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(54) Title: *CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING METABOLIC PATHWAY PROTEINS

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



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***CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING METABOLIC PATHWAY PROTEINS**

Related Applications

5 The present application is an continuation in part of U.S. Patent Application 09/606,740, filed June 23, 2000. This application is also a continuation in part of U.S. Patent Application 09/603,124, filed June 23, 2000. The present application claims priority to prior filed U.S. Provisional Patent Application Serial No. 60/141031, filed June 25, 1999, U.S. Provisional Patent Application Serial No. 60/142101, filed July 2, 10 1999, U.S. Provisional Patent Application Serial No. 60/148613, filed August 12, 1999, U.S. Provisional Patent Application Serial No. 60/187970, filed March 9, 2000, and also to German Patent Application No. 19931420.9, filed July 8, 1999. The entire contents of all of the aforementioned applications are hereby expressly incorporated herein by this reference.

15

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', 20 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 large-scale culture of bacteria developed to produce and secrete large quantities of a particular desired molecule. One particularly useful 25 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.

30

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 (*e.g.*, amino acids, such as, for example, lysine and methionine), 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.

- 5 These novel nucleic acid molecules encode proteins, referred to herein as metabolic pathway (MP) 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
10 terpenoids. The MP 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 MP nucleic acids of the invention, or modification of the sequence of the MP nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a
15 microorganism (*e.g.*, to improve the yield or production of one or more fine chemicals from a *Corynebacterium* or *Brevibacterium* species). In a preferred embodiment, the MP genes of the invention are combined with one or more genes involved in the same or different metabolic pathway to modulate the production of one or more fine chemicals from a microorganism.

- 20 The MP 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 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
25 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. 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
30 significant clinical relevance.

The MP nucleic acid molecules of the invention may also serve as reference 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 MP proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing an enzymatic step involved in the metabolism of certain fine chemicals, including amino acids, *e.g.*, lysine and methionine, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. 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 *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 direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation. Specifically, alterations in *C. glutamicum* metabolic pathways for amino acids, *e.g.*, lysine and methionine, vitamins, cofactors, nucleotides, and trehalose may have a direct impact on the overall production of one or more of these desired compounds from this organism. For example, optimizing the activity of a lysine or a methionine biosynthetic pathway protein or decreasing the activity of a lysine or methionine degradative pathway protein may result in an increase in the yield or efficiency of production of lysine or methionine from such an engineered organism. Alterations in the proteins involved in these metabolic pathways may also have an indirect impact on the production or efficiency of production of a desired fine chemical. For example, a reaction which is in competition for an intermediate necessary for the production of a desired molecule may be eliminated, or a pathway necessary for the production of a particular intermediate for a desired compound may be optimized. Further, modulations in the biosynthesis or degradation of, for example, an amino acid, *e.g.*, lysine or methionine, a vitamin, or a nucleotide may increase the overall ability of the microorganism to rapidly grow and divide, thus increasing the number and/or production capacities of the microorganism in culture and thereby increasing the possible yield of the desired fine chemical.

The nucleic acid and protein molecules of the invention, alone or in combination with one or more nucleic acid and protein molecules of the same or different metabolic pathway, may be utilized to directly improve the production or efficiency of production of one or more desired fine chemicals from *Corynebacterium glutamicum* (e.g., methionine or lysine). Using recombinant genetic techniques well known in the art, one or more of the biosynthetic or degradative enzymes of the invention for amino acids, e.g., lysine and methionine, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, or trehalose may be manipulated such that its function is modulated. For example, a biosynthetic enzyme may be improved in efficiency, or its allosteric control region destroyed such that feedback inhibition of production of the compound is prevented. Similarly, a degradative enzyme may be deleted or modified by substitution, deletion, or addition such that its degradative activity is lessened for the desired compound without impairing the viability of the cell. In each case, the overall yield or rate of production of the desired fine chemical may be increased.

It is also possible that such alterations in the protein and nucleotide molecules of the invention may improve the production of other fine chemicals besides the amino acids, e.g., lysine and methionine, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose through indirect mechanisms. Metabolism of any one compound is necessarily intertwined with other biosynthetic and degradative pathways within the cell, and necessary cofactors, intermediates, or substrates in one pathway are likely supplied or limited by another such pathway. Therefore, by modulating the activity of one or more of the proteins of the invention, the production or efficiency of activity of another fine chemical biosynthetic or degradative pathway may be impacted. For example, amino acids serve as the structural units of all proteins, yet may be present intracellularly in levels which are limiting for protein synthesis; therefore, by increasing the efficiency of production or the yields of one or more amino acids within the cell, proteins, such as biosynthetic or degradative proteins, may be more readily synthesized. Likewise, an alteration in a metabolic pathway enzyme such that a particular side reaction becomes more or less favored may result in the over- or under-production of one or more compounds which are utilized as intermediates or substrates for the production of a desired fine chemical.

This invention provides novel nucleic acid molecules which encode proteins, referred to herein as metabolic pathway ("MP") proteins, which are capable of, for

example, performing an enzymatic step involved in the metabolism of molecules important for the normal functioning of cells, such as amino acids, *e.g.*, lysine and methionine, vitamins, cofactors, nucleotides and nucleosides, or trehalose. Nucleic acid molecules encoding an MP protein are referred to herein as MP nucleic acid molecules.

- 5 In a preferred embodiment, an MP protein, alone or in combination with one or more proteins of the same or different metabolic pathway, performs an enzymatic step related to the metabolism of one or more of the following: amino acids, *e.g.*, lysine and methionine, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. Examples of such proteins include those encoded by the genes set forth in Table 1.
- 10 Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an MP protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of MP-encoding nucleic acid (*e.g.*, DNA or mRNA). In particularly preferred embodiments,
- 15 the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth as the odd-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:5), or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or
- 20 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 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99%, 99.7% or
- 25 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, or SEQ ID NO:5), 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, or SEQ ID NO:6). The preferred MP
- 30 proteins of the present invention also preferably possess at least one of the MP 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

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, such as SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6), *e.g.*, sufficiently homologous to an amino acid sequence of the invention such that the protein or portion thereof maintains an MP activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to perform an enzymatic reaction in a amino acid, *e.g.*, lysine or methionine, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway. In one embodiment, the protein encoded by the nucleic acid molecule 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 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99%, 99.7% or more homologous to an amino acid sequence of the invention (*e.g.*, an entire amino acid sequence selected from those having an even-numbered SEQ ID NO in the Sequence Listing, such as SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6). 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-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:5).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an MP fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of one of the even-numbered SEQ ID NOs in the Sequence Listing, such as SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6) and is able to catalyze a reaction in a metabolic pathway for an amino acid, *e.g.*, lysine or methionine, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose, or one or more of the activities set forth in Table 1, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

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, such as SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:5). 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* MP protein, or a biologically active
5 portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, alone or in combination with one or more nucleic acid molecules involved in the same or different pathway, and host cells into which such vectors have been introduced. In one embodiment, such a
10 host cell is used to produce an MP protein by culturing the host cell in a suitable medium. The MP 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 one or more MP genes, alone or in combination with one or more genes involved in the same or different metabolic pathway, have been introduced
15 or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding one or more wild-type or mutated MP sequences as transgenes alone or in combination with one or more nucleic acid molecules involved in the same or different metabolic pathway. In another embodiment, one or more endogenous MP genes within the genome of the
20 microorganism have been altered, *e.g.*, functionally disrupted, by homologous recombination with one or more altered MP genes. In another embodiment, one or more endogenous or introduced MP genes, alone or in combination with one or more genes of the same or different metabolic pathway in a microorganism have been altered by one or more point mutations, deletions, or inversions, but still encode functional MP proteins.
25 In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of one or more MP genes in a microorganism, alone or in combination with one or more MP genes or in combination with one or more genes of the same or different metabolic pathway, has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of one or more MP genes is
30 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 and

methionine being particularly preferred. In a particularly preferred embodiment, the MP gene is the *metZ* gene (SEQ ID NO:1), *metC* gene (SEQ ID NO:3), or the RXA00657 gene (SEQ ID NO:5), alone or in combination with one or more MP genes of the invention or in combination with one or more genes involved in methionine and/or lysine metabolism.

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 sequences set forth in Table 1 and in the Sequence Listing as SEQ ID NOs 1 through 122) 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 MP protein or portion, *e.g.*, biologically active portion, thereof. In a preferred embodiment, the isolated MP protein or portion thereof, alone or in combination with one or more MP proteins of the invention or in combination with one or more proteins of the same or different metabolic pathway, can catalyze an enzymatic reaction involved in one or more pathways for the metabolism of an amino acid, *e.g.*, lysine or methionine, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose. In another preferred embodiment, the isolated MP 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 as SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6) such that the protein or portion thereof maintains the ability to catalyze an enzymatic reaction involved in one or more pathways for the metabolism of an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose.

The invention also provides an isolated preparation of an MP protein. In preferred embodiments, the MP protein comprises an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing such as SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6). 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 such as SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6) (encoded by an open reading frame set forth in a corresponding odd-numbered SEQ ID NO: of the Sequence Listing such as SEQ ID

NO:1, SEQ ID NO:3, or SEQ ID NO:5). In yet another embodiment, the protein 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%,
5 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%, 99.7% 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 such as SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6). In other embodiments, the isolated MP protein comprises an
10 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 such as SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6) and is able to catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway either alone or in
15 combination one or more MP proteins of the invention or any protein of the same or different metabolic pathway, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated MP 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%, 51%, 52%, 53%, 54%, 55%, 56%, 57%,
20 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%, 98%, 99%, 99.7% or more homologous to a nucleotide sequence of one of the even-numbered
25 SEQ ID NOs set forth in the Sequence Listing. It is also preferred that the preferred forms of MP proteins also have one or more of the MP bioactivities described herein.

The MP polypeptide, or a biologically active portion thereof, can be operatively linked to a non-MP polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the MP protein alone. In other
30 preferred embodiments, this fusion protein, when introduced into a *C. glutamicum* pathway for the metabolism of an amino acid, vitamin, cofactor, nutraceutical, results in increased yields and/or efficiency of production of a desired fine chemical from *C. glutamicum*. In particularly preferred embodiments, integration of this fusion protein

into an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway of a host cell modulates production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which
5 modulate the activity of an MP protein, either by interacting with the protein itself or a substrate or binding partner of the MP protein, or by modulating the transcription or translation of an MP 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 one or more vectors
10 directing the expression of one or more MP nucleic acid molecules of the either alone or in combination one or more MP nucleic acid molecules of the invention or any nucleic acid molecule of the same or different metabolic pathway, such that a fine chemical 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
15 expression of an MP 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 *Brevibacterium*, or is selected from those strains set forth in Table 3. In another preferred embodiment, the MP genes is the *metZ* gene (SEQ ID NO:1), *metC* gene (SEQ ID NO:3), or the gene
20 designated as RXA00657 (SEQ ID NO:5) (see Table 1), alone or in combination with one or more MP nucleic acid molecules of the invention or with one or more genes involved in methionine and/or lysine metabolism. In yet another preferred embodiment, the fine chemical is an amino acid, *e.g.*, L-lysine and L-methionine.

Another aspect of the invention pertains to methods for modulating production of
25 a molecule from a microorganism. Such methods include contacting the cell with an agent which modulates MP protein activity or MP 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* amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose
30 metabolic pathways, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates MP protein activity can be an agent which stimulates MP protein activity or MP nucleic acid expression. Examples of agents which stimulate MP protein activity or MP nucleic acid expression

include small molecules, active MP proteins, and nucleic acids encoding MP proteins that have been introduced into the cell. Examples of agents which inhibit MP activity or expression include small molecules and antisense MP nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a
5 desired compound from a cell, involving the introduction of a wild-type or mutant MP gene into a cell, either alone or in combination one or more MP nucleic acid molecules of the invention or any nucleic acid molecule of the same or different metabolic pathway, 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
10 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
15 acid are L-lysine and L-methionine. In another preferred embodiment, said gene is the *metZ* gene (SEQ ID NO:1), *metC* gene (SEQ ID NO:3), or the RXA00657 gene (SEQ ID NO:5), alone or in combination with one or more MP nucleic acid molecules of the invention or with one or more genes involved in methionine and/or lysine metabolism.

20 **Detailed Description of the Invention**

The present invention provides MP nucleic acid and protein molecules which are involved in the metabolism of certain fine chemicals in *Corynebacterium glutamicum*, including amino acids, *e.g.*, lysine and methionine, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. The molecules of the invention may be utilized
25 in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (*e.g.*, where modulation of the activity of a lysine or methionine biosynthesis protein has a direct impact on the production or efficiency of production of lysine or methionine from that organism), or may have an indirect impact which nonetheless results in an increase of yield or efficiency of production of the
30 desired compound (*e.g.*, where modulation of the activity of a nucleotide biosynthesis protein has an impact on the production of an organic acid or a fatty acid from the bacterium, perhaps due to improved growth or an increased supply of necessary co-factors, energy compounds, or precursor molecules). The MP molecules may be utilized

alone or in combination with other MP molecules of the invention, or in combination with other molecules involved in the same or a different metabolic pathway (*e.g.*, lysine or methionine metabolism). In a preferred embodiment, the MP molecules are the *metZ* (SEQ ID NO:1), *metC* (SEQ ID NO:3), or RXA00657 (SEQ ID NO:5) nucleic acid molecules and the proteins encoded by these nucleic acid molecules (SEQ ID NO:2, SEQ ID NO:4 and SEQ ID NO:6, respectively). Aspects of the invention are further explicated below.

I. Fine Chemicals

10 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, 15 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, 20 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 – 25 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-

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:

- 5 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
10 (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
15 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
20 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,
25 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
30 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 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.

The biosynthetic pathways leading to methionine have been studied in diverse organisms. The first step, acylation of homoserine, is common to all of the organisms, even though the source of the transferred acyl groups is different. *Escherichia coli* and the related species use succinyl-CoA (Michaeli, S. and Ron, E. Z. (1981) *Mol. Gen. Genet.* 182, 349-354), while *Saccharomyces cerevisiae* (Langin, T., et al. (1986) *Gene* 49, 283-293), *Brevibacterium flavum* (Miyajima, R. and Shiio, I. (1973) *J. Biochem.* 73, 1061-1068; Ozaki, H. and Shiio, I. (1982) *J. Biochem.* 91, 1163-1171), *C. glutamicum* (Park, S.-D., et al. (1998) *Mol. Cells* 8, 286-294), and *Leptospira meyeri* (Belfaiza, J. et al. (1998) 180, 250-255; Bourhy, P., et al. (1997) *J. Bacteriol.* 179, 4396-4398) use acetyl-CoA as the acyl donor. Formation of homocysteine from acylhomoserine can occur in two different ways. *E. coli* uses the transsulfuration pathway which is catalyzed by cystathionine γ -synthase (the product of *metB*) and cystathionine β -lyase

(the product of *metC*). *S. cerevisiae* (Cherest, H. and Surdin-Kerjan, Y. (1992) *Genetics* 130, 51-58), *B. flavum* (Ozaki, H. and Shiio, I. (1982) *J. Biochem.* 91, 1163-1171), *Pseudomonas aeruginosa* (Foglino, M., *et al.* (1995) *Microbiology* 141, 431-439), and *L. meyeri* (Belfaiza, J., *et al.* (1998) *J. Bacteriol.* 180, 250-255) utilize the direct

5 sulfhydrylation pathway which is catalyzed by acylhomoserine sulfhydrylase. Unlike closely related *B. flavum* which uses only the direct sulfhydrylation pathway, enzyme activities of the transsulfuration pathway have been detected in the extracts of the *C. glutamicum* cells and the pathway has been proposed to be the route for methionine biosynthesis in the organism (Hwang, B-J., *et al.* (1999) *Mol. Cells* 9, 300-308; Kase, H.

10 and Nakayama, K. (1974) *Agr. Biol. Chem.* 38, 2021-2030; Park, S.-D., *et al.* 1998) *Mol. Cells* 8, 286-294).

Although some genes involved in methionine biosynthesis in *C. glutamicum* have been isolated, information on the biosynthesis of methionine in *C. glutamicum* is still very limited. No genes other than *metA* and *metB* have been isolated from the

15 organism. To understand the biosynthetic pathways leading to methionine in *C. glutamicum*, we have isolated and characterized the *metC* gene (SEQ ID NO:3) and the *metZ* (also called *metY*) gene (SEQ ID NO:1) of *C. glutamicum* (see Table 1).

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

20 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,

25 in which the presence of a particular amino acid serves to slow or entirely stop its own 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.

30

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 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 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" 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 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 & Sons; 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: 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, pyridoxa-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 panthotenic 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 panthothante, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B₅), pantetheine (and its derivatives) and coenzyme A.

10 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 is 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. 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 (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 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

5 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
10 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
15 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
20 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 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
25 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
30 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 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 many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. 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 MP nucleic acid and protein molecules (see Table 1), which play a role in or function in one or more cellular metabolic pathways. In one embodiment, the MP molecules catalyze an enzymatic reaction involving one or more amino acid, *e.g.*, lysine or methionine, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways. In a preferred embodiment, the activity of one or more MP molecules of the present invention, alone or in combination with molecules involved in the same or different metabolic pathway (*e.g.*, methionine or lysine metabolism), in one or more *C. glutamicum* metabolic pathways for amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides or trehalose has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the MP molecules of the invention are modulated in activity, such that the *C. glutamicum* metabolic pathways in which the MP proteins of the invention are involved are modulated in efficiency or output, which either directly or indirectly modulates the production or efficiency of production of a desired fine chemical by *C. glutamicum*. In a preferred embodiment, the fine chemical is an amino acid, *e.g.*, lysine or methionine. In another preferred embodiment, the MP molecules are metZ, metY, and/or RXA00657 (see Table 1).

The language, "MP protein" or "MP polypeptide" includes proteins which play a role in, *e.g.*, catalyze an enzymatic reaction, in one or more amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside or trehalose metabolic pathways. Examples of MP proteins include those encoded by the MP genes set forth in Table 1 and by the odd-numbered SEQ ID NOs. The terms "MP gene" or "MP nucleic acid sequence" include nucleic acid sequences encoding an MP protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of MP 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 products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. 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.

The MP molecules of the present invention may be combined with one or more MP molecules of the invention or one or more molecules of the same or different metabolic pathway to increase the yield of a desired fine chemical. In a preferred embodiment, the fine chemical is an amino acid, *e.g.*, lysine or methionine. Alternatively, or in addition, a byproduct which is not desired may be reduced by combination or disruption of MP molecules or other metabolic molecules (*e.g.*, molecules involved in lysine or methionine metabolism). MP molecules combined with other molecules of the same or a different metabolic pathway may be altered in their nucleotide sequence and in the corresponding amino acid sequence to alter their activity under physiological conditions, which leads to an increase in productivity and/or yield of a desired fine chemical. In a further embodiment, an MP molecule in its original or in its above-described altered form may be combined with other molecules of the same or a different metabolic pathway which are altered in their nucleotide sequence in such a way that their activity is altered under physiological conditions which leads to an increase in productivity and/or yield of a desired fine chemical, *e.g.*, an amino acid such as methionine or lysine.

In another embodiment, the MP molecules of the invention, alone or in combination with one or more molecules of the same or different metabolic pathway, are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. Using recombinant genetic techniques, one or more of the biosynthetic or degradative enzymes of the invention for amino acids, *e.g.*, lysine or methionine, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, or trehalose may be manipulated such that its function is modulated. For example, a biosynthetic enzyme may be improved in efficiency, or its allosteric control region destroyed such that feedback inhibition of production of the compound is prevented. Similarly, a degradative enzyme may be deleted or modified by substitution, deletion, or addition such that its degradative activity is lessened for the desired compound without impairing the viability of the cell. In each case, the overall yield or rate of production of one of these desired fine chemicals may be increased.

It is also possible that such alterations in the protein and nucleotide molecules of the invention may improve the production of other fine chemicals besides the amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. Metabolism of any one compound is necessarily intertwined with other biosynthetic and degradative pathways within the cell, and necessary cofactors, intermediates, or substrates in one pathway are likely supplied or limited by another such pathway. Therefore, by modulating the activity of one or more of the proteins of the invention, the production or efficiency of activity of another fine chemical biosynthetic or degradative pathway may be impacted. For example, amino acids serve as the structural units of all proteins, yet may be present intracellularly in levels which are limiting for protein synthesis; therefore, by increasing the efficiency of production or the yields of one or more amino acids within the cell, proteins, such as biosynthetic or degradative proteins, may be more readily synthesized. Likewise, an alteration in a metabolic pathway enzyme such that a particular side reaction becomes more or less favored may result in the over- or under-production of one or more compounds which are utilized as intermediates or substrates for the production of a desired fine chemical.

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* MP DNAs and the predicted amino acid sequences of the *C.*

glutamicum MP 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 metabolic pathway proteins, *e.g.*, proteins involved in the methionine or lysine metabolic pathways.

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 (*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%, 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%, 98%, 99%, 99.7% or more homologous to the selected amino acid sequence.

An MP protein of the invention, or a biologically active portion or fragment thereof, alone or in combination with one or more proteins of the same or different metabolic pathway, can catalyze an enzymatic reaction in one or more amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways, or have one or more of the activities set forth in Table 1 (*e.g.*, metabolism of methionine or lysine biosynthesis).

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 MP 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 MP-encoding nucleic acid (*e.g.*, MP 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 genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated MP 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 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 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* MP DNA can be isolated from a *C. glutamicum* library using all or portion of one of the odd-numbered SEQ ID NO sequences of the Sequence Listing as a hybridization probe and standard hybridization techniques (*e.g.*, as described in Sambrook, J., Fritsch, 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 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 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 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 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 MP nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*, 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* MP DNAs of the invention. This DNA comprises sequences encoding MP 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 nucleic acid sequences of the Sequence Listing.

For the purposes of this application, it will be understood that some of the MP nucleic acid and amino acid sequences set forth in the Sequence Listing have an identifying RXA, RXN, RXS, or RXC number having the designation "RXA", "RXN", "RXS", or "RXC" followed by 5 digits (*i.e.*, RXA, RXN, RXS, or RXC). Each of the nucleic acid sequences 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, RXS, or RXC 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, RXS, or RXC 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 RXA00115 is set forth in SEQ ID NO:69, while the amino acid sequence which it encodes is set forth as SEQ ID NO:70. The sequences of the nucleic acid molecules of the invention are identified by the same RXA, RXN, RXS, or RXC designations as the amino acid molecules which they encode, such that they can be readily correlated. For example, the amino acid sequences designated RXA00115, RXN00403, and RXS03158 are translations of the coding regions of the nucleotide sequences of nucleic acid molecules RXA00115, RXN00403, and RXS03158, respectively. The correspondence between the RXA, RXN, RXS, and RXC nucleotide and 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, RXN, RXS, or RXC designation. For example, SEQ ID NO:77, designated, as indicated on Table 1, as "F RXA00254", is an F-designated gene.

Also listed on Table 1 are the *metZ* (or *metY*) and *metC* genes (designated as SEQ ID NO:1 and SEQ ID NO:3, respectively). The corresponding amino acid sequence encoded by the *metZ* and *metC* genes are designated as SEQ ID NO:2 and SEQ ID NO:5, respectively.

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2.

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 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%,

- 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
- 5 about 95%, 96%, 97%, 98%, 99%, 99.7% 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 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
- 10 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.*, hybridizes under stringent conditions, to one of the nucleotide sequences of the invention, or a portion thereof.
- 15 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 or a fragment encoding a biologically active portion of an MP protein. The nucleotide sequences determined from the cloning of the MP genes from *C. glutamicum* allows for
- 20 the generation of probes and primers designed for use in identifying and/or cloning MP homologues in other cell types and organisms, as well as MP homologues from other *Corynebacteria* or related species. The probe/primer typically comprises 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 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 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 MP homologues.
- 30 Probes based on the MP 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.* 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 MP protein, such as by measuring a level of an MP-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting MP mRNA levels or determining whether a genomic MP gene has been mutated or deleted.

- 5 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 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 catalyze an enzymatic reaction in an amino acid, vitamin,
- 10 cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway. As used 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
- 15 Listing) amino acid residues to an amino acid sequence of the invention such that the protein or portion thereof is able to catalyze an enzymatic reaction in a *C. glutamicum* amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside or trehalose metabolic pathway. Protein members of such metabolic pathways, as described herein, function to catalyze the biosynthesis or degradation of one or more of: amino acids,
- 20 vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, or trehalose. Examples of such activities are also described herein. Thus, "the function of an MP protein" contributes to the overall functioning of one or more such metabolic pathway and contributes, either directly or indirectly, to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of MP protein activities are set
- 25 forth in Table 1.

- In another embodiment, the protein 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%,
- 30 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99%, 99.7% 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 MP nucleic acid molecules of the invention are preferably biologically active portions of one of the MP proteins. As used herein, the term "biologically active portion of an MP protein" is intended to include a portion, *e.g.*, a domain/motif, of an MP protein that catalyzes an enzymatic reaction in one or more *C. glutamicum* amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways, or has an activity as set forth in Table 1. To determine whether an MP protein or a biologically active portion thereof can catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, 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 MP 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 MP protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the MP 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 MP 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 sequence 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 Table 2, which was 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 Table 2). For example, the invention includes a nucleotide sequence which is greater than and/or at least 45% identical to the nucleotide sequence designated RXA00657 SEQ ID NO:5

5 One of ordinary skill in the art would be able to 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

10 acid sequences having percent identities greater than the lower threshold so calculated (*e.g.*, 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 91%, 92%, 93%,

15 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99%, 99.7% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* MP nucleotide sequences set forth in the Sequence Listing as odd-numbered SEQ ID NOs, it will be appreciated by one of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the

20 amino acid sequences of MP proteins may exist within a population (*e.g.*, the *C. glutamicum* population). Such genetic polymorphism in the MP 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 MP protein, preferably a *C. glutamicum* MP protein. Such

25 natural variations can typically result in 1-5% variance in the nucleotide sequence of the MP gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in MP that are the result of natural variation and that do not alter the functional activity of MP proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum*

30 homologues of the *C. glutamicum* MP DNA of the invention can be isolated based on their homology to the *C. glutamicum* MP 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

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 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 one 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* MP protein.

In addition to naturally-occurring variants of the MP 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 MP protein, without altering the functional ability of the MP 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 MP proteins (*e.g.*, an even-
30 numbered SEQ ID NO: of the Sequence Listing) without altering the activity of said MP protein, whereas an "essential" amino acid residue is required for MP protein activity. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-

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

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding MP proteins that contain changes in amino acid residues that are not essential for MP activity. Such MP 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 MP 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 catalyzing an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, 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%, 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%, 98%, 99%, 99.7% 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 of 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).

An isolated nucleic acid molecule encoding an MP 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 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 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, 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 MP protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an MP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an MP activity described herein to identify mutants that retain MP activity. Following mutagenesis of the nucleotide sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, 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 MP proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which 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 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 MP 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 MP 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 SEQ ID NO.:1 (*metZ*) comprises nucleotides 363 to 1673). In another

5 embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding MP. 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 MP disclosed herein (*e.g.*, the

10 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 MP mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of MP mRNA. For

15 example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of MP 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

20 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

25 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-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine,

30 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'-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
5 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
10 to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an MP 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
15 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
20 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
25 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-methylribonucleotide (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).

30 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 MP mRNA transcripts to thereby inhibit translation of MP mRNA. A ribozyme having specificity for an MP-encoding nucleic acid can be designed based upon the nucleotide sequence of an MP DNA disclosed herein (*i.e.*, SEQ ID NO:1

- 5 (*metZ*). 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 MP-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, MP mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of
- 10 RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

Alternatively, MP gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an MP nucleotide sequence (*e.g.*, an MP promoter and/or enhancers) to form triple helical structures that prevent transcription of an MP gene in target cells. See generally, Helene, C. (1991) *Anticancer*

15 *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.

Another aspect of the invention pertains to combinations of genes involved in methionine and/or lysine metabolism and the use of to combinations of genes involved in methionine and/or lysine metabolism in the methods of the invention. Preferred

20 combinations are the combination of *metZ* with *metC*, *metB* (encoding Cystathionine-Synthase), *metA* (encoding homoserine-O-acetyltransferase), *metE* (encoding Methionine Synthase), *metH* (encoding Methionine Synthase), *hom* (encoding homoserine dehydrogenase), *asd* (encoding aspartatesemialdehyd dehydrogenase), *lysC* /*ask* (encoding aspartokinase) and rxa00657 (herein designated as SEQ ID NO.:5),

25 *dapA*, (gene encoding DIHYDRODIPICOLINATE SYNTHASE), *dapB* (gene encoding DIHYDRODIPICOLINATE REDUCTASE), *dapC* (gene encoding 2,3,4,5-tetrahydropyridine-2-carboxylate N—succinyltransferase), *dapD/argD* (gene encoding acetylornithine transaminase), *dapE* (gene encoding succinyldiaminopimelate desuccinylase), *dapF* (gene encoding diaminopimelate epimerase), *lysA* (gene encoding

30 diaminopimelate decarboxylase), *ddh* (gene encoding diaminopimelate dehydrogenase), *lysE* (gene encoding for the lysine exporter), *lysG* (gene encoding for the exporter regulator), *hsk* (gene encoding homoserine kinase) as well as genes involved in anaplerotic reaction such as *ppc* (gene encoding phosphoenolpyruvate carboxylase),

ppcK (gene encoding phosphoenolpyruvate carboxykinase), *pycA* (gene encoding pyruvate carboxylase), *accD*, *accA*, *accB*, *accC* (genes encoding for subunits of acetyl-CoA-carboxylase), as well as genes of the pentose-phosphate pathway, *gpdh* genes encoding glucose-6-phosphate-dehydrogenase, *opcA*, *pgdh* (gene encoding 6-phosphogluconate-dehydrogenase), *ta* (gene encoding transaldolase), *tk* (gene encoding gene encoding transketolase), *pgl* (gene encoding 6-PHOSPHOGLUCONOLACTONASE), *rlpe* (gene encoding RIBULOSE-PHOSPHATE 3-EPIMERASE) *rpe* (gene encoding RIBOSE 5-PHOSPHATE EPIMERASE) or combinations of the above-mentioned genes of the pentose-phosphate-pathways, or other MP genes of the invention.

The genes may be altered in their nucleotide sequence and in the corresponding amino acid sequence resulting in derivatives in such a way that their activity is altered under physiological conditions which leads to an increase in productivity and/or yield of a desired fine chemical, *e.g.*, an amino acid such as methionine or lysine. One class of such alterations or derivatives is well known for the nucleotide sequence of the *ask* gene encoding aspartokinase. These alterations lead to removal of feed back inhibition by the amino acids lysine and threonine and subsequently to lysine overproduction. In a preferred embodiment the *metZ* gene or altered forms of the *metZ* gene are used in a *Corynebacterium* strain in combination with *ask*, *hom*, *metA* and *metH* or derivatives of these genes. In another preferred embodiment *metZ* or altered forms of the *metZ* gene are used in a *Corynebacterium* strain in combination with *ask*, *hom*, *metA* and *metE* or derivatives of these genes. In a more preferred embodiment, the gene combinations *metZ* or altered forms of the *metZ* gene are combined with *ask*, *hom*, *metA* and *metH* or derivatives of these genes, or *metZ* is combined with *ask*, *hom*, *metA* and *metE* or derivatives of these genes in a *Corynebacterium* strain and sulfur sources such as sulfates, thiosulfates, sulfites and also more reduced sulfur sources such as H₂S and sulfides and derivatives are used in the growth medium. Also, sulfur sources such as methyl mercaptan, methanesulfonic acid, thioglycolates, thiocyanates, thiourea, sulfur containing amino acids such as cysteine and other sulfur containing compounds can be used. Another aspect of the invention pertains to the use of the above mentioned gene combinations in a *Corynebacterium* strain which is, before or after introduction of the genes, mutagenized by radiation or by mutagenic chemicals well-known to one of ordinary skill in the art and selected for resistance against high concentrations of the fine

chemical of interest, *e.g.* lysine or methionine or analogues of the desired fine chemical such as the methionine analogues ethionine, methyl methionine, or others. In another embodiment, the gene combinations mentioned above can be expressed in a *Corynebacterium* strain having particular gene disruptions. Preferred are gene disruptions that encode proteins that favor carbon flux to undesired metabolites. Where methionine is the desired fine chemical the formation of lysine may be unfavorable. In such a case the combination of the above mentioned genes should proceed in a *Corynebacterium* strain bearing a gene disruption of the *lysA* gene (encoding diaminopimelate decarboxylase) or the *ddh* gene (encoding the meso-diaminopimelate dehydrogenase catalysing the conversion of tetrahydropicolinate to meso-diaminopimelate). In a preferred embodiment, a favorable combination of the above-mentioned genes are all altered in such a way that their gene products are not feed back inhibited by end products or metabolites of the biosynthetic pathway leading to the desired fine chemical. In the case that the desired fine chemical is methionine, the combinations may be expressed in a strain previously treated with mutagenic agents or radiation and selected for the above-mentioned resistance. Additionally, the strain should be grown in a growth medium containing one or more of the above mentioned sulfur sources.

In another embodiment of the invention, a gene was identified from the genome of *Corynebacterium glutamicum* as a gene coding for a hypothetical transcriptional regulatory protein. This gene is described as RXA00657. The nucleotide sequence of RXA00657 corresponds to SEQ ID NO:5. The amino acid sequence of RXA00657 corresponds to SEQ ID NO:6. It was found that when the RXA00657 gene, as well as upstream and downstream regulatory regions described in the examples, was cloned into a vector capable of replicating in *Corynebacterium glutamicum* and transformed and expressed in a lysine producing strain such as ATCC13286, that this strain produced more lysine compared to the strain transformed with the same plasmid lacking the aforementioned nucleotide fragment RXA00657. In addition to the observation that the lysine titer was increased in the mentioned strain, the selectivity determined by the molar amount of lysine produced compared to the molar amount of sucrose consumed was increased (see Example 14). Overexpression of RXA00657 in combination with the overexpression of other genes either directly involved in the lysine specific pathway

such as *lysC*, *dapA*, *dapB*, *dapC*, *dapD*, *dapF*, *ddh*, *lysE*, *lysG*, and *lysR* results in an increase in the production of lysine compared to RXA00657 alone.

B. Recombinant Expression Vectors and Host Cells

5 Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an MP protein (or a portion thereof) or combinations of genes wherein at least one gene encodes for an MP protein. 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",
10 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 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
15 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
20 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. 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.

25 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
30 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, repressor binding sites, activator binding sites, enhancers and other expression control elements (*e.g.*, terminators, polyadenylation signals, or other elements of mRNA secondary structure). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression* 5 *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-, 10 *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*, *usp*, STLS1, B33, *nos* or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by one of 15 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 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.*, MP proteins, mutant forms of MP proteins, 20 fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of MP proteins in prokaryotic or eukaryotic cells. For example, MP genes 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) 25 "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 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), 30 algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* -mediated transformation of *Arabidopsis 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.

- 5 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 typically
10 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 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
15 moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

- 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
20 (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the MP protein is cloned into a 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.
25 Recombinant MP protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

- 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-
30 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 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 host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7

5 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 of *Bacillus* species. Several plasmids of use in the transfer of genetic information into

10 *Corynebacterium* include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018).

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*

15 *Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another 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

20 sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the MP 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)

25 *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and 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

30 University Press: Cambridge, and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York (ISBN 0 444 904018).

Alternatively, the MP 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) *Virology* 170:31-39).

In another embodiment, the MP proteins of the invention may be expressed in
5 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
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
10 plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHlac+,
pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier:
New York ISBN 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
15 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
20 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
25 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)
30 *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 a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to MP 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 MP 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 those 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

5 "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, transposon or other DNA) into a host cell, including calcium phosphate or calcium

10 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.

15 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

20 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 MP protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable

25 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 MP gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the MP gene. Preferably, this MP gene is a *Corynebacterium glutamicum* MP gene, but it can be a homologue

30 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 MP 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 MP 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 MP protein). In the homologous recombination vector, the altered portion
5 of the MP gene is flanked at its 5' and 3' ends by additional nucleic acid of the MP gene to allow for homologous recombination to occur between the exogenous MP gene carried by the vector and an endogenous MP gene in a microorganism. The additional flanking MP nucleic acid is of sufficient length for successful homologous
10 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 vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced MP gene has homologously recombined with the endogenous MP gene are selected, using art-known techniques.

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

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

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 MP protein. Accordingly, the invention

further provides methods for producing MP 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 MP protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered MP protein) in a suitable medium until MP protein is produced. In another embodiment, the method further comprises isolating MP proteins from the medium or the host cell.

C. Isolated MP Proteins

Another aspect of the invention pertains to isolated MP 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 preparations of MP 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 MP protein having less than about 30% (by dry weight) of non-MP protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-MP protein, still more preferably less than about 10% of non-MP protein, and most preferably less than about 5% non-MP protein. When the MP 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 preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of MP 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 MP protein having less than about 30% (by dry weight) of chemical precursors or non-MP chemicals, more preferably less than about 20% chemical precursors or non-MP chemicals, still more preferably less than about 10% chemical precursors or non-MP chemicals, and most preferably less than about 5% chemical precursors or non-MP chemicals. In preferred embodiments, isolated proteins or

biologically active portions thereof lack contaminating proteins from the same organism from which the MP protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* MP protein in a microorganism such as *C. glutamicum*.

- 5 An isolated MP protein or a portion thereof of the invention can catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or has one or more of the activities set forth in Table 1. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of the
- 10 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 catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an MP protein of
- 15 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 MP protein has an amino acid sequence which is encoded by a 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
- 20 preferred embodiment, the MP 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 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
- 25 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99%, 99.7% or more homologous to one of the nucleic acid sequences of the invention, or a portion thereof. 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 identity values using a
- 30 combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred MP proteins of the present invention also preferably possess at least one of the MP activities described herein. For example, a preferred MP 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 which can catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or which has one or more of the activities set forth in Table 1.

5 In other embodiments, the MP 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 MP 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%, 99.7% or more homologous to an entire amino acid sequence of the invention and which has at least one of the MP 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 MP protein include peptides comprising amino
25 acid sequences derived from the amino acid sequence of an MP 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 MP protein, which include fewer amino acids than a full length MP protein or the full length protein which is homologous to an MP protein, and exhibit at least one activity of an MP protein. Typically, biologically
30 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 MP protein. Moreover, other 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 MP protein include one or more selected domains/motifs or portions thereof having biological activity.

MP 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 MP protein is expressed in the host cell. The MP protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an MP protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native MP protein can be isolated from cells (*e.g.*, endothelial cells), for example using an anti-MP antibody, which can be produced by standard techniques utilizing an MP protein or fragment thereof of this invention.

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

Preferably, an MP 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

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.

- 5 Alternatively, PCR amplification of gene fragments can be carried out using anchor 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*, eds. Ausubel *et al.* John Wiley & Sons: 1992). Moreover, many expression vectors are commercially
10 available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An MP-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the MP protein.

- Homologues of the MP protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the MP protein. As used herein, the term "homologue"
15 refers to a variant form of the MP protein which acts as an agonist or antagonist of the activity of the MP protein. An agonist of the MP protein can retain substantially the same, or a subset, of the biological activities of the MP protein. An antagonist of the MP protein can inhibit one or more of the activities of the naturally occurring form of the MP protein, by, for example, competitively binding to a downstream or upstream
20 member of the MP cascade which includes the MP protein. Thus, the *C. glutamicum* MP protein and homologues thereof of the present invention may modulate the activity of one or more metabolic pathways in which MP proteins play a role in this microorganism.

- In an alternative embodiment, homologues of the MP protein can be identified
25 by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the MP protein for MP protein agonist or antagonist activity. In one embodiment, a variegated library of MP variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of MP variants can be produced by, for example, enzymatically ligating a mixture of synthetic
30 oligonucleotides into gene sequences such that a degenerate set of potential MP sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of MP sequences therein. There are a variety of methods which can be used to produce libraries of potential MP

homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a 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 MP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; 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 MP protein coding can be used to generate a variegated population of MP fragments for screening and subsequent selection of homologues of an MP protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an MP 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 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 MP 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 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 MP 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 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 frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify MP 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 variegated MP library, using methods well known in the art.

D. Uses and Methods of the Invention

5 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 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 MP protein
10 regions required for function; modulation of an MP protein activity; modulation of the activity of an MP pathway; and modulation of cellular production of a desired compound, such as a fine chemical.

 The MP 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
15 close relative thereof. Also, they may be used to identify the 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
20 which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is not pathogenic to humans, it is related to species which are human pathogens, 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
25 disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli 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 spleen, result in the systemic pathology of the
30 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.

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 *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 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 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 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 MP nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic processes in which 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 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 engineering studies and may

give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

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

The invention also provides methods for screening molecules which modulate the activity of an MP protein, either by interacting with the protein itself or a substrate or binding partner of the MP protein, or by modulating the transcription or translation of an MP nucleic acid molecule of the invention. In such methods, a microorganism expressing one or more MP 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 MP protein is assessed.

When the desired fine chemical to be isolated from large-scale fermentative culture of *C. glutamicum* is an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose, modulation of the activity or efficiency of activity of one or more of the proteins of the invention by recombinant genetic mechanisms may directly impact the production of one of these fine chemicals. For example, in the case of an enzyme in a biosynthetic pathway for a desired amino acid, improvement in efficiency or activity of the enzyme (including the presence of multiple copies of the gene) should lead to an increased production or efficiency of production of that desired amino acid. In the case of an enzyme in a biosynthetic pathway for an amino acid whose synthesis is in competition with the synthesis of a desired amino acid, any decrease in the efficiency or activity of this enzyme (including deletion of the gene) should result in an increase in production or efficiency of production of the desired amino acid, due to decreased competition for intermediate compounds and/or energy. In the case of an enzyme in a degradation pathway for a desired amino acid, any decrease in efficiency or activity of the enzyme should result in a greater yield or efficiency of production of the desired product due to a decrease in its degradation. Lastly, mutagenesis of an enzyme involved in the biosynthesis of a desired amino acid such that this enzyme is no longer is capable of feedback inhibition should result in increased yields or efficiency of production of the desired amino acid. The same should apply to the biosynthetic and

degradative enzymes of the invention involved in the metabolism of vitamins, cofactors, nutraceuticals, nucleotides, nucleosides and trehalose.

Similarly, when the desired fine chemical is not one of the aforementioned compounds, the modulation of activity of one of the proteins of the invention may still
5 impact the yield and/or efficiency of production of the compound from large-scale culture of *C. glutamicum*. The metabolic pathways of any organism are closely interconnected; the intermediate used by one pathway is often supplied by a different pathway. Enzyme expression and function may be regulated based on the cellular levels of a compound from a different metabolic process, and the cellular levels of molecules
10 necessary for basic growth, such as amino acids and nucleotides, may critically affect the viability of the microorganism in large-scale culture. Thus, modulation of an amino acid biosynthesis enzyme, for example, such that it is no longer responsive to feedback inhibition or such that it is improved in efficiency or turnover may result in increased cellular levels of one or more amino acids. In turn, this increased pool of amino acids
15 provides not only an increased supply of molecules necessary for protein synthesis, but also of molecules which are utilized as intermediates and precursors in a number of other biosynthetic pathways. If a particular amino acid had been limiting in the cell, its increased production might increase the ability of the cell to perform numerous other metabolic reactions, as well as enabling the cell to more efficiently produce proteins of
20 all kinds, possibly increasing the overall growth rate or survival ability of the cell in large scale culture. Increased viability improves the number of cells capable of producing the desired fine chemical in fermentative culture, thereby increasing the yield of this compound. Similar processes are possible by the modulation of activity of a degradative enzyme of the invention such that the enzyme no longer catalyzes, or
25 catalyzes less efficiently, the degradation of a cellular compound which is important for the biosynthesis of a desired compound, or which will enable the cell to grow and reproduce more efficiently in large-scale culture. It should be emphasized that optimizing the degradative activity or decreasing the biosynthetic activity of certain molecules of the invention may also have a beneficial effect on the production of certain
30 fine chemicals from *C. glutamicum*. For example, by decreasing the efficiency of activity of a biosynthetic enzyme in a pathway which competes with the biosynthetic pathway of a desired compound for one or more intermediates, more of those intermediates should be available for conversion to the desired product. A similar

situation may call for the improvement of degradative ability or efficiency of one or more proteins of the invention.

