtc	atc	aaa	tcg	ctt	tagaccacgc	aaaaagcctc				1080

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Leu Arg Ala Glu His Val Val Ile Lys Ser Leu
 310 315 320

aaa

1083

<210> 56

<211> 320

<212> PRT

<213> Corynebacterium glutamicum

<400> 56

Met Ile Leu Thr Val Thr Ala Ser Pro Tyr Leu Leu Ser Thr Asn Glu
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Leu Asp Gly Thr Ile Glu Ile Gly Glu Ala Asn Lys Ile Arg Gln Val
 20 25 30

Ser Thr Val Ala Gly Gly Phe Gly Thr Gly Val Ala Ala Thr Leu Phe
 35 40 45

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

His Tyr Met Arg Leu Val Thr Phe Ala Gly Leu Pro His Glu Ile Ile
 65 70 75 80

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

Gly Asn Glu Thr Lys Phe Lys Asp Ser Pro Met Pro Leu Asp Val Ser
 100 105 110

Gln Leu Ala Ile Leu Arg Asp Leu Val Val Arg Arg Ala Glu Asp Ala
 115 120 125

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

Trp Phe Val Asp Val Val Arg Ser Leu Arg Leu Tyr His Pro His Val
 145 150 155 160

Lys Val Ala Ile Ala Ala Thr Gly Ala Ala Leu Arg Ala Val Ile Arg
 165 170 175

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

Ile Glu Ile Ala Thr Gly Leu Glu Pro Lys Thr Leu Arg Gly Pro Trp
 195 200 205

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

Asp Ser Gly Val Thr Glu Val Leu Val Thr Asn Lys Arg Thr Glu Ser
 225 230 235 240

Leu Tyr Val Ser Glu Ser Glu Ser Leu Leu Ala Ser Tyr Asp Ser Thr
 245 250 255

Pro Gly Lys Gln Gly Val Asn Trp Arg Glu Ser Phe Thr Ala Gly Phe

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260	265	270
Leu Ala Ala Ser Asn Asp Gly Lys Ser Thr Glu Asp Ser Val Ile Asn		
275	280	285
Ala Val Ala Tyr Ala Asn Ala Glu Gly Ser Glu Trp Asp Asn Tyr Ile		
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Pro Thr Pro Asp Lys Leu Arg Ala Glu His Val Val Ile Lys Ser Leu		
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 Met Ile Ile Thr Phe
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 Thr Pro Asn Pro Ser Ile Asp Ser Thr Leu Ser Leu Gly Glu Glu Leu
 10 15 20
 tcc cgt gga tcc gtc caa cga ctt gat tcc gtc acc gct gtc gca ggt 211
 Ser Arg Gly Ser Val Gln Arg Leu Asp Ser Val Thr Ala Val Ala Gly
 25 30 35
 ggt aaa ggc atc aat gtc gcc cac gct gtc ttg ctt gcg ggc ttt gaa 259
 Gly Lys Gly Ile Asn Val Ala His Ala Val Leu Leu Ala Gly Phe Glu
 40 45 50
 acc ttg gct gtg ttc cca gcc ggc aag ctc gac ccc ttc gtc cca ctg 307
 Thr Leu Ala Val Phe Pro Ala Gly Lys Leu Asp Pro Phe Val Pro Leu
 55 60 65
 gtc cgc gac atc ggc ttg ccc gtg gaa act gtt gtg atc aac aag aac 355
 Val Arg Asp Ile Gly Leu Pro Val Glu Thr Val Val Ile Asn Lys Asn
 70 75 80 85
 gtc cgc acc aac acc aca gtc acc gaa ccg gac ggc acc acc acc aag 403
 Val Arg Thr Asn Thr Thr Val Thr Glu Pro Asp Gly Thr Thr Thr Lys
 90 95 100
 ctc aac ggc ccc ggc gcg ccg ctc agc gag cag aag ctc cgt agc ttg 451
 Leu Asn Gly Pro Gly Ala Pro Leu Ser Glu Gln Lys Leu Arg Ser Leu
 105 110 115
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Leu	Ala	Gly	Ser	Leu	Pro	Pro	Gly	Ala	Pro	Val	Asp	Trp	Tyr	Ala	Arg		
		135					140				145						
ctc	acc	gcg	ttg	atc	cat	tca	gca	cgc	cct	gac	gtt	cgc	gtg	gct	gtc	595	
Leu	Thr	Ala	Leu	Ile	His	Ser	Ala	Arg	Pro	Asp	Val	Arg	Val	Ala	Val		
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gat	acc	tca	gac	aag	cca	ctg	atg	gcg	ttg	ggc	gag	agc	ttg	gat	aca	643	
Asp	Thr	Ser	Asp	Lys	Pro	Leu	Met	Ala	Leu	Gly	Glu	Ser	Leu	Asp	Thr		
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cct	ggc	gct	gct	ccg	aac	ctg	att	aag	cca	aat	ggc	ctg	gaa	ctg	ggc	691	
Pro	Gly	Ala	Ala	Pro	Asn	Leu	Ile	Lys	Pro	Asn	Gly	Leu	Glu	Leu	Gly		
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Gln	Leu	Ala	Asn	Thr	Asp	Gly	Glu	Glu	Leu	Glu	Ala	Arg	Ala	Ala	Gln		
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Gly	Asp	Tyr	Asp	Ala	Ile	Ile	Ala	Ala	Ala	Asp	Val	Leu	Val	Asn	Arg		
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Gly	Ile	Glu	Gln	Val	Leu	Val	Thr	Leu	Gly	Ala	Ala	Gly	Ala	Val	Leu		
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gtc	aac	gca	gaa	ggc	gcg	tgg	act	gct	act	tct	cca	aag	att	gat	gtt	883	
Val	Asn	Ala	Glu	Gly	Ala	Trp	Thr	Ala	Thr	Ser	Pro	Lys	Ile	Asp	Val		
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Val	Ser	Thr	Val	Gly	Ala	Gly	Asp	Cys	Ala	Leu	Ala	Gly	Phe	Val	Met		
			265					270					275				
gca	cgt	tcc	cag	aag	aaa	aca	ctg	gag	gaa	tct	ctg	ctg	aat	gcc	gtg	979	
Ala	Arg	Ser	Gln	Lys	Lys	Thr	Leu	Glu	Glu	Ser	Leu	Leu	Asn	Ala	Val		
		280					285					290					
tct	tac	ggc	tcg	act	gcg	gcg	tct	ctt	cct	ggc	act	acc	att	cct	cgt	1027	
Ser	Tyr	Gly	Ser	Thr	Ala	Ala	Ser	Leu	Pro	Gly	Thr	Thr	Ile	Pro	Arg		
		295				300					305						
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Pro	Asp	Gln	Leu	Ala	Thr	Ala	Gly	Ala	Thr	Val	Thr	Gln	Val	Lys	Gly		
					315					320					325		
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Leu	Lys	Glu	Ser	Ala													
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<212> PRT

<213> Corynebacterium glutamicum

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<210> 59
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 Met Pro Ile Ala Thr
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 ccc gag gtc tat aac gag atg ctc gat cgt gct aag gaa ggc gga ttc 163
 Pro Glu Val Tyr Asn Glu Met Leu Asp Arg Ala Lys Glu Gly Gly Phe
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 gcc ttc cca gcc atc aac tgc acc tcc tcg gaa acc atc aac gca gct 211
 Ala Phe Pro Ala Ile Asn Cys Thr Ser Ser Glu Thr Ile Asn Ala Ala
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 ctc aag ggc ttc gca gag gct gaa tct gac gga atc atc cag ttc tcc 259
 Leu Lys Gly Phe Ala Glu Ala Glu Ser Asp Gly Ile Ile Gln Phe Ser
 40 45 50
 acc ggt ggt gca gag ttc ggt tcc ggc ctg gca gta aag aac aag gtc 307
 Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ala Val Lys Asn Lys Val
 55 60 65
 aag ggc gca gtt gcg ctt gca gcc ttc gcc cac gag gca gca aag agc 355
 Lys Gly Ala Val Ala Leu Ala Ala Phe Ala His Glu Ala Ala Lys Ser
 70 75 80 85
 tac ggc atc aac gtt gct ctg cac act gac cac tgc cag aag gaa gtc 403
 Tyr Gly Ile Asn Val Ala Leu His Thr Asp His Cys Gln Lys Glu Val
 90 95 100
 ctg gac gag tac gtc cgc cca ctg ctg gct atc tcc cag gag cgc gtc 451
 Leu Asp Glu Tyr Val Arg Pro Leu Leu Ala Ile Ser Gln Glu Arg Val
 105 110 115
 gac cgc ggc gag ctt cca ctg ttc cag tcc cac atg tgg gat ggt tcc 499
 Asp Arg Gly Glu Leu Pro Leu Phe Gln Ser His Met Trp Asp Gly Ser
 120 125 130
 gct gtc cca atc gac gag aac ctc gaa atc gca cag gag ctg ctg gct 547
 Ala Val Pro Ile Asp Glu Asn Leu Glu Ile Ala Gln Glu Leu Leu Ala
 135 140 145
 aag gcc aag gca gcg aac atc atc ttg gaa gtt gag atc ggt gtt gtc 595
 Lys Ala Lys Ala Ala Asn Ile Ile Leu Glu Val Glu Ile Gly Val Val
 150 155 160 165

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ggt ggc gaa gaa gac ggc gtt gag gct aag gct ggc gca aac ctc tac 643
 Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala Gly Ala Asn Leu Tyr
 170 175 180

acc tcc cca gaa gac ttt gag aag acc atc gat gca atc ggc acc ggt 691
 Thr Ser Pro Glu Asp Phe Glu Lys Thr Ile Asp Ala Ile Gly Thr Gly
 185 190 195

gag aag ggc cgc tac ctg cta gca gct acc ttc ggt aac gtc cac ggc 739
 Glu Lys Gly Arg Tyr Leu Leu Ala Ala Thr Phe Gly Asn Val His Gly
 200 205 210

gtt tac aag cca ggc aac gtc aag ctg cgc cca gag gtc ctc ctt gag 787
 Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro Glu Val Leu Leu Glu
 215 220 225

ggc cag cag gtt gca cgc aag aag ctt gga ctt gca gac gac gca ctt 835
 Gly Gln Gln Val Ala Arg Lys Lys Leu Gly Leu Ala Asp Asp Ala Leu
 230 235 240 245

cca ttc gac ttc gtc ttc cac ggt ggc tca ggc tcc gag aag gaa aag 883
 Pro Phe Asp Phe Val Phe His Gly Gly Ser Gly Ser Glu Lys Glu Lys
 250 255 260

atc gaa gag gcg ctg acc tac ggc gtc atc aag atg aac gtt gat act 931
 Ile Glu Glu Ala Leu Thr Tyr Gly Val Ile Lys Met Asn Val Asp Thr
 265 270 275

gac acc cag tac gca ttc acc cgc cca atc gtc tcc cac atg ttt gag 979
 Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val Ser His Met Phe Glu
 280 285 290

aac tac aac ggc gtt ctc aag atc gac ggc gag gtc gga aac aag aag 1027
 Asn Tyr Asn Gly Val Leu Lys Ile Asp Gly Glu Val Gly Asn Lys Lys
 295 300 305

gct tac gac cca cgc tct tac atg aag aag gct gag cag agc atg tct 1075
 Ala Tyr Asp Pro Arg Ser Tyr Met Lys Lys Ala Glu Gln Ser Met Ser
 310 315 320 325

gag cgc att atc gag tct tgc cag gac ctc aag tct gtt gga aag acc 1123
 Glu Arg Ile Ile Glu Ser Cys Gln Asp Leu Lys Ser Val Gly Lys Thr
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<212> PRT

<213> Corynebacterium glutamicum

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 20 25 30

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PCT/IB00/00943

Thr Ile Asn Ala Ala Leu Lys Gly Phe Ala Glu Ala Glu Ser Asp Gly
 35 40 45
 Ile Ile Gln Phe Ser Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ala
 50 55 60
 Val Lys Asn Lys Val Lys Gly Ala Val Ala Leu Ala Ala Phe Ala His
 65 70 75 80
 Glu Ala Ala Lys Ser Tyr Gly Ile Asn Val Ala Leu His Thr Asp His
 85 90 95
 Cys Gln Lys Glu Val Leu Asp Glu Tyr Val Arg Pro Leu Leu Ala Ile
 100 105 110
 Ser Gln Glu Arg Val Asp Arg Gly Glu Leu Pro Leu Phe Gln Ser His
 115 120 125
 Met Trp Asp Gly Ser Ala Val Pro Ile Asp Glu Asn Leu Glu Ile Ala
 130 135 140
 Gln Glu Leu Leu Ala Lys Ala Lys Ala Ala Asn Ile Ile Leu Glu Val
 145 150 155 160
 Glu Ile Gly Val Val Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala
 165 170 175
 Gly Ala Asn Leu Tyr Thr Ser Pro Glu Asp Phe Glu Lys Thr Ile Asp
 180 185 190
 Ala Ile Gly Thr Gly Glu Lys Gly Arg Tyr Leu Leu Ala Ala Thr Phe
 195 200 205
 Gly Asn Val His Gly Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro
 210 215 220
 Glu Val Leu Leu Glu Gly Gln Gln Val Ala Arg Lys Lys Leu Gly Leu
 225 230 235 240
 Ala Asp Asp Ala Leu Pro Phe Asp Phe Val Phe His Gly Gly Ser Gly
 245 250 255
 Ser Glu Lys Glu Lys Ile Glu Glu Ala Leu Thr Tyr Gly Val Ile Lys
 260 265 270
 Met Asn Val Asp Thr Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val
 275 280 285
 Ser His Met Phe Glu Asn Tyr Asn Gly Val Leu Lys Ile Asp Gly Glu
 290 295 300
 Val Gly Asn Lys Lys Ala Tyr Asp Pro Arg Ser Tyr Met Lys Lys Ala
 305 310 315 320
 Glu Gln Ser Met Ser Glu Arg Ile Ile Glu Ser Cys Gln Asp Leu Lys
 325 330 335
 Ser Val Gly Lys Thr Thr Ser Lys
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ctt atc gct ggt aac tgg aag atg aac ctg gat cac cag cag gca atc																163
Leu Ile Ala Gly Asn Trp Lys Met Asn Leu Asp His Gln Gln Ala Ile																
ggc act gtt cag aag ctt gca ttc gcc ctt cca aag gaa tac ttc gag																211
Gly Thr Val Gln Lys Leu Ala Phe Ala Leu Pro Lys Glu Tyr Phe Glu																
aag gtt gac gtt gca gtc acc gtt cct ttc act gac atc cgc tcc gtc																259
Lys Val Asp Val Ala Val Thr Val Pro Phe Thr Asp Ile Arg Ser Val																
cag act ctc gtt gag ggc gac aag ctt gag gtc act ttc ggt gct cag																307
Gln Thr Leu Val Glu Gly Asp Lys Leu Glu Val Thr Phe Gly Ala Gln																
gac gtc tcc cag cac gag tcc ggt gcg tac acc ggt gaa gtt tct gca																355
Asp Val Ser Gln His Glu Ser Gly Ala Tyr Thr Gly Glu Val Ser Ala																
agc atg ctg gca aag ttg aac tgc tct tgg gtt gtc gtt gga cac tcc																403
Ser Met Leu Ala Lys Leu Asn Cys Ser Trp Val Val Val Gly His Ser																
gag cgc cgc gag tac cac aac gag tct gat gag ttg gtt gct gcg aag																451
Glu Arg Arg Glu Tyr His Asn Glu Ser Asp Glu Leu Val Ala Ala Lys																
gca aag gca gct ctg tcc aac ggc atc agc ccg atc gtc tgc gtt ggt																499
Ala Lys Ala Ala Leu Ser Asn Gly Ile Ser Pro Ile Val Cys Val Gly																
gag cca ctg gaa atc cgt gaa gct ggc acc cac gtt gag tac gtc gtc																547
Glu Pro Leu Glu Ile Arg Glu Ala Gly Thr His Val Glu Tyr Val Val																
gag cag acc cgt aag tcc ctt gct ggc ctg gat gct gct gag ctg gcc																595
Glu Gln Thr Arg Lys Ser Leu Ala Gly Leu Asp Ala Ala Glu Leu Ala																
aac acc gtt atc gcg tat gag cca gtg tgg gct atc ggc acc ggt aag																643
Asn Thr Val Ile Ala Tyr Glu Pro Val Trp Ala Ile Gly Thr Gly Lys																

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gtt gct tcc gca gct gac gct cag gaa gtg tgc aag gct atc cgc ggt 691
 Val Ala Ser Ala Ala Asp Ala Gln Glu Val Cys Lys Ala Ile Arg Gly
 185 190 195

ctg atc gtg gag ctt gca ggc gac gag gtc gct gag ggc ctg cgt att 739
 Leu Ile Val Glu Leu Ala Gly Asp Glu Val Ala Glu Gly Leu Arg Ile
 200 205 210

ctt tac ggt ggt tct gtt aag gca gaa acc gtc gct gag atc gtc ggt 787
 Leu Tyr Gly Gly Ser Val Lys Ala Glu Thr Val Ala Glu Ile Val Gly
 215 220 225

cag cct gac gtc gac ggc gga ctt gtc ggt ggc gct tcc ctc gac ggt 835
 Gln Pro Asp Val Asp Gly Gly Leu Val Gly Gly Ala Ser Leu Asp Gly
 230 235 240 245

gaa gca ttc gcc aag ctg gct gcc aac gct gcg agc gtt gct 877
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 250 255

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Lys Glu Tyr Phe Glu Lys Val Asp Val Ala Val Thr Val Pro Phe Thr
 35 40 45

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

Thr Phe Gly Ala Gln Asp Val Ser Gln His Glu Ser Gly Ala Tyr Thr
 65 70 75 80

Gly Glu Val Ser Ala Ser Met Leu Ala Lys Leu Asn Cys Ser Trp Val
 85 90 95

Val Val Gly His Ser Glu Arg Arg Glu Tyr His Asn Glu Ser Asp Glu
 100 105 110

Leu Val Ala Ala Lys Ala Lys Ala Ala Leu Ser Asn Gly Ile Ser Pro
 115 120 125

Ile Val Cys Val Gly Glu Pro Leu Glu Ile Arg Glu Ala Gly Thr His
 130 135 140

Val Glu Tyr Val Val Glu Gln Thr Arg Lys Ser Leu Ala Gly Leu Asp
 145 150 155 160

Ala Ala Glu Leu Ala Asn Thr Val Ile Ala Tyr Glu Pro Val Trp Ala
 165 170 175

Ile Gly Thr Gly Lys Val Ala Ser Ala Ala Asp Ala Gln Glu Val Cys
 180 185 190

Lys Ala Ile Arg Gly Leu Ile Val Glu Leu Ala Gly Asp Glu Val Ala
 195 200 205

Glu Gly Leu Arg Ile Leu Tyr Gly Gly Ser Val Lys Ala Glu Thr Val
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 Met Thr His Asn His
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aag gac tgg aac gat cgc att gca gtt gcg gag gaa atg gtg ccg ttg 163
 Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu Glu Met Val Pro Leu
 10 15 20

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 Ile Gly Arg Leu His Arg Asn Asn Asn Val Val Val Ser Val Phe Gly
 25 30 35

cgt ctc ctt gtg aat gtc tca gac atc gat atc atc aag tct cac cgc 259
 Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile Ile Lys Ser His Arg
 40 45 50

tac gcc cgc cac atc ata tcc aag gaa ctt cca ctg gaa agc tcc ttg 307
 Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro Leu Glu Ser Ser Leu
 55 60 65

gat att ttg cgc gaa ctg gta gat atg aac ctt ggt acc gca tcg atc 355
 Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu Gly Thr Ala Ser Ile
 70 75 80 85

gac ctg gga cag ctg gcc tac agc ttc gaa gaa tcc gaa agc acc gac 403
 Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu Ser Glu Ser Thr Asp
 90 95 100

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acc	gac	atc	aac	cca	act	gat	atc	gtg	ctg	tac	ggt	ttc	ggc	cgc	atc	499
Thr	Asp	Ile	Asn	Pro	Thr	Asp	Ile	Val	Leu	Tyr	Gly	Phe	Gly	Arg	Ile	
		120					125					130				
ggt	cgc	ctg	ctg	gcc	cgc	atc	ctg	gtt	tcc	cgc	gag	gca	ctg	tat	gac	547
Gly	Arg	Leu	Leu	Ala	Arg	Ile	Leu	Val	Ser	Arg	Glu	Ala	Leu	Tyr	Asp	
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ggt	gct	cgt	ctg	cgc	gcc	atc	gtg	gtc	cgc	aaa	aat	ggt	gaa	gaa	gac	595
Gly	Ala	Arg	Leu	Arg	Ala	Ile	Val	Val	Arg	Lys	Asn	Gly	Glu	Glu	Asp	
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ctg	gtc	aag	cgc	gca	tcc	ttg	ctg	cgt	cgt	gat	tct	gtc	cac	ggt	gga	643
Leu	Val	Lys	Arg	Ala	Ser	Leu	Leu	Arg	Arg	Asp	Ser	Val	His	Gly	Gly	
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Phe	Asp	Gly	Thr	Ile	Thr	Thr	Asp	Tyr	Asp	Asn	Asn	Ile	Ile	Trp	Ala	
			185					190					195			
aac	ggc	acc	cca	atc	aag	gtc	atc	tac	tcc	aat	gac	cca	gcc	acc	att	739
Asn	Gly	Thr	Pro	Ile	Lys	Val	Ile	Tyr	Ser	Asn	Asp	Pro	Ala	Thr	Ile	
		200					205					210				
gat	tac	acc	gaa	tac	ggc	atc	aat	gac	gcc	gtc	gtg	gta	gac	aac	acc	787
Asp	Tyr	Thr	Glu	Tyr	Gly	Ile	Asn	Asp	Ala	Val	Val	Val	Asp	Asn	Thr	
	215					220					225					
ggc	cgc	tgg	cgt	gac	cgc	gaa	ggc	ctg	tcc	cag	cac	ctc	aag	tcc	aag	835
Gly	Arg	Trp	Arg	Asp	Arg	Glu	Gly	Leu	Ser	Gln	His	Leu	Lys	Ser	Lys	
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ggc	gtt	gcc	aag	gtt	gta	ctc	acc	gcg	ccg	ggc	aag	ggc	gat	ctg	aag	883
Gly	Val	Ala	Lys	Val	Val	Leu	Thr	Ala	Pro	Gly	Lys	Gly	Asp	Leu	Lys	
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aac	atc	gtg	tac	ggc	atc	aac	cac	acc	gac	atc	acc	gca	gat	gat	cag	931
Asn	Ile	Val	Tyr	Gly	Ile	Asn	His	Thr	Asp	Ile	Thr	Ala	Asp	Asp	Gln	
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atc	gtt	tcc	gca	gca	tca	tgc	acc	acc	aat	gcc	att	acc	cca	gtg	ctc	979
Ile	Val	Ser	Ala	Ala	Ser	Cys	Thr	Thr	Asn	Ala	Ile	Thr	Pro	Val	Leu	
		280					285					290				
aag	gtg	atc	aat	gat	cgc	tac	ggc	gtg	gaa	ttc	ggc	cac	gta	gaa	acc	1027
Lys	Val	Ile	Asn	Asp	Arg	Tyr	Gly	Val	Glu	Phe	Gly	His	Val	Glu	Thr	
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gtt	cac	tcc	ttc	acc	aat	gac	cag	aac	ctg	atc	gac	aac	ttc	cac	aag	1075
Val	His	Ser	Phe	Thr	Asn	Asp	Gln	Asn	Leu	Ile	Asp	Asn	Phe	His	Lys	
310					315					320					325	
ggt	tct	cgc	cgt	ggt	cgc	gca	gca	ggt	ctg	aat	atg	gtt	ctc	acc	gaa	1123
Gly	Ser	Arg	Arg	Gly	Arg	Ala	Ala	Gly	Leu	Asn	Met	Val	Leu	Thr	Glu	
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acc	ggc	gct	gca	aag	gct	gta	tcc	aag	gcg	ctt	cca	gag	ctg	gaa	ggc	1171

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PCT/IB00/00943

Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu Pro Glu Leu Glu Gly
 345 350 355
 aag ctc acc ggc aat gcc atc cgc gtt cct acc cct gac gtg tcc atg 1219
 Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr Pro Asp Val Ser Met
 360 365 370
 gct gtg ctc aac ttg acc ctg aac acg gag gtg gac cgc gat gag gtc 1267
 Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val Asp Arg Asp Glu Val
 375 380 385
 aac gag ttc ctc cgc cgt gtg tcc ctg cac tct gac ttg cgc cag caa 1315
 Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser Asp Leu Arg Gln Gln
 390 395 400 405
 atc gac tgg atc cgt tcc cca gag gtt gtt tcc act gac ttc gtg ggc 1363
 Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser Thr Asp Phe Val Gly
 410 415 420
 acc acc cac gcg ggc atc gtt gat ggt cta gcc acc atc gca acc ggt 1411
 Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala Thr Ile Ala Thr Gly
 425 430 435
 cgc cac ctg gtg ctt tac gtg tgg tac gac aac gag ttc ggc tac tcc 1459
 Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn Glu Phe Gly Tyr Ser
 440 445 450
 aac cag gtc att cgc atc gtc gag gag atc gcc ggc gtg cgt cct cgc 1507
 Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala Gly Val Arg Pro Arg
 455 460 465
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 cac 1563

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 <213> Corynebacterium glutamicum

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

Ser	Glu	Ser	Thr	Asp	Leu	Arg	Ala	Phe	Leu	Glu	Asp	Ala	Leu	Ala	Pro			
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Glu	Ala	Leu	Tyr	Asp	Gly	Ala	Arg	Leu	Arg	Ala	Ile	Val	Val	Arg	Lys			
145					150					155					160			
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Ser	Val	His	Gly	Gly	Phe	Asp	Gly	Thr	Ile	Thr	Thr	Asp	Tyr	Asp	Asn			
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Asn	Ile	Ile	Trp	Ala	Asn	Gly	Thr	Pro	Ile	Lys	Val	Ile	Tyr	Ser	Asn			
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	210					215					220							
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225					230					235					240			
His	Leu	Lys	Ser	Lys	Gly	Val	Ala	Lys	Val	Val	Leu	Thr	Ala	Pro	Gly			
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Lys	Gly	Asp	Leu	Lys	Asn	Ile	Val	Tyr	Gly	Ile	Asn	His	Thr	Asp	Ile			
			260					265					270					
Thr	Ala	Asp	Asp	Gln	Ile	Val	Ser	Ala	Ala	Ser	Cys	Thr	Thr	Asn	Ala			
		275					280					285						
Ile	Thr	Pro	Val	Leu	Lys	Val	Ile	Asn	Asp	Arg	Tyr	Gly	Val	Glu	Phe			
	290					295					300							
Gly	His	Val	Glu	Thr	Val	His	Ser	Phe	Thr	Asn	Asp	Gln	Asn	Leu	Ile			
305					310					315					320			
Asp	Asn	Phe	His	Lys	Gly	Ser	Arg	Arg	Gly	Arg	Ala	Ala	Gly	Leu	Asn			
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Pro	Glu	Leu	Glu	Gly	Lys	Leu	Thr	Gly	Asn	Ala	Ile	Arg	Val	Pro	Thr			
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Pro	Asp	Val	Ser	Met	Ala	Val	Leu	Asn	Leu	Thr	Leu	Asn	Thr	Glu	Val			
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Asp	Arg	Asp	Glu	Val	Asn	Glu	Phe	Leu	Arg	Arg	Val	Ser	Leu	His	Ser			
385					390					395					400			
Asp	Leu	Arg	Gln	Gln	Ile	Asp	Trp	Ile	Arg	Ser	Pro	Glu	Val	Val	Ser			
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Thr Asp Phe Val Gly Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala
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Thr Ile Ala Thr Gly Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn
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Glu Phe Gly Tyr Ser Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala
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Gly Val Arg Pro Arg Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
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 Met Thr His Asn His
 1 5

aag gac tgg aac gat cgc att gca gtt gcg gag gaa atg gtg ccg ttg 163
 Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu Glu Met Val Pro Leu
 10 15 20

atc ggg cgc ctg cac cgc aac aac aac gtg gtg gtt tcc gta ttc ggt 211
 Ile Gly Arg Leu His Arg Asn Asn Asn Val Val Val Ser Val Phe Gly
 25 30 35

cgt ctc ctt gtg aat gtc tca gac atc gat atc atc aag tct cac cgc 259
 Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile Ile Lys Ser His Arg
 40 45 50

tac gcc cgc cac atc ata tcc aag gaa ctt cca ctg gaa agc tcc ttg 307
 Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro Leu Glu Ser Ser Leu
 55 60 65

gat att ttg cgc gaa ctg gta gat atg aac ctt ggt acc gca tcg atc 355
 Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu Gly Thr Ala Ser Ile
 70 75 80 85

gac ctg gga cag ctg gcc tac agc ttc gaa gaa tcc gaa agc acc gac 403
 Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu Ser Glu Ser Thr Asp
 90 95 100

ctg cgt gcc ttc ctg gag gac gct ctc gcg ccg gtc att ggt gcg gaa 451
 Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro Val Ile Gly Ala Glu
 105 110 115

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acc gac atc aac cca act gat atc gtg ctg tac ggt ttc ggc cgc atc	499
Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr Gly Phe Gly Arg Ile	
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Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg Glu Ala Leu Tyr Asp	
135 140 145	
ggt gct cgt ctg cgc gcc atc gtg gtc cgc aaa aat ggt gaa gaa gac	595
Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys Asn Gly Glu Glu Asp	
150 155 160 165	
ctg gtc aag cgc gca tcc ttg ctg cgt cgt gat tct gtc cac ggt gga	643
Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp Ser Val His Gly Gly	
170 175 180	
ttc gat ggc acc atc acc acc gat tat gac aac aac atc atc tgg gcc	691
Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn Asn Ile Ile Trp Ala	
185 190 195	
aac ggc acc cca atc aag gtc atc tac tcc aat gac cca gcc acc att	739
Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn Asp Pro Ala Thr Ile	
200 205 210	
gat tac acc gaa tac ggc atc aat gac gcc gtc gtg gta gac aac acc	787
Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val Val Val Asp Asn Thr	
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Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln His Leu Lys Ser Lys	
230 235 240 245	
ggc gtt gcc aag gtt gta ctc acc gcg ccg ggc aag ggc gat ctg aag	883
Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly Lys Gly Asp Leu Lys	
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aac atc gtg tac ggc atc aac cac acc gac atc acc gca gat gat cag	931
Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile Thr Ala Asp Asp Gln	
265 270 275	
atc gtt tcc gca gca tca tgc acc acc aat gcc att acc cca gtg ctc	979
Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala Ile Thr Pro Val Leu	
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aag gtg atc aat gat cgc tac ggc gtg gaa ttc ggc cac gta gaa acc	1027
Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe Gly His Val Glu Thr	
295 300 305	
gtt cac tcc ttc acc aat gac cag aac ctg atc gac aac ttc cac aag	1075
Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile Asp Asn Phe His Lys	
310 315 320 325	
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Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn Met Val Leu Thr Glu	
330 335 340	
acc ggc gct gca aag gct gta tcc aag gcg ctt cca gag ctg gaa ggc	1171
Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu Pro Glu Leu Glu Gly	
345 350 355	
aag ctc acc ggc aat gcc atc cgc gtt cct acc cct gac gtg tcc atg	1219

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Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr Pro Asp Val Ser Met
 360 365 370
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 Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val Asp Arg Asp Glu Val
 375 380 385
 aac gag ttc ctc cgc cgt gtg tcc ctg cac tct gac ttg cgc cag caa 1315
 Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser Asp Leu Arg Gln Gln
 390 395 400 405
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 Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser Thr Asp Phe Val Gly
 410 415 420
 acc acc cac gcg ggc atc gtt gat ggt cta gcc acc atc gca acc ggt 1411
 Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala Thr Ile Ala Thr Gly
 425 430 435
 cgc cac ctg gtg ctt tac gtg tgg tac gac aac gag ttc ggc tac tcc 1459
 Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn Glu Phe Gly Tyr Ser
 440 445 450
 aac cag gtc att cgc atc gtc gag gag atc gcc ggc gtg cgt cct cgc 1507
 Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala Gly Val Arg Pro Arg
 455 460 465
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 Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
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 cac 1563

<210> 66

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<212> PRT

<213> Corynebacterium glutamicum

<400> 66

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 35 40 45
 Ile Lys Ser His Arg Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro
 50 55 60
 Leu Glu Ser Ser Leu Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu
 65 70 75 80
 Gly Thr Ala Ser Ile Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu
 85 90 95
 Ser Glu Ser Thr Asp Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro
 100 105 110

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Asn	Gly	Glu	Glu	Asp	Leu	Val	Lys	Arg	Ala	Ser	Leu	Leu	Arg	Arg	Asp
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Ser	Val	His	Gly	Gly	Phe	Asp	Gly	Thr	Ile	Thr	Thr	Asp	Tyr	Asp	Asn
			180					185					190		
Asn	Ile	Ile	Trp	Ala	Asn	Gly	Thr	Pro	Ile	Lys	Val	Ile	Tyr	Ser	Asn
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Asp	Pro	Ala	Thr	Ile	Asp	Tyr	Thr	Glu	Tyr	Gly	Ile	Asn	Asp	Ala	Val
	210					215					220				
Val	Val	Asp	Asn	Thr	Gly	Arg	Trp	Arg	Asp	Arg	Glu	Gly	Leu	Ser	Gln
225					230					235					240
His	Leu	Lys	Ser	Lys	Gly	Val	Ala	Lys	Val	Val	Leu	Thr	Ala	Pro	Gly
				245					250					255	
Lys	Gly	Asp	Leu	Lys	Asn	Ile	Val	Tyr	Gly	Ile	Asn	His	Thr	Asp	Ile
			260					265					270		
Thr	Ala	Asp	Asp	Gln	Ile	Val	Ser	Ala	Ala	Ser	Cys	Thr	Thr	Asn	Ala
		275					280					285			
Ile	Thr	Pro	Val	Leu	Lys	Val	Ile	Asn	Asp	Arg	Tyr	Gly	Val	Glu	Phe
	290					295					300				
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305					310					315					320
Asp	Asn	Phe	His	Lys	Gly	Ser	Arg	Arg	Gly	Arg	Ala	Ala	Gly	Leu	Asn
				325					330					335	
Met	Val	Leu	Thr	Glu	Thr	Gly	Ala	Ala	Lys	Ala	Val	Ser	Lys	Ala	Leu
			340					345					350		
Pro	Glu	Leu	Glu	Gly	Lys	Leu	Thr	Gly	Asn	Ala	Ile	Arg	Val	Pro	Thr
		355					360					365			
Pro	Asp	Val	Ser	Met	Ala	Val	Leu	Asn	Leu	Thr	Leu	Asn	Thr	Glu	Val
	370					375					380				
Asp	Arg	Asp	Glu	Val	Asn	Glu	Phe	Leu	Arg	Arg	Val	Ser	Leu	His	Ser
385					390					395					400
Asp	Leu	Arg	Gln	Gln	Ile	Asp	Trp	Ile	Arg	Ser	Pro	Glu	Val	Val	Ser
			405					410						415	
Thr	Asp	Phe	Val	Gly	Thr	Thr	His	Ala	Gly	Ile	Val	Asp	Gly	Leu	Ala
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						Met	Thr	Ile	Arg	Val							
						1				5							
ggt	att	aac	gga	ttt	ggc	cgt	atc	gga	cgt	aac	ttc	ttc	cgc	gca	gtt	163	
Gly	Ile	Asn	Gly	Phe	Gly	Arg	Ile	Gly	Arg	Asn	Phe	Phe	Arg	Ala	Val		
				10					15					20			
ctg	gag	cgc	agc	gac	gat	ctc	gag	gta	gtt	gca	gtc	aac	gac	ctc	acc	211	
Leu	Glu	Arg	Ser	Asp	Asp	Leu	Glu	Val	Val	Ala	Val	Asn	Asp	Leu	Thr		
				25					30					35			
gac	aac	aag	acc	ctt	tcc	acc	ctt	ctc	aag	ttc	gac	tcc	atc	atg	ggc	259	
Asp	Asn	Lys	Thr	Leu	Ser	Thr	Leu	Leu	Lys	Phe	Asp	Ser	Ile	Met	Gly		
			40					45					50				
cgc	ctt	ggc	cag	gaa	gtt	gaa	tac	gac	gat	gac	tcc	atc	acc	gtt	ggt	307	
Arg	Leu	Gly	Gln	Glu	Val	Glu	Tyr	Asp	Asp	Asp	Ser	Ile	Thr	Val	Gly		
		55					60					65					
ggc	aag	cgc	atc	gct	gtt	tac	gca	gag	cgc	gat	cca	aag	aac	ctg	gac	355	
Gly	Lys	Arg	Ile	Ala	Val	Tyr	Ala	Glu	Arg	Asp	Pro	Lys	Asn	Leu	Asp		
70					75					80					85		
tgg	gct	gca	cac	aac	gtt	gac	atc	gtg	atc	gag	tcc	acc	ggc	ttc	ttc	403	
Trp	Ala	Ala	His	Asn	Val	Asp	Ile	Val	Ile	Glu	Ser	Thr	Gly	Phe	Phe		
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acc	gat	gca	aac	gcg	gct	aag	gct	cac	atc	gaa	gca	ggt	gcc	aag	aag	451	
Thr	Asp	Ala	Asn	Ala	Ala	Lys	Ala	His	Ile	Glu	Ala	Gly	Ala	Lys	Lys		
			105					110					115				
gtc	atc	atc	tcc	gca	cca	gca	agc	aac	gaa	gac	gca	acc	ttc	gtt	tac	499	
Val	Ile	Ile	Ser	Ala	Pro	Ala	Ser	Asn	Glu	Asp	Ala	Thr	Phe	Val	Tyr		
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Gly	Val	Asn	His	Glu	Ser	Tyr	Asp	Pro	Glu	Asn	His	Asn	Val	Ile	Ser	
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ggc	gca	tct	tgc	acc	acc	aac	tgc	ctc	gca	cca	atg	gca	aag	gtc	cta	595
Gly	Ala	Ser	Cys	Thr	Thr	Asn	Cys	Leu	Ala	Pro	Met	Ala	Lys	Val	Leu	
150					155					160					165	
aac	gac	aag	ttc	ggc	atc	gag	aac	ggc	ctc	atg	acc	acc	gtt	cac	gca	643
Asn	Asp	Lys	Phe	Gly	Ile	Glu	Asn	Gly	Leu	Met	Thr	Thr	Val	His	Ala	
				170					175					180		
tac	act	ggc	gac	cag	cgc	ctg	cac	gat	gca	cct	cac	cgc	gac	ctg	cgt	691
Tyr	Thr	Gly	Asp	Gln	Arg	Leu	His	Asp	Ala	Pro	His	Arg	Asp	Leu	Arg	
			185					190					195			
cgt	gca	cgt	gca	gca	gca	gtc	aac	atc	gtt	cct	acc	tcc	acc	ggt	gca	739
Arg	Ala	Arg	Ala	Ala	Ala	Val	Asn	Ile	Val	Pro	Thr	Ser	Thr	Gly	Ala	
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gct	aag	gct	gtt	gct	ctg	gtt	ctc	cca	gag	ctc	aag	ggc	aag	ctt	gac	787
Ala	Lys	Ala	Val	Ala	Leu	Val	Leu	Pro	Glu	Leu	Lys	Gly	Lys	Leu	Asp	
	215					220					225					
ggc	tac	gca	ctt	cgc	gtt	cca	gtt	atc	acc	ggt	tcc	gca	acc	gac	ctg	835
Gly	Tyr	Ala	Leu	Arg	Val	Pro	Val	Ile	Thr	Gly	Ser	Ala	Thr	Asp	Leu	
230					235					240					245	
acc	ttc	aac	acc	aag	tct	gag	gtc	acc	gtt	gag	tcc	atc	aac	gct	gca	883
Thr	Phe	Asn	Thr	Lys	Ser	Glu	Val	Thr	Val	Glu	Ser	Ile	Asn	Ala	Ala	
				250					255					260		
atc	aag	gaa	gct	gca	gtc	ggc	gag	ttc	ggc	gag	acc	ctg	gct	tac	tcc	931
Ile	Lys	Glu	Ala	Ala	Val	Gly	Glu	Phe	Gly	Glu	Thr	Leu	Ala	Tyr	Ser	
			265					270					275			
gaa	gag	cca	ctg	gtt	tcc	acc	gac	atc	gtc	cac	gat	tcc	cac	ggc	tcc	979
Glu	Glu	Pro	Leu	Val	Ser	Thr	Asp	Ile	Val	His	Asp	Ser	His	Gly	Ser	
		280					285					290				
atc	ttc	gac	gct	ggc	ctg	acc	aag	gtc	tcc	ggc	aac	acc	gtc	aag	gtt	1027
Ile	Phe	Asp	Ala	Gly	Leu	Thr	Lys	Val	Ser	Gly	Asn	Thr	Val	Lys	Val	
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Val	Ser	Trp	Tyr	Asp	Asn	Glu	Trp	Gly	Tyr	Thr	Cys	Gln	Leu	Leu	Arg	
310					315					320					325	
ctg	acc	gag	ctc	gta	gct	tcc	aag	ctc	taattagttc	acatcgctaa						1122
Leu	Thr	Glu	Leu	Val	Ala	Ser	Lys	Leu								
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cgt

1125

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<211> 334

<212> PRT

<213> Corynebacterium glutamicum

<400> 68

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Val	Asn	Asp	Leu	Thr	Asp	Asn	Lys	Thr	Leu	Ser	Thr	Leu	Leu	Lys	Phe	35	40	45	
Asp	Ser	Ile	Met	Gly	Arg	Leu	Gly	Gln	Glu	Val	Glu	Tyr	Asp	Asp	Asp	50	55	60	
Ser	Ile	Thr	Val	Gly	Gly	Lys	Arg	Ile	Ala	Val	Tyr	Ala	Glu	Arg	Asp	65	70	75	80
Pro	Lys	Asn	Leu	Asp	Trp	Ala	Ala	His	Asn	Val	Asp	Ile	Val	Ile	Glu	85	90	95	
Ser	Thr	Gly	Phe	Phe	Thr	Asp	Ala	Asn	Ala	Ala	Lys	Ala	His	Ile	Glu	100	105	110	
Ala	Gly	Ala	Lys	Lys	Val	Ile	Ile	Ser	Ala	Pro	Ala	Ser	Asn	Glu	Asp	115	120	125	
Ala	Thr	Phe	Val	Tyr	Gly	Val	Asn	His	Glu	Ser	Tyr	Asp	Pro	Glu	Asn	130	135	140	
His	Asn	Val	Ile	Ser	Gly	Ala	Ser	Cys	Thr	Thr	Asn	Cys	Leu	Ala	Pro	145	150	155	160
Met	Ala	Lys	Val	Leu	Asn	Asp	Lys	Phe	Gly	Ile	Glu	Asn	Gly	Leu	Met	165	170	175	
Thr	Thr	Val	His	Ala	Tyr	Thr	Gly	Asp	Gln	Arg	Leu	His	Asp	Ala	Pro	180	185	190	
His	Arg	Asp	Leu	Arg	Arg	Ala	Arg	Ala	Ala	Ala	Val	Asn	Ile	Val	Pro	195	200	205	
Thr	Ser	Thr	Gly	Ala	Ala	Lys	Ala	Val	Ala	Leu	Val	Leu	Pro	Glu	Leu	210	215	220	
Lys	Gly	Lys	Leu	Asp	Gly	Tyr	Ala	Leu	Arg	Val	Pro	Val	Ile	Thr	Gly	225	230	235	240
Ser	Ala	Thr	Asp	Leu	Thr	Phe	Asn	Thr	Lys	Ser	Glu	Val	Thr	Val	Glu	245	250	255	
Ser	Ile	Asn	Ala	Ala	Ile	Lys	Glu	Ala	Ala	Val	Gly	Glu	Phe	Gly	Glu	260	265	270	
Thr	Leu	Ala	Tyr	Ser	Glu	Glu	Pro	Leu	Val	Ser	Thr	Asp	Ile	Val	His	275	280	285	
Asp	Ser	His	Gly	Ser	Ile	Phe	Asp	Ala	Gly	Leu	Thr	Lys	Val	Ser	Gly	290	295	300	
Asn	Thr	Val	Lys	Val	Val	Ser	Trp	Tyr	Asp	Asn	Glu	Trp	Gly	Tyr	Thr	305	310	315	320
Cys	Gln	Leu	Leu	Arg	Leu	Thr	Glu	Leu	Val	Ala	Ser	Lys	Leu						

325

330

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 <211> 1338
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1315)
 <223> RXA02257

<400> 69

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gaagaatttt ttaaacaatc aaatctccaa ggagtacggc atg gct gtt aag acc 115
 Met Ala Val Lys Thr
 1 5

ctc aag gac ttg ctc gac gaa ggc gta gac gga cgc cac gtc atc gtt 163
 Leu Lys Asp Leu Leu Asp Glu Gly Val Asp Gly Arg His Val Ile Val
 10 15 20

cga tct gac ttc aat gtt ccc ctc aac gat gac cgc gag atc acc gat 211
 Arg Ser Asp Phe Asn Val Pro Leu Asn Asp Asp Arg Glu Ile Thr Asp
 25 30 35

aag ggc cga atc att gcc tcc cta cca acc ctt aaa gca ctg agc gaa 259
 Lys Gly Arg Ile Ile Ala Ser Leu Pro Thr Leu Lys Ala Leu Ser Glu
 40 45 50

ggt ggc gca aag gtc atc gtc atg gct cac ctt ggc cgc cca aag ggc 307
 Gly Gly Ala Lys Val Ile Val Met Ala His Leu Gly Arg Pro Lys Gly
 55 60 65

gag gtc aac gag aag tac tcc ctc gca cct gtc gct gag gca ctc tcc 355
 Glu Val Asn Glu Lys Tyr Ser Leu Ala Pro Val Ala Glu Ala Leu Ser
 70 75 80 85

gat gag ctt ggc cag tac gtt gca ctt gcc gca gac gtt gtt ggc gaa 403
 Asp Glu Leu Gly Gln Tyr Val Ala Leu Ala Ala Asp Val Val Gly Glu
 90 95 100

gac gca cac gag cgc gca aac ggc ctg acc gag ggc gac atc ctg ctc 451
 Asp Ala His Glu Arg Ala Asn Gly Leu Thr Glu Gly Asp Ile Leu Leu
 105 110 115

ctg gag aac gtg cgc ttc gac cca cgc gaa acc tcc aag gac gag gca 499
 Leu Glu Asn Val Arg Phe Asp Pro Arg Glu Thr Ser Lys Asp Glu Ala
 120 125 130

gag cgc acc gct ttc gct cag gag ctc gca gct ctt gca gca gac aac 547
 Glu Arg Thr Ala Phe Ala Gln Glu Leu Ala Ala Leu Ala Ala Asp Asn
 135 140 145

ggc gca ttc gtt tct gac ggc ttc ggt gtt gtc cac cgc gca cag acc 595
 Gly Ala Phe Val Ser Asp Gly Phe Gly Val Val His Arg Ala Gln Thr
 150 155 160 165

tcc gtc tac gac att gca aag ttg ctg cca cac tac gct ggc gga ctg 643

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Ser	Val	Tyr	Asp	Ile	Ala	Lys	Leu	Leu	Pro	His	Tyr	Ala	Gly	Gly	Leu	
				170					175					180		
gta	gag	acc	gag	att	tcc	gtt	ctg	gaa	aag	atc	gca	gaa	tca	cca	gag	691
Val	Glu	Thr	Glu	Ile	Ser	Val	Leu	Glu	Lys	Ile	Ala	Glu	Ser	Pro	Glu	
			185					190					195			
gca	cca	tac	gta	gtg	gtt	ctc	ggt	gga	tcc	aag	gtc	tct	gac	aag	atc	739
Ala	Pro	Tyr	Val	Val	Val	Leu	Gly	Gly	Ser	Lys	Val	Ser	Asp	Lys	Ile	
		200					205					210				
ggt	gtt	att	gag	gcg	ctg	gct	gcc	aag	gct	gac	aag	atc	atc	gtc	ggt	787
Gly	Val	Ile	Glu	Ala	Leu	Ala	Ala	Lys	Ala	Asp	Lys	Ile	Ile	Val	Gly	
	215					220				225						
ggc	ggc	atg	tgc	tac	acc	ttc	ctc	gca	gct	cag	gga	cac	aac	gtt	cag	835
Gly	Gly	Met	Cys	Tyr	Thr	Phe	Leu	Ala	Ala	Gln	Gly	His	Asn	Val	Gln	
230					235					240					245	
cag	tcc	ctc	ctg	cag	gaa	gaa	atg	aag	gct	acc	tgc	acc	gac	ctg	ctc	883
Gln	Ser	Leu	Leu	Gln	Glu	Glu	Met	Lys	Ala	Thr	Cys	Thr	Asp	Leu	Leu	
				250					255					260		
gca	cgc	ttc	ggt	gac	aag	atc	gtt	ctc	cca	gtt	gac	ctg	gtt	gca	gca	931
Ala	Arg	Phe	Gly	Asp	Lys	Ile	Val	Leu	Pro	Val	Asp	Leu	Val	Ala	Ala	
			265					270					275			
tcc	gaa	ttt	aac	aag	gac	gca	gag	aag	cag	atc	gtt	gac	ctg	gac	tcc	979
Ser	Glu	Phe	Asn	Lys	Asp	Ala	Glu	Lys	Gln	Ile	Val	Asp	Leu	Asp	Ser	
		280					285					290				
atc	cca	gaa	ggc	tgg	atg	tct	ctt	gac	atc	gga	cca	gag	tcc	gtc	aag	1027
Ile	Pro	Glu	Gly	Trp	Met	Ser	Leu	Asp	Ile	Gly	Pro	Glu	Ser	Val	Lys	
	295					300				305						
aac	ttc	ggt	gag	gtt	ctc	agc	acc	gct	aag	acc	atc	ttc	tgg	aac	ggc	1075
Asn	Phe	Gly	Glu	Val	Leu	Ser	Thr	Ala	Lys	Thr	Ile	Phe	Trp	Asn	Gly	
310					315					320					325	
cca	atg	ggc	gtg	ttc	gag	ttc	gca	gca	ttc	tct	gaa	ggc	acc	cgc	ggc	1123
Pro	Met	Gly	Val	Phe	Glu	Phe	Ala	Ala	Phe	Ser	Glu	Gly	Thr	Arg	Gly	
				330					335					340		
atc	gcc	cag	gcc	atc	atc	gat	gca	act	gca	ggc	aac	gac	gca	ttc	tcc	1171
Ile	Ala	Gln	Ala	Ile	Ile	Asp	Ala	Thr	Ala	Gly	Asn	Asp	Ala	Phe	Ser	
			345					350					355			
gtt	gtt	ggc	ggt	ggc	gac	tcc	gca	gca	tcc	gtt	cgc	gtg	ctc	ggc	ctg	1219
Val	Val	Gly	Gly	Gly	Asp	Ser	Ala	Ala	Ser	Val	Arg	Val	Leu	Gly	Leu	
		360					365				370					
aac	gaa	gac	ggc	ttc	tcc	cac	atc	tcc	acc	ggt	ggt	ggc	gca	tcc	ctc	1267
Asn	Glu	Asp	Gly	Phe	Ser	His	Ile	Ser	Thr	Gly	Gly	Gly	Ala	Ser	Leu	
	375					380				385						
gag	tac	ctt	gaa	ggc	aag	gaa	ctc	cca	ggc	gtt	gca	att	ctc	gct	cag	1315
Glu	Tyr	Leu	Glu	Gly	Lys	Glu	Leu	Pro	Gly	Val	Ala	Ile	Leu	Ala	Gln	
390					395				400						405	
taa	atc	cgac	acg	gcc	cttt	gtt										1338

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<210> 70

<211> 405

<212> PRT

<213> Corynebacterium glutamicum

<400> 70

Met	Ala	Val	Lys	Thr	Leu	Lys	Asp	Leu	Leu	Asp	Glu	Gly	Val	Asp	Gly	1	5	10	15
Arg	His	Val	Ile	Val	Arg	Ser	Asp	Phe	Asn	Val	Pro	Leu	Asn	Asp	Asp	20	25	30	
Arg	Glu	Ile	Thr	Asp	Lys	Gly	Arg	Ile	Ile	Ala	Ser	Leu	Pro	Thr	Leu	35	40	45	
Lys	Ala	Leu	Ser	Glu	Gly	Gly	Ala	Lys	Val	Ile	Val	Met	Ala	His	Leu	50	55	60	
Gly	Arg	Pro	Lys	Gly	Glu	Val	Asn	Glu	Lys	Tyr	Ser	Leu	Ala	Pro	Val	65	70	75	80
Ala	Glu	Ala	Leu	Ser	Asp	Glu	Leu	Gly	Gln	Tyr	Val	Ala	Leu	Ala	Ala	85	90	95	
Asp	Val	Val	Gly	Glu	Asp	Ala	His	Glu	Arg	Ala	Asn	Gly	Leu	Thr	Glu	100	105	110	
Gly	Asp	Ile	Leu	Leu	Leu	Glu	Asn	Val	Arg	Phe	Asp	Pro	Arg	Glu	Thr	115	120	125	
Ser	Lys	Asp	Glu	Ala	Glu	Arg	Thr	Ala	Phe	Ala	Gln	Glu	Leu	Ala	Ala	130	135	140	
Leu	Ala	Ala	Asp	Asn	Gly	Ala	Phe	Val	Ser	Asp	Gly	Phe	Gly	Val	Val	145	150	155	160
His	Arg	Ala	Gln	Thr	Ser	Val	Tyr	Asp	Ile	Ala	Lys	Leu	Leu	Pro	His	165	170	175	
Tyr	Ala	Gly	Gly	Leu	Val	Glu	Thr	Glu	Ile	Ser	Val	Leu	Glu	Lys	Ile	180	185	190	
Ala	Glu	Ser	Pro	Glu	Ala	Pro	Tyr	Val	Val	Val	Leu	Gly	Gly	Ser	Lys	195	200	205	
Val	Ser	Asp	Lys	Ile	Gly	Val	Ile	Glu	Ala	Leu	Ala	Ala	Lys	Ala	Asp	210	215	220	
Lys	Ile	Ile	Val	Gly	Gly	Gly	Met	Cys	Tyr	Thr	Phe	Leu	Ala	Ala	Gln	225	230	235	240
Gly	His	Asn	Val	Gln	Gln	Ser	Leu	Leu	Gln	Glu	Glu	Met	Lys	Ala	Thr	245	250	255	
Cys	Thr	Asp	Leu	Leu	Ala	Arg	Phe	Gly	Asp	Lys	Ile	Val	Leu	Pro	Val	260	265	270	
Asp	Leu	Val	Ala	Ala	Ser	Glu	Phe	Asn	Lys	Asp	Ala	Glu	Lys	Gln	Ile	275	280	285	

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Val Asp Leu Asp Ser Ile Pro Glu Gly Trp Met Ser Leu Asp Ile Gly
 290 295 300

Pro Glu Ser Val Lys Asn Phe Gly Glu Val Leu Ser Thr Ala Lys Thr
 305 310 315 320

Ile Phe Trp Asn Gly Pro Met Gly Val Phe Glu Phe Ala Ala Phe Ser
 325 330 335

Glu Gly Thr Arg Gly Ile Ala Gln Ala Ile Ile Asp Ala Thr Ala Gly
 340 345 350

Asn Asp Ala Phe Ser Val Val Gly Gly Gly Asp Ser Ala Ala Ser Val
 355 360 365

Arg Val Leu Gly Leu Asn Glu Asp Gly Phe Ser His Ile Ser Thr Gly
 370 375 380

Gly Gly Ala Ser Leu Glu Tyr Leu Glu Gly Lys Glu Leu Pro Gly Val
 385 390 395 400

Ala Ile Leu Ala Gln
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1375)
 <223> RXA00235

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 Val Ala Glu Ile Met
 1 5

cac gta ttc gct cgc gaa att ctc gac tcc cgc ggt aac cca acc gtc 163
 His Val Phe Ala Arg Glu Ile Leu Asp Ser Arg Gly Asn Pro Thr Val
 10 15 20

gag gca gag gtt ttc ctg gat gac ggt tcc cac ggt gtc gca ggt gtt 211
 Glu Ala Glu Val Phe Leu Asp Asp Gly Ser His Gly Val Ala Gly Val
 25 30 35

cca tcc ggc gca tcc acc ggc gtc cac gag gct cat gag ctg cgt gac 259
 Pro Ser Gly Ala Ser Thr Gly Val His Glu Ala His Glu Leu Arg Asp
 40 45 50

ggt ggc gat cgc tac ctg ggc aag ggc gtt ttg aag gca gtt gaa aac 307
 Gly Gly Asp Arg Tyr Leu Gly Lys Gly Val Leu Lys Ala Val Glu Asn
 55 60 65

gtc aac gaa gaa atc ggc gac gag ctc gct ggc cta gag gct gac gat 355
 Val Asn Glu Glu Ile Gly Asp Glu Leu Ala Gly Leu Glu Ala Asp Asp
 70 75 80 85

cag cgc ctc atc gac gaa gca atg atc aag ctt gat ggc acc gcc aac	403
Gln Arg Leu Ile Asp Glu Ala Met Ile Lys Leu Asp Gly Thr Ala Asn	
90 95 100	
aag tcc cgc ctg ggt gca aac gca atc ctt ggt gtt tcc atg gct gtt	451
Lys Ser Arg Leu Gly Ala Asn Ala Ile Leu Gly Val Ser Met Ala Val	
105 110 115	
gca aag gct gct gct gat tcc gca ggc ctc cca ctg ttc cgc tac atc	499
Ala Lys Ala Ala Ala Asp Ser Ala Gly Leu Pro Leu Phe Arg Tyr Ile	
120 125 130	
ggt gga cca aac gca cac gtt ctt cca gtt cca atg atg aac atc atc	547
Gly Gly Pro Asn Ala His Val Leu Pro Val Pro Met Met Asn Ile Ile	
135 140 145	
acc ggt ggc gct cac gct gac tcc ggt gtt gac gtt cag gaa ttc atg	595
Thr Gly Gly Ala His Ala Asp Ser Gly Val Asp Val Gln Glu Phe Met	
150 155 160 165	
atc gct cca atc ggt gca gag acc ttc tct gag gct ctc cgc aac ggc	643
Ile Ala Pro Ile Gly Ala Glu Thr Phe Ser Glu Ala Leu Arg Asn Gly	
170 175 180	
gcg gag gtc tac cac gca ctg aag tcc gtc atc aag gaa aag ggc ctg	691
Ala Glu Val Tyr His Ala Leu Lys Ser Val Ile Lys Glu Lys Gly Leu	
185 190 195	
tcc acc gga ctt ggc gat gag ggc ggc ttc gct cct tcc gtc ggc tcc	739
Ser Thr Gly Leu Gly Asp Glu Gly Gly Phe Ala Pro Ser Val Gly Ser	
200 205 210	
acc cgt gag gct ctt gac ctt atc gtt gag gca atc gag aag gct ggc	787
Thr Arg Glu Ala Leu Asp Leu Ile Val Glu Ala Ile Glu Lys Ala Gly	
215 220 225	
ttc acc cca ggc aag gac atc gct ctt gct ctg gac gtt gct tcc tct	835
Phe Thr Pro Gly Lys Asp Ile Ala Leu Ala Leu Asp Val Ala Ser Ser	
230 235 240 245	
gag ttc ttc aag gac ggc acc tac cac ttc gaa ggt ggc cag cac tcc	883
Glu Phe Phe Lys Asp Gly Thr Tyr His Phe Glu Gly Gly Gln His Ser	
250 255 260	
gca gct gag atg gca aac gtt tac gct gag ctc gtt gac gcg tac cca	931
Ala Ala Glu Met Ala Asn Val Tyr Ala Glu Leu Val Asp Ala Tyr Pro	
265 270 275	
atc gtc tcc atc gag gac cca ctg cag gaa gat gac tgg gag ggt tac	979
Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp Asp Trp Glu Gly Tyr	
280 285 290	
acc aac ctc acc gca acc atc ggc gac aag gtt cag atc gtt ggc gac	1027
Thr Asn Leu Thr Ala Thr Ile Gly Asp Lys Val Gln Ile Val Gly Asp	
295 300 305	
gac ttc ttc gtc acc aac cct gag cgc ctg aag gag ggc atc gct aag	1075
Asp Phe Phe Val Thr Asn Pro Glu Arg Leu Lys Glu Gly Ile Ala Lys	
310 315 320 325	

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aag gct gcc aac tcc atc ctg gtt aag gtg aac cag atc ggt acc ctc 1123
Lys Ala Ala Asn Ser Ile Leu Val Lys Val Asn Gln Ile Gly Thr Leu
330 335 340

acc gag acc ttc gac gct gtc gac atg gct cac cgc gca ggc tac acc 1171
Thr Glu Thr Phe Asp Ala Val Asp Met Ala His Arg Ala Gly Tyr Thr
345 350 355

tcc atg atg tcc cac cgt tcc ggt gag acc gag gac acc acc att gct 1219
Ser Met Met Ser His Arg Ser Gly Glu Thr Glu Asp Thr Thr Ile Ala
360 365 370

gac ctc gca gtt gca ctc aac tgt ggc cag atc aag act ggt gct cca 1267
Asp Leu Ala Val Ala Leu Asn Cys Gly Gln Ile Lys Thr Gly Ala Pro
375 380 385

gca cgt tcc gac cgt gtc gca aag tac aac cag ctt ctc cgc atc gag 1315
Ala Arg Ser Asp Arg Val Ala Lys Tyr Asn Gln Leu Leu Arg Ile Glu
390 395 400 405

cag ctg ctt ggc gac gcc ggc gtc tac gca ggt cgc agc gca ttc cca 1363
Gln Leu Leu Gly Asp Ala Gly Val Tyr Ala Gly Arg Ser Ala Phe Pro
410 415 420

cgc ttt cag ggc taaataaaaag cgcttttcga cgc 1398
Arg Phe Gln Gly
425

<210> 72
<211> 425
<212> PRT
<213> Corynebacterium glutamicum

<400> 72
Val Ala Glu Ile Met His Val Phe Ala Arg Glu Ile Leu Asp Ser Arg
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Gly Asn Pro Thr Val Glu Ala Glu Val Phe Leu Asp Asp Gly Ser His
20 25 30
Gly Val Ala Gly Val Pro Ser Gly Ala Ser Thr Gly Val His Glu Ala
35 40 45
His Glu Leu Arg Asp Gly Gly Asp Arg Tyr Leu Gly Lys Gly Val Leu
50 55 60
Lys Ala Val Glu Asn Val Asn Glu Glu Ile Gly Asp Glu Leu Ala Gly
65 70 75 80
Leu Glu Ala Asp Asp Gln Arg Leu Ile Asp Glu Ala Met Ile Lys Leu
85 90 95
Asp Gly Thr Ala Asn Lys Ser Arg Leu Gly Ala Asn Ala Ile Leu Gly
100 105 110
Val Ser Met Ala Val Ala Lys Ala Ala Ala Asp Ser Ala Gly Leu Pro
115 120 125
Leu Phe Arg Tyr Ile Gly Gly Pro Asn Ala His Val Leu Pro Val Pro
130 135 140

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Met Met Asn Ile Ile Thr Gly Gly Ala His Ala Asp Ser Gly Val Asp
 145 150 155 160
 Val Gln Glu Phe Met Ile Ala Pro Ile Gly Ala Glu Thr Phe Ser Glu
 165 170 175
 Ala Leu Arg Asn Gly Ala Glu Val Tyr His Ala Leu Lys Ser Val Ile
 180 185 190
 Lys Glu Lys Gly Leu Ser Thr Gly Leu Gly Asp Glu Gly Gly Phe Ala
 195 200 205
 Pro Ser Val Gly Ser Thr Arg Glu Ala Leu Asp Leu Ile Val Glu Ala
 210 215 220
 Ile Glu Lys Ala Gly Phe Thr Pro Gly Lys Asp Ile Ala Leu Ala Leu
 225 230 235 240
 Asp Val Ala Ser Ser Glu Phe Phe Lys Asp Gly Thr Tyr His Phe Glu
 245 250 255
 Gly Gly Gln His Ser Ala Ala Glu Met Ala Asn Val Tyr Ala Glu Leu
 260 265 270
 Val Asp Ala Tyr Pro Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp
 275 280 285
 Asp Trp Glu Gly Tyr Thr Asn Leu Thr Ala Thr Ile Gly Asp Lys Val
 290 295 300
 Gln Ile Val Gly Asp Asp Phe Phe Val Thr Asn Pro Glu Arg Leu Lys
 305 310 315 320
 Glu Gly Ile Ala Lys Lys Ala Ala Asn Ser Ile Leu Val Lys Val Asn
 325 330 335
 Gln Ile Gly Thr Leu Thr Glu Thr Phe Asp Ala Val Asp Met Ala His
 340 345 350
 Arg Ala Gly Tyr Thr Ser Met Met Ser His Arg Ser Gly Glu Thr Glu
 355 360 365
 Asp Thr Thr Ile Ala Asp Leu Ala Val Ala Leu Asn Cys Gly Gln Ile
 370 375 380
 Lys Thr Gly Ala Pro Ala Arg Ser Asp Arg Val Ala Lys Tyr Asn Gln
 385 390 395 400
 Leu Leu Arg Ile Glu Gln Leu Leu Gly Asp Ala Gly Val Tyr Ala Gly
 405 410 415
 Arg Ser Ala Phe Pro Arg Phe Gln Gly
 420 425

<210> 73

<211> 1554

<212> DNA

<213> Corynebacterium glutamicum

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<220>

<221> CDS

<222> (101)..(1531)

<223> RXA01093

<400> 73

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 Met Gly Val Asp Arg
 1 5

cga act aag att gta tgt acc cta ggc cca gcg gtg gct agt gca gat 163
 Arg Thr Lys Ile Val Cys Thr Leu Gly Pro Ala Val Ala Ser Ala Asp
 10 15 20

gga att ctg cgt ttg gta gaa gac ggc atg gat gtt gct cgc ctc aac 211
 Gly Ile Leu Arg Leu Val Glu Asp Gly Met Asp Val Ala Arg Leu Asn
 25 30 35

ttc tcc cat ggt gac cac cca gat cat gag caa aac tac aag tgg gtc 259
 Phe Ser His Gly Asp His Pro Asp His Glu Gln Asn Tyr Lys Trp Val
 40 45 50

cgc gag gcg gcg gag aag act ggc cgt gca gtc ggt att ctc gca gac 307
 Arg Glu Ala Ala Glu Lys Thr Gly Arg Ala Val Gly Ile Leu Ala Asp
 55 60 65

ctc caa gga ccg aag atc cgt ctt ggc cgt ttc act gac ggc gca acc 355
 Leu Gln Gly Pro Lys Ile Arg Leu Gly Arg Phe Thr Asp Gly Ala Thr
 70 75 80 85

gtg tgg gaa aac ggc gag acc att cgg atc acc gtt gac gat gta gag 403
 Val Trp Glu Asn Gly Glu Thr Ile Arg Ile Thr Val Asp Asp Val Glu
 90 95 100

gga acg cac gat cgt gtg tcc acc acc tac aag aat ctg gca aaa gac 451
 Gly Thr His Asp Arg Val Ser Thr Thr Tyr Lys Asn Leu Ala Lys Asp
 105 110 115

gcg aag cca ggc gac cgc ctg ctc gtt gat gac ggc aag gtt ggc ctc 499
 Ala Lys Pro Gly Asp Arg Leu Leu Val Asp Asp Gly Lys Val Gly Leu
 120 125 130

gtc tgc gtt tcc gtc gaa ggt aac gac gtc atc tgt gag gtt gtt gag 547
 Val Cys Val Ser Val Glu Gly Asn Asp Val Ile Cys Glu Val Val Glu
 135 140 145

ggc gga cca gtc tcc aac aac aag ggt gtt tcc ctg cca ggt atg gat 595
 Gly Gly Pro Val Ser Asn Asn Lys Gly Val Ser Leu Pro Gly Met Asp
 150 155 160 165

att tcc gta cct gca ctg tcc gaa aag gat atc cgt gac ctg cgc ttc 643
 Ile Ser Val Pro Ala Leu Ser Glu Lys Asp Ile Arg Asp Leu Arg Phe
 170 175 180

gcc ctg aag ctc ggc gtg gac ttt att gca ctg tcc ttc gta cgt tcc 691
 Ala Leu Lys Leu Gly Val Asp Phe Ile Ala Leu Ser Phe Val Arg Ser
 185 190 195

cca gca gat gct gaa ctc gtt cac aag atc atg gac gaa gaa ggt cgt 739

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Pro	Ala	Asp	Ala	Glu	Leu	Val	His	Lys	Ile	Met	Asp	Glu	Glu	Gly	Arg	
		200					205					210				
cgt	gtt	cct	gtg	atc	gcc	aag	ctg	gaa	aag	cca	gag	gct	gtc	acc	tcc	787
Arg	Val	Pro	Val	Ile	Ala	Lys	Leu	Glu	Lys	Pro	Glu	Ala	Val	Thr	Ser	
	215					220				225						
ctc	gag	cca	atc	gtg	ttg	gca	ttc	gac	gcc	gtc	atg	gtt	gct	cgt	ggc	835
Leu	Glu	Pro	Ile	Val	Leu	Ala	Phe	Asp	Ala	Val	Met	Val	Ala	Arg	Gly	
230					235					240					245	
gac	ctc	ggc	gtt	gag	gtt	cct	ctg	gag	gag	gtt	cca	ctg	gtt	cag	aag	883
Asp	Leu	Gly	Val	Glu	Val	Pro	Leu	Glu	Glu	Val	Pro	Leu	Val	Gln	Lys	
				250					255					260		
cgc	gca	atc	cag	att	gcc	cgt	gag	aac	gca	aag	cca	gtt	atc	gtg	gca	931
Arg	Ala	Ile	Gln	Ile	Ala	Arg	Glu	Asn	Ala	Lys	Pro	Val	Ile	Val	Ala	
			265					270					275			
acc	cag	atg	ctg	gat	tcc	atg	att	gag	aac	tcc	cgc	cca	acc	cgt	gcg	979
Thr	Gln	Met	Leu	Asp	Ser	Met	Ile	Glu	Asn	Ser	Arg	Pro	Thr	Arg	Ala	
		280					285					290				
gaa	gct	tct	gac	gtg	gca	aac	gct	gtg	ctc	gat	ggc	gca	gat	gct	gtc	1027
Glu	Ala	Ser	Asp	Val	Ala	Asn	Ala	Val	Leu	Asp	Gly	Ala	Asp	Ala	Val	
	295					300					305					
atg	ctt	tct	ggt	gaa	act	tca	gtg	ggc	aaa	gat	ccg	cac	aac	gtt	gtg	1075
Met	Leu	Ser	Gly	Glu	Thr	Ser	Val	Gly	Lys	Asp	Pro	His	Asn	Val	Val	
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Arg	Thr	Met	Ser	Arg	Ile	Val	Arg	Phe	Ala	Glu	Thr	Asp	Gly	Arg	Val	
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Ser	Ala	Arg	Asp	Ile	Ala	Glu	Arg	Leu	Asn	Ala	Arg	Ala	Leu	Val	Ala	
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Phe	Thr	Thr	Ser	Gly	Asp	Thr	Ala	Lys	Arg	Val	Ala	Arg	Leu	His	Ser	
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Asp	Thr	Asp	Asp	Met	Met	Arg	Glu	Val	Asp	Arg	Ala	Leu	Leu	Ala	Met	
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Pro Gly Val Thr Gly Asn Thr Asn Met Ile His Val His Leu Leu Gly			
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 35 40 45
 Asn Tyr Lys Trp Val Arg Glu Ala Ala Glu Lys Thr Gly Arg Ala Val
 50 55 60
 Gly Ile Leu Ala Asp Leu Gln Gly Pro Lys Ile Arg Leu Gly Arg Phe
 65 70 75 80
 Thr Asp Gly Ala Thr Val Trp Glu Asn Gly Glu Thr Ile Arg Ile Thr
 85 90 95
 Val Asp Asp Val Glu Gly Thr His Asp Arg Val Ser Thr Thr Tyr Lys
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 Asn Leu Ala Lys Asp Ala Lys Pro Gly Asp Arg Leu Leu Val Asp Asp
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 Gly Lys Val Gly Leu Val Cys Val Ser Val Glu Gly Asn Asp Val Ile
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 Cys Glu Val Val Glu Gly Gly Pro Val Ser Asn Asn Lys Gly Val Ser
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 Leu Pro Gly Met Asp Ile Ser Val Pro Ala Leu Ser Glu Lys Asp Ile
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 Arg Asp Leu Arg Phe Ala Leu Lys Leu Gly Val Asp Phe Ile Ala Leu
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 Ser Phe Val Arg Ser Pro Ala Asp Ala Glu Leu Val His Lys Ile Met
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 Asp Glu Glu Gly Arg Arg Val Pro Val Ile Ala Lys Leu Glu Lys Pro
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 Glu Ala Val Thr Ser Leu Glu Pro Ile Val Leu Ala Phe Asp Ala Val
 225 230 235 240