This aforementioned list of mutagenesis strategies for MP proteins to result in increased yields of a desired compound is not meant to be limiting; variations on these mutagenesis strategies will be readily apparent to one of ordinary skill in the art. By these mechanisms, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated MP 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 natural product of *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. Preferred compounds to be produced by *Corynebacterium glutamicum* strains are the amino acids L-lysine and L-methionine.

In one embodiment, the *metC* gene encoding cystathionine β -lyase, the third enzyme in the methionine biosynthetic pathway, was isolated from *Corynebacterium glutamicum*. The translational product of the gene showed no significant homology with that of *metC* gene from other organisms. Introduction of the plasmid containing the *metC* gene into *C. glutamicum* resulted in a 5-fold increase in the activity of cystathionine β -lyase. The protein product, now designated MetC (corresponding to SEQ ID NO:4), which encodes a protein product of 35,574 Daltons and consists of 325 amino acids, is identical to the previously reported *aecD* gene (Rossol, I. and Puhler, A. (1992) *J. Bacteriology* 174, 2968-2977) except the existence of two different amino acids. Like *aecD* gene, when present in multiple copies, *metC* gene conferred resistance to S-(β -aminoethyl)-cysteine which is a toxic lysine analog. However, genetic and biochemical evidences suggest that the natural activity of *metC* gene product is to mediate methionine biosynthesis in *C. glutamicum*. Mutant strains of *metC* were constructed and the strains showed methionine prototrophy. The mutant strains completely lost their ability to show resistance to S-(γ -aminoethyl)-cysteine. These results show that, in addition to the transsulfuration, which is another biosynthetic pathway, the direct sulphydrylation pathway is functional in *C. glutamicum* as a parallel biosynthetic route for methionine.

In yet another embodiment, it is also shown that the additional sulfhydrylation pathway is catalyzed by *O*-acetylhomoserine sulfhydrylase. The presence of the pathway is demonstrated by the isolation of the corresponding *metZ* (or *metY*) gene and enzyme (corresponding to SEQ ID NO:1 and SEQ ID NO:2, respectively). Among the eukaryotes, fungi and yeast species have been reported to have both the transsulfuration and direct sulfhydrylation pathway. Thus far, no prokaryotic organism which possesses both pathways has been found. Unlike *E. coli* which only possesses single biosynthetic route for lysine, *C. glutamicum* possesses two parallel biosynthetic pathways for the amino acid. The biosynthetic pathway for methionine in *C. glutamicum* is analogous to that of lysine in that aspect.

The gene *metZ* is located in the upstream region of *metA*, which is the gene encoding the enzyme catalysing the first step of methionine biosynthesis (Park, S.-D., *et al.* (1998) *Mol. Cells* 8, 286-294). Regions upstream and downstream of *metA* were sequenced to identify other *met* genes. It appears that *metZ* and *metA* form an operon. Expression of the genes encoding MetA and MetZ leads to overproduction of the corresponding polypeptides.

Surprisingly, *metZ* clones can complement methionine auxotrophic *Escherichia coli metB* mutant strains. This shows that the protein product of *metZ* catalyzes a step that can bypass the step catalyzed by the protein product of *metB*. *MetZ* was also disrupted and the mutant strain showed methionine prototrophy. *Corynebacterium glutamicum metB* and *metZ* double mutants were also constructed. The double mutant is auxotrophic for methionine. Thus, *metZ* encodes a protein catalysing the reaction from O-Acetyl-Homoserine to Homocysteine, which is one step in the sulfhydrylation pathway of methionine biosynthesis. *Corynebacterium glutamicum* contains both the transsulfuration and the sulfhydrylation pathway of methionine biosynthesis.

Introduction of *metZ* into *C. glutamicum* resulted in the expression of a 47,000 Dalton protein. Combined introduction of *metZ* and *metA* in *C. glutamicum* resulted in the appearance of *metA* and *metZ* proteins as shown by gel electrophoresis. If the *Corynebacterium* strain is a lysine overproducer, introduction of a plasmid containing *metZ* and *metA* resulted in a lower lysine titer but accumulation of homocysteine and methionine is detected.

In another embodiment *metZ* and *metA* were introduced into *Corynebacterium glutamicum* strains together with the *hom* gene, encoding the homoserine dehydrogenase, catalysing the conversion from aspartate semialdehyde to homoserine. Different *hom* genes from different organisms were chosen for this experiment. The *Corynebacterium glutamicum* *hom* gene can be used as well as *hom* genes from other procaryotes like *Escherichia coli* or *Bacillus subtilis* or the *hom* gene of eukaryotes such as *Saccharomyces cerevisiae*, *Shizosaccharomyces pombe*, *Ashbya gossypii* or algae, higher plants or animals. It may be that the *hom* gene is insensitive against feed back inhibition mediated by any metabolites that occur in the biosynthetic routes of the amino acids of the aspartate family, like aspartate, lysine, threonine or methionine. Such metabolites are for example aspartate, lysine, methionine, threonine, aspartyl-phosphate, aspartate semialdehyd, homoserine, cystathionine, homocysteine or any other metabolite that occurs in this biosynthetic routes. In addition to the metabolites, the homoserine dehydrogenase may be insensitive against inhibition by analogues of all those metabolites or even against other compounds involved in this metabolism as there are other amino acids like cysteine or cofactors like vitamin B12 and all of its derivatives and S-adenosylmethionine and its metabolites and derivatives and analogues. The insensitivity of the homoserine dehydrogenase against all these, a part of these or only one of these compounds may either be its natural attitude or it may be the result from one or more mutations that resulted from classical mutation and selection using chemicals or irradiation or other mutagens. The mutations could also be introduced into the *hom* gene using gene technology, for example the introduction of site specific point mutations or by any method aforementioned for the MP or MP encoding DNA-sequences.

When a *hom* gene was combined with the *metZ* and *metA* genes and introduced into a *Corynebacterium glutamicum* strain that is a lysine overproducer, lysine accumulation was reduced and homocysteine and methionine accumulation was enhanced. A further enhancement of homocysteine and methionine concentrations can be achieved, if a lysine overproducing *Corynebacterium glutamicum* strain is used and a disruption of the *ddh* gene or the *lysA* gene was introduced prior to the transformation with DNA containing a *hom* gene and *metZ* and *metA* in combination. The overproduction of homocysteine and methionine was possible using different sulfur sources. Sulfates, thiosulfates, sulfites and also more reduced sulfur sources like H₂S and sulfides and derivatives could be used. Also, organic sulfur sources like methyl mercaptan,

thioglycolates, thiocyanates, thiourea, sulfur containing amino acids like cysteine and other sulfur containing compounds can be used to achieve homocysteine and methionine overproduction.

In another embodiment, the *metC* gene was introduced into a *Corynebacterium*
5 *glutamicum* strain using aforementioned methods. The *metC* gene can be transformed into the strain in combination with other genes like *metB*, *metA* and *metA*. The *hom* gene can also be added. When the *hom* gene, the *met C*, *metA* and *metB* genes were combined on a vector and introduced into a *Corynebacterium glutamicum* strain, homocysteine and methionine overproduction was achieved. The overproduction of homocysteine and
10 methionine was possible using different sulfur sources. Sulfates, thiosulfates, sulfites and also more reduced sulfur sources like H₂S and sulfides and derivatives could be used. Also, organic sulfur sources like methyl mercaptan, thioglycolates, thiocyanates, thiourea, sulfur containing amino acids like cysteine and other sulfur containing compounds can be used to achieve homocysteine and methionine overproduction.

15

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.

Exemplification

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Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC13032

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, 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 (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 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 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 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 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
5 prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

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

10 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.)
15 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 library
20 specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

For the isolation of *metC* clones, *E. coli* JE6839 cells were transformed with the library DNA and plated onto the M9 minimal medium containing ampicillin and appropriate supplements. The plates were incubated at 37°C for 5 days. Colonies were
25 isolated and screened for the plasmid content. The complete nucleotide sequence of the isolated *metC* gene was determined by methods well-known to one of ordinary skill in the art.

Example 3: DNA Sequencing and Computational Functional Analysis

30 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' (SEQ ID NO:123) or 5'-GTAAAACGACGGCCAGT-3' (SEQ ID NO:124).

5 **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 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.

15 **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 an origin of 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

5 *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.* (1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for

10 *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 *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

15 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 overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

20 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 methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through

25 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 homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional

30 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: 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 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.* (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 SDS-acrylamide gel electrophoresis, were employed. The overproduction of *metC* and *metZ* in combination with *metA* in *Corynebacterium glutamicum* was demonstrated by this method. Western blot may also 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 Escherichia coli and Genetically Modified Corynebacterium glutamicum — Media and Culture Conditions

E. coli strains are routinely grown in MB and LB broth, respectively (Follettie, M. T., *et al.* (1993) *J. Bacteriol.* 175, 4096-4103). Minimal media for *E. coli* is M9 and modified MCGC (Yoshihama, M., *et al.* (1985) *J. Bacteriol.* 162, 591-507). Glucose was

added to a final concentration of 1%. Antibiotics were added in the following amounts (micrograms per milliliter): ampicillin, 50; kanamycin, 25; nalidixic acid, 25. Amino acids, vitamins, and other supplements were added in the following amounts: methionine, 9.3 mM; arginine, 9.3 mM; histidine, 9.3 mM; thiamine, 0.05 mM. *E. coli* cells were
5 routinely grown at 37°C, respectively.

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)
10 “The Genus *Corynebacterium*, in: The Prokaryotes, 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
15 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 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
20 which contain these compounds. Exemplary nitrogen sources include ammonia gas or 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.

The overproduction of sulfur containing amino acids like homocysteine and
25 methionine was made possible using different sulfur sources. Sulfates, thiosulfates, sulfites and also more reduced sulfur sources like H_2S and sulfides and derivatives can be used. Also, organic sulfur sources like methyl mercaptan, thioglycolates, thiocyanates, thiourea, sulfur containing amino acids like cysteine and other sulfur containing compounds can be used to achieve homocysteine and methionine overproduction

30 Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt, 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 acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently
5 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 Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0
10 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 necessary, separately. All media components can be present at the beginning of growth,
15 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 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media.
20 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 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
25 compounds have high buffer capacities. If a fermentor is utilized for culturing the microorganisms, 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
30 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.

- 5 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, 10 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.

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

- 15 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, 20 applications and examples for the determination of many enzyme activities may be 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 25 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. 30 352-363.

Cell extracts from *Corynebacterium glutamicum* were prepared as described previously (Park, S.-D., *et al.* (1998) *Mol. Cells* 8, 286-294). Cystathionine β-lyase was assayed as follows. The assay mixture contained 100 mM Tris-HCl (pH8.5), 0.1 mM

- NADH, 1 mM *L*-cystathionine, 5 units of *L*-lactate dehydrogenase, and appropriate amounts of crude extract. Optical changes were monitored at 340 nm. Assay for *S*-(β -aminoethyl)-cysteine (AEC) resistance was carried out as described in Rossol, I. and Pühler, A. (1992) *J. Bacteriol.* 174, 2968-77. The results of cystathionin β -lyase assays
- 5 from extracts of different *Corynebacterium glutamicum* strains as well as results of AEC resistance assays of the same strain are summarized in Table 5, below.

Table 5. Expression of cystathionine β -lyase^a

Strains	Properties	Activity (nmol min ⁻¹ mg ⁻¹)	Growth on MM ^b	Resistance to AEC ^c
<i>C. glutamicum</i> ASO19E12	-	146	+	+
<i>C. glutamicum</i> ASO19E12/pMT1	Empty vector	145	+	+
<i>C. glutamicum</i> ASO19E12/pSL173	<i>metC</i> clone	797	+	++
<i>C. glutamicum</i> HL457	<i>metC</i> mutant ^d	19	+	-
<i>C. glutamicum</i> HL459	<i>metC</i> mutant ^d	23	+	-
<i>E. coli</i> JE6839	<i>metC</i> mutant	21	-	<u>ND</u> ^e

5 ^a The enzyme was induced by growth to the stationary phase on the minimal medium containing 1% glucose. Cells were harvested, disrupted, and assayed for the activity as described in the Materials and Methods.

^b MCGC minimal media was used. Growth was monitored on plates.

^c Cells were grown on plates containing 40 mM *S*-(β -aminoethyl)-cysteine (AEC) for 5 days.

10 ^d The mutants were generated in this study.

^e Not determined.

The ability of the *metC* clones to express cystathionine β -lyase was tested by enzymatic assay. Crude extracts prepared from the *C. glutamicum* ASO19E12 cells
15 harboring plasmid pSL173 were assayed. Cells harboring the plasmid showed approximately a 5-fold increase in the activity of cystathionine β -lyase compared to those harboring the empty vector pMT1 (Table 5), apparently due to the gene-dose effect. SDS-PAGE analysis of crude extracts revealed a putative cystathionine β -lyase band with approximate M_r of 41,000. Intensity of each putative cystathionine β -lyase
20 band agreed with the complementation and enzymatic assay data (Table 5). As described above, a region of *metC* appeared to be nearly identical to the previously reported *aecD*. Since the *aecD* gene was isolated on the basis of its ability to confer resistance to *S*-(β -aminoethyl)-cysteine (AEC), a toxic lysine analogue, we tested the protein product of *metC* for the presence of the activity. As shown in Table 5, cells overexpressing
25 cystathionine β -lyase showed increased resistance to AEC. The strain carrying a mutation in *metC* gene (see below) completely lost its ability to show a resistant phenotype to AEC.

Assay for *O*-acetylhomoserine sulphydrylase was performed as follows (Belfaiza, J.,
et al. (1998) *J. Bacteriol.* 180, 250-255; Ravanel, S., M. Droux, and R. Douce (1995)
30 *Arch. Biochem. Biophys.* 316, 572-584; Foglino, M. (1995) *Microbiology* 141, 431-439). Assay mixture of 0.1 ml contained 20 mM MOPS-NaOH (pH7.5), 10 mM *O*-

acetylhomoserine, 2 mM Na₂S in 50 mM NaOH, and an appropriate amount of enzyme. Immediately after the addition of Na₂S which was added last, the reaction mixture was overlaid with 50 ul of mineral oil. After 30 minute incubation at 30°C, the reaction was stopped by boiling the mixture for 3 minutes. Homocysteine produced in the

5 reaction was quantified as previously described (Yamagata, S. (1987) *Method Enzymol.* 143, 478-483.). Reaction mixture of 0.1 ml was taken and mixed with 0.1 ml of H₂O, 0.6 ml of saturated NaCl, 0.1 ml of 1.5 M Na₂CO₃ containing 67 mM KCN, and 0.1 ml of 2% nitroprusside. After 1 minute incubation at room temperature, optical density was measured at 520 nm. *Corynebacterium* cells harboring additional copies of the *metZ*

10 gene, e.g., a plasmid containing the *metZ* gene, exhibited significantly higher *metZ* enzyme activities than the same type of *Corynebacterium* cells without additional copies of the *metZ* gene.

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).

15 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.

20 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.

25 **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

30 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, 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.

25 **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*

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) *Biotehnologiya* 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* 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 MP nucleic acid molecules of the invention. BLAST protein searches can be performed with the
5 XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to MP 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
10 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
15 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
20 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 Blossum 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
25 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
30 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 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 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 (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 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 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, 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 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 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 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 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 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 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), *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as 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: 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 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, fluorescent labels may be employed. These labeled proteins can be extracted, isolated
5 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 of other proteins in the same gel or in other gels. Comparisons of proteins on gels can
10 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 standard techniques may be employed. For example, N- and/or C-terminal amino acid
15 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.

The information obtained by these methods can be used to compare patterns of
20 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, such as to compare the behavior of various organisms in a given (e.g., metabolic)
25 situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

Example 14: Cloning of Genes by Application of the Polymerase Chain Reaction (PCR)

30 Genes can be amplified using specific oligonucleotides comprising either nucleotide sequences homologous to sequences of *Corynebacterium glutamicum* or other strains as well as recognition sites of restriction enzymes well known in the art (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). These oligonucleotides can be used to amplify specific DNA-fragments containing parts of the chromosome of mentioned strains using DNA-polymerases such as *T. aquaticus* DNA-polymerase, *P. furiosus* DNA-polymerase, or *P. woesei* DNA-polymerase and dNTPs nucleotides in an appropriate buffer solution as described by the manufacturer.

Gene fragments such as coding sequences from RXA00657 including appropriate upstream and downstream regions not contained in the coding region of the mentioned gene can be amplified using the aforementioned technologies. Furthermore, these fragments can be purified from unincorporated oligonucleotides and nucleotides. DNA restriction enzymes can be used to produce protruding ends that can be used to ligate DNA fragments to vectors digested with complementary enzymes or compatible enzymes producing ends that can be used to ligate the DNA into the vectors mentioned 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 *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). Oligonucleotides used as primers for the amplification of upstream DNA sequence, the coding region sequence and the downstream region of RXA00657 were as follows:

TCGGGTATCCGCGCTACACTTAGA (SEQ ID NO:121);
GGAAACCGGGGCATCGAAACTTA (SEQ ID NO:122).

Corynebacterium glutamicum chromosomal DNA with an amount of 200ng was used as a template in a 100µl reaction volume containing 2,5U Pfu Turbo-Polymerase™ (Stratagene™), and 200µM dNTP-nucleotides. The PCR was performed on a PCR-Cycler™ (Perkin Elmer 2400™) using the following temperature/time protocol:

1 cycle: 94 °C: 2 min.;
20 cycle: 94°C : 1 min.;
52°C: 1 min, 72°C: 1.5 min.,
1 cycle: 72 °C: 5 min.

Primers were removed from the resulting amplified DNA fragment and the resulting fragment was cloned into the blunt EcoRV site of pBS KS (Stratagene™). The fragment was excised by digestion with the restriction enzymes BamHI/XhoI and ligated

into a BamHI SalI digested vector pB (SEQ ID NO.:125). The resulting vector is called pB RXA00657.

Resulting recombinant vectors can be analyzed using standard techniques described in *e.g.*, 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), and can be transferred into *C. glutamicum* using aforementioned techniques.

A *Corynebacterium* strain (ATCC 13286) was treated for a transformation as described. 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.* (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 *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Transformation of a bacterial strain such as *Corynebacterium glutamicum* strain (ATCC 13286) was performed with a plasmid pB containing the aforementioned DNA regions of RXA00657 (SEQ ID NO.:6) and in another case with the vector pB (SEQ ID NO.:) carrying no additional insertion of nucleic acids.

The resulting strains were plated on and isolated from CM-Medium (10 g/l Glucose 2,5 g/l NaCl, 2,0 g/l Urea, 10 g/l Bacto Peptone (Difco/Becton Dickinson/Sparks USATM), 5 g/l yeast extract (Difco/Becton Dickinson/Sparks USATM), 5g/l meat extract (Difco/Becton Dickinson/Sparks USATM), 22g/l Agar (Difco/Becton Dickinson/Sparks USATM) and 15µg/ml kanamycin sulfate (Serva, Germany) with a adjusted with NaOH to pH of 6.8.

Strains isolated from the aforementioned agar medium were inoculated in 10 ml in a 100ml shake flask containing no baffles in liquid medium containing 100 g/l sucrose 50g/l (NH₄)₂SO₄, 2,5 g/l NaCl, 2,0 g/l Urea, 10 g/l Bacto Peptone (Difco/Becton Dickinson/Sparks USA), 5 g/l yeast extract (Difco/Becton Dickinson/Sparks USA), 5g/l meat extract (Difco/Becton Dickinson/Sparks USA), and

25g/l CaCO₃ (Riedel de Haen, Germany) . Medium was adjusted with NaOH to pH of 6.8.

Strains were incubated at 30°C for 48h. Supernatants of incubations were prepared by centrifugation 20' at 12,000 rpm in an Eppendorf™ microcentrifuge. Liquid supernatants were diluted and subjected to amino acid analysis (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).

The results are shown in Table 6, below.

10

Results: Table 6:

Strain ATCC 13286	Plasmid contained	pB	pB RXA00657
lysine produced (g/l)		13.5	14.93
Selectivity (mol lysine/mol consumed Saccharose)		0.235	0.25

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 the invention described herein. Such equivalents are intended to be encompassed by the following claims.

TABLE 1: Included Genes

Lysine biosynthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
5	6	RXA00657				AMINOACID BIOSYNTHESIS REGULATOR
7	8	RXA02229	GR00653	2793	3617	DIAMINOPELMATE EPIMERASE (EC 5.1.1.7)
9	10	RXS02970				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
11	12	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
13	14	RXC02390				MEMBRANE SPANNING PROTEIN INVOLVED IN LYSINE METABOLISM
15	16	RXC01796				MEMBRANE ASSOCIATED PROTEIN INVOLVED IN LYSINE METABOLISM
17	18	RXC01207				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF LYSINE AND THREONINE
19	20	RXC00657				TRANSCRIPTIONAL REGULATOR INVOLVED IN LYSINE METABOLISM
21	22	RXC00552				CYTOSOLIC PROTEIN INVOLVED IN LYSINE METABOLISM

Lysine biosynthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
23	24	RXA00534	GR00137	4758	3496	ASPARTOKINASE ALPHA AND BETA SUBUNITS (EC 2.7.2.4)
25	26	RXA00533	GR00137	3469	2438	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE (EC 1.2.1.11)
27	28	RXA02843	GR00842	543	4	2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
29	30	RXA02022	GR00613	2063	3169	SUCCINYL-DIAMINOPELMATE DESUCCINYLASE (EC 3.5.1.18)
31	32	RXA00044	GR00007	3458	4393	DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52)
33	34	RXA00863	GR00236	896	1639	DIHYDRODIPICOLINATE REDUCTASE (EC 1.3.1.26)
35	36	RXA00864	GR00236	1694	2443	probable 2,3-dihydrodipicolinate N-C6-lyase (cyclizing) (EC 4.3.3.-) - Corynebacterium glutamicum
37	38	RXA02843	GR00842	543	4	2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
39	40	RXN00355	VV0135	31980	30961	MESO-DIAMINOPELMATE D-DEHYDROGENASE
41	42	F RXA00352	GR00068	861	4	MESO-DIAMINOPELMATE D-DEHYDROGENASE (EC 1.4.1.16)
43	44	RXA00972	GR00274	3	1379	DIAMINOPELMATE DECARBOXYLASE (EC 4.1.1.20)
45	46	RXA02653	GR00752	5237	7234	DIAMINOPELMATE DECARBOXYLASE (EC 4.1.1.20)
47	48	RXA01393	GR00408	4249	3380	LYSINE EXPORT REGULATOR PROTEIN
49	50	RXA00241	GR00036	5443	6945	L-LYSINE TRANSPORT PROTEIN
51	52	RXA01394	GR00408	4320	5018	LYSINE EXPORTER PROTEIN
53	54	RXA00865	GR00236	2647	3549	DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52)

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
55	56	RXS02021				2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
57	58	RXS02157				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
59	60	RXC00733				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN LYSINE METABOLISM
61	62	RXC00861				PROTEIN INVOLVED IN LYSINE METABOLISM
63	64	RXC00866				ZN-DEPENDENT HYDROLASE INVOLVED IN LYSINE METABOLISM
65	66	RXC02095				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN LYSINE METABOLISM
67	68	RXC03185				PROTEIN INVOLVED IN LYSINE METABOLISM

Metabolism of methionine and S-adenosyl methionine

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
1	2	metZ or met				O-ACETYLMOMOSERINE SULFHYDRYLASE (EC 4.2.99.10)
3	4	metC				Cystathionine-γ-lyase
69	70	RXA00115	GR00017	5359	4313	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.31)
71	72	RXN00403	VW0086	70041	68911	HOMOSERINE O-ACETYLTRANSFERASE
73	74	F RXA00403	GR00088	723	1832	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.11)
75	76	RXS03158				CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
77	78	F RXA00254	GR00038	2404	1811	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
79	80	RXA02532	GR00726	3085	2039	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
81	82	RXS03159				CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
83	84	F RXA02768	GR00770	1919	2521	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
85	86	RXA00216	GR00032	16286	15297	5-methyltetrahydrofolate-homocysteine methyltransferase (methionine synthetase)
87	94	RXA02197	GR00645	4552	4025	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
89	90	RXN02198	VW0302	9228	11726	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
91	91	F RXA02198	GR00646	2483	6	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
93	94	RXN03074	VW0042	2238	1741	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
95	96	F RXA02906	GR10044	1142	645	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
97	98	RXN00132	VW0124	3612	5045	ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
99	100	F RXA00132	GR00020	7728	7624	ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
101	102	F RXA01371	GR00398	2339	3634	ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
103	104	RXN02085				ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
105	106	F RXA02085	GR00629	3496	5295	ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
107	108	F RXA02086	GR00629	5252	5731	ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
109	110	RXN02648				ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
111	112	F RXA02648	GR00751	5254	4730	ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
113	114	F RXA02658	GR00752	14764	15447	ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
115	116	RXC02238				ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
117	118	RXC00128				ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)

S-2adenosyl methionine (SAM) Biosynthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
119	120	RXA02240	GR00654	7160	8380	S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6)

TABLE 2: GENES IDENTIFIED FROM GENBANK

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate 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	dtsR		Kimura, E. et al. "Molecular cloning of a novel gene, dtsR, 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	dtsR1; dtsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkl	transketolase	
AB024708	glbB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF036932	aroD	3-dehydroquinate dehydratase	
AF038548	pyc	Pyruvate carboxylase	
AF038651	dciAE; 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)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate 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	Dehydroquinate 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)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
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		
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 Corynebacterium glutamicum," <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 Corynebacterium glutamicum; 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	mqo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from Corynebacterium glutamicum," <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 Corynebacterium glutamicum: The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
DI7429		Transposable element IS31831	Vertes et al. "Isolation and characterization of IS31831, a transposable element from Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the Corynebacterium glutamicum (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
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

GenBank™ Accession No.	Gene Name	Gene Function	Reference
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
E06827		Mutated aspartokinase alpha subunit	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 membraneous 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

GenBank™ Accession No.	Gene Name	Gene Function	Reference
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
E13655		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
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. "Isolation and synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
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>FEBS 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	Jeften, 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 5S 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)
M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of Corynebacterium glutamicum 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)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
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	accD; brnQ; yhbW	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbW	Rosol, I. et al. "The Corynebacterium glutamicum accD 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 Corynebacterium glutamicum 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 Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthranelate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum 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 Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The Corynebacterium glutamicum cglIM gene encoding a 5-cytosine in an McrBC-deficient Escherichia coli strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the Corynebacterium glutamicum 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 Corynebacterium glutamicum 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 Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
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	thtK; aceBC	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-bisphosphate 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)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X54223		AttB-related 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)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the Corynebacterium glutamicum lysA gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990)
X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component I	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)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X66078	cop1	Psl protein	Joliff, G. et al. "Cloning and nucleotide sequence of the csp1 gene encoding PS1, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i> : The deduced N-terminal region of PS1 is similar to the <i>Mycobacterium</i> 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 <i>Corynebacterium glutamicum</i> 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 <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a <i>Corynebacterium glutamicum</i> IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)
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

GenBank™ Accession No.	Gene Name	Gene Function	Reference
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)
X82061	16S rDNA	16S ribosomal RNA	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)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
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)
X90360		Promoter fragment F22	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)
X90361		Promoter fragment F34	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)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from <i>C. glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X90363		Promoter fragment F45	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)
X90364		Promoter fragment F64	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)
X90365		Promoter fragment F75	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)
X90366		Promoter fragment PF101	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)
X90367		Promoter fragment PF104	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)
X90368		Promoter fragment PF109	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)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <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 <i>Corynebacterium glutamicum</i> 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 <i>Corynebacterium glutamicum</i> , 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	Vrjic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)
X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-	Sahm, H. et al. "D-pantothenate synthesis in <i>Corynebacterium glutamicum</i> and use of panBC and genes encoding L-valine synthesis for D-pantothenate

GenBank™ Accession No.	Gene Name	alanine ligase; xylulokinase Gene Function	overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	Reference
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer <i>Brevibacterium lactofermentum</i> (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 <i>Brevibacterium lactofermentum</i> ," <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 <i>Corynebacterium glutamicum</i> ," <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 <i>Brevibacterium lactofermentum</i> ," <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 <i>Corynebacterium glutamicum</i> 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 <i>Brevibacterium lactofermentum</i> ," <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 <i>Corynebacterium glutamicum</i> proline 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 <i>Corynebacterium glutamicum</i> : 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 <i>Corynebacterium glutamicum</i> ," <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)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
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 Corynephage 304L	Moreau, S. et al. "Analysis of the integration functions of φ304L: An integrase module among corynephages," <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	fujikense	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	Other origin
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								
Corynebacterium	Glutamicum*									ASO19
Corynebacterium	Glutamicum**									ASO19 E12
Corynebacterium	Glutamicum***									HL457
Corynebacterium	Glutamicum****									HL459

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, Saitama, Japan.

* Spontaneous rifampin-resistant mutant of *C. glutamicum* ATCC13059^d Yoshihama et al., 1985

** Restriction-deficient variant of ASO19 Follett et al., 1993

*** *metC*-disrupted mutant of ASO19E12 This study

**** *metC*-disrupted mutant of ASO19E12 This study

TABLE 4: ALIGNMENT RESULTS

ID #	length (NT)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rx000657	906	GB_BA1:AF064700	3481	AF064700	Rhodococcus sp. NO1-1 CpsS and CprR genes, complete cds.	Rhodococcus sp	40,265	15-Jul-98
metz	1314	GB_BA2:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	61,278	23-Jun-99
metc	978	GB_BA2:CORCSLYS	2821	M89931	Corynebacterium glutamicum beta C-S lyase (aecD) and branched-chain amino acid uptake	Corynebacterium glutamicum	99,591	04-JUN-1998
rx000023	3579	GB_EST33:AI776129	483	AI776129	EST1257217 tomato resistant, Cornell Lycopersicon esculentum cDNA clone	Lycopersicon esculentum	40,956	29-Jun-99
		GB_EST33:AI776129	483	AI776129	cLER17D3, mRNA sequence.	Lycopersicon esculentum	40,956	29-Jun-99
		GB_EST33:AI776129	483	AI776129	EST257217 tomato resistant, Cornell Lycopersicon esculentum cDNA clone	Lycopersicon esculentum	40,956	29-Jun-99
		GB_EST33:AI776129	483	AI776129	cLER17D3, mRNA sequence.	Lycopersicon esculentum	40,956	29-Jun-99
rx000044	1059	EM_PAT:E11760	6911	E11760	Base sequence of sucrose gene.	Corynebacterium glutamicum	42,979	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:126124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	42,979	07-OCT-1996
		GB_BA2:ECOUW89	176195	U00006	E. coli chromosomal region from 89.2 to 92.8 minutes.	Escherichia coli	39,097	17-DEC-1993
rx000064	1401	GB_PAT:E16763	2517	E16763	gDNA encoding aspartate transferase (AAT).	Corynebacterium glutamicum	95,429	28-Jul-99
		GB_HTG2:AC007892	134257	AC007892	Drosophila melanogaster chromosome 3 clone BACR02O03 (D797) RPCI-98	Drosophila melanogaster	31,111	2-Aug-99
		GB_HTG2:AC007892	134257	AC007892	02.O.3 map 99B-99B strain y; cn bw sp, *** SEQUENCING IN PROGRESS			
		GB_HTG2:AC007892	134257	AC007892	***, 113 unordered pieces.			
rx000072		GB_HTG2:AC007892	134257	AC007892	Drosophila melanogaster chromosome 3 clone BACR02O03 (D797) RPCI-98	Drosophila melanogaster	31,111	2-Aug-99
		GB_HTG2:AC007892	134257	AC007892	02.O.3 map 99B-99B strain y; cn bw sp, *** SEQUENCING IN PROGRESS***,			
		GB_HTG2:AC007892	134257	AC007892	113 unordered pieces.			
rx000105	798	GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	37,753	17-Jun-98
		GB_BA1:ECU29581	71128	U29581	Escherichia coli k-12 genome; approximately 63 to 64 minutes.	Escherichia coli	35,669	14-Jan-97
		GB_BA2:AE000366	10405	AE000366	Escherichia coli k-12 MG1655 section 256 of 400 of the complete genome.	Escherichia coli	35,669	12-Nov-98
rx000106	579	GB_EST15:AA494237	367	AA494237	ng83104.s1 NCL CGAP_P16 Homo sapiens cDNA clone IMAGE:941407	Homo sapiens	42,896	20-Aug-97
		GB_EST15:AA494237	367	AA494237	similar to SW:DYR_LACCA P00381 DIHYDROFOLATE REDUCTASE ;			
		GB_EST15:AA494237	367	AA494237	mRNA sequence.			
		GB_BA2:AF161327	2021	AF161327	Corynebacterium diphtheriae histidine kinase ChrS (chrS) and response	Corynebacterium diphtheriae	40,210	9-Sep-99
		GB_PAT:AR041189	654	AR041189	regulator ChrA (chrA) genes, complete cds.	Unknown.	41,176	29-Sep-99
rx000115	1170	GB_PAT:AR041189	654	AR041189	Sequence 4 from patent US 5811286.	Unknown.	41,176	29-Sep-99
		GB_PAT:AR041189	654	AR041189	Homo sapiens chromosome 17, clone HRPK.472_J_18, complete sequence.	Homo sapiens	36,783	30-MAR-1999
		GB_PAT:AR041189	654	AR041189	Homo sapiens chromosome 17, clone HRPK.472_J_18, complete sequence.	Homo sapiens	36,783	30-MAR-1999
		GB_HTG3:AC008537	170030	AC008537	Homo sapiens chromosome 19 clone CIT-HSPC_490E21, *** SEQUENCING	Homo sapiens	40,296	2-Sep-99
		GB_HTG3:AC008537	170030	AC008537	IN PROGRESS ***, 93 unordered pieces.	Homo sapiens	40,296	2-Sep-99
		GB_HTG3:AC008537	170030	AC008537	Homo sapiens chromosome 19 clone CIT-HSPC_490E21, *** SEQUENCING	Homo sapiens	40,296	2-Sep-99
		GB_HTG3:AC008537	170030	AC008537	IN PROGRESS ***, 93 unordered pieces.	Homo sapiens	40,296	2-Sep-99

	Accession	Gene ID	Gene Name	Species	Date
rx000116	GB_BA2:AF062345	16458	AF062345	Caulobacter crescentus Sst1 (sst1), S-layer protein subunit (rsaA), ABC transporter (rsaD), membrane forming unit (rsaE), putative GDP-mannose-4,6-dehydratase (lpsA), putative acetyltransferase (lpsB), putative perosamine synthetase (lpsC), putative mannitoltransferase (lpsD), putative mannitoltransferase (lpsE), outer membrane protein (rsaF), and putative perosamine transferase (lpsE) genes, complete cds.	19-OCT-1999
	GB_PAT:118647	3300	118647	Unknown.	07-OCT-1996
	GB_GSS13:AQ446197	751	AQ446197	Oryza sativa	8-Apr-99
rx000131	GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis	17-Jun-98
	GB_BA1:SAR7932	15176	AJ007932	Streptomyces argillaceus	15-Jun-99
	GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis	17-Jun-98
rx000132	GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis	17-Jun-98
	GB_IN2:TUVU0872	1882	UJ0872	Trichomonas vaginalis S-adenosyl-L-homocysteine hydrolase gene, complete cds.	31-OCT-1996
	GB_HTG6:AC010706	169265	AC010706	Drosophila melanogaster chromosome X clone BACR36D15 (D887) RPCI-98 36.D.15 map 13C-13E strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***; 74 unordered pieces.	22-Nov-99
rx000145	GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	18-Jun-98
	GB_BA1:PSEPYRBX	2273	L19649	Pseudomonas aeruginosa aspartate transcarbamoylase (pyrB) and dihydroorotase-like (pyrX) genes, complete cds's.	26-Jul-93
	GB_BA1:LLPYRBDNA	1468	X84262	L.leichmannii pyrB gene.	29-Apr-97
rx000146	GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	18-Jun-98
	GB_BA1:MTCY154	13935	Z98209	Mycobacterium tuberculosis H37Rv complete genome; segment 121/162.	17-Jun-98
	GB_BA1:MSGY154	40221	AD000002	Mycobacterium tuberculosis sequence from clone y154.	03-DEC-1996
rx000147	GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	18-Jun-98
	GB_BA1:MSGB937CS	38914	L78820	Mycobacterium leprae cosmid B937 DNA sequence.	15-Jun-96
	GB_BA1:PAU81259	7285	U81259	Pseudomonas aeruginosa dihydroadipic acid reductase (dapB) gene, partial cds, carbamoylphosphate synthetase small subunit (carA) and carbamoylphosphate synthetase large subunit (carB) genes, complete cds, and FtsJ homolog (ftsJ) gene, partial cds.	23-DEC-1996
rx000156	GB_BA1:SC9B10	33320	AL008204	Streptomyces coelicolor cosmid 9B10.	10-Feb-99
	GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain G1R10 transcriptional regulator (mav81) gene, partial cds, aconitase (acon), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.	26-MAR-1998
	GB_BA1:D85417	7984	D85417	Propionibacterium freudenreichii hemY, hemH, hemB, hemX, hemR and hemL genes, complete cds.	6-Feb-99
rx000166	GB_HTG3:AC008167	174223	AC008167	Homo sapiens clone NH0172O13, *** SEQUENCING IN PROGRESS ***; 7 unordered pieces.	21-Aug-99
	GB_HTG3:AC008167	174223	AC008167	Homo sapiens clone NH0172O13, *** SEQUENCING IN PROGRESS ***; 7 unordered pieces.	21-Aug-99
	GB_HTG4:AC010118	80605	AC010118	Drosophila melanogaster chromosome 3L/62B1 clone RPCI98-10D15, *** SEQUENCING IN PROGRESS ***; 51 unordered pieces.	16-OCT-1999

TABLE 4: ALIGNMENT RESULTS

rx00198	672	GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	92,113	13-MAR-1999
		GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	93,702	13-MAR-1999
		GB_EST24:AI232702	528	AI232702	EST229390 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone RKICF35 3' end, mRNA sequence.	Rattus sp.	34,221	31-Jan-99
rx00216	1113	GB_HTG2:HSDJ850E9	117353	AL121758	Homo sapiens chromosome 20 clone RP5-850E9, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	37,965	03-DEC-1999
		GB_HTG2:HSDJ850E9	117353	AL121758	Homo sapiens chromosome 20 clone RP5-850E9, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	37,965	03-DEC-1999
		GB_PR2:CNS01DSA	159400	AL121766	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-412H8 of RPCI-11 library from chromosome 14 of Homo sapiens (Human), complete sequence.	Homo sapiens	38,796	11-Nov-99
rx00219	1065	GB_HTG2:AC005079_0	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS *** 3 unordered pieces.	Homo sapiens	38,227	22-Nov-98
		GB_HTG2:AC005079_1	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS *** 3 unordered pieces.	Homo sapiens	38,227	22-Nov-98
		GB_HTG2:AC005079_1	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS *** 3 unordered pieces.	Homo sapiens	38,227	22-Nov-98
rx00223	1212	GB_BA1:PPEA3NIF	19771	X99694	Plasmid pEA3 nitrogen fixation genes.	Enterobacter agglomerans	48,826	2-Aug-96
		GB_BA2:AF128444	2477	AF128444	Rhodobacter capsulatus molybdenum cofactor biosynthetic gene cluster, partial sequence.	Rhodobacter capsulatus	40,135	22-MAR-1999
		GB_HTG4:AC010111	138938	AC010111	Drosophila melanogaster chromosome 3L/70C1 clone RPCI98-9B18, *** SEQUENCING IN PROGRESS *** 64 unordered pieces.	Drosophila melanogaster	39,527	16-OCT-1999
rx00229	803	GB_BA2:AF124518	1758	AF124518	Corynebacterium glutamicum 3-dehydroquinase (aroD) and shikimate dehydrogenase (aroE) genes, complete cds.	Corynebacterium glutamicum	98,237	18-MAY-1999
		GB_PR3:AC004593	150221	AC004593	Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.	Homo sapiens	36,616	18-Apr-98
		GB_HTG2:AC006907	188972	AC006907	Caenorhabditis elegans clone Y76B12, *** SEQUENCING IN PROGRESS *** 25 unordered pieces.	Caenorhabditis elegans	37,095	26-Feb-99
rx00241	1626	GB_BA1:CGLYSI	4232	X60312	C-glutamicum lysI gene for L-lysine permease.	Corynebacterium glutamicum	100,000	30-Jan-92
		GB_HTG1:PFMAL13P1	192581	AL049180	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Plasmodium falciparum	34,947	11-Aug-99
		GB_HTG1:PFMAL13P1	192581	AL049180	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Plasmodium falciparum	34,947	11-Aug-99
rx00262	1197	GB_IN2:EHU89655	3219	U89655	Entamoeba histolytica unconventional myosin IB mRNA, complete cds.	Entamoeba histolytica	36,496	23-MAY-1997
		GB_IN2:EHU89655	3219	U89655	Entamoeba histolytica unconventional myosin IB mRNA, complete cds.	Entamoeba histolytica	37,544	23-MAY-1997
rx00266	531	GB_RO:AF016190	2939	AF016190	Mus musculus connexin-36 (Cx36) gene, complete cds.	Mus musculus	41,856	9-Feb-99
		EM_PAT:E09719	3505	E09719	DNA encoding precursor protein of alkaline cellulase.	Bacillus sp.	34,741	08-OCT-1997 (Rel. 52, Created)
rx00278	1155	GB_PAT:E02133	3494	E02133	gDNA encoding alkaline cellulase.	Bacillus sp.	34,741	29-Sep-97
		GB_IN1:CELK05F6	36912	AF040653	Caenorhabditis elegans cosmid K05F6.	Caenorhabditis elegans	36,943	6-Jan-98