Met Val Ala Arg Gly Asp Leu Gly Val Glu Val Pro Leu Glu Glu Val
 245 250 255
 Pro Leu Val Gln Lys Arg Ala Ile Gln Ile Ala Arg Glu Asn Ala Lys
 260 265 270
 Pro Val Ile Val Ala Thr Gln Met Leu Asp Ser Met Ile Glu Asn Ser
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 Arg Pro Thr Arg Ala Glu Ala Ser Asp Val Ala Asn Ala Val Leu Asp
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 Gly Ala Asp Ala Val Met Leu Ser Gly Glu Thr Ser Val Gly Lys Asp
 305 310 315 320
 Pro His Asn Val Val Arg Thr Met Ser Arg Ile Val Arg Phe Ala Glu
 325 330 335
 Thr Asp Gly Arg Val Pro Asp Leu Thr His Ile Pro Arg Thr Lys Arg
 340 345 350
 Gly Val Ile Ser Tyr Ser Ala Arg Asp Ile Ala Glu Arg Leu Asn Ala
 355 360 365
 Arg Ala Leu Val Ala Phe Thr Thr Ser Gly Asp Thr Ala Lys Arg Val
 370 375 380
 Ala Arg Leu His Ser His Leu Pro Leu Leu Val Phe Thr Pro Asn Glu
 385 390 395 400
 Ala Val Arg Ser Glu Leu Ala Leu Thr Trp Gly Ala Thr Thr Phe Leu
 405 410 415
 Cys Pro Pro Val Ser Asp Thr Asp Asp Met Met Arg Glu Val Asp Arg
 420 425 430
 Ala Leu Leu Ala Met Pro Glu Tyr Asn Lys Gly Asp Met Met Val Val
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<223> RXN02675

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

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	250	255	260	
cca gaa tgg ttc gac aaa cta gaa atc ggc agc gtc atc aac gtc cca	Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser Val Ile Asn Val Pro	931		
	265	270	275	
gac acc cgc gga tcc cgc cga gca ttc acc gtg acc agg gtt ttt gat	Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val Thr Arg Val Phe Asp	979		
	280	285	290	
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	295	300	305	
acc ctc ctg gaa cac aac tac gac cgc tcc cgg gtc tac ggc atc ccc	Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg Val Tyr Gly Ile Pro	1075		
	310	315	320	325
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	330	335	340	
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	345	350	355	
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	375	380	385	
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	390	395	400	405
acc cac gcc cgc cca caa ggc gta aac ctg gcc gca tac aag gga atc	Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala Ala Tyr Lys Gly Ile	1363		
	410	415	420	
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	425	430	435	
ctc caa cac ctg cgc ttt gtc gtc aaa tac gcc gac atc gca gcc atc	Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala Asp Ile Ala Ala Ile	1459		
	440	445	450	
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	455	460	465	
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acc ggc atg cgc cac gaa aac ttc ggc atc atg atc gcc cgc gga gac 1651
Thr Gly Met Arg His Glu Asn Phe Gly Ile Met Ile Ala Arg Gly Asp
      505                      510                      515

ctc gcc gtc gaa ctc ggc ttc gac cgc atg gca gaa gtc ccc caa ctg 1699
Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala Glu Val Pro Gln Leu
      520                      525                      530

atc atg gcc ctt gcc gaa gcc gcc cac gtc cca acc atc ttg gcc acc 1747
Ile Met Ala Leu Ala Glu Ala Ala His Val Pro Thr Ile Leu Ala Thr
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caa gtc ctg gaa aac atg gcc aaa aac gga ctc cca tct cgc gca gaa 1795
Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser Arg Ala Glu
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atc acc gac gca gca atg gca ctt cgc gct gaa tgc gtc atg ctg aac 1843
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aag gga cca cac atc aac gac gcc atc aag gtc ctc acc gaa atg agc 1891
Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr Glu Met Ser
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cgc aaa ctt ggt gca tcc caa cga aag agt agg ctg ctg ctg cgc aag 1939
Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu Leu Arg Lys
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Ala Ile Gly Gln Val Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu
      35                      40                      45

Met His Tyr Ala His Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln
      50                      55                      60

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

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

Asp Ile Ala Ala Ile Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr
450 455 460

Leu Leu Gln Ala Leu Ala Asp Ile Gly Asp Pro Val Ala Val Glu Arg
465 470 475 480

Leu Gly Leu Val Leu Lys Ile Glu Thr Ile Pro Gly Tyr Glu Gly Leu
485 490 495

Ala Gln Ile Leu Leu Thr Gly Met Arg His Glu Asn Phe Gly Ile Met
500 505 510

Ile Ala Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala
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Glu Val Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro
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Thr Ile Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu
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Pro Ser Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu
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Cys Val Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val
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Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala Glu Val
20 25 30

ccc caa ctg atc atg gcc ctt gca gaa gcc gcc cac gtc cca acc atc 144
Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro Thr Ile

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Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser			
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cgc gca gaa atc acc gac gca gca atg gca ctt cgc gct gaa tgc gtc			240
Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val			
65	70	75	80
atg ctg aac aag gga cca cac atc aac gac gcc atc aag gtc ctc acc			288
Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr			
	85	90	95
gaa atg agc cgc aaa ctt ggt gca tcc caa cga aag agt agg ctg ctg			336
Glu Met Ser Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu			
	100	105	110
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cgt 386

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 Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser
 50 55 60
 Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val
 65 70 75 80
 Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr
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Gln	Asp	Ile	Leu	Gln	Glu	Ile	Lys	Thr	Glu	Leu	Asp	Glu	Leu	Ile	Leu	
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gaa	ctt	gat	gag	gtg	aca	caa	act	cac	agc	gag	gcc	atc	ggg	cag	gtc	211
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Leu	Arg	Thr	Lys	Asp	Leu	Arg	Gly	Leu	Gln	Gln	Arg	Leu	Ser	Ser	Val	
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Gly	Ala	Thr	Arg	Leu	Thr	Thr	Thr	Glu	Pro	Ala	Val	Gln	Ala	Arg	Leu	
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Tyr	Pro	Pro	Ser	Asp	Val	Val	Asp	Ala	Phe	Glu	Asp	Ala	Asp	Glu	Ile	
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		120					125					130				

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Pro	Ser	Cys	Ile	Met	Val	Thr	Leu	Pro	Thr	Glu	Ala	Ala	Thr	Asp	Ile	
	135					140					145					

gaa	ctt	gtc	cgt	ggc	ttc	gcc	aaa	agc	ggc	atg	aat	cta	gct	cgc	atc	595
Glu	Leu	Val	Arg	Gly	Phe	Ala	Lys	Ser	Gly	Met	Asn	Leu	Ala	Arg	Ile	
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Val	His	Thr	Val	Ala	Glu	Glu	Val	Gly	Arg	Glu	Ile	Arg	Val	Ser	Met	
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Glu	Val	Gly	Arg	Ala	Arg	Val	Thr	Arg	Asp	Glu	Thr	Gly	Lys	Val	Leu	
	215					220					225					
acg	ccc	gca	aaa	ctg	tgg	atc	acc	gcc	cac	ggc	tcc	gaa	cca	gtc	cca	835
Thr	Pro	Ala	Lys	Leu	Trp	Ile	Thr	Ala	His	Gly	Ser	Glu	Pro	Val	Pro	
230					235					240					245	
gcc	ccc	gaa	agc	ctg	ccc	ggt	cgc	ccc	gct	ctg	ccg	att	gaa	gtc	acc	883
Ala	Pro	Glu	Ser	Leu	Pro	Gly	Arg	Pro	Ala	Leu	Pro	Ile	Glu	Val	Thr	
				250					255					260		
cca	gaa	tgg	ttc	gac	aaa	cta	gaa	atc	ggc	agc	gtc	atc	aac	gtc	cca	931
Pro	Glu	Trp	Phe	Asp	Lys	Leu	Glu	Ile	Gly	Ser	Val	Ile	Asn	Val	Pro	
			265					270					275			
gac	acc	cgc	gga	tcc	cgc	cga	gca	ttc	acc	gtg	acc	agg	gtt	ttt	gat	979
Asp	Thr	Arg	Gly	Ser	Arg	Arg	Ala	Phe	Thr	Val	Thr	Arg	Val	Phe	Asp	
		280					285					290				
ggc	gcg	gtc	ctc	gcc	gaa	ggc	cca	caa	aaa	gcc	tac	atc	tcc	aac	ggc	1027
Gly	Ala	Val	Leu	Ala	Glu	Gly	Pro	Gln	Lys	Ala	Tyr	Ile	Ser	Asn	Gly	
	295					300					305					
acc	ctc	ctg	gaa	cac	aac	tac	gac	cgc	tcc	cgg	gtc	tac	ggc	atc	ccc	1075
Thr	Leu	Leu	Glu	His	Asn	Tyr	Asp	Arg	Ser	Arg	Val	Tyr	Gly	Ile	Pro	
310					315					320					325	
gcc	gta	gtt	cag	cgc	atc	aac	ctc	aaa	gtc	ggc	gac	cgc	ctc	atc	ctt	1123
Ala	Val	Val	Gln	Arg	Ile	Asn	Leu	Lys	Val	Gly	Asp	Arg	Leu	Ile	Leu	
				330					335					340		
acc	gac	gaa	gaa	ctc	acc	tac	gat	cca	tcc	ctc	gga	tcc	ggc	cgc	aca	1171
Thr	Asp	Glu	Glu	Leu	Thr	Tyr	Asp	Pro	Ser	Leu	Gly	Ser	Gly	Arg	Thr	
			345					350					355			
cca	cgc	atc	agc	tgc	acc	ctt	cca	caa	gca	gtc	gat	gca	att	aaa	gtc	1219
Pro	Arg	Ile	Ser	Cys	Thr	Leu	Pro	Gln	Ala	Val	Asp	Ala	Ile	Lys	Val	
		360					365					370				
ggg	cac	cgc	gtg	ctt	ttc	gac	gac	gga	gcc	atc	gcc	gca	gtc	tgc	atc	1267
Gly	His	Arg	Val	Leu	Phe	Asp	Asp	Gly	Ala	Ile	Ala	Ala	Val	Cys	Ile	
	375					380					385					
gac	aag	acc	tcc	act	gcc	gac	ggc	cac	aac	gac	gta	gaa	ttg	gaa	gtc	1315
Asp	Lys	Thr	Ser	Thr	Ala	Asp	Gly	His	Asn	Asp	Val	Glu	Leu	Glu	Val	
390					395					400					405	
acc	cac	gcc	cgc	cca	caa	ggc	gta	aac	ctg	gcc	gca	tac	aag	gga	atc	1363
Thr	His	Ala	Arg	Pro	Gln	Gly	Val	Asn	Leu	Ala	Ala	Tyr	Lys	Gly	Ile	
				410					415					420		
aac	ctc	cca	gac	tcc	gaa	ctt	cca	ctc	cca	agc	ctc	act	gaa	gaa	gac	1411
Asn	Leu	Pro	Asp	Ser	Glu	Leu	Pro	Leu	Pro	Ser	Leu	Thr	Glu	Glu	Asp	
			425					430					435			
ctc	caa	cac	ctg	cgc	ttt	gtc	gtc	aaa	tac	gcc	gac	atc	gca	gcc	atc	1459
Leu	Gln	His	Leu	Arg	Phe	Val	Val	Lys	Tyr	Ala	Asp	Ile	Ala	Ala	Ile	

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440	445	450	
tcc ttc atc cga aac gtc gcc gac gtg gaa tac ctc ctc caa gca ctc			1507
Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr Leu Leu Gln Ala Leu			
455	460	465	

gcc gac atc gga gat	1522
Ala Asp Ile Gly Asp	
470	

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 80	
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Asp Glu Leu Ile Leu Glu Leu Asp Glu Val Thr Gln Thr His Ser Glu	
20 25 30	
Ala Ile Gly Gln Val Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu	
35 40 45	
Met His Tyr Ala His Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln	
50 55 60	
Arg Leu Ser Ser Val Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala	
65 70 75 80	
Val Gln Ala Arg Leu Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala	
85 90 95	
Gly Glu Gly Pro Leu Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu	
100 105 110	
Asp Ala Asp Glu Ile Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu	
115 120 125	
Pro Leu Pro Asp Thr Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu	
130 135 140	
Ala Ala Thr Asp Ile Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met	
145 150 155 160	
Asn Leu Ala Arg Ile Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys	
165 170 175	
Gln Met Ile Asp Asn Val His Thr Val Ala Glu Glu Val Gly Arg Glu	
180 185 190	
Ile Arg Val Ser Met Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu	
195 200 205	
Ile Ala Pro Gly Ala Glu Val Gly Arg Ala Arg Val Thr Arg Asp Glu	
210 215 220	
Thr Gly Lys Val Leu Thr Pro Ala Lys Leu Trp Ile Thr Ala His Gly	
225 230 235 240	

Ser Glu Pro Val Pro Ala Pro Glu Ser Leu Pro Gly Arg Pro Ala Leu
 245 250 255
 Pro Ile Glu Val Thr Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser
 260 265 270
 Val Ile Asn Val Pro Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val
 275 280 285
 Thr Arg Val Phe Asp Gly Ala Val Leu Ala Glu Gly Pro Gln Lys Ala
 290 295 300
 Tyr Ile Ser Asn Gly Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg
 305 310 315 320
 Val Tyr Gly Ile Pro Ala Val Val Gln Arg Ile Asn Leu Lys Val Gly
 325 330 335
 Asp Arg Leu Ile Leu Thr Asp Glu Glu Leu Thr Tyr Asp Pro Ser Leu
 340 345 350
 Gly Ser Gly Arg Thr Pro Arg Ile Ser Cys Thr Leu Pro Gln Ala Val
 355 360 365
 Asp Ala Ile Lys Val Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile
 370 375 380
 Ala Ala Val Cys Ile Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp
 385 390 395 400
 Val Glu Leu Glu Val Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala
 405 410 415
 Ala Tyr Lys Gly Ile Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser
 420 425 430
 Leu Thr Glu Glu Asp Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala
 435 440 445
 Asp Ile Ala Ala Ile Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr
 450 455 460
 Leu Leu Gln Ala Leu Ala Asp Ile Gly Asp
 465 470

<210> 81
 <211> 2022
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1999)
 <223> RXA00682

<400> 81
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 cgcacatctttt cgtcgaaaag catctaaaag gagtttgacc atg gct aat aaa tct 115

120

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230		235		240		245	
gtc gac ctt ggc ctg caa act cac ttt gcc aac ccg gat gat ccg caa							883
Val Asp Leu Gly Leu Gln Thr His Phe Ala Asn Pro Asp Asp Pro Gln							
		250		255		260	
gct acc ttg gct gct atc gca aag gca gaa ggc ggc gcg aca tgg ata							931
Ala Thr Leu Ala Ala Ile Ala Lys Ala Glu Gly Gly Ala Thr Trp Ile							
		265		270		275	
gcg cgc tgg gaa gaa gca caa gat ccg tgg ttc aac ttc acc gtc ggt							979
Ala Arg Trp Glu Glu Ala Gln Asp Pro Trp Phe Asn Phe Thr Val Gly							
		280		285		290	
aat ggc ttc tac ggt cac gat aaa tac tgg atc gag cac ctg gaa ctt							1027
Asn Gly Phe Tyr Gly His Asp Lys Tyr Trp Ile Glu His Leu Glu Leu							
		295		300		305	
cca ctg ggg tac atc gcg gat tac atc cgc cgc cta gat gaa ggc caa							1075
Pro Leu Gly Tyr Ile Ala Asp Tyr Ile Arg Arg Leu Asp Glu Gly Gln							
		310		315		320	325
acc atc tcc cgc ccg aaa gat gaa ctc atc gca gaa aag gaa cgc gtg							1123
Thr Ile Ser Arg Pro Lys Asp Glu Leu Ile Ala Glu Lys Glu Arg Val							
		330		335		340	
gtg gaa gaa tac cgc gac ctt ttg gat gga gaa caa ctc gcg cag ttt							1171
Val Glu Glu Tyr Arg Asp Leu Leu Asp Gly Glu Gln Leu Ala Gln Phe							
		345		350		355	
gat gct aaa tgc ggc ctc gct gct act gca tac ccc tat gtg gaa aac							1219
Asp Ala Lys Cys Gly Leu Ala Ala Thr Ala Tyr Pro Tyr Val Glu Asn							
		360		365		370	
cat aac ttc tac atc gag cac tgg acc atg tca gta ttt tgg cgc aaa							1267
His Asn Phe Tyr Ile Glu His Trp Thr Met Ser Val Phe Trp Arg Lys							
		375		380		385	
gta cgc gaa ctt tcc cgc act ctc cag ggc tac ggt ttc tgg gag aac							1315
Val Arg Glu Leu Ser Arg Thr Leu Gln Gly Tyr Gly Phe Trp Glu Asn							
		390		395		400	405
gag gat gac atg ttg tac ctc aac cgc act gaa gtc cgc gat gtc ctc							1363
Glu Asp Asp Met Leu Tyr Leu Asn Arg Thr Glu Val Arg Asp Val Leu							
		410		415		420	
ttc gac ctg gct act gcg tgg ggt gtc ggc gca ccc ggt ggt cca att							1411
Phe Asp Leu Ala Thr Ala Trp Gly Val Gly Ala Pro Gly Gly Pro Ile							
		425		430		435	
ggc acg atc att tgg ccg gaa gaa att gag cga aga aaa gca att gtc							1459
Gly Thr Ile Ile Trp Pro Glu Glu Ile Glu Arg Arg Lys Ala Ile Val							
		440		445		450	
acc gct ttg aaa act gcc cga cca gcg cca gct ctt aac act cct cca							1507
Thr Ala Leu Lys Thr Ala Arg Pro Ala Pro Ala Leu Asn Thr Pro Pro							
		455		460		465	
gag tcc atc acc gaa cct ttc acc cgc atg ctc tgg gga atc acc acc							1555
Glu Ser Ile Thr Glu Pro Phe Thr Arg Met Leu Trp Gly Ile Thr Thr							
		470		475		480	485

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gaa cag gtg caa tca tgg ttg ggc aat gac gag gat gcc gaa gaa gga 1603
 Glu Gln Val Gln Ser Trp Leu Gly Asn Asp Glu Asp Ala Glu Glu Gly
 490 495 500

acc ctt aaa ggc atg gct gca tcc cct ggt gtg gtg gaa ggc tac gct 1651
 Thr Leu Lys Gly Met Ala Ala Ser Pro Gly Val Val Glu Gly Tyr Ala
 505 510 515

cga gta att ctc agc gca gat gac ctt tca gaa atc cag cag gat gaa 1699
 Arg Val Ile Leu Ser Ala Asp Asp Leu Ser Glu Ile Gln Gln Asp Glu
 520 525 530

atc ctc gtt gcc cct gta aca gca cct tct tgg ggc cca atc ttt ggc 1747
 Ile Leu Val Ala Pro Val Thr Ala Pro Ser Trp Gly Pro Ile Phe Gly
 535 540 545

aaa atc aag gca aca gtc act gat att ggt ggc atg atg agc cat gct 1795
 Lys Ile Lys Ala Thr Val Thr Asp Ile Gly Gly Met Met Ser His Ala
 550 555 560 565

gcg atc gtg tgc cgc gaa tac ggc ttg ccg gct gtt act gga act ggc 1843
 Ala Ile Val Cys Arg Glu Tyr Gly Leu Pro Ala Val Thr Gly Thr Gly
 570 575 580

gct gca tcc acc acc atc aaa acc ggc gat tac ctc aag gtc gat gga 1891
 Ala Ala Ser Thr Thr Ile Lys Thr Gly Asp Tyr Leu Lys Val Asp Gly
 585 590 595

acc aag ggc aag gtt gtc att gtt gat cca gat gcg cca cgc atc gaa 1939
 Thr Lys Gly Lys Val Val Ile Val Asp Pro Asp Ala Pro Arg Ile Glu
 600 605 610

gga ccc ggc gcg cac agc cat gcg cac tca gta gca gca cat ggg gtg 1987
 Gly Pro Gly Ala His Ser His Ala His Ser Val Ala Ala His Gly Val
 615 620 625

gat aca cat gcc tagtccacgc actgttctta tca 2022
 Asp Thr His Ala
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<210> 82

<211> 633

<212> PRT

<213> Corynebacterium glutamicum

<400> 82

Met Ala Asn Lys Ser Phe Pro Lys Pro Ser Asp Leu Pro Val Pro Lys
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Gly Ala Glu Gly Trp Glu Asp Leu Tyr Pro Tyr Tyr Leu Val Phe Gln
 20 25 30

Asp Lys Leu Met Asp Gln Glu Asn Glu Lys Phe Trp Phe Cys Asp Ser
 35 40 45

Gln His Trp Pro Thr Val Phe Lys Pro Phe Glu Thr Ile Gly Gly Glu
 50 55 60

Phe Ala Val Lys Cys Leu Gly Gln Tyr Asn Ala Arg His Leu Met Ile

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PCT/IB00/00943

65					70						75				80
Pro	Asn	Ala	Asn	Gly	Ile	Glu	Phe	Arg	Val	His	Leu	Gly	Tyr	Leu	Tyr
				85					90					95	
Met	Ser	Pro	Ile	Pro	Val	Pro	Glu	Asp	Gln	Ile	Ala	Glu	Arg	Val	Pro
			100					105					110		
Met	Phe	Gln	Glu	Arg	Ile	Thr	His	Tyr	Phe	Gln	Asn	Trp	Glu	Pro	Met
		115					120					125			
Leu	Ala	Asn	Trp	Lys	Glu	Arg	Val	Leu	Gly	Thr	Ile	Asn	Glu	Leu	Glu
	130					135					140				
Ser	Leu	Glu	Phe	Lys	Pro	Leu	Pro	Asp	Tyr	Val	Pro	Ile	Asp	Asp	Ile
145					150					155					160
Val	Ser	Gly	Lys	Ala	Lys	Asp	Gly	Thr	Glu	Val	Leu	Met	Glu	Asn	Phe
				165					170					175	
Asp	Arg	Leu	Ile	Gln	Leu	Ala	Tyr	Gln	Asn	Trp	Gln	Tyr	His	Phe	Glu
			180					185					190		
Phe	Leu	Asn	Leu	Gly	Tyr	Ile	Ala	Tyr	Leu	Asp	Phe	Phe	Asn	Phe	Cys
		195					200					205			
Lys	Glu	Val	Phe	Pro	Asp	Ile	Pro	Asp	Gln	Ser	Ile	Ser	Met	Met	Val
	210					215					220				
Gln	Gly	Val	Asp	Met	Glu	Leu	Phe	Arg	Pro	Asp	Asp	Glu	Leu	Lys	Ile
225					230					235					240
Leu	Ala	Gln	Leu	Ala	Val	Asp	Leu	Gly	Leu	Gln	Thr	His	Phe	Ala	Asn
				245					250					255	
Pro	Asp	Asp	Pro	Gln	Ala	Thr	Leu	Ala	Ala	Ile	Ala	Lys	Ala	Glu	Gly
			260					265					270		
Gly	Ala	Thr	Trp	Ile	Ala	Arg	Trp	Glu	Glu	Ala	Gln	Asp	Pro	Trp	Phe
		275					280					285			
Asn	Phe	Thr	Val	Gly	Asn	Gly	Phe	Tyr	Gly	His	Asp	Lys	Tyr	Trp	Ile
	290					295					300				
Glu	His	Leu	Glu	Leu	Pro	Leu	Gly	Tyr	Ile	Ala	Asp	Tyr	Ile	Arg	Arg
305					310					315					320
Leu	Asp	Glu	Gly	Gln	Thr	Ile	Ser	Arg	Pro	Lys	Asp	Glu	Leu	Ile	Ala
				325					330					335	
Glu	Lys	Glu	Arg	Val	Val	Glu	Glu	Tyr	Arg	Asp	Leu	Leu	Asp	Gly	Glu
			340					345					350		
Gln	Leu	Ala	Gln	Phe	Asp	Ala	Lys	Cys	Gly	Leu	Ala	Ala	Thr	Ala	Tyr
		355					360					365			
Pro	Tyr	Val	Glu	Asn	His	Asn	Phe	Tyr	Ile	Glu	His	Trp	Thr	Met	Ser
	370					375					380				
Val	Phe	Trp	Arg	Lys	Val	Arg	Glu	Leu	Ser	Arg	Thr	Leu	Gln	Gly	Tyr
385					390					395					400

Gly Phe Trp Glu Asn Glu Asp Asp Met Leu Tyr Leu Asn Arg Thr Glu
 405 410 415
 Val Arg Asp Val Leu Phe Asp Leu Ala Thr Ala Trp Gly Val Gly Ala
 420 425 430
 Pro Gly Gly Pro Ile Gly Thr Ile Ile Trp Pro Glu Glu Ile Glu Arg
 435 440 445
 Arg Lys Ala Ile Val Thr Ala Leu Lys Thr Ala Arg Pro Ala Pro Ala
 450 455 460
 Leu Asn Thr Pro Pro Glu Ser Ile Thr Glu Pro Phe Thr Arg Met Leu
 465 470 475 480
 Trp Gly Ile Thr Thr Glu Gln Val Gln Ser Trp Leu Gly Asn Asp Glu
 485 490 495
 Asp Ala Glu Glu Gly Thr Leu Lys Gly Met Ala Ala Ser Pro Gly Val
 500 505 510
 Val Glu Gly Tyr Ala Arg Val Ile Leu Ser Ala Asp Asp Leu Ser Glu
 515 520 525
 Ile Gln Gln Asp Glu Ile Leu Val Ala Pro Val Thr Ala Pro Ser Trp
 530 535 540
 Gly Pro Ile Phe Gly Lys Ile Lys Ala Thr Val Thr Asp Ile Gly Gly
 545 550 555 560
 Met Met Ser His Ala Ala Ile Val Cys Arg Glu Tyr Gly Leu Pro Ala
 565 570 575
 Val Thr Gly Thr Gly Ala Ala Ser Thr Thr Ile Lys Thr Gly Asp Tyr
 580 585 590
 Leu Lys Val Asp Gly Thr Lys Gly Lys Val Val Ile Val Asp Pro Asp
 595 600 605
 Ala Pro Arg Ile Glu Gly Pro Gly Ala His Ser His Ala His Ser Val
 610 615 620
 Ala Ala His Gly Val Asp Thr His Ala
 625 630

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 <211> 1215
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1192)
 <223> RXA00683

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											Met 1	Thr	Asn	Ser	Leu 5	
aac Asn	atc Ile	ccg Pro	ttt Phe	gtc Val 10	cag Gln	cgc Arg	ttc Phe	gat Asp	gaa Glu 15	ggc Gly	ctg Leu	gat Asp	cct Pro	gtt Val 20	cta Leu	163
gaa Glu	gta Val	ctc Leu	ggg Gly 25	ggc Gly	aag Lys	ggc Gly	gct Ala	tca Ser 30	cta Leu	gtc Val	acc Thr	atg Met	aca Thr 35	gat Asp	gct Ala	211
gga Gly	atg Met	ccc Pro 40	gtt Val	cca Pro	cct Pro	gga Gly	ttt Phe 45	gtg Val	gtc Val	act Thr	act Thr	gcc Ala 50	agc Ser	ttt Phe	gat Asp	259
gaa Glu	ttc Phe 55	atc Ile	cgt Arg	gaa Glu	gca Ala	ggg Gly 60	gtt Val	gct Ala	gaa Glu	cac His	atc Ile 65	gat Asp	aaa Lys	ttc Phe	cta Leu	307
aac Asn 70	gat Asp	ctc Leu	gat Asp	gca Ala	gaa Glu 75	gat Asp	gtt Val	aag Lys	gaa Glu	gtg Val 80	gat Asp	cga Arg	gtt Val	tct Ser	gcg Ala 85	355
atc Ile	atc Ile	cgc Arg	gat Asp	gag Glu 90	ctg Leu	tgc Cys	agt Ser	ctt Leu	gac Asp 95	gtt Val	cca Pro	gag Glu	aat Asn	gct Ala 100	cgt Arg	403
ttc Phe	gca Ala	gtg Val	cac His 105	cag Gln	gct Ala	tat Tyr	cgc Arg	gat Asp 110	ctc Leu	atg Met	gaa Glu	cga Arg	tgc Cys 115	ggg Gly	ggc Gly	451
gac Asp	gtc Val	ccg Pro 120	gtt Val	gct Ala	gtc Val	cgg Arg	tca Ser 125	tcg Ser	gcc Ala	act Thr	gcc Ala	gaa Glu 130	gat Asp	ctg Leu	ccc Pro	499
gat Asp	gct Ala 135	tcc Ser	ttc Phe	gca Ala	ggg Gly	caa Gln 140	cag Gln	gac Asp	acc Thr	tat Tyr	ctg Leu 145	tgg Trp	caa Gln	gtc Val	ggg Gly	547
ttg Leu 150	agc Ser	gct Ala	gtc Val	act Thr	gaa Glu 155	cac His	atc Ile	cgt Arg	aaa Lys	tgc Cys 160	tgg Trp	gct Ala	tcg Ser	ctg Leu	ttc Phe 165	595
act Thr	tcc Ser	cgt Arg	gcc Ala	att Ile 170	atc Ile	tac Tyr	cgt Arg	ctg Leu	aaa Lys 175	aac Asn	aac Asn	atc Ile	ccc Pro	aat Asn 180	gag Glu	643
ggc Gly	ctc Leu	tcc Ser	atg Met 185	gcg Ala	gta Val	gtt Val	gtt Val	caa Gln 190	aaa Lys	atg Met	gtc Val	aac Asn	tct Ser 195	cgt Arg	gtc Val	691
gca Ala	ggc Gly	gtg Val 200	gca Ala	atc Ile	act Thr	atg Met 205	aat Asn	cct Pro	tcc Ser	aac Asn	ggc Gly	gac Asp 210	cgc Arg	tcg Ser	aag Lys	739
atc Ile	acc Thr 215	atc Ile	gat Asp	tcc Ser	tca Ser	tgg Trp 220	ggg Gly	gtt Val	ggg Gly	gaa Glu 225	atg Met	gtg Val	gtc Val	tca Ser	ggg Gly	787
gaa Glu	gtg Val	aca Thr	cca Pro	gac Asp	aat Asn	atc Ile	ttg Leu	ctg Leu	gac Asp	aag Lys	atc Ile	acg Thr	ctg Leu	cag Gln	gtt Val	835

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230	235	240	245	
gtc tcc gaa cac att gga agc aaa cac gct gaa ctc atc ccc gat gcc	Val Ser Glu His Ile Gly Ser Lys His Ala Glu Leu Ile Pro Asp Ala	883		
	250	255	260	
acc agt gga agc ctc gtg gaa aag ccc gtt gat gaa gaa cgc gca aac	Thr Ser Gly Ser Leu Val Glu Lys Pro Val Asp Glu Glu Arg Ala Asn	931		
	265	270	275	
cgc cgc agt ctg act gat gag gaa atg ctc gct gtg gca caa atg gct	Arg Arg Ser Leu Thr Asp Glu Glu Met Leu Ala Val Ala Gln Met Ala	979		
	280	285	290	
aag cgt gca gaa aaa cac tac aag tgc cca caa gat atc gaa tgg gcg	Lys Arg Ala Glu Lys His Tyr Lys Cys Pro Gln Asp Ile Glu Trp Ala	1027		
	295	300	305	
ctg gac gct gat ctg cca gat gga gaa aac ctt ctg tta ttg caa tcc	Leu Asp Ala Asp Leu Pro Asp Gly Glu Asn Leu Leu Leu Leu Gln Ser	1075		
	310	315	320	325
cgc ccg gaa act atc cac tcc aac ggt gtg aag aag gaa acc cca act	Arg Pro Glu Thr Ile His Ser Asn Gly Val Lys Lys Glu Thr Pro Thr	1123		
	330	335	340	
ccg cag gct gcc aaa acc ata ggc acc ttc gat ttc agc tca atc acc	Pro Gln Ala Ala Lys Thr Ile Gly Thr Phe Asp Phe Ser Ser Ile Thr	1171		
	345	350	355	
gtc gca atg acc ggc acg aag taaaaccacc gcattcttttc gtc	Val Ala Met Thr Gly Thr Lys	1215		
	360			

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<211> 364

<212> PRT

<213> Corynebacterium glutamicum

<400> 84

Met Thr Asn Ser Leu Asn Ile Pro Phe Val Gln Arg Phe Asp Glu Gly	1	5	10	15
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Thr Met Thr Asp Ala Gly Met Pro Val Pro Pro Gly Phe Val Val Thr	35	40	45	
Thr Ala Ser Phe Asp Glu Phe Ile Arg Glu Ala Gly Val Ala Glu His	50	55	60	
Ile Asp Lys Phe Leu Asn Asp Leu Asp Ala Glu Asp Val Lys Glu Val	65	70	75	80
Asp Arg Val Ser Ala Ile Ile Arg Asp Glu Leu Cys Ser Leu Asp Val	85	90	95	
Pro Glu Asn Ala Arg Phe Ala Val His Gln Ala Tyr Arg Asp Leu Met	100	105	110	

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

<210> 85
 <211> 1860
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1837)
 <223> RXN00635