	GB_BA1:CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	36,658	9-Apr-97
rrxa00295	GB_RO:RNU30789	3510	U30789	Rattus norvegicus clone N27 mRNA.	Rattus norvegicus	38,190	20-Aug-96
	GB_BA2:CGU31281	1614	U31281	Corynebacterium glutamicum biotin synthase (bioB) gene, complete cds.	Corynebacterium glutamicum	99,111	21-Nov-96
	GB_BA1:BRLBIOBA	1647	D14084	Brevibacterium flavum gene for biotin synthetase, complete cds.	Corynebacterium glutamicum	98,489	3-Feb-99
	GB_PAT:E03937	1005	E03937	DNA sequence encoding Brevibacterium flavum biotin-synthase.	Corynebacterium glutamicum	98,207	29-Sep-97
	GB_BA1:MTCV427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mycobacterium tuberculosis	35,615	24-Jun-99
	GB_BA1:MSGB32CS	36404	L78818	Mycobacterium leprae cosmid B32 DNA sequence.	Mycobacterium leprae	60,917	15-Jun-96
rrxa00324	GB_BA1:MTCV427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mycobacterium tuberculosis	44,606	24-Jun-99
	GB_BA1:MSGB32CS	36404	L78818	Mycobacterium leprae cosmid B32 DNA sequence.	Mycobacterium leprae	52,516	15-Jun-96
	GB_BA1:MTCV427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mycobacterium tuberculosis	38,079	24-Jun-99
	GB_OM:BOVELA	3242	J02717	Bovine elastin a mRNA, complete cds.	Bos taurus	39,351	27-Apr-93
	GB_BA1:CGTHRC	3120	X56037	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2).	Corynebacterium glutamicum	99,808	17-Jun-97
		GB_PAT:109078	3146	I09078	Sequence 4 from Patent WO 8809819.	Unknown.	99,617
rrxa00335	GB_BA1:BLTHRESYN	1892	Z29563	Brevibacterium lactofermentum; ATCC 13869; DNA (genomic);	Corynebacterium glutamicum	99,170	20-Sep-95
	GB_BA1:CGGLNA	3686	Y13221	Corynebacterium glutamicum glnA gene.	Corynebacterium glutamicum	100,000	28-Aug-97
	GB_BA2:AF005635	1690	AF005635	Corynebacterium glutamicum glutamine synthetase (glnA) gene, complete cds.	Corynebacterium glutamicum	98,906	14-Jun-99
	GB_BA1:MSGB27CS	38793	L78817	Mycobacterium leprae cosmid B27 DNA sequence.	Mycobacterium leprae	66,345	15-Jun-96
rrxa00336	GB_EST27:AI455217	624	AI455217	LD21828.3prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD21828 3prime, mRNA sequence.	Drosophila melanogaster	34,510	09-MAR-1999
	GB_BA2:SSU30252	2891	U30252	Synechococcus PCC7942 nucleoside diphosphate kinase and ORF2 protein genes, complete cds, ORF1 protein gene, partial cds, and neutral site 1 for vector use.	Synechococcus PCC7942	37,084	29-OCT-1999
	GB_EST21:AA911262	581	AA911262	oe75a02.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1417418 3' similar to gb:A18757 UROKINASE PLASMINOGEN ACTIVATOR SURFACE RECEPTOR, GPI-ANCHORED (HUMAN);, mRNA sequence.	Homo sapiens	37,500	21-Apr-98
rrxa00351	GB_BA1:MLU15187	36138	U15187	Mycobacterium leprae cosmid L286.	Mycobacterium leprae	52,972	09-MAR-1995
	GB_IN2:AC004373	72722	AC004373	Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.	Drosophila melanogaster	46,341	17-Jul-98
rrxa00365	GB_IN2:AF145653	3197	AF145653	Drosophila melanogaster clone GH08860 BcDNA.GH08860 (BcDNA.GH08860) mRNA, complete cds.	Drosophila melanogaster	49,471	14-Jun-99
	GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	96,556	13-MAR-1999
	GB_BA1:MTCY1A6	37751	Z83864	Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.	Mycobacterium tuberculosis	39,496	17-Jun-98
rrxa00366	GB_BA1:SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	37,946	16-Aug-99
	GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	99,374	13-MAR-1999
	GB_BA1:MTCY1A6	37751	Z83864	Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.	Mycobacterium tuberculosis	41,333	17-Jun-98
	GB_BA1:SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	37,554	16-Aug-99

TABLE 4: ALIGNMENT RESULTS

rx00367	4653	GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gtb and gtd genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	99,312	13-MAR-1999
		GB_BA1:MTCY1A6	37751	Z83864	Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.	Mycobacterium tuberculosis	36,971	17-Jun-98
		GB_BA1:SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	37,905	16-Aug-99
rx00371	1917	GB_VI:SBVORFS	7568	M89923	Sugarcane bacilliform virus ORF 1,2, and 3 DNA, complete cds.	Sugarcane bacilliform virus	35,843	12-Jun-93
		GB_EST37:AI967505	380	AI967505	Ljirpest03-215-c10 Ljirp Lambda HybZap two-hybrid library Lotus japonicus cDNA clone LP215-03-c10 5' similar to 60S ribosomal protein L39, mRNA sequence.	Sugarcane bacilliform virus	42,593	24-Aug-99
rx00377	1245	GB_IN1:CELK09H9	37881	AF043700	Caenorhabditis elegans cosmid K09H9.	Caenorhabditis elegans	34,295	22-Jan-98
		GB_BA1:CCU13664	1678	U13664	Caulobacter crescentus uroporphyrinogen decarboxylase homolog (heme) gene, partial cds.	Caulobacter crescentus	36,832	24-MAR-1995
		GB_PL1:ANSDGENE	1299	Y08866	A.nidulans sD gene.	Emericella nidulans	39,603	17-OCT-1996
		GB_GSS4:AQ730303	483	AQ730303	HS_5505_B1_C04_TTA RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1081 Col=7 Row=F, genomic survey sequence.	Homo sapiens	36,728	15-Jul-99
rx00382	1425	GB_BA1:PAHEML	4444	X82072	P.aeruginosa hemL gene.	Pseudomonas aeruginosa	54,175	18-DEC-1995
		GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	61,143	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	61,143	03-DEC-1996
rx00383	1467	GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	43,981	27-Aug-99
		GB_HTG2:AC006269	167171	AC006269	Homo sapiens chromosome 17 clone hRPK.515_E_23 map 17, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	35,444	10-Jun-99
		GB_HTG2:AC007638	178053	AC007638	Homo sapiens chromosome 17 clone hRPK.515_O_17 map 17, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.	Homo sapiens	34,821	22-MAY-1999
rx00391	843	GB_EST38:AW017053	613	AW017053	EST272398 Schistosoma mansoni male, Phil LoVerde/Joel Merrick Schistosoma mansoni cDNA clone SMMAS14 5' end, mRNA sequence.	Schistosoma mansoni	40,472	10-Sep-99
		GB_PAT:AR065852	32207	AR065852	Sequence 20 from patent US 5849564.	Unknown.	38,586	29-Sep-99
		GB_VI:AF148805	28559	AF148805	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds.	Kaposi's sarcoma-associated herpesvirus	38,509	2-Aug-99
rx00393	1017	GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	36,308	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	39,282	03-DEC-1996
		GB_BA1:MLB1306	7762	Y13803	Mycobacterium leprae cosmid B1306 DNA.	Mycobacterium leprae	39,228	24-Jun-97
rx00402	623	GB_BA2:AF052652	2096	AF052652	Corynebacterium glutamicum homoserine O-acetyltransferase (metA) gene, complete cds.	Corynebacterium glutamicum	99,672	19-MAR-1998
		GB_BA2:AF109162	4514	AF109162	Corynebacterium diphtheriae heme uptake locus, complete sequence.	Corynebacterium diphtheriae	40,830	8-Jun-99
		GB_BA2:AF092918	20758	AF092918	Pseudomonas alcaligenes outer membrane Xcp-secretion system gene cluster.	Pseudomonas alcaligenes	50,161	06-DEC-1998
rx00403	1254	GB_BA2:AF052652	2096	AF052652	Corynebacterium glutamicum homoserine O-acetyltransferase (metA) gene, complete cds.	Corynebacterium glutamicum	99,920	19-MAR-1998
		GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	52,898	23-Jun-99
		GB_EST23:AI111288	750	AI111288	SWOvAMCAQ02A05SK Onchocerca volvulus adult male cDNA (SAW98MLW-OvAM) Onchocerca volvulus cDNA clone SWOvAMCAQ02A05 5' mRNA sequence.	Mycobacterium tuberculosis	37,565	31-Aug-98

TABLE 4: ALIGNMENT RESULTS

rx00405	613	GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	57,259	23-Jun-99
		GB_PR4:AC005145	143678	AC005145	Homo sapiens Xp22-166-169 GSHB-323A23 (Genome Systems Human BAC library) complete sequence.	Homo sapiens	34,179	08-DEC-1998
rx00420	1587	GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	40,169	23-Jun-99
		GB_BA1:MTY13D12	37085	Z80343	Mycobacterium tuberculosis H37Rv complete genome; segment 156/162.	Mycobacterium tuberculosis	62,031	17-Jun-98
		GB_BA1:MSGY126	37164	AD000012	Mycobacterium tuberculosis sequence from clone y126.	Mycobacterium tuberculosis	61,902	10-DEC-1996
		GB_BA1:MSG8971CS	37566	L78821	Mycobacterium leprae cosmid B971 DNA sequence.	Mycobacterium leprae	39,651	15-Jun-96
rx00435	1296	GB_BA1:AFACBBTZ	2760	M68904	Alcaligenes eutrophus chromosomal transketolase (cbbTc) and phosphoglycolate phosphatase (cbbZc) genes, complete cds.	Ralstonia eutropha	38,677	27-Jul-94
		GB_HTG4:AC009541	169583	AC009541	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces.	Homo sapiens	36,335	12-OCT-1999
		GB_HTG4:AC009541	169583	AC009541	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces.	Homo sapiens	36,335	12-OCT-1999
rx00437	579	GB_PR4:AC005951	155450	AC005951	Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.	Homo sapiens	31,738	18-Nov-98
		GB_BA1:SC2A11	22789	AL031184	Streptomyces coelicolor cosmid 2A11.	Streptomyces coelicolor	43,262	5-Aug-98
		GB_PR4:AC005951	155450	AC005951	Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.	Homo sapiens	37,647	18-Nov-98
rx00439	591	GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	37,088	23-Jun-99
		GB_PL2:AF167358	1022	AF167358	Rumex acetosa expansin (EXP3) gene, partial cds.	Rumex acetosa	45,538	17-Aug-99
		GB_HTG3:AC009120	269445	AC009120	Homo sapiens chromosome 16 clone RPC1-1_484E3, *** SEQUENCING IN PROGRESS ***, 34 unordered pieces.	Homo sapiens	43,276	3-Aug-99
rx00440	582	GB_BA2:SKZ86111	7860	Z86111	Streptomyces lividans rpsP, trmD, rplS, sipW, sipX, sipY, sipZ, mutT genes and 4 open reading frames.	Streptomyces lividans	43,080	27-OCT-1999
		GB_BA1:SC2E1	38962	AL023797	Streptomyces coelicolor cosmid 2E1.	Streptomyces coelicolor	42,931	4-Jun-98
		GB_BA1:SC2E1	38962	AL023797	Streptomyces coelicolor cosmid 2E1.	Streptomyces coelicolor	36,702	4-Jun-98
rx00441	1287	GB_PR2:HS173D1	117338	AL031984	Human DNA sequence from clone 173D1 on chromosome 1p36.21-36.33. Contains ESTs, STSs and GSSs, complete sequence.	Homo sapiens	38,027	23-Nov-99
		GB_HTG2:HSDJ719K3	267114	AL109931	Homo sapiens chromosome X clone RP4-719K3 map q21.1-21.31, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	34,521	03-DEC-1999
		GB_HTG2:HSDJ719K3	267114	AL109931	Homo sapiens chromosome X clone RP4-719K3 map q21.1-21.31, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	34,521	03-DEC-1999
rx00446	987	GB_BA1:SCD78	36224	AL034355	Streptomyces coelicolor cosmid D78.	Streptomyces coelicolor	56,410	26-Nov-98
		GB_HTG4:AC009367	226055	AC009367	Drosophila melanogaster chromosome 3L/76A2 clone RPC198-48B15, *** SEQUENCING IN PROGRESS ***, 44 unordered pieces.	Drosophila melanogaster	34,959	16-OCT-1999
		GB_HTG4:AC009367	226055	AC009367	Drosophila melanogaster chromosome 3L/76A2 clone RPC198-48B15, *** SEQUENCING IN PROGRESS ***, 44 unordered pieces.	Drosophila melanogaster	34,959	16-OCT-1999
rx00448	1143	GB_PR3:AC003670	88945	AC003670	Homo sapiens 12q13.1 PAC RPC11-130F5 (Roswell Park Cancer Institute Human PAC library) complete sequence.	Homo sapiens	35,682	9-Jun-98
		GB_HTG2:AF029367	148676	AF029367	Homo sapiens chromosome 12 clone RPC1-1 130F5 map 12q13.1, *** SEQUENCING IN PROGRESS ***, 156 unordered pieces.	Homo sapiens	31,373	18-OCT-1997
		GB_HTG2:AF029367	148676	AF029367	Homo sapiens chromosome 12 clone RPC1-1 130F5 map 12q13.1, *** SEQUENCING IN PROGRESS ***, 156 unordered pieces.	Homo sapiens	31,373	18-OCT-1997

TABLE 4: ALIGNMENT RESULTS

rx00450	424	GB_HTG2:AC007824	133361	AC007824	Drosophila melanogaster chromosome 3 clone BACR02L16 (D715) RPCI-98 02.L.16 map 89E-90A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 91 unordered pieces.	Drosophila melanogaster	40,000	2-Aug-99
		GB_HTG2:AC007824	133361	AC007824	Drosophila melanogaster chromosome 3 clone BACR02L16 (D715) RPCI-98 02.L.16 map 89E-90A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 91 unordered pieces.	Drosophila melanogaster	40,000	2-Aug-99
		GB_EST35:A1818057	412	A1818057	wk14a08.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2412278 3' similar to gb:Y00764 UBIQUINOL-CYTOCHROME C REDUCTASE 11 KD PROTEIN (HUMAN); mRNA sequence.	Homo sapiens	35,714	24-Aug-99
rx00461	975	GB_BA1:MLCB1779	43254	Z98271	Mycobacterium leprae cosmid B1779.	Mycobacterium leprae	39,308	8-Aug-97
		GB_IN1:DMC86E4	29352	AL021086	Drosophila melanogaster cosmid clone 86E4.	Drosophila melanogaster	37,487	27-Apr-99
		GB_GSS15:AQ640325	467	AQ640325	927P1-2H3.TP 927P1 Trypanosoma brucei genomic clone 927P1-2H3, genomic survey sequence.	Trypanosoma brucei	38,116	8-Jul-99
rx00465								
rx00487	1692	GB_BA1:BAGUAA	3866	Y10499	B.ammonia genes guaA gene.	Corynebacterium ammonia genes	74,259	8-Jan-98
		GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	37,248	01-MAR-1994
rx00488	1641	GB_BA1:MTCV78	33818	Z77165	Mycobacterium tuberculosis H37Rv complete genome; segment 145/162.	Mycobacterium tuberculosis	39,725	17-Jun-98
		GB_BA1:MTCV78	33818	Z77165	Mycobacterium tuberculosis H37Rv complete genome; segment 145/162.	Mycobacterium tuberculosis	39,451	17-Jun-98
		GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	39,178	01-MAR-1994
		GB_BA1:SCAJ10601	4692	AJ010601	Streptomyces coelicolor A3(2) DNA for whiD and whiK loci.	Streptomyces coelicolor	60,835	17-Sep-98
rx00489	1245	GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	38,041	01-MAR-1994
		GB_HTG2:HS225E12	126464	AL031772	Homo sapiens chromosome 6 clone RP1-225E12 map q24, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	36,756	03-DEC-1999
		GB_HTG2:HS225E12	126464	AL031772	Homo sapiens chromosome 6 clone RP1-225E12 map q24, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	36,756	03-DEC-1999
rx00533	1155	GB_BA1:CGLYS	2803	X57226	C. glutamicum lysC-alpha, lysC-beta and asd genes for aspartokinase-alpha and -beta subunits, and aspartate beta semialdehyde dehydrogenase, respectively (EC 2.7.2.4; EC 1.2.1.11).	Corynebacterium glutamicum	99,913	17-Feb-97
		GB_BA1:CGCYSCASD	1591	X82928	C. glutamicum aspartate-semialdehyde dehydrogenase gene.	Corynebacterium glutamicum	99,221	17-Feb-97
rx00534	1386	GB_PAT:A07546	2112	A07546	Recombinant DNA fragment (PstI-XhoI).	synthetic construct	99,391	30-Jul-93
		GB_BA1:CGLYS	2803	X57226	C. glutamicum lysC-alpha, lysC-beta and asd genes for aspartokinase-alpha and -beta subunits, and aspartate beta semialdehyde dehydrogenase, respectively (EC 2.7.2.4; EC 1.2.1.11).	Corynebacterium glutamicum	99,856	17-Feb-97
		GB_BA1:CORASKD	2957	L16848	Corynebacterium flavum aspartokinase (ask), and aspartate-semialdehyde dehydrogenase (asd) genes, complete cds.	Corynebacterium flavesens	98,701	11-Jun-93
		GB_PAT:E14514	1643	E14514	DNA encoding Brevibacterium aspartokinase.	Corynebacterium glutamicum	98,773	28-Jul-99
rx00535	1494	GB_BA1:CGLYUA	3492	X70959	C. glutamicum gene leuA for isopropylmalate synthase.	Corynebacterium glutamicum	100,000	10-Feb-99
		GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	68,003	24-Jun-99
		GB_BA1:MTU88526	2412	U88526	Mycobacterium tuberculosis putative alpha-isopropyl malate synthase (leuA) gene, complete cds.	Mycobacterium tuberculosis	68,185	26-Feb-97

TABLE 4: ALIGNMENT RESULTS

rx00537	2409	GB_BA2:SCD25	41622	AL118514	Streptomyces coelicolor cosmid D25.	Streptomyces coelicolor A3(2)	63,187	21-Sep-99
		GB_BA1:BTCY7H7A	10451	Z95618	Mycobacterium tuberculosis H37Rv complete genome; segment 39/162.	Mycobacterium tuberculosis	62,401	17-Jun-98
		GB_BA1:MTU34956	2462	U34956	Mycobacterium tuberculosis phosphoribosylformylglycinamide synthase (purL) gene, complete cds.	Mycobacterium tuberculosis	62,205	28-Jan-97
rx00541	792	GB_PAT:192052	2115	I92052	Sequence 19 from patent US 5726299.	Unknown.	98,359	01-DEC-1998
		GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	62,468	24-Jun-97
		GB_BA1:BTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome; segment 36/162.	Mycobacterium tuberculosis	60,814	17-Jun-98
rx00558	1470	GB_BA1:BAPURF	1885	X91252	B.ammoniaenes purF gene.	Corynebacterium ammoniagenes	66,095	5-Jun-97
		GB_BA1:MLU15182	40123	U15182	Mycobacterium leprae cosmid B2266.	Mycobacterium leprae	64,315	09-MAR-1995
		GB_BA1:BTCY7H7A	10451	Z95618	Mycobacterium tuberculosis H37Rv complete genome; segment 39/162.	Mycobacterium tuberculosis	64,863	17-Jun-98
rx00579	1983	GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	98,810	05-DEC-1998
		EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	98,810	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	98,810	24-Jun-98
rx00580	1425	GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	99,368	24-Jun-98
		GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	99,368	05-DEC-1998
		EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	99,368	08-OCT-1997 (Rel. 52, Created)
rx00581	1092	GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	37,071	24-Jun-98
		EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	37,071	08-OCT-1997 (Rel. 52, Created)
rx00584	1248	GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	37,071	05-DEC-1998
		GB_BA1:CORAHPS	2570	L07603	Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene, complete cds.	Corynebacterium glutamicum	98,236	26-Apr-93
		GB_BA1:AOPCZA361	37941	AJ223998	Amycolatopsis orientalis cosmid PCZA361.	Amycolatopsis orientalis	54,553	29-MAR-1999
		GB_BA1:D90714	14358	D90714	Escherichia coli genomic DNA. (16.8 - 17.1 min).	Escherichia coli	53,312	7-Feb-99
rx00618	1230	GB_EST19:AA802737	280	AA802737	GM06236.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM06236 5prime, mRNA sequence.	Drosophila melanogaster	39,928	25-Nov-98
		GB_EST28:A1534381	581	A1534381	SD07186.5prime SD Drosophila melanogaster Schneider L2 cell culture pOT2 Drosophila melanogaster cDNA clone SD07186 5prime similar to X89858: Ani FBgn0011558 PID:g927407 SPTREMBL:Q24240, mRNA sequence.	Drosophila melanogaster	41,136	18-MAR-1999
rx00619	1551	GB_IN1:DMANILLIN	4029	X89858	D.melanogaster mRNA for anillin protein.	Drosophila melanogaster	34,398	8-Nov-95
		GB_BA1:BTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome; segment 36/162.	Mycobacterium tuberculosis	62,776	17-Jun-98
		GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	61,831	24-Jun-97
		GB_PAT:A60305	1845	A60305	Sequence 5 from Patent WO9708323.	unidentified	61,785	06-MAR-1998
rx00620	1014	GB_PL2:AF063247	1450	AF063247	Pneumocystis carinii f. sp. ratti enolase mRNA, complete cds.	Pneumocystis carinii f. sp. ratti	41,060	5-Jan-99
		GB_BA1:STMAPP	2069	M91546	Streptomyces lividans aminopeptidase P (PepP) gene, complete cds.	Streptomyces lividans	37,126	12-Jun-93

TABLE 4: ALIGNMENT RESULTS

	GB_HTG3:AC008763	214575	AC008763	Homo sapiens chromosome 19 contig E1_3214H19, *** SEQUENCING IN PROGRESS ***; 21 unordered pieces.	Homo sapiens	40,020	3-Aug-99
rx00624	810	GB_IN1:CEY41E3	150641	Z95559	Caenorhabditis elegans cosmid Y41E3, complete sequence.	Caenorhabditis elegans	36,986
		GB_EST13:AA362167	372	AA362167	EST71561 Macrophage 1 Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	38,378
		GB_IN1:CEY41E3	150641	Z95559	Caenorhabditis elegans cosmid Y41E3, complete sequence.	Caenorhabditis elegans	37,694
	1386	GB_BA1:MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome; segment 36/162.	Mycobacterium tuberculosis	57,971
		GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	58,806
rx00632	795	GB_BA1:MLU15167	36138	U15167	Mycobacterium leprae cosmid L296.	Mycobacterium leprae	38,007
		GB_BA1:BRLBIOAD	2272	D14083	Brevibacterium flavum genes for 7,8-diaminopelargonic acid aminotransferase and dethiobiotin synthetase, complete cds.	Corynebacterium glutamicum	97,358
		GB_PAT:E04041	675	E04041	DNA sequence coding for dethiobiotinsynthetase.	Corynebacterium glutamicum	98,074
		GB_PAT:E04040	1272	E04040	DNA sequence coding for diamino pelargonic acid aminotransferase.	Corynebacterium glutamicum	93,814
	1392	GB_BA1:BRLBIOAD	2272	D14083	Brevibacterium flavum genes for 7,8-diaminopelargonic acid aminotransferase and dethiobiotin synthetase, complete cds.	Corynebacterium glutamicum	95,690
rx00688	666	GB_PAT:E04040	1272	E04040	DNA sequence coding for diamino pelargonic acid aminotransferase.	Corynebacterium glutamicum	95,755
		GB_BA2:EHU38519	1290	U38519	Erwinia herbicola adenosylmethionine-8-amino-7-oxononanoate transaminase (bioA) gene, complete cds.	Erwinia herbicola	55,564
		GB_BA1:MTV041	28826	AL021958	Mycobacterium tuberculosis H37Rv complete genome; segment 35/162.	Mycobacterium tuberculosis	60,030
		GB_BA1:BRLSECY	1516	D14162	Brevibacterium flavum gene for SecY protein (complete cds) and gene or adenylate kinase (partial cds).	Corynebacterium glutamicum	99,563
		GB_BA2:MBU77912	7163	U77912	Mycobacterium bovis MBE50a gene, partial cds; and MBE50b, MBE50c, preprotein translocase SecY subunit (secY), adenylate kinase (ack), methionine aminopeptidase (map), RNA polymerase ECF sigma factor (sigE50), MBE50d, and MBE50e genes, complete cds.	Mycobacterium bovis	60,030
rx00708	930	GB_BA2:AF157493	25454	AF157493	Zymomonas mobilis ZM4 fosmid clone 42D7, complete sequence.	Zymomonas mobilis	39,116
		GB_PAT:I00836	1853	I00836	Sequence 1 from Patent US 4758514.	Unknown.	47,419
		GB_PAT:E00311	1853	E00311	DNA coding of 2,5-diketoglucuronic acid reductase.	unidentified	47,419
	1083	GB_PAT:I78753	1187	I78753	Sequence 9 from patent US 5693781.	Unknown.	37,814
		GB_PAT:I92042	1187	I92042	Sequence 9 from patent US 5726299.	Unknown.	37,814
rx00718	831	GB_BA1:MTCH125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	50,647
		GB_BA1:MTCH125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	55,228
		GB_BA1:MTCH125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	40,300
		GB_GSS12:AQ420755	671	AQ420755	RPC1-11-168G18 TJ RPC1-11 Homo sapiens genomic clone RPC1-11-168G18, genomic survey sequence.	Homo sapiens	35,750
	1035	GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPC1-98 48.D.10 map 34A-34A strain y; on bw sp, *** SEQUENCING IN PROGRESS ***; 78 unordered pieces.	Drosophila melanogaster	40,634
rx00727		GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPC1-98 48.D.10 map 34A-34A strain y; on bw sp, *** SEQUENCING IN PROGRESS***; 78 unordered pieces.	Drosophila melanogaster	40,634
		GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPC1-98 48.D.10 map 34A-34A strain y; on bw sp, *** SEQUENCING IN PROGRESS***; 78 unordered pieces.	Drosophila melanogaster	33,888
		GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPC1-98 48.D.10 map 34A-34A strain y; on bw sp, *** SEQUENCING IN PROGRESS***; 78 unordered pieces.	Drosophila melanogaster	33,888
		GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPC1-98 48.D.10 map 34A-34A strain y; on bw sp, *** SEQUENCING IN PROGRESS***; 78 unordered pieces.	Drosophila melanogaster	33,888
		GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPC1-98 48.D.10 map 34A-34A strain y; on bw sp, *** SEQUENCING IN PROGRESS***; 78 unordered pieces.	Drosophila melanogaster	33,888

TABLE 4: ALIGNMENT RESULTS

rx00766	966	GB_HTG2:AC006789	83823	AC006789	Caenorhabditis elegans clone Y49F6, *** SEQUENCING IN PROGRESS ***	2 Caenorhabditis elegans unordered pieces.	36,737	25-Feb-99
		GB_HTG2:AC006789	83823	AC006789	Caenorhabditis elegans clone Y49F6, *** SEQUENCING IN PROGRESS ***	2 Caenorhabditis elegans unordered pieces.	36,737	25-Feb-99
rx00770	1293	GB_BA1:D90810	20476	D90810	E.coli genomic DNA, Kohara clone #319(37.4-37.8 min.).	Escherichia coli	36,526	29-MAY-1997
		GB_BA1:MTV043	68848	AL022004	Mycobacterium tuberculosis H37Rv complete genome; segment 40/162.	Mycobacterium tuberculosis	66,193	24-Jun-99
		GB_BA1:MLU15182	40123	U15182	Mycobacterium leprae cosmid B2266.	Mycobacterium leprae	61,443	09-MAR-1995
		GB_BA2:SCD25	41622	AL118514	Streptomyces coelicolor cosmid D25.	Streptomyces coelicolor A3(2)	59,938	21-Sep-99
rx00779	1056	GB_HTG1:CER08A5	51920	Z82281	Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS ***	Caenorhabditis elegans	64,896	14-OCT-1998
		GB_HTG1:CER08A5	51920	Z82281	Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS ***	Caenorhabditis elegans	64,896	14-OCT-1998
rx00780	669	GB_PL2:AF078693	1492	AF078693	Chlamydomonas reinhardtii putative O-acetylserine(thiol)lyase precursor (Crys-1A) mRNA, nuclear gene encoding organellar protein, complete cds.	Chlamydomonas reinhardtii	57,970	3-Nov-99
		GB_BA1:MTCY98	31225	Z83860	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162.	Mycobacterium tuberculosis	54,410	17-Jun-98
		GB_BA1:AVNIFREG	7099	M60090	Azotobacter chroococcum nifU, nifS, nifV, nifP, nifW, nifZ and nifM genes, complete cds.	Azotobacter chroococcum	51,729	26-Apr-93
rx00838	1023	GB_BA2:AF001780	6701	AF001780	Cyanotheca PCC 8801 NifP (nifP), nitrogenase (nifB), FdxN (fdxN), NifS (nifS) and NifU (nifU) genes, complete cds, and NifH (nifH) gene, partial cds.	Cyanotheca PCC8801	36,309	08-MAR-1999
		GB_EST1:Z30506	329	Z30506	ATTS2430 AC16H Arabidopsis thaliana cDNA clone TAI306 3', mRNA sequence.	Arabidopsis thaliana	44,308	11-MAR-1994
		GB_PL2:AC006258	110469	AC006258	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence.	Arabidopsis thaliana	35,571	28-DEC-1998
		GB_EST37:A1998439	455	A1998439	701545695 A, thaliana, Columbia Col-0, rosette-2 Arabidopsis thaliana cDNA clone 701545695, mRNA sequence.	Arabidopsis thaliana	36,044	8-Sep-99
rx00863	867	GB_BA1:BLDAPAB	3572	Z21502	B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	Corynebacterium glutamicum	99,539	16-Aug-93
		GB_PAT:E16749	2001	E16749	gDNA encoding dihydrodipicolinate synthase (DDPS).	Corynebacterium glutamicum	99,539	28-Jul-99
		GB_PAT:E14520	2001	E14520	DNA encoding Brevibacterium dihydrodipicolinic acid synthase.	Corynebacterium glutamicum	99,539	28-Jul-99
rx00864	873	GB_BA1:BLDAPAB	3572	Z21502	B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	Corynebacterium glutamicum	99,885	16-Aug-93
		GB_BA1:CGDAPB	1902	X67737	C.glutamicum dapB gene for dihydrodipicolinate reductase.	Corynebacterium glutamicum	100,000	1-Apr-93
		GB_PAT:E14520	2001	E14520	DNA encoding Brevibacterium dihydrodipicolinic acid synthase.	Corynebacterium glutamicum	100,000	28-Jul-99
rx00865	1026	GB_BA1:BLDAPAB	3572	Z21502	B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	Corynebacterium glutamicum	100,000	16-Aug-93
		GB_PAT:E16752	1411	E16752	gDNA encoding dihydrodipicolinate reductase (DDPR).	Corynebacterium glutamicum	99,805	28-Jul-99
		GB_PAT:AR038113	1411	AR038113	Sequence 18 from patent US 5804414.	Unknown.	99,805	29-Sep-99
rx00867	650	GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	39,179	17-Jun-98
		GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	39,482	22-Aug-97
		GB_BA1:SAU19858	2838	U19858	Streptomyces antibioticus guanosine pentaphosphate synthetase (gpsl) gene, complete cds.	Streptomyces antibioticus	69,706	25-OCT-1996
rx00873	779	GB_BA1:SCO001206	9184	AJ001206	Streptomyces coelicolor A3(2), glycogen metabolism cluster II.	Streptomyces coelicolor	63,415	29-MAR-1999
		GB_BA1:SCO001205	9589	AJ001205	Streptomyces coelicolor A3(2) glycogen metabolism clusterI.	Streptomyces coelicolor	61,617	29-MAR-1999

TABLE 4: ALIGNMENT RESULTS

rx00884	1263	GB_BA1:D78198	2304	D78198	Pimelobacter sp. DNA for trehalose synthase, complete cds.	Pimelobacter sp.	60,594	5-Feb-99
		GB_BA1:MTCY253	41230	Z81368	Mycobacterium tuberculosis H37Rv complete genome; segment 106/162.	Mycobacterium tuberculosis	37,785	17-Jun-98
		GB_BA1:MSGY222	41156	AD000010	Mycobacterium tuberculosis sequence from clone y222.	Mycobacterium tuberculosis	38,006	03-DEC-1996
		GB_GSS15:AQ654600	468	AQ654600	Sheared DNA-1014. TF Sheared DNA Trypanosoma brucei genomic clone	Trypanosoma brucei	33,974	22-Jun-99
rx00891	1102	GB_BA1:MTCI418B	11700	Z96071	Sheared DNA-1014, genomic survey sequence.			
		GB_BA1:SCO001206	9184	AJ001206	Mycobacterium tuberculosis H37Rv complete genome; segment 7/162.	Mycobacterium tuberculosis	63,297	18-Jun-98
		GB_BA1:SCO001205	9589	AJ001205	Streptomyces coelicolor A3(2), glycogen metabolism cluster II.	Streptomyces coelicolor	61,965	29-MAR-1999
rx00952	963	EM_PAT:E10963	3118	E10963	Streptomyces coelicolor A3(2) glycogen metabolism cluster I.	Streptomyces coelicolor	61,727	29-MAR-1999
					gDNA encoding tryptophan synthase.	Corynebacterium glutamicum	99,688	08-OCT-1997 (Rel. 52, Created)
rx00954	644	GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	98,847	10-Feb-99
		GB_PAT:E01688	7725	E01688	Genomic DNA of trp operon of prebacterium latophelmentam.	unidentified	98,428	29-Sep-97
		GB_PAT:E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,758	29-Sep-97
		GB_PAT:E01688	7725	E01688	Genomic DNA of trp operon of prebacterium latophelmentam.	unidentified	98,758	29-Sep-97
rx00955	1545	GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	98,758	10-Feb-99
		GB_PAT:E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,372	29-Sep-97
		GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	98,372	10-Feb-99
		GB_PAT:E01688	7725	E01688	Genomic DNA of trp operon of prebacterium latophelmentam.	unidentified	98,242	29-Sep-97
rx00956	1237	EM_PAT:E10963	3118	E10963	gDNA encoding tryptophan synthase.	Corynebacterium glutamicum	98,949	08-OCT-1997 (Rel. 52, Created)
rx00957	1677	GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	99,107	10-Feb-99
		GB_PAT:E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,945	29-Sep-97
		GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	99,165	10-Feb-99
		GB_PAT:E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,927	29-Sep-97
		GB_PAT:E01688	7725	E01688	Genomic DNA of trp operon of prebacterium latophelmentam.	unidentified	98,867	29-Sep-97
rx00958	747	GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	98,792	10-Feb-99
		GB_PAT:E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,792	29-Sep-97
		GB_PAT:E01688	7725	E01688	Genomic DNA of trp operon of prebacterium latophelmentam.	unidentified	98,658	29-Sep-97
rx00970	1050	GB_BA1:CGHOMTHR	3685	Y00546	Corynebacterium glutamicum hom-thrB genes for homoserine dehydrogenase and homoserine kinase.	Corynebacterium glutamicum	99,905	12-Sep-93
		GB_PAT:109077	3685	I09077	Sequence 1 from Patent WO 8809819.	Unknown.	99,810	02-DEC-1994
		GB_PAT:E01358	2615	E01358	DNA encoding for homoserine dehydrogenase(HDH)and homoserine kinase(HK).	Corynebacterium glutamicum	97,524	29-Sep-97
rx00972	1458	GB_PAT:E16755	3579	E16755	gDNA encoding diaminopimelate decarboxylase (DDC) and arginyl-tRNA synthase.	Corynebacterium glutamicum	99,931	28-Jul-99
		GB_PAT:AR038110	3579	AR038110	Sequence 15 from patent US 5804414.	Unknown.	99,931	29-Sep-99
		GB_PAT:E14508	3579	E14508	DNA encoding Brevibacterium diaminopimelic acid decarboxylase and arginyl-tRNA synthase.	Corynebacterium glutamicum	99,931	28-Jul-99
rx00981	753	GB_OV:GGA245664	512	AJ245664	Gallus gallus partial mRNA for ATP-citrate lyase (ACL gene).	Gallus gallus	37,538	28-Sep-99
		GB_PL2:AC007887	159434	AC007887	Genomic sequence for Arabidopsis thaliana BAC F1504 from chromosome I, complete sequence.	Arabidopsis thaliana	37,600	04-OCT-1999

TABLE 4: ALIGNMENT RESULTS

GB_GSS1:CNS00RNW	542	AL087338	Arabidopsis thaliana genome survey sequence T7 end of BAC F14D7 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.	Arabidopsis thaliana	41,264	28-Jun-99
GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	40,773	17-Jun-98
GB_BA1:SCVALSFP	3619	Y13070	S.coelicolor valS, fpgs, ndk genes.	Streptomyces coelicolor	58,119	03-MAR-1998
GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	38,167	17-Jun-98
GB_BA2:CGU31225	1817	U31225	Corynebacterium glutamicum L-proline:NADP+ 5-oxidoeductase (proC) gene, complete cds.	Corynebacterium glutamicum	40,841	2-Aug-96
GB_HTG1:CEY39C12	282838	AL009026	Caenorhabditis elegans chromosome IV clone Y39C12, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	36,416	26-OCT-1999
GB_IN1:CEB0001	39416	Z69634	Caenorhabditis elegans cosmid B0001, complete sequence.	Caenorhabditis elegans	36,416	2-Sep-99
GB_HTG2:AC005052	144734	AC005052	Homo sapiens clone RG038K21, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	39,172	12-Jun-98
GB_HTG2:AC005052	144734	AC005052	Homo sapiens clone RG038K21, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	39,172	12-Jun-98
GB_GSS9:AQ171808	512	AQ171808	HS_3179_A1_G03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3179 Col=5 Row=M, genomic survey sequence.	Homo sapiens	34,661	17-OCT-1998
GB_BA1:SC1C2	42210	AL031124	Streptomyces coelicolor cosmid 1C2.	Streptomyces coelicolor	68,275	15-Jan-99
GB_BA1:ATLEUCD	2982	X84647	A.tetichomyceticus leuC and leuD genes.	Actinoplanes teichomyceticus	65,935	04-OCT-1995
GB_BA1:MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	Mycobacterium tuberculosis	40,454	23-Jun-99
GB_BA1:MLCB637	44882	Z99263	Mycobacterium leprae cosmid B637.	Mycobacterium leprae	38,636	17-Sep-97
GB_BA1:MTCV349	43523	Z83018	Mycobacterium tuberculosis H37Rv complete genome; segment 131/162.	Mycobacterium tuberculosis	51,989	17-Jun-98
GB_BA1:SPUNG MUTX	1172	Z21702	S.pneumoniae ung gene and mutX genes encoding uracil-DNA glycosylase and 8-oxodGTP nucleoside triphosphatase.	Streptococcus pneumoniae	38,088	15-Jun-94
GB_BA1:BACOUTB	1004	M15811	Bacillus subtilis outB gene encoding a sporulation protein, complete cds.	Bacillus subtilis	53,723	26-Apr-93
GB_PR4:AC007938	167237	AC007938	Homo sapiens clone UWGC:djs201 from 7q31, complete sequence.	Homo sapiens	34,322	1-Jul-99
GB_PL2:ATAC006282	92577	AC006282	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence.	Arabidopsis thaliana	36,181	13-MAR-1999
GB_BA2:AF112535	4363	AF112535	Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), NrdI (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds.	Corynebacterium glutamicum	99,820	5-Aug-99
GB_BA1:CANRDFGEN	6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	Corynebacterium ammoniagenes	75,966	18-Apr-98
GB_BA1:MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	Mycobacterium tuberculosis	38,296	23-Jun-99
GB_BA2:AF112535	4363	AF112535	Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), NrdI (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds.	Corynebacterium glutamicum	100,000	5-Aug-99
GB_BA1:CANRDFGEN	6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	Corynebacterium ammoniagenes	65,511	18-Apr-98
GB_BA1:STNRD	4894	X73226	S.typhimurium nrdEF operon.	Salmonella typhimurium	52,477	03-MAR-1997
GB_IN2:AF063412	1093	AF063412	Limnadia lenticularis elongation factor 1-alpha mRNA, partial cds.	Limnadia lenticularis	43,750	29-MAR-1999
GB_PR3:HS24M15	134539	Z94055	Human DNA sequence from PAC 24M15 on chromosome 1. Contains tenascin-R (restictin), EST.	Homo sapiens	37,475	23-Nov-99
GB_IN2:ARU85702	1240	U85702	Anathix ralla elongation factor-1 alpha (EF-1a) gene, partial cds.	Anathix ralla	37,319	16-Jul-97

TABLE 4: ALIGNMENT RESULTS

rx01095	857	GB_BA1:MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162.	Mycobacterium tuberculosis	43,243	17-Jun-98
		GB_HTG5:AC011632	175917	AC011632	Homo sapiens clone RP11-3N13, WORKING DRAFT SEQUENCE, 9 unordered pieces.	Homo sapiens	36,471	19-Nov-99
		GB_HTG5:AC011632	175917	AC011632	Homo sapiens clone RP11-3N13, WORKING DRAFT SEQUENCE, 9 unordered pieces.	Homo sapiens	36,836	19-Nov-99
rx01097	477	GB_BA2:AF030405	774	AF030405	Corynebacterium glutamicum cyclase (hisF) gene, complete cds.	Corynebacterium glutamicum	100,000	13-Nov-97
		GB_BA2:AF030405	774	AF030405	Corynebacterium glutamicum cyclase (hisF) gene, complete cds.	Corynebacterium glutamicum	41,206	13-Nov-97
rx01098	897	GB_BA2:AF030405	774	AF030405	Corynebacterium glutamicum cyclase (hisF) gene, complete cds.	Corynebacterium glutamicum	97,933	13-Nov-97
		GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	40,972	10-DEC-1996
		GB_BA1:MLCB1610	40055	AL049913	Mycobacterium leprae cosmid B1610.	Mycobacterium leprae	61,366	27-Aug-99
rx01100	861	GB_BA2:AF051846	738	AF051846	Corynebacterium glutamicum phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase (hisA) gene, complete cds.	Corynebacterium glutamicum	97,154	12-MAR-1998
		GB_BA2:AF060558	636	AF060558	Corynebacterium glutamicum glutamine amidotransferase (hisH) gene, complete cds.	Corynebacterium glutamicum	95,455	29-Apr-98
rx01101	756	GB_BA2:AF060558	636	AF060558	Homo sapiens chromosome 1 clone RP1-140A9, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	30,523	23-Nov-99
		GB_BA1:SC4G6	36917	AL096884	Corynebacterium glutamicum glutamine amidotransferase (hisH) gene, complete cds.	Corynebacterium glutamicum	94,462	29-Apr-98
		GB_BA1:STMHISOPA	3981	M31628	Streptomyces coelicolor cosmid 4G6.	Streptomyces coelicolor A3(2)	38,378	23-Jul-99
rx01104	729	GB_BA1:STMHISOPA	3981	M31628	S.coelicolor histidine biosynthesis operon encoding hisD, partial cds., and hisC, hisB, hisH, and hisA genes, complete cds.	Streptomyces coelicolor	60,053	26-Apr-93
		GB_BA1:SC4G6	36917	AL096884	S.coelicolor histidine biosynthesis operon encoding hisD, partial cds., and hisC, hisB, hisH, and hisA genes, complete cds.	Streptomyces coelicolor	58,333	26-Apr-93
		GB_BA1:MTCY336	32437	Z95586	Streptomyces coelicolor cosmid 4G6.	Streptomyces coelicolor A3(2)	39,045	23-Jul-99
rx01105	1221	GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	60,364	24-Jun-99
		GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	60,931	24-Jun-99
		GB_BA1:MLCB1610	40055	AL049913	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	36,851	10-DEC-1996
rx01106	1449	GB_BA1:MSGY223	42061	AD000019	Mycobacterium leprae cosmid B1610.	Mycobacterium leprae	60,902	27-Aug-99
		GB_BA1:MSHISC	2298	X65542	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	37,233	10-DEC-1996
		GB_BA1:MTCY336	32437	Z95586	M.smegmatis genes hisD and hisC for histidinol dehydrogenase and histidinol-phosphate aminotransferase, respectively.	Mycobacterium smegmatis	60,111	30-Jun-93
rx01145	1137	GB_BA1:CORAI	4705	L09232	Corynebacterium glutamicum H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	58,420	24-Jun-99
		GB_BA1:BRILVCA	1364	D14551	Corynebacterium glutamicum acetoxy acid synthase (ilvB) and (ilvN) genes, and acetoxy acid isomerase (ilvC) gene, complete cds.	Corynebacterium glutamicum	100,000	23-Feb-95
		GB_PAT:E08232	1017	E08232	Brevibacterium flavum ilvC gene for acetoxy acid isomerase, complete cds.	Corynebacterium glutamicum	99,560	3-Feb-99
rx01162	1449	GB_PAT:A60299	2869	A60299	DNA encoding acetoxy acid isomerase.	Corynebacterium glutamicum	99,803	29-Sep-97
		GB_PR3:HS24E5	35506	Z82185	Sequence 18 from Patent WO9706261.	Aspergillus niger	38,675	06-MAR-1998
					Human DNA sequence from Fosmid 24E5 on chromosome 22q11.2-qter contains parvalbumin, ESTs, STS.	Homo sapiens	36,204	23-Nov-99