<400> 85

128

atc ggg cat gcg ctg ggt ggt aag cag tac atc cag cat gag aat ccg 835
Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile Gln His Glu Asn Pro
230 235 240 245
ttt gag gtc ggc atg tct ggc ctg ctt ggt tac ggc gcc tgc gtg gat 883
Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr Gly Ala Cys Val Asp
250 255 260
gcg tcc aat gag gcg gat ctg ctg att cta ttg ggt acg gat ttc cct 931
Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu Gly Thr Asp Phe Pro
265 270 275
tat tct gat ttc ctt cct aaa gac aac gtt gcc cag gtg gat atc aac 979
Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala Gln Val Asp Ile Asn
280 285 290
ggt gcg cac att ggt cga cgt acc acg gtg aag tat ccg gtg acc ggt 1027
Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys Tyr Pro Val Thr Gly
295 300 305
gat gtt gct gca aca atc gaa aat att ttg cct cat gtg aag gaa aaa 1075
Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro His Val Lys Glu Lys
310 315 320 325
aca gat cgt tcc ttc ctt gat cgg atg ctc aag gca cac gag cgt aag 1123
Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys Ala His Glu Arg Lys
330 335 340
ttg agc tcg gtg gta gag acg tac aca cat aac gtc gag aag cat gtg 1171
Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn Val Glu Lys His Val
345 350 355
cct att cac cct gaa tac gtt gcc tct att ttg aac gag ctg gcg gat 1219
Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu Asn Glu Leu Ala Asp
360 365 370
aag gat gcg gtg ttt act gtg gat acc ggc atg tgc aat gtg tgg cat 1267
Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met Cys Asn Val Trp His
375 380 385
gcg agg tac atc gag aat ccg gag gga acg cgc gac ttt gtg ggt tca 1315
Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg Asp Phe Val Gly Ser
390 395 400 405
ttc cgc cac ggc acg atg gct aat gcg ttg cct cat gcg att ggt gcg 1363
Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro His Ala Ile Gly Ala
410 415 420
caa agt gtt gat cga aac cgc cag gtg atc gcg atg tgt ggc gat ggt 1411
Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala Met Cys Gly Asp Gly
425 430 435
ggt ttg ggc atg ctg ctg ggt gag ctt ctg acc gtt aag ctg cac caa 1459
Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr Val Lys Leu His Gln
440 445 450
ctt ccg ctg aag gct gtg gtg ttt aac aac agt tct ttg ggc atg gtg 1507
Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser Ser Leu Gly Met Val
455 460 465

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aag ttg gag atg ctc gtg gag gga cag cca gaa ttt ggt act gac cat 1555
Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu Phe Gly Thr Asp His
470 475 480 485

gag gaa gtg aat ttc gca gag att gcg gcg gct gcg ggt atc aaa tcg 1603
Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala Ala Gly Ile Lys Ser
490 495 500

gta cgc atc acc gat ccg aag aaa gtt cgc gag cag cta gct gag gca 1651
Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu Gln Leu Ala Glu Ala
505 510 515

ttg gca tat cct gga cct gta ctg atc gat atc gtc acg gat cct aat 1699
Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile Val Thr Asp Pro Asn
520 525 530

gcg ctg tcg atc cca cca acc atc acg tgg gaa cag gtc atg gga ttc 1747
Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu Gln Val Met Gly Phe
535 540 545

agc aag gcg gcc acc cga acc gtc ttt ggt gga gga gta gga gcg atg 1795
Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly Gly Val Gly Ala Met
550 555 560 565

atc gat ctg gcc cgt tcg aac ata agg aat att cct act cca 1837
Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile Pro Thr Pro
570 575

tgatgattga tacacctgct gtt 1860

<210> 86

<211> 579

<212> PRT

<213> Corynebacterium glutamicum

<400> 86

Met Ala His Ser Tyr Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln
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Gly Val Lys Arg Ile Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile
20 25 30

Val Asp Ala Val Arg Gln Ser Asp Ile Glu Trp Val His Val Arg Asn
35 40 45

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

Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu
65 70 75 80

Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala
85 90 95

Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln
100 105 110

Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
115 120 125

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Met	Val	Asn	Gly	Gly	Glu	Gln	Gly	Glu	Arg	Ile	Leu	His	His	Ala	Ile
130						135					140				
Gln	Ser	Thr	Met	Ala	Gly	Lys	Gly	Val	Ser	Val	Val	Val	Ile	Pro	Gly
145					150					155					160
Asp	Ile	Ala	Lys	Glu	Asp	Ala	Gly	Asp	Gly	Thr	Tyr	Ser	Asn	Ser	Thr
				165					170					175	
Ile	Ser	Ser	Gly	Thr	Pro	Val	Val	Phe	Pro	Asp	Pro	Thr	Glu	Ala	Ala
			180					185					190		
Ala	Leu	Val	Glu	Ala	Ile	Asn	Asn	Ala	Lys	Ser	Val	Thr	Leu	Phe	Cys
		195					200					205			
Gly	Ala	Gly	Val	Lys	Asn	Ala	Arg	Ala	Gln	Val	Leu	Glu	Leu	Ala	Glu
	210					215					220				
Lys	Ile	Lys	Ser	Pro	Ile	Gly	His	Ala	Leu	Gly	Gly	Lys	Gln	Tyr	Ile
225					230					235					240
Gln	His	Glu	Asn	Pro	Phe	Glu	Val	Gly	Met	Ser	Gly	Leu	Leu	Gly	Tyr
				245					250					255	
Gly	Ala	Cys	Val	Asp	Ala	Ser	Asn	Glu	Ala	Asp	Leu	Leu	Ile	Leu	Leu
			260					265					270		
Gly	Thr	Asp	Phe	Pro	Tyr	Ser	Asp	Phe	Leu	Pro	Lys	Asp	Asn	Val	Ala
		275					280					285			
Gln	Val	Asp	Ile	Asn	Gly	Ala	His	Ile	Gly	Arg	Arg	Thr	Thr	Val	Lys
	290					295					300				
Tyr	Pro	Val	Thr	Gly	Asp	Val	Ala	Ala	Thr	Ile	Glu	Asn	Ile	Leu	Pro
305					310					315					320
His	Val	Lys	Glu	Lys	Thr	Asp	Arg	Ser	Phe	Leu	Asp	Arg	Met	Leu	Lys
				325					330					335	
Ala	His	Glu	Arg	Lys	Leu	Ser	Ser	Val	Val	Glu	Thr	Tyr	Thr	His	Asn
			340					345					350		
Val	Glu	Lys	His	Val	Pro	Ile	His	Pro	Glu	Tyr	Val	Ala	Ser	Ile	Leu
		355					360					365			
Asn	Glu	Leu	Ala	Asp	Lys	Asp	Ala	Val	Phe	Thr	Val	Asp	Thr	Gly	Met
		370				375					380				
Cys	Asn	Val	Trp	His	Ala	Arg	Tyr	Ile	Glu	Asn	Pro	Glu	Gly	Thr	Arg
385					390					395					400
Asp	Phe	Val	Gly	Ser	Phe	Arg	His	Gly	Thr	Met	Ala	Asn	Ala	Leu	Pro
				405					410					415	
His	Ala	Ile	Gly	Ala	Gln	Ser	Val	Asp	Arg	Asn	Arg	Gln	Val	Ile	Ala
			420					425					430		
Met	Cys	Gly	Asp	Gly	Gly	Leu	Gly	Met	Leu	Leu	Gly	Glu	Leu	Leu	Thr
		435					440					445			
Val	Lys	Leu	His	Gln	Leu	Pro	Leu	Lys	Ala	Val	Val	Phe	Asn	Asn	Ser

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450		455		460
Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu				
465		470		480
Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala				
	485		490	495
Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu				
	500		505	510
Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile				
	515		520	525
Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu				
	530		535	540
Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly				
545		550		560
Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile				
	565		570	575
Pro Thr Pro				

<210> 87
 <211> 552
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (88)..(552)
 <223> FRXA02807

<400> 87
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 caatagccat aacgttgagg agttcagatg gca cac agc tac gca gaa caa tta 114
 Met Ala His Ser Tyr Ala Glu Gln Leu
 1 5
 att gac act ttg gaa gct caa ggt gtg aag cga att tat ggt ttg gtg 162
 Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile Tyr Gly Leu Val
 10 15 20 25
 ggt gac agc ctt aat ccg atc gtg gat gct gtc cgc caa tca gat att 210
 Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg Gln Ser Asp Ile
 30 35 40
 gag tgg gtg cac gtt cga aat gag gaa gcg gcg gcg ttt gca gcc ggt 258
 Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala Phe Ala Ala Gly
 45 50 55
 gcg gaa tcg ttg atc act ggg gag ctg gca gta tgt gct gct tct tgt 306
 Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys Ala Ala Ser Cys
 60 65 70
 ggt cct gga aac aca cac ctg att cag ggt ctt tat gat tcg cat cga 354

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Gly	Pro	Gly	Asn	Thr	His	Leu	Ile	Gln	Gly	Leu	Tyr	Asp	Ser	His	Arg	
	75					80					85					
aat	ggt	gcg	aag	gtg	ttg	gcc	atc	gct	agc	cat	att	ccg	agt	gcc	cag	402
Asn	Gly	Ala	Lys	Val	Leu	Ala	Ile	Ala	Ser	His	Ile	Pro	Ser	Ala	Gln	
90					95					100					105	
att	ggt	tcg	acg	ttc	ttc	cag	gaa	acg	cat	ccg	gag	att	ttg	ttt	aag	450
Ile	Gly	Ser	Thr	Phe	Phe	Gln	Glu	Thr	His	Pro	Glu	Ile	Leu	Phe	Lys	
				110					115					120		
gaa	tgc	tct	ggt	tac	tgc	gag	atg	gtg	aat	ggt	ggt	gag	cag	ggt	gaa	498
Glu	Cys	Ser	Gly	Tyr	Cys	Glu	Met	Val	Asn	Gly	Gly	Glu	Gln	Gly	Glu	
			125					130					135			
cgc	att	ttg	cat	cac	gcg	att	cag	tcc	acc	atg	gcg	ggt	aaa	ggt	gtg	546
Arg	Ile	Leu	His	His	Ala	Ile	Gln	Ser	Thr	Met	Ala	Gly	Lys	Gly	Val	
		140					145					150				
tcg	gtg															552
Ser	Val															
	155															

<210> 88

<211> 155

<212> PRT

<213> Corynebacterium glutamicum

<400> 88

Met	Ala	His	Ser	Tyr	Ala	Glu	Gln	Leu	Ile	Asp	Thr	Leu	Glu	Ala	Gln	
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Gly	Val	Lys	Arg	Ile	Tyr	Gly	Leu	Val	Gly	Asp	Ser	Leu	Asn	Pro	Ile	
			20					25					30			
Val	Asp	Ala	Val	Arg	Gln	Ser	Asp	Ile	Glu	Trp	Val	His	Val	Arg	Asn	
		35					40					45				
Glu	Glu	Ala	Ala	Ala	Phe	Ala	Ala	Gly	Ala	Glu	Ser	Leu	Ile	Thr	Gly	
	50					55					60					
Glu	Leu	Ala	Val	Cys	Ala	Ala	Ser	Cys	Gly	Pro	Gly	Asn	Thr	His	Leu	
65				70					75						80	
Ile	Gln	Gly	Leu	Tyr	Asp	Ser	His	Arg	Asn	Gly	Ala	Lys	Val	Leu	Ala	
			85						90					95		
Ile	Ala	Ser	His	Ile	Pro	Ser	Ala	Gln	Ile	Gly	Ser	Thr	Phe	Phe	Gln	
		100						105					110			
Glu	Thr	His	Pro	Glu	Ile	Leu	Phe	Lys	Glu	Cys	Ser	Gly	Tyr	Cys	Glu	
		115					120					125				
Met	Val	Asn	Gly	Gly	Glu	Gln	Gly	Glu	Arg	Ile	Leu	His	His	Ala	Ile	
	130					135					140					
Gln	Ser	Thr	Met	Ala	Gly	Lys	Gly	Val	Ser	Val						
145					150					155						

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PCT/IB00/00943

<210> 89
 <211> 944
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(921)
 <223> FRXA00635

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 cag gtg gat atc aac ggt gcg cac att ggt cga cgt acc acg gtg aag 96
 Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
 20 25 30
 tat ccg gtg acc ggt gat gtt gct gca aca atc gaa aat att ttg cct 144
 Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
 35 40 45
 cat gtg aag gaa aaa aca gat cgt tcc ttc ctt gat cgg atg ctc aag 192
 His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
 50 55 60
 gca cac gag cgt aag ttg agc tcg gtg gta gag acg tac aca cat aac 240
 Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
 65 70 75 80
 gtc gag aag cat gtg cct att cac cct gaa tac gtt gcc tct att ttg 288
 Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
 85 90 95
 aac gag ctg gcg gat aag gat gcg gtg ttt act gtg gat acc ggc atg 336
 Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
 100 105 110
 tgc aat gtg tgg cat gcg agg tac atc gag aat ccg gag gga acg cgc 384
 Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
 115 120 125
 gac ttt gtg ggt tca ttc cgc cac ggc acg atg gct aat gcg ttg cct 432
 Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
 130 135 140
 cat gcg att ggt gcg caa agt gtt gat cga aac cgc cag gtg atc gcg 480
 His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
 145 150 155 160
 atg tgt ggc gat ggt ggt ttg ggc atg ctg ctg ggt gag ctt ctg acc 528
 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
 165 170 175
 gtt aag ctg cac caa ctt ccg ctg aag gct gtg gtg ttt aac aac agt 576
 Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
 180 185 190
 tct ttg ggc atg gtg aag ttg gag atg ctc gtg gag gga cag cca gaa 624
 Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu

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195	200	205	
ttt ggt act gac cat gag gaa gtg aat ttc gca gag att gcg gcg gct			672
Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala			
210	215	220	
gcg ggt atc aaa tcg gta cgc atc acc gat ccg aag aaa gtt cgc gag			720
Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu			
225	230	235	240
cag cta gct gag gca ttg gca tat cct gga cct gta ctg atc gat atc			768
Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile			
	245	250	255
gtc acg gat cct aat gcg ctg tcg atc cca cca acc atc acg tgg gaa			816
Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu			
	260	265	270
cag gtc atg gga ttc agc aag gcg gcc acc cga acc gtc ttt ggt gga			864
Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly			
	275	280	285
gga gta gga gcg atg atc gat ctg gcc cgt tcg aac ata agg aat att			912
Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile			
	290	295	300
cct act cca tgatgattga tacacctgct gtt			944
Pro Thr Pro			
305			

<210> 90

<211> 307

<212> PRT

<213> Corynebacterium glutamicum

<400> 90

Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala	
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Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys	
20	30
Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro	
35	45
His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys	
50	60
Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn	
65	80
Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu	
85	95
Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met	
100	110
Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg	
115	125

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PCT/IB00/00943

Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
 130 135 140
 His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
 145 150 155 160
 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
 165 170 175
 Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
 180 185 190
 Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu
 195 200 205
 Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala
 210 215 220
 Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu
 225 230 235 240
 Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile
 245 250 255
 Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu
 260 265 270
 Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly
 275 280 285
 Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile
 290 295 300
 Pro Thr Pro
 305

<210> 91
 <211> 954
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(931)
 <223> RXN03044

<400> 91
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 ccagcgcacc ggtgactcca tctgggcagc agccgatcag atg gca cgt ggc ttc 115
 Met Ala Arg Gly Phe
 1 5
 ctc ttg ggc gct acc gca ggt cgc acc acc ctg acc ggt gaa ggc ctc 163
 Leu Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu
 10 15 20
 cag cac atg gat gga cac tcc cct gtc ttg gct tcc acc aac gag ggt 211
 Gln His Met Asp Gly His Ser Pro Val Leu Ala Ser Thr Asn Glu Gly
 25 30 35

gtc gag acc tac gac cca tcc ttt gcg tac gag atc gca cac ctg gtt	259
Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu Ile Ala His Leu Val	
40 45 50	
cac cgt ggc atc gac cgc atg tac ggc cca ggc aag ggt gaa gat gtt	307
His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly Lys Gly Glu Asp Val	
55 60 65	
atc tac tac atc acc atc tac aac gag cca acc cca cag cca gct gag	355
Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr Pro Gln Pro Ala Glu	
70 75 80 85	
cca gaa gga ctg gac gta gaa ggc ctg cac aag ggc atc tac ctc tac	403
Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys Gly Ile Tyr Leu Tyr	
90 95 100	
tcc cgc ggt gaa ggc acc ggc cat gag gca aac atc ttg gct tcc ggt	451
Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn Ile Leu Ala Ser Gly	
105 110 115	
gtt ggt atg cag tgg gct ctc aag gct gca tcc atc ctt gag gct gac	499
Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser Ile Leu Glu Ala Asp	
120 125 130	
tac gga gtt cgt gcc aac att tac tcc gct act tct tgg gtt aac ttg	547
Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr Ser Trp Val Asn Leu	
135 140 145	
gct cgc gat ggc gct gct cgt aac aag gca cag ctg cgc aac cca ggt	595
Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln Leu Arg Asn Pro Gly	
150 155 160 165	
gca gat gct ggc gag gca ttc gta acc acc cag ctg aag cag acc tcc	643
Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln Leu Lys Gln Thr Ser	
170 175 180	
ggc cca tac gtt gca gtg tct gac ttc tcc act gat ctg cca aac cag	691
Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln	
185 190 195	
atc cgt gaa tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc	739
Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly	
200 205 210	
ttc ggt ttc tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc	787
Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile	
215 220 225	
gac gct gag tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa	835
Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu	
230 235 240 245	
ggc aag atc gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag	883
Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys	
250 255 260	
ttg gat gat cct acg agt gtt tcc gta gat cca aac gct cct gag gaa	931
Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu	
265 270 275	

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PCT/IB00/00943

taaatcacct caaggacag ata

954

<210> 92

<211> 277

<212> PRT

<213> Corynebacterium glutamicum

<400> 92

Met	Ala	Arg	Gly	Phe	Leu	Leu	Gly	Ala	Thr	Ala	Gly	Arg	Thr	Thr	Leu
1				5					10					15	

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

Ser	Thr	Asn	Glu	Gly	Val	Glu	Thr	Tyr	Asp	Pro	Ser	Phe	Ala	Tyr	Glu
		35					40					45			

Ile	Ala	His	Leu	Val	His	Arg	Gly	Ile	Asp	Arg	Met	Tyr	Gly	Pro	Gly
	50					55					60				

Lys	Gly	Glu	Asp	Val	Ile	Tyr	Tyr	Ile	Thr	Ile	Tyr	Asn	Glu	Pro	Thr
65					70					75					80

Pro	Gln	Pro	Ala	Glu	Pro	Glu	Gly	Leu	Asp	Val	Glu	Gly	Leu	His	Lys
				85					90					95	

Gly	Ile	Tyr	Leu	Tyr	Ser	Arg	Gly	Glu	Gly	Thr	Gly	His	Glu	Ala	Asn
			100					105					110		

Ile	Leu	Ala	Ser	Gly	Val	Gly	Met	Gln	Trp	Ala	Leu	Lys	Ala	Ala	Ser
		115					120					125			

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

Ser	Trp	Val	Asn	Leu	Ala	Arg	Asp	Gly	Ala	Ala	Arg	Asn	Lys	Ala	Gln
145				150						155					160

Leu	Arg	Asn	Pro	Gly	Ala	Asp	Ala	Gly	Glu	Ala	Phe	Val	Thr	Thr	Gln
				165					170					175	

Leu	Lys	Gln	Thr	Ser	Gly	Pro	Tyr	Val	Ala	Val	Ser	Asp	Phe	Ser	Thr
			180					185					190		

Asp	Leu	Pro	Asn	Gln	Ile	Arg	Glu	Trp	Val	Pro	Gly	Asp	Tyr	Thr	Val
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Leu	Gly	Ala	Asp	Gly	Phe	Gly	Phe	Ser	Asp	Thr	Arg	Pro	Ala	Ala	Arg
	210					215					220				

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

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

Ala	Glu	Lys	Phe	Lys	Leu	Asp	Asp	Pro	Thr	Ser	Val	Ser	Val	Asp	Pro
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Asn Ala Pro Glu Glu

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275

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 tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc ttc ggt ttc 96
 Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
 20 25 30
 tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc gac gct gag 144
 Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
 35 40 45
 tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa ggc aag atc 192
 Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
 50 55 60
 gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag ttg gat gat 240
 Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
 65 70 75 80
 cct acg agt gtt tcc gta gat cca aac gct cct gag gaa taaatcacct 289
 Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
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 35 40 45
 Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
 50 55 60
 Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
 65 70 75 80

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Met Ala Arg Gly Phe																15
1																5
ttt ttg ggc gct acc gca ggt cgc acc acc ttg acc ggt gaa ggc ctc																163
Phe Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu																20
10																15
cag cac atg gat gga cac tcc cct gtt ttg gct tcc acc aac gag ggt																211
Gln His Met Asp Gly His Ser Pro Val Leu Ala Ser Thr Asn Glu Gly																25
30																35
gtc gag acc tac gac cca tcc ttt gcg tac gag atc gca cac ctg gtt																259
Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu Ile Ala His Leu Val																40
45																50
cac cgt ggc atc gac cgc atg tac ggc cca ggc aag ggt gaa gat gtt																307
His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly Lys Gly Glu Asp Val																55
60																65
atc tac tac atc acc atc tac aac gag cca acc cca cag cca gct gag																355
Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr Pro Gln Pro Ala Glu																70
75																80
cca gaa gga ctg gac gta gaa ggc ctg cac aag ggc atc tac ctc tac																403
Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys Gly Ile Tyr Leu Tyr																90
95																100
tcc cgc ggt gaa ggc acc ggc cat gag gca aac atc ttg gct tcc ggt																451
Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn Ile Leu Ala Ser Gly																105
110																115
gtt ggt atg cag tgg gct ctc aag gct gca tcc atc ctt gag gct gac																499
Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser Ile Leu Glu Ala Asp																120
125																130
tac gga gtt cgt gcc aac att tac tcc gct act tct tgg gtt aac ttg																547
Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr Ser Trp Val Asn Leu																135
140																145
gct cgc gat ggc gct gct cgt aac aag gca cag ctg cgc aac cca ggt																595
Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln Leu Arg Asn Pro Gly																150
155																160
165																

gca gat gct ggc gag gca ttc gta acc acc cag ctg aag cag acc tcc 643
 Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln Leu Lys Gln Thr Ser
 170 175 180

ggc cca tac gtt gca gtg tct gac ttc tcc act gat ctg cca aac cag 691
 Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln
 185 190 195

atc cgt gaa tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc 739
 Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly
 200 205 210

ttc ggt ttc tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc 787
 Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile
 215 220 225

gac gct gag tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa 835
 Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu
 230 235 240 245

ggc aag atc gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag 883
 Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys
 250 255 260

ttg gat gat cct acg agt gtt tcc gta gat cca aac gct cct gag gaa 931
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 <213> Corynebacterium glutamicum

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Ser Thr Asn Glu Gly Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu
 35 40 45

Ile Ala His Leu Val His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly
 50 55 60

Lys Gly Glu Asp Val Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr
 65 70 75 80

Pro Gln Pro Ala Glu Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys
 85 90 95

Gly Ile Tyr Leu Tyr Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn
 100 105 110

Ile Leu Ala Ser Gly Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser
 115 120 125

Ile Leu Glu Ala Asp Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr
 130 135 140
 Ser Trp Val Asn Leu Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln
 145 150 155 160
 Leu Arg Asn Pro Gly Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln
 165 170 175
 Leu Lys Gln Thr Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr
 180 185 190
 Asp Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val
 195 200 205
 Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg
 210 215 220
 Arg Phe Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn
 225 230 235 240
 Ser Leu Ala Arg Glu Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala
 245 250 255
 Ala Glu Lys Phe Lys Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro
 260 265 270
 Asn Ala Pro Glu Glu
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(508)
 <223> RXN03086

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 Met Ala Asp Gln Ala
 1 5
 aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc 163
 Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg
 10 15 20
 gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac 211
 Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn
 25 30 35
 gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa 259
 Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu
 40 45 50

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cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307
 Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys
 55 60 65

cgc gta tct ctt ccc cca atg acg tca acc gac tac gtc aac acc att 355
 Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile
 70 75 80 85

cca acc tct atg gaa cct gaa ttc cca ggc gat gag gaa atg gag aag 403
 Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp Glu Glu Met Glu Lys
 90 95 100

cgt tac cgt cgt tgg att cgc tgg aac gca gcc atc atg gtt cac cgc 451
 Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala Ile Met Val His Arg
 105 110 115

gct cag cga cca ggc atc ggc gtc ggc gga cac att tcc act tac gca 499
 Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His Ile Ser Thr Tyr Ala
 120 125 130

ggc gca gcc 508
 Gly Ala Ala
 135

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 <213> Corynebacterium glutamicum

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 20 25 30

Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln
 35 40 45

Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
 50 55 60

Arg Ala Ser Ala Lys Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp
 65 70 75 80

Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp
 85 90 95

Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala
 100 105 110

Ile Met Val His Arg Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His
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Ile Ser Thr Tyr Ala Gly Ala Ala
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<210> 99
 <211> 508

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(508)

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				Met Ala Asp Gln Ala	
				1 5	

aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc	163
Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg	
10 15 20	

gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac	211
Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn	
25 30 35	

gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa	259
Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu	
40 45 50	

cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag	307
Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys	
55 60 65	

cgc gta tct ctt ccc cca atg acg tca acc gac tac gtc aac acc att	355
Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile	
70 75 80 85	

cca acc tct atg gaa cct gaa ttc cca ggc gat gag gaa atg gag aag	403
Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp Glu Glu Met Glu Lys	
90 95 100	

cgt tac cgt cgt tgg att cgc tgg aac gca gcc atc atg gtt cac cgc	451
Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala Ile Met Val His Arg	
105 110 115	

gct cag cga cca ggc atc ggc gtc ggc gga cac att tcc act tac gca	499
Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His Ile Ser Thr Tyr Ala	
120 125 130	

ggc gca gcc	508
Gly Ala Ala	
135	

<210> 100

<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 100

Met Ala Asp Gln Ala Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn
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Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp
 20 25 30
 Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln
 35 40 45
 Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
 50 55 60
 Arg Ala Ser Ala Lys Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp
 65 70 75 80
 Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp
 85 90 95
 Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala
 100 105 110
 Ile Met Val His Arg Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His
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 Ile Ser Thr Tyr Ala Gly Ala Ala
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<210> 101
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <223> RXN03043

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 1 5 10 15
 ccg tcc tac cct cac cca cac ggt atg aag gac ttc tgg gag ttc cca 96
 Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro
 20 25 30
 act gtg tcc atg ggt ctt ggc cca atg gat gcc att tac cag gca cgt 144
 Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg
 35 40 45
 ttc aac cgc tac ctc gaa aac cgt ggc atc aag gac acc tct gac cag 192
 Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
 50 55 60
 cac gtc tgg gcc ttc ctt ggc gac ggc gaa atg gac gag cca gaa tca 240
 His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
 65 70 75 80
 cgt ggt ctc atc cag cag gct gca ctg aac aac ctg gac aac ctg acc 288
 Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
 85 90 95
 ttc gtg gtt aac tgc aac ctg cag cgt ctc gac gga cct gtc cgc ggt 336

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aac	acc	aag	atc	atc	cag	gaa	ctc	gag	tcc	ttc	ttc	cgt	ggc	gca	ggc	384
Asn	Thr	Lys	Ile	Ile	Gln	Glu	Leu	Glu	Ser	Phe	Phe	Arg	Gly	Ala	Gly	
		115					120					125				
tgg	tct	gtg	atc	aag	gtt	gtt	tgg	ggc	cgc	gag	tgg	gat	gaa	ctt	ctg	432
Trp	Ser	Val	Ile	Lys	Val	Val	Trp	Gly	Arg	Glu	Trp	Asp	Glu	Leu	Leu	
	130						135				140					
gag	aag	gac	cag	gat	ggc	gca	ctt	gtt	gag	atc	atg	aac	aac	acc	tcc	480
Glu	Lys	Asp	Gln	Asp	Gly	Ala	Leu	Val	Glu	Ile	Met	Asn	Asn	Thr	Ser	
145					150					155					160	
gat	ggc	gac	tac	cag	acc	ttc	aag	gct	aac	gac	ggc	gca	tat	gtt	cgt	528
Asp	Gly	Asp	Tyr	Gln	Thr	Phe	Lys	Ala	Asn	Asp	Gly	Ala	Tyr	Val	Arg	
				165					170					175		
gag	cac	ttc	ttc	gga	cgt	gac	cca	cgc	acc	gca	aag	ctc	gtt	gag	aac	576
Glu	His	Phe	Phe	Gly	Arg	Asp	Pro	Arg	Thr	Ala	Lys	Leu	Val	Glu	Asn	
			180					185					190			
atg	acc	gac	gaa	gaa	atc	tgg	aag	ctt	cca	cgt	ggc	ggc	cac	gat	tac	624
Met	Thr	Asp	Glu	Glu	Ile	Trp	Lys	Leu	Pro	Arg	Gly	Gly	His	Asp	Tyr	
		195					200					205				
cgc	aag	gtt	tac	gca	gcc	tac	aag	cga	gct	ctt	gag	acc	aag	gat	cgc	672
Arg	Lys	Val	Tyr	Ala	Ala	Tyr	Lys	Arg	Ala	Leu	Glu	Thr	Lys	Asp	Arg	
	210					215					220					
cca	acc	gtc	atc	ctt	gct	cac	acc	att	aag	ggc	tac	gga	ctc	ggc	cac	720
Pro	Thr	Val	Ile	Leu	Ala	His	Thr	Ile	Lys	Gly	Tyr	Gly	Leu	Gly	His	
225					230					235					240	
aac	ttc	gaa	ggc	cgt	aac	gca	acc	cac	cag	atg	aag	aag	ctg	acg	ctt	768
Asn	Phe	Glu	Gly	Arg	Asn	Ala	Thr	His	Gln	Met	Lys	Lys	Leu	Thr	Leu	
				245					250					255		
gat	gat	ctg	aag	ttg	ttc	cgc	gac	aag	cag	ggc	atc	cca	atc	acc	gat	816
Asp	Asp	Leu	Lys	Leu	Phe	Arg	Asp	Lys	Gln	Gly	Ile	Pro	Ile	Thr	Asp	
			260					265					270			
gag	cag	ctg	gag	aag	gat	cct	tac	ctt	cct	cct	tac	tac	cac	cca	ggc	864
Glu	Gln	Leu	Glu	Lys	Asp	Pro	Tyr	Leu	Pro	Pro	Tyr	Tyr	His	Pro	Gly	
		275					280					285				
gaa	gac	gct	cct	gaa	atc	aag	tac	atg	aag	gaa	cgt	cgc	gca	gcg	ctc	912
Glu	Asp	Ala	Pro	Glu	Ile	Lys	Tyr	Met	Lys	Glu	Arg	Arg	Ala	Ala	Leu	
	290					295					300					
ggc	ggc	tac	ctg	cca	gag	cgt	cgt	gag	aac	tac	gat	cca	att	cag	gtt	960
Gly	Gly	Tyr	Leu	Pro	Glu	Arg	Arg	Glu	Asn	Tyr	Asp	Pro	Ile	Gln	Val	
305					310					315					320	
cca	cca	ctg	gat	aag	ctt	cgc	tct	gtc	cgt	aag	ggc	tcc	ggc	aag	cag	1008
Pro	Pro	Leu	Asp	Lys	Leu	Arg	Ser	Val	Arg	Lys	Gly	Ser	Gly	Lys	Gln	
				325					330					335		
cag	atc	gct	acc	acc	atg	gcg	act	gtt	cgt	acc	ttc	aag	gaa	ctg	atg	1056
Gln	Ile	Ala	Thr	Thr	Met	Ala	Thr	Val	Arg	Thr	Phe	Lys	Glu	Leu	Met	

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340	345	350	
cgc gat aag ggc ttg gct gat	cgc ctt gtc cca atc att	cct gat gag	1104
Arg Asp Lys Gly Leu Ala Asp	Arg Leu Val Pro Ile Ile	Pro Asp Glu	
355	360	365	
gca cgt acc ttc ggt ctt gac	tct tgg ttc cca acc ttg	aag atc tac	1152
Ala Arg Thr Phe Gly Leu Asp	Ser Trp Phe Pro Thr Leu	Lys Ile Tyr	
370	375	380	
aac ccg cac ggt cag aac tac	gtg cct gtt gac cac gac	ctg atg ctc	1200
Asn Pro His Gly Gln Asn Tyr	Val Pro Val Asp His Asp	Leu Met Leu	
385	390	400	
tcc tac cgt gag gca cct gaa	gga cag atc ctg cac gaa	ggc atc aac	1248
Ser Tyr Arg Glu Ala Pro Glu	Gly Gln Ile Leu His Glu	Gly Ile Asn	
405	410	415	
gag gct ggt tcc gtg gca tcg	ttc atc gct gcg ggt acc	tcc tac gcc	1296
Glu Ala Gly Ser Val Ala Ser	Phe Ile Ala Ala Gly Thr	Ser Tyr Ala	
420	425	430	
acc cac ggc aag gcc atg att	ccg ctg tac atc ttc tac	tcg atg ttc	1344
Thr His Gly Lys Ala Met Ile	Pro Leu Tyr Ile Phe Tyr	Ser Met Phe	
435	440	445	
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Gly Ile Pro Ala His Arg			
450			

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<211> 454

<212> PRT

<213> Corynebacterium glutamicum

<400> 102

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Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg	
35 40 45	
Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln	
50 55 60	
His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser	
65 70 75 80	
Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr	
85 90 95	
Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly	
100 105 110	
Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly	
115 120 125	

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Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu
 130 135 140
 Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser
 145 150 155 160
 Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg
 165 170 175
 Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn
 180 185 190
 Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr
 195 200 205
 Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg
 210 215 220
 Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His
 225 230 235 240
 Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu
 245 250 255
 Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp
 260 265 270
 Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly
 275 280 285
 Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu
 290 295 300
 Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val
 305 310 315 320
 Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln
 325 330 335
 Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met
 340 345 350
 Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu
 355 360 365
 Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr
 370 375 380
 Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu
 385 390 395 400
 Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn
 405 410 415
 Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr Ser Tyr Ala
 420 425 430
 Thr His Gly Lys Ala Met Ile Pro Leu Tyr Ile Phe Tyr Ser Met Phe
 435 440 445
 Gly Ile Pro Ala His Arg

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450

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (1)..(1287)
 <223> FRXA02897

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 ccg tcc tac cct cac cca cac ggt atg aag gac ttc tgg gag ttc cca 96
 Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro
 20 25 30
 act gtg tcc atg ggt ctt ggc cca atg gat gcc att tac cag gca cgt 144
 Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg
 35 40 45
 ttc aac cgc tac ctc gaa aac cgt ggc atc aag gac acc tct gac cag 192
 Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
 50 55 60
 cac gtc tgg gcc ttc ctt ggc gac ggc gaa atg gac gag cca gaa tca 240
 His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
 65 70 75 80
 cgt ggt ctc atc cag cag gct gca ctg aac aac ctg gac aac ctg acc 288
 Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
 85 90 95
 ttc gtg gtt aac tgc aac ctg cag cgt ctc gac gga cct gtc cgc ggt 336
 Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly
 100 105 110
 aac acc aag atc atc cag gaa ctc gag tcc ttc ttc cgt ggc gca ggc 384
 Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly
 115 120 125
 tgg tct gtg atc aag gtt gtt tgg ggt cgc gag tgg gat gaa ctt ctg 432
 Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu
 130 135 140
 gag aag gac cag gat ggt gca ctt gtt gag atc atg aac aac acc tcc 480
 Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser
 145 150 155 160
 gat ggt gac tac cag acc ttc aag gct aac gac ggc gca tat gtt cgt 528
 Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg
 165 170 175
 gag cac ttc ttc gga cgt gac cca cgc acc gca aag ctc gtt gag aac 576
 Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn
 180 185 190

atg acc gac gaa gaa atc tgg aag ctt cca cgt ggc ggc cac gat tac	624
Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr	
195 200 205	
cgc aag gtt tac gca gcc tac aag cga gct ctt gag acc aag gat cgc	672
Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg	
210 215 220	
cca acc gtc atc ctt gct cac acc att aag ggc tac gga ctc ggc cac	720
Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His	
225 230 235 240	
aac ttc gaa ggc cgt aac gca acc cac cag atg aag aag ctg acg ctt	768
Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu	
245 250 255	
gat gat ctg aag ttg ttc cgc gac aag cag ggc atc cca atc acc gat	816
Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp	
260 265 270	
gag cag ctg gag aag gat cct tac ctt cct cct tac tac cac cca ggt	864
Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly	
275 280 285	
gaa gac gct cct gaa atc aag tac atg aag gaa cgt cgc gca gcg ctc	912
Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu	
290 295 300	
ggt ggc tac ctg cca gag cgt cgt gag aac tac gat cca att cag gtt	960
Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val	
305 310 315 320	
cca cca ctg gat aag ctt cgc tct gtc cgt aag ggc tcc ggc aag cag	1008
Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln	
325 330 335	
cag atc gct acc acc atg gcg act gtt cgt acc ttc aag gaa ctg atg	1056
Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met	
340 345 350	
cgc gat aag ggc ttg gct gat cgc ctt gtc cca atc att cct gat gag	1104
Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu	
355 360 365	
gca cgt acc ttc ggt ctt gac tct tgg ttc cca acc ttg aag atc tac	1152
Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr	
370 375 380	
aac ccg cac ggt cag aac tac gtg cct gtt gac cac gac ctg atg ctc	1200
Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu	
385 390 395 400	
tcc tac cgt gag gca cct gaa gga cag atc ctg cac gaa ggc atc aac	1248
Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn	
405 410 415	
gag gct ggt tcc gtg gca tcg ttc atc gct gcg ggt acc	1287
Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr	
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<210> 104
 <211> 429
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 104