TABLE 4: ALIGNMENT RESULTS

rx01208	846	GB_PR3:AC005265	43900	AC005265	Homo sapiens chromosome 19, cosmid F19750, complete sequence.	Homo sapiens	38,363	6-Jul-98
		GB_HTG2:AC004965	323792	AC004965	Homo sapiens clone DJ1106H14, *** SEQUENCING IN PROGRESS ***	Homo sapiens	36,058	12-Jun-98
		GB_HTG2:AC004965	323792	AC004965	unordered pieces.			
		GB_HTG2:AC004965	323792	AC004965	Homo sapiens clone DJ1106H14, *** SEQUENCING IN PROGRESS ***	Homo sapiens	36,058	12-Jun-98
		GB_PL2:TAU55859	2397	U55859	unordered pieces.			
rx01209	1528	GB_HTG3:AC011469	113436	AC011469	Triticum aestivum heat shock protein 80 mRNA, complete cds.	Triticum aestivum	37,269	1-Feb-99
		GB_HTG3:AC011469	113436	AC011469	Homo sapiens chromosome 19 clone CIT-HSPC_475D23, *** SEQUENCING IN PROGRESS ***	Homo sapiens	40,000	07-OCT-1999
		GB_HTG3:AC011469	113436	AC011469	IN PROGRESS ***			
		GB_HTG3:AC011469	113436	AC011469	Homo sapiens chromosome 19 clone CIT-HSPC_475D23, *** SEQUENCING IN PROGRESS ***	Homo sapiens	40,000	07-OCT-1999
		GB_PL1:AB010077	77380	AB010077	IN PROGRESS ***			
		GB_PL1:AB010077	77380	AB010077	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence.	Arabidopsis thaliana	36,803	20-Nov-99
rx01215	1098	GB_BA1:MTCY10G2	38970	Z92539	Mycobacterium tuberculosis H37Rv complete genome; segment 47/162.	Mycobacterium tuberculosis	37,047	17-Jun-98
		GB_IN1:LEIPRPP	1887	M76553	Leishmania donovani phosphoribosylpyrophosphate synthetase gene, complete cds.	Leishmania donovani	50,738	7-Jun-93
		GB_HTG2:HSJ799D16	130149	AL050344	Homo sapiens chromosome 1 clone RP4-799D16 map p34.3-36.1, *** SEQUENCING IN PROGRESS ***	Homo sapiens	38,135	29-Nov-99
		GB_BA1:MTCY48	35377	Z74020	SEQUENCING IN PROGRESS ***			
rx01239	2556	GB_PR2:AB029032	6377	AB029032	Mycobacterium tuberculosis H37Rv complete genome; segment 69/162.	Mycobacterium tuberculosis	38,139	17-Jun-98
		GB_GSS9:AQ107201	355	AQ107201	Homo sapiens mRNA for KIAA1109 protein, partial cds.	Homo sapiens	39,394	4-Aug-99
		GB_PL2:F508	99923	AC005990	HS_3098_A1_C03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3098 Col=5 Row=E, genomic survey sequence.	Homo sapiens	41,408	28-Aug-98
rx01253	873	GB_PL2:F508	99923	AC005990	Arabidopsis thaliana chromosome 1 BAC F508 sequence, complete sequence.	Arabidopsis thaliana	36,118	23-DEC-1998
		GB_PL2:F508	99923	AC005990	Arabidopsis thaliana chromosome 1 BAC F508 sequence, complete sequence.	Arabidopsis thaliana	35,574	23-DEC-1998
rx01321	1044	GB_IN1:CELC06G1	31205	U41014	Caenorhabditis elegans cosmid C06G1.	Caenorhabditis elegans	38,560	30-Nov-95
		GB_GSS14:AQ518843	441	AQ518843	HS_5106_A1_D10_SP6E RPCL-11 Human Male BAC Library Homo sapiens genomic clone Plate=682 Col=19 Row=G, genomic survey sequence.	Homo sapiens	41,121	05-MAY-1999
		GB_HTG2:AC007473	194859	AC007473	Drosophila melanogaster chromosome 2 clone BACR38D12 (D590) RPCL-98	Drosophila melanogaster	40,634	2-Aug-99
		GB_HTG2:AC007473	194859	AC007473	38.D.12 map 48A-48B strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***			
		GB_HTG4:AC011696	115847	AC011696	Drosophila melanogaster chromosome 2 clone BACR35F01 (D1156) RPCL-98	Drosophila melanogaster	38,290	26-OCT-1999
		GB_PL2:ATAC005167	83260	AC005167	35.F.1 map 48A-48C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***			
rx01352	706	GB_PL2:ATAC005167	83260	AC005167	108 unordered pieces.	Arabidopsis thaliana	34,311	15-OCT-1998
		GB_PL2:ATAC005825	97380	AC005825	complete sequence.	Arabidopsis thaliana	34,311	12-Apr-99
		GB_HTG3:AC011150	127222	AC011150	Arabidopsis thaliana chromosome II BAC T24/21 genomic sequence, complete sequence.	Arabidopsis thaliana	37,722	01-OCT-1999
rx01360	259	GB_EST32:A1725583	728	A1725583	Homo sapiens clone 4_K_17, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	38,492	11-Jun-99
		GB_PR2:HS227P17	82951	Z81007	BNLGH12371 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (U86081) root hair defective 3 [Arabidopsis thaliana], mRNA sequence.	Gossypium hirsutum	39,738	23-Nov-99
		GB_PR2:HS227P17	82951	Z81007	Human DNA sequence from PAC 227P17, between markers DXS6791 and DXS8038 on chromosome X contains CpG island, EST.	Homo sapiens		

TABLE 4: ALIGNMENT RESULTS

GB_EST34:AV171099	173	AV171099	AV171099 Mus musculus head C57BL/6J 14, 17 day embryo Mus musculus cDNA clone 3200002M11, mRNA sequence.	Mus musculus	46,237	6-Jul-99
GB_RO:AB008915S1	530	AB008915	Mus musculus mGpi1 gene, exon 1.	Mus musculus	45,574	28-Sep-99
GB_EST22:AI050532	293	AI050532	uc83d10.y1 Sugano mouse kidney mika Mus musculus cDNA clone IMAGE:1432243 5' similar to TR:O35120 O35120 MGPI1P. ; mRNA sequence.	Mus musculus	44,097	9-Jul-98
GB_RO:AB008895	3062	AB008895	Mus musculus mRNA for mGpi1p, complete cds.	Mus musculus	41,316	23-Nov-97
GB_PL1:AB005237	87835	AB005237	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence.	Arabidopsis thaliana	36,606	20-Nov-99
GB_GSS5:AQ766840	491	AQ766840	HS_2026_A2_C09_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=18 Row=E, genomic survey sequence.	Homo sapiens	37,916	28-Jul-99
GB_BA1:MTV043	68848	AL022004	Mycobacterium tuberculosis H37Rv complete genome; segment 40/162.	Mycobacterium tuberculosis	37,419	24-Jun-99
GB_BA1:CGLYSE	2374	X96471	C.glutamicum lysE and lysG genes.	Corynebacterium glutamicum	34,831	24-Feb-97
GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	35,138	27-Jul-98
GB_PR3:AC004054	112184	AC004054	Homo sapiens chromosome 4 clone B220G8 map 4q21, complete sequence.	Homo sapiens	37,277	9-Jul-98
GB_BA1:CGLYSEG	2374	X96471	C.glutamicum lysE and lysG genes.	Corynebacterium glutamicum	100,000	24-Feb-97
GB_GSS5:AQ769223	500	AQ769223	HS_3155_B2_G10_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3155 Col=20 Row=N, genomic survey sequence.	Homo sapiens	38,400	28-Jul-99
GB_BA1:CGLYSEG	2374	X96471	C.glutamicum lysE and lysG genes.	Corynebacterium glutamicum	33,665	24-Feb-97
GB_BA1:SC3C3	31382	AL031231	Streptomyces coelicolor cosmid 3C3.	Streptomyces coelicolor	62,726	10-Aug-98
GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	39,159	22-Aug-97
GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	37,340	17-Jun-98
GB_BA1:D90827	18886	D90827	E.coli genomic DNA, Kohara clone #336(41.2-41.6 min.).	Escherichia coli	58,517	21-MAR-1997
GB_BA1:D90828	14590	D90828	E.coli genomic DNA, Kohara clone #336gap(41.6-41.9 min.).	Escherichia coli	56,151	21-MAR-1997
GB_BA2:AE000279	10855	AE000279	Escherichia coli K-12 MG1655 section 169 of 400 of the complete genome.	Escherichia coli	58,021	12-Nov-98
GB_BA1:SCH10	39524	AL049754	Streptomyces coelicolor cosmid H10.	Streptomyces coelicolor	39,037	04-MAY-1999
GB_BA1:MTY13E10	35019	Z95324	Mycobacterium tuberculosis H37Rv complete genome; segment 18/162.	Mycobacterium tuberculosis	40,130	17-Jun-98
GB_BA1:MLCB4	36310	AL023514	Mycobacterium leprae cosmid B4.	Mycobacterium leprae	37,752	27-Aug-99
GB_BA1:MTCY98	31225	Z83860	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162.	Mycobacterium tuberculosis	39,057	17-Jun-98
GB_BA1:MSGB1229CS	30670	L78812	Mycobacterium leprae cosmid B1229 DNA sequence.	Mycobacterium leprae	54,382	15-Jun-96
GB_BA2:AF027507	5168	AF027507	Mycobacterium smegmatis dGTPase (dgt), and primase (dnaG) genes, complete cds; IRNA-Asn gene, complete sequence.	Mycobacterium smegmatis	52,941	16-Jan-98
GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	40,941	17-Jun-98
GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	38,451	22-Aug-97
GB_BA1:SC3C3	31382	AL031231	Streptomyces coelicolor cosmid 3C3.	Streptomyces coelicolor	61,194	10-Aug-98
GB_BA1:CORFADS	1547	D37867	Corynebacterium ammoniagenes gene for FAD synthetase, complete cds.	Corynebacterium ammoniagenes	58,021	8-Feb-99
GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	38,414	22-Aug-97
GB_BA1:SC10A7	39739	AL078618	Streptomyces coelicolor cosmid 10A7.	Streptomyces coelicolor	36,930	9-Jun-99
GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	37,062	17-Jun-98

TABLE 4: ALIGNMENT RESULTS

rx01508	1662	GB_EST13:AA356956	255	AA356956	EST65614 Jurkat T-cells III Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	37,647	21-Apr-97
		GB_OV:OMDNAPRO1	7327	X92380	O.mossambicus prolactin I gene.	Tilapia mossambica	38,289	19-OCT-1995
		GB_IN1:CEF28C12	14653	Z93380	Caenorhabditis elegans cosmid F28C12, complete sequence.	Caenorhabditis elegans	37,984	23-Nov-98
		GB_IN1:CEF28C12	14653	Z93380	Caenorhabditis elegans cosmid F28C12, complete sequence.	Caenorhabditis elegans	38,469	23-Nov-98
rx01512	723	GB_BA1:SCE9	37730	AL049841	Streptomyces coelicolor cosmid E9.	Streptomyces coelicolor	39,021	19-MAY-1999
		GB_BA1:MAU88875	840	U88875	Mycobacterium avium hypoxanthine-guanine phosphoribosyl transferase gene, complete cds.	Mycobacterium avium	57,521	05-MAR-1997
rx01514	711	GB_BA1:MTY15C10	33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome; segment 154/162.	Mycobacterium tuberculosis	40,086	17-Jun-98
		GB_BA1:MTY7H7B	24244	Z95557	Mycobacterium tuberculosis H37Rv complete genome; segment 153/162.	Mycobacterium tuberculosis	43,343	18-Jun-98
		GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae	38,177	27-Aug-99
		GB_PL1:EGGTPCHI	242	Z49757	E.gracilis mRNA for GTP cyclohydrolase I (core region).	Euglena gracilis	64,876	20-OCT-1995
rx01515	975	GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	38,943	17-Apr-96
		GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	37,500	17-Apr-96
		GB_BA1:MTCY49	39430	Z73966	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162.	Mycobacterium tuberculosis	38,010	24-Jun-99
rx01516	513	GB_IN1:DME238847	5419	AJ238847	Drosophila melanogaster mRNA for drosophila dodeca-satellite protein 1 (DDP).	Drosophila melanogaster	36,346	13-Aug-99
		GB_HTG3:AC009210	103814	AC009210	Drosophila melanogaster chromosome 2 clone BACR0106 (D1054) RPCI-98 01.1.6 map 55D-55D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***.	Drosophila melanogaster	37,897	20-Aug-99
rx01517	600	GB_IN2:AF132179	4842	AF132179	Drosophila melanogaster clone LD21677 unknown mRNA.	Drosophila melanogaster	36,149	3-Jun-99
		GB_PL2:F6H8	82596	AF178045	Arabidopsis thaliana BAC F6H8.	Arabidopsis thaliana	35,846	19-Aug-99
		GB_PL2:AF038831	647	AF038831	Sorosporium saporariae internal transcribed spacer 1, 5.8S ribosomal RNA gene; and internal transcribed spacer 2, complete sequence.	Sorosporium saporariae	40,566	13-Apr-99
		GB_PL2:ATAC005957	108355	AC005957	Arabidopsis thaliana chromosome II BAC T15J14 genomic sequence, complete sequence.	Arabidopsis thaliana	38,095	7-Jan-99
rx01521	921	GB_BA1:ANANIFBH	5936	J05111	Anabaena sp. (clone AnH20.1) nitrogen fixation operon nifB, fdxN, nifS, nifU, and nifH genes, complete cds.	Anabaena sp.	38,206	26-Apr-93
		GB_PR2:AC002461	197273	AC002461	Human BAC clone RG20416 from 7q31, complete sequence.	Homo sapiens	36,623	20-Aug-97
		GB_PR2:AC002461	197273	AC002461	Human BAC clone RG20416 from 7q31, complete sequence.	Homo sapiens	34,719	20-Aug-97
rx01528	651	GB_RO:MM437P9	165901	AL049866	Mus musculus chromosome X, clone 437P9.	Mus musculus	37,500	29-Jun-99
		GB_PR3:AC005740	186780	AC005740	Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.	Homo sapiens	37,031	01-OCT-1998
		GB_PR3:AC005740	186780	AC005740	Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.	Homo sapiens	38,035	01-OCT-1998
rx01551	1998	GB_BA1:MTY22G10	35420	Z84724	Mycobacterium tuberculosis H37Rv complete genome; segment 21/162.	Mycobacterium tuberculosis	38,371	17-Jun-98
		GB_BA2:ECOUW89	176195	U00006	E. coli chromosomal region from 89.2 to 92.8 minutes.	Escherichia coli	38,064	17-DEC-1993
		GB_BA1:SCQ11	15441	AL096823	Streptomyces coelicolor cosmid Q11.	Streptomyces coelicolor	60,775	8-Jul-99
rx01561	1053	GB_IN1:CEY62H9A	47396	AL032630	Caenorhabditis elegans cosmid Y62H9A, complete sequence.	Caenorhabditis elegans	38,514	2-Sep-99
		GB_PR4:HSU51003	3202	U51003	Homo sapiens DLX-2 (DLX-2) gene, complete cds.	Homo sapiens	37,730	07-DEC-1999
		GB_OM:PIGDAO1	395	M18444	Pig D-aminop acid oxidase (DAO) gene, exon 1.	Sus scrofa	39,340	27-Apr-93
rx01599	1785	GB_BA1:MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	63,300	17-Jun-98
		GB_BA1:U00021	39193	U00021	Mycobacterium leprae cosmid L247.	Mycobacterium leprae	36,756	29-Sep-94
		GB_BA1:MLCB1351	38936	Z95117	Mycobacterium leprae cosmid B1351.	Mycobacterium leprae	36,756	24-Jun-97

TABLE 4: ALIGNMENT RESULTS

rx01617	795	GB_PR2:HSMTM0	217657	AL034384	Human chromosome Xq28, cosmid clones 7H3, 14D7, C1230, 11E7, F1096, A12197, 12G8, A09100; complete sequence bases 1..217657.	Homo sapiens	40,811	5-Jul-99
		GB_PR2:HS13D10	153147	AL021407	Homo sapiens DNA sequence from PAC 13D10 on chromosome 6p22.3-23. Contains CpG island.	Homo sapiens	38,768	23-Nov-99
rx01657	723	GB_PR2:HSMTM0	217657	AL034384	Human chromosome Xq28, cosmid clones 7H3, 14D7, C1230, 11E7, F1096, A12197, 12G8, A09100; complete sequence bases 1..217657.	Homo sapiens	39,018	5-Jul-99
		GB_BA1:MTCY1A10	25949	Z95387	Mycobacterium tuberculosis H37Rv complete genome; segment 117/162.	Mycobacterium tuberculosis	40,656	17-Jun-98
		GB_EST6:D79278	392	D79278	HUM213D06B Human aorta polyA+ (TFujiiwara) Homo sapiens cDNA clone GEN-213D06 5'. mRNA sequence.	Homo sapiens	44,262	9-Feb-96
rx01660	675	GB_BA2:AF129925	10243	AF129925	Thiobacillus ferrooxidans carboxysome operon, complete cds.	Thiobacillus ferrooxidans	40,709	17-MAY-1999
		GB_BA1:MTV013	11364	AL021309	Mycobacterium tuberculosis H37Rv complete genome; segment 134/162.	Mycobacterium tuberculosis	40,986	17-Jun-98
		GB_RO:MMFV1	6480	X97719	M.musculus retrovirus restriction gene Fv1.	Mus musculus	35,364	29-Aug-96
		GB_PAT:A67508	6480	A67508	Sequence 1 from Patent WO9743410.	Mus musculus	35,364	05-MAY-1999
rx01678	651	GB_VI:TVU95309	600	U95309	Tula virus O64 nucleocapsid protein gene, partial cds.	Tula virus	41,894	28-OCT-1997
		GB_VI:TVU95303	600	U95303	Tula virus O52 nucleocapsid protein gene, partial cds.	Tula virus	41,712	28-OCT-1997
		GB_VI:TVU95302	600	U95302	Tula virus O24 nucleocapsid protein gene, partial cds.	Tula virus	39,576	28-OCT-1997
rx01679	1359	GB_EST5:H91843	362	H91843	ys81e01.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:221208 3' similar to gb:X63749_ma1 GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-1 (HUMAN); mRNA sequence.	Homo sapiens	39,157	29-Nov-95
		GB_STS:G26925	362	G26925	human STS SHGC-30023, sequence tagged site.	Homo sapiens	39,157	14-Jun-96
		GB_PL2:AF139451	1202	AF139451	Gossypium robinsonii CelA2 pseudogene, partial sequence.	Gossypium robinsonii	38,910	1-Jun-99
rx01690	1224	GB_BA1:SC1C2	42210	AL031124	Streptomyces coelicolor cosmid 1C2.	Streptomyces coelicolor	60,644	15-Jan-99
		GB_EST22:A064232	493	A064232	GH04563.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH04563 5prime, mRNA sequence.	Drosophila melanogaster	38,037	24-Nov-98
rx01692	873	GB_IN2:AF117896	1020	AF117896	Drosophila melanogaster neuropeptide F (npf) gene, complete cds.	Drosophila melanogaster	36,122	2-Jul-99
		GB_BA2:AF067123	1034	AF067123	Lactobacillus reuteri cobalamin biosynthesis protein J (cbiJ) gene, partial cds; and uroporphyrin-III C-methyltransferase (sumT) gene, complete cds.	Lactobacillus reuteri	48,079	3-Jun-98
		GB_RO:RATNFHPEP	3085	M37227	Rat heavy neurofilament (NF-H) polypeptide, partial cds.	Rattus norvegicus	37,093	27-Apr-93
		GB_RO:RSNFH	3085	X13804	Rat mRNA for heavy neurofilament polypeptide NF-H C-terminus.	Rattus sp.	37,093	14-Jul-95
rx01698	1353	GB_BA2:AF124600	4115	AF124600	Corynebacterium glutamicum chorismate synthase (aroC), shikimate kinase (aroK), and 3-dehydroquinate synthase (aroB) genes, complete cds; and putative cytoplasmic peptidase (pepQ) gene, partial cds.	Corynebacterium glutamicum	100,000	04-MAY-1999
		GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	36,323	17-Jun-98
		GB_BA1:MSGB937CS	38914	L78820	Mycobacterium leprae cosmid B937 DNA sequence.	Mycobacterium leprae	62,780	15-Jun-96
rx01699	693	GB_BA2:AF124600	4115	AF124600	Corynebacterium glutamicum chorismate synthase (aroC), shikimate kinase (aroK), and 3-dehydroquinate synthase (aroB) genes, complete cds; and putative cytoplasmic peptidase (pepQ) gene, partial cds.	Corynebacterium glutamicum	100,000	04-MAY-1999
		GB_BA2:AF016585	41097	AF016585	Streptomyces caelestis cytochrome P-450 hydroxylase homolog (nidI) gene, partial cds; polyketide synthase modules 1 through 7 (nidA) genes, complete cds; and N-methyltransferase homolog gene, partial cds.	Streptomyces caelestis	40,260	07-DEC-1997
		GB_EST9:C19712	399	C19712	C19712 Rice panicle at ripening stage Oryza sativa cDNA clone E10821_1A, mRNA sequence.	Oryza sativa	45,425	24-OCT-1996
rx01712	805	GB_EST21:AA952466	278	AA952466	TENS1404 T. cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 1404 5', mRNA sequence.	Trypanosoma cruzi	40,876	29-OCT-1998

TABLE 4: ALIGNMENT RESULTS

GB_EST21:AA952466	278	AA952466	TENS1404 T. cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 1404 5', mRNA sequence.	41,367	29-OCT-1998
GB_HTG1:HSDJ534K7	154416	AL109925	Homo sapiens chromosome 1 clone RP4-534K7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	35,651	23-Nov-99
GB_HTG1:HSDJ534K7	154416	AL109925	Homo sapiens chromosome 1 clone RP4-534K7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	35,651	23-Nov-99
GB_EST27:AI447108	431	AI447108	mq91e08.x1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:586118 3', mRNA sequence.	39,671	09-MAR-1999
GB_PR4:AC006322	179640	AC006322	Homo sapiens PAC clone DJ1060B11 from 7q11.23-q21.1, complete sequence.	35,817	18-MAR-1999
GB_PL2:TM018A10	106184	AF013294	Arabidopsis thaliana BAC TM018A10.	35,698	12-Jul-97
GB_PR4:AC006322	179640	AC006322	Homo sapiens PAC clone DJ1060B11 from 7q11.23-q21.1, complete sequence.	37,243	18-MAR-1999
GB_EST3:R46227	443	R46227	yg52a03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36000 3', mRNA sequence.	42,812	22-MAY-1995
GB_EST3:R46227	443	R46227	yg52a03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36000 3', mRNA sequence.	42,655	22-MAY-1995
GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	59,294	17-Jun-98
GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	57,584	22-Aug-97
GB_BA1:SC5F7	40024	AL096872	Streptomyces coelicolor cosmid 5F7.	61,810	22-Jul-99
GB_EST21:AA918454	416	AA918454	om38c02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1543298 3' similar to WP:F28F8.3 CE09757 SMALL NUCLEAR RIBONUCLEOPROTEIN E.; mRNA sequence.	39,655	23-Jun-98
GB_EST4:H34042	345	H34042	EST110563 Rat PC-12 cells, NGF-treated (9 days) Rattus sp. cDNA clone RPNB181 5' end, mRNA sequence.	35,942	2-Apr-98
GB_EST20:AA899038	450	AA899038	NCP6G8T7 Perithecial Neurospora crassa cDNA clone NP6G8 3' end, mRNA sequence.	40,000	12-Apr-98
GB_BA1:AP000063	185300	AP000063	Aeropyrum pernix genomic DNA, section 6/7.	40,067	22-Jun-99
GB_HTG4:AC010694	115857	AC010694	Drosophila melanogaster clone RPC198-6H2, *** SEQUENCING IN PROGRESS ***, 75 unordered pieces.	35,450	16-OCT-1999
GB_HTG4:AC010694	115857	AC010694	Drosophila melanogaster clone RPC198-6H2, *** SEQUENCING IN PROGRESS ***, 75 unordered pieces.	35,450	16-OCT-1999
GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, ocd gene and 5' soxA gene.	100,000	7-Jan-99
GB_RO:RATALGL	7601	M24108	Rattus norvegicus (clone A2U42) alpha2u globulin gene, exons 1-7.	38,692	15-DEC-1994
GB_OV:APIGY2	1381	X78272	Anas platyrhynchos (Super M) IgY upslon heavy chain gene, exon 2.	36,962	15-Feb-99
GB_EST30:AI629479	353	AI629479	486101D10.x1 486 - leaf primordia cDNA library from Hake lab Zea mays cDNA, mRNA sequence.	38,109	26-Apr-99
GB_STS:G48245	515	G48245	SHGC-62915 Human Homo sapiens STS genomic, sequence tagged site.	37,021	26-MAR-1999
GB_GSS3:B49052	515	B49052	RPC11-4112.TV RPC11-11 Homo sapiens genomic clone RPC11-11-4112, genomic survey sequence.	37,021	8-Apr-99

TABLE 4: ALIGNMENT RESULTS

rx01850	1470	GB_BA2:ECUJW67_0	110000	U18997	Escherichia coli K-12 chromosomal region from 67.4 to 76.0 minutes.	Escherichia coli	37,196	U18997
		GB_BA2:AE000392	10345	AE000392	Escherichia coli K-12 MG1655 section 282 of 400 of the complete genome.	Escherichia coli	38,021	12-Nov-98
		GB_BA2:U32715	13136	U32715	Haemophilus influenzae Rd section 30 of 163 of the complete genome.	Haemophilus influenzae Rd	39,860	29-MAY-1998
rx01878	1002	GB_HTG1:CEY64F11	177748	Z99776	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	37,564	14-OCT-1998
		GB_HTG1:CEY64F11	177748	Z99776	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	37,564	14-OCT-1998
		GB_HTG1:CEY64F11	177748	Z99776	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	37,576	14-OCT-1998
rx01892	852	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	35,910	19-Jun-98
		GB_BA1:MLCB250	40603	Z97369	Mycobacterium leprae cosmid B250.	Mycobacterium leprae	64,260	27-Aug-99
		GB_BA1:MSGB1529CS	36985	L78824	Mycobacterium leprae cosmid B1529 DNA sequence.	Mycobacterium leprae	64,260	15-Jun-96
rx01894	978	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	37,229	19-Jun-98
		GB_IN1:CELF46H5	38886	U41543	Caenorhabditis elegans cosmid F46H5.	Caenorhabditis elegans	38,525	29-Nov-96
		GB_HTG3:AC009204	115633	AC009204	Drosophila melanogaster chromosome 2 clone BACR03E19 (D1033) RPCI-98 03.E.19 map 36E-37C strain y; on bw sp, *** SEQUENCING IN PROGRESS ***, 94 unordered pieces.	Drosophila melanogaster	31,579	18-Aug-99
rx01920	1125	GB_BA2:AF112536	1798	AF112536	Corynebacterium glutamicum ribonucleotide reductase beta-chain (nrdF) gene, complete cds.	Corynebacterium glutamicum	99,733	5-Aug-99
		GB_BA1:CANRDFGEN	6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	Corynebacterium ammoniagenes	70,321	18-Apr-98
		GB_BA2:AF050168	1228	AF050168	Corynebacterium ammoniagenes ribonucleoside diphosphate reductase small subunit (nrdF) gene, complete cds.	Corynebacterium ammoniagenes	72,082	23-Apr-98
rx01928	960	GB_BA1:CGPAN	2164	X96580	C.glutamicum panB, panC & xylB genes.	Corynebacterium glutamicum	100,000	11-MAY-1999
		GB_PL1:AP000423	154478	AP000423	Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain:Columbia.	Chloroplast Arabidopsis thaliana	35,917	15-Sep-99
		GB_PL1:AP000423	154478	AP000423	Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain:Columbia.	Chloroplast Arabidopsis thaliana	33,925	15-Sep-99
rx01929	936	GB_BA1:CGPAN	2164	X96580	C.glutamicum panB, panC & xylB genes.	Corynebacterium glutamicum	100,000	11-MAY-1999
		GB_BA1:XCU33548	8429	U33548	Xanthomonas campestris hrpB pathogenicity locus proteins HrpB1, HrpB2, HrpB3, HrpB4, HrpB5, HrpB6, HrpB7, HrpB8, HrpA1, and ORF62 genes, complete cds.	Xanthomonas campestris pv. vesicatoria	38,749	19-Sep-95
rx01940	1059	GB_BA1:XANHRPB6A	1329	M99174	Xanthomonas campestris hrpB6 gene, complete cds.	Xanthomonas campestris	39,305	14-Sep-93
		GB_IN2:CFU43371	1060	U43371	Critidia fasciculata inosine-uridine preferring nucleoside hydrolase (IUNH) gene, complete cds.	Critidia fasciculata	61,417	18-Jun-96
		GB_BA2:AE001467	11601	AE001467	Helicobacter pylori, strain J99 section 28 of 132 of the complete genome.	Helicobacter pylori J99	38,560	20-Jan-99
		GB_RO:AF175967	3492	AF175967	Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.	Mus musculus	40,275	26-Sep-99
rx02022	1230	GB_BA1:CGDAPE	1966	X81379	C.glutamicum dapE gene and orf2.	Corynebacterium glutamicum	100,000	8-Aug-95
		GB_BA1:CGDNAAROP	2612	X85965	C.glutamicum ORF3 and aroP gene.	Corynebacterium glutamicum	38,889	30-Nov-97
		GB_BA1:APU47055	6469	U47055	Anabaena PCC7120 nitrogen fixation proteins (nifE, nifN, nifX, nifW) genes, complete cds, and nitrogenase (nifK) and hesA genes, partial cds.	Anabaena PCC7120	36,647	17-Feb-96
rx02024	859	GB_BA1:MTIC364	29540	Z93777	Mycobacterium tuberculosis H37Rv complete genome; segment 52/162.	Mycobacterium tuberculosis	59,415	17-Jun-98

GB_BA1:MSGB1912CS	35503	L01536	M. leprae genomic dna sequence, cosmid b1912.	Mycobacterium leprae	57,093	14-Jun-96
GB_BA1:MLU15180	38675	U15180	Mycobacterium leprae cosmid B1756.	Mycobacterium leprae	57,210	09-MAR-1995
GB_BA1:CGGDHA	2037	X72855	C.glutamicum GDHA gene.	Corynebacterium glutamicum	99,317	24-MAY-1993
GB_BA1:CGGDH	2037	X59404	Corynebacterium glutamicum, gdh gen for glutamate dehydrogenase.	Corynebacterium glutamicum	94,387	30-Jul-99
GB_BA1:PAE18494	1628	Y18494	Pseudomonas aeruginosa gdhA gene, strain PAC1.	Pseudomonas aeruginosa	82,247	6-Feb-99
GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	38,442	17-Jun-98
GB_BA1:MLCB33	42224	Z94723	Mycobacterium leprae cosmid B33.	Mycobacterium leprae	56,486	24-Jun-97
GB_BA1:ECOUW85	91414	M87049	E. coli genomic sequence of the region from 84.5 to 86.5 minutes.	Escherichia coli	52,127	29-MAY-1995
GB_EST14:AA448146	452	AA448146	zw82h01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782737 5', Homo sapiens mRNA sequence.	Homo sapiens	34,163	4-Jun-97
GB_EST17:AA641937	444	AA641937	ns18b10.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1183963 5', Homo sapiens mRNA sequence.	Homo sapiens	35,586	27-OCT-1997
GB_PR3:AC003074	143029	AC003074	Human PAC clone DJ0596009 from 7p15, complete sequence.	Homo sapiens	31,917	6-Nov-97
GB_BA1:SC1A6	37620	AL023496	Streptomyces coelicolor cosmid 1A6.	Streptomyces coelicolor	35,818	13-Jan-99
GB_PR4:AC005553	179651	AC005553	Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence.	Homo sapiens	34,274	31-DEC-1998
GB_EST3:R49746	397	R49746	yg71g10.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:38768 5' similar to gb:V00567 BETA-2-MICROGLOBULIN PRECURSOR (HUMAN);, mRNA sequence.	Homo sapiens	41,162	18-MAY-1995
GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	50,791	24-MAR-1999
GB_BA1:U00010	41171	U00010	Mycobacterium leprae cosmid B1170.	Mycobacterium leprae	37,563	01-MAR-1994
GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	39,504	24-Jun-99
GB_HTG3:AC010579	157658	AC010579	Drosophila melanogaster chromosome 3 clone BACR09D08 (D1101) RPCI-98 09.D.8 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 121 unordered pieces.	Drosophila melanogaster	37,909	24-Sep-99
GB_GSS3:B09839	1191	B09839	T12A12-Sp6 TAmu Arabidopsis thaliana genomic clone T12A12, genomic survey sequence.	Arabidopsis thaliana	37,843	14-MAY-1997
GB_HTG3:AC010579	157658	AC010579	Drosophila melanogaster chromosome 3 clone BACR09D08 (D1101) RPCI-98 09.D.8 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 121 unordered pieces.	Drosophila melanogaster	37,909	24-Sep-99
GB_BA1:SCSECYDNA	6154	X83011	S.coelicolor secY locus DNA.	Streptomyces coelicolor	36,533	02-MAR-1998
GB_EST32:AI731596	568	AI731596	BNLGH10185 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AC004005) putative ribosomal protein L7 [Arabidopsis thaliana], mRNA sequence.	Gossypium hirsutum	33,451	11-Jun-99
GB_BA1:SCSECYDNA	6154	X83011	S.coelicolor secY locus DNA.	Streptomyces coelicolor	36,756	02-MAR-1998

TABLE 4: ALIGNMENT RESULTS

rx02135	1197	GB_PR3:HS525L6	168111	AL023807	Human DNA sequence from clone RP3-325L6 on chromosome 6p22.3-23 Contains CA repeat, STSs, GSSs and a CpG island, complete sequence.	Homo sapiens	34,365	23-Nov-99
		GB_PL2:ATF21P8	85785	AL022347	Arabidopsis thaliana DNA chromosome 4, BAC clone F21P8 (ESSA project).	Arabidopsis thaliana	34,325	9-Jun-99
rx02136	645	GB_PL2:U89959	106973	U89959	Arabidopsis thaliana BAC T7123, complete sequence.	Arabidopsis thaliana	33,874	26-Jun-98
		GB_PL2:ATAC005819	57752	AC005819	Arabidopsis thaliana chromosome II BAC T3A4 genomic sequence, complete sequence.	Arabidopsis thaliana	34,123	3-Nov-98
		GB_PL2:F15K9	71097	AC005278	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence.	Arabidopsis thaliana	31,260	7-Nov-98
rx02139	1962	GB_PL2:U89959	106973	U89959	Arabidopsis thaliana BAC T7123, complete sequence.	Arabidopsis thaliana	34,281	26-Jun-98
		GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	62,904	17-Jun-98
		GB_BA1:MSGB1554CS	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	36,648	15-Jun-96
rx02153	903	GB_BA1:MSGB1551CS	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	36,648	15-Jun-96
		GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamyphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,104	1-Jul-98
		GB_BA1:AF005242	1044	AF005242	Corynebacterium glutamicum N-acetylglutamate-5-semialdehyde dehydrogenase (argC) gene, complete cds.	Corynebacterium glutamicum	99,224	2-Jul-97
		GB_BA1:CGARGCJBD	4355	X86157	C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
rx02154	414	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamyphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	98,551	1-Jul-98
		GB_BA1:AF005242	1044	AF005242	Corynebacterium glutamicum N-acetylglutamate-5-semialdehyde dehydrogenase (argC) gene, complete cds.	Corynebacterium glutamicum	98,477	2-Jul-97
		GB_BA1:CGARGCJBD	4355	X86157	C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
rx02155	1287	GB_BA1:CGARGCJBD	4355	X86157	C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	99,767	25-Jul-96
		GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamyphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,378	1-Jul-98
		GB_BA1:MSGB1133CS	42106	L78811	Mycobacterium leprae cosmid B1133 DNA sequence.	Mycobacterium leprae	55,504	15-Jun-96

TABLE 4: ALIGNMENT RESULTS

rx02156	1074	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	100,000	1-Jul-98
		GB_BA1:CGARGCJBD	4355	X86157	C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
		GB_BA2:AE001816	10007	AE001816	Thermotoga maritima section 128 of 136 of the complete genome.	Thermotoga maritima	50,238	2-Jun-99
rx02157	1296	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,612	1-Jul-98
		GB_BA1:CGARGCJBD	4355	X86157	C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	99,612	25-Jul-96
		GB_BA1:MTCY06H11	38000	Z85982	Mycobacterium tuberculosis H37Rv complete genome; segment 73/162.	Mycobacterium tuberculosis	57,278	17-Jun-98
rx02158	1080	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	100,000	1-Jul-98
		GB_BA2:AF031518	2045	AF031518	Corynebacterium glutamicum ornithine carbamoyltransferase (argF) gene, complete cds.	Corynebacterium glutamicum	99,898	5-Jan-99
		GB_BA1:CGARGCJBD	4355	X86157	C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
rx02159	636	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,843	1-Jul-98
		GB_BA2:AF031518	2045	AF031518	Corynebacterium glutamicum ornithine carbamoyltransferase (argF) gene, complete cds.	Corynebacterium glutamicum	88,679	5-Jan-99
		GB_BA2:AF041436	516	AF041436	Corynebacterium glutamicum arginine repressor (argR) gene, complete cds.	Corynebacterium glutamicum	100,000	5-Jan-99
rx02160	1326	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,774	1-Jul-98
		GB_BA2:AF030520	1206	AF030520	Corynebacterium glutamicum argininosuccinate synthetase (argG) gene, complete cds.	Corynebacterium glutamicum	99,834	19-Nov-97
		GB_BA1:SCARGGH	1909	Z49111	S.clavuligerus argG gene and argH gene (partial).	Streptomyces clavuligerus	65,913	22-Apr-96

TABLE 4: ALIGNMENT RESULTS

rx02162	1554	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	88,524	1-Jul-98
		GB_BA2:AF048764	1437	AF048764	Corynebacterium glutamicum argininosuccinate lyase (argH) gene, complete cds.	Corynebacterium glutamicum	87,561	1-Jul-98
rx02176	1251	GB_BA1:MTCY06H11	38000	Z85982	Mycobacterium tuberculosis H37Rv complete genome; segment 73/162.	Mycobacterium tuberculosis	64,732	17-Jun-98
		GB_BA1:MTCY31	37630	Z73101	Mycobacterium tuberculosis H37Rv complete genome; segment 41/162.	Mycobacterium tuberculosis	36,998	17-Jun-98
		GB_BA1:CGGLTG	3013	X86112	C.glutamicum glt gene for citrate synthase and ORF.	Corynebacterium glutamicum	39,910	17-Feb-95
		GB_PL2:PGU65399	2700	U65399	Basidiomycete CECT 20197 phenoloxidase (pox1) gene, complete cds.	basidiomycete CECT 20197	38,474	19-Jul-97
rx02189	861	GB_PR3:AC002468	115888	AC002468	Human Chromosome 15q26.1 PAC clone pDJ417d7, complete sequence.	Homo sapiens	35,941	16-Sep-98
		GB_BA1:MSGB1970CS	39399	L78815	Mycobacterium leprae cosmid B1970 DNA sequence.	Mycobacterium leprae	40,286	15-Jun-96
rx02193	1701	GB_PR3:AC002468	115888	AC002468	Human Chromosome 15q26.1 PAC clone pDJ417d7, complete sequence.	Homo sapiens	33,689	16-Sep-98
		GB_BA1:BRLASPA	1987	D25316	Brevibacterium flavum aspA gene for aspartase, complete cds.	Corynebacterium glutamicum	99,353	6-Feb-99
		GB_PAT:E04307	1581	E04307	DNA encoding Brevibacterium flavum aspartase.	Corynebacterium glutamicum	99,367	29-Sep-97
		GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	37,651	17-Apr-96
rx02194	966	GB_BA2:AF050166	840	AF050166	Corynebacterium glutamicum ATP phosphoribosyltransferase (hisG) gene, complete cds.	Corynebacterium glutamicum	98,214	5-Jan-99
		GB_BA1:BRLASPA	1987	D25316	Brevibacterium flavum aspA gene for aspartase, complete cds.	Corynebacterium glutamicum	93,805	6-Feb-99
		GB_PAT:E08649	188	E08649	DNA encoding part of aspartase from coryneform bacteria.	Corynebacterium glutamicum	100,000	29-Sep-97
rx02195	393	GB_BA2:AF086704	264	AF086704	Corynebacterium glutamicum phosphoribosyl-ATP-pyrophosphohydrolase (hisE) gene, complete cds.	Corynebacterium glutamicum	100,000	8-Feb-99
		GB_BA1:EAY17145	6019	Y17145	Eubacterium acidaminophilum grdR, grdI, grdH genes and partial ldc, grdT genes.	Eubacterium acidaminophilum	39,075	5-Aug-98
rx02197	551	GB_STS:G01195	332	G01195	fruit fly STS Dm1930 clone DS06959 T7.	Drosophila melanogaster	35,542	28-Feb-95
		GB_BA1:MTCY261	27322	Z97559	Mycobacterium tuberculosis H37Rv complete genome; segment 95/162.	Mycobacterium tuberculosis	33,938	17-Jun-98
		GB_BA1:MLCB2533	40245	AL035310	Mycobacterium leprae cosmid B2533.	Mycobacterium leprae	65,517	27-Aug-99
		GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	36,770	01-MAR-1994
rx02198	2599	GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	38,674	01-MAR-1994
		GB_BA1:MLCB2533	40245	AL035310	Mycobacterium leprae cosmid B2533.	Mycobacterium leprae	65,465	27-Aug-99
		GB_BA1:MTCY261	27322	Z97559	Mycobacterium tuberculosis H37Rv complete genome; segment 95/162.	Mycobacterium tuberculosis	37,577	17-Jun-98
rx02208	1025	GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	59,823	01-MAR-1994
		GB_BA1:AP000063	185300	AP000063	Aeropyrum pernix genomic DNA, section 6/7.	Aeropyrum pernix	39,442	22-Jun-99
		GB_PR4:AC006236	127593	AC006236	Homo sapiens chromosome 17, clone hC1T:162_E_12, complete sequence.	Homo sapiens	37,191	29-DEC-1998
rx02229	948	GB_BA1:MSGY154	40221	AD000002	Mycobacterium tuberculosis sequence from clone y154.	Mycobacterium tuberculosis	53,541	03-DEC-1996
		GB_BA1:MTCY154	13935	Z98209	Mycobacterium tuberculosis H37Rv complete genome; segment 121/162.	Mycobacterium tuberculosis	40,407	17-Jun-98
		GB_BA1:U00019	36033	U00019	Mycobacterium leprae cosmid B2235.	Mycobacterium leprae	40,541	01-MAR-1994
rx02234	3462	GB_BA1:MSGB937CS	38914	L78820	Mycobacterium leprae cosmid B937 DNA sequence.	Mycobacterium leprae	66,027	15-Jun-96
		GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	71,723	18-Jun-98
		GB_BA2:U01072	4393	U01072	Mycobacterium bovis BCG orotidine-5'-monophosphate decarboxylase (uraA) gene.	Mycobacterium bovis	67,101	22-DEC-1993

TABLE 4: ALIGNMENT RESULTS

rx02235	727	GB_BA1:MSU91572	960	U91572	Mycobacterium smegmatis carbamoyl phosphate synthetase (pyrAB) gene, partial cds and orotidine 5'-monophosphate decarboxylase (pyrF) gene, complete cds.	Mycobacterium smegmatis	60,870	22-MAR-1997
		GB_HTG3:AC009364	192791	AC009364	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 57 unordered pieces.	Homo sapiens	37,994	1-Sep-99
		GB_HTG3:AC009364	192791	AC009364	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 57 unordered pieces.	Homo sapiens	37,994	1-Sep-99
rx02237	693	GB_BA1:MTCY21B4	39150	Z80108	Mycobacterium tuberculosis H37Rv complete genome; segment 62/162.	Mycobacterium tuberculosis	55,844	23-Jun-98
		GB_BA2:AF077324	5228	AF077324	Rhodococcus equi strain 103 plasmid RE-VP1 fragment f.	Rhodococcus equi	41,185	5-Nov-98
		GB_EST22:AU017763	586	AU017763	AU017763 Mouse two-cell stage embryo cDNA Mus musculus cDNA clone J0744A04 3', mRNA sequence.	Mus musculus	38,616	19-OCT-1998
rx02239	1389	GB_BA1:MTCY21B4	39150	Z80108	Mycobacterium tuberculosis H37Rv complete genome; segment 62/162.	Mycobacterium tuberculosis	55,282	23-Jun-98
		GB_HTG3:AC010745	193862	AC010745	Homo sapiens clone NH0549D18, *** SEQUENCING IN PROGRESS ***; 30 unordered pieces.	Homo sapiens	36,772	21-Sep-99
		GB_HTG3:AC010745	193862	AC010745	Homo sapiens clone NH0549D18, *** SEQUENCING IN PROGRESS ***; 30 unordered pieces.	Homo sapiens	36,772	21-Sep-99
rx02240	1344	EM_PAT:E09855	1239	E09855	gDNA encoding S-adenosylmethionine synthetase.	Corynebacterium glutamicum	99,515	07-OCT-1997 (Rel. 52, Created)
		GB_PAT:A37831	5392	A37831	Sequence 1 from Patent WO9408014.	Streptomyces pristinaespiralis	63,568	05-MAR-1997
		GB_BA2:AF117274	2303	AF117274	Streptomyces spectabilis flavoprotein homolog Dfp (dfp) gene, partial cds; and S-adenosylmethionine synthetase (metK) gene, complete cds.	Streptomyces spectabilis	65,000	31-MAR-1999
rx02246	1107	EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	52,909	03-OCT-1997 (Rel. 52, Created)
		GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	52,909	29-Sep-97
		GB_PAT:132742	5589	132742	Sequence 1 from patent US 5589355.	Unknown.	52,909	6-Feb-97
		GB_PAT:132743	2689	132743	Sequence 2 from patent US 5589355.	Unknown.	57,937	6-Feb-97
		EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	57,937	03-OCT-1997 (Rel. 52, Created)
rx02248	1389	GB_PAT:132742	5589	132742	Sequence 1 from patent US 5589355.	Unknown.	57,937	6-Feb-97
		EM_PAT:132742	5589	132742	Sequence 1 from patent US 5589355.	Unknown.	61,843	6-Feb-97
		EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	61,843	03-OCT-1997 (Rel. 52, Created)
		GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	61,843	29-Sep-97
rx02249	600	GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	64,346	29-Sep-97
		GB_PAT:132742	5589	132742	Sequence 1 from patent US 5589355.	Unknown.	64,346	6-Feb-97
		GB_PAT:132743	2689	132743	Sequence 2 from patent US 5589355.	Unknown.	64,346	6-Feb-97

TABLE 4: ALIGNMENT RESULTS

rx02250	643	GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	56,318	29-Sep-97
		GB_PAT:132742	5589	132742	Sequence 1 from patent US 5589335.	Unknown.	56,318	6-Feb-97
		EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	56,318	03-OCT-1997 (Rel. 52, Created)
rx02262	1269	GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	100,000	7-Jan-99
		GB_BA1:CGAMTGENE 2028	X93513	X93513	C.glutamicum amt gene.	Corynebacterium glutamicum	100,000	29-MAY-1996
rx02263	488	GB_Vi:HEHCMVCG	229354	X17403	Human cytomegalovirus strain AD169 complete genome.	human herpesvirus 5	38,651	10-Feb-99
		GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	100,000	7-Jan-99
		GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	37,526	7-Jan-99
rx02272	1368	EM_PAT:E09373	1591	E09373	Creatinine deiminase gene.	Bacillus sp.	96,928	08-OCT-1997 (Rel. 52, Created)
rx02281	1545	GB_BA1:D38505	1591	D38505	Bacillus sp. gene for creatinine deaminase, complete cds.	Bacillus sp.	96,781	7-Aug-98
		GB_HTG2:AC006595	146070	AC006595	Homo sapiens, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.	Homo sapiens	36,264	20-Feb-99
		GB_GSS12:AQ411010	551	AQ411010	HS_2257_B1_H02_MR CIT Approved Human Genomic Sperm Library D	Homo sapiens	36,197	17-MAR-1999
					Homo sapiens genomic clone Plate=2257 Col=3 Row=P, genomic survey sequence.			
		GB_EST23:A1128623	363	A1128623	qa62c01.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1691328 3', mRNA sequence.	Homo sapiens	37,017	05-OCT-1998
		GB_PL2:ATAC007019	102335	AC007019	Arabidopsis thaliana chromosome II BAC F7D8 genomic sequence, complete sequence.	Arabidopsis thaliana	33,988	16-MAR-1999
rx02299	531	GB_BA2:AF116184	540	AF116184	Corynebacterium glutamicum L-aspartate-alpha-decarboxylase precursor (panD) gene, complete cds.	Corynebacterium glutamicum	100,000	02-MAY-1999
		GB_GSS9:AQ164310	507	AQ164310	HS_2171_A2_E01_MR CIT Approved Human Genomic Sperm Library D	Homo sapiens	37,278	16-OCT-1998
					Homo sapiens genomic clone Plate=2171 Col=2 Row=I, genomic survey sequence.			
rx02311	813	GB_Vi:MH68TKH	4557	X93468	Murine herpesvirus type 68 thymidine kinase and glycoprotein H genes.	murine herpesvirus 68	40,298	3-Sep-96
		GB_HTG4:AC006091	176878	AC006091	Drosophila melanogaster chromosome 3 clone BACR48G05 (D475) RPCL-98	Drosophila melanogaster	36,454	27-OCT-1999
					48.G.5 map 91F1-91F13 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.			
		GB_HTG4:AC006091	176878	AC006091	Drosophila melanogaster chromosome 3 clone BACR48G05 (D475) RPCL-98	Drosophila melanogaster	36,454	27-OCT-1999
					48.G.5 map 91F1-91F13 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.			

TABLE 4: ALIGNMENT RESULTS

GB_BA2:RRU65510	16259	U65510	Rhodospirillum rubrum CO-induced hydrogenase operon (cooM, cooK, cooL, cooX, cooU, cooH) genes, iron sulfur protein (cooF) gene, carbon monoxide dehydrogenase (cooS) gene, carbon monoxide dehydrogenase accessory proteins (cooC, cooT, cooJ) genes, putative transcriptional activator (cooA) gene, nicotinate-nucleotide pyrophosphorylase (nadC) gene, complete cds, L-aspartate oxidase (nadB) gene, and alkyl hydroperoxide reductase (ahpC) gene, partial cds.	Rhodospirillum rubrum	37,828	9-Apr-97
rx02315	1752	GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	03-DEC-1996
		GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	17-Jun-98
rx02318	402	GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	03-DEC-1996
		GB_HTG3:AC011348	111083	AC011348	Homo sapiens chromosome 5 clone CIT-HSPC_303E13, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.	06-OCT-1999
		GB_HTG3:AC011348	111083	AC011348	Homo sapiens chromosome 5 clone CIT-HSPC_303E13, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.	06-OCT-1999
		GB_HTG3:AC011412	89234	AC011412	Homo sapiens chromosome 5 clone CIT978SKB_81K21, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.	06-OCT-1999
rx02319	1080	GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	03-DEC-1996
		GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	17-Jun-98
		GB_EST23:A117213	476	A117213	ub83h02.r1 Soares 2NbMT Mus musculus cDNA clone IMAGE:1395123 5'mRNA sequence.	2-Sep-98
rx02345	1320	GB_BA1:BAPURKE	2582	X91189	B.ammoniaenes purK and purE genes.	14-Jan-97
rx02350	618	GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	10-Feb-99
		GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	10-Feb-99
		GB_BA1:BAPURKE	2582	X91189	B.ammoniaenes purK and purE genes.	14-Jan-97
rx02373	1038	GB_PL1:SC130KEXV	129528	X94335	S.cerevisiae 130kb DNA fragment from chromosome XV.	15-Jul-97
		GB_PL1:SCXVORFS	50984	X90518	S.cerevisiae DNA of 51 Kb from chromosome XV right arm.	1-Nov-95
		GB_PAT:E00311	1853	E00311	DNA coding of 2,5-diketogluconic acid reductase.	29-Sep-97
		GB_PAT:I06030	1853	I06030	Sequence 4 from Patent EP 0305608.	02-DEC-1994
		GB_PAT:I00836	1853	I00836	Sequence 1 from Patent US 4758514.	21-MAY-1993
rx02375	1350	GB_BA2:CGU31230	3005	U31230	Corynebacterium glutamicum Obg protein homolog gene, partial cds, gamma glutamyl kinase (proB) gene, complete cds, and (unkdh) gene, complete cds.	2-Aug-96
		GB_HTG3:AC009946	169072	AC009946	Homo sapiens clone NH0012C17, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces.	8-Sep-99
		GB_HTG3:AC009946	169072	AC009946	Homo sapiens clone NH0012C17, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces.	8-Sep-99
rx02380	777	GB_BA1:MTCY253	41230	Z81368	Mycobacterium tuberculosis H37Rv complete genome; segment 106/162.	17-Jun-98
		GB_HTG4:AC010658	120754	AC010658	Drosophila melanogaster chromosome 3L/75C1 clone RPC198-3B20, *** SEQUENCING IN PROGRESS ***, 78 unordered pieces.	16-OCT-1999
		GB_HTG4:AC010658	120754	AC010658	Drosophila melanogaster chromosome 3L/75C1 clone RPC198-3B20, *** SEQUENCING IN PROGRESS ***, 78 unordered pieces.	16-OCT-1999

TABLE 4: ALIGNMENT RESULTS

rx02382	1419	GB_BA1:CGPROAGEN	1783	X82929	C-glutamicum proA gene.	Corynebacterium glutamicum	98,802	23-Jan-97
		GB_BA1:MTCY428	26914	Z81451	Mycobacterium tuberculosis H37Rv complete genome; segment 107/162.	Mycobacterium tuberculosis	38,054	17-Jun-98
		GB_BA2:CGU31230	3005	U31230	Corynebacterium glutamicum Opg protein homolog gene, partial cds, gamma glutamyl kinase (proB) gene, complete cds, and (unkdh) gene, complete cds.	Corynebacterium glutamicum	98,529	2-Aug-96
rx02400	693	GB_BA1:CGACEA	2427	X75504	C-glutamicum aceA gene and thiX genes (partial).	Corynebacterium glutamicum	100,000	9-Sep-94
		GB_PAT:I86191	2135	I86191	Sequence 3 from patent US 5700661.	Unknown.	100,000	10-Jun-98
		GB_PAT:I13693	2135	I13693	Sequence 3 from patent US 5439822.	Unknown.	100,000	26-Sep-95
rx02432	1098	GB_GSS15:AQ606842	574	AQ606842	HS_5404_B2_E07_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=980 Col=14 Row=J, genomic survey sequence.	Homo sapiens	39,716	10-Jun-99
		GB_EST1:T05804	406	T05804	EST03693 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDG63 similar to EST containing Alu repeat, mRNA sequence.	Homo sapiens	37,915	30-Jun-93
		GB_PL1:AB006699	77363	AB006699	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence.	Arabidopsis thaliana	35,526	20-Nov-99
rx02458	1413	GB_BA2:AF114233	1852	AF114233	Corynebacterium glutamicum 5-enolpyruvylshikimate 3-phosphate synthase (aroA) gene, complete cds.	Corynebacterium glutamicum	100,000	7-Feb-99
		GB_EST37:AW013061	578	AW013061	ODT-0033 Winter flounder ovary Pleuronectes americanus cDNA clone ODT-0033 5' similar to FRUCTOSE-BISPHOSPHATE ALDOLASE B (LIVER), mRNA sequence.	Pleuronectes americanus	39,175	10-Sep-99
rx02469	1554	GB_GSS15:AQ650027	728	AQ650027	Sheared DNA-5L2, TF Sheared DNA Trypanosoma brucei genomic clone Sheared DNA-5L2, genomic survey sequence.	Trypanosoma brucei	39,281	22-Jun-99
		GB_BA1:MTCY359	36021	Z83859	Mycobacterium tuberculosis H37Rv complete genome; segment 84/162.	Mycobacterium tuberculosis	39,634	17-Jun-98
		GB_BA1:MLCB1788	39228	AL008609	Mycobacterium leprae cosmid B1788.	Mycobacterium leprae	59,343	27-Aug-99
		GB_BA1:SCAJ10601	4692	AJ010601	Streptomyces coelicolor A3(2) DNA for whiD and whiK loci.	Streptomyces coelicolor	48,899	17-Sep-98
rx02497	1050	GB_BA2:CGU31224	422	U31224	Corynebacterium glutamicum (ppx) gene, partial cds.	Corynebacterium glutamicum	96,445	2-Aug-96
		GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	59,429	17-Jun-98
		GB_BA1:SCE7	16911	AL049819	Streptomyces coelicolor cosmid E7.	Streptomyces coelicolor	39,510	10-MAY-1999
rx02499	933	GB_BA2:CGU31225	1817	U31225	Corynebacterium glutamicum L-proline:NADP+ 5-oxidoeductase (proC) gene, complete cds.	Corynebacterium glutamicum	97,749	2-Aug-96
		GB_BA1:NG17PILA	1920	X13965	Neisseria gonorrhoeae pilA gene.	Neisseria gonorrhoeae	43,249	30-Sep-93
		GB_HTG2:AC007984	129715	AC007984	Drosophila melanogaster chromosome 3 clone BACR05C10 (D781) RPCI-98 05.C.10 map 97D-97E strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** , 87 unordered pieces.	Drosophila melanogaster	33,406	2-Aug-99
rx02501	1188	GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	39,357	17-Jun-98
		GB_BA1:U00018	42991	U00018	Mycobacterium leprae cosmid B2168.	Mycobacterium leprae	51,768	01-MAR-1994
		GB_Vi:HE1CG	152261	X14112	Herpes simplex virus (HSV) type 1 complete genome.	human herpesvirus 1	39,378	17-Apr-97
rx02503	522	GB_PR3:AC005328	35414	AC005328	Homo sapiens chromosome 19, cosmid R26660, complete sequence.	Homo sapiens	39,922	28-Jul-98
		GB_PR3:AC005545	43514	AC005545	Homo sapiens chromosome 19, cosmid R26634, complete sequence.	Homo sapiens	39,922	3-Sep-98
		GB_PR3:AC005328	35414	AC005328	Homo sapiens chromosome 19, cosmid R26660, complete sequence.	Homo sapiens	34,911	28-Jul-98
rx02504	681	GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	54,940	17-Jun-98
		GB_PR3:AC005328	35414	AC005328	Homo sapiens chromosome 19, cosmid R26660, complete sequence.	Homo sapiens	41,265	28-Jul-98
		GB_PR3:AC005545	43514	AC005545	Homo sapiens chromosome 19, cosmid R26634, complete sequence.	Homo sapiens	41,265	3-Sep-98
rx02516	1386	GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	37,723	04-DEC-1998

TABLE 4: ALIGNMENT RESULTS

rx02517	570	GB_BA1:U00013 GB_BA1:MTV007 GB_BA1:MLCL536 GB_BA1:U00013 GB_BA1:SCC22 GB_OV:AF137219 GB_EST30:AI645057	35881 32806 36224 35881 22115 831 301	U00013 AL021184 Z39125 U00013 AL096839 AF137219 AI645057	Mycobacterium leprae cosmid B1496. Mycobacterium tuberculosis H37Rv complete genome; segment 64/162. Mycobacterium leprae cosmid L536. Mycobacterium leprae cosmid B1496. Streptomyces coelicolor cosmid C22. Amia calva mixed lineage leukemia-like protein (MLl) gene, partial cds. vs52a10.y1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1149882 5', mRNA sequence.	Mycobacterium leprae Mycobacterium tuberculosis Mycobacterium leprae Mycobacterium leprae Streptomyces coelicolor Amia calva Mus musculus	37,723 61,335 37,018 37,018 37,071 36,853 41,860	01-MAR-1994 17-Jun-98 04-DEC-1998 01-MAR-1994 12-Jul-99 7-Sep-99 29-Apr-99
rx02532	1170	GB_EST20:AA822595 GB_HTG2:AF130866 GB_HTG2:AF130866 GB_PL1:ATT12J5	429 118874 118874 84499	AA822595 AF130866 AF130866 AL035522	Mus musculus cDNA clone IMAGE:1149882 5', mRNA sequence. Homo sapiens chromosome 8 clone PAC 172N13 map 8q24, *** SEQUENCING IN PROGRESS ***, in unordered pieces. Homo sapiens chromosome 8 clone PAC 172N13 map 8q24, *** SEQUENCING IN PROGRESS ***, in unordered pieces. Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5 (ESSAII project).	Mus musculus Homo sapiens Homo sapiens Arabidopsis thaliana	42,353 40,754 40,754 35,063	17-Feb-98 21-MAR-1999 21-MAR-1999 24-Feb-99
rx02550	1434	GB_BA1:MTCV279 GB_BA1:MSGB1970CS GB_BA2:SC2H4	9150 39399 25970	Z97991 L78815 AL031514	Mycobacterium tuberculosis H37Rv complete genome; segment 17/162. Mycobacterium leprae cosmid B1970 DNA sequence. Streptomyces coelicolor cosmid 2H4.	Mycobacterium tuberculosis Mycobacterium leprae Streptomyces coelicolor A3(2)	37,773 39,024 37,906	17-Jun-98 15-Jun-96 19-OCT-1999
rx02559	1026	GB_BA1:MTV004 GB_PAT:J28684 GB_BA1:MTU27357	69350 5100 5100	AL009198 I28584 U27357	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162. Sequence 1 from patent US 5573915. Mycobacterium tuberculosis cyclopropane mycolic acid synthase (cma1) gene, complete cds.	Mycobacterium tuberculosis Unknown. Mycobacterium tuberculosis	47,358 39,138 39,138	18-Jun-98 6-Feb-97 26-Sep-95
rx02622	1683	GB_BA2:AE001780 GB_OV:AF064564 GB_OV:AF064564	11957 49254 49254	AE001780 AF064564 AF064564	Thermotoga maritima section 92 of 136 of the complete genome. Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds. Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds.	Thermotoga maritima Fugu rubripes Fugu rubripes	44,914 39,732 36,703	2-Jun-99 17-Aug-99 17-Aug-99
rx02623	714	GB_GSS5:AQ818728 GB_HTG5:AC011083 GB_GSS6:AQ826948 GB_Vi:BRSMGP	444 198586 544 462	AQ818728 AC011083 AQ826948 M86652	HS_5268_A1_G09_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=844 Col=17 Row=M, genomic survey sequence. Homo sapiens chromosome 9 clone RP11-111M7 map 9, WORKING DRAFT SEQUENCE, 51 unordered pieces. HS_5014_A2_C12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=590 Col=24 Row=E, genomic survey sequence. Bovine respiratory syncytial virus membrane glycoprotein mRNA, complete cds.	Homo sapiens Homo sapiens Homo sapiens Bovine respiratory syncytial virus	38,801 35,714 39,146 37,013	26-Aug-99 19-Nov-99 27-Aug-99 28-Apr-93
rx02629	708	GB_Vi:BRSMGP GB_Vi:BRSMGP	462 462	M86652 M86652	Bovine respiratory syncytial virus membrane glycoprotein mRNA, complete cds. Bovine respiratory syncytial virus	Bovine respiratory syncytial virus Bovine respiratory syncytial virus	37,013 37,013	28-Apr-93 28-Apr-93

TABLE 4: ALIGNMENT RESULTS

rx02645	1953	GB_PAT:A45577 GB_PAT:A45581 GB_BA1:CORILVA	1925 1925 1925	A45577 A45581 L01508	Sequence 1 from Patent WO9519442. Sequence 5 from Patent WO9519442. Corynebacterium glutamicum threonine dehydratase (ilvA) gene, complete cds.	Corynebacterium glutamicum Corynebacterium glutamicum Corynebacterium glutamicum	39,130 39,130 39,130	07-MAR-1997 07-MAR-1997 26-Apr-93
rx02646	1392	GB_BA1:CORILVA	1925	L01508	Corynebacterium glutamicum threonine dehydratase (ilvA) gene, complete cds.	Corynebacterium glutamicum	99,138	26-Apr-93
rx02648	1326	GB_PAT:A45585 GB_PAT:A45583 GB_OV:ICTCNC GB_EST11:AA265464	1925 1925 2049 345	A45585 A45583 M83111 AA265464	Sequence 9 from Patent WO9519442. Sequence 7 from Patent WO9519442. Ictalurus punctatus cyclic nucleotide-gated channel RNA sequence. mx91c06.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:693706 5', mRNA sequence.	Corynebacterium glutamicum Corynebacterium glutamicum Corynebacterium glutamicum Ictalurus punctatus Mus musculus	99,066 99,066 38,402 38,655	07-MAR-1997 07-MAR-1997 24-MAY-1993 20-MAR-1997
rx02653		GB_GSS8:AQ006950	480	AQ006950	CIT-HSP-2294E14. TR CIT-HSP Homo sapiens genomic clone 2294E14, genomic survey sequence.	Homo sapiens	36,074	27-Jun-98
rx02687	1068	GB_BA1:CORPHEA GB_PAT:E04483 GB_PAT:E06110 GB_PL1:HVC4H GB_PR2:HS310H5	1088 948 948 59748 29718	M13774 E04483 E06110 Y14573 Z69705	C-glutamicum pheA gene encoding prephenate dehydratase, complete cds. DNA encoding prephenate dehydratase. DNA encoding prephenate dehydratase. Hordeum vulgare DNA for chromosome 4H. Human DNA sequence from cosmid 310H5 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains EST and CpG island.	Corynebacterium glutamicum Corynebacterium glutamicum Corynebacterium glutamicum Hordeum vulgare Homo sapiens	99,715 98,523 98,523 36,593 36,089	26-Apr-93 29-Sep-97 29-Sep-97 25-MAR-1999 22-Nov-99
rx02754	1461	GB_PR3:AC004754 GB_HTG2:AC008223	39188 130212	AC004754 AC008223	Homo sapiens chromosome 16, cosmid clone RT286 (LANL), complete sequence. Drosophila melanogaster chromosome 3 clone BACR16118 (D815) RPCI-98 16.1.18 map 95A-95A strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Homo sapiens Drosophila melanogaster	36,089 32,757	28-MAY-1998 2-Aug-99
rx02758	1422	GB_HTG2:AC008223 GB_BA1:MTCY71 GB_HTG5:AC011678 GB_HTG5:AC011678 GB_BA2:AF064070	130212 42729 171967 171967 23183	AC008223 Z92771 AC011678 AC011678 AF064070	Drosophila melanogaster chromosome 3 clone BACR16118 (D815) RPCI-98 16.1.18 map 95A-95A strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces. Mycobacterium tuberculosis H37Rv complete genome; segment 141/162. Homo sapiens clone 14_B_7, *** SEQUENCING IN PROGRESS***, 20 unordered pieces. Homo sapiens clone 14_B_7, *** SEQUENCING IN PROGRESS***, 20 unordered pieces. Burkholderia pseudomallei putative dihydroorotase (pyrC) gene, partial cds; putative 1-acyl-sn-glycerol-3-phosphate acyltransferase (plsC), putative diadenosine tetraphosphatase (apah), complete cds; type II O-antigen biosynthesis gene cluster, complete sequence; putative undecaprenyl phosphate N-acetylglucosaminyltransferase, and putative UDP-glucose 4-epimerase genes, complete cds; and putative galactosyl transferase gene, partial cds.	Drosophila melanogaster Mycobacterium tuberculosis Homo sapiens Homo sapiens Burkholderia pseudomallei	32,757 37,838 35,331 33,807 36,929	2-Aug-99 10-Feb-99 5-Nov-99 5-Nov-99 20-Jan-99

TABLE 4: ALIGNMENT RESULTS

rx02771	678	GB_BA2:AF038651	4077	AF038651	Corynebacterium glutamicum dipeptide-binding protein (dciAE) gene, partial cds; adenine phosphoribosyltransferase (apt) and GTP pyrophosphokinase (rel) genes, complete cds; and unknown gene.	Corynebacterium glutamicum	99,852	14-Sep-98
		GB_IN1:CELT19B4	37121	U80438	Caenorhabditis elegans cosmid T19B4.	Caenorhabditis elegans	43,836	04-DEC-1996
		GB_EST36:AV193572	360	AV193572	AV193572 Yujii Kohara unpublished cDNA:Strain N2 hermaphrodite embryo	Caenorhabditis elegans	48,588	22-Jul-99
rx02772	1158	GB_BA2:AF038651	4077	AF038651	Caenorhabditis elegans cDNA clone yk618h8 5', mRNA sequence.	Corynebacterium glutamicum	99,914	14-Sep-98
		GB_BA1:MTCY227	35946	Z77724	Corynebacterium glutamicum dipeptide-binding protein (dciAE) gene, partial cds; adenine phosphoribosyltransferase (apt) and GTP pyrophosphokinase (rel) genes, complete cds; and unknown gene.	Mycobacterium tuberculosis	38,339	17-Jun-98
		GB_BA1:U00011	40429	U00011	Mycobacterium tuberculosis H37Rv complete genome; segment 114/162.	Mycobacterium leprae	38,996	01-MAR-1994
rx02790	1266	GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	37,640	17-Jun-98
		GB_PR4:AC006581	172931	AC006581	Homo sapiens 12p21 BAC RPC11-259O18 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	37,906	3-Jun-99
rx02791	951	GB_PR4:AC006581	172931	AC006581	Homo sapiens 12p21 BAC RPC11-259O18 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	35,280	3-Jun-99
		GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	39,765	17-Jun-98
		GB_OV:CHKCEK2	3694	M35195	Chicken tyrosine kinase (cek2) mRNA, complete cds.	Gallus gallus	38,937	28-Apr-93
		GB_BA1:MSASDASK	5037	Z17372	M.smegmatis asd, ask-alpha, and ask-beta genes.	Mycobacterium smegmatis	38,495	9-Aug-94
rx02802	1194	GB_EST24:AI223401	169	AI223401	qq48g01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838448 3' similar to WP:C25D7.8 CE08394 ; mRNA sequence.	Homo sapiens	40,828	27-OCT-1998
		GB_EST24:AI223401	169	AI223401	qq48g01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838448 3' similar to WP:C25D7.8 CE08394 ; mRNA sequence.	Homo sapiens	40,828	27-OCT-1998
rx02814	494	GB_BA1:MTCY7D11	22070	Z95120	Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.	Mycobacterium tuberculosis	58,418	17-Jun-98
		GB_BA1:MTCY7D11	22070	Z95120	Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.	Mycobacterium tuberculosis	40,496	17-Jun-98
		GB_PR1:HSAJ2962	778	AJ002962	Homo sapiens mRNA for hB-FABP.	Homo sapiens	39,826	8-Jan-98
rx02843	608	GB_BA1:CGAJ4934	1160	AJ004934	Corynebacterium glutamicum depD gene, complete CDS.	Corynebacterium glutamicum	100,000	17-Jun-98
		GB_BA1:MTCI364	29540	Z93777	Mycobacterium tuberculosis H37Rv complete genome; segment 52/162.	Mycobacterium tuberculosis	37,710	17-Jun-98
		GB_BA1:MLU15180	38675	U15180	Mycobacterium leprae cosmid BT756.	Mycobacterium leprae	39,626	09-MAR-1995
rx03205	963	GB_BA1:BLSIGBGN	2906	Z49824	B.lactofermentum orf1 gene and sigB gene.	Corynebacterium glutamicum	98,854	25-Apr-96
		GB_EST21:AA980237	377	AA980237	ua32a12.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1348414 5' similar to TR:Q61025 Q61025 HYPOTHETICAL 15.2 KD PROTEIN. ; mRNA sequence.	Mus musculus	41,489	27-MAY-1998
		GB_EST23:AI158316	371	AI158316	ud27c05.r1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1447112 5' mRNA sequence.	Mus musculus	38,005	30-Sep-98
rx03223	1237	GB_IN1:LMFL2743	38368	AL031910	Leishmania major Friedlin chromosome 4 cosmid L2743.	Leishmania major	39,869	15-DEC-1999
		GB_PR3:HSDJ61B2	119666	AL096710	Human DNA sequence from clone RP1-61B2 on chromosome 6p11.2-12.3 Contains isoforms 1 and 3 of BPAG1 (bullous pemphigoid antigen 1 (230/240kD), an exon of a gene similar to murine MACF cytoskeletal protein, STSs and GSSs, complete sequence.	Homo sapiens	34,930	17-DEC-1999

TABLE 4: ALIGNMENT RESULTS

GB_PR3:HSDJ61B2	119666	AL096710	Human DNA sequence from clone RP1-61B2 on chromosome 6p11.2-12.3 Contains isoforms 1 and 3 of BPAG1 (bullous pemphigoid antigen 1 (230/240kD), an exon of a gene similar to murine MACF cytoskeletal protein, STs and GSSs, complete sequence.	Homo sapiens	34,634	17-DEC-1999

What is claimed:

1. 1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding a metabolic pathway protein selected from the group consisting of a nucleic acid molecule comprising the nucleotide sequence set forth in SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:5.
2. The isolated nucleic acid molecule of claim 1, wherein said metabolic pathway protein is involved in the metabolism of an amino acid.
3. 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 SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6.
4. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence set forth in SEQ ID NO:6, or a complement thereof.
5. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 65% homologous to a nucleotide sequence set forth in SEQ ID NO:1, or a complement thereof.
6. 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 set forth in SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:5.
7. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-6 under stringent conditions.
8. An isolated nucleic acid molecule comprising the nucleic acid molecule of claim 1, or a portion thereof, and a nucleotide sequence encoding a heterologous polypeptide.
9. A vector comprising the nucleic acid molecule of claim 1.
10. The vector of claim 9, further comprising one or more metabolic pathway nucleic acid molecules.
11. The vector of claim 9 or 10, which is an expression vector.

12. A host cell transfected with the expression vector of claim 9 or 10.
13. The vector of claim 10, wherein the second metabolic pathway nucleic acid
5 molecule is selected from the group consisting of a nucleic acid molecule
comprising the nucleotide sequence set forth in the odd-numbered sequences listed
in Table 1, excluding any F-designated nucleic acid molecules.
14. The host cell of claim 12, wherein said cell is a microorganism.
- 10 15. The host cell of claim 12, wherein said cell belongs to the genus *Corynebacterium*
or *Brevibacterium*.
16. The host cell of claim 12, wherein the expression of said nucleic acid molecules
15 results in the modulation in production of a fine chemical from said cell.
17. The host cell of claim 16, wherein said fine chemical is an amino acid.
18. The host cell of claim 17, wherein said amino acid is methionine or lysine.
- 20 19. A method of producing a polypeptide comprising culturing the host cell of claim 12
in an appropriate culture medium to, thereby, produce the polypeptide.
20. An isolated metabolic pathway polypeptide from *Corynebacterium glutamicum*, or a
25 portion thereof.
21. The protein of claim 20, wherein said polypeptide is selected from the group of
metabolic pathway proteins which participate in the metabolism of an amino acid.
- 30 22. The protein of claim 21, wherein said amino acid is methionine or lysine.
23. An isolated nucleic acid molecule from *Corynebacterium glutamicum* which
encodes a metabolic pathway protein comprising the amino acid sequence set forth
in SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6.
- 35 24. 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 in SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6.

25. The isolated polypeptide of claim 23, further comprising heterologous amino acid sequences.
- 5 26. An isolated polypeptide comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence set forth in SEQ ID NO:5, or a complement thereof.
- 10 27. An isolated polypeptide comprising a nucleotide sequence which is at least 65% homologous to a nucleotide sequence set forth in SEQ ID NO:1, or a complement thereof.
- 15 28. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 9 or 10, such that the fine chemical is produced.
- 20 29. The method of claim 28, wherein said cell is cultured in the presence of a sulfur source.
- 30 30. The method of claim 28, wherein said method further comprises the step of recovering the fine chemical from said culture.
31. The method of claim 28, wherein said fine chemical is an amino acid.
- 25 32. The method of claim 31, wherein said amino acid is methionine or lysine.
33. The method of claim 28, wherein said method further comprises the step of transfecting said cell with the vector of claim 9 or 10, to result in a cell containing said vector.
- 30 34. The method of claim 28, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
- 35 35. The method of claim 27, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium lilium*, *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*
ketosoreductum, *Brevibacterium lactofermentum*, *Brevibacterium linens*,
5 *Brevibacterium paraffinolyticum*, and those strains set forth in Table 3.

36. 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
10 1-6.

37. 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
1-6, alone or in combination with another metabolic pathway nucleic acid selected from
15 the group consisting of a nucleic acid molecule comprising the nucleotide sequence set
forth in the odd-numbered sequences listed in Table 1, excluding any F-designated
nucleic acid molecules.

38. A method for producing a fine chemical, comprising culturing a cell whose genomic
20 DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims
1-6, alone or in combination with one or more metabolic pathway nucleic acid molecule.

39. The method of claim 36, wherein the metabolic pathway nucleic acid molecule is
selected from the group consisting of *metZ*, *metC*, *metB*, *metA*, *metE*, *metH*, *hom*, *asd*,
25 *lysC*, *lysC/ask*, *rxn00657*, *dapA*, *dapB*, *dapC*, *dapD/argD*, *dapE*, *dapF*, *lysA*, *ddh*, *lysE*,
lysG, *lysR*, *hsk*, *ppc*, *pycA*, *accD*, *accA*, *accB*, *accC*, *gpdh* genes encoding glucose-6-
phosphate-dehydrogenase, *opcA*, *pgdh*, *ta*, *tk*, *pgl*, *rlpe*, *rpe* or any combination of the
above-mentioned genes.

30 40. The method of claim 35 or 36, wherein said metabolic pathway is methionine or
lysine metabolism.

41. A method of modulating the yield of a fine chemical from a cell comprising, introducing one or more metabolic pathway genes into a cell, thereby modulating the yield of a fine chemical.

5 42. The method of claim 41, wherein said metabolic pathway gene or genes are integrated into the chromosome of the cell.

43. The method of claim 41, wherein said metabolic pathway gene or genes are maintained on a plasmid.

10

44. The method of claim 41, wherein said fine chemical is an amino acid.

45. The method of claim 44, wherein said amino acid is methionine or lysine.

15 46. The method of claim 41, wherein said metabolic pathway gene or genes are selected from the group consisting of the nucleic acid molecule of any one of claims 1-6.

47. The method of claim 41, wherein the nucleotide sequence of said metabolic pathway gene or genes has been mutated to increase yield of a fine chemical.

20

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 Gly Ala Glu Leu Val Ala Val His Thr Trp Met Asp Met Gln Val Gln
 185 190 195
 gca tca ctt gca ggt ctt gca gct gct caa cag cag tgg gat gaa gtg 739
 Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln Gln Trp Asp Glu Val
 200 205 210
 gaa cgt cag caa acc gac atg ctg atc gaa cgc ctc gca cca ctg gtg 787
 Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg Leu Ala Pro Leu Val
 215 220 225
 gaa aag tac cca agt gta acc gtc aag aag atc atc acc cgt gac cgc 835
 Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile Ile Thr Arg Asp Arg
 230 235 240 245
 cca gtt cgc gca ctt gca gaa gca tct gaa aac gcg cag ctc cta gtc 883
 Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn Ala Gln Leu Leu Val
 250 255 260
 gtt ggt tcc cat ggt cgt ggc gga ttt aag ggc atg ctc ctt ggc tcc 931
 Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly Met Leu Leu Gly Ser
 265 270 275
 acc tcc cgc gca ctg ctg caa tcc gca ccg tgc cca atg atg gtg gtt 979
 Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys Pro Met Met Val Val
 280 285 290
 cgc cca cct gag aag att aag aag tag tttcttttaa gtttcgatgc cccggtt 1033
 Arg Pro Pro Glu Lys Ile Lys Lys
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<212> PRT

<213> Corynebacterium glutamicum

<400> 6

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 Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr
 35 40 45
 Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala
 50 55 60

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

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<211> 948

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(925)

<223> RXA02229

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aagccttgga gattttgggt ctacaatagc gaggggtgaat ttg acc atc ccc ttt 115

	Leu	Thr	Ile	Pro	Phe	
	1				5	
gcc aaa ggc cac gcc acc gaa aac gac ttc atc atc atc ccc gat gag						163
Ala Lys Gly His Ala Thr Glu Asn Asp Phe Ile Ile Ile Pro Asp Glu						
	10				20	
gat gcg cgc cta gat tta act cca gaa atg gtg gtc acg ctg tgt gac						211
Asp Ala Arg Leu Asp Leu Thr Pro Glu Met Val Val Thr Leu Cys Asp						
	25				35	
cgc cgc gcc ggg atc ggt gct gat ggt atc ctc cgc gtg gtt aaa gct						259
Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu Arg Val Val Lys Ala						
	40				50	
gca gac gta gaa ggc tcc acg gtc gac cca tcg ctg tgg ttc atg gat						307
Ala Asp Val Glu Gly Ser Thr Val Asp Pro Ser Leu Trp Phe Met Asp						
	55				65	
tac cgc aac gcc gat gga tct ttg gct gaa atg tgc ggc aat ggt gtg						355
Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met Cys Gly Asn Gly Val						
	70				80	85
cgc ctg ttc gcg cac tgg ctg tac tcc cgc ggt ctt gtt gat aat acg						403
Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly Leu Val Asp Asn Thr						
	90				95	100
agc ttt gat atc ggt acc cgc gcc ggt gtc cgc cac gtt gat att ttg						451
Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg His Val Asp Ile Leu						
	105				110	115
cag gca gat caa cat tct gcg cag gtc cgc gtt gat atg ggc atc cct						499
Gln Ala Asp Gln His Ser Ala Gln Val Arg Val Asp Met Gly Ile Pro						
	120				125	130
gac gtc acg gga tta tcc acc tgc gac atc aac ggc caa gta ttc gct						547
Asp Val Thr Gly Leu Ser Thr Cys Asp Ile Asn Gly Gln Val Phe Ala						
	135				140	145
ggc ctt ggc gtt gat atg ggt aac cca cac cta gcg tgc gtt gtg ccg						595
Gly Leu Gly Val Asp Met Gly Asn Pro His Leu Ala Cys Val Val Pro						
	150				155	160
ggc tta agt gcg tcg gct ctt gcc gat atg gaa ctg cgc gca cct acg						643
Gly Leu Ser Ala Ser Ala Leu Ala Asp Met Glu Leu Arg Ala Pro Thr						
	170				175	180
ttt gat cag gaa ttc ttc ccc cac ggt gtg aac gta gaa atc gtc aca						691
Phe Asp Gln Glu Phe Phe Pro His Gly Val Asn Val Glu Ile Val Thr						
	185				190	195
gaa tta gaa gat gac gca gta tcg atg cgc gtg tgg gaa cgc gga gtg						739
Glu Leu Glu Asp Asp Ala Val Ser Met Arg Val Trp Glu Arg Gly Val						
	200				205	210
ggc gaa acc cgc tcc tgt ggc acg gga acc gtt gct gca gcg tgt gct						787
Gly Glu Thr Arg Ser Cys Gly Thr Gly Thr Val Ala Ala Ala Cys Ala						
	215				220	225
gct tta gct gat gct gga ttg gga gaa ggc aca gct aaa gtg tgc gtt						835
Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr Ala Lys Val Cys Val						

Ala Ala Ala Cys Ala Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr
 225 230 235 240
 Ala Lys Val Cys Val Pro Arg Gly Glu Val Glu Val Gln Ile Phe Asp
 245 250 255
 Asp Gly Ser Thr Leu Thr Gly Pro Ser Ala Ile Ile Ala Leu Gly Glu
 260 265 270
 Val Gln Ile
 275

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1468)
 <223> RXS02970

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

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly 135 140 145	547
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly 150 155 160 165	595
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr 170 175 180	643
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser 185 190 195	691
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys 200 205 210	739
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala 215 220 225	787
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro 230 235 240 245	835
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile 250 255 260	883
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys 265 270 275	931
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile 280 285 290	979
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile 295 300 305	1027
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser 310 315 320 325	1075
ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys 330 335 340	1123
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala 345 350 355	1171
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu 360 365 370	1219

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gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca 1267
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa 1315
Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
390 395 400 405

ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac 1363
Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His
410 415 420

atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg 1411
Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu
425 430 435

gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg 1459
Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly
440 445 450

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Ala Leu Phe
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<212> PRT
<213> Corynebacterium glutamicum

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20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
35 40 45

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

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
145 150 155 160

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His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
 165 170 175
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
 180 185 190
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
 195 200 205
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
 370 375 380
 Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
 385 390 395 400
 Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser
 405 410 415
 Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu
 420 425 430
 Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu
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 Leu Thr Phe Ala Gly Ala Leu Phe
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<210> 11
 <211> 1330
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1330)

<223> FRXA01009

<400> 11

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                                   Leu Ala Leu Lys Gly
                                   1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
                        10 15 20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
                        25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
                        40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
                        55 60 65

atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
                        70 75 80 85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
                        90 95 100

cgg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
                        105 110 115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
                        120 125 130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
                        135 140 145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
                        150 155 160 165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
                        170 175 180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser
                        185 190 195

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tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
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200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
280 285 290	
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc	1027
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile	
295 300 305	
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc	1075
Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser	
310 315 320 325	
ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag	1123
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys	
330 335 340	
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct	1171
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala	
345 350 355	
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa	1219
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu	
360 365 370	
gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca	1267
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala	
375 380 385	
gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa	1315
Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu	
390 395 400 405	
ttc aag gaa cgc ggc	1330
Phe Lys Glu Arg Gly	
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<210> 12
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 <212> PRT