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Pro	Ser	Tyr	Pro	His	Pro	His	Gly	Met	Lys	Asp	Phe	Trp	Glu	Phe	Pro
			20					25					30		
Thr	Val	Ser	Met	Gly	Leu	Gly	Pro	Met	Asp	Ala	Ile	Tyr	Gln	Ala	Arg
		35					40					45			
Phe	Asn	Arg	Tyr	Leu	Glu	Asn	Arg	Gly	Ile	Lys	Asp	Thr	Ser	Asp	Gln
	50					55					60				
His	Val	Trp	Ala	Phe	Leu	Gly	Asp	Gly	Glu	Met	Asp	Glu	Pro	Glu	Ser
65					70					75					80
Arg	Gly	Leu	Ile	Gln	Gln	Ala	Ala	Leu	Asn	Asn	Leu	Asp	Asn	Leu	Thr
				85					90					95	
Phe	Val	Val	Asn	Cys	Asn	Leu	Gln	Arg	Leu	Asp	Gly	Pro	Val	Arg	Gly
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Asn	Thr	Lys	Ile	Ile	Gln	Glu	Leu	Glu	Ser	Phe	Phe	Arg	Gly	Ala	Gly
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Trp	Ser	Val	Ile	Lys	Val	Val	Trp	Gly	Arg	Glu	Trp	Asp	Glu	Leu	Leu
	130					135					140				
Glu	Lys	Asp	Gln	Asp	Gly	Ala	Leu	Val	Glu	Ile	Met	Asn	Asn	Thr	Ser
145					150					155					160
Asp	Gly	Asp	Tyr	Gln	Thr	Phe	Lys	Ala	Asn	Asp	Gly	Ala	Tyr	Val	Arg
				165					170					175	
Glu	His	Phe	Phe	Gly	Arg	Asp	Pro	Arg	Thr	Ala	Lys	Leu	Val	Glu	Asn
			180					185					190		
Met	Thr	Asp	Glu	Glu	Ile	Trp	Lys	Leu	Pro	Arg	Gly	Gly	His	Asp	Tyr
		195					200					205			
Arg	Lys	Val	Tyr	Ala	Ala	Tyr	Lys	Arg	Ala	Leu	Glu	Thr	Lys	Asp	Arg
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Pro	Thr	Val	Ile	Leu	Ala	His	Thr	Ile	Lys	Gly	Tyr	Gly	Leu	Gly	His
225					230					235					240
Asn	Phe	Glu	Gly	Arg	Asn	Ala	Thr	His	Gln	Met	Lys	Lys	Leu	Thr	Leu
				245					250					255	
Asp	Asp	Leu	Lys	Leu	Phe	Arg	Asp	Lys	Gln	Gly	Ile	Pro	Ile	Thr	Asp
		260						265					270		
Glu	Gln	Leu	Glu	Lys	Asp	Pro	Tyr	Leu	Pro	Pro	Tyr	Tyr	His	Pro	Gly
		275					280					285			

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Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu
 290 295 300
 Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val
 305 310 315 320
 Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln
 325 330 335
 Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met
 340 345 350
 Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu
 355 360 365
 Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr
 370 375 380
 Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu
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 Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn
 405 410 415
 Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr
 420 425

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (88)..(1110)
 <223> RXN03083

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 Met Ala Lys Arg Ile Val Ile Ile Gly
 1 5
 ggt gga cct gca ggc tat gaa gcc gca ctc gca ggc gct aaa tac ggt 162
 Gly Gly Pro Ala Gly Tyr Glu Ala Ala Leu Ala Gly Ala Lys Tyr Gly
 10 15 20 25
 gca gaa gtt acc gtt att gaa gat gtc gga gtt ggc gga tcc gca gtc 210
 Ala Glu Val Thr Val Ile Glu Asp Val Gly Val Gly Gly Ser Ala Val
 30 35 40
 acc atg gac tgt gta cct tca aag tcc ttc atc gct ggt acc ggt atc 258
 Thr Met Asp Cys Val Pro Ser Lys Ser Phe Ile Ala Gly Thr Gly Ile
 45 50 55
 aaa acc gac ctc cga cgt gct gat gac atg gga ctt aac cgt ggg ctt 306
 Lys Thr Asp Leu Arg Arg Ala Asp Asp Met Gly Leu Asn Arg Gly Leu
 60 65 70

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gga	aaa	gca	cac	cta	gaa	atc	gat	gca	ctg	aac	atc	cgt	gtg	aag	gac	354
Gly	Lys	Ala	His	Leu	Glu	Ile	Asp	Ala	Leu	Asn	Ile	Arg	Val	Lys	Asp	
	75					80					85					
ctt	gcg	aaa	gca	cag	tcc	gaa	gat	atc	ttg	ggc	cag	ctg	cag	cgc	tca	402
Leu	Ala	Lys	Ala	Gln	Ser	Glu	Asp	Ile	Leu	Gly	Gln	Leu	Gln	Arg	Ser	
	90				95					100					105	
gat	gtc	cgc	atg	att	aac	ggg	gtg	ggc	cgc	ttt	gat	gat	tac	aac	acc	450
Asp	Val	Arg	Met	Ile	Asn	Gly	Val	Gly	Arg	Phe	Asp	Asp	Tyr	Asn	Thr	
				110					115					120		
aag	caa	acc	acc	cac	tac	att	aaa	gtc	acc	cac	agc	gat	ggc	tcc	gaa	498
Lys	Gln	Thr	Thr	His	Tyr	Ile	Lys	Val	Thr	His	Ser	Asp	Gly	Ser	Glu	
				125				130					135			
gaa	acc	gtt	gag	tgc	gat	ctg	gtg	ctg	gtt	gca	act	ggg	gca	acc	ccc	546
Glu	Thr	Val	Glu	Cys	Asp	Leu	Val	Leu	Val	Ala	Thr	Gly	Ala	Thr	Pro	
		140					145					150				
cgc	att	ctt	aaa	ggg	gca	gag	cca	gac	ggc	gag	cgc	atc	ttg	acc	tgg	594
Arg	Ile	Leu	Lys	Gly	Ala	Glu	Pro	Asp	Gly	Glu	Arg	Ile	Leu	Thr	Trp	
	155					160					165					
cgt	cag	gtc	tac	gac	att	gaa	gaa	ctc	ccc	acc	cac	ctt	atc	gtg	gtt	642
Arg	Gln	Val	Tyr	Asp	Ile	Glu	Glu	Leu	Pro	Thr	His	Leu	Ile	Val	Val	
	170				175					180					185	
ggg	tcc	ggg	gtg	acc	ggg	gca	gaa	ttt	gtc	tct	gca	ttt	gct	gaa	ctc	690
Gly	Ser	Gly	Val	Thr	Gly	Ala	Glu	Phe	Val	Ser	Ala	Phe	Ala	Glu	Leu	
				190					195					200		
ggc	gtc	aaa	gtc	acc	atg	gtg	gca	tcc	cgt	gac	cgc	att	ttg	cct	cac	738
Gly	Val	Lys	Val	Thr	Met	Val	Ala	Ser	Arg	Asp	Arg	Ile	Leu	Pro	His	
			205					210					215			
gat	gac	gca	gat	gcc	gca	gac	gtg	ctg	gaa	acc	gtt	ctg	gct	gag	cgc	786
Asp	Asp	Ala	Asp	Ala	Ala	Asp	Val	Leu	Glu	Thr	Val	Leu	Ala	Glu	Arg	
		220					225					230				
gga	gta	tcc	ctg	gaa	aag	cat	gcc	cgc	gtg	gag	tct	gtc	acc	cgc	acc	834
Gly	Val	Ser	Leu	Glu	Lys	His	Ala	Arg	Val	Glu	Ser	Val	Thr	Arg	Thr	
	235					240					245					
gaa	gac	ggg	ggc	gtg	tgt	gtt	cgc	act	gct	gac	gga	cga	gaa	atc	tac	882
Glu	Asp	Gly	Gly	Val	Cys	Val	Arg	Thr	Ala	Asp	Gly	Arg	Glu	Ile	Tyr	
	250				255					260					265	
ggg	tct	cac	gca	ttg	atg	act	gtt	ggg	tcc	att	cca	aac	acg	gca	gat	930
Gly	Ser	His	Ala	Leu	Met	Thr	Val	Gly	Ser	Ile	Pro	Asn	Thr	Ala	Asp	
				270					275					280		
ctt	ggc	ctg	gag	aac	atc	ggg	gtt	gag	ctg	gca	cca	tcc	ggc	cat	atc	978
Leu	Gly	Leu	Glu	Asn	Ile	Gly	Val	Glu	Leu	Ala	Pro	Ser	Gly	His	Ile	
			285					290					295			
aag	gtt	gac	cgg	tct	ccc	gca	cca	aca	tcc	ccg	gtg	tgt	acg	cag	cag	1026
Lys	Val	Asp	Arg	Ser	Pro	Ala	Pro	Thr	Ser	Pro	Val	Cys	Thr	Gln	Gln	
		300					305					310				
gtg	act	gta	ctg	acc	tat	tcc	cac	tgg	cgt	ccg	ttg	cag	cga	tgc	agg	1074

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Val Thr Val Leu Thr Tyr Ser His Trp Arg Pro Leu Gln Arg Cys Arg
 315 320 325

gcc gta tcg cca tgt atc acg cac tcg gtg aag gcg tgagcccat 1120
 Ala Val Ser Pro Cys Ile Thr His Ser Val Lys Ala
 330 335 340

ccgtttgaag act 1133

<210> 106

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 106

Met Ala Lys Arg Ile Val Ile Ile Gly Gly Gly Pro Ala Gly Tyr Glu
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Ala Ala Leu Ala Gly Ala Lys Tyr Gly Ala Glu Val Thr Val Ile Glu
 20 25 30

Asp Val Gly Val Gly Gly Ser Ala Val Thr Met Asp Cys Val Pro Ser
 35 40 45

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

Asp Asp Met Gly Leu Asn Arg Gly Leu Gly Lys Ala His Leu Glu Ile
 65 70 75 80

Asp Ala Leu Asn Ile Arg Val Lys Asp Leu Ala Lys Ala Gln Ser Glu
 85 90 95

Asp Ile Leu Gly Gln Leu Gln Arg Ser Asp Val Arg Met Ile Asn Gly
 100 105 110

Val Gly Arg Phe Asp Asp Tyr Asn Thr Lys Gln Thr Thr His Tyr Ile
 115 120 125

Lys Val Thr His Ser Asp Gly Ser Glu Glu Thr Val Glu Cys Asp Leu
 130 135 140

Val Leu Val Ala Thr Gly Ala Thr Pro Arg Ile Leu Lys Gly Ala Glu
 145 150 155 160

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

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

Glu Phe Val Ser Ala Phe Ala Glu Leu Gly Val Lys Val Thr Met Val
 195 200 205

Ala Ser Arg Asp Arg Ile Leu Pro His Asp Asp Ala Asp Ala Ala Asp
 210 215 220

Val Leu Glu Thr Val Leu Ala Glu Arg Gly Val Ser Leu Glu Lys His
 225 230 235 240

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Ala Arg Val Glu Ser Val Thr Arg Thr Glu Asp Gly Gly Val Cys Val
 245 250 255

Arg Thr Ala Asp Gly Arg Glu Ile Tyr Gly Ser His Ala Leu Met Thr
 260 265 270

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

Val Glu Leu Ala Pro Ser Gly His Ile Lys Val Asp Arg Ser Pro Ala
 290 295 300

Pro Thr Ser Pro Val Cys Thr Gln Gln Val Thr Val Leu Thr Tyr Ser
 305 310 315 320

His Trp Arg Pro Leu Gln Arg Cys Arg Ala Val Ser Pro Cys Ile Thr
 325 330 335

His Ser Val Lys Ala
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<210> 107
 <211> 1518
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (89)..(1495)
 <223> FRXA02853

<400> 107
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cccagctcac acgtgtggag gtgccttaatg gca aag agg atc gta att atc ggc 115
 Met Ala Lys Arg Ile Val Ile Ile Gly
 1 5

ggt gga cct gca ggc tat gaa gcc gca ctc gca ggc gct aaa tac ggt 163
 Gly Gly Pro Ala Gly Tyr Glu Ala Ala Leu Ala Gly Ala Lys Tyr Gly
 10 15 20 25

gca gaa gtt acc gtt att gaa gat gtc gga gtt ggc gga tcc gca gtc 211
 Ala Glu Val Thr Val Ile Glu Asp Val Gly Val Gly Gly Ser Ala Val
 30 35 40

acc atg gac tgt gta cct tca aag tcc ttc atc gct ggt acc ggt atc 259
 Thr Met Asp Cys Val Pro Ser Lys Ser Phe Ile Ala Gly Thr Gly Ile
 45 50 55

aaa acc gac ctc cga cgt gct gat gac atg gga ctt aac cgt ggg ctt 307
 Lys Thr Asp Leu Arg Arg Ala Asp Asp Met Gly Leu Asn Arg Gly Leu
 60 65 70

gga aaa gca cac cta gaa atc gat gca ctg aac atc cgt gtg aag gac 355
 Gly Lys Ala His Leu Glu Ile Asp Ala Leu Asn Ile Arg Val Lys Asp
 75 80 85

ctt gcg aaa gca cag tcc gaa gat atc ttg ggc cag ctg cag cgc tca 403
 Leu Ala Lys Ala Gln Ser Glu Asp Ile Leu Gly Gln Leu Gln Arg Ser

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90	95	100	105	
gat gtc cgc atg att aac ggt gtg ggc cgc ttt gat gat tac aac acc	451			
Asp Val Arg Met Ile Asn Gly Val Gly Arg Phe Asp Asp Tyr Asn Thr				
110 115 120				
aag caa acc acc cac tac att aaa gtc acc cac agc gat ggc tcc gaa	499			
Lys Gln Thr Thr His Tyr Ile Lys Val Thr His Ser Asp Gly Ser Glu				
125 130 135				
gaa acc gtt gag tgc gat ctg gtg ctg gtt gca act ggt gca acc ccc	547			
Glu Thr Val Glu Cys Asp Leu Val Leu Val Ala Thr Gly Ala Thr Pro				
140 145 150				
cgc att ctt aaa ggt gca gag cca gac ggc gag cgc atc ttg acc tgg	595			
Arg Ile Leu Lys Gly Ala Glu Pro Asp Gly Glu Arg Ile Leu Thr Trp				
155 160 165				
cgt cag gtc tac gac att gaa gaa ctc ccc acc cac ctt atc gtg gtt	643			
Arg Gln Val Tyr Asp Ile Glu Glu Leu Pro Thr His Leu Ile Val Val				
170 175 180 185				
ggt tcc ggt gtg acc ggt gcg gaa ttt gtc tct gcg ttt gct gaa ctc	691			
Gly Ser Gly Val Thr Gly Ala Glu Phe Val Ser Ala Phe Ala Glu Leu				
190 195 200				
ggc gtc aaa gtc acc atg gtg gca tcc cgt gac cgc att ttg cct cac	739			
Gly Val Lys Val Thr Met Val Ala Ser Arg Asp Arg Ile Leu Pro His				
205 210 215				
gat gac gca gat gcc gca gac gtg ctg gaa acc gtt ctg gct gag cgc	787			
Asp Asp Ala Asp Ala Asp Val Leu Glu Thr Val Leu Ala Glu Arg				
220 225 230				
gga gta tcc ctg gaa aag cat gcc cgc gtg gag tct gtc acc cgc acc	835			
Gly Val Ser Leu Glu Lys His Ala Arg Val Glu Ser Val Thr Arg Thr				
235 240 245				
gaa gac ggt ggc gtg tgt gtt cgc act gct gac gga cga gaa atc tac	883			
Glu Asp Gly Gly Val Cys Val Arg Thr Ala Asp Gly Arg Glu Ile Tyr				
250 255 260 265				
ggt tct cac gcg ttg atg act gtt ggt tcc att cca aac acg gca gat	931			
Gly Ser His Ala Leu Met Thr Val Gly Ser Ile Pro Asn Thr Ala Asp				
270 275 280				
ctt ggc ctg gag aac atc ggt gtt gag ctg gca cca tcc ggc cat atc	979			
Leu Gly Leu Glu Asn Ile Gly Val Glu Leu Ala Pro Ser Gly His Ile				
285 290 295				
aag gtt gac cgn gtc tcc cgc acc aac atc ccc ggt gtg tac gca gca	1027			
Lys Val Asp Arg Val Ser Arg Thr Asn Ile Pro Gly Val Tyr Ala Ala				
300 305 310				
ggt gac tgt act gac cta ttc cca ctg gcg tcc gtt gca gcg atg cag	1075			
Gly Asp Cys Thr Asp Leu Phe Pro Leu Ala Ser Val Ala Ala Met Gln				
315 320 325				
ggc cgt atc gcc atg tat cac gca ctc ggt gaa ggc gtg agc ccc atc	1123			
Gly Arg Ile Ala Met Tyr His Ala Leu Gly Glu Gly Val Ser Pro Ile				
330 335 340 345				

cgt ttg aag act gtt gcc acc gca gtg ttt acc cgc cca gag atc gca 1171
 Arg Leu Lys Thr Val Ala Thr Ala Val Phe Thr Arg Pro Glu Ile Ala
 350 355 360

gca gta ggt atc acc cat gca caa gtt gat tcc ggc gaa gtg tct gct 1219
 Ala Val Gly Ile Thr His Ala Gln Val Asp Ser Gly Glu Val Ser Ala
 365 370 375

cgc gtg att gtg ctt cct ttg gct act aac cca cgc gcc aag atg cgt 1267
 Arg Val Ile Val Leu Pro Leu Ala Thr Asn Pro Arg Ala Lys Met Arg
 380 385 390

tcc ctg cgc cac ggt ttt gtg aag ctg ttc tgc cgc cgt aac tct ggc 1315
 Ser Leu Arg His Gly Phe Val Lys Leu Phe Cys Arg Arg Asn Ser Gly
 395 400 405

ctg atc atc ggt ggt gtc gtg gtg gca ccg acc gcg tct gag ctg atc 1363
 Leu Ile Ile Gly Gly Val Val Val Ala Pro Thr Ala Ser Glu Leu Ile
 410 415 420 425

cta ccg atc gct gtg gca gtg acc aac cgt ctg aca gtt gct gat ctg 1411
 Leu Pro Ile Ala Val Ala Val Thr Asn Arg Leu Thr Val Ala Asp Leu
 430 435 440

gct gat acc ttc gcg gtg tac cca tca ttg tca ggt tcg att act gaa 1459
 Ala Asp Thr Phe Ala Val Tyr Pro Ser Leu Ser Gly Ser Ile Thr Glu
 445 450 455

gca gca cgt cag ctg gtt caa cat gat gat cta ggc taatttttct 1505
 Ala Ala Arg Gln Leu Val Gln His Asp Asp Leu Gly
 460 465

gagtccttaga ttt 1518

<210> 108
 <211> 469
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 108
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Asp Val Gly Val Gly Gly Ser Ala Val Thr Met Asp Cys Val Pro Ser
 35 40 45

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

Asp Asp Met Gly Leu Asn Arg Gly Leu Gly Lys Ala His Leu Glu Ile
 65 70 75 80

Asp Ala Leu Asn Ile Arg Val Lys Asp Leu Ala Lys Ala Gln Ser Glu
 85 90 95

Asp Ile Leu Gly Gln Leu Gln Arg Ser Asp Val Arg Met Ile Asn Gly

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Val	Gly	Arg	Phe	Asp	Asp	Tyr	Asn	Thr	Lys	Gln	Thr	Thr	His	Tyr	Ile
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Lys	Val	Thr	His	Ser	Asp	Gly	Ser	Glu	Glu	Thr	Val	Glu	Cys	Asp	Leu
	130					135					140				
Val	Leu	Val	Ala	Thr	Gly	Ala	Thr	Pro	Arg	Ile	Leu	Lys	Gly	Ala	Glu
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Pro	Asp	Gly	Glu	Arg	Ile	Leu	Thr	Trp	Arg	Gln	Val	Tyr	Asp	Ile	Glu
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Glu	Leu	Pro	Thr	His	Leu	Ile	Val	Val	Gly	Ser	Gly	Val	Thr	Gly	Ala
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Glu	Phe	Val	Ser	Ala	Phe	Ala	Glu	Leu	Gly	Val	Lys	Val	Thr	Met	Val
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Ala	Ser	Arg	Asp	Arg	Ile	Leu	Pro	His	Asp	Asp	Ala	Asp	Ala	Ala	Asp
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Val	Leu	Glu	Thr	Val	Leu	Ala	Glu	Arg	Gly	Val	Ser	Leu	Glu	Lys	His
225					230					235					240
Ala	Arg	Val	Glu	Ser	Val	Thr	Arg	Thr	Glu	Asp	Gly	Gly	Val	Cys	Val
				245					250					255	
Arg	Thr	Ala	Asp	Gly	Arg	Glu	Ile	Tyr	Gly	Ser	His	Ala	Leu	Met	Thr
			260					265					270		
Val	Gly	Ser	Ile	Pro	Asn	Thr	Ala	Asp	Leu	Gly	Leu	Glu	Asn	Ile	Gly
		275					280					285			
Val	Glu	Leu	Ala	Pro	Ser	Gly	His	Ile	Lys	Val	Asp	Arg	Val	Ser	Arg
	290					295					300				
Thr	Asn	Ile	Pro	Gly	Val	Tyr	Ala	Ala	Gly	Asp	Cys	Thr	Asp	Leu	Phe
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Pro	Leu	Ala	Ser	Val	Ala	Ala	Met	Gln	Gly	Arg	Ile	Ala	Met	Tyr	His
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Ala	Leu	Gly	Glu	Gly	Val	Ser	Pro	Ile	Arg	Leu	Lys	Thr	Val	Ala	Thr
			340					345					350		
Ala	Val	Phe	Thr	Arg	Pro	Glu	Ile	Ala	Ala	Val	Gly	Ile	Thr	His	Ala
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Gln	Val	Asp	Ser	Gly	Glu	Val	Ser	Ala	Arg	Val	Ile	Val	Leu	Pro	Leu
	370					375					380				
Ala	Thr	Asn	Pro	Arg	Ala	Lys	Met	Arg	Ser	Leu	Arg	His	Gly	Phe	Val
385					390					395					400
Lys	Leu	Phe	Cys	Arg	Arg	Asn	Ser	Gly	Leu	Ile	Ile	Gly	Gly	Val	Val
				405					410					415	
Val	Ala	Pro	Thr	Ala	Ser	Glu	Leu	Ile	Leu	Pro	Ile	Ala	Val	Ala	Val
			420					425					430		

Thr Asn Arg Leu Thr Val Ala Asp Leu Ala Asp Thr Phe Ala Val Tyr
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His Asp Asp Leu Gly
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<223> RXA02259

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 Val Phe Lys Val Val
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atg act gat ttt tta cgc gat gac atc agg ttc ctc ggt caa atc ctc 163
 Met Thr Asp Phe Leu Arg Asp Asp Ile Arg Phe Leu Gly Gln Ile Leu
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ggt gag gta att gcg gaa caa gaa ggc cag gag gtt tat gaa ctg gtc 211
 Gly Glu Val Ile Ala Glu Gln Glu Gly Gln Glu Val Tyr Glu Leu Val
 25 30 35

gaa caa gcg cgc ctg act tct ttt gat atc gcc aag ggc aac gcc gaa 259
 Glu Gln Ala Arg Leu Thr Ser Phe Asp Ile Ala Lys Gly Asn Ala Glu
 40 45 50

atg gat agc ctg gtt cag gtt ttc gac ggc att act cca gcc aag gca 307
 Met Asp Ser Leu Val Gln Val Phe Asp Gly Ile Thr Pro Ala Lys Ala
 55 60 65

aca ccg att gct cgc gca ttt tcc cac ttc gct ctg ctg gct aac ctg 355
 Thr Pro Ile Ala Arg Ala Phe Ser His Phe Ala Leu Leu Ala Asn Leu
 70 75 80 85

gcg gaa gac ctc tac gat gaa gag ctt cgt gaa cag gct ctc gat gca 403
 Ala Glu Asp Leu Tyr Asp Glu Glu Leu Arg Glu Gln Ala Leu Asp Ala
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ggc gac acc cct ccg gac agc act ctt gat gcc acc tgg ctg aaa ctc 451
 Gly Asp Thr Pro Pro Asp Ser Thr Leu Asp Ala Thr Trp Leu Lys Leu
 105 110 115

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 Asn Glu Gly Asn Val Gly Ala Glu Ala Val Ala Asp Val Leu Arg Asn
 120 125 130

gct gag gtg gcg ccg gtt ctg act gcg cac cca act gag act cgc cgc 547

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Arg	Thr	Val	Phe	Asp	Ala	Gln	Lys	Trp	Ile	Thr	Thr	His	Met	Arg	Glu		
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cgc	cac	gct	ttg	cag	tct	gcg	gag	cct	acc	gct	cgt	acg	caa	agc	aag	643	
Arg	His	Ala	Leu	Gln	Ser	Ala	Glu	Pro	Thr	Ala	Arg	Thr	Gln	Ser	Lys		
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Leu	Asp	Glu	Ile	Glu	Lys	Asn	Ile	Arg	Arg	Arg	Ile	Thr	Ile	Leu	Trp		
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cag	acc	gcg	ttg	att	cgt	gtg	gcc	cgc	cca	cgt	atc	gag	gac	gag	atc	739	
Gln	Thr	Ala	Leu	Ile	Arg	Val	Ala	Arg	Pro	Arg	Ile	Glu	Asp	Glu	Ile		
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gaa	gta	ggg	ctg	cgc	tac	tac	aag	ctg	agc	ctt	ttg	gaa	gag	att	cca	787	
Glu	Val	Gly	Leu	Arg	Tyr	Tyr	Lys	Leu	Ser	Leu	Leu	Glu	Glu	Ile	Pro		
	215					220				225							
cgt	atc	aac	cgt	gat	gtg	gct	gtt	gag	ctt	cgt	gag	cgt	ttc	ggc	gag	835	
Arg	Ile	Asn	Arg	Asp	Val	Ala	Val	Glu	Leu	Arg	Glu	Arg	Phe	Gly	Glu		
230					235					240					245		
ggt	gtt	cct	ttg	aag	ccc	gtg	gtc	aag	cca	ggt	tcc	tgg	att	ggt	gga	883	
Gly	Val	Pro	Leu	Lys	Pro	Val	Val	Lys	Pro	Gly	Ser	Trp	Ile	Gly	Gly		
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gac	cac	gac	ggt	aac	cct	tat	gtc	acc	gcg	gaa	aca	gtt	gag	tat	tcc	931	
Asp	His	Asp	Gly	Asn	Pro	Tyr	Val	Thr	Ala	Glu	Thr	Val	Glu	Tyr	Ser		
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act	cac	cgc	gct	gcg	gaa	acc	gtg	ctc	aag	tac	tat	gca	cgc	cag	ctg	979	
Thr	His	Arg	Ala	Ala	Glu	Thr	Val	Leu	Lys	Tyr	Tyr	Ala	Arg	Gln	Leu		
		280					285					290					
cat	tcc	ctc	gag	cat	gag	ctc	agc	ctg	tcg	gac	cgc	atg	aat	aag	gtc	1027	
His	Ser	Leu	Glu	His	Glu	Leu	Ser	Leu	Ser	Asp	Arg	Met	Asn	Lys	Val		
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Thr	Pro	Gln	Leu	Leu	Ala	Leu	Ala	Asp	Ala	Gly	His	Asn	Asp	Val	Pro		
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Ser	Arg	Val	Asp	Glu	Pro	Tyr	Arg	Arg	Ala	Val	His	Gly	Val	Arg	Gly		
				330				335					340				
cgt	atc	ctc	gcg	acg	acg	gcc	gag	ctg	atc	ggc	gag	gac	gcc	gtt	gag	1171	
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Gly	Val	Trp	Phe	Lys	Val	Phe	Thr	Pro	Tyr	Ala	Ser	Pro	Glu	Glu	Phe		
		360					365					370					
tta	aac	gat	gcg	ttg	acc	att	gat	cat	tct	ctg	cgt	gaa	tcc	aag	gac	1267	
Leu	Asn	Asp	Ala	Leu	Thr	Ile	Asp	His	Ser	Leu	Arg	Glu	Ser	Lys	Asp		

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agc ttt gga ttc aac ctt tac gca ctg gat ctg cgc caa aac tcc gaa Ser Phe Gly Phe Asn Leu Tyr Ala Leu Asp Leu Arg Gln Asn Ser Glu 410 415 420			1363
agc tac gag gac gtc ctc acc gag ctt ttc gaa cgc gcc caa gtc acc Ser Tyr Glu Asp Val Leu Thr Glu Leu Phe Glu Arg Ala Gln Val Thr 425 430 435			1411
gca aac tac cgc gag ctg tct gaa gca gag aag ctt gag gtg ctg ctg Ala Asn Tyr Arg Glu Leu Ser Glu Ala Glu Lys Leu Glu Val Leu Leu 440 445 450			1459
aag gaa ctg cgc agc cct cgt ccg ctg atc ccg cac ggt tca gat gaa Lys Glu Leu Arg Ser Pro Arg Pro Leu Ile Pro His Gly Ser Asp Glu 455 460 465			1507
tac agc gag gtc acc gac cgc gag ctc ggc atc ttc cgc acc gcg tcg Tyr Ser Glu Val Thr Asp Arg Glu Leu Gly Ile Phe Arg Thr Ala Ser 470 475 480 485			1555
gag gct gtt aag aaa ttc ggg cca cgg atg gtg cct cac tgc atc atc Glu Ala Val Lys Lys Phe Gly Pro Arg Met Val Pro His Cys Ile Ile 490 495 500			1603
tcc atg gca tca tcg gtc acc gat gtg ctc gag ccg atg gtg ttg ctc Ser Met Ala Ser Ser Val Thr Asp Val Leu Glu Pro Met Val Leu Leu 505 510 515			1651
aag gaa ttc gga ctc atc gca gcc aac ggc gac aac cca cgc ggc acc Lys Glu Phe Gly Leu Ile Ala Ala Asn Gly Asp Asn Pro Arg Gly Thr 520 525 530			1699
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gcc gga atc ctc gac gaa ctg tgg aaa att gat ctc tac cgc aac tac Ala Gly Ile Leu Asp Glu Leu Trp Lys Ile Asp Leu Tyr Arg Asn Tyr 550 555 560 565			1795
ctc ctg cag cgc gac aac gtc cag gaa gtc atg ctc ggt tac tcc gat Leu Leu Gln Arg Asp Asn Val Gln Glu Val Met Leu Gly Tyr Ser Asp 570 575 580			1843
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gcg gaa ctg cag ctc gtc gaa cta tgc cga tca gcc ggg gtc aag ctt Ala Glu Leu Gln Leu Val Glu Leu Cys Arg Ser Ala Gly Val Lys Leu 600 605 610			1939
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Ser Tyr Asp Ala Ile Leu Ala Gln Pro Arg Gly Ala Val Gln Gly Ser	
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gtg cgc atc acc gag cag ggc gag atc atc tcc gct aag tac ggc aac	2083
Val Arg Ile Thr Glu Gln Gly Glu Ile Ile Ser Ala Lys Tyr Gly Asn	
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ccc gaa acc gcg cgc cga aac ctc gaa gcc ctg gtc tca gcc acg ctt	2131
Pro Glu Thr Ala Arg Arg Asn Leu Glu Ala Leu Val Ser Ala Thr Leu	
665 670 675	
gag gca tcg ctt ctc gac gtc tcc gaa ctc acc gat cac caa cgc gcg	2179
Glu Ala Ser Leu Leu Asp Val Ser Glu Leu Thr Asp His Gln Arg Ala	
680 685 690	
tac gac atc atg agt gag atc tct gag ctc agc ttg aag aag tac gcc	2227
Tyr Asp Ile Met Ser Glu Ile Ser Glu Leu Ser Leu Lys Lys Tyr Ala	
695 700 705	
tcc ttg gtg cac gag gat caa ggc ttc atc gat tac ttc acc cag tcc	2275
Ser Leu Val His Glu Asp Gln Gly Phe Ile Asp Tyr Phe Thr Gln Ser	
710 715 720 725	
acg ccg ctg cag gag att gga tcc ctc aac atc gga tcc agg cct tcc	2323
Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile Gly Ser Arg Pro Ser	
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tca cgc aag cag acc tcc tcg gtg gaa gat ttg cga gcc atc cca tgg	2371
Ser Arg Lys Gln Thr Ser Ser Val Glu Asp Leu Arg Ala Ile Pro Trp	
745 750 755	
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Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu Pro Gly Trp Phe Gly	
760 765 770	
gtc gga acc gca tta gag cag tgg att ggc gaa ggg gag cag gcc acc	2467
Val Gly Thr Ala Leu Glu Gln Trp Ile Gly Glu Gly Glu Gln Ala Thr	
775 780 785	
caa cgc att gcc gag ctg caa aca ctc aat gag tcc tgg cca ttt ttc	2515
Gln Arg Ile Ala Glu Leu Gln Thr Leu Asn Glu Ser Trp Pro Phe Phe	
790 795 800 805	
acc tca gtg ttg gat aac atg gct cag gtg atg tcc aag gca gag ctg	2563
Thr Ser Val Leu Asp Asn Met Ala Gln Val Met Ser Lys Ala Glu Leu	
810 815 820	
cgt ttg gca aag ctc tac gca gac ctg atc cca gat acg gaa gta gcc	2611
Arg Leu Ala Lys Leu Tyr Ala Asp Leu Ile Pro Asp Thr Glu Val Ala	
825 830 835	
gag cga gtc tat tcc gtc atc cgc gag gag tac ttc ctg acc aag aag	2659
Glu Arg Val Tyr Ser Val Ile Arg Glu Glu Tyr Phe Leu Thr Lys Lys	
840 845 850	
atg ttc tgc gta atc acc ggc tct gat gat ctg ctt gat gac aac cca	2707
Met Phe Cys Val Ile Thr Gly Ser Asp Asp Leu Leu Asp Asp Asn Pro	
855 860 865	