<213> Corynebacterium glutamicum

<400> 12

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Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
          35          40          45

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

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65          70          75          80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
          85          90          95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
          100          105          110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
          115          120          125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
          130          135          140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
          145          150          155          160

His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
          165          170          175

Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
          180          185          190

Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
          195          200          205

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
          210          215          220

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

Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
          245          250          255

Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
          260          265          270

Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
          275          280          285

Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
          290          295          300

Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly

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Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
                      325                      330                      335

Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
                      340                      345                      350

Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
                      355                      360                      365

Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
                      370                      375                      380

Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
385                      390                      395                      400

Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly
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<210> 13
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<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(769)
<223> RXC02390

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Val Glu Trp Thr Ala
1 5

ttt ggc acc ctg att ctg ctc aat ttg gtg ggc agt tta tcc ccg ggg 163
Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly Ser Leu Ser Pro Gly
10 15 20

cct gat acc ttt ttc ctc ctc cgc tta gcc acc cgc tcc aga gcg cac 211
Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr Arg Ser Arg Ala His
25 30 35

gcg atc gct ggc gtc gcc ggc atc gtc acc gga ctc acg gtg tgg gtg 259
Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly Leu Thr Val Trp Val
40 45 50

acg ctg acg gtc gtg gga gca gcg gcg ctg ctc acc act tat ccg tcg 307
Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu Thr Thr Tyr Pro Ser
55 60 65

att ctc gga atc atc cag ctc gtc ggc ggc acg tac cta agc ttc att 355
Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr Tyr Leu Ser Phe Ile
70 75 80 85

ggg tac aag ttg ctg cgc tcg gcg tcg aga gag ctt atc gac gcc cgc 403
Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu Leu Ile Asp Ala Arg
90 95 100

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cag ttc cgt ttc aac gcc gat gcc cga cct atc ccg gat gcg gta gaa 451
 Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile Pro Asp Ala Val Glu
 105 110 115

 gca ctg gga acc cgc act cag gta tat cga caa ggt ttg gcc acc aac 499
 Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln Gly Leu Ala Thr Asn
 120 125 130

 ctg tca aac cct aaa gtt gtc atg tac ttc gcg gca att ctg gct ccg 547
 Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala Ala Ile Leu Ala Pro
 135 140 145

 ttg atg cca gcg cac cca tca ccg gtg ctg gcg ttc tct atc atc gtg 595
 Leu Met Pro Ala His Pro Ser Pro Val Leu Ala Phe Ser Ile Ile Val
 150 155 160 165

 gcg att tta gtg cag acc ttt gtt acc ttc tct gct gtg tgc ctc att 643
 Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser Ala Val Cys Leu Ile
 170 175 180

 gtc tct acg gag cgt gtg cgc aaa gca atg ctg cgt gca ggt ccc tgg 691
 Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu Arg Ala Gly Pro Trp
 185 190 195

 ttt gac ctg ctt gct ggc gtt gtc ttc ctc gtt gtg ggt gtg act ctg 739
 Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val Val Gly Val Thr Leu
 200 205 210

 ctg tat gaa ggc ctg acc ggt tta ctc ggg taaaggcata aaaaatggct 789
 Leu Tyr Glu Gly Leu Thr Gly Leu Leu Gly
 215 220

 tcc 792

<210> 14
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 14
 Val Glu Trp Thr Ala Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly
 1 5 10 15

 Ser Leu Ser Pro Gly Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr
 20 25 30

 Arg Ser Arg Ala His Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly
 35 40 45

 Leu Thr Val Trp Val Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu
 50 55 60

 Thr Thr Tyr Pro Ser Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr
 65 70 75 80

 Tyr Leu Ser Phe Ile Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu
 85 90 95

 Leu Ile Asp Ala Arg Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile

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                100                105                110
Pro  Asp  Ala  Val  Glu  Ala  Leu  Gly  Thr  Arg  Thr  Gln  Val  Tyr  Arg  Gln
      115                120                125

Gly  Leu  Ala  Thr  Asn  Leu  Ser  Asn  Pro  Lys  Val  Val  Met  Tyr  Phe  Ala
      130                135                140

Ala  Ile  Leu  Ala  Pro  Leu  Met  Pro  Ala  His  Pro  Ser  Pro  Val  Leu  Ala
      145                150                155                160

Phe  Ser  Ile  Ile  Val  Ala  Ile  Leu  Val  Gln  Thr  Phe  Val  Thr  Phe  Ser
      165                170                175

Ala  Val  Cys  Leu  Ile  Val  Ser  Thr  Glu  Arg  Val  Arg  Lys  Ala  Met  Leu
      180                185                190

Arg  Ala  Gly  Pro  Trp  Phe  Asp  Leu  Leu  Ala  Gly  Val  Val  Phe  Leu  Val
      195                200                205

Val  Gly  Val  Thr  Leu  Leu  Tyr  Glu  Gly  Leu  Thr  Gly  Leu  Leu  Gly
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<211> 897
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(874)
<223> RXC01796

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ttggtgcggc atcgggtggc tgctactagt cgggctcttc ttg ctc ctt ggc ggt 115
                        Leu Leu Leu Gly Gly
                        1 5

aac cct gcc gag atc gac cag gtt tta ggt ggc gat caa acc cag atc 163
Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly Asp Gln Thr Gln Ile
      10                15                20

gag tct gga gag tcc acc gga gcc ggc gac ttt gat cac tgc caa acc 211
Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe Asp His Cys Gln Thr
      25                30                35

ggc gca gat gcc aac gcc agt gat gat tgt cgc ctt tac tac acc tca 259
Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg Leu Tyr Tyr Thr Ser
      40                45                50

ttc tcc gtc aat gaa atg tgg cag act ttg ctt cca gct cag gct ggt 307
Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu Pro Ala Gln Ala Gly
      55                60                65

atc gaa tac acc gag ccg aca ttg act ctt ttc aaa aac tcc acc caa 355
Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe Lys Asn Ser Thr Gln
      70                75                80                85

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acc ggc tgc ggt ttc gct tct gcg tcc act ggg ccg ttt tac tgt ccg 403
Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly Pro Phe Tyr Cys Pro
          90                      95                      100

tca gac caa gat gct tat ttt gac ttg act ttc ttc gat cag atg cgt 451
Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe Phe Asp Gln Met Arg
          105                      110                      115

cag ttc ggt gca gaa aac gcc ccg ctt gcc cag atg tac atc gtg gcg 499
Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln Met Tyr Ile Val Ala
          120                      125                      130

cac gag tac ggc cac cac gtc caa aac ctc gag ggc aca ctc gga ctg 547
His Glu Tyr Gly His His Val Gln Asn Leu Glu Gly Thr Leu Gly Leu
          135                      140                      145

tcc aat tac aac gat ccg ggc gct gat tcc aac gcc gtc aag atc gag 595
Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn Ala Val Lys Ile Glu
          150                      155                      160                      165

ttg cag gcc gat tgc tac gca ggc att tgg gct aat cac tcc agc gaa 643
Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala Asn His Ser Ser Glu
          170                      175                      180

ggc ccg gat ccg cta ctc caa ccc atc acc gaa tct gag cta gat tcc 691
Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu Ser Glu Leu Asp Ser
          185                      190                      195

gct ctc ctt gct gca agc gcc gtg ggc gac gac aat atc cag caa cga 739
Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp Asn Ile Gln Gln Arg
          200                      205                      210

tcc ggt ggc gat gtc aat cct gaa agc tgg act cac ggc tca tcg cag 787
Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr His Gly Ser Ser Gln
          215                      220                      225

cag cgc aaa gac gcg ttc ctc gcc ggc tac aac acc ggc cag atg agc 835
Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn Thr Gly Gln Met Ser
          230                      235                      240                      245

gcc tgc gac ttc ctc ggc cgg ggc gtc tac aac gac gct taaagcattg 884
Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn Asp Ala
          250                      255

cttttcgacg tct 897

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<210> 16

<211> 258

<212> PRT

<213> Corynebacterium glutamicum

<400> 16

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Leu Leu Leu Gly Gly Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly
 1          5          10          15

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Asp Gln Thr Gln Ile Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe
          20          25          30

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Asp His Cys Gln Thr Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg
          35          40          45

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

<210> 17

<211> 771

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(748)

<223> RXC01207

<400> 17

cttcgatgac tcaccggcag agcgcgtttt gttacagcgc gtaaactgtg actttgaaaa 60

atTTTTgaac aatccgtaca ccaacttcag gagaaaaaca gtg agc aga atc tat 115

 Val Ser Arg Ile Tyr
 1 5

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gac tgt gcc gac caa gac tcc cgt gca gca ggc cta aag gcg gct gtc 163
Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val
      10                      15                      20

gat gca gtc aaa gcc ggt cag ctc gtt gtc ctt ccc acg gat acc ctt 211
Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu
      25                      30                      35

tat gga ctc ggc tgc gac gct ttc aac aac gag gca gta gcc aac ctt 259
Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu
      40                      45                      50

ctg gcc acc aaa cac cgt ggc ccc gat atg ccc gtt cca gtg ctc gtc 307
Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val
      55                      60                      65

ggc agc tgg gac acc att caa gga ctt gtg cac tcc tat tct gcg cag 355
Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln
      70                      75                      80                      85

gca aaa gcg ctt gtg gag gcg ttc tgg cct ggt gga ctg tcc atc atc 403
Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile
      90                      95                      100

gtt ccg cag gca cca agc ctt ccg tgg aac ctt ggc gat acc cgt ggc 451
Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly
      105                      110                      115

acc gta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg 499
Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu
      120                      125                      130

cgc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat 547
Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His
      135                      140                      145

act cct cca acc acc gtg ctg gag gct cgt cag cag ctc aac caa aat 595
Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln Gln Leu Asn Gln Asn
      150                      155                      160                      165

gtc gct gtc tac ctc gat ggt ggc gaa tgc gcg ctg gcc acc cct tca 643
Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser
      170                      175                      180

acc atc gtg gat att tca ggc ccc gca cca aag att ttg cgt gag ggt 691
Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly
      185                      190                      195

gcc atc agc gca gaa cgc gtt ggc gaa gta ctt gga gtg tcg gca gaa 739
Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu Gly Val Ser Ala Glu
      200                      205                      210

agc ctg cgc taaatgggag tcggtttcgc ggg 771
Ser Leu Arg
      215

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<210> 18

<211> 216

<212> PRT

<213> Corynebacterium glutamicum

<400> 18

Val Ser Arg Ile Tyr Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly
 1 5 10 15

Leu Lys Ala Ala Val Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu
 20 25 30

Pro Thr Asp Thr Leu Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu
 35 40 45

Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro
 50 55 60

Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His
 65 70 75 80

Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly
 85 90 95

Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu
 100 105 110

Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val
 115 120 125

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

Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln
 145 150 155 160

Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala
 165 170 175

Leu Ala Thr Pro Ser Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys
 180 185 190

Ile Leu Arg Glu Gly Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu
 195 200 205

Gly Val Ser Ala Glu Ser Leu Arg
 210 215

<210> 19

<211> 1026

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1003)

<223> RXC00657

<400> 19

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tgtaacgcag gattcaccaa tcaatgaaag gtcgaccgac atg agc act gaa gac 115
 Met Ser Thr Glu Asp
 1 5

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

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cca gtt cgc gca ctt gca gaa gca tct gaa aac gcg cag ctc cta gtc 883
Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn Ala Gln Leu Leu Val
                250                255                260

gtt ggt tcc cat ggt cgt ggc gga ttt aag ggc atg ctc ctt ggc tcc 931
Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly Met Leu Leu Gly Ser
                265                270                275

acc tcc cgc gca ctg ctg caa tcc gca ccg tgc cca atg atg gtg gtt 979
Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys Pro Met Met Val Val
                280                285                290

cgc cca cct gag aag att aag aag tagttttcttt taagtttcga tgc 1026
Arg Pro Pro Glu Lys Ile Lys Lys
                295                300

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<210> 20

<211> 301

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 20

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

Ser Lys Gln Ala Val Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly
                20                25                30

Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr
                35                40                45

Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala
 50                55                60

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

Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile
                85                90                95

Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly
                100                105                110

Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser
                115                120                125

Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu
                130                135                140

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

Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala
                165                170                175

Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met
                180                185                190

Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln
                195                200                205

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Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg
 210 215 220

Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile
 225 230 235 240

Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn
 245 250 255

Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly
 260 265 270

Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys
 275 280 285

Pro Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys
 290 295 300

<210> 21
 <211> 1059
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1036)
 <223> RXC00552

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gtttttaagg tagccacaca tcgcactaga ctgaagaact gtg gct acc tca aaa 115
 Val Ala Thr Ser Lys
 1 5

att ctt ctt tat tac gca ttc acc ccg ctc tct gac cct aaa gcg gtt 163
 Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser Asp Pro Lys Ala Val
 10 15 20

cag ctg tgg cag cgt gag ctc tgc gag tca ctg aat ctt cgt ggc cgc 211
 Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu Asn Leu Arg Gly Arg
 25 30 35

atc ctg atc tcc act cac ggc atc aat gga acc gtg ggc gga gat att 259
 Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr Val Gly Gly Asp Ile
 40 45 50

gat gat tgc aag gcg tac att aaa aag acc cgc gag tac cca ggt ttc 307
 Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg Glu Tyr Pro Gly Phe
 55 60 65

aac cgc atg cag ttt aag tgg tcc gag ggt ggc gct gag gat ttc cca 355
 Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly Ala Glu Asp Phe Pro
 70 75 80 85

aag ctc agt gtc aaa gtc cgc gat gag atc gtt gcc ttc ggc gct cca 403
 Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val Ala Phe Gly Ala Pro
 90 95 100

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gat gag ctc aaa gtg gat gaa aac ggc gtc gtc ggt ggc ggc gtt cac 451
Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val Gly Gly Gly Val His
      105                      110                      115

ctg aaa cca cag cag gtc aat gag ctt gtg gaa gcc cgt ggc gat gaa 499
Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu Ala Arg Gly Asp Glu
      120                      125                      130

gtt gtg ttc ttt gac ggc cgc aac gca atg gaa gcc cag atc ggc aag 547
Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu Ala Gln Ile Gly Lys
      135                      140                      145

ttc aag gac gct gtt gtc cct gac gta gaa acc act cat gat ttc atc 595
Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr Thr His Asp Phe Ile
      150                      155                      160                      165

gca gaa att gag tct gga aaa tac gac gat ctc aaa gac aag cct gtg 643
Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu Lys Asp Lys Pro Val
      170                      175                      180

gtc acc tac tgc acc ggc gga att cgt tgt gag atc ctg agt tca ctc 691
Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu Ile Leu Ser Ser Leu
      185                      190                      195

atg atc aac cgt ggt ttc aaa gag gtc tac caa atc gat ggc ggc atc 739
Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln Ile Asp Gly Gly Ile
      200                      205                      210

gtt cgc tac ggc gag cag ttt ggc aac aag ggc ctg tgg gaa ggc tcc 787
Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly Leu Trp Glu Gly Ser
      215                      220                      225

ctc tac gtt ttc gat aag cgc atg cat atg gaa ttc ggc gag gat tac 835
Leu Tyr Val Phe Asp Lys Arg Met His Met Glu Phe Gly Glu Asp Tyr
      230                      235                      240                      245

aaa gag gtc gga cac tgc atc cat tgc gat act ccc acc aac aaa ttt 883
Lys Glu Val Gly His Cys Ile His Cys Asp Thr Pro Thr Asn Lys Phe
      250                      255                      260

gag cac tgc ctc aac gaa gat gat tgc cgc gag ctc gtg ttg atg tgc 931
Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys
      265                      270                      275

cct gat tgc ttc gcc aat gtt gag acc cgt cat tgc aag cgc gaa cgc 979
Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg
      280                      285                      290

tgt gca gca att gct gcg gat ttc gct gag caa gga att gat ccg ctc 1027
Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu
      295                      300                      305

gtt act tct taaaaagggg atggtggctg ggt 1059
Val Thr Ser
310

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<210> 22

<211> 312

<212> PRT

<213> Corynebacterium glutamicum

<400> 22

Val Ala Thr Ser Lys Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser
 1 5 10 15
 Asp Pro Lys Ala Val Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu
 20 25 30
 Asn Leu Arg Gly Arg Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr
 35 40 45
 Val Gly Gly Asp Ile Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg
 50 55 60
 Glu Tyr Pro Gly Phe Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly
 65 70 75 80
 Ala Glu Asp Phe Pro Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val
 85 90 95
 Ala Phe Gly Ala Pro Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val
 100 105 110
 Gly Gly Gly Val His Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu
 115 120 125
 Ala Arg Gly Asp Glu Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu
 130 135 140
 Ala Gln Ile Gly Lys Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr
 145 150 155 160
 Thr His Asp Phe Ile Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu
 165 170 175
 Lys Asp Lys Pro Val Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu
 180 185 190
 Ile Leu Ser Ser Leu Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln
 195 200 205
 Ile Asp Gly Gly Ile Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly
 210 215 220
 Leu Trp Glu Gly Ser Leu Tyr Val Phe Asp Lys Arg Met His Met Glu
 225 230 235 240
 Phe Gly Glu Asp Tyr Lys Glu Val Gly His Cys Ile His Cys Asp Thr
 245 250 255
 Pro Thr Asn Lys Phe Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu
 260 265 270
 Leu Val Leu Met Cys Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His
 275 280 285
 Cys Lys Arg Glu Arg Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln
 290 295 300
 Gly Ile Asp Pro Leu Val Thr Ser
 305 310


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<210> 23
<211> 1386
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1363)
<223> RXA00534
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<400> 23																	
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Lys	Ile	Cys	Ile	Val	Ala	Gly	Phe	Gln	Gly	Val	Asn	Lys	Glu	Thr	Arg
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Leu	Ala	Ala	Ala	Leu	Asn	Ala	Asp	Val	Cys	Glu	Ile	Tyr	Ser	Asp	Val
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Asp	Gly	Val	Tyr	Thr	Ala	Asp	Pro	Arg	Ile	Val	Pro	Asn	Ala	Gln	Lys
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Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
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Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
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 Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly Thr Glu Ile Glu Val
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Lys Asp Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys
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Gln Tyr Ala Pro Leu Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn
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Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His
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Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala
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Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp

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 Val Pro Thr Pro Leu Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly
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 Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg
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 Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val
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 Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile
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 Val Asn Ser Glu Leu
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 Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu Pro Gly Val Glu Val
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 ttc cgc ttc aac aac aac gtt ctt gct cgc acg aac agg gga ttg gcc 307
 Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr Asn Arg Gly Leu Ala
 55 60 65
 tcg agg gtc atg ctt gct ggt cat atc gat aca gtg ccg atc gcg gac 355
 Ser Arg Val Met Leu Ala Gly His Ile Asp Thr Val Pro Ile Ala Asp
 70 75 80 85
 aat ctg cca agc cgt gtg gaa gac ggc atc atg tat ggc tgt ggc acc 403
 Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met Tyr Gly Cys Gly Thr
 90 95 100
 gtc gat atg aaa tct ggg ttg gcg gtg tat ttg cat act ttt gcc acc 451
 Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu His Thr Phe Ala Thr
 105 110 115
 ttg gcc acg tog act gag ctt aaa cat gat ctg acg ctg att gcg tat 499
 Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu Thr Leu Ile Ala Tyr
 120 125 130
 gag tgc gag gaa gtt gct gat cac ctc aat ggt ttg ggc cac att cgc 547
 Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly Leu Gly His Ile Arg

135	140	145	
gat gag cat ccg gag tgg ttg gcg gct gat ttg gcg ttg ttg ggt gag Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu Ala Leu Leu Gly Glu 150 155 160 165			595
cct act ggc ggc tgg att gag gcg ggc tgc cag ggc aat ctg cgc atc Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln Gly Asn Leu Arg Ile 170 175 180			643
aag gtg acg gcg cat ggt gtg cgt gcc cat tcg gcg aga agc tgg ttg Lys Val Thr Ala His Gly Val Arg Ala His Ser Ala Arg Ser Trp Leu 185 190 195			691
ggt gat aat gcg atg cat aag ttg tcg ccg atc att tcg aag gtt gct Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile Ile Ser Lys Val Ala 200 205 210			739
gcg tat aag gcc gca gaa gtc aac att gat ggc ttg acc tac cgt gaa Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly Leu Thr Tyr Arg Glu 215 220 225			787
ggc ctc aac atc gtt ttc tgc gaa tcg ggc gtg gca aac aac gtc att Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val Ala Asn Asn Val Ile 230 235 240 245			835
cca gac ctc gcg tgg atg aac ctc aac ttc cgt ttc gcg ccg aat cgc Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg Phe Ala Pro Asn Arg 250 255 260			883
gat ctc aac gag gcg atc gag cat gtc gtc gaa acg ctt gag ctt gac Asp Leu Asn Glu Ala Ile Glu His Val Val Glu Thr Leu Glu Leu Asp 265 270 275			931
ggt caa gac ggc atc gaa tgg gcc gta gaa gac ggg gca ggc ggt gcc Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp Gly Ala Gly Gly Ala 280 285 290			979
ctt cca ggc ttg ggg cag cag gtg aca agc ggg ctt atc gac gcc gtc Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly Leu Ile Asp Ala Val 295 300 305			1027
ggc cgc gaa aaa atc cgc gca aaa ttc ggc tgg acc gat gtc tca cgt Gly Arg Glu Lys Ile Arg Ala Lys Phe Gly Trp Thr Asp Val Ser Arg 310 315 320 325			1075
ttt tca gcc atg gga att cca gcc cta aac ttt ggc gct ggt gat cca Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe Gly Ala Gly Asp Pro 330 335 340			1123
agt ttc gcg cat aaa cgc gac gag cag tgc cca gtg gag caa atc acg Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro Val Glu Gln Ile Thr 345 350 355			1171
gat gtg gca gca att ttg aag cag tac ctg agc gag taaccgcatt Asp Val Ala Ala Ile Leu Lys Gln Tyr Leu Ser Glu 360 365			1217
cgggggttatc gtg			1230

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<211> 369

<212> PRT

<213> Corynebacterium glutamicum

<400> 30

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Val	Leu	Thr	Gln	Arg	Leu	Val	Asp	Ile	Pro	Ser	Pro	Ser	Gly	Gln	Glu
			20					25					30		

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

Pro	Gly	Val	Glu	Val	Phe	Arg	Phe	Asn	Asn	Asn	Val	Leu	Ala	Arg	Thr
	50					55					60				

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

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

Tyr	Gly	Cys	Gly	Thr	Val	Asp	Met	Lys	Ser	Gly	Leu	Ala	Val	Tyr	Leu
			100					105					110		

His	Thr	Phe	Ala	Thr	Leu	Ala	Thr	Ser	Thr	Glu	Leu	Lys	His	Asp	Leu
		115					120					125			

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

Leu	Gly	His	Ile	Arg	Asp	Glu	His	Pro	Glu	Trp	Leu	Ala	Ala	Asp	Leu
145					150					155					160

Ala	Leu	Leu	Gly	Glu	Pro	Thr	Gly	Gly	Trp	Ile	Glu	Ala	Gly	Cys	Gln
				165					170					175	

Gly	Asn	Leu	Arg	Ile	Lys	Val	Thr	Ala	His	Gly	Val	Arg	Ala	His	Ser
		180						185					190		

Ala	Arg	Ser	Trp	Leu	Gly	Asp	Asn	Ala	Met	His	Lys	Leu	Ser	Pro	Ile
		195					200					205			

Ile	Ser	Lys	Val	Ala	Ala	Tyr	Lys	Ala	Ala	Glu	Val	Asn	Ile	Asp	Gly
	210					215					220				

Leu	Thr	Tyr	Arg	Glu	Gly	Leu	Asn	Ile	Val	Phe	Cys	Glu	Ser	Gly	Val
225					230					235					240

Ala	Asn	Asn	Val	Ile	Pro	Asp	Leu	Ala	Trp	Met	Asn	Leu	Asn	Phe	Arg
			245						250					255	

Phe	Ala	Pro	Asn	Arg	Asp	Leu	Asn	Glu	Ala	Ile	Glu	His	Val	Val	Glu
			260					265					270		

Thr	Leu	Glu	Leu	Asp	Gly	Gln	Asp	Gly	Ile	Glu	Trp	Ala	Val	Glu	Asp
	275						280					285			

Gly	Ala	Gly	Gly	Ala	Leu	Pro	Gly	Leu	Gly	Gln	Gln	Val	Thr	Ser	Gly

290	295	300
Leu Ile Asp Ala Val Gly Arg Glu Lys Ile Arg Ala Lys Phe Gly Trp		
305	310	315 320
Thr Asp Val Ser Arg Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe		
	325	330 335
Gly Ala Gly Asp Pro Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro		
	340	345 350
Val Glu Gln Ile Thr Asp Val Ala Ala Ile Leu Lys Gln Tyr Leu Ser		
	355	360 365
Glu		

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1036)
 <223> RXA00044

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ttctcaccgc cactcggtcc ctcaaccac aaggagcacc atg gct tcc gca act 115
 Met Ala Ser Ala Thr
 1 5

ttc acc ggc gtg atc cca ccc gta atg acc cca ctc cac gcc gac ggc 163
 Phe Thr Gly Val Ile Pro Pro Val Met Thr Pro Leu His Ala Asp Gly
 10 15 20

agt gtg gat gta gaa agc ctc cgc aag ctc gtt gac cac ctc atc aat 211
 Ser Val Asp Val Glu Ser Leu Arg Lys Leu Val Asp His Leu Ile Asn
 25 30 35

ggc ggc gtc gac gga ctt ttc gca ctg ggc tcc tca ggc gaa gcg gca 259
 Gly Gly Val Asp Gly Leu Phe Ala Leu Gly Ser Ser Gly Glu Ala Ala
 40 45 50

ttc ctc acc cgc gcc cag cgc aaa ctc gca ctg acc acc atc atc gag 307
 Phe Leu Thr Arg Ala Gln Arg Lys Leu Ala Leu Thr Thr Ile Ile Glu
 55 60 65

cac acc gca ggc cgc gtt ccc gta act gct ggt gtc att gaa acc acc 355
 His Thr Ala Gly Arg Val Pro Val Thr Ala Gly Val Ile Glu Thr Thr
 70 75 80 85

act gct cgc gtg att gag ctc gtg gaa gat gcc ctg gag gct ggt gcc 403
 Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala Leu Glu Ala Gly Ala
 90 95 100

gaa ggc ctc gtt gcc act gca cct ttc tac acc cgc acc cac gat gtg 451
 Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr Arg Thr His Asp Val

105	110	115	
gaa att gaa gaa cac ttc cgc aag atc cac gcc gcc gct cca gag ctt Glu Ile Glu Glu His Phe Arg Lys Ile His Ala Ala Ala Pro Glu Leu 120 125 130			499
cca ctg ttt gcc tac aac atc cca gtg tgc gtg cac tcc aac ctc aac Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val His Ser Asn Leu Asn 135 140 145			547
cca gtc atg ctt ttg acg ctg gcc aag gat gcc gtt ctt gca gcc acc Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly Val Leu Ala Gly Thr 150 155 160 165			595
aag gat tcc agt gcc aat gat gcc gca atc cgc tca ctg atc gaa gct Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg Ser Leu Ile Glu Ala 170 175 180			643
cgt gat gat gct gga ctc act gag cag ttc aag atc ctc acc gcc agc Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys Ile Leu Thr Gly Ser 185 190 195			691
gaa acc acc gtt gat ttc gcc tac ctt gcg ggt gcc gat gga gtt gtc Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly Ala Asp Gly Val Val 200 205 210			739
cca gcc ctg gcc aat gtt gat cct gca gca tac gca gct tta gca aaa Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr Ala Ala Leu Ala Lys 215 220 225			787
ctc tgc ctc gat gga aag tgg gca gaa gct gct gct ttg cag aag cgc Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala Ala Leu Gln Lys Arg 230 235 240 245			835
atc aac cac ctc ttc cac atc gtc ttc gtg gga gac acc tcc cat atg Ile Asn His Leu Phe His Ile Val Phe Val Gly Asp Thr Ser His Met 250 255 260			883
tcc gga tcc agc gct ggt ttg gcc ggt ttc aag aca gca ctc gca cac Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys Thr Ala Leu Ala His 265 270 275			931
ctt gcc att att gaa tcc aat gcg atg gca gtt cct cac cag agc ctc Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val Pro His Gln Ser Leu 280 285 290			979
agc gac gaa gaa act gct cgc att cac gcc att gtt gat gaa ttc ctg Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile Val Asp Glu Phe Leu 295 300 305			1027
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<210> 32

<211> 312

<212> PRT

<213> Corynebacterium glutamicum

<400> 32

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 20 25 30
 Asp His Leu Ile Asn Gly Gly Val Asp Gly Leu Phe Ala Leu Gly Ser
 35 40 45
 Ser Gly Glu Ala Ala Phe Leu Thr Arg Ala Gln Arg Lys Leu Ala Leu
 50 55 60
 Thr Thr Ile Ile Glu His Thr Ala Gly Arg Val Pro Val Thr Ala Gly
 65 70 75 80
 Val Ile Glu Thr Thr Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala
 85 90 95
 Leu Glu Ala Gly Ala Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr
 100 105 110
 Arg Thr His Asp Val Glu Ile Glu Glu His Phe Arg Lys Ile His Ala
 115 120 125
 Ala Ala Pro Glu Leu Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val
 130 135 140
 His Ser Asn Leu Asn Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly
 145 150 155 160
 Val Leu Ala Gly Thr Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg
 165 170 175
 Ser Leu Ile Glu Ala Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys
 180 185 190
 Ile Leu Thr Gly Ser Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly
 195 200 205
 Ala Asp Gly Val Val Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr
 210 215 220
 Ala Ala Leu Ala Lys Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala
 225 230 235 240
 Ala Leu Gln Lys Arg Ile Asn His Leu Phe His Ile Val Phe Val Gly
 245 250 255
 Asp Thr Ser His Met Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys
 260 265 270
 Thr Ala Leu Ala His Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val
 275 280 285
 Pro His Gln Ser Leu Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile
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 Val Asp Glu Phe Leu Tyr Thr Ala
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<211> 867
<212> DNA
<213> Corynebacterium glutamicum
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<223> RXA00863
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Met Gly Ile Lys Val																	5
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ggc gtt ctc gga gcc aaa ggc cgt gtt ggt caa act att gtg gca gca												163					
Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln Thr Ile Val Ala Ala																	
10 15 20																	
gtc aat gag tcc gac gat ctg gag ctt gtt gca gag atc ggc gtc gac												211					
Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala Glu Ile Gly Val Asp																	
25 30 35																	
gat gat ttg agc ctt ctg gta gac aac ggc gct gaa gtt gtc gtt gac												259					
Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala Glu Val Val Val Asp																	
40 45 50																	
ttc acc act cct aac gct gtg atg ggc aac ctg gag ttc tgc atc aac												307					
Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu Glu Phe Cys Ile Asn																	
55 60 65																	
aac ggc att tct gcg gtt gtt gga acc acg ggc ttc gat gat gct cgt												355					
Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly Phe Asp Asp Ala Arg																	
70 75 80 85																	
ttg gag cag gtt cgc gac tgg ctt gaa gga aaa gac aat gtc ggt gtt												403					
Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys Asp Asn Val Gly Val																	
90 95 100																	
ctg atc gca cct aac ttt gct atc tct gcg gtg ttg acc atg gtc ttt												451					
Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val Leu Thr Met Val Phe																	
105 110 115																	
tcc aag cag gct gcc cgc ttc ttc gaa tca gct gaa gtt att gag ctg												499					
Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala Glu Val Ile Glu Leu																	
120 125 130																	
cac cac ccc aac aag ctg gat gca cct tca ggc acc gcg atc cac act												547					
His His Pro Asn Lys Leu Asp Ala Pro Ser Gly Thr Ala Ile His Thr																	
135 140 145																	
gct cag ggc att gct gcg gca cgc aaa gaa gca ggc atg gac gca cag												595					
Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala Gly Met Asp Ala Gln																	
150 155 160 165																	
cca gat gcg acc gag cag gca ctt gag ggt tcc cgt ggc gca agc gta												643					
Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser Arg Gly Ala Ser Val																	
170 175 180																	

gat gga atc ccg gtt cat gca gtc cgc atg tcc ggc atg gtt gct cac 691
 Asp Gly Ile Pro Val His Ala Val Arg Met Ser Gly Met Val Ala His
 185 190 195
 gag caa gtt atc ttt ggc acc cag ggt cag acc ttg acc atc aag cag 739
 Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr Leu Thr Ile Lys Gln
 200 205 210
 gac tcc tat gat cgc aac tca ttt gca cca ggt gtc ttg gtg ggt gtg 787
 Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly Val Leu Val Gly Val
 215 220 225
 cgc aac att gca cag cac cca ggc cta gtc gta gga ctt gag cat tac 835
 Arg Asn Ile Ala Gln His Pro Gly Leu Val Val Gly Leu Glu His Tyr
 230 235 240 245
 cta ggc ctg taaaggctca tttcagcagc ggg 867
 Leu Gly Leu

<210> 34
 <211> 248
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 34
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 20 25 30
 Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala
 35 40 45
 Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu
 50 55 60
 Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly
 65 70 75 80
 Phe Asp Asp Ala Arg Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys
 85 90 95
 Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val
 100 105 110
 Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala
 115 120 125
 Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly
 130 135 140
 Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Arg Lys Glu Ala
 145 150 155 160
 Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser
 165 170 175
 Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser


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                180                185                190
Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr
      195                200                205

Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly
      210                215                220

Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val
      225                230                235                240

Gly Leu Glu His Tyr Leu Gly Leu
      245

<210> 35
<211> 873
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(850)
<223> RXA00864

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                        Val Ala Glu Gln Val
                        1                    5

aaa ttg agc gtg gag ttg ata gcg tgc agt tct ttt act cca ccc gct 163
Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser Phe Thr Pro Pro Ala
                        10                15                20

gat gtt gag tgg tca act gat gtt gag ggc gcg gaa gca ctc gtc gag 211
Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala Glu Ala Leu Val Glu
                        25                30                35

ttt gcg ggt cgt gcc tgc tac gaa act ttt gat aag ccg aac cct cga 259
Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp Lys Pro Asn Pro Arg
                        40                45                50

act gct tcc aat gct gcg tat ctg cgc cac atc atg gaa gtg ggg cac 307
Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile Met Glu Val Gly His
                        55                60                65

act gct ttg ctt gag cat gcc aat gcc acg atg tat atc cga ggc att 355
Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met Tyr Ile Arg Gly Ile
      70                75                80                85

tct cgg tcc gcg acc cat gaa ttg gtc cga cac cgc cat ttt tcc ttc 403
Ser Arg Ser Ala Thr His Glu Leu Val Arg His Arg His Phe Ser Phe
                        90                95                100

tct caa ctg tct cag cgt ttc gtg cac agc gga gaa tcg gaa gta gtg 451
Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly Glu Ser Glu Val Val
      105                110                115

gtg ccc act ctc atc gat gaa gat ccg cag ttg cgt gaa ctt ttc atg 499

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Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu Arg Glu Leu Phe Met
 120 125 130

cac gcc atg gat gag tct cgg ttc gct ttc aat gag ctg ctt aat gcg 547
 His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn Glu Leu Leu Asn Ala
 135 140 145

ctg gaa gaa aaa ctt ggc gat gaa ccg aat gca ctt tta agg aaa aag 595
 Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala Leu Leu Arg Lys Lys
 150 155 160 165

cag gct cgt caa gca gct cgc gct gtg ctg ccc aac gct aca gag tcc 643
 Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro Asn Ala Thr Glu Ser
 170 175 180

aga atc gtg gtg tct gga aac ttc cgc acc tgg agg cat ttc att ggc 691
 Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp Arg His Phe Ile Gly
 185 190 195

atg cga gcc agt gaa cat gca gac gtc gaa atc cgc gaa gta gcg gta 739
 Met Arg Ala Ser Glu His Ala Asp Val Glu Ile Arg Glu Val Ala Val
 200 205 210

gaa tgt tta aga aag ctg cag gta gca gcg cca act gtt ttc ggt gat 787
 Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro Thr Val Phe Gly Asp
 215 220 225

ttt gag att gaa act ttg gca gac gga tgc caa atg gca aca agc ccg 835
 Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln Met Ala Thr Ser Pro
 230 235 240 245

tat gtc atg gac ttt taacgcaaag ctcacaccca cga 873
 Tyr Val Met Asp Phe
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<210> 36

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

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 20 25 30

Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp
 35 40 45

Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile
 50 55 60

Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met
 65 70 75 80

Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His
 85 90 95

Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly

100	105	110
Glu Ser Glu Val Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu		
115	120	125
Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn		
130	135	140
Glu Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala		
145	150	155
Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro		
165	170	175
Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp		
180	185	190
Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile		
195	200	205
Arg Glu Val Ala Val Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro		
210	215	220
Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln		
225	230	235
Met Ala Thr Ser Pro Tyr Val Met Asp Phe		
245	250	

<210> 37

<211> 608

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (69)..(608)

<223> RXA02843

<400> 37

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Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser

1

5

10

acc ggc gac gtc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac 158

Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp

15

20

25

30

cag tcc gcg ctc aca cct cta gaa ggc gtc gat gaa gat cga aac gtc 206

Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val

35

40

45

acc cgc aaa atc gtg acg aca act atc gac acc gac gca gcc ccc acc 254

Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr

50

55

60

gac acc tac gat gca tgg ctg cgc ctt cac ctc ctc tcc cac cgc gtt 302

Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val

65	70	75	
ttc cgc cct cac acc atc aac cta gac ggc att ttc ggc ctc ctc aac			350
Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn			
80	85	90	
aat gtc gtg tgg acc aac ttc gga ccg tgc gca gtt gac ggt ttc gca			398
Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala			
95	100	105	110
ctc acc cgc gcg cgc ctg tca cgc cga ggc caa gtt acg gtt tat agc			446
Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser			
115	120	125	
gtc gac aag ttc cca cgc atg gtc gac tat gtg gtt ccc tcg ggc gtg			494
Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val			
130	135	140	
cgc atc ggt gac gcc gac cgc gtc cga ctt ggc gcg tac ctg gca gat			542
Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp			
145	150	155	
ggc acc acc gtg atg cat gag ggc ttc gtg aac ttc aac gct ggc acg			590
Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr			
160	165	170	
ctc ggc gct tcc atg gtt			608
Leu Gly Ala Ser Met Val			
175	180		

<210> 38

<211> 180

<212> PRT

<213> Corynebacterium glutamicum

<400> 38

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20	30
Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val Thr Arg	
35	45
Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr	
50	60
Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg	
65	80
Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val	
85	95
Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr	
100	110
Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp	
115	125

Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile
 130 135 140

Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr
 145 150 155 160

Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr Leu Gly
 165 170 175

Ala Ser Met Val
 180

<210> 39
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1120)
 <223> RXN00355

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ggctcctgatg aaagagatgt ccctgaatca tcacttaagt atg cat ctc ggt aag 115
 Met His Leu Gly Lys
 1 5

ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163
 Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met
 10 15 20

acc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc 211
 Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser
 25 30 35

gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc 259
 Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met Asp Leu Val Gly Ile
 40 45 50

ttc tcg cgc cgg gcc acc ctc gac aca aag acg cca gtc ttt gat gtc 307
 Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr Pro Val Phe Asp Val
 55 60 65

gcc gac gtg gac aag cac gcc gac gac gtg gac gtg ctg ttc ctg tgc 355
 Ala Asp Val Asp Lys His Ala Asp Asp Val Asp Val Leu Phe Leu Cys
 70 75 80 85

atg ggc tcc gcc acc gac atc cct gag cag gca cca aag ttc gcg cag 403
 Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro Lys Phe Ala Gln
 90 95 100

ttc gcc tgc acc gta gac acc tac gac aac cac cgc gac atc cca cgc 451
 Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His Arg Asp Ile Pro Arg
 105 110 115

cac cgc cag gtc atg aac gaa gcc gcc acc gca gcc ggc aac gtt gca 499
 His Arg Gln Val Met Asn Glu Ala Ala Thr Ala Ala Gly Asn Val Ala
 120 125 130

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ctg gtc tct acc ggc tgg gat cca gga atg ttc tcc atc aac cgc gtc 547
Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser Ile Asn Arg Val
135 140 145

tac gca gcg gca gtc tta gcc gag cac cag cag cac acc ttc tgg ggc 595
Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln His Thr Phe Trp Gly
150 155 160 165

cca ggt ttg tca cag ggc cac tcc gat gct ttg cga cgc atc cct ggc 643
Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu Arg Arg Ile Pro Gly
170 175 180

gtt caa aag gca gtc cag tac acc ctc cca tcc gaa gac gcc ctg gaa 691
Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser Glu Asp Ala Leu Glu
185 190 195

aag gcc cgc cgc ggc gaa gcc ggc gac ctt acc gga aag caa acc cac 739
Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr Gly Lys Gln Thr His
200 205 210

aag cgc caa tgc ttc gtg gtt gcc gac gcg gcc gat cac gag cgc atc 787
Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala Asp His Glu Arg Ile
215 220 225

gaa aac gac atc cgc acc atg cct gat tac ttc gtt gcc tac gaa gtc 835
Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe Val Gly Tyr Glu Val
230 235 240 245

gaa gtc aac ttc atc gac gaa gca acc ttc gac tcc gag cac acc ggc 883
Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ser Glu His Thr Gly
250 255 260

atg cca cac ggt ggc cac gtg att acc acc ggc gac acc ggt ggc ttc 931
Met Pro His Gly Gly His Val Ile Thr Thr Gly Asp Thr Gly Gly Phe
265 270 275

aac cac acc gtg gaa tac atc ctc aag ctg gac cga aac cca gat ttc 979
Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp Arg Asn Pro Asp Phe
280 285 290

acc gct tcc tca cag atc gct ttc ggt cgc gca gct cac cgc atg aag 1027
Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala Ala His Arg Met Lys
295 300 305

cag cag ggc caa agc gga gct ttc acc gtc ctc gaa gtt gct cca tac 1075
Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu Glu Val Ala Pro Tyr
310 315 320 325

ctg ctc tcc cca gag aac ttg gac gat ctg atc gca cgc gac gtc 1120
Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile Ala Arg Asp Val
330 335 340

taatttagct cgaggggcaa gga 1143

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<210> 40

<211> 340

<212> PRT

<213> Corynebacterium glutamicum

<400> 40

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

Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met
          35           40           45

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

Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp
          65           70           75           80

Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala
          85           90           95

Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His
          100          105          110

Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala
          115          120          125

Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe
          130          135          140

Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln
          145          150          155          160

His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu
          165          170          175

Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser
          180          185          190

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

Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala
          210          215          220

Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe
          225          230          235          240

Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp
          245          250          255

Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly
          260          265          270

Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp
          275          280          285

Arg Asn Pro Asp Phe Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala
          290          295          300

Ala His Arg Met Lys Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu
          305          310          315          320

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Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile
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Ala Arg Asp Val
 340

<210> 41

<211> 958

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(958)

<223> FRXA00352

<400> 41

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ggtcctgatg aaagagatgt ccctgaatca tcatctaagt atg cat ctc ggt aag 115
 Met His Leu Gly Lys
 1 5

ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163
 Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met
 10 15 20

acc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc 211
 Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser
 25 30 35

gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc 259
 Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met Asp Leu Val Gly Ile
 40 45 50

ttc tcg cgc cgg gcc acc ctc gac aca aag acg cca gtc ttt gat gtc 307
 Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr Pro Val Phe Asp Val
 55 60 65

gcc gac gtg gac aag cac gcc gac gac gtg gac gtg ctg ttc ctg tgc 355
 Ala Asp Val Asp Lys His Ala Asp Asp Val Asp Val Leu Phe Leu Cys
 70 75 80 85

atg ggc tcc gcc acc gac atc cct gag cag gca cca aag ttc gcg cag 403
 Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro Lys Phe Ala Gln
 90 95 100

ttc gcc tgc acc gta gac acc tac gac aac cac cgc gac atc cca cgc 451
 Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His Arg Asp Ile Pro Arg
 105 110 115

cac cgc cag gtc atg aac gaa gcc gcc acc gca gcc ggc aac gtt gca 499
 His Arg Gln Val Met Asn Glu Ala Ala Thr Ala Ala Gly Asn Val Ala
 120 125 130

ctg gtc tct acc ggc tgg gat cca gga atg ttc tcc atc aac cgc gtc 547
 Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser Ile Asn Arg Val
 135 140 145

tac gca gcg gca gtc tta gcc gag cac cag cag cac acc ttc tgg ggc 595

Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln His Thr Phe Trp Gly
 150 155 160 165
 cca ggt ttg tca cag ggc cac tcc gat gct ttg cga cgc atc cct ggc 643
 Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu Arg Arg Ile Pro Gly
 170 175 180
 gtt caa aag gca gtc cag tac acc ctc cca tcc gaa gac gcc ctg gaa 691
 Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser Glu Asp Ala Leu Glu
 185 190 195
 aag gcc cgc cgc ggc gaa gcc tgc gac ctt acc gga aag caa acc cac 739
 Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr Gly Lys Gln Thr His
 200 205 210
 aag cgc caa tgc ttc gtg gtt gcc gac gcg gcc gat cac gag cgc atc 787
 Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala Asp His Glu Arg Ile
 215 220 225
 gaa aac gac atc cgc acc atg cct gat tac ttc gtt ggc tac gaa gtc 835
 Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe Val Gly Tyr Glu Val
 230 235 240 245
 gaa gtc aac ttc atc gac gaa gca acc ttc gac tcc gag cac acc ggc 883
 Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ser Glu His Thr Gly
 250 255 260
 atg cca cac ggt ggc cac gtg att acc acc ggc gac acc ggt ggc ttc 931
 Met Pro His Gly Gly His Val Ile Thr Thr Gly Asp Thr Gly Gly Phe
 265 270 275
 aac cac acc gtg gaa tac atc ctc aag 958
 Asn His Thr Val Glu Tyr Ile Leu Lys
 280 285

<210> 42

<211> 286

<212> PRT

<213> Corynebacterium glutamicum

<400> 42

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

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

<210> 43
 <211> 1400
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1377)
 <223> RXA00972

<400> 43
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 1 5 10 15
 aca gtt gaa aat ttc aat gaa ctt ccc gca cac gta tgg oca cgc aat 96
 Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro Arg Asn
 20 25 30
 gcc gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg cct ctg 144
 Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu
 35 40 45
 cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc gac gag 192
 Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu

50	55	60	
gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc ggt gga Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly 65 70 75 80			240
cca ggc aat gtg cac tac gca tct aaa gcg ttc ctg acc aag acc att Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile 85 90 95			288
gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gca tcc atc Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile 100 105 110			336
aac gaa ctg ggc att gcc ctg gcc gct ggt ttc ccc gcc agc cgt atc Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile 115 120 125			384
acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg ttg gtt Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val 130 135 140			432
caa aac ggt gtg gga cac gtg gtg ctg gac tcc gca cag gaa cta gaa Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu 145 150 155 160			480
ctg ttg gat tac gtt gcc gct ggt gaa ggc aag att cag gac gtg ttg Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu 165 170 175			528
atc cgc gta aag cca ggc atc gaa gca cac acc cac gag ttc atc gcc Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe Ile Ala 180 185 190			576
act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc ggt tcc Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser 195 200 205			624
gca ttc gaa gca gca aaa gcc gcc aac aac gca gaa aac ctg aac ctg Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu 210 215 220			672
gtt ggc ctg cac tgc cac gtt ggt tcc cag gtg ttc gac gcc gaa ggc Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Glu Gly 225 230 235 240			720
ttc aag ctg gca gca gaa cgc gtg ttg ggc ctg tac tca cag atc cac Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His 245 250 255			768
agc gaa ctg ggc gtt gcc ctt cct gaa ctg gat ctc ggt ggc gga tac Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr 260 265 270			816
ggc att gcc tat acc gca gct gaa gaa cca ctc aac gtc gca gaa gtt Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val 275 280 285			864
gcc tcc gac ctg ctc acc gca gtc gga aaa atg gca gcg gaa cta ggc Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly 290 295 300			912

atc gac gca cca acc gtg ctt gtt gag ccc ggc cgc gct atc gca ggc 960
 Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly
 305 310 315 320
 ccc tcc acc gtg acc atc tac gaa gtc ggc acc acc aaa gac gtc cac 1008
 Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His
 325 330 335
 gta gac gac gac aaa acc cgc cgt tac atc gcc gtg gac gga ggc atg 1056
 Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly Gly Met
 340 345 350
 tcc gac aac atc cgc cca gca ctc tac ggg tcc gaa tac gac gcc cgc 1104
 Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp Ala Arg
 355 360 365
 gta gta tcc cgc ttc gcc gaa gga gac cca gta agc acc cgc atc gtg 1152
 Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val
 370 375 380
 ggc tcc cac tgc gaa tcc ggc gat atc ctg atc aac gat gaa atc tac 1200
 Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr
 385 390 395 400
 cca tct gac atc acc agc ggc gac ttc ctt gca ctc gca gcc acc ggc 1248
 Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly
 405 410 415
 gca tac tgc tac gcc atg agc tcc cgc tac aac gcc ttc aca cgg ccc 1296
 Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro
 420 425 430
 gcc gtc gtg tcc gtc cgc gct ggc agc tcc cgc ctc atg ctg cgc cgc 1344
 Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu Arg Arg
 435 440 445
 gaa acg ctc gac gac atc ctc tca cta gag gca taacgctttt cgacgcctga 1397
 Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala
 450 455
 ccc 1400

<210> 44
 <211> 459
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 44
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 20 25 30
 Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu
 35 40 45
 Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu
 50 55 60

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Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly
 65              70              75              80

Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile
              85              90              95

Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile
              100              105              110

Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile
              115              120              125

Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val
 130              135              140

Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu
 145              150              155              160

Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu
              165              170              175

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

Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser
 195              200              205

Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu
 210              215              220

Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Glu Gly
 225              230              235              240

Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His
              245              250              255

Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr
 260              265              270

Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val
 275              280              285

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

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

Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His
              325              330              335

Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly Gly Met
 340              345              350

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

Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val
 370              375              380

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Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr
 385 390 395 400
 Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly
 405 410 415
 Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro
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 Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu Arg Arg
 435 440 445
 Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala
 450 455

<210> 45
 <211> 2121
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2098)
 <223> RXA02653

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 Met Ile Pro Lys Pro
 1 5
 gac gtg acc gac tta tat tta gag gac ctc tta aat gag ggt tog gaa 163
 Asp Val Thr Asp Leu Tyr Leu Glu Asp Leu Leu Asn Glu Gly Ser Glu
 10 15 20
 aag att cgg tcc gcc aag gat ctt tcc gaa ctt agg aca gtt cta aaa 211
 Lys Ile Arg Ser Ala Lys Asp Leu Ser Glu Leu Arg Thr Val Leu Lys
 25 30 35
 gag gtt tcc tcc caa att cag gaa cga gct ggg aaa aaa gat gaa gaa 259
 Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly Lys Lys Asp Glu Glu
 40 45 50
 tgg gga atg ggg gcc act tgg cgg gag ctg tac ccc agc atc gtg gaa 307
 Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr Pro Ser Ile Val Glu
 55 60 65
 cgc gct tcc tac gaa ggg cgt gac agc cta atc gga ttt gat cac tta 355
 Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile Gly Phe Asp His Leu
 70 75 80 85
 gcc cgg gaa atg gaa aga tta gcc ttc ggc cca cca tcc gaa agt ttt 403
 Ala Arg Glu Met Glu Arg Leu Ala Phe Gly Pro Pro Ser Glu Ser Phe
 90 95 100
 gaa tac ctc caa gaa ctc gta aaa tcc gga gtg gta gac atc act cac 451
 Glu Tyr Leu Gln Glu Leu Val Lys Ser Gly Val Val Asp Ile Thr His
 105 110 115

ctg cat cgt ggc cgg gaa cca	ctg aca gat tta gtt cgt gaa ctt gaa	499
Leu His Arg Gly Arg Glu Pro	Leu Thr Asp Leu Val Arg Glu Leu Glu	
120	125 130	
ata act gtg gtg ata gac gct gtt ctt ccc ccg ccg gga gta gtg cca	547	
Ile Thr Val Val Ile Asp Ala Val Leu Pro Pro Pro Gly Val Val Pro		
135	140 145	
ggc aca ttg gtg cac aat ttg gta aaa gag gga tat gcc aga atg cgt	595	
Gly Thr Leu Val His Asn Leu Val Lys Glu Gly Tyr Ala Arg Met Arg		
150	155 160 165	
cct ggg act cgg ggg tta gat gta gcg gct gac ggc acc gtt caa ggg	643	
Pro Gly Thr Arg Gly Leu Asp Val Ala Ala Asp Gly Thr Val Gln Gly		
170	175 180	
caa cga cat ttg gct gca gtc gga cgg atg acg gaa gat gtg gtt ttg	691	
Gln Arg His Leu Ala Ala Val Gly Arg Met Thr Glu Asp Val Val Leu		
185	190 195	
ggt aat gac aca ttg tcg cga tca tta cat gac ata atc ccg aag tgg	739	
Gly Asn Asp Thr Leu Ser Arg Ser Leu His Asp Ile Ile Pro Lys Trp		
200	205 210	
gct cgt cga gtt atc cgc gac gcg agc acg tat ccc gat agg gta cat	787	
Ala Arg Arg Val Ile Arg Asp Ala Ser Thr Tyr Pro Asp Arg Val His		
215	220 225	
ggt act cca ccg ctt ccg gca cgg ttg gaa ccc tgg gcg gaa aag ctc	835	
Gly Thr Pro Pro Leu Pro Ala Arg Leu Glu Pro Trp Ala Glu Lys Leu		
230	235 240 245	
act tca gat ccg gcc aca tgc cgc cac ctg att gaa gaa ttc ggg agt	883	
Thr Ser Asp Pro Ala Thr Cys Arg His Leu Ile Glu Glu Phe Gly Ser		
250	255 260	
cct gtg aat gta ctc cat tca ggt tct atg cct cgt aat ata aat gag	931	
Pro Val Asn Val Leu His Ser Gly Ser Met Pro Arg Asn Ile Asn Glu		
265	270 275	
ttg gtt gac gcc ggc att cag atg ggg gtg gat act cga ata ttt ttt	979	
Leu Val Asp Ala Gly Ile Gln Met Gly Val Asp Thr Arg Ile Phe Phe		
280	285 290	
gcc cgc aaa gcg aat aag ggt ctt acc ttc gtt gat gcc gtt aaa gac	1027	
Ala Arg Lys Ala Asn Lys Gly Leu Thr Phe Val Asp Ala Val Lys Asp		
295	300 305	
acc ggt cat ggt gta gat gta gcc agt gaa cga gag tta tct cag gtg	1075	
Thr Gly His Gly Val Asp Val Ala Ser Glu Arg Glu Leu Ser Gln Val		
310	315 320 325	
ctt aat cgt gga gtc cca gga gag cgg atc att cta tcc gca gct atc	1123	
Leu Asn Arg Gly Val Pro Gly Glu Arg Ile Ile Leu Ser Ala Ala Ile		
330	335 340	
aaa ccg gac aga cta ttg gca tta gcg atc gaa aat ggc gtg atc atc	1171	
Lys Pro Asp Arg Leu Leu Ala Leu Ala Ile Glu Asn Gly Val Ile Ile		
345	350 355	
tct gtg gat tcg cgt gat gaa tta gat cgc att tcg gct ttg gtt ggt	1219	

Ser	Val	Asp	Ser	Arg	Asp	Glu	Leu	Asp	Arg	Ile	Ser	Ala	Leu	Val	Gly		
		360					365					370					
gac	cgc	gtt	gca	cga	gtt	gcg	cct	aga	gta	gct	cca	gat	cct	gca	gtc	1267	
Asp	Arg	Val	Ala	Arg	Val	Ala	Pro	Arg	Val	Ala	Pro	Asp	Pro	Ala	Val		
		375				380					385						
tta	cct	cca	act	aga	ttt	ggt	gag	cgt	gct	gca	gac	tgg	ggt	aat	cgg	1315	
Leu	Pro	Pro	Thr	Arg	Phe	Gly	Glu	Arg	Ala	Ala	Asp	Trp	Gly	Asn	Arg		
		390			395				400					405			
ctt	acc	gag	gtg	ata	ccc	ggc	gtg	gat	att	gtg	ggt	ctt	cac	gtt	cac	1363	
Leu	Thr	Glu	Val	Ile	Pro	Gly	Val	Asp	Ile	Val	Gly	Leu	His	Val	His		
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ctc	cat	ggc	tat	gct	gca	aaa	gac	cgt	gct	ctg	gct	ctg	cag	gaa	tgt	1411	
Leu	His	Gly	Tyr	Ala	Ala	Lys	Asp	Arg	Ala	Leu	Ala	Leu	Gln	Glu	Cys		
			425					430					435				
tgc	caa	ctc	gtc	gat	tct	ctc	aga	gaa	tgc	ggg	cat	tcc	cca	cag	ttt	1459	
Cys	Gln	Leu	Val	Asp	Ser	Leu	Arg	Glu	Cys	Gly	His	Ser	Pro	Gln	Phe		
		440					445					450					
att	gac	ctt	gga	gga	ggg	gtg	cct	atg	agc	tac	att	gaa	tct	gag	gaa	1507	
Ile	Asp	Leu	Gly	Gly	Gly	Val	Pro	Met	Ser	Tyr	Ile	Glu	Ser	Glu	Glu		
	455					460					465						
gat	tgg	atc	cgt	tat	caa	tcc	gct	aaa	tct	gcg	act	tca	gcc	ggg	tat	1555	
Asp	Trp	Ile	Arg	Tyr	Gln	Ser	Ala	Lys	Ser	Ala	Thr	Ser	Ala	Gly	Tyr		
	470				475				480					485			
gcc	gaa	tcc	ttt	acg	tgg	aaa	gac	gat	ccg	tta	tct	aat	acg	tac	ccg	1603	
Ala	Glu	Ser	Phe	Thr	Trp	Lys	Asp	Asp	Pro	Leu	Ser	Asn	Thr	Tyr	Pro		
				490					495					500			
ttc	tat	cag	acc	cca	gtg	cgc	ggt	aat	tgg	ttg	aaa	gac	gtg	ctt	tct	1651	
Phe	Tyr	Gln	Thr	Pro	Val	Arg	Gly	Asn	Trp	Leu	Lys	Asp	Val	Leu	Ser		
		505						510					515				
aag	ggg	gta	gct	cag	atg	ctc	att	gac	cgg	gga	ttg	cgg	tta	cac	ata	1699	
Lys	Gly	Val	Ala	Gln	Met	Leu	Ile	Asp	Arg	Gly	Leu	Arg	Leu	His	Ile		
		520				525						530					
gag	cct	ggt	cga	agt	tta	cta	gat	ggg	tgt	ggc	gtc	act	ctt	gcc	gaa	1747	
Glu	Pro	Gly	Arg	Ser	Leu	Leu	Asp	Gly	Cys	Gly	Val	Thr	Leu	Ala	Glu		
	535					540					545						
gtt	gct	ttt	gtg	aaa	acc	cga	agt	gac	ggg	ttg	cct	cta	gtg	gga	ctg	1795	
Val	Ala	Phe	Val	Lys	Thr	Arg	Ser	Asp	Gly	Leu	Pro	Leu	Val	Gly	Leu		
	550				555				560					565			
gct	atg	aac	cga	acg	cag	tgc	cgg	act	aca	tcc	gat	gat	ttt	ctc	att	1843	
Ala	Met	Asn	Arg	Thr	Gln	Cys	Arg	Thr	Thr	Ser	Asp	Asp	Phe	Leu	Ile		
				570					575					580			
gat	ccc	ctg	cat	atc	act	gac	ggt	gat	gta	ggc	gag	gaa	atc	gaa	gca	1891	
Asp	Pro	Leu	His	Ile	Thr	Asp	Gly	Asp	Val	Gly	Glu	Glu	Ile	Glu	Ala		
			585					590					595				
tat	cta	gtg	ggt	gcc	tac	tgc	atc	gaa	gat	gag	ctg	att	tta	cgc	cgg	1939	
Tyr	Leu	Val	Gly	Ala	Tyr	Cys	Ile	Glu	Asp	Glu	Leu	Ile	Leu	Arg	Arg		

600	605	610	
cga atc cgc ttc ccg aga gga gtc aaa cca gga gat atc atc gga att			1987
Arg Ile Arg Phe Pro Arg Gly Val Lys Pro Gly Asp Ile Ile Gly Ile			
615	620	625	
cct aac acc gca gga tac ttc atg cat atc ttg gaa agt gca tcg cac			2035
Pro Asn Thr Ala Gly Tyr Phe Met His Ile Leu Glu Ser Ala Ser His			
630	635	640	645
caa atc ccg ttg gcg aaa aat gta gtg tgg ccg gag ggg cag tta gac			2083
Gln Ile Pro Leu Ala Lys Asn Val Val Trp Pro Glu Gly Gln Leu Asp			
650	655	660	
gat atc gat gcg gat taagacataa ccattcgcta atc			2121
Asp Ile Asp Ala Asp			
665			
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Asn Glu Gly Ser Glu Lys Ile Arg Ser Ala Lys Asp Leu Ser Glu Leu			
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Arg Thr Val Leu Lys Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly			
35	40	45	
Lys Lys Asp Glu Glu Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr			
50	55	60	
Pro Ser Ile Val Glu Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile			
65	70	75	80
Gly Phe Asp His Leu Ala Arg Glu Met Glu Arg Leu Ala Phe Gly Pro			
85	90	95	
Pro Ser Glu Ser Phe Glu Tyr Leu Gln Glu Leu Val Lys Ser Gly Val			
100	105	110	
Val Asp Ile Thr His Leu His Arg Gly Arg Glu Pro Leu Thr Asp Leu			
115	120	125	
Val Arg Glu Leu Glu Ile Thr Val Val Ile Asp Ala Val Leu Pro Pro			
130	135	140	
Pro Gly Val Val Pro Gly Thr Leu Val His Asn Leu Val Lys Glu Gly			
145	150	155	160
Tyr Ala Arg Met Arg Pro Gly Thr Arg Gly Leu Asp Val Ala Ala Asp			
165	170	175	
Gly Thr Val Gln Gly Gln Arg His Leu Ala Ala Val Gly Arg Met Thr			
180	185	190	

Glu Asp Val Val Leu Gly Asn Asp Thr Leu Ser Arg Ser Leu His Asp
 195 200 205
 Ile Ile Pro Lys Trp Ala Arg Arg Val Ile Arg Asp Ala Ser Thr Tyr
 210 215 220
 Pro Asp Arg Val His Gly Thr Pro Pro Leu Pro Ala Arg Leu Glu Pro
 225 230 235 240
 Trp Ala Glu Lys Leu Thr Ser Asp Pro Ala Thr Cys Arg His Leu Ile
 245 250 255
 Glu Glu Phe Gly Ser Pro Val Asn Val Leu His Ser Gly Ser Met Pro
 260 265 270
 Arg Asn Ile Asn Glu Leu Val Asp Ala Gly Ile Gln Met Gly Val Asp
 275 280 285
 Thr Arg Ile Phe Phe Ala Arg Lys Ala Asn Lys Gly Leu Thr Phe Val
 290 295 300
 Asp Ala Val Lys Asp Thr Gly His Gly Val Asp Val Ala Ser Glu Arg
 305 310 315 320
 Glu Leu Ser Gln Val Leu Asn Arg Gly Val Pro Gly Glu Arg Ile Ile
 325 330 335
 Leu Ser Ala Ala Ile Lys Pro Asp Arg Leu Leu Ala Leu Ala Ile Glu
 340 345 350
 Asn Gly Val Ile Ile Ser Val Asp Ser Arg Asp Glu Leu Asp Arg Ile
 355 360 365
 Ser Ala Leu Val Gly Asp Arg Val Ala Arg Val Ala Pro Arg Val Ala
 370 375 380
 Pro Asp Pro Ala Val Leu Pro Pro Thr Arg Phe Gly Glu Arg Ala Ala
 385 390 395 400
 Asp Trp Gly Asn Arg Leu Thr Glu Val Ile Pro Gly Val Asp Ile Val
 405 410 415
 Gly Leu His Val His Leu His Gly Tyr Ala Ala Lys Asp Arg Ala Leu
 420 425 430
 Ala Leu Gln Glu Cys Cys Gln Leu Val Asp Ser Leu Arg Glu Cys Gly
 435 440 445
 His Ser Pro Gln Phe Ile Asp Leu Gly Gly Gly Val Pro Met Ser Tyr
 450 455 460
 Ile Glu Ser Glu Glu Asp Trp Ile Arg Tyr Gln Ser Ala Lys Ser Ala
 465 470 475 480
 Thr Ser Ala Gly Tyr Ala Glu Ser Phe Thr Trp Lys Asp Asp Pro Leu
 485 490 495
 Ser Asn Thr Tyr Pro Phe Tyr Gln Thr Pro Val Arg Gly Asn Trp Leu
 500 505 510
 Lys Asp Val Leu Ser Lys Gly Val Ala Gln Met Leu Ile Asp Arg Gly

515		520		525
Leu Arg Leu His Ile Glu Pro Gly Arg Ser Leu Leu Asp Gly Cys Gly				
530		535		540
Val Thr Leu Ala Glu Val Ala Phe Val Lys Thr Arg Ser Asp Gly Leu				
545		550		555
Pro Leu Val Gly Leu Ala Met Asn Arg Thr Gln Cys Arg Thr Thr Ser				
	565		570	575
Asp Asp Phe Leu Ile Asp Pro Leu His Ile Thr Asp Gly Asp Val Gly				
	580		585	590
Glu Glu Ile Glu Ala Tyr Leu Val Gly Ala Tyr Cys Ile Glu Asp Glu				
	595		600	605
Leu Ile Leu Arg Arg Arg Ile Arg Phe Pro Arg Gly Val Lys Pro Gly				
	610		615	620
Asp Ile Ile Gly Ile Pro Asn Thr Ala Gly Tyr Phe Met His Ile Leu				
	625		630	635
Glu Ser Ala Ser His Gln Ile Pro Leu Ala Lys Asn Val Val Trp Pro				
	645		650	655
Glu Gly Gln Leu Asp Asp Ile Asp Ala Asp				
	660		665	

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 <223> RXA01393

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 agtaaaatga ttggttctta acatggttta atatagcttc atg aac ccc att caa 115
 Met Asn Pro Ile Gln
 1 5
 ctg gac act ttg ctc tca atc att gat gaa ggc agc ttc gaa ggc gcc 163
 Leu Asp Thr Leu Leu Ser Ile Ile Asp Glu Gly Ser Phe Glu Gly Ala
 10 15 20
 tcc tta gcc ctt tcc att tcc ccc tcg gcg gtg agt cag cgc gtt aaa 211
 Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys
 25 30 35
 gct ctc gag cat cac gtg ggt cga gtg ttg gta tcg cgc acc caa ccg 259
 Ala Leu Glu His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro
 40 45 50
 gcc aaa gca acc gaa gcg ggt gaa gtc ctt gtg caa gca gcg cgg aaa 307
 Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys

55	60	65	
atg gtg ttg ctg caa gca gaa act aaa gcg caa cta tct gga cgc ctt			355
Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln Leu Ser Gly Arg Leu			
70	75	80	85
gct gaa atc ccg tta acc atc gcc atc aac gca gat tcg cta tcc aca			403
Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala Asp Ser Leu Ser Thr			
	90	95	100
tgg ttt cct ccc gtg ttc aac gag gta gct tct tgg ggt gga gca acg			451
Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr			
	105	110	115
ctc acg ctg cgc ttg gaa gat gaa gcg cac aca tta tcc ttg ctg cgg			499
Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr Leu Ser Leu Leu Arg			
	120	125	130
cgt gga gat gtt tta gga gcg gta acc cgt gaa gct aat ccc gtg gcg			547
Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala			
	135	140	145
gga tgt gaa gta gta gaa ctt gga acc atg cgc cac ttg gcc att gca			595
Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala			
	150	155	160
acc ccc tca ttg cgg gat gcc tac atg gtt gat ggg aaa cta gat tgg			643
Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp			
	170	175	180
gct gcg atg ccc gtc tta cgc ttc ggt ccc aaa gat gtg ctt caa gac			691
Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp			
	185	190	195
cgt gac ctg gac ggg cgc gtc gat ggt cct gtg ggg cgc agg cgc gta			739
Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val Gly Arg Arg Val			
	200	205	210
tcc att gtc ccg tcg gcg gaa ggt ttt ggt gag gca att cgc cga ggc			787
Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu Ala Ile Arg Arg Gly			
	215	220	225
ctt ggt tgg gga ctt ctt ccc gaa acc caa gct gct ccc atg cta aaa			835
Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala Ala Pro Met Leu Lys			
	230	235	240
gca gga gaa gtg atc ctc ctc gat gag ata ccc att gac aca ccg atg			883
Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro Ile Asp Thr Pro Met			
	250	255	260
tat tgg caa cga tgg cgc ctg gaa tct aga tct cta gct aga ctc aca			931
Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser Leu Ala Arg Leu Thr			
	265	270	275
gac gcc gtc gtt gat gca gca atc gag gga ttg cgg cct tagttacttc			980
Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu Arg Pro			
	280	285	290
tgaaaagggtt cag			993

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<211> 290

<212> PRT

<213> Corynebacterium glutamicum

<400> 48

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Ser Phe Glu Gly Ala Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val
 20 25 30

Ser Gln Arg Val Lys Ala Leu Glu His His Val Gly Arg Val Leu Val
 35 40 45

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

Gln Ala Ala Arg Lys Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln
 65 70 75 80

Leu Ser Gly Arg Leu Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala
 85 90 95

Asp Ser Leu Ser Thr Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser
 100 105 110

Trp Gly Gly Ala Thr Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr
 115 120 125

Leu Ser Leu Leu Arg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu
 130 135 140

Ala Asn Pro Val Ala Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg
 145 150 155 160

His Leu Ala Ile Ala Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp
 165 170 175

Gly Lys Leu Asp Trp Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys
 180 185 190

Asp Val Leu Gln Asp Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val
 195 200 205

Gly Arg Arg Arg Val Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu
 210 215 220

Ala Ile Arg Arg Gly Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala
 225 230 235 240

Ala Pro Met Leu Lys Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro
 245 250 255

Ile Asp Thr Pro Met Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser
 260 265 270

Leu Ala Arg Leu Thr Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu
 275 280 285

Arg Pro

Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro Leu Leu Cys Phe Ile	170	175	180	
atc ctt gtt gca ttc ttg ggc ttt agc tgg gag aag ttc act gtt gat	185	190	195	691
Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu Lys Phe Thr Val Asp				
tta tgg gcg cgt gat ggt ggc gtg ggc agc att ttt gat cag gtg cgc	200	205	210	739
Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile Phe Asp Gln Val Arg				
ggc atc atg gtg tac acc gtg tgg gtg ttc atc ggt atc gaa ggt gca	215	220	225	787
Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile Gly Ile Glu Gly Ala				
tcg gta tat tcc cgc cag gca cgc tca cgc agt gat gtc agc cga gct	230	235	240	835
Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser Asp Val Ser Arg Ala				
acc gtg att ggt ttt gtg gct gtt ctc ctt ttg ctg gtg tcg att tct	250	255	260	883
Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu Leu Val Ser Ile Ser				
tcg ctg agc ttc ggt gta ctg acc caa caa gag ctc gct gcg tta cca	265	270	275	931
Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu Leu Ala Ala Leu Pro				
gat aat tcc atg gcg tcg gtg ctc gaa gct gtt gtt ggt cca tgg ggt	280	285	290	979
Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val Val Gly Pro Trp Gly				
gcc gca ttg att tcg ttg ggt ctg tgt ctt tcg gtt ctt ggg gcc tat	295	300	305	1027
Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser Val Leu Gly Ala Tyr				
gtg tcc tgg cag atg ctc tgc gca gaa cca ctg gcg ttg atg gca atg	310	315	320	1075
Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu Ala Leu Met Ala Met				
gat ggc ctc att cca agc aaa atc ggg gcc atc aac agc cgc ggt gct	330	335	340	1123
Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile Asn Ser Arg Gly Ala				
gcc tgg atg gct cag ctg atc tcc acc atc gtg att cag att ttc atc	345	350	355	1171
Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val Ile Gln Ile Phe Ile				
atc att ttc ttc ctc aac gag acc acc tac gtc tcc atg gtg caa ttg	360	365	370	1219
Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val Ser Met Val Gln Leu				
gct acc aac cta tac ttg gtg cct tac ctg ttc tot gcc ttt tat ctg	375	380	385	1267
Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe Ser Ala Phe Tyr Leu				
gtc atg ctg gca aca cgt gga aaa gga atc acc cac cca cat gcc ggc	390	395	400	1315
Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr His Pro His Ala Gly				
aca cgt ttt gat gat tcc ggt cca gag ata tcc cgc cga gaa aac cgc				1363
Thr Arg Phe Asp Asp Ser Gly Pro Glu Ile Ser Arg Arg Glu Asn Arg				

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                410                415                420
aaa cac ctc atc gtc ggt tta gta gca acg gtg tat tca gtg tgg ctg 1411
Lys His Leu Ile Val Gly Leu Val Ala Thr Val Tyr Ser Val Trp Leu
                425                430                435

ttt tac gct gca gaa ccg cag ttt gtc ctc ttc gga gcc atg gcg atg 1459
Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe Gly Ala Met Ala Met
                440                445                450

ctt ccc ggc tta atc ccc tat gtg tgg aca agg att tat cgt ggc gaa 1507
Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg Ile Tyr Arg Gly Glu
                455                460                465

cag gtg ttt aac cgc ttt gaa atc ggc gtg gtt gtt gtc ctg gtc gtt 1555
Gln Val Phe Asn Arg Phe Glu Ile Gly Val Val Val Val Leu Val Val
                470                475                480                485

gct gcc agc gcg ggc gtt att ggt ttg gtc aac gga tca cta tcg ctt 1603
Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn Gly Ser Leu Ser Leu
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taaacaccga aaccttcctg cta 1626

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<213> Corynebacterium glutamicum

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Thr Val Gly Ala Gly Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val
                35                40                45

Ala Gly Pro Gly Ala Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly
                50                55                60

Met Leu Ser Val Ala Phe Val Phe His Val Leu Ala Arg Arg Lys Pro
  65                70                75                80

His Leu Asp Ser Gly Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp
                85                90                95

Tyr Val Gly Phe Ser Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile
                100                105                110

Ala Gln Val Gly Tyr Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr
                115                120                125

Val Pro Leu Phe Ser Gln Asp His Pro Phe Val Ser Ala Leu Ala Val
  130                135                140

Ser Ala Leu Thr Trp Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser
  145                150                155                160

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

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Gly Ser Leu Ser Leu
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<223> RXA01394

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                                   Met Glu Ile Phe Ile
                                   1 5

aca ggt ctg ctt ttg ggg gcc agt ctt tta ctg tcc atc gga ccg cag 163
Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Leu Ser Ile Gly Pro Gln
                                   10 15 20

aat gta ctg gtg att aaa caa gga att aag cgc gaa gga ctc att gcg 211
Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg Glu Gly Leu Ile Ala
                                   25 30 35

gtt ctt ctc gtg tgt tta att tct gac gtc ttt ttg ttc atc gcc ggc 259
Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe Leu Phe Ile Ala Gly
                                   40 45 50

acc ttg ggc gtt gat ctt ttg tcc aat gcc gcg ccg atc gtg ctc gat 307
Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala Pro Ile Val Leu Asp
                                   55 60 65

att atg cgc tgg ggt ggc atc gct tac ctg tta tgg ttt gcc gtc atg 355
Ile Met Arg Trp Gly Gly Ile Ala Tyr Leu Leu Trp Phe Ala Val Met
                                   70 75 80 85

gca gcg aaa gac gcc atg aca aac aag gtg gaa gcg cca cag atc att 403
Ala Ala Lys Asp Ala Met Thr Asn Lys Val Glu Ala Pro Gln Ile Ile
                                   90 95 100

gaa gaa aca gaa cca acc gtg ccc gat gac acg cct ttg ggc ggt tcg 451
Glu Glu Thr Glu Pro Thr Val Pro Asp Asp Thr Pro Leu Gly Gly Ser
                                   105 110 115

gcg gtg gcc act gac acg cgc aac cgg gtg cgg gtg gag gtg agc gtc 499
Ala Val Ala Thr Asp Thr Arg Asn Arg Val Arg Val Glu Val Ser Val
                                   120 125 130

gat aag cag cgg gtt tgg gta aag ccc atg ttg atg gca atc gtg ctg 547
Asp Lys Gln Arg Val Trp Val Lys Pro Met Leu Met Ala Ile Val Leu
                                   135 140 145

acc tgg ttg aac ccg aat gcg tat ttg gac gcg ttt gtg ttt atc gcc 595
Thr Trp Leu Asn Pro Asn Ala Tyr Leu Asp Ala Phe Val Phe Ile Gly

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150                      155                      160                      165
ggc gtc ggc gcg caa tac ggc gac acc gga cgg tgg att ttc gcc gct 643
Gly Val Gly Ala Gln Tyr Gly Asp Thr Gly Arg Trp Ile Phe Ala Ala
                      170                      175                      180

ggc gcg ttc gcg gca agc ctg atc tgg ttc ccg ctg gtg ggt ttc ggc 691
Gly Ala Phe Ala Ala Ser Leu Ile Trp Phe Pro Leu Val Gly Phe Gly
                      185                      190                      195

gca gca gca ttg tca cgc ccg ctg tcc agc ccc aag gtg tgg cgc tgg 739
Ala Ala Ala Leu Ser Arg Pro Leu Ser Ser Pro Lys Val Trp Arg Trp
                      200                      205                      210

atc aac gtc gtc gtg gca gtt gtg atg acc gca ttg gcc atc aaa ctg 787
Ile Asn Val Val Val Ala Val Val Met Thr Ala Leu Ala Ile Lys Leu
                      215                      220                      225

atg ttg atg ggt tagttttcgc gggttttgga atc 822
Met Leu Met Gly
230

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<210> 52

<211> 233

<212> PRT

<213> Corynebacterium glutamicum

<400> 52

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Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Leu
  1                      5                      10                      15

Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg
                      20                      25                      30

Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe
                      35                      40                      45

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

Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala Tyr Leu Leu
                      65                      70                      75                      80

Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn Lys Val Glu
                      85                      90                      95

Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro Asp Asp Thr
                      100                      105                      110

Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn Arg Val Arg
                      115                      120                      125

Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys Pro Met Leu
                      130                      135                      140

Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr Leu Asp Ala
                      145                      150                      155                      160

Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp Thr Gly Arg
                      165                      170                      175

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<400> 53																		
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ttta	accccc	aaatg	aggga	agaag	gtaac	cttga	actct	atg	agc	aca	ggt	tta	115					
								Met	Ser	Thr	Gly	Leu	5					
								1										
aca	gct	aag	acc	gga	gta	gag	cac	ttc	ggc	acc	gtt	gga	gta	gca	atg	163		
Thr	Ala	Lys	Thr	Gly	Val	Glu	His	Phe	Gly	Thr	Val	Gly	Val	Ala	Met			
				10					15					20				
gtt	act	cca	ttc	acg	gaa	tcc	gga	gac	atc	gat	atc	gct	gct	ggc	cgc	211		
Val	Thr	Pro	Phe	Thr	Glu	Ser	Gly	Asp	Ile	Asp	Ile	Ala	Ala	Gly	Arg			
			25					30					35					
gaa	gtc	gog	gct	tat	ttg	gtt	gat	aag	ggc	ttg	gat	tct	ttg	gtt	ctc	259		
Glu	Val	Ala	Ala	Tyr	Leu	Val	Asp	Lys	Gly	Leu	Asp	Ser	Leu	Val	Leu			
		40					45					50						
gcg	ggc	acc	act	ggt	gaa	tcc	cca	acg	aca	acc	gcc	gct	gaa	aaa	cta	307		
Ala	Gly	Thr	Thr	Gly	Glu	Ser	Pro	Thr	Thr	Thr	Ala	Ala	Glu	Lys	Leu			
	55					60					65							
gaa	ctg	ctc	aag	gcc	gtt	cgt	gag	gaa	gtt	ggg	gat	cgg	gcg	aag	ctc	355		
Glu	Leu	Leu	Lys	Ala	Val	Arg	Glu	Glu	Val	Gly	Asp	Arg	Ala	Lys	Leu			
70					75					80					85			
atc	gcc	ggt	gtc	gga	acc	aac	aac	acg	cgg	aca	tct	gtg	gaa	ctt	gcg	403		
Ile	Ala	Gly	Val	Gly	Thr	Asn	Asn	Thr	Arg	Thr	Ser	Val	Glu	Leu	Ala			
				90					95					100				
gaa	gct	gct	gct	tct	gct	ggc	gca	gac	ggc	ctt	tta	gtt	gta	act	cct	451		
Glu	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Asp	Gly	Leu	Leu	Val	Val	Thr	Pro			
			105					110					115					
tat	tac	tcc	aag	ccg	agc	caa	gag	gga	ttg	ctg	gcg	cac	ttc	ggt	gca	499		
Tyr	Tyr	Ser	Lys	Pro	Ser	Gln	Glu	Gly	Leu	Leu	Ala	His	Phe	Gly	Ala			

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120          125          130
att gct gca gca aca gag gtt cca att tgt ctc tat gac att cct ggt 547
Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu Tyr Asp Ile Pro Gly
135          140          145

cgg tca ggt att cca att gag tct gat acc atg aga cgc ctg agt gaa 595
Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met Arg Arg Leu Ser Glu
150          155          160

tta cct acg att ttg gcg gtc aag gac gcc aag ggt gac ctc gtt gca 643
Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys Gly Asp Leu Val Ala
170          175          180

gcc acg tca ttg atc aaa gaa acg gga ctt gcc tgg tat tca ggc gat 691
Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala Trp Tyr Ser Gly Asp
185          190          195

gac cca cta aac ctt gtt tgg ctt gct ttg ggc gga tca ggt ttc att 739
Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly Gly Ser Gly Phe Ile
200          205          210

tcc gta att gga cat gca gcc ccc aca gca tta cgt gag ttg tac aca 787
Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu Arg Glu Leu Tyr Thr
215          220          225

agc ttc gag gaa ggc gac ctc gtc cgt gcg cgg gaa atc aac gcc aaa 835
Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg Glu Ile Asn Ala Lys
230          235          240

cta tca ccg ctg gta gct gcc caa ggt cgc ttg ggt gga gtc agc ttg 883
Leu*Ser Pro Leu Val Ala Ala Gln Gly Arg Leu Gly Gly Val Ser Leu
250          255          260

gca aaa gct gct ctg cgt ctg cag ggc atc aac gta gga gat cct cga 931
Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn Val Gly Asp Pro Arg
265          270          275

ctt cca att atg gct cca aat gag cag gaa ctt gag gct ctc cga gaa 979
Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu Glu Ala Leu Arg Glu
280          285          290

gac atg aaa aaa gct gga gtt cta taaatatgaa tgattccoga aat 1026
Asp Met Lys Lys Ala Gly Val Leu
295          300

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<210> 54

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 54

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Met Ser Thr Gly Leu Thr Ala Lys Thr Gly Val Glu His Phe Gly Thr
1          5          10          15

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Val Gly Val Ala Met Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp
20          25          30

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Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu
35          40          45

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

<210> 55

<211> 1071

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1048)

<223> RXS02021

<400> 55

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aaaccttagt taaaacatga tggaagcggg cgattaaaaa atg agt gaa aac att 115
                                         Met Ser Glu Asn Ile
                                         1 5
cgc gga gcc caa gca gtt gga atc gca aat atc gcc atg gac ggg acc 163
Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile Ala Met Asp Gly Thr
                        10 15 20
atc ctg gac acg tgg tac cca gaa ccc caa att ttc aac ccg gat cag 211
Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile Phe Asn Pro Asp Gln
                        25 30 35
tgg gct gaa cgc tac cca ttg gaa gtg ggc acc aca cgc ctc gga gca 259
Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr Thr Arg Leu Gly Ala
                        40 45 50
aac gaa ctc acc cca cgg atg ctg cag ttg gta aaa ctg gac caa gat 307
Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val Lys Leu Asp Gln Asp
                        55 60 65
cgc ctc gtc gaa cag gta gca gtc cgc acc gtt atc ccc gat ctg tct 355
Arg Leu Val Glu Gln Val Ala Val Arg Thr Val Ile Pro Asp Leu Ser
                        70 75 80 85
caa cct cca gta gac gcg cac gat gtt tac ctg cgc ctc cac ctg ctt 403
Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu Arg Leu His Leu Leu
                        90 95 100
tcc cac cgg ctg gtc cgc ccc cac gaa atg cac atg caa aac acc ttg 451
Ser His Arg Leu Val Arg Pro His Glu Met His Met Gln Asn Thr Leu
                        105 110 115
gag ctg ctg tcc gac gtg gtg tgg aca aac aag ggc cct tgc ctt cct 499
Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys Gly Pro Cys Leu Pro
                        120 125 130
gaa aac ttt gag tgg gtg cgt ggt gct ctg cgg tcc cgc gga ctc atc 547
Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg Ser Arg Gly Leu Ile
                        135 140 145
cac gtc tac tgt gtg gac cgt ctt ccc cgc atg gtc gac tat gtg gtt 595
His Val Tyr Cys Val Asp Arg Leu Pro Arg Met Val Asp Tyr Val Val
                        150 155 160 165
ccc cct gga gtc cgc atc tcc gaa gca gaa cgc gtg cgc cta ggt gca 643
Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg Val Arg Leu Gly Ala
                        170 175 180
tac ctt gct ccg ggt acc tct gtg ctg cgt gaa ggt ttc gtg tct ttc 691
Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu Gly Phe Val Ser Phe
                        185 190 195
aac tcc ggc acc ttg ggt gcc gca aag gtg gaa ggc cgc ctg agt tcc 739
Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu Gly Arg Leu Ser Ser
                        200 205 210
ggt gtg gtc atc ggt gaa ggt tcc gag att gga ctg tct tct act att 787
Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly Leu Ser Ser Thr Ile
                        215 220 225

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cag tcc ccg aga gat gaa cag cgc cgc cgt ttg ccg ttg agc atc ggc 835
 Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu Pro Leu Ser Ile Gly
 230 235 240 245

caa aac tgc aac ttt ggt gtc agc tcc gga atc atc gga gtc agt ctg 883
 Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile Ile Gly Val Ser Leu
 250 255 260

gga gac aat tgc gac atc gga aat aac att gtc ttg gat gga gat acc 931
 Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val Leu Asp Gly Asp Thr
 265 270 275

ccc att tgg ttc gca gcc gat gag gag tta cgc act atc gac tcc atc 979
 Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg Thr Ile Asp Ser Ile
 280 285 290

gaa ggc caa gca aat tgg tca atc aag cgt gaa tcc ggc ttc cat gag 1027
 Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu Ser Gly Phe His Glu
 295 300 305

cca gtt gcc cgc ctc aaa gct tgacccattt tcataaccag tgc 1071
 Pro Val Ala Arg Leu Lys Ala
 310 315