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aac gtg atc cag gta gag atg atg cga cgc tac cga aaa ggc gac caa 2803
 Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr Arg Lys Gly Asp Gln
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 Ser Glu Gln Val Ser Arg Asn Ile Gln Leu Thr Met Asn Gly Leu Ser
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 Lys Gly Asn Ala Glu Met Asp Ser Leu Val Gln Val Phe Asp Gly Ile
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 Thr Pro Ala Lys Ala Thr Pro Ile Ala Arg Ala Phe Ser His Phe Ala
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 Gln Ala Leu Asp Ala Gly Asp Thr Pro Pro Asp Ser Thr Leu Asp Ala
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 Thr Trp Leu Lys Leu Asn Glu Gly Asn Val Gly Ala Glu Ala Val Ala
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 Asp Val Leu Arg Asn Ala Glu Val Ala Pro Val Leu Thr Ala His Pro
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 Thr His Met Arg Glu Arg His Ala Leu Gln Ser Ala Glu Pro Thr Ala
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 Arg Thr Gln Ser Lys Leu Asp Glu Ile Glu Lys Asn Ile Arg Arg Arg
 180 185 190
 Ile Thr Ile Leu Trp Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg
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Thr	Val	Glu	Tyr	Ser	Thr	His	Arg	Ala	Ala	Glu	Thr	Val	Leu	Lys	Tyr	275	280	285	
Tyr	Ala	Arg	Gln	Leu	His	Ser	Leu	Glu	His	Glu	Leu	Ser	Leu	Ser	Asp	290	295	300	
Arg	Met	Asn	Lys	Val	Thr	Pro	Gln	Leu	Leu	Ala	Leu	Ala	Asp	Ala	Gly	305	310	315	320
His	Asn	Asp	Val	Pro	Ser	Arg	Val	Asp	Glu	Pro	Tyr	Arg	Arg	Ala	Val	325	330	335	
His	Gly	Val	Arg	Gly	Arg	Ile	Leu	Ala	Thr	Thr	Ala	Glu	Leu	Ile	Gly	340	345	350	
Glu	Asp	Ala	Val	Glu	Gly	Val	Trp	Phe	Lys	Val	Phe	Thr	Pro	Tyr	Ala	355	360	365	
Ser	Pro	Glu	Glu	Phe	Leu	Asn	Asp	Ala	Leu	Thr	Ile	Asp	His	Ser	Leu	370	375	380	
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Ile	Ser	Ala	Ile	Glu	Ser	Phe	Gly	Phe	Asn	Leu	Tyr	Ala	Leu	Asp	Leu	405	410	415	
Arg	Gln	Asn	Ser	Glu	Ser	Tyr	Glu	Asp	Val	Leu	Thr	Glu	Leu	Phe	Glu	420	425	430	
Arg	Ala	Gln	Val	Thr	Ala	Asn	Tyr	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Lys	435	440	445	
Leu	Glu	Val	Leu	Leu	Lys	Glu	Leu	Arg	Ser	Pro	Arg	Pro	Leu	Ile	Pro	450	455	460	
His	Gly	Ser	Asp	Glu	Tyr	Ser	Glu	Val	Thr	Asp	Arg	Glu	Leu	Gly	Ile	465	470	475	480
Phe	Arg	Thr	Ala	Ser	Glu	Ala	Val	Lys	Lys	Phe	Gly	Pro	Arg	Met	Val	485	490	495	
Pro	His	Cys	Ile	Ile	Ser	Met	Ala	Ser	Ser	Val	Thr	Asp	Val	Leu	Glu	500	505	510	
Pro	Met	Val	Leu	Leu	Lys	Glu	Phe	Gly	Leu	Ile	Ala	Ala	Asn	Gly	Asp	515	520	525	

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Leu	Tyr	Arg	Asn	Tyr	Leu	Leu	Gln	Arg	Asp	Asn	Val	Gln	Glu	Val	Met
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Leu	Gly	Tyr	Ser	Asp	Ser	Asn	Lys	Asp	Gly	Gly	Tyr	Phe	Ser	Ala	Asn
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Trp	Ala	Leu	Tyr	Asp	Ala	Glu	Leu	Gln	Leu	Val	Glu	Leu	Cys	Arg	Ser
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Ala	Gly	Val	Lys	Leu	Arg	Leu	Phe	His	Gly	Arg	Gly	Gly	Thr	Val	Gly
	610					615					620				
Arg	Gly	Gly	Gly	Pro	Ser	Tyr	Asp	Ala	Ile	Leu	Ala	Gln	Pro	Arg	Gly
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Ala	Val	Gln	Gly	Ser	Val	Arg	Ile	Thr	Glu	Gln	Gly	Glu	Ile	Ile	Ser
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Ala	Lys	Tyr	Gly	Asn	Pro	Glu	Thr	Ala	Arg	Arg	Asn	Leu	Glu	Ala	Leu
			660					665					670		
Val	Ser	Ala	Thr	Leu	Glu	Ala	Ser	Leu	Leu	Asp	Val	Ser	Glu	Leu	Thr
		675					680					685			
Asp	His	Gln	Arg	Ala	Tyr	Asp	Ile	Met	Ser	Glu	Ile	Ser	Glu	Leu	Ser
	690					695					700				
Leu	Lys	Lys	Tyr	Ala	Ser	Leu	Val	His	Glu	Asp	Gln	Gly	Phe	Ile	Asp
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Tyr	Phe	Thr	Gln	Ser	Thr	Pro	Leu	Gln	Glu	Ile	Gly	Ser	Leu	Asn	Ile
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Gly	Ser	Arg	Pro	Ser	Ser	Arg	Lys	Gln	Thr	Ser	Ser	Val	Glu	Asp	Leu
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Pro	Gly	Trp	Phe	Gly	Val	Gly	Thr	Ala	Leu	Glu	Gln	Trp	Ile	Gly	Glu
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Gly	Glu	Gln	Ala	Thr	Gln	Arg	Ile	Ala	Glu	Leu	Gln	Thr	Leu	Asn	Glu
785					790					795					800
Ser	Trp	Pro	Phe	Phe	Thr	Ser	Val	Leu	Asp	Asn	Met	Ala	Gln	Val	Met
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Ser	Lys	Ala	Glu	Leu	Arg	Leu	Ala	Lys	Leu	Tyr	Ala	Asp	Leu	Ile	Pro
			820					825					830		
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Tyr Leu Leu Pro Leu Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr			
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Arg Lys Gly Asp Gln Ser Glu Gln Val Ser Arg Asn Ile Gln Leu Thr			
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 Met Leu Gly Arg Pro
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 acc aag gtc acc cca tcc tcc aag gtt gtt ggc gac ctc gca ctc cac 163
 Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly Asp Leu Ala Leu His
 10 15 20
 ctc gtt ggt gcg ggt gtg gat cca gca gac ttt gct gcc gat cca caa 211
 Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe Ala Ala Asp Pro Gln
 25 30 35
 aag tac gac atc cca gac tct gtc atc gcg ttc ctg cgc ggc gag ctt 259
 Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe Leu Arg Gly Glu Leu
 40 45 50
 ggt aac cct cca ggt ggc tgg cca gag cca ctg cgc acc cgc gca ctg 307
 Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu Arg Thr Arg Ala Leu
 55 60 65
 gaa ggc cgc tcc gaa ggc aag gca cct ctg acg gaa gtt cct gag gaa 355
 Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr Glu Val Pro Glu Glu
 70 75 80 85
 gag cag gcg cac ctc gac gct gat gat tcc aag gaa cgt cgc aat agc 403
 Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys Glu Arg Arg Asn Ser
 90 95 100
 ctc aac cgc ctg ctg ttc ccg aag cca acc gaa gag ttc ctc gag cac 451
 Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu Glu Phe Leu Glu His
 105 110 115
 cgt cgc cgc ttc ggc aac acc tct gcg ctg gat gat cgt gaa ttc ttc 499

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Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp Asp Arg Glu Phe Phe
 120 125 130
 tac ggc ctg gtc gaa ggc cgc gag act ttg atc cgc ctg cca gat gtg 547
 Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile Arg Leu Pro Asp Val
 135 140 145
 cgc acc cca ctg ctt gtt cgc ctg gat gcg atc tct gag cca gac gat 595
 Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile Ser Glu Pro Asp Asp
 150 155 160 165
 aag ggt atg cgc aat gtt gtg gcc aac gtc aac ggc cag atc cgc cca 643
 Lys Gly Met Arg Asn Val Val Ala Asn Val Asn Gly Gln Ile Arg Pro
 170 175 180
 atg cgt gtg cgt gac cgc tcc gtt gag tct gtc acc gca acc gca gaa 691
 Met Arg Val Arg Asp Arg Ser Val Glu Ser Val Thr Ala Thr Ala Glu
 185 190 195
 aag gca gat tcc tcc aac aag ggc cat gtt gct gca cca ttc gct ggt 739
 Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala Ala Pro Phe Ala Gly
 200 205 210
 gtt gtc acc gtg act gtt gct gaa ggt gat gag gtc aag gct gga gat 787
 Val Val Thr Val Thr Val Ala Glu Gly Asp Glu Val Lys Ala Gly Asp
 215 220 225
 gca gtc gca atc atc gag gct atg aag atg gaa gca aca atc act gct 835
 Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu Ala Thr Ile Thr Ala
 230 235 240 245
 tct gtt gac ggc aaa atc gat cgc gtt gtg gtt cct gct gca acg aag 883
 Ser Val Asp Gly Lys Ile Asp Arg Val Val Val Pro Ala Ala Thr Lys
 250 255 260
 gtg gaa ggt ggc gac ttg atc gtc gtc gtt tcc taaacctttc tgtaaaaagc 936
 Val Glu Gly Gly Asp Leu Ile Val Val Val Ser
 265 270
 ccc 939

<210> 112

<211> 272

<212> PRT

<213> Corynebacterium glutamicum

<400> 112

Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly
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 20 25 30
 Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe
 35 40 45
 Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu
 50 55 60
 Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr

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65		70		75		80
Glu Val Pro Glu	Glu Glu Gln Ala His Leu Asp	Ala Asp Asp Ser Lys				
	85		90			95
Glu Arg Arg Asn Ser Leu Asn Arg	Leu Leu Phe Pro Lys Pro Thr Glu					
	100		105			110
Glu Phe Leu Glu His Arg Arg Arg	Phe Gly Asn Thr Ser Ala Leu Asp					
	115		120			125
Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly	Arg Glu Thr Leu Ile					
	130		135			140
Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val	Arg Leu Asp Ala Ile					
	145		150			155
Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val	Ala Asn Val Asn					
	165		170			175
Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg	Ser Val Glu Ser Val					
	180		185			190
Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys	Gly His Val Ala					
	195		200			205
Ala Pro Phe Ala Gly Val Val Thr Val Thr Val	Ala Glu Gly Asp Glu					
	210		215			220
Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met	Glu					
	225		230			235
Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp Arg Val Val Val						
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Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val Val Val Ser						
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<210> 113
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(916)
 <223> FRXA02326

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 Met Leu Gly Arg Pro
 1 5
 acc aag gtc acc cca tcc tcc aag gtt gtt ggc gac ctc gca ctc cac 163
 Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly Asp Leu Ala Leu His

10							15							20		
ctc	ggt	ggt	gcg	ggt	gtg	gat	cca	gca	gac	ttt	gct	gcc	gat	cca	caa	211
Leu	Val	Gly	Ala	Gly	Val	Asp	Pro	Ala	Asp	Phe	Ala	Ala	Asp	Pro	Gln	
			25					30					35			
aag	tac	gac	atc	cca	gac	tct	gtc	atc	gcg	ttc	ctg	cgc	ggc	gag	ctt	259
Lys	Tyr	Asp	Ile	Pro	Asp	Ser	Val	Ile	Ala	Phe	Leu	Arg	Gly	Glu	Leu	
		40					45					50				
ggt	aac	cct	cca	ggt	ggc	tgg	cca	gag	cca	ctg	cgc	acc	cgc	gca	ctg	307
Gly	Asn	Pro	Pro	Gly	Gly	Trp	Pro	Glu	Pro	Leu	Arg	Thr	Arg	Ala	Leu	
	55					60					65					
gaa	ggc	cgc	tcc	gaa	ggc	aag	gca	cct	ctg	acg	gaa	gtt	cct	gag	gaa	355
Glu	Gly	Arg	Ser	Glu	Gly	Lys	Ala	Pro	Leu	Thr	Glu	Val	Pro	Glu	Glu	
	70				75					80					85	
gag	cag	gcg	cac	ctc	gac	gct	gat	gat	tcc	aag	gaa	cgt	cgc	aat	agc	403
Glu	Gln	Ala	His	Leu	Asp	Ala	Asp	Asp	Ser	Lys	Glu	Arg	Arg	Asn	Ser	
				90					95					100		
ctc	aac	cgc	ctg	ctg	ttc	ccg	aag	cca	acc	gaa	gag	ttc	ctc	gag	cac	451
Leu	Asn	Arg	Leu	Leu	Phe	Pro	Lys	Pro	Thr	Glu	Glu	Phe	Leu	Glu	His	
			105					110					115			
cgt	cgc	cgc	ttc	ggc	aac	acc	tct	gcg	ctg	gat	gat	cgt	gaa	ttc	ttc	499
Arg	Arg	Arg	Phe	Gly	Asn	Thr	Ser	Ala	Leu	Asp	Asp	Arg	Glu	Phe	Phe	
		120					125					130				
tac	ggc	ctg	gtc	gaa	ggc	cgc	gag	act	ttg	atc	cgc	ctg	cca	gat	gtg	547
Tyr	Gly	Leu	Val	Glu	Gly	Arg	Glu	Thr	Leu	Ile	Arg	Leu	Pro	Asp	Val	
	135					140					145					
cgc	acc	cca	ctg	ctt	gtt	cgc	ctg	gat	gcg	atc	tct	gag	cca	gac	gat	595
Arg	Thr	Pro	Leu	Leu	Val	Arg	Leu	Asp	Ala	Ile	Ser	Glu	Pro	Asp	Asp	
	150				155					160					165	
aag	ggt	atg	cgc	aat	gtt	gtg	gcc	aac	gtc	aac	ggc	cag	atc	cgc	cca	643
Lys	Gly	Met	Arg	Asn	Val	Val	Ala	Asn	Val	Asn	Gly	Gln	Ile	Arg	Pro	
				170					175					180		
atg	cgt	gtg	cgt	gac	cgc	tcc	gtt	gag	tct	gtc	acc	gca	acc	gca	gaa	691
Met	Arg	Val	Arg	Asp	Arg	Ser	Val	Glu	Ser	Val	Thr	Ala	Thr	Ala	Glu	
			185					190					195			
aag	gca	gat	tcc	tcc	aac	aag	ggc	cat	gtt	gct	gca	cca	ttc	gct	ggt	739
Lys	Ala	Asp	Ser	Ser	Asn	Lys	Gly	His	Val	Ala	Ala	Pro	Phe	Ala	Gly	
		200					205					210				
gtt	gtc	acc	gtg	act	gtt	gct	gaa	ggt	gat	gag	gtc	aag	gct	gga	gat	787
Val	Val	Thr	Val	Thr	Val	Ala	Glu	Gly	Asp	Glu	Val	Lys	Ala	Gly	Asp	
	215					220					225					
gca	gtc	gca	atc	atc	gag	gct	atg	aag	atg	gaa	gca	aca	atc	act	gct	835
Ala	Val	Ala	Ile	Ile	Glu	Ala	Met	Lys	Met	Glu	Ala	Thr	Ile	Thr	Ala	
	230				235					240					245	
tct	gtt	gac	ggc	aaa	atc	gat	cgc	gtt	gtg	gtt	cct	gct	gca	acg	aag	883
Ser	Val	Asp	Gly	Lys	Ile	Asp	Arg	Val	Val	Val	Pro	Ala	Ala	Thr	Lys	
				250					255					260		

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gtg gaa ggt ggc gac ttg atc gtc gtc gtt tcc taaacctttc tgtaaaaagc 936
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 265 270

ccc

939

<210> 114
 <211> 272
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 114
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 Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe
 20 25 30
 Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe
 35 40 45
 Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu
 50 55 60
 Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr
 65 70 75 80
 Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys
 85 90 95
 Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu
 100 105 110
 Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp
 115 120 125
 Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile
 130 135 140
 Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile
 145 150 155 160
 Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn
 165 170 175
 Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val
 180 185 190
 Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala
 195 200 205
 Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu Gly Asp Glu
 210 215 220
 Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu
 225 230 235 240
 Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp Arg Val Val Val
 245 250 255

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

<210> 115
 <211> 1083
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1060)
 <223> RXN02327

<400> 115
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 ggcagttact gataccacct tccgcgatgc acaccagtct ttg ctt gcg acc cga 115
 Leu Leu Ala Thr Arg
 1 5
 gtc cgc tca ttc gca ctg aag cct gcg gca gag gcc gtc gca aag ctg 163
 Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu Ala Val Ala Lys Leu
 10 15 20
 act cct gag ctt ttg tcc gtg gag gcc tgg ggc ggc gcg acc tac gat 211
 Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly Ala Thr Tyr Asp
 25 30 35
 gtg gcg atg cgt ttc ctc ttt gag gat ccg tgg gac agg ctc gac gag 259
 Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp Asp Arg Leu Asp Glu
 40 45 50
 ctg cgc gag gcg atg ccg aat gta aac att cag atg ctg ctt cgc ggc 307
 Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln Met Leu Leu Arg Gly
 55 60 65
 cgc aac acc gtg gga tac acc ccg tac cca gac tcc gtc tgc cgc gcg 355
 Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp Ser Val Cys Arg Ala
 70 75 80 85
 ttt gtt aag gaa gct gcc agc tcc ggc gtg gac atc ttc cgc atc ttc 403
 Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp Ile Phe Arg Ile Phe
 90 95 100
 gac gcg ctt aac gac gtc tcc cag atg cgt cca gca atc gac gca gtc 451
 Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro Ala Ile Asp Ala Val
 105 110 115
 ctg gag acc aac acc gcg gta gcc gag gtg gct atg gct tat tct ggt 499
 Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala Met Ala Tyr Ser Gly
 120 125 130
 gat ctc tct gat cca aat gaa aag ctc tac acc ctg gat tac tac cta 547
 Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu
 135 140 145

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aag atg gca gag gag atc gtc aag tct ggc gct cac atc ttg gcc att 595
Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala His Ile Leu Ala Ile
150                      155                      160                      165

aag gat atg gct ggt ctg ctt cgc cca gct gcg gta acc aag ctg gtc 643
Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala Val Thr Lys Leu Val
170                      175                      180

acc gca ctg cgc cgt gaa ttc gat ctg cca gtg cac gtg cac acc cac 691
Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val His Val His Thr His
185                      190                      195

gac act gcg ggt ggc cag ctg gca acc tac ttt gct gca gct caa gct 739
Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe Ala Ala Ala Gln Ala
200                      205                      210

ggt gca gat gct gtt gac ggt gct tcc ggc acc act gtc tgg cac cac 787
Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr Thr Val Trp His His
215                      220                      225

ctc cca agc cat ccc ttg tct gcc att gtt gct gca ttc gcg cac acc 835
Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala Ala Phe Ala His Thr
230                      235                      240                      245

cgt cgc gat acc ggt ttg agc ctc gag gct gtt tct gac ctc gag ccg 883
Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val Ser Asp Leu Glu Pro
250                      255                      260

tac tgg gaa gca gtg cgc gga ctg tac ctg cca ttt gag tct gga acc 931
Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro Phe Glu Ser Gly Thr
265                      270                      275

cca ggc cca acc ggt cgc gtc tac cgc cac gaa atc cca ggc gga cag 979
Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu Ile Pro Gly Gly Gln
280                      285                      290

ttg tcc aac ctg cgt gca cag gcc acc gca ctg ggc ctt gcg gat cgt 1027
Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu Gly Leu Ala Asp Arg
295                      300                      305

ttc gaa ctc atc gaa gac aac tac gca agc cgt taatgagatg ctgggacgcc 1080
Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ser Arg
310                      315                      320

caa 1083

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<210> 116

<211> 320

<212> PRT

<213> Corynebacterium glutamicum

<400> 116

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Leu Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu
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Ala Val Ala Lys Leu Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly
20                      25                      30

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Gly Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp
35                      40                      45

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Asp Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln
 50 55 60
 Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp
 65 70 75 80
 Ser Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp
 85 90 95
 Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro
 100 105 110
 Ala Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala
 115 120 125
 Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr
 130 135 140
 Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala
 145 150 155 160
 His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala
 165 170 175
 Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val
 180 185 190
 His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe
 195 200 205
 Ala Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr
 210 215 220
 Thr Val Trp His His Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala
 225 230 235 240
 Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val
 245 250 255
 Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro
 260 265 270
 Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu
 275 280 285
 Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu
 290 295 300
 Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ser Arg
 305 310 315 320

<210> 117

<211> 1083

<212> DNA

<213> Corynebacterium glutamicum

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PCT/IB00/00943

<220>

<221> CDS

<222> (101)..(1060)

<223> FRXA02327

<400> 117

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 Leu Leu Ala Thr Arg
 1 5

gtc cgc tca ttc gca ctg aag cct gcg gca gag gcc gtc gca aag ctg 163
 Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu Ala Val Ala Lys Leu
 10 15 20

act cct gag ctt ttg tcc gtg gag gcc tgg ggc ggc gcg acc tac gat 211
 Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly Ala Thr Tyr Asp
 25 30 35

gtg gcg atg cgt ttc ctc ttt gag gat ccg tgg gac agg ctc gac gag 259
 Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp Asp Arg Leu Asp Glu
 40 45 50

ctg cgc gag gcg atg ccg aat gta aac att cag atg ctg ctt cgc ggc 307
 Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln Met Leu Leu Arg Gly
 55 60 65

cgc aac acc gtg gga tac acc ccg tac cca gac tcc gtc tgc cgc gcg 355
 Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp Ser Val Cys Arg Ala
 70 75 80 85

ttt gtt aag gaa gct gcc agc tcc ggc gtg gac atc ttc cgc atc ttc 403
 Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp Ile Phe Arg Ile Phe
 90 95 100

gac gcg ctt aac gac gtc tcc cag atg cgt cca gca atc gac gca gtc 451
 Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro Ala Ile Asp Ala Val
 105 110 115

ctg gag acc aac acc gcg gta gcc gag gtg gct atg gct tat tct ggt 499
 Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala Met Ala Tyr Ser Gly
 120 125 130

gat ctc tct gat cca aat gaa aag ctc tac acc ctg gat tac tac cta 547
 Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu
 135 140 145

aag atg gca gag gag atc gtc aag tct ggc gct cac atc ttg gcc att 595
 Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala His Ile Leu Ala Ile
 150 155 160 165

aag gat atg gct ggt ctg ctt cgc cca gct gcg gta acc aag ctg gtc 643
 Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala Val Thr Lys Leu Val
 170 175 180

acc gca ctg cgc cgt gaa ttc gat ctg cca gtg cac gtg cac acc cac 691
 Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val His Val His Thr His
 185 190 195

gac act gcg ggt ggc cag ctg gca acc tac ttt gct gca gct caa gct 739

WO 01/00844

PCT/IB00/00943

Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe Ala Ala Ala Gln Ala
 200 205 210
 ggt gca gat gct gtt gac ggt gct tcc ggc acc act gtc tgg cac cac 787
 Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr Thr Val Trp His His
 215 220 225
 ctc cca agc cat ccc ttg tct gcc att gtt gct gca ttc gcg cac acc 835
 Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala Ala Phe Ala His Thr
 230 235 240 245
 cgt cgc gat acc ggt ttg agc ctc gag gct gtt tct gac ctc gag ccg 883
 Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val Ser Asp Leu Glu Pro
 250 255 260
 tac tgg gaa gca gtg cgc gga ctg tac ctg cca ttt gag tct gga acc 931
 Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro Phe Glu Ser Gly Thr
 265 270 275
 cca ggc cca acc ggt cgc gtc tac cgc cac gaa atc cca ggc gga cag 979
 Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu Ile Pro Gly Gly Gln
 280 285 290
 ttg tcc aac ctg cgt gca cag gcc acc gca ctg ggc ctt gcg gat cgt 1027
 Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu Gly Leu Ala Asp Arg
 295 300 305
 ttc gaa ctc atc gaa gac aac tac gca agc cgt taatgagatg ctgggacgcc 1080
 Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ser Arg
 310 315 320
 caa 1083

<210> 118

<211> 320

<212> PRT

<213> Corynebacterium glutamicum

<400> 118

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 20 25 30
 Gly Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp
 35 40 45
 Asp Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln
 50 55 60
 Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp
 65 70 75 80
 Ser Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp
 85 90 95
 Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro
 100 105 110

WO 01/00844

PCT/IB00/00943

Ala Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala
115 120 125

Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr
130 135 140

Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala
145 150 155 160

His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala
165 170 175

Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val
180 185 190

His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe
195 200 205

Ala Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr
210 215 220

Thr Val Trp His His Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala
225 230 235 240

Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val
245 250 255

Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro
260 265 270

Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu
275 280 285

Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu
290 295 300

Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ser Arg
305 310 315 320

<210> 119
<211> 1719
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1696)
<223> RXN02328

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Val Thr Ala Ile Thr
1 5

ctt ggc ggt ctc ttg ttg aaa gga ata att act cta gtg tcg act cac 163

Leu	Gly	Gly	Leu	Leu	Leu	Lys	Gly	Ile	Ile	Thr	Leu	Val	Ser	Thr	His	
				10					15					20		
aca	tct	tca	acg	ctt	cca	gca	ttc	aaa	aag	atc	ttg	gta	gca	aac	cgc	211
Thr	Ser	Ser	Thr	Leu	Pro	Ala	Phe	Lys	Lys	Ile	Leu	Val	Ala	Asn	Arg	
			25					30					35			
ggc	gaa	atc	gcg	gtc	cgt	gct	ttc	cgt	gca	gca	ctc	gaa	acc	ggc	gca	259
Gly	Glu	Ile	Ala	Val	Arg	Ala	Phe	Arg	Ala	Ala	Leu	Glu	Thr	Gly	Ala	
		40					45					50				
gcc	acg	gta	gct	att	tac	ccc	cgt	gaa	gat	cgg	gga	tca	ttc	cac	cgc	307
Ala	Thr	Val	Ala	Ile	Tyr	Pro	Arg	Glu	Asp	Arg	Gly	Ser	Phe	His	Arg	
	55					60					65					
tct	ttt	gct	tct	gaa	gct	gtc	cgc	att	ggc	acc	gaa	ggc	tca	cca	gtc	355
Ser	Phe	Ala	Ser	Glu	Ala	Val	Arg	Ile	Gly	Thr	Glu	Gly	Ser	Pro	Val	
70					75				80						85	
aag	gcg	tac	ctg	gac	atc	gat	gaa	att	atc	ggc	gca	gct	aaa	aaa	gtt	403
Lys	Ala	Tyr	Leu	Asp	Ile	Asp	Glu	Ile	Ile	Gly	Ala	Ala	Lys	Lys	Val	
				90					95					100		
aaa	gca	gat	gcc	att	tac	ccg	gga	tac	ggc	ttc	ctg	tct	gaa	aat	gcc	451
Lys	Ala	Asp	Ala	Ile	Tyr	Pro	Gly	Tyr	Gly	Phe	Leu	Ser	Glu	Asn	Ala	
			105					110					115			
cag	ctt	gcc	cgc	gag	tgt	gcg	gaa	aac	ggc	att	act	ttt	att	ggc	cca	499
Gln	Leu	Ala	Arg	Glu	Cys	Ala	Glu	Asn	Gly	Ile	Thr	Phe	Ile	Gly	Pro	
		120					125					130				
acc	cca	gag	gtt	ctt	gat	ctc	acc	ggc	gat	aag	tct	cgc	gcg	gta	acc	547
Thr	Pro	Glu	Val	Leu	Asp	Leu	Thr	Gly	Asp	Lys	Ser	Arg	Ala	Val	Thr	
	135					140					145					
gcc	gcg	aag	aag	gct	ggc	ctg	cca	gtt	ttg	gcg	gaa	tcc	acc	ccg	agc	595
Ala	Ala	Lys	Lys	Ala	Gly	Leu	Pro	Val	Leu	Ala	Glu	Ser	Thr	Pro	Ser	
150					155					160					165	
aaa	aac	atc	gat	gag	atc	gtt	aaa	agc	gct	gaa	ggc	cag	act	tac	ccc	643
Lys	Asn	Ile	Asp	Glu	Ile	Val	Lys	Ser	Ala	Glu	Gly	Gln	Thr	Tyr	Pro	
				170					175					180		
atc	ttt	gtg	aag	gca	gtt	gcc	ggc	ggc	ggc	gga	cgc	ggc	atg	cgt	ttt	691
Ile	Phe	Val	Lys	Ala	Val	Ala	Gly	Gly	Gly	Gly	Arg	Gly	Met	Arg	Phe	
			185					190					195			
gtt	gct	tca	cct	gat	gag	ctt	cgc	aaa	tta	gca	aca	gaa	gca	tct	cgt	739
Val	Ala	Ser	Pro	Asp	Glu	Leu	Arg	Lys	Leu	Ala	Thr	Glu	Ala	Ser	Arg	
		200					205					210				
gaa	gct	gaa	gcg	gct	ttc	ggc	gat	ggc	gcg	gta	tat	gtc	gaa	cgt	gct	787
Glu	Ala	Glu	Ala	Ala	Phe	Gly	Asp	Gly	Ala	Val	Tyr	Val	Glu	Arg	Ala	
	215					220				225						
gtg	att	aac	cct	cag	cat	att	gaa	gtg	cag	atc	ctt	ggc	gat	cac	act	835
Val	Ile	Asn	Pro	Gln	His	Ile	Glu	Val	Gln	Ile	Leu	Gly	Asp	His	Thr	
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gga	gaa	gtt	gta	cac	ctt	tat	gaa	cgt	gac	tgc	tca	ctg	cag	cgt	cgt	883
Gly	Glu	Val	Val	His	Leu	Tyr	Glu	Arg	Asp	Cys	Ser	Leu	Gln	Arg	Arg	

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250						255						260						
cac	caa	aaa	gtt	gtc	gaa	att	gcg	cca	gca	cag	cat	ttg	gat	cca	gaa	931		
His	Gln	Lys	Val	Val	Glu	Ile	Ala	Pro	Ala	Gln	His	Leu	Asp	Pro	Glu			
			265					270					275					
ctg	cgt	gat	cgc	att	tgt	gcg	gat	gca	gta	aag	ttc	tgc	cgc	tcc	att	979		
Leu	Arg	Asp	Arg	Ile	Cys	Ala	Asp	Ala	Val	Lys	Phe	Cys	Arg	Ser	Ile			
		280					285					290						
ggt	tac	cag	ggc	gcg	gga	acc	gtg	gaa	ttc	ttg	gtc	gat	gaa	aag	ggc	1027		
Gly	Tyr	Gln	Gly	Ala	Gly	Thr	Val	Glu	Phe	Leu	Val	Asp	Glu	Lys	Gly			
	295					300					305							
aac	cac	gtc	ttc	atc	gaa	atg	aac	cca	cgt	atc	cag	gtt	gag	cac	acc	1075		
Asn	His	Val	Phe	Ile	Glu	Met	Asn	Pro	Arg	Ile	Gln	Val	Glu	His	Thr			
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gtg	act	gaa	gaa	gtc	acc	gag	gtg	gac	ctg	gtg	aag	gcg	cag	atg	cgc	1123		
Val	Thr	Glu	Glu	Val	Thr	Glu	Val	Asp	Leu	Val	Lys	Ala	Gln	Met	Arg			
				330					335					340				
ttg	gct	gct	ggc	gca	acc	ttg	aag	gaa	ttg	ggc	ctg	acc	caa	gat	aag	1171		
Leu	Ala	Ala	Gly	Ala	Thr	Leu	Lys	Glu	Leu	Gly	Leu	Thr	Gln	Asp	Lys			
			345					350					355					
atc	aag	acc	cac	ggc	gca	gca	ctg	cag	tgc	cgc	atc	acc	acg	gaa	gat	1219		
Ile	Lys	Thr	His	Gly	Ala	Ala	Leu	Gln	Cys	Arg	Ile	Thr	Thr	Glu	Asp			
		360					365					370						
cca	aac	aac	ggc	ttc	cgc	cca	gat	acc	gga	act	atc	acc	gcg	tac	cgc	1267		
Pro	Asn	Asn	Gly	Phe	Arg	Pro	Asp	Thr	Gly	Thr	Ile	Thr	Ala	Tyr	Arg			
	375					380					385							
tca	cca	ggc	gga	gct	ggc	gtt	cgt	ctt	gac	ggc	gca	gct	cag	ctc	ggc	1315		
Ser	Pro	Gly	Gly	Ala	Gly	Val	Arg	Leu	Asp	Gly	Ala	Ala	Gln	Leu	Gly			
390					395					400				405				
ggc	gaa	atc	acc	gca	cac	ttt	gac	tcc	atg	ctg	gtg	aaa	atg	acc	tgc	1363		
Gly	Glu	Ile	Thr	Ala	His	Phe	Asp	Ser	Met	Leu	Val	Lys	Met	Thr	Cys			
				410				415						420				
cgt	ggc	tcc	gac	ttt	gaa	act	gct	gtt	gct	cgt	gca	cag	cgc	gcg	ttg	1411		
Arg	Gly	Ser	Asp	Phe	Glu	Thr	Ala	Val	Ala	Arg	Ala	Gln	Arg	Ala	Leu			
			425					430					435					
gct	gag	ttc	acc	gtg	tct	ggc	gtt	gca	acc	aac	att	ggc	ttc	ttg	cgt	1459		
Ala	Glu	Phe	Thr	Val	Ser	Gly	Val	Ala	Thr	Asn	Ile	Gly	Phe	Leu	Arg			
		440					445					450						
gcg	ttg	ctg	cgg	gaa	gag	gac	ttc	act	tcc	aag	cgc	atc	gcc	acc	gga	1507		
Ala	Leu	Leu	Arg	Glu	Glu	Asp	Phe	Thr	Ser	Lys	Arg	Ile	Ala	Thr	Gly			
	455					460					465							
ttc	att	gcc	gat	cac	ccg	cac	ctc	ctt	cag	gct	cca	cct	gct	gat	gat	1555		
Phe	Ile	Ala	Asp	His	Pro	His	Leu	Leu	Gln	Ala	Pro	Pro	Ala	Asp	Asp			
470					475					480				485				
gag	cag	gga	cgc	atc	ctg	gat	tac	ttg	gca	gat	gtc	acc	gtg	aac	aag	1603		
Glu	Gln	Gly	Arg	Ile	Leu	Asp	Tyr	Leu	Ala	Asp	Val	Thr	Val	Asn	Lys			
				490					495					500				

cct cat ggt gtg cgt cca aag gat gtt gca gct cct atc gat aag ctg 1651
 Pro His Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu
 505 510 515

cct aac atc aag gat ctg cca ctg cca cgc ggt tcc cgt gac cgc 1696
 Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg
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<211> 532

<212> PRT

<213> Corynebacterium glutamicum

<400> 120

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 20 25 30

Leu Val Ala Asn Arg Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala
 35 40 45

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

Gly Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr
 65 70 75 80

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

Ala Ala Lys Lys Val Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe
 100 105 110

Leu Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile
 115 120 125

Thr Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys
 130 135 140

Ser Arg Ala Val Thr Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala
 145 150 155 160

Glu Ser Thr Pro Ser Lys Asn Ile Asp Glu Ile Val Lys Ser Ala Glu
 165 170 175

Gly Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly
 180 185 190

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

Thr Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly Ala Val
 210 215 220

Tyr Val Glu Arg Ala Val Ile Asn Pro Gln His Ile Glu Val Gln Ile

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225					230						235				240
Leu	Gly	Asp	His	Thr	Gly	Glu	Val	Val	His	Leu	Tyr	Glu	Arg	Asp	Cys
				245					250					255	
Ser	Leu	Gln	Arg	Arg	His	Gln	Lys	Val	Val	Glu	Ile	Ala	Pro	Ala	Gln
			260					265					270		
His	Leu	Asp	Pro	Glu	Leu	Arg	Asp	Arg	Ile	Cys	Ala	Asp	Ala	Val	Lys
		275					280					285			
Phe	Cys	Arg	Ser	Ile	Gly	Tyr	Gln	Gly	Ala	Gly	Thr	Val	Glu	Phe	Leu
	290					295					300				
Val	Asp	Glu	Lys	Gly	Asn	His	Val	Phe	Ile	Glu	Met	Asn	Pro	Arg	Ile
305					310					315					320
Gln	Val	Glu	His	Thr	Val	Thr	Glu	Glu	Val	Thr	Glu	Val	Asp	Leu	Val
				325					330					335	
Lys	Ala	Gln	Met	Arg	Leu	Ala	Ala	Gly	Ala	Thr	Leu	Lys	Glu	Leu	Gly
			340					345					350		
Leu	Thr	Gln	Asp	Lys	Ile	Lys	Thr	His	Gly	Ala	Ala	Leu	Gln	Cys	Arg
		355					360					365			
Ile	Thr	Thr	Glu	Asp	Pro	Asn	Asn	Gly	Phe	Arg	Pro	Asp	Thr	Gly	Thr
	370					375					380				
Ile	Thr	Ala	Tyr	Arg	Ser	Pro	Gly	Gly	Ala	Gly	Val	Arg	Leu	Asp	Gly
385					390					395					400
Ala	Ala	Gln	Leu	Gly	Gly	Glu	Ile	Thr	Ala	His	Phe	Asp	Ser	Met	Leu
				405					410					415	
Val	Lys	Met	Thr	Cys	Arg	Gly	Ser	Asp	Phe	Glu	Thr	Ala	Val	Ala	Arg
			420					425					430		
Ala	Gln	Arg	Ala	Leu	Ala	Glu	Phe	Thr	Val	Ser	Gly	Val	Ala	Thr	Asn
		435					440					445			
Ile	Gly	Phe	Leu	Arg	Ala	Leu	Leu	Arg	Glu	Glu	Asp	Phe	Thr	Ser	Lys
	450					455					460				
Arg	Ile	Ala	Thr	Gly	Phe	Ile	Ala	Asp	His	Pro	His	Leu	Leu	Gln	Ala
465					470					475					480
Pro	Pro	Ala	Asp	Asp	Glu	Gln	Gly	Arg	Ile	Leu	Asp	Tyr	Leu	Ala	Asp
				485					490					495	
Val	Thr	Val	Asn	Lys	Pro	His	Gly	Val	Arg	Pro	Lys	Asp	Val	Ala	Ala
			500					505					510		
Pro	Ile	Asp	Lys	Leu	Pro	Asn	Ile	Lys	Asp	Leu	Pro	Leu	Pro	Arg	Gly
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<210> 121

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<211> 1406

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1383)

<223> FRXA02328

<400> 121

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tac	ctg	gac	atc	gat	gaa	att	atc	ggc	gca	gct	aaa	aaa	gtt	aaa	gca	96
Tyr	Leu	Asp	Ile	Asp	Glu	Ile	Ile	Gly	Ala	Ala	Lys	Lys	Val	Lys	Ala	
			20					25					30			

gat	gcc	att	tac	ccg	gga	tac	ggc	ttc	ctg	tct	gaa	aat	gcc	cag	ctt	144
Asp	Ala	Ile	Tyr	Pro	Gly	Tyr	Gly	Phe	Leu	Ser	Glu	Asn	Ala	Gln	Leu	
		35					40					45				

gcc	cgc	gag	tgt	gcg	gaa	aac	ggc	att	act	ttt	att	ggc	cca	acc	cca	192
Ala	Arg	Glu	Cys	Ala	Glu	Asn	Gly	Ile	Thr	Phe	Ile	Gly	Pro	Thr	Pro	
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gag	gtt	ctt	gat	ctc	acc	ggc	gat	aag	tct	cgc	gcg	gta	acc	gcc	gcg	240
Glu	Val	Leu	Asp	Leu	Thr	Gly	Asp	Lys	Ser	Arg	Ala	Val	Thr	Ala	Ala	
65					70				75						80	

aag	aag	gct	ggc	ctg	cca	gtt	ttg	gcg	gaa	tcc	acc	ccg	agc	aaa	aac	288
Lys	Lys	Ala	Gly	Leu	Pro	Val	Leu	Ala	Glu	Ser	Thr	Pro	Ser	Lys	Asn	
				85				90						95		

atc	gat	gag	atc	gtt	aaa	agc	gct	gaa	ggc	cag	act	tac	ccc	atc	ttt	336
Ile	Asp	Glu	Ile	Val	Lys	Ser	Ala	Glu	Gly	Gln	Thr	Tyr	Pro	Ile	Phe	
			100					105					110			

gtg	aag	gca	gtt	gcc	ggc	ggc	ggc	gga	cgc	ggc	atg	cgt	ttt	gtt	gct	384
Val	Lys	Ala	Val	Ala	Gly	Gly	Gly	Gly	Arg	Gly	Met	Arg	Phe	Val	Ala	
		115				120						125				

tca	cct	gat	gag	ctt	cgc	aaa	tta	gca	aca	gaa	gca	tct	cgt	gaa	gct	432
Ser	Pro	Asp	Glu	Leu	Arg	Lys	Leu	Ala	Thr	Glu	Ala	Ser	Arg	Glu	Ala	
	130					135					140					

gaa	gcg	gct	ttc	ggc	gat	ggc	gcg	gta	tat	gtc	gaa	cgt	gct	gtg	att	480
Glu	Ala	Ala	Phe	Gly	Asp	Gly	Ala	Val	Tyr	Val	Glu	Arg	Ala	Val	Ile	
145				150						155					160	

aac	cct	cag	cat	att	gaa	gtg	cag	atc	ctt	ggc	gat	cac	act	gga	gaa	528
Asn	Pro	Gln	His	Ile	Glu	Val	Gln	Ile	Leu	Gly	Asp	His	Thr	Gly	Glu	
			165					170						175		

gtt	gta	cac	ctt	tat	gaa	cgt	gac	tgc	tca	ctg	cag	cgt	cgt	cac	caa	576
Val	Val	His	Leu	Tyr	Glu	Arg	Asp	Cys	Ser	Leu	Gln	Arg	Arg	His	Gln	
			180				185						190			

aaa	gtt	gtc	gaa	att	gcg	cca	gca	cag	cat	ttg	gat	cca	gaa	ctg	cgt	624
Lys	Val	Val	Glu	Ile	Ala	Pro	Ala	Gln	His	Leu	Asp	Pro	Glu	Leu	Arg	
		195				200						205				

gat	cgc	att	tgt	gcg	gat	gca	gta	aag	ttc	tgc	cgc	tcc	att	ggt	tac	672
Asp	Arg	Ile	Cys	Ala	Asp	Ala	Val	Lys	Phe	Cys	Arg	Ser	Ile	Gly	Tyr	
	210					215					220					
cag	ggc	gcg	gga	acc	gtg	gaa	ttc	ttg	gtc	gat	gaa	aag	ggc	aac	cac	720
Gln	Gly	Ala	Gly	Thr	Val	Glu	Phe	Leu	Val	Asp	Glu	Lys	Gly	Asn	His	
225					230					235					240	
gtc	ttc	atc	gaa	atg	aac	cca	cgt	atc	cag	gtt	gag	cac	acc	gtg	act	768
Val	Phe	Ile	Glu	Met	Asn	Pro	Arg	Ile	Gln	Val	Glu	His	Thr	Val	Thr	
				245					250					255		
gaa	gaa	gtc	acc	gag	gtg	gac	ctg	gtg	aag	gcg	cag	atg	cgc	ttg	gct	816
Glu	Glu	Val	Thr	Glu	Val	Asp	Leu	Val	Lys	Ala	Gln	Met	Arg	Leu	Ala	
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gct	ggt	gca	acc	ttg	aag	gaa	ttg	ggt	ctg	acc	caa	gat	aag	atc	aag	864
Ala	Gly	Ala	Thr	Leu	Lys	Glu	Leu	Gly	Leu	Thr	Gln	Asp	Lys	Ile	Lys	
		275					280					285				
acc	cac	ggt	gca	gca	ctg	cag	tgc	cgc	atc	acc	acg	gaa	gat	cca	aac	912
Thr	His	Gly	Ala	Ala	Leu	Gln	Cys	Arg	Ile	Thr	Thr	Glu	Asp	Pro	Asn	
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aac	ggc	ttc	cgc	cca	gat	acc	gga	act	atc	acc	gcg	tac	cgc	tca	cca	960
Asn	Gly	Phe	Arg	Pro	Asp	Thr	Gly	Thr	Ile	Thr	Ala	Tyr	Arg	Ser	Pro	
305					310					315					320	
ggc	gga	gct	ggc	gtt	cgt	ctt	gac	ggt	gca	gct	cag	ctc	ggt	ggc	gaa	1008
Gly	Gly	Ala	Gly	Val	Arg	Leu	Asp	Gly	Ala	Ala	Gln	Leu	Gly	Gly	Glu	
				325					330					335		
atc	acc	gca	cac	ttt	gac	tcc	atg	ctg	gtg	aaa	atg	acc	tgc	cgt	ggt	1056
Ile	Thr	Ala	His	Phe	Asp	Ser	Met	Leu	Val	Lys	Met	Thr	Cys	Arg	Gly	
			340					345					350			
tcc	gac	ttt	gaa	act	gct	gtt	gct	cgt	gca	cag	cgc	gcg	ttg	gct	gag	1104
Ser	Asp	Phe	Glu	Thr	Ala	Val	Ala	Arg	Ala	Gln	Arg	Ala	Leu	Ala	Glu	
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ttc	acc	gtg	tct	ggt	gtt	gca	acc	aac	att	ggt	ttc	ttg	cgt	gcg	ttg	1152
Phe	Thr	Val	Ser	Gly	Val	Ala	Thr	Asn	Ile	Gly	Phe	Leu	Arg	Ala	Leu	
	370					375					380					
ctg	cgg	gaa	gag	gac	ttc	act	tcc	aag	cgc	atc	gcc	acc	gga	ttc	att	1200
Leu	Arg	Glu	Glu	Asp	Phe	Thr	Ser	Lys	Arg	Ile	Ala	Thr	Gly	Phe	Ile	
385					390					395					400	
gcc	gat	cac	ccg	cac	ctc	ctt	cag	gct	cca	cct	gct	gat	gat	gag	cag	1248
Ala	Asp	His	Pro	His	Leu	Leu	Gln	Ala	Pro	Pro	Ala	Asp	Asp	Glu	Gln	
				405					410					415		
gga	cgc	atc	ctg	gat	tac	ttg	gca	gat	gtc	acc	gtg	aac	aag	cct	cat	1296
Gly	Arg	Ile	Leu	Asp	Tyr	Leu	Ala	Asp	Val	Thr	Val	Asn	Lys	Pro	His	
			420					425					430			
ggt	gtg	cgt	cca	aag	gat	gtt	gca	gct	cct	atc	gat	aag	ctg	cct	aac	1344
Gly	Val	Arg	Pro	Lys	Asp	Val	Ala	Ala	Pro	Ile	Asp	Lys	Leu	Pro	Asn	
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tggcccagcc gcg 1406

<210> 122

<211> 461

<212> PRT

<213> Corynebacterium glutamicum

<400> 122

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Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala Gln Leu
 35 40 45

Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro Thr Pro
 50 55 60

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

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

Ile Asp Glu Ile Val Lys Ser Ala Glu Gly Gln Thr Tyr Pro Ile Phe
 100 105 110

Val Lys Ala Val Ala Gly Gly Gly Gly Arg Gly Met Arg Phe Val Ala
 115 120 125

Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr Glu Ala Ser Arg Glu Ala
 130 135 140

Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr Val Glu Arg Ala Val Ile
 145 150 155 160

Asn Pro Gln His Ile Glu Val Gln Ile Leu Gly Asp His Thr Gly Glu
 165 170 175

Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg His Gln
 180 185 190

Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro Glu Leu Arg
 195 200 205

Asp Arg Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser Ile Gly Tyr
 210 215 220

Gln Gly Ala Gly Thr Val Glu Phe Leu Val Asp Glu Lys Gly Asn His
 225 230 235 240

Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His Thr Val Thr
 245 250 255

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

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1324)
 <223> RXN01048

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 gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115
 Met Thr Ile Asp Leu
 1 5
 cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163
 Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His
 10 15 20

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gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg	211
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met	
25 30 35	
cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa	259
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu	
40 45 50	
gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga	307
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly	
55 60 65	
aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc	355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly	
70 75 80 85	
gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag	403
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln	
90 95 100	
ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac	451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp	
105 110 115	
gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct	499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro	
120 125 130	
tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc	547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe	
135 140 145	
gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac	595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His	
150 155 160 165	
gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac	643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn	
170 175 180	
tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att	691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile	
185 190 195	
tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac	739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn	
200 205 210	
gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac	787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His	
215 220 225	
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag	835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys	
230 235 240 245	
acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc	883
Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly	
250 255 260	
gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct	931

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Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala
 265 270 275

ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca 979
 Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro
 280 285 290

acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc 1027
 Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val
 295 300 305

gcg acc ggg cgc tct gac ctg cct aac cag atc aac aac gtg ctg gcg 1075
 Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala
 310 315 320 325

ttc cca gga att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc 1123
 Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile
 330 335 340

acc ccc gag atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag 1171
 Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln
 345 350 355

ctg agg acc tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc 1219
 Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro
 360 365 370

gcg ttg ccc caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc 1267
 Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg
 375 380 385

aaa acg ctt aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg 1315
 Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala
 390 395 400 405

cca ata ttt taagagcaaaa cttgaggccc aca 1347
 Pro Ile Phe

<210> 124

<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 124

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu
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Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
 20 25 30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
 35 40 45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr
 50 55 60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
 65 70 75 80

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Val	Leu	Gly	Leu	Gly	Asp	Ile	Gly	Pro	Gln	Ala	Ser	Leu	Pro	Val	Met
				85					90					95	
Glu	Gly	Lys	Ala	Gln	Leu	Phe	Ser	Ser	Phe	Ala	Gly	Leu	Lys	Ala	Ile
			100					105					110		
Pro	Ile	Val	Leu	Asp	Val	His	Asp	Val	Asp	Ala	Leu	Val	Glu	Thr	Ile
		115					120					125			
Ala	Ala	Ile	Ala	Pro	Ser	Phe	Gly	Ala	Ile	Asn	Leu	Glu	Asp	Ile	Ser
	130					135					140				
Ala	Pro	Arg	Cys	Phe	Glu	Val	Glu	Arg	Arg	Leu	Ile	Glu	Arg	Leu	Asp
145					150					155					160
Ile	Pro	Val	Met	His	Asp	Asp	Gln	His	Gly	Thr	Ala	Val	Val	Ile	Leu
				165					170					175	
Ala	Ala	Leu	Arg	Asn	Ser	Leu	Lys	Leu	Leu	Asp	Arg	Lys	Ile	Glu	Asp
			180					185					190		
Leu	Lys	Ile	Val	Ile	Ser	Gly	Ala	Gly	Ala	Ala	Gly	Val	Ala	Ala	Val
		195					200					205			
Asp	Met	Leu	Thr	Asn	Ala	Gly	Ala	Thr	Asp	Ile	Val	Val	Leu	Asp	Ser
	210					215					220				
Arg	Gly	Ile	Ile	His	Asp	Ser	Arg	Glu	Asp	Leu	Ser	Pro	Val	Lys	Ala
225					230					235					240
Ala	Leu	Ala	Glu	Lys	Thr	Asn	Pro	Arg	Gly	Ile	Ser	Gly	Gly	Ile	Asn
				245					250					255	
Glu	Ala	Phe	Thr	Gly	Ala	Asp	Leu	Phe	Ile	Gly	Val	Ser	Gly	Gly	Asn
			260					265					270		
Ile	Gly	Glu	Asp	Ala	Leu	Lys	Leu	Met	Ala	Pro	Glu	Pro	Ile	Leu	Phe
		275					280					285			
Thr	Leu	Ala	Asn	Pro	Thr	Pro	Glu	Ile	Asp	Pro	Glu	Leu	Ser	Gln	Lys
	290					295					300				
Tyr	Gly	Ala	Ile	Val	Ala	Thr	Gly	Arg	Ser	Asp	Leu	Pro	Asn	Gln	Ile
305					310					315					320
Asn	Asn	Val	Leu	Ala	Phe	Pro	Gly	Ile	Phe	Ala	Gly	Ala	Leu	Ala	Ala
				325					330					335	
Lys	Ala	Lys	Lys	Ile	Thr	Pro	Glu	Met	Lys	Leu	Ala	Ala	Gln	Arg	Gln
			340					345					350		
Ser	Gln	Thr	Ser	Gln	Leu	Arg	Thr	Ser	Arg	Ser	Ala	Ala	Ser	Cys	Leu
		355					360					365			
Pro	Pro	Trp	Ile	Pro	Ala	Leu	Pro	Gln	Gln	Ser	Arg	Gln	Leu	Ser	Arg
	370					375					380				
Pro	Ser	Pro	Lys	Arg	Lys	Thr	Leu	Lys	Asn	Leu	Leu	Ile	Asp	Ala	Ser
385					390					395					400
Leu	Pro	Val	Glu	Ala	Pro	Ile	Phe								

405

<210> 125
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(288)
 <223> FRXA01048

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 1 5 10 15
 att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc acc ccc gag 96
 Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
 20 25 30
 atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag ctg agg acc 144
 Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
 35 40 45
 tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc gcg ttg ccc 192
 Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
 50 55 60
 caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc aaa acg ctt 240
 Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
 65 70 75 80
 aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg cca ata ttt 288
 Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
 85 90 95
 taagagcaaa cttgaggccc aca 311

<210> 126
 <211> 96
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 126
 Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
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 Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
 20 25 30
 Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
 35 40 45
 Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
 50 55 60
 Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
 65 70 75 80

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gag	gtg	gag	cgc	cgc	ctc	atc	gag	cgt	ctc	gat	att	cca	gtt	atg	cac	595
Glu	Val	Glu	Arg	Arg	Leu	Ile	Glu	Arg	Leu	Asp	Ile	Pro	Val	Met	His	
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gat	gac	cag	cac	ggc	acc	gct	gtg	gtt	atc	ctc	gct	gcg	ctg	cgc	aac	643
Asp	Asp	Gln	His	Gly	Thr	Ala	Val	Val	Ile	Leu	Ala	Ala	Leu	Arg	Asn	
				170					175					180		
tcc	ctg	aag	ctg	ctg	gat	cgc	aag	atc	gaa	gac	ctc	aag	att	gtt	att	691
Ser	Leu	Lys	Leu	Leu	Asp	Arg	Lys	Ile	Glu	Asp	Leu	Lys	Ile	Val	Ile	
			185					190					195			
tcc	ggc	gca	ggc	gca	gcg	ggc	gtt	gca	gct	gta	gat	atg	ctg	acc	aac	739
Ser	Gly	Ala	Gly	Ala	Ala	Gly	Val	Ala	Ala	Val	Asp	Met	Leu	Thr	Asn	
		200					205					210				
gct	gga	gca	acc	gac	atc	gtg	gtt	ctt	gat	tcc	cga	ggc	atc	atc	cac	787
Ala	Gly	Ala	Thr	Asp	Ile	Val	Val	Leu	Asp	Ser	Arg	Gly	Ile	Ile	His	
	215					220					225					
gac	agc	cgt	gag	gat	ctt	tcc	cca	gtt	aag	gct	gct	ctt	gca	gag	aag	835
Asp	Ser	Arg	Glu	Asp	Leu	Ser	Pro	Val	Lys	Ala	Ala	Leu	Ala	Glu	Lys	
230					235					240					245	
acc	aac	cct	cgt	ggc	atc	agc	ggt	ggc	atc	aat	gag	gct	ttc	acc	ggc	883
Thr	Asn	Pro	Arg	Gly	Ile	Ser	Gly	Gly	Ile	Asn	Glu	Ala	Phe	Thr	Gly	
			250						255					260		
gcg	gac	ctg	ttc	att	ggc	gtg	tcc	ggc	ggc	aac	atc	ggc	gag	gac	gct	931
Ala	Asp	Leu	Phe	Ile	Gly	Val	Ser	Gly	Gly	Asn	Ile	Gly	Glu	Asp	Ala	
			265					270					275			
ctc	aaa	ctc	atg	gcc	ccg	gag	cca	atc	ctg	ttc	acc	ctg	gcg	aac	cca	979
Leu	Lys	Leu	Met	Ala	Pro	Glu	Pro	Ile	Leu	Phe	Thr	Leu	Ala	Asn	Pro	
		280					285					290				
acc	cca	gag	atc	gat	cct	gag	ctg	tct	cag	aag	tac	ggc	gcc	atc	gtc	1027
Thr	Pro	Glu	Ile	Asp	Pro	Glu	Leu	Ser	Gln	Lys	Tyr	Gly	Ala	Ile	Val	
	295					300					305					
gcg	acc	ggg	ccg	gtc	ttg	acc	tgc	cta	acc	aga	tca					1063
Ala	Thr	Gly	Pro	Val	Leu	Thr	Cys	Leu	Thr	Arg	Ser					
310					315					320						

<210> 128

<211> 321

<212> PRT

<213> Corynebacterium glutamicum

<400> 128

Met	Thr	Ile	Asp	Leu	Gln	Arg	Ser	Thr	Gln	Asn	Leu	Thr	His	Glu	Glu
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Ile	Phe	Glu	Ala	His	Glu	Gly	Gly	Lys	Leu	Ser	Ile	Ser	Ser	Thr	Arg
			20					25					30		

Pro	Leu	Arg	Asp	Met	Arg	Asp	Leu	Ser	Leu	Ala	Tyr	Thr	Pro	Gly	Val
		35					40					45			

Ala	Gln	Val	Cys	Glu	Ala	Ile	Lys	Glu	Asp	Pro	Glu	Val	Ala	Arg	Thr

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50					55					60					
His	Thr	Gly	Ile	Gly	Asn	Thr	Val	Ala	Val	Ile	Ser	Asp	Gly	Thr	Ala
65					70					75					80
Val	Leu	Gly	Leu	Gly	Asp	Ile	Gly	Pro	Gln	Ala	Ser	Leu	Pro	Val	Met
				85					90					95	
Glu	Gly	Lys	Ala	Gln	Leu	Phe	Ser	Ser	Phe	Ala	Gly	Leu	Lys	Ala	Ile
			100					105					110		
Pro	Ile	Val	Leu	Asp	Val	His	Asp	Val	Asp	Ala	Leu	Val	Glu	Thr	Ile
		115					120					125			
Ala	Ala	Ile	Ala	Pro	Ser	Phe	Gly	Ala	Ile	Asn	Leu	Glu	Asp	Ile	Ser
		130				135					140				
Ala	Pro	Arg	Cys	Phe	Glu	Val	Glu	Arg	Arg	Leu	Ile	Glu	Arg	Leu	Asp
145					150					155					160
Ile	Pro	Val	Met	His	Asp	Asp	Gln	His	Gly	Thr	Ala	Val	Val	Ile	Leu
				165					170					175	
Ala	Ala	Leu	Arg	Asn	Ser	Leu	Lys	Leu	Leu	Asp	Arg	Lys	Ile	Glu	Asp
			180					185					190		
Leu	Lys	Ile	Val	Ile	Ser	Gly	Ala	Gly	Ala	Ala	Gly	Val	Ala	Ala	Val
		195					200					205			
Asp	Met	Leu	Thr	Asn	Ala	Gly	Ala	Thr	Asp	Ile	Val	Val	Leu	Asp	Ser
	210					215					220				
Arg	Gly	Ile	Ile	His	Asp	Ser	Arg	Glu	Asp	Leu	Ser	Pro	Val	Lys	Ala
225					230					235					240
Ala	Leu	Ala	Glu	Lys	Thr	Asn	Pro	Arg	Gly	Ile	Ser	Gly	Gly	Ile	Asn
				245					250					255	
Glu	Ala	Phe	Thr	Gly	Ala	Asp	Leu	Phe	Ile	Gly	Val	Ser	Gly	Gly	Asn
			260					265					270		
Ile	Gly	Glu	Asp	Ala	Leu	Lys	Leu	Met	Ala	Pro	Glu	Pro	Ile	Leu	Phe
		275					280					285			
Thr	Leu	Ala	Asn	Pro	Thr	Pro	Glu	Ile	Asp	Pro	Glu	Leu	Ser	Gln	Lys
	290					295					300				
Tyr	Gly	Ala	Ile	Val	Ala	Thr	Gly	Pro	Val	Leu	Thr	Cys	Leu	Thr	Arg
305					310					315					320
Ser															

<210> 129

<211> 1065

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

WO 01/00844

PCT/IB00/00943

<222> (101)..(1042)

<223> RXA02694

<400> 129

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tgggttgtcc	ggttagggaa	atcaggaagt	gggatcgaaa	atg	aaa	gaa	acc	gtc	115
				Met	Lys	Glu	Thr	Val	
				1				5	

ggt	aac	aag	att	gtc	ctc	att	ggc	gca	gga	gat	gtt	gga	gtt	gca	tac	163
Gly	Asn	Lys	Ile	Val	Leu	Ile	Gly	Ala	Gly	Asp	Val	Gly	Val	Ala	Tyr	
			10					15					20			

gca	tac	gca	ctg	atc	aac	cag	ggc	atg	gca	gat	cac	ctt	gcg	atc	atc	211
Ala	Tyr	Ala	Leu	Ile	Asn	Gln	Gly	Met	Ala	Asp	His	Leu	Ala	Ile	Ile	
			25					30					35			

gac	atc	gat	gaa	aag	aaa	ctc	gaa	ggc	aac	gtc	atg	gac	tta	aac	cat	259
Asp	Ile	Asp	Glu	Lys	Lys	Leu	Glu	Gly	Asn	Val	Met	Asp	Leu	Asn	His	
			40				45					50				

ggt	gtt	gtg	tgg	gcc	gat	tcc	cgc	acc	cgc	gtc	acc	aag	ggc	acc	tac	307
Gly	Val	Val	Trp	Ala	Asp	Ser	Arg	Thr	Arg	Val	Thr	Lys	Gly	Thr	Tyr	
	55					60					65					

gct	gac	tgc	gaa	gac	gca	gcc	atg	gtt	gtc	att	tgt	gcc	ggc	gca	gcc	355
Ala	Asp	Cys	Glu	Asp	Ala	Ala	Met	Val	Val	Ile	Cys	Ala	Gly	Ala	Ala	
70					75					80					85	

caa	aag	cca	ggc	gag	acc	cgc	ctc	cag	ctg	gtg	gac	aaa	aac	gtc	aag	403
Gln	Lys	Pro	Gly	Glu	Thr	Arg	Leu	Gln	Leu	Val	Asp	Lys	Asn	Val	Lys	
				90					95					100		

att	atg	aaa	tcc	atc	gtc	ggc	gat	gtc	atg	gac	agc	gga	ttc	gac	ggc	451
Ile	Met	Lys	Ser	Ile	Val	Gly	Asp	Val	Met	Asp	Ser	Gly	Phe	Asp	Gly	
			105					110					115			

atc	ttc	ctc	gtg	gcg	tcc	aac	cca	gtg	gat	atc	ctg	acc	tac	gca	gtg	499
Ile	Phe	Leu	Val	Ala	Ser	Asn	Pro	Val	Asp	Ile	Leu	Thr	Tyr	Ala	Val	
		120					125					130				

tgg	aaa	ttc	tcc	ggc	ttg	gaa	tgg	aac	cgc	gtg	atc	ggc	tcc	gga	act	547
Trp	Lys	Phe	Ser	Gly	Leu	Glu	Trp	Asn	Arg	Val	Ile	Gly	Ser	Gly	Thr	
	135					140					145					

gtc	ctg	gac	tcc	gct	cga	ttc	cgc	tac	atg	ctg	ggc	gaa	ctc	tac	gaa	595
Val	Leu	Asp	Ser	Ala	Arg	Phe	Arg	Tyr	Met	Leu	Gly	Glu	Leu	Tyr	Glu	
150					155					160					165	

gtg	gca	cca	agc	tcc	gtc	cac	gcc	tac	atc	atc	ggc	gaa	cac	ggc	gac	643
Val	Ala	Pro	Ser	Ser	Val	His	Ala	Tyr	Ile	Ile	Gly	Glu	His	Gly	Asp	
				170					175					180		

act	gaa	ctt	cca	gtc	ctg	tcc	tcc	gcg	acc	atc	gca	ggc	gta	tcg	ctt	691
Thr	Glu	Leu	Pro	Val	Leu	Ser	Ser	Ala	Thr	Ile	Ala	Gly	Val	Ser	Leu	
			185					190					195			

agc	cga	atg	ctg	gac	aaa	gac	cca	gag	ctt	gag	ggc	cgt	cta	gag	aaa	739
Ser	Arg	Met	Leu	Asp	Lys	Asp	Pro	Glu	Leu	Glu	Gly	Arg	Leu	Glu	Lys	
		200					205					210				

att ttc gaa gac acc cgc gac gct gcc tat cac att atc gac gcc aag 787
 Ile Phe Glu Asp Thr Arg Asp Ala Ala Tyr His Ile Ile Asp Ala Lys
 215 220 225

 ggc tcc act tcc tac ggc atc ggc atg ggt ctt gct cgc atc acc cgc 835
 Gly Ser Thr Ser Tyr Gly Ile Gly Met Gly Leu Ala Arg Ile Thr Arg
 230 235 240 245

 gca atc cta cag aac caa gac gtt gca gtc cca gtc tct gca ctg ctc 883
 Ala Ile Leu Gln Asn Gln Asp Val Ala Val Pro Val Ser Ala Leu Leu
 250 255 260

 cac ggt gaa tac ggt gag gaa gac atc tac atc ggc acc cca gct gtg 931
 His Gly Glu Tyr Gly Glu Glu Asp Ile Tyr Ile Gly Thr Pro Ala Val
 265 270 275

 gtg aac cgc cga ggc atc cgc cgc gtt gtc gaa cta gaa atc acc gac 979
 Val Asn Arg Arg Gly Ile Arg Arg Val Val Glu Leu Glu Ile Thr Asp
 280 285 290

 cac gag atg gaa cgc ttc aag cat tcc gca aat acc ctg cgc gaa att 1027
 His Glu Met Glu Arg Phe Lys His Ser Ala Asn Thr Leu Arg Glu Ile
 295 300 305

 cag aag cag ttc ttc taaatctttg gcgcctagtt ggc 1065
 Gln Lys Gln Phe Phe
 310

<210> 130

<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<400> 130

Met Lys Glu Thr Val Gly Asn Lys Ile Val Leu Ile Gly Ala Gly Asp
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 Val Gly Val Ala Tyr Ala Tyr Ala Leu Ile Asn Gln Gly Met Ala Asp
 20 25 30

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

 Met Asp Leu Asn His Gly Val Val Trp Ala Asp Ser Arg Thr Arg Val
 50 55 60

 Thr Lys Gly Thr Tyr Ala Asp Cys Glu Asp Ala Ala Met Val Val Ile
 65 70 75 80

 Cys Ala Gly Ala Ala Gln Lys Pro Gly Glu Thr Arg Leu Gln Leu Val
 85 90 95

 Asp Lys Asn Val Lys Ile Met Lys Ser Ile Val Gly Asp Val Met Asp
 100 105 110

 Ser Gly Phe Asp Gly Ile Phe Leu Val Ala Ser Asn Pro Val Asp Ile
 115 120 125

 Leu Thr Tyr Ala Val Trp Lys Phe Ser Gly Leu Glu Trp Asn Arg Val

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130 135 140
 Ile Gly Ser Gly Thr Val Leu Asp Ser Ala Arg Phe Arg Tyr Met Leu
 145 150 155 160
 Gly Glu Leu Tyr Glu Val Ala Pro Ser Ser Val His Ala Tyr Ile Ile
 165 170 175
 Gly Glu His Gly Asp Thr Glu Leu Pro Val Leu Ser Ser Ala Thr Ile
 180 185 190
 Ala Gly Val Ser Leu Ser Arg Met Leu Asp Lys Asp Pro Glu Leu Glu
 195 200 205
 Gly Arg Leu Glu Lys Ile Phe Glu Asp Thr Arg Asp Ala Ala Tyr His
 210 215 220
 Ile Ile Asp Ala Lys Gly Ser Thr Ser Tyr Gly Ile Gly Met Gly Leu
 225 230 235 240
 Ala Arg Ile Thr Arg Ala Ile Leu Gln Asn Gln Asp Val Ala Val Pro
 245 250 255
 Val Ser Ala Leu Leu His Gly Glu Tyr Gly Glu Glu Asp Ile Tyr Ile
 260 265 270
 Gly Thr Pro Ala Val Val Asn Arg Arg Gly Ile Arg Arg Val Val Glu
 275 280 285
 Leu Glu Ile Thr Asp His Glu Met Glu Arg Phe Lys His Ser Ala Asn
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 Thr Leu Arg Glu Ile Gln Lys Gln Phe Phe
 305 310

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 <213> Corynebacterium glutamicum

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 <223> RXN00296

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 Met Thr His Thr Ile
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 aaa ttc aac aga ctc gac cca gaa gta ttt agc cag cat tct cgc gcg 163
 Lys Phe Asn Arg Leu Asp Pro Glu Val Phe Ser Gln His Ser Arg Ala
 10 15 20
 aag ctg cgc acg gat atg aca acc cgt gca gca tat tct tct gat gca 211
 Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala Tyr Ser Ser Asp Ala
 25 30 35

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gga att ttt aga cgc gtc cct gca gct gta gct gaa cca gaa aat gtg	259
Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu Asn Val	
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gaa caa att cgt gat gcc att gct gtt gcg gtg gca cga ggg tgg tct	307
Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val Ala Arg Gly Trp Ser	
55 60 65	
gtt gtt ggg cgc ggt gga gga agc tcg gtt gct gga aat gcg atc ggt	355
Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala Gly Asn Ala Ile Gly	
70 75 80 85	
gaa ggt ttg atc atc gat acg tca cgc tat ttc aac cgc att tta gat	403
Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe Asn Arg Ile Leu Asp	
90 95 100	
att gat cca gtt gca caa act gca gtt gtg gaa ccc ggt gtg gtg tgt	451
Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu Pro Gly Val Val Cys	
105 110 115	
gat gcc ttg cgc gat gca gcc gca gaa ttc gga tta act tac ggc ccg	499
Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly Leu Thr Tyr Gly Pro	
120 125 130	
gat cct tcc acg cat tcc cgg tgc acg atc ggt ggc atg gtt gcc aac	547
Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly Gly Met Val Ala Asn	
135 140 145	
aat gcg tgt ggt tca cac tcg gtt gca ttc ggt aca gct gcg gaa aat	595
Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly Thr Ala Ala Glu Asn	
150 155 160 165	
ctc gtg gat gtc acg ctc atg ctc agc gat ggc cga gaa gtc act gtg	643
Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly Arg Glu Val Thr Val	
170 175 180	
aca aaa gat ggc tgc gat gat gct gag atc aat cag aag ctc acc gac	691
Thr Lys Asp Gly Cys Asp Asp Ala Glu Ile Asn Gln Lys Leu Thr Asp	
185 190 195	
tta gcg tcc aag aat cag gac ctt att agt aaa gaa ctg ggt cgt ttc	739
Leu Ala Ser Lys Asn Gln Asp Leu Ile Ser Lys Glu Leu Gly Arg Phe	
200 205 210	
cct cgc caa gtg tcg ggc tac ggt ttg cat tat ctt gcc cac gac atg	787
Pro Arg Gln Val Ser Gly Tyr Gly Leu His Tyr Leu Ala His Asp Met	
215 220 225	
gcc aaa gca atg gcg ggc acc gag gga acc att gga atc att act cgg	835
Ala Lys Ala Met Ala Gly Thr Glu Gly Thr Ile Gly Ile Ile Thr Arg	
230 235 240 245	
ttg acg gtg aag ttg gtt cca aca ccc aaa gtg aaa gcg ctt gct gtc	883
Leu Thr Val Lys Leu Val Pro Thr Pro Lys Val Lys Ala Leu Ala Val	
250 255 260	
ctg gct ttc gac acg gtt ttt gac gcc gcc cga gca gcc gcc aaa ttg	931
Leu Ala Phe Asp Thr Val Phe Asp Ala Ala Arg Ala Ala Ala Lys Leu	
265 270 275	
cga ctg cct ggg gta gca acc att gaa ggc atg ggc gga gat ctc ctc	979

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gct	gcg	ctg	cgc	agt	aaa	cag	gga	caa	tca	gaa	gct	ggg	cag	aat	ctt	1027
Ala	Ala	Leu	Arg	Ser	Lys	Gln	Gly	Gln	Ser	Glu	Ala	Gly	Gln	Asn	Leu	
	295					300				305						
cca	gga	aac	cgc	atc	ggc	att	gaa	gcc	ggc	gga	tgg	ttg	tac	tgc	gag	1075
Pro	Gly	Asn	Arg	Ile	Gly	Ile	Glu	Ala	Gly	Gly	Trp	Leu	Tyr	Cys	Glu	
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aca	gga	agt	gac	acc	ctg	cag	gcc	gcg	gta	caa	gcc	gcc	gag	gaa	gtc	1123
Thr	Gly	Ser	Asp	Thr	Leu	Gln	Ala	Ala	Val	Gln	Ala	Ala	Glu	Glu	Val	
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gca	acc	gcc	gtt	gac	acc	att	gat	tac	gtg	gtc	gtg	tct	gag	cct	tct	1171
Ala	Thr	Ala	Val	Asp	Thr	Ile	Asp	Tyr	Val	Val	Val	Ser	Glu	Pro	Ser	
			345				350						355			
gaa	atg	cgg	gaa	ttg	tgg	cgc	atc	cgt	gaa	tcc	tcg	gcg	ggc	att	gtc	1219
Glu	Met	Arg	Glu	Leu	Trp	Arg	Ile	Arg	Glu	Ser	Ser	Ala	Gly	Ile	Val	
	360					365						370				
acg	cgc	tta	gct	gat	ggc	ggg	gaa	gcg	tgg	ccg	aat	tgg	gaa	gac	tcg	1267
Thr	Arg	Leu	Ala	Asp	Gly	Gly	Glu	Ala	Trp	Pro	Asn	Trp	Glu	Asp	Ser	
	375					380					385					
gcg	gtg	cct	cca	gag	aat	tta	gct	gat	tat	ctc	cgc	gat	ctt	tat	gcg	1315
Ala	Val	Pro	Pro	Glu	Asn	Leu	Ala	Asp	Tyr	Leu	Arg	Asp	Leu	Tyr	Ala	
390					395					400					405	
ctg	atg	gat	aag	ttc	gat	tac	cag	ggt	att	cca	ttt	gga	cac	ttt	gga	1363
Leu	Met	Asp	Lys	Phe	Asp	Tyr	Gln	Gly	Ile	Pro	Phe	Gly	His	Phe	Gly	
				410					415					420		
gaa	ggc	tgc	gtc	cac	gtt	cgc	atc	agt	ttt	gat	ttc	tct	acc	aag	gaa	1411
Glu	Gly	Cys	Val	His	Val	Arg	Ile	Ser	Phe	Asp	Phe	Ser	Thr	Lys	Glu	
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ggc	ctg	aag	aaa	ttc	gag	gcg	ttc	atg	aat	gaa	gcc	tcc	acc	ttg	gtg	1459
Gly	Leu	Lys	Lys	Phe	Glu	Ala	Phe	Met	Asn	Glu	Ala	Ser	Thr	Leu	Val	
	440					445						450				
gcg	tct	tat	ggt	ggc	agc	ctc	tcg	ggc	gag	cat	gga	gac	ggt	cgc	gcc	1507
Ala	Ser	Tyr	Gly	Gly	Ser	Leu	Ser	Gly	Glu	His	Gly	Asp	Gly	Arg	Ala	
	455					460					465					
cgc	tca	tcc	ttc	ctt	gac	cgc	atg	tat	tca	gca	gaa	atg	cgt	gca	ctc	1555
Arg	Ser	Ser	Phe	Leu	Asp	Arg	Met	Tyr	Ser	Ala	Glu	Met	Arg	Ala	Leu	
470					475					480					485	
ttc	gaa	gaa	ttc	aag	ctg	att	ttc	gat	ccc	cag	cgc	atc	ttc	aat	ccg	1603
Phe	Glu	Glu	Phe	Lys	Leu	Ile	Phe	Asp	Pro	Gln	Arg	Ile	Phe	Asn	Pro	
				490					495					500		
gga	gtg	ttg	gtc	tgg	gca	gat	cct	gtc	atg	caa	gga	ctt	cgc	atg	gac	1651
Gly	Val	Leu	Val	Trp	Ala	Asp	Pro	Val	Met	Gln	Gly	Leu	Arg	Met	Asp	
			505					510					515			
ccg	ggc	cag	cgc	gcc	ctc	gac	atc	acg	ccc	gta	cac	aaa	ttc	tct	aaa	1699
Pro	Gly	Gln	Arg	Ala	Leu	Asp	Ile	Thr	Pro	Val	His	Lys	Phe	Ser	Lys	

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gac	aaa	ggt	tcc	atg	atc	aac	gcg	gtg	aat	cgc	tgc	gtg	ggt	gta	tcc	1747		
Asp	Lys	Gly	Ser	Met	Ile	Asn	Ala	Val	Asn	Arg	Cys	Val	Gly	Val	Ser			
	535						540				545							
gca	tgc	cgc	tca	gaa	tcc	gac	gcg	atg	tgc	ccg	tcc	ttc	caa	atc	acc	1795		
Ala	Cys	Arg	Ser	Glu	Ser	Asp	Ala	Met	Cys	Pro	Ser	Phe	Gln	Ile	Thr			
	550				555					560					565			
ggc	gac	gaa	gta	cat	tcc	acc	aga	ggc	cgc	gcc	cgc	ttg	ctc	tct	gag	1843		
Gly	Asp	Glu	Val	His	Ser	Thr	Arg	Gly	Arg	Ala	Arg	Leu	Leu	Ser	Glu			
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Met	Phe	Arg	Gly	Glu	Ser	Ile	Ala	Asp	Gly	Tyr	Arg	Ser	Glu	Glu	Val			
			585					590					595					
aat	gaa	gcc	ctt	gac	ctg	tgc	ctt	tcc	tgc	aaa	gca	tgc	gca	tcg	gaa	1939		
Asn	Glu	Ala	Leu	Asp	Leu	Cys	Leu	Ser	Cys	Lys	Ala	Cys	Ala	Ser	Glu			
		600					605					610						
tgt	cca	gtc	aac	gtc	gac	atg	tcc	acc	tac	aaa	gcc	gaa	ttc	ctg	gac	1987		
Cys	Pro	Val	Asn	Val	Asp	Met	Ser	Thr	Tyr	Lys	Ala	Glu	Phe	Leu	Asp			
	615					620					625							
aaa	cac	tac	gcc	ggc	cga	ctt	cgc	ccc	atg	gcc	cat	tac	gtc	atg	ggc	2035		
Lys	His	Tyr	Ala	Gly	Arg	Leu	Arg	Pro	Met	Ala	His	Tyr	Val	Met	Gly			
	630				635					640					645			
tgg	ctg	ccg	ctt	ctg	gga	cac	gtt	gcc	cat	aaa	ata	ccg	ctt	ctt	cct	2083		
Trp	Leu	Pro	Leu	Leu	Gly	His	Val	Ala	His	Lys	Ile	Pro	Leu	Leu	Pro			
				650					655					660				
acg	ctt	atc	gac	gcc	acc	atg	cag	tca	gca	ctc	acc	gcc	cca	gtg	gtg	2131		
Thr	Leu	Ile	Asp	Ala	Thr	Met	Gln	Ser	Ala	Leu	Thr	Ala	Pro	Val	Val			
			665					670					675					
cgc	aag	gtc	ggc	ggg	ctc	gct	gat	cgc	ccg	ttg	att	tcc	ttc	gcc	cac	2179		
Arg	Lys	Val	Gly	Gly	Leu	Ala	Asp	Arg	Pro	Leu	Ile	Ser	Phe	Ala	His			
		680					685					690						
cgc	tcg	ctg	cgc	aag	tac	aag	ccg	aag	aaa	aac	tca	ggt	gaa	acg	gtg	2227		
Arg	Ser	Leu	Arg	Lys	Tyr	Lys	Pro	Lys	Lys	Asn	Ser	Gly	Glu	Thr	Val			
	695					700				705								
gtg	ctg	tgg	ccc	gat	tcc	ttc	aac	acc	aac	ctc	gac	acc	gga	cca	gct	2275		
Val	Leu	Trp	Pro	Asp	Ser	Phe	Asn	Thr	Asn	Leu	Asp	Thr	Gly	Pro	Ala			
	710				715					720					725			
cac	gca	gcg	atc	aaa	act	ctt	gaa	gcc	ctc	ggt	tac	aac	gtg	gtc	atc	2323		
His	Ala	Ala	Ile	Lys	Thr	Leu	Glu	Ala	Leu	Gly	Tyr	Asn	Val	Val	Ile			
			730						735					740				
cca	gat	ggc	ttc	gtc	tgc	tgt	gga	ctc	acc	tgg	cat	tcc	acc	ggc	caa	2371		
Pro	Asp	Gly	Phe	Val	Cys	Cys	Gly	Leu	Thr	Trp	His	Ser	Thr	Gly	Gln			
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ttg	agc	atg	aca	aag	aaa	gtc	cta	gaa	caa	acg	gcg	aaa	gtg	atg	aaa	2419		
Leu	Ser	Met	Thr	Lys	Lys	Val	Leu	Glu	Gln	Thr	Ala	Lys	Val	Met	Lys			
		760					765					770						


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ccc tac ctg gac caa ggt cta aca gtc gtt ggt ttg gaa cct tcg tgc 2467
Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly Leu Glu Pro Ser Cys
    775                                780                                785

acc gtc atg ctt caa gat gag gca aca gaa ctc tcc gat aac cct gat 2515
Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu Ser Asp Asn Pro Asp
    790                                795                                800                                805

ctg gca cgc ctt gca gca ctg acc aaa cca ttc gct gag gtc atc gca 2563
Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe Ala Glu Val Ile Ala
    810                                815                                820

cca aag atc acc gag cta gtc gag tct gga agc ctc cag cta aca gaa 2611
Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser Leu Gln Leu Thr Glu
    825                                830                                835

tca act gcg ctt acc cag gtg cac tgc cac gag cgt tcg cta ggc gac 2659
Ser Thr Ala Leu Thr Gln Val His Cys His Glu Arg Ser Leu Gly Asp
    840                                845                                850

cca caa caa tcg gca ctc gtt ctt gaa gct ttg ggt gta aaa gat gaa 2707
Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu Gly Val Lys Asp Glu
    855                                860                                865

caa att gcc act ggt tgt tgc ggg ctt gcc gga aac tgg ggc ttt gaa 2755
Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly Asn Trp Gly Phe Glu
    870                                875                                880                                885

aaa gac cac gct gaa atg tcc ttc gca ctt ggt gaa cga gag ctg ttc 2803
Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly Glu Arg Glu Leu Phe
    890                                895                                900

ccc aag gtc aga aaa gca gaa gga cat gtg att gct gac ggt ttc tcc 2851
Pro Lys Val Arg Lys Ala Glu Gly His Val Ile Ala Asp Gly Phe Ser
    905                                910                                915

tgc cgc acc cag atc gaa caa ggc acc gga aaa caa gca acg cac ctt 2899
Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys Gln Ala Thr His Leu
    920                                925                                930

gca gag gtg gtc tta agc atc ttg gag caa aac aac atg gca caa 2944
Ala Glu Val Val Leu Ser Ile Leu Glu Gln Asn Asn Met Ala Gln
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<211> 948

<212> PRT

<213> Corynebacterium glutamicum

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Gln His Ser Arg Ala Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala
      20              25              30

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Tyr Ser Ser Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala

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Ala	Arg	Gly	Trp	Ser	Val	Val	Gly	Arg	Gly	Gly	Gly	Ser	Ser	Val	Ala
65					70					75					80
Gly	Asn	Ala	Ile	Gly	Glu	Gly	Leu	Ile	Ile	Asp	Thr	Ser	Arg	Tyr	Phe
				85					90					95	
Asn	Arg	Ile	Leu	Asp	Ile	Asp	Pro	Val	Ala	Gln	Thr	Ala	Val	Val	Glu
			100					105					110		
Pro	Gly	Val	Val	Cys	Asp	Ala	Leu	Arg	Asp	Ala	Ala	Ala	Glu	Phe	Gly
		115					120					125			
Leu	Thr	Tyr	Gly	Pro	Asp	Pro	Ser	Thr	His	Ser	Arg	Cys	Thr	Ile	Gly
	130					135					140				
Gly	Met	Val	Ala	Asn	Asn	Ala	Cys	Gly	Ser	His	Ser	Val	Ala	Phe	Gly
145						150					155				160
Thr	Ala	Ala	Glu	Asn	Leu	Val	Asp	Val	Thr	Leu	Met	Leu	Ser	Asp	Gly
				165					170					175	
Arg	Glu	Val	Thr	Val	Thr	Lys	Asp	Gly	Cys	Asp	Asp	Ala	Glu	Ile	Asn
			180					185					190		
Gln	Lys	Leu	Thr	Asp	Leu	Ala	Ser	Lys	Asn	Gln	Asp	Leu	Ile	Ser	Lys
		195					200					205			
Glu	Leu	Gly	Arg	Phe	Pro	Arg	Gln	Val	Ser	Gly	Tyr	Gly	Leu	His	Tyr
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Leu	Ala	His	Asp	Met	Ala	Lys	Ala	Met	Ala	Gly	Thr	Glu	Gly	Thr	Ile
225						230					235				240
Gly	Ile	Ile	Thr	Arg	Leu	Thr	Val	Lys	Leu	Val	Pro	Thr	Pro	Lys	Val
				245					250					255	
Lys	Ala	Leu	Ala	Val	Leu	Ala	Phe	Asp	Thr	Val	Phe	Asp	Ala	Ala	Arg
			260					265					270		
Ala	Ala	Ala	Lys	Leu	Arg	Leu	Pro	Gly	Val	Ala	Thr	Ile	Glu	Gly	Met
		275					280					285			
Gly	Gly	Asp	Leu	Leu	Ala	Ala	Leu	Arg	Ser	Lys	Gln	Gly	Gln	Ser	Glu
	290					295					300				
Ala	Gly	Gln	Asn	Leu	Pro	Gly	Asn	Arg	Ile	Gly	Ile	Glu	Ala	Gly	Gly
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Trp	Leu	Tyr	Cys	Glu	Thr	Gly	Ser	Asp	Thr	Leu	Gln	Ala	Ala	Val	Gln
				325					330					335	
Ala	Ala	Glu	Glu	Val	Ala	Thr	Ala	Val	Asp	Thr	Ile	Asp	Tyr	Val	Val
			340					345					350		
Val	Ser	Glu	Pro	Ser	Glu	Met	Arg	Glu	Leu	Trp	Arg	Ile	Arg	Glu	Ser
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Ser Ala Gly Ile Val Thr Arg Leu Ala Asp Gly Gly Glu Ala Trp Pro
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 Asn Trp Glu Asp Ser Ala Val Pro Pro Glu Asn Leu Ala Asp Tyr Leu
 385 390 395 400
 Arg Asp Leu Tyr Ala Leu Met Asp Lys Phe Asp Tyr Gln Gly Ile Pro
 405 410 415
 Phe Gly His Phe Gly Glu Gly Cys Val His Val Arg Ile Ser Phe Asp
 420 425 430
 Phe Ser Thr Lys Glu Gly Leu Lys Lys Phe Glu Ala Phe Met Asn Glu
 435 440 445
 Ala Ser Thr Leu Val Ala Ser Tyr Gly Gly Ser Leu Ser Gly Glu His
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 Gly Asp Gly Arg Ala Arg Ser Ser Phe Leu Asp Arg Met Tyr Ser Ala
 465 470 475 480
 Glu Met Arg Ala Leu Phe Glu Glu Phe Lys Leu Ile Phe Asp Pro Gln
 485 490 495
 Arg Ile Phe Asn Pro Gly Val Leu Val Trp Ala Asp Pro Val Met Gln
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 Gly Leu Arg Met Asp Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val
 515 520 525
 His Lys Phe Ser Lys Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg
 530 535 540
 Cys Val Gly Val Ser Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro
 545 550 555 560
 Ser Phe Gln Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala
 565 570 575
 Arg Leu Leu Ser Glu Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr
 580 585 590
 Arg Ser Glu Glu Val Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys
 595 600 605
 Ala Cys Ala Ser Glu Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys
 610 615 620
 Ala Glu Phe Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala
 625 630 635 640
 His Tyr Val Met Gly Trp Leu Pro Leu Leu Gly His Val Ala His Lys
 645 650 655
 Ile Pro Leu Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu
 660 665 670
 Thr Ala Pro Val Val Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu
 675 680 685

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Ile Ser Phe Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn
 690 695 700
 Ser Gly Glu Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu
 705 710 715 720
 Asp Thr Gly Pro Ala His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly
 725 730 735
 Tyr Asn Val Val Ile Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp
 740 745 750
 His Ser Thr Gly Gln Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr
 755 760 765
 Ala Lys Val Met Lys Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly
 770 775 780
 Leu Glu Pro Ser Cys Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu
 785 790 795 800
 Ser Asp Asn Pro Asp Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe
 805 810 815
 Ala Glu Val Ile Ala Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser
 820 825 830
 Leu Gln Leu Thr Glu Ser Thr Ala Leu Thr Gln Val His Cys His Glu
 835 840 845
 Arg Ser Leu Gly Asp Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu
 850 855 860
 Gly Val Lys Asp Glu Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly
 865 870 875 880
 Asn Trp Gly Phe Glu Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly
 885 890 895
 Glu Arg Glu Leu Phe Pro Lys Val Arg Lys Ala Glu Gly His Val Ile
 900 905 910
 Ala Asp Gly Phe Ser Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys
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 <213> Corynebacterium glutamicum

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 <223> FRXA00296

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Arg Ala Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala Tyr Ser Ser	
20 25 30	
gat gca gga att ttt aga cgc gtc cct gca gct gta gct gaa cca gaa	144
Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu	
35 40 45	
aat gtg gaa caa att cgt gat gcc att gct gtt gcg gtg gca cga ggg	192
Asn Val Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val Ala Arg Gly	
50 55 60	
tgg tct gtt gtt ggg cgc ggt gga gga agc tcg gtt gct gga aat gcg	240
Trp Ser Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala Gly Asn Ala	
65 70 75 80	
atc ggt gaa ggt ttg atc atc gat acg tca cgc tat ttc aac cgc att	288
Ile Gly Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe Asn Arg Ile	
85 90 95	
tta gat att gat cca gtt gca caa act gca gtt gtg gaa ccc ggt gtg	336
Leu Asp Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu Pro Gly Val	
100 105 110	
gtg tgt gat gcc ttg cgc gat gca gcc gca gaa ttc gga tta act tac	384
Val Cys Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly Leu Thr Tyr	
115 120 125	
ggc ccg gat cct tcc acg cat tcc cgg tgc acg atc ggt ggc atg gtt	432
Gly Pro Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly Gly Met Val	
130 135 140	
gcc aac aat gcg tgt ggt tca cac tcg gtt gca ttc ggt aca gct gcg	480
Ala Asn Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly Thr Ala Ala	
145 150 155 160	
gaa aat ctc gtg gat gtc acg ctc atg ctc agc gat ggc cga gaa gtc	528
Glu Asn Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly Arg Glu Val	
165 170 175	
act gtg aca aaa gat ggc tgc gat gat gct gag atc aat cag aag ctc	576
Thr Val Thr Lys Asp Gly Cys Asp Asp Ala Glu Ile Asn Gln Lys Leu	
180 185 190	
acc gac tta gcg tcc aag aat cag gac ctt att agt aaa gaa ctg ggt	624
Thr Asp Leu Ala Ser Lys Asn Gln Asp Leu Ile Ser Lys Glu Leu Gly	
195 200 205	
cgt ttc cct cgc caa gtg tcg ggc tac ggt ttg cat tat ctt gcc cac	672
Arg Phe Pro Arg Gln Val Ser Gly Tyr Gly Leu His Tyr Leu Ala His	
210 215 220	
gac atg gcc aaa gca atg gcg ggc acc gag gga acc att gga atc att	720
Asp Met Ala Lys Ala Met Ala Gly Thr Glu Gly Thr Ile Gly Ile Ile	
225 230 235 240	

act cgg ttg acg gtg aag ttg gtt cca aca ccc aaa gtg aaa gcg ctt	768
Thr Arg Leu Thr Val Lys Leu Val Pro Thr Pro Lys Val Lys Ala Leu	
245 250 255	
gct gtc ctg gct ttc gac acg gtt ttt gac gcc gcc cga gca gcc gcc	816
Ala Val Leu Ala Phe Asp Thr Val Phe Asp Ala Ala Arg Ala Ala Ala	
260 265 270	
aaa ttg cga ctg cct ggg gta gca acc att gaa ggc atg ggc gga gat	864
Lys Leu Arg Leu Pro Gly Val Ala Thr Ile Glu Gly Met Gly Gly Asp	
275 280 285	
ctc ctc gct gcg ctg cgc agt aaa cag gga caa tca gaa gct ggg cag	912
Leu Leu Ala Ala Leu Arg Ser Lys Gln Gly Gln Ser Glu Ala Gly Gln	
290 295 300	
aat ctt cca gga aac cgc atc ggc att gaa gcc ggc gga tgg ttg tac	960
Asn Leu Pro Gly Asn Arg Ile Gly Ile Glu Ala Gly Gly Trp Leu Tyr	
305 310 315 320	
tgc gag aca gga agt gac acc ctg cag gcc gcg gta caa gcc gcc gag	1008
Cys Glu Thr Gly Ser Asp Thr Leu Gln Ala Ala Val Gln Ala Ala Glu	
325 330 335	
gaa gtc gca acc gcc gtt gac acc att gat tac gtg gtc gtg tct gag	1056
Glu Val Ala Thr Ala Val Asp Thr Ile Asp Tyr Val Val Val Ser Glu	
340 345 350	
cct tct gaa atg cgg gaa ttg tgg cgc atc cgt gaa tcc tcg gcg ggc	1104
Pro Ser Glu Met Arg Glu Leu Trp Arg Ile Arg Glu Ser Ser Ala Gly	
355 360 365	
att gtc acg cgc tta gct gat ggt ggg gaa gcg tgg ccg aat tgg gaa	1152
Ile Val Thr Arg Leu Ala Asp Gly Gly Glu Ala Trp Pro Asn Trp Glu	
370 375 380	
gac tcg gcg gtg cct cca gag aat tta gct gat tat ctc cgc gat ctt	1200
Asp Ser Ala Val Pro Pro Glu Asn Leu Ala Asp Tyr Leu Arg Asp Leu	
385 390 395 400	
tat gcg ctg atg gat aag ttc gat tac cag ggt att cca ttt gga cac	1248
Tyr Ala Leu Met Asp Lys Phe Asp Tyr Gln Gly Ile Pro Phe Gly His	
405 410 415	
ttt gga gaa ggc tgc gtc cac gtt cgc atc agt ttt gat ttc tct acc	1296
Phe Gly Glu Gly Cys Val His Val Arg Ile Ser Phe Asp Phe Ser Thr	
420 425 430	
aag gaa ggc ctg aag aaa ttc gag gcg ttc atg aat gaa gcc tcc acc	1344
Lys Glu Gly Leu Lys Lys Phe Glu Ala Phe Met Asn Glu Ala Ser Thr	
435 440 445	
ttg gtg gcg tct tat ggt ggc agc ctc tcg ggc gag cat gga gac ggt	1392
Leu Val Ala Ser Tyr Gly Gly Ser Leu Ser Gly Glu His Gly Asp Gly	
450 455 460	
cgc gcc cgc tca tcc ttc ctt gac cgc atg tat tca gca gaa atg cgt	1440
Arg Ala Arg Ser Ser Phe Leu Asp Arg Met Tyr Ser Ala Glu Met Arg	
465 470 475 480	

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gca ctc ttc gaa gaa ttc aag ctg att ttc gat ccc cag cgc atc ttc	1488
Ala Leu Phe Glu Glu Phe Lys Leu Ile Phe Asp Pro Gln Arg Ile Phe	
485 490 495	
aat ccg gga gtg ttg gtc tgg gca gat cct gtc atg caa gga ctt cgc	1536
Asn Pro Gly Val Leu Val Trp Ala Asp Pro Val Met Gln Gly Leu Arg	
500 505 510	
atg gac ccg ggc cag cgc gcc ctc gac atc acg ccc gta cac aaa ttc	1584
Met Asp Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val His Lys Phe	
515 520 525	
tct aaa gac aaa ggt tcc atg atc aac gcg gtg aat cgc tgc gtg ggt	1632
Ser Lys Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg Cys Val Gly	
530 535 540	
gta tcc gca tgc cgc tca gaa tcc gac gcg atg tgc ccg tcc ttc caa	1680
Val Ser Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro Ser Phe Gln	
545 550 555 560	
atc acc ggc gac gaa gta cat tcc acc aga ggc cgc gcc cgc ttg ctc	1728
Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala Arg Leu Leu	
565 570 575	
tct gag atg ttc cgc ggt gaa tcc atc gcc gac ggc tac cgc agc gaa	1776
Ser Glu Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr Arg Ser Glu	
580 585 590	
gaa gtc aat gaa gcc ctt gac ctg tgc ctt tcc tgc aaa gca tgc gca	1824
Glu Val Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys Ala Cys Ala	
595 600 605	
tcg gaa tgt cca gtc aac gtc gac atg tcc acc tac aaa gcc gaa ttc	1872
Ser Glu Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys Ala Glu Phe	
610 615 620	
ctg gac aaa cac tac gcc ggc cga ctt cgc ccc atg gcc cat tac gtc	1920
Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala His Tyr Val	
625 630 635 640	
atg ggc tgg ctg ccg ctt ctg gga cac gtt gcc cat aaa ata ccg ctt	1968
Met Gly Trp Leu Pro Leu Leu Gly His Val Ala His Lys Ile Pro Leu	
645 650 655	
ctt cct acg ctt atc gac gcc acc atg cag tca gca ctc acc gcc cca	2016
Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu Thr Ala Pro	
660 665 670	
gtg gtg cgc aag gtc ggc ggg ctc gct gat cgc ccg ttg att tcc ttc	2064
Val Val Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu Ile Ser Phe	
675 680 685	
gcc cac cgc tcg ctg cgc aag tac aag ccg aag aaa aac tca ggt gaa	2112
Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn Ser Gly Glu	
690 695 700	
acg gtg gtg ctg tgg ccc gat tcc ttc aac acc aac ctc gac acc gga	2160
Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu Asp Thr Gly	
705 710 715 720	
cca gct cac gca gcg atc aaa act ctt gaa gcc ctc ggt tac aac gtg	2208

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Pro	Ala	His	Ala	Ala	Ile	Lys	Thr	Leu	Glu	Ala	Leu	Gly	Tyr	Asn	Val	
				725					730					735		
gtc	atc	cca	gat	ggc	ttc	gtc	tgc	tgt	gga	ctc	acc	tgg	cat	tcc	acc	2256
Val	Ile	Pro	Asp	Gly	Phe	Val	Cys	Cys	Gly	Leu	Thr	Trp	His	Ser	Thr	
			740				745						750			
ggc	caa	ttg	agc	atg	aca	aag	aaa	gtc	cta	gaa	caa	acg	gcg	aaa	gtg	2304
Gly	Gln	Leu	Ser	Met	Thr	Lys	Lys	Val	Leu	Glu	Gln	Thr	Ala	Lys	Val	
		755				760						765				
atg	aaa	ccc	tac	ctg	gac	caa	ggc	cta	aca	gtc	gtt	ggc	ttg	gaa	cct	2352
Met	Lys	Pro	Tyr	Leu	Asp	Gln	Gly	Leu	Thr	Val	Val	Gly	Leu	Glu	Pro	
	770					775					780					
tcg	tgc	acc	gtc	atg	ctt	caa	gat	gag	gca	aca	gaa	ctc	tcc	gat	aac	2400
Ser	Cys	Thr	Val	Met	Leu	Gln	Asp	Glu	Ala	Thr	Glu	Leu	Ser	Asp	Asn	
785					790				795						800	
cct	gat	ctg	gca	cgc	ctt	gca	gca	ctg	acc	aaa	cca	ttc	gct	gag	gtc	2448
Pro	Asp	Leu	Ala	Arg	Leu	Ala	Ala	Leu	Thr	Lys	Pro	Phe	Ala	Glu	Val	
				805					810					815		
atc	gca	cca	aag	atc	acc	gag	cta	gtc	gag	tct	gga	agc	ctc	cag	cta	2496
Ile	Ala	Pro	Lys	Ile	Thr	Glu	Leu	Val	Glu	Ser	Gly	Ser	Leu	Gln	Leu	
			820					825					830			
aca	gaa	tca	act	gcg	ctt	acc	cag	gtg	cac	tgc	cac	gag	cgt	tcg	cta	2544
Thr	Glu	Ser	Thr	Ala	Leu	Thr	Gln	Val	His	Cys	His	Glu	Arg	Ser	Leu	
		835					840					845				
ggc	gac	cca	caa	caa	tcg	gca	ctc	gtt	ctt	gaa	gct	ttg	ggc	gta	aaa	2592
Gly	Asp	Pro	Gln	Gln	Ser	Ala	Leu	Val	Leu	Glu	Ala	Leu	Gly	Val	Lys	
	850					855					860					
gat	gaa	caa	att	gcc	act	ggc	tgt	tgc	ggg	ctt	gcc	gga	aac	tgg	ggc	2640
Asp	Glu	Gln	Ile	Ala	Thr	Gly	Cys	Cys	Gly	Leu	Ala	Gly	Asn	Trp	Gly	
865					870					875					880	
ttt	gaa	aaa	gac	cac	gct	gaa	atg	tcc	ttc	gca	ctt	ggc	gaa	cga	gag	2688
Phe	Glu	Lys	Asp	His	Ala	Glu	Met	Ser	Phe	Ala	Leu	Gly	Glu	Arg	Glu	
				885					890					895		
ctg	ttc	ccc	aag	gtc	aga	aaa	gca	gaa	gga	cat	gtg	att	gct	gac	ggc	2736
Leu	Phe	Pro	Lys	Val	Arg	Lys	Ala	Glu	Gly	His	Val	Ile	Ala	Asp	Gly	
			900					905					910			
ttc	tcc	tgc	cgc	acc	cag	atc	gaa	caa	ggc	acc	gga	aaa	caa	gca	acg	2784
Phe	Ser	Cys	Arg	Thr	Gln	Ile	Glu	Gln	Gly	Thr	Gly	Lys	Gln	Ala	Thr	
		915					920					925				
cac	ctt	gca	gag	gtg	gtc	tta	agc	atc	ttg	gag	caa	aac	aac	atg	gca	2832
His	Leu	Ala	Glu	Val	Val	Leu	Ser	Ile	Leu	Glu	Gln	Asn	Asn	Met	Ala	
	930					935					940					
caa	taacgatcat	gcaacaggtg	ctc													2858
Gln																
945																

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DEMANDES OU BREVETS VOLUMINEUX

**LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVETS
COMPREND PLUS D'UN TOME.**

CECI EST LE TOME __1__ DE __3__

NOTE: Pour les tomes additionels, veuillez contacter le Bureau Canadien des Brevets.

JUMBO APPLICATIONS / PATENTS

**THIS SECTION OF THE APPLICATION / PATENT CONTAINS MORE
THAN ONE VOLUME.**

THIS IS VOLUME __1__ OF __3__

NOTE: For additional volumes please contact the Canadian Patent Office.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding an
5 SMP protein, or a portion thereof, provided that the nucleic acid molecule does not
consist of any of the F-designated genes set forth in Table 1.
2. The isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule
encodes an SMP protein involved in the production of a fine chemical.
- 10 3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the
group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the
Sequence Listing, or a portion thereof, provided that the nucleic acid molecule does
not consist of any of the F-designated genes set forth in Table 1.
- 15 4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected
from the group consisting of those sequences set forth as even-numbered SEQ ID
NOs of the Sequence Listing,, provided that the nucleic acid molecule does not
consist of any of the F-designated genes set forth in Table 1.
- 20 5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant
of a polypeptide selected from the group of amino acid sequences consisting of those
sequences set forth in as even-numbered SEQ ID NOs of the Sequence Listing,
provided that the nucleic acid molecule does not consist of any of the F-designated
25 genes set forth in Table 1.
6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least
50% homologous to a nucleotide sequence selected from the group consisting of
those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or
30 a portion thereof, provided that the nucleic acid molecule does not consist of any of
the F-designated genes set forth in Table 1.

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7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.
9. An isolated nucleic acid molecule comprising the nucleic acid molecule of any one of claims 1-8 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.
10. A vector comprising the nucleic acid molecule of any one of claims 1-9.
11. The vector of claim 10, which is an expression vector.
12. A host cell transfected with the expression vector of claim 11.
13. The host cell of claim 12, wherein said cell is a microorganism.
14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.
16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

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17. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.

5 18. An isolated SMP polypeptide from *Corynebacterium glutamicum*, or a portion thereof.

19. The polypeptide of claim 18, wherein said polypeptide is involved in the production of a fine chemical.

10

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1,

15

21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the amino acid sequence is not encoded
20 by any of the F-designated genes set forth in Table 1.

22. The isolated polypeptide of any of claims 18-21, further comprising heterologous amino acid sequences.

25 23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.

30

24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those

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sequences as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

- 5 25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.
26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.
- 10 27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.
- 15 28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium, lilium*,
20 *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*,
Corynebacterium acetophilum, *Corynebacterium ammoniagenes*, *Corynebacterium fujiokense*, *Corynebacterium nitrilophilus*, *Brevibacterium ammoniagenes*,
Brevibacterium butanicum, *Brevibacterium divaricatum*, *Brevibacterium flavum*,
Brevibacterium healii, *Brevibacterium ketoglutamicum*, *Brevibacterium*
25 *ketosoreductum*, *Brevibacterium lactofermentum*, *Brevibacterium linens*,
Brevibacterium paraffinolyticum, and those strains set forth in Table 3.
30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.
- 30 31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine

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and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

5 32. The method of claim 25, wherein said fine chemical is an amino acid.

33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine,
10 tyrosine, phenylalanine, and tryptophan.

34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.

15

35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more of SEQ ID NOs 1 through 782 of the Sequence Listing in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1,
20 thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.

36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the
25 Sequence Listing, wherein the nucleic acid molecule is disrupted.

35. 37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs in the Sequence Listing, wherein the nucleic acid molecule comprises one or more
30 nucleic acid modifications from the sequence set forth as odd-numbered SEQ ID NOs of the Sequence Listing s.

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38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the regulatory region of the nucleic acid molecule is modified
5 relative to the wild-type regulatory region of the molecule.