<210> 56
 <211> 316
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 56
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 20 25 30

Phe Asn Pro Asp Gln Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr
 35 40 45

Thr Arg Leu Gly Ala Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val
 50 55 60

Lys Leu Asp Gln Asp Arg Leu Val Glu Gln Val Ala Val Arg Thr Val
 65 70 75 80

Ile Pro Asp Leu Ser Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu
 85 90 95

Arg Leu His Leu Leu Ser His Arg Leu Val Arg Pro His Glu Met His
 100 105 110

Met Gln Asn Thr Leu Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys
 115 120 125

Gly Pro Cys Leu Pro Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg
 130 135 140

Ser Arg Gly Leu Ile His Val Tyr Cys Val Asp Arg Leu Pro Arg Met
 145 150 155 160

Val Asp Tyr Val Val Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg
 165 170 175

Val Arg Leu Gly Ala Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu
 180 185 190

Gly Phe Val Ser Phe Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu
 195 200 205

Gly Arg Leu Ser Ser Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly
 210 215 220

Leu Ser Ser Thr Ile Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu
 225 230 235 240

Pro Leu Ser Ile Gly Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile
 245 250 255

Ile Gly Val Ser Leu Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val
 260 265 270

Leu Asp Gly Asp Thr Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg
 275 280 285

Thr Ile Asp Ser Ile Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu
 290 295 300

Ser Gly Phe His Glu Pro Val Ala Arg Leu Lys Ala
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<210> 57

<211> 1296

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> {101}..(1273)

<223> RXS02157

<400> 57

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caccgttttt agaaaagacg acaaggatgg ggaactgtaa atg agc acg ctg gaa 115
 Met Ser Thr Leu Glu
 1 5

act tgg cca cag gtc att att aat acg tac ggc acc cca cca gtt gag 163
 Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu
 10 15 20

ctg gtg tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc 211
 Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val
 25 30 35

tac atc gac ttg ctc gcg ggc atc gca gtc aac gcg ttg ggc cac gcc 259
 Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala
 40 45 50

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

Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala
 295 300 305
 cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt 1075
 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val
 310 315 320 325
 gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc 1123
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg
 330 335 340
 gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att 1171
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile
 345 350 355
 ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg 1219
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val
 360 365 370
 atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca 1267
 Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr
 375 380 385
 atc gca taaaggactc aaacttatga ctt 1296
 Ile Ala
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 <213> Corynebacterium glutamicum
 <400> 58
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 20 25 30
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 35 40 45
 Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
 50 55 60
 Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
 65 70 75 80
 Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
 85 90 95
 Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
 100 105 110
 Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg
 115 120 125
 Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu
 130 135 140

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

<210> 59

<211> 1008

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(985)

<223> RXC00733

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	Met Ser Asn Thr Ala	
	1 5	
ggc ccc cgc ggg cgt tcc cat cag gca gac gcc gcg ccg aat caa aag	163	
Gly Pro Arg Gly Arg Ser His Gln Ala Asp Ala Ala Pro Asn Gln Lys		
	10 15 20	
gca cag aat ttc gga cca tct gcc aaa agg ctt ttc gga att cta ggc	211	
Ala Gln Asn Phe Gly Pro Ser Ala Lys Arg Leu Phe Gly Ile Leu Gly		
	25 30 35	
cat gac cgt aac acc tta att ttt gtt atc ttc cta gcc gtc ctg agc	259	
His Asp Arg Asn Thr Leu Ile Phe Val Ile Phe Leu Ala Val Leu Ser		
	40 45 50	
gtt gga ctt acc gtc ttg ggc cca tgg ttg ctg ggt aaa gcc acc aac	307	
Val Gly Leu Thr Val Leu Gly Pro Trp Leu Leu Gly Lys Ala Thr Asn		
	55 60 65	
gtg gtg ttt gaa gga ttc cta tct aag cgc atg ccg gct ggt gcg tca	355	
Val Val Phe Glu Gly Phe Leu Ser Lys Arg Met Pro Ala Gly Ala Ser		
	70 75 80 85	
aag gaa gat atc atc gcg cag ttg cag gct gca ggt aaa cat aat cag	403	
Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala Gly Lys His Asn Gln		
	90 95 100	
gct tcc atg atg gaa gac atg aac ctt gtt cca gcc tca ggc att gat	451	
Ala Ser Met Met Glu Asp Met Asn Leu Val Pro Gly Ser Gly Ile Asp		
	105 110 115	
ttt gaa aaa tta gcc atg atc ctc gga ctg gtg atc ggt gct tat ctc	499	
Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val Ile Gly Ala Tyr Leu		
	120 125 130	
atc ggt agc ctg ttg tcg ttg ttc cag gcg ccg atg ctc aac cgc atc	547	
Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg Met Leu Asn Arg Ile		
	135 140 145	
gtg caa agt gcc atg cac cgg ctg cgc atg gag gtg gag gaa aaa atc	595	
Val Gln Ser Ala Met His Arg Leu Arg Met Glu Val Glu Glu Lys Ile		
	150 155 160 165	
cac cgc cta ccg ctg agc tat ttc gat tcc atc aaa cgt ggt gat ctg	643	
His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile Lys Arg Gly Asp Leu		
	170 175 180	
ctt agc cgt gtg acc aac gat gtg gat aat atc ggt caa tcc ctg caa	691	
Leu Ser Arg Val Thr Asn Asp Val Asp Asn Ile Gly Gln Ser Leu Gln		
	185 190 195	
caa acc ttg tca cag gcg atc act tcc cta ctg acc gtc atc ggt gtg	739	
Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu Thr Val Ile Gly Val		
	200 205 210	
ttg gtg atg atg ttt atc atc tcc cca ctg ctc gca ctc gtg gcg ctg	787	
Leu Val Met Met Phe Ile Ile Ser Pro Leu Leu Ala Leu Val Ala Leu		
	215 220 225	

gta tcc att ccg gtc acc atc gtg gtc act gtg gtg gtt gcg agc cgt 835
 Val Ser Ile Pro Val Thr Ile Val Val Thr Val Val Val Ala Ser Arg
 230 235 240 245

tcc cag aaa ctc ttt gcg gaa cag tgg aag cag acc ggt att ttg aat 883
 Ser Gln Lys Leu Phe Ala Glu Gln Trp Lys Gln Thr Gly Ile Leu Asn
 250 255 260

gcg cgc ctg gag gaa acc tac tct ggc cac gcc gtg gtt aag gtt ttc 931
 Ala Arg Leu Glu Glu Thr Tyr Ser Gly His Ala Val Val Lys Val Phe
 265 270 275

gga cac caa aag gat gtt caa gaa gca ttc gag gaa gaa aat caa gct 979
 Gly His Gln Lys Asp Val Gln Glu Ala Phe Glu Glu Glu Asn Gln Ala
 280 285 290

tgt gta taaggccagc tttggtgccc agt 1008
 Cys Val
 295

<210> 60
 <211> 295
 <212> PRT
 <213> Corynebacterium glutamicum

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

	180		185		190										
Gly	Gln	Ser	Leu	Gln	Gln	Thr	Leu	Ser	Gln	Ala	Ile	Thr	Ser	Leu	Leu
	195						200					205			
Thr	Val	Ile	Gly	Val	Leu	Val	Met	Met	Phe	Ile	Ile	Ser	Pro	Leu	Leu
	210					215					220				
Ala	Leu	Val	Ala	Leu	Val	Ser	Ile	Pro	Val	Thr	Ile	Val	Val	Thr	Val
	225				230					235					240
Val	Val	Ala	Ser	Arg	Ser	Gln	Lys	Leu	Phe	Ala	Glu	Gln	Trp	Lys	Gln
			245						250					255	
Thr	Gly	Ile	Leu	Asn	Ala	Arg	Leu	Glu	Glu	Thr	Tyr	Ser	Gly	His	Ala
			260					265					270		
Val	Val	Lys	Val	Phe	Gly	His	Gln	Lys	Asp	Val	Gln	Glu	Ala	Phe	Glu
		275					280					285			
Glu	Glu	Asn	Gln	Ala	Cys	Val									
	290					295									

<210> 61
 <211> 426
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(426)
 <223> RXC00861

<400> 61
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 Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
 1 5 10 15

cct atg gct gcg ctg tct cgc atg gcg cgt cgt gag cac cga cag atc 96
 Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
 20 25 30

act gtc cgt gat gga gac ttg att atc ctt tct tcc tcc ctg gtt cca 144
 Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
 35 40 45

ggt aac gaa gaa gca gtg ttc ggt gtc atc aac atg ctg gct cag atc 192
 Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
 50 55 60

ggt gca act gtt gtt acc ggt cgc gac gcc aag gtg cac acc tcg ggc 240
 Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
 65 70 75 80

cac ggc tac tcc gga gag ctg ttg ttc ttg tac aac gcc gct cgt ccg 288
 His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
 85 90 95

aag aac gct atg cct gtc cac ggc gag tgg cgc cac ctg cgc gcc aac 336
 Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn

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          100              105              110
aag gaa ctg gct atc tcc act ggt gtt aac cgc gac aac gtt gtg ctt 384
Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu
      115              120              125

gca caa aac ggt gtt gtg gtt gat atg gtc aac ggt cgc gca 426
Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
      130              135              140

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<210> 62

<211> 142

<212> PRT

<213> Corynebacterium glutamicum

<400> 62

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

Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
      20              25              30

Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
      35              40              45

Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
      50              55              60

Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
      65              70              75              80

His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
      85              90              95

Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
      100              105              110

Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu
      115              120              125

Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
      130              135              140

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<210> 63

<211> 1066

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1066)

<223> RXC00866

<400> 63

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ctctccgaga agacatgaaa aaagctggag ttctataaat atg aat gat tcc cga 115
Met Asn Asp Ser Arg
      1              5

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

ttc acc ttg gct ctg att gca gct aag tgt aag gaa cac cgt cag cgt 883
 Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys Glu His Arg Gln Arg
 250 255 260
 ccg aag ctg atc gag gtc aac gag cag tcc aat gag gac cgc gga ccg 931
 Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn Glu Asp Arg Gly Pro
 265 270 275
 ttc aac att cgc ttc tgg gct gtt aac cac tcc atc cca gac tgc ctt 979
 Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser Ile Pro Asp Cys Leu
 280 285 290
 ggt ctt gct atc aag act cct gct ggt ttg gtc atc cac acc ggt gac 1027
 Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val Ile His Thr Gly Asp
 295 300 305
 atc aag ctg gat cag act cct cct gat gga cgc cca act 1066
 Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg Pro Thr
 310 315 320

<210> 64

<211> 322

<212> PRT

<213> Corynebacterium glutamicum

<400> 64

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

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

<210> 65
 <211> 1527
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1504)
 <223> RXC02095

<400> 65
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 tactcccca acagggtcaa aaatactgaa aggtctacgc atg aaa act gag caa 115
 Met Lys Thr Glu Gln
 1 5
 tcc caa aaa gca caa tta gcc cct aag aaa gca cct gaa aag cca caa 163
 Ser Gln Lys Ala Gln Leu Ala Pro Lys Lys Ala Pro Glu Lys Pro Gln
 10 15 20
 cgc atc cgc caa ctt att tcc gtg gcg tgg cag cga cct tgg ctc acc 211
 Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln Arg Pro Trp Leu Thr
 25 30 35
 tca ttc acc gta atc agc gct tta gct gca acg ttg ttt gaa ctt aca 259
 Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr Leu Phe Glu Leu Thr
 40 45 50
 ctt cct ctt ttg acc ggt ggc gcc atc gat atc gcg ctc gga aat acc 307
 Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile Ala Leu Gly Asn Thr

55	60	65	
gga gat act tta acc act gac ctg ctg gac cgg ttc act ccg agt gga Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg Phe Thr Pro Ser Gly 70 75 80 85			355
tta agc gtg ttg acc agc gtc att gcc ctt atc gtg ctt ctc gcg ttg Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile Val Leu Leu Ala Leu 90 95 100			403
ctt cgc tat gcc agt caa ttt gga cgg cga tac acc gca ggc aag ctc Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr Thr Ala Gly Lys Leu 105 110 115			451
agc atg ggg gta cag cat gat gtc cgg ctt aaa acg atg cgc tca ttg Ser Met Gly Val Gln His Asp Val Arg Leu Lys Thr Met Arg Ser Leu 120 125 130			499
cag aac ctc gat ggg cca ggt cag gac tct att cgc aca ggc caa gta Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile Arg Thr Gly Gln Val 135 140 145			547
gtc agt cgg tcc att tcg gat atc aac atg gtg caa agc ctt gtg gcg Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val Gln Ser Leu Val Ala 150 155 160 165			595
atg ttg ccg atg ttg atc gga aat gtg gtc aag ctt gtg ctc act ttg Met Leu Pro Met Leu Ile Gly Asn Val Val Lys Leu Val Leu Thr Leu 170 175 180			643
gtg atc atg ctg gct att tcc ccg ccg ctg acc atc atc gct gca gtg Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr Ile Ile Ala Ala Val 185 190 195			691
ttg gtg cct ttg ctg ttg tgg gcc gtg gcc tat tcg cga aaa gcg ctt Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr Ser Arg Lys Ala Leu 200 205 210			739
ttt gcg tcc acg tgg tcg gcc cag caa aag gct gcg gat ctg acc act Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala Ala Asp Leu Thr Thr 215 220 225			787
cat gtg gaa gaa act gtc acg ggt atc cgc gtg gtc aag gca ttt gcg His Val Glu Glu Thr Val Thr Gly Ile Arg Val Val Lys Ala Phe Ala 230 235 240 245			835
cag gaa gac cgc gag acc gac aaa ttg gat ctc acc gca cgt gag tta Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu Thr Ala Arg Glu Leu 250 255 260			883
ttt gcc cag cgc atg cgc act gca cgt ctg acg gca aag ttc atc ccc Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr Ala Lys Phe Ile Pro 265 270 275			931
atg gtt gag cag ctt ccg cag ctt gct ttg gtg gtc aac att gtt ggc Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val Val Asn Ile Val Gly 280 285 290			979
ggt ggc tat ttg gcc atg act ggt cac atc acg gtg ggc acg ttt gtg Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr Val Gly Thr Phe Val 295 300 305			1027

gcg ttt tct tcc tat ctc act agc ttg tgc gcg gtg gct agg tcc ctg 1075
 Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala Val Ala Arg Ser Leu
 310 315 320 325
 tcg ggc atg ctc atg cgc gtg cag ttg gcg ctg tct tct gtg gag cgc 1123
 Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu Ser Ser Val Glu Arg
 330 335 340
 atc ttt gaa gtc att gat ctt cag cct gaa cgc acc gat cct gca cac 1171
 Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg Thr Asp Pro Ala His
 345 350 355
 ccc ctg tca ctt ccc gac act ccc ctg ggt ctg tgc ttc aac aac gta 1219
 Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu Ser Phe Asn Asn Val
 360 365 370
 gat ttc cgt ggg att ctc aac ggt ttt gag ctg ggt gtt cag gcc ggt 1267
 Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu Gly Val Gln Ala Gly
 375 380 385
 gaa acc gtt gtg ttg gtg ggc cct cca ggt tca ggc aag acc atg gct 1315
 Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser Gly Lys Thr Met Ala
 390 395 400 405
 gtg cag ctt gct gga aac ttt tat caa cca gac agc ggc cac atc gcc 1363
 Val Gln Leu Ala Gly Asn Phe Tyr Gln Pro Asp Ser Gly His Ile Ala
 410 415 420
 ttt gat agc aac ggc cat cgc act cgc ttc gac gac ctc acc cac agc 1411
 Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp Asp Leu Thr His Ser
 425 430 435
 gat atc cgc agg aat ctc atc gcg gtt ttt gat gag ccg ttc ttg tac 1459
 Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp Glu Pro Phe Leu Tyr
 440 445 450
 tcc tcc tcc ata ccg cga gaa cat ctc gat ggg ttt gga tgt cag 1504
 Ser Ser Ser Ile Pro Arg Glu His Leu Asp Gly Phe Gly Cys Gln
 455 460 465
 tgatgagcag atcgaacacg cag 1527

<210> 66

<211> 468

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 66

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 20 25 30
 Arg Pro Trp Leu Thr Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr
 35 40 45
 Leu Phe Glu Leu Thr Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile
 50 55 60

Ala Leu Gly Asn Thr Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg
 65 70 75 80
 Phe Thr Pro Ser Gly Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile
 85 90 95
 Val Leu Leu Ala Leu Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr
 100 105 110
 Thr Ala Gly Lys Leu Ser Met Gly Val Gln His Asp Val Arg Leu Lys
 115 120 125
 Thr Met Arg Ser Leu Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile
 130 135 140
 Arg Thr Gly Gln Val Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val
 145 150 155 160
 Gln Ser Leu Val Ala Met Leu Pro Met Leu Ile Gly Asn Val Val Lys
 165 170 175
 Leu Val Leu Thr Leu Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr
 180 185 190
 Ile Ile Ala Ala Val Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr
 195 200 205
 Ser Arg Lys Ala Leu Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala
 210 215 220
 Ala Asp Leu Thr Thr His Val Glu Glu Thr Val Thr Gly Ile Arg Val
 225 230 235 240
 Val Lys Ala Phe Ala Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu
 245 250 255
 Thr Ala Arg Glu Leu Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr
 260 265 270
 Ala Lys Phe Ile Pro Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val
 275 280 285
 Val Asn Ile Val Gly Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr
 290 295 300
 Val Gly Thr Phe Val Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala
 305 310 315 320
 Val Ala Arg Ser Leu Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu
 325 330 335
 Ser Ser Val Glu Arg Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg
 340 345 350
 Thr Asp Pro Ala His Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu
 355 360 365
 Ser Phe Asn Asn Val Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu
 370 375 380

Gly Val Gln Ala Gly Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser
 385 390 395 400

Gly Lys Thr Met Ala Val Gln Leu Ala Gly Asn Phe Tyr Gln Pro Asp
 405 410 415

Ser Gly His Ile Ala Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp
 420 425 430

Asp Leu Thr His Ser Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp
 435 440 445

Glu Pro Phe Leu Tyr Ser Ser Ser Ile Pro Arg Glu His Leu Asp Gly
 450 455 460

Phe Gly Cys Gln
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<210> 67
 <211> 295
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (84)..(272)
 <223> RXC03185

<400> 67
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 Met Asn Asp Leu Ala Ala Glu Gly Glu Asn
 1 5 10

gat cct tac cgc atg gtt cag cag ctg cgc cgc aag ctc tct cgc ttc 161
 Asp Pro Tyr Arg Met Val Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe
 15 20 25

gtc gag cag aag tgg aag cgc cag ccg gtc atc atg cca acc gtc att 209
 Val Glu Gln Lys Trp Lys Arg Gln Pro Val Ile Met Pro Thr Val Ile
 30 35 40

ccg atg act gcg gaa acc acg cac atc ggt gac gat gag gtt cgc gct 257
 Pro Met Thr Ala Glu Thr Thr His Ile Gly Asp Asp Glu Val Arg Ala
 45 50 55

tca cgc gag tcc ctg taaaagcatt tcgcttttcg acg 295
 Ser Arg Glu Ser Leu
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<210> 68
 <211> 63
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 68
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Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe Val Glu Gln Lys Trp Lys
 20 25 30

Arg Gln Pro Val Ile Met Pro Thr Val Ile Pro Met Thr Ala Glu Thr
 35 40 45

Thr His Ile Gly Asp Asp Glu Val Arg Ala Ser Arg Glu Ser Leu
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<210> 69

<211> 1170

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1147)

<223> RXA00115

<400> 69

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 Met Leu Asp Asn Ser
 1 5

ttt tac acc gca gag gtt cag ggc cca tac gaa acc gct tcc att ggc 163
 Phe Tyr Thr Ala Glu Val Gln Gly Pro Tyr Glu Thr Ala Ser Ile Gly
 10 15 20

cgg ctc gaa ctc gaa gaa ggg ggt gtg att gag gat tgc tgg ttg gct 211
 Arg Leu Glu Leu Glu Glu Gly Gly Val Ile Glu Asp Cys Trp Leu Ala
 25 30 35

tac gct aca gct gga acg ctc aac gag gac aag tcc aac gcc atc ctc 259
 Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys Ser Asn Ala Ile Leu
 40 45 50

att ccg acg tgg tac tcc gga acc cat cag acc tgg ttc cag cag tac 307
 Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr Trp Phe Gln Gln Tyr
 55 60 65

atc ggc act gat cat gcg ctg gat cca tca aag tat ttc atc atc tcc 355
 Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys Tyr Phe Ile Ile Ser
 70 75 80 85

atc aac caa atc ggt aat ggt ttg tcg gtc tcc cct gcc aac acg gct 403
 Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser Pro Ala Asn Thr Ala
 90 95 100

gat gac agc atc tcg atg tcc aag ttc ccg aat gtt cgc att ggt gat 451
 Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn Val Arg Ile Gly Asp
 105 110 115

gat gtc gtt gcc cag gac cgg ctc ttg cgc caa gag ttt ggt att acc 499
 Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln Glu Phe Gly Ile Thr
 120 125 130

gag ctc ttt gcc gtc gtt ggt ggt tcg atg ggt gcg cag caa acc tat 547


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Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly Ala Gln Gln Thr Tyr
135                               140                               145

gag tgg att gtt cgc ttc cct gac caa gtt cat cga gca gct ccg atc 595
Glu Trp Ile Val Arg Phe Pro Asp Gln Val His Arg Ala Ala Pro Ile
150                               155                               160                               165

gcg ggc act gcg aag aac act cct cat gat ttc atc ttc acc cag act 643
Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe Ile Phe Thr Gln Thr
170                               175                               180

ctt aat gag acc gtt gag gcc gat cca ggg ttc aat ggc ggc gaa tac 691
Leu Asn Glu Thr Val Glu Ala Asp Pro Gly Phe Asn Gly Gly Glu Tyr
185                               190                               195

tcc tcc cat gaa gag gta gct gat gga ctt cgc cgt caa tcg cat ctt 739
Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg Arg Gln Ser His Leu
200                               205                               210

tgg gct gcc atg gga ttt tcc aca gag ttc tgg aag cag gag gca tgg 787
Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp Lys Gln Glu Ala Trp
215                               220                               225

cgt cgc ctg gga ctt gaa agt aag gag tca gtg ctc gcg gac ttc ctg 835
Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val Leu Ala Asp Phe Leu
230                               235                               240                               245

gat ccg ctg ttc atg tcc atg gat cct aat acc ttg ctc aac aac gct 883
Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr Leu Leu Asn Asn Ala
250                               255                               260

tgg aag tgg cag cat ggc gat gtc tct cgc cac acc ggc ggc gac ttg 931
Trp Lys Trp Gln His Gly Asp Val Ser Arg His Thr Gly Gly Asp Leu
265                               270                               275

gca gcg gct ctt ggc cga gtg aag gct aag acc ttc gtt atg ccc atc 979
Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr Phe Val Met Pro Ile
280                               285                               290

agc gag gac atg ttc ttt cct gtt cgt gac tgt gcc gca gaa caa gca 1027
Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys Ala Ala Glu Gln Ala
295                               300                               305

ctc atc cca ggc agc gag ctt cga gtg atc gaa gac atc gcc ggt cac 1075
Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu Asp Ile Ala Gly His
310                               315                               320                               325

ctt ggg ott ttt aac gtc tct gag aat tac atc cca cag atc gac aaa 1123
Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile Pro Gln Ile Asp Lys
330                               335                               340

aat ctg aaa gag ctg ttc gag agc taaacactga tgtcaaagag cct 1170
Asn Leu Lys Glu Leu Phe Glu Ser
345

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<210> 70

<211> 349

<212> PRT

<213> Corynebacterium glutamicum

<400> 70

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Met Leu Asp Asn Ser Phe Tyr Thr Ala Glu Val Gln Gly Pro Tyr Glu
 1           5           10           15

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

Asp Cys Trp Leu Ala Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys
      35           40           45

Ser Asn Ala Ile Leu Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr
      50           55           60

Trp Phe Gln Gln Tyr Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys
      65           70           75           80

Tyr Phe Ile Ile Ser Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser
      85           90           95

Pro Ala Asn Thr Ala Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn
      100          105          110

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

Glu Phe Gly Ile Thr Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly
      130          135          140

Ala Gln Gln Thr Tyr Glu Trp Ile Val Arg Phe Pro Asp Gln Val His
      145          150          155          160

Arg Ala Ala Pro Ile Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe
      165          170          175

Ile Phe Thr Gln Thr Leu Asn Glu Thr Val Glu Ala Asp Pro Gly Phe
      180          185          190

Asn Gly Gly Glu Tyr Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg
      195          200          205

Arg Gln Ser His Leu Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp
      210          215          220

Lys Gln Glu Ala Trp Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val
      225          230          235          240

Leu Ala Asp Phe Leu Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr
      245          250          255

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

Thr Gly Gly Asp Leu Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr
      275          280          285

Phe Val Met Pro Ile Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys
      290          295          300

Ala Ala Glu Gln Ala Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu
      305          310          315          320

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Asp Ile Ala Gly His Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile
 325 330 335

Pro Gln Ile Asp Lys Asn Leu Lys Glu Leu Phe Glu Ser
 340 345

<210> 71

<211> 1254

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1231)

<223> RXN00403

<400> 71

tttttcagac tcgtgagaat gcaaactaga ctagacagag ctgtccatat acactggacg 60

aagtttttagt cttgtccacc cagaacaggc ggttatttttc atg ccc acc ctc gcg 115
 Met Pro Thr Leu Ala
 1 5

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163
 Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
 10 15 20

gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt 211
 Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly
 25 30 35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259
 Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu
 40 45 50

cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307
 His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu
 55 60 65

ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355
 Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys
 70 75 80 85

acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg 403
 Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met
 90 95 100

cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att 451
 His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile
 105 110 115

cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc 499
 Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile
 120 125 130

acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc 547
 Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr
 135 140 145

cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt 595

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Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val
150                               155                               160                               165

ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc 643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser
                               170                               175                               180

gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac 691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn
                               185                               190                               195

tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga 739
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg
                               200                               205                               210

cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc 787
Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg
                               215                               220                               225

ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc 835
Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg
230                               235                               240                               245

aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca 883
Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala
                               250                               255                               260

gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931
Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr
                               265                               270                               275

gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979
Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn
                               280                               285                               290

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat 1027
Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp
295                               300                               305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac 1075
Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
310                               315                               320                               325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac 1123
Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
                               330                               335                               340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac 1171
Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
                               345                               350                               355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg acc tac atc 1219
Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser Thr Tyr Ile
                               360                               365                               370

gag ttc tac atc taataggtat ttacgacaaa tag 1254
Glu Phe Tyr Ile
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<210> 72

<211> 377

<212> PRT

<213> Corynebacterium glutamicum

<400> 72

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Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly
  1              5              10              15

Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
      20              25              30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
      35              40              45

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

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

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
      85              90              95

Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
      100              105              110

Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
      115              120              125

Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
      130              135              140

Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
      145              150              155              160

Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
      165              170              175

Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
      180              185              190

Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
      195              200              205

Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
      210              215              220

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

Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
      245              250              255

Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
      260              265              270

Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
      275              280              285

Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
      290              295              300

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Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320

His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335

Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
 340 345 350

Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
 355 360 365

Pro Ser Thr Tyr Ile Glu Phe Tyr Ile
 370 375

<210> 73
 <211> 1210
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1210)
 <223> FRXA00403

<400> 73
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aagtttttagt cttgtccacc cagaacaggc ggttattttc atg ccc acc ctc gcg 115
 Met Pro Thr Leu Ala
 1 5

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163
 Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
 10 15 20

gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt 211
 Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly
 25 30 35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259
 Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu
 40 45 50

cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307
 His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu
 55 60 65

ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355
 Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys
 70 75 80 85

acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg 403
 Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met
 90 95 100

cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att 451
 His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile
 105 110 115

cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc	499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile	
120 125 130	
acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc	547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr	
135 140 145	
cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt	595
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val	
150 155 160 165	
ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc	643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser	
170 175 180	
gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac	691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn	
185 190 195	
tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga	739
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg	
200 205 210	
cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc	787
Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg	
215 220 225	
ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc	835
Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg	
230 235 240 245	
aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca	883
Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala	
250 255 260	
gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc	931
Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr	
265 270 275	
gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac	979
Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn	
280 285 290	
aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat	1027
Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp	
295 300 305	
acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac	1075
Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn	
310 315 320 325	
ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac	1123
Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His	
330 335 340	
gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac	1171
Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn	
345 350 355	

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg 1210
 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser
 360 365 370

<210> 74
 <211> 370
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 74
 Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly
 1 5 10 15
 Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
 20 25 30
 Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95
 Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
 115 120 125
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
 180 185 190
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
 195 200 205
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
 210 215 220
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270

Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
 340 345 350
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
 355 360 365
 Pro Ser
 370

<210> 75
 <211> 687
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(664)
 <223> RXS03158

<400> 75
 caaagctcac cgaaggcacc aacgccaagt tggttgttga caacaccttg gcatcccat 60
 acctgcagca gccactaaaa ctgcgcgcac acgcaagtcc ttg cac tcc acc acc 115
 Leu His Ser Thr Thr
 1 5
 aag tac atc gaa gga cac tcc gac gtt gtt ggc ggc ctt gtg ggt acc 163
 Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly Gly Leu Val Gly Thr
 10 15 20
 aac gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc 211
 Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile
 25 30 35
 gga ccg atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc 259
 Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu
 40 45 50
 aag acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag 307
 Lys Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys
 55 60 65
 atc gcg gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctc tac 355
 Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr
 70 75 80 85
 cca ggt ctg aag aac cac cca ggc cac gaa gtc gca gcg aag cag atg 403

Pro Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met
 90 95 100

aag cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa 451
 Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu
 105 110 115

gca gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag 499
 Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu
 120 125 130

tcc ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc 547
 Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr
 135 140 145

cac cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg 595
 His Gln Ser Ala Ala Glu Ser Gln Leu Glu Val Pro Arg Asp Leu Val
 150 155 160 165

cgc atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc 643
 Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val
 170 175 180

gag cag gcc ctc aat aac ctt tagaaactat ttggcggcaa gca 687
 Glu Gln Ala Leu Asn Asn Leu
 185

<210> 76

<211> 188

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 76

Leu His Ser Thr Thr Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly
 1 5 10 15

Gly Leu Val Gly Thr Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe
 20 25 30

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

Thr Ala Arg Gly Leu Lys Thr Leu Ala Val Arg Met Asp Arg His Cys
 50 55 60

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

Ser Thr Val Leu Tyr Pro Gly Leu Lys Asn His Pro Gly His Glu Val
 85 90 95

Ala Ala Lys Gln Met Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe
 100 105 110

Ala Gly Gly Glu Glu Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu
 115 120 125

Ile Cys Leu Ala Glu Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His
 130 135 140

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

Pro Arg Asp Leu Val Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp
165 170 175

Leu Leu Ala Asp Val Glu Gln Ala Leu Asn Asn Leu
180 185

<210> 77

<211> 617

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(594)

<223> FRXA00254

<400> 77

cag cca cta aaa ctc ggc gca cac gca gtc ttg cac tcc acc acc aag 48
Gln Pro Leu Lys Leu Gly Ala His Ala Val Leu His Ser Thr Thr Lys
1 5 10 15

tac atc gga gga cac tcc gac gtt gtt ggc ggc ctt gtg gtt acc aac 96
Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn
20 25 30

gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc gga 144
Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly
35 40 45

cag atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc aag 192
Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys
50 55 60

acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag atc 240
Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile
65 70 75 80

gcg gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctc tac cca 288
Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro
85 90 95

ggt ctg aag aac cac cca ggc cac gaa gtc gca gcg aag cag atg aag 336
Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys
100 105 110

cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa gca 384
Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala
115 120 125

gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag tcc 432
Ala Lys Lys Phe Cys Thr Thr Lys Leu Ile Cys Leu Ala Glu Ser
130 135 140

ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc cac 480
Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His
145 150 155 160

cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg cgc 528
 Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg
 165 170 175

atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc gag 576
 Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu
 180 185 190

cag gcc ctc aat aac ctt tagaaactat ttggcggcaa gca 617
 Gln Ala Leu Asn Asn Leu
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<210> 78

<211> 198

<212> PRT

<213> Corynebacterium glutamicum

<400> 78

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

Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly
 35 40 45

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

Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile
 65 70 75 80

Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro
 85 90 95

Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys
 100 105 110

Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala
 115 120 125

Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser
 130 135 140

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

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

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

Gln Ala Leu Asn Asn Leu
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<210> 79

<211> 1170

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1147)

<223> RXA02532

<400> 79

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tgtgcaagcg ggacggccag ccagaactcc tggcgcccg atg aac cca cct atc 115
                                         Met Asn Pro Pro Ile
                                         1 5
acg ttg tcc agc act tat gtt cat gat tca gaa aaa gct tat ggg cgc 163
Thr Leu Ser Ser Thr Tyr Val His Asp Ser Glu Lys Ala Tyr Gly Arg
                        10 15 20
gat ggc aat gat gga tgg ggt gca ttt gag gct gcc atg gga act cta 211
Asp Gly Asn Asp Gly Trp Gly Ala Phe Glu Ala Ala Met Gly Thr Leu
                        25 30 35
gat ggt ggg ttc gcg gta tct tat tct tca ggt ttg gca gcg gca acg 259
Asp Gly Gly Phe Ala Val Ser Tyr Ser Ser Gly Leu Ala Ala Ala Thr
                        40 45 50
tcg att gct gat ttg gtt cct act ggt ggc aca gtt gtt tta cct aaa 307
Ser Ile Ala Asp Leu Val Pro Thr Gly Gly Thr Val Val Leu Pro Lys
                        55 60 65
gct gcc tat tat ggc gtg acc aat att ttc gcc agg atg gaa gcc cgc 355
Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe Ala Arg Met Glu Ala Arg
                        70 75 80 85
gga agg ctg aag gtt cga act gtt gat gca gac aat acc gaa gaa gtg 403
Gly Arg Leu Lys Val Arg Thr Val Asp Ala Asp Asn Thr Glu Glu Val
                        90 95 100
att gct gct gct caa ggt gca gat gtg gtg tgg gtg gaa tcg atc gct 451
Ile Ala Ala Ala Gln Gly Ala Asp Val Val Trp Val Glu Ser Ile Ala
                        105 110 115
aat ccg acg atg gtg gta gct gat atc cct gca ata gtc gac ggt gtg 499
Asn Pro Thr Met Val Val Ala Asp Ile Pro Ala Ile Val Asp Gly Val
                        120 125 130
cgt ggg ctt gga gtt ttg act gtc gtt gac gcg act ttc gca acg cca 547
Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala Thr Phe Ala Thr Pro
                        135 140 145
ctt cgt caa cgt cca ttg gaa ctt ggt gct gat att gtg ctt tac tcg 595
Leu Arg Gln Arg Pro Leu Glu Leu Gly Ala Asp Ile Val Leu Tyr Ser
                        150 155 160 165
gca acc aaa ctt atc ggt gga cac tct gat ctt ctt ctt gga gtc gca 643
Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu Leu Leu Gly Val Ala
                        170 175 180
gtg tgc aag tct gag cac cat gcg cag ttt ctt gcc act cac cgt cat 691
Val Cys Lys Ser Glu His His Ala Gln Phe Leu Ala Thr His Arg His

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gat cat ggt tca gtg ccg gga ggt ctt gaa gcg ttt ctt gct ctc cgt				739
Asp His Gly Ser Val Pro Gly Gly Leu Glu Ala Phe Leu Ala Leu Arg				
	200	205	210	
gga ttg tat tcc ttg gcg gtg cgt ctt gat cga gca gaa tcc aac gca				787
Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg Ala Glu Ser Asn Ala				
	215	220	225	
gca gaa ctt tcg cgg cga ctt aac gcg cat cct tcg gtt acc cgc gtc				835
Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro Ser Val Thr Arg Val				
	230	235	240	245
aat tat cca gga ctt cct gat gat ccc caa cat gaa aaa gcc gtg cga				883
Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His Glu Lys Ala Val Arg				
	250	255	260	
gtc cta ccc tct gga tgt gga aac atg ttg tca ttt gag ctt gat gca				931
Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser Phe Glu Leu Asp Ala				
	265	270	275	
aca cct gaa cga act gat gag att ctc gaa agc ctg tca ctt tta acc				979
Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser Leu Ser Leu Leu Thr				
	280	285	290	
cac gcg acc agt tgg gga ggt gtg gaa aca gcc att gaa cgt cgc acc				1027
His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala Ile Glu Arg Arg Thr				
	295	300	305	
agg cgg gat gct gaa gtg gtg gca gaa gta ccg atg act ctt tgc cgc				1075
Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro Met Thr Leu Cys Arg				
	310	315	320	325
gtt tcc gta gga att gaa gac gtt gaa gat cta tgg gaa gac ctc aac				1123
Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu Trp Glu Asp Leu Asn				
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gcc tca atc gac aaa gtt ctg ggt tagaactcgt agccagtaac cag				1170
Ala Ser Ile Asp Lys Val Leu Gly				
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<211> 349

<212> PRT

<213> Corynebacterium glutamicum

<400> 80

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Lys	Ala	Tyr	Gly	Arg	Asp	Gly	Asn	Asp	Gly	Trp	Gly	Ala	Phe	Glu	Ala
	20						25					30			

Ala	Met	Gly	Thr	Leu	Asp	Gly	Gly	Phe	Ala	Val	Ser	Tyr	Ser	Ser	Gly
	35						40					45			

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

Val Val Leu Pro Lys Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe Ala
 65 70 75 80
 Arg Met Glu Ala Arg Gly Arg Leu Lys Val Arg Thr Val Asp Ala Asp
 85 90 95
 Asn Thr Glu Glu Val Ile Ala Ala Ala Gln Gly Ala Asp Val Val Trp
 100 105 110
 Val Glu Ser Ile Ala Asn Pro Thr Met Val Val Ala Asp Ile Pro Ala
 115 120 125
 Ile Val Asp Gly Val Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala
 130 135 140
 Thr Phe Ala Thr Pro Leu Arg Gln Arg Pro Leu Glu Leu Gly Ala Asp
 145 150 155 160
 Ile Val Leu Tyr Ser Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu
 165 170 175
 Leu Leu Gly Val Ala Val Cys Lys Ser Glu His His Ala Gln Phe Leu
 180 185 190
 Ala Thr His Arg His Asp His Gly Ser Val Pro Gly Gly Leu Glu Ala
 195 200 205
 Phe Leu Ala Leu Arg Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg
 210 215 220
 Ala Glu Ser Asn Ala Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro
 225 230 235 240
 Ser Val Thr Arg Val Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His
 245 250 255
 Glu Lys Ala Val Arg Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser
 260 265 270
 Phe Glu Leu Asp Ala Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser
 275 280 285
 Leu Ser Leu Leu Thr His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala
 290 295 300
 Ile Glu Arg Arg Thr Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro
 305 310 315 320
 Met Thr Leu Cys Arg Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu
 325 330 335
 Trp Glu Asp Leu Asn Ala Ser Ile Asp Lys Val Leu Gly
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<210> 81

<211> 861

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(838)

<223> RXS03159

<400> 81

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tttagggcca tagaattctg attacaggag ttgatctacc ttg tct ttt gac cca 115
                                         Leu Ser Phe Asp Pro
                                         1       5

aac acc cag ggt ttc tcc act gca tcg att cac gct ggg tat gag cca 163
Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro
              10              15              20

gac gac tac tac ggt tcg att aac acc cca atc tat gcc tcc acc acc 211
Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr
              25              30              35

ttc gcg cag aac gct cca aac gaa ctg cgc aaa ggc tac gag tac acc 259
Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr
              40              45              50

cgt gtg ggc aac ccc acc atc gtg gca tta gag cag acc gtc gca gca 307
Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala
              55              60              65

ctc gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg gct gca 355
Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala
              70              75              80              85

acc gac atc ctg ttc cgc atc atc ctc aag ccg ggc gat cac atc gtc 403
Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val
              90              95              100

ctc ggc aac gat gct tac ggc gga acc tac cgc ctg atc gac acc gta 451
Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val
              105              110              115

ttc acc gca tgg ggc gtc gaa tac acc gtt gtt gat acc tcc gtc gtg 499
Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val
              120              125              130

gaa gag gtc aag gca gcg atc aag gac aac acc aag ctg atc tgg gtg 547
Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Leu Ile Trp Val
              135              140              145

gaa acc cca acc aac cca gca ctt ggc atc acc gac atc gaa gca gta 595
Glu Thr Pro Thr Asn Pro Ala Leu Gly Ile Thr Asp Ile Glu Ala Val
              150              155              160              165

gca aag ctc acc gaa ggc acc aac gcc aag ttg gtt gtt gac aac acc 643
Ala Lys Leu Thr Glu Gly Thr Asn Ala Lys Leu Val Val Asp Asn Thr
              170              175              180

ttg gca tcc cca tac ctg cag cag cca cta aaa ctc ggc gca cac gca 691
Leu Ala Ser Pro Tyr Leu Gln Gln Pro Leu Lys Leu Gly Ala His Ala
              185              190              195

agt cct tgc act cca cca cca agt aca tcg aag gac act ccg acg ttg 739
Ser Pro Cys Thr Pro Pro Pro Ser Thr Ser Lys Asp Thr Pro Thr Leu

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200	205	210	
ttg gcg gcc ttg tgg gta cca acg acc agg aaa tgg acg aag aac tgc			787
Leu Ala Ala Leu Trp Val Pro Thr Thr Arg Lys Trp Thr Lys Asn Cys			
215	220	225	
tgt tca tgc agg gcg gca tcg gac cga tcc cat cag ttt tcg atg cat			835
Cys Ser Cys Arg Ala Ala Ser Asp Arg Ser His Gln Phe Ser Met His			
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acc tgaccgcccg tggcctcaag acc			861
Thr			
<210> 82			
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<213> Corynebacterium glutamicum			
<400> 82			
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	20	25	30
Tyr Ala Ser Thr Thr Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys			
	35	40	45
Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu			
	50	55	60
Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser			
	65	70	75
Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro			
	85	90	95
Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg			
	100	105	110
Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val			
	115	120	125
Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr			
	130	135	140
Lys Leu Ile Trp Val Glu Thr Pro Thr Asn Pro Ala Leu Gly Ile Thr			
	145	150	155
Asp Ile Glu Ala Val Ala Lys Leu Thr Glu Gly Thr Asn Ala Lys Leu			
	165	170	175
Val Val Asp Asn Thr Leu Ala Ser Pro Tyr Leu Gln Gln Pro Leu Lys			
	180	185	190
Leu Gly Ala His Ala Ser Pro Cys Thr Pro Pro Pro Ser Thr Ser Lys			
	195	200	205
Asp Thr Pro Thr Leu Leu Ala Ala Leu Trp Val Pro Thr Thr Arg Lys			

210 215 220

Trp Thr Lys Asn Cys Cys Ser Cys Arg Ala Ala Ser Asp Arg Ser His
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Gln Phe Ser Met His Thr
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<210> 83
 <211> 703
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(703)
 <223> FRXA02768

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 <223> All occurrences of n = any nucleotide

<220>
 <223> All occurrences of Xaa = any amino acid

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tttagggcca tagaattctg attacaggag ttgatctacc ttg tct ttt gac cca 115
 Leu Ser Phe Asp Pro
 1 5

aac acc cag ggt ttc tcc act gca tcg att cac gct ggg tat gag cca 163
 Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro
 10 15 20

gac gac tac tac ggt tcg att aac acc cca atc tat gcc tcc acc acc 211
 Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr
 25 30 35

ttc gcg cag aac gct cca aac gaa ctg cgc aaa ggc tac gag tac acc 259
 Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr
 40 45 50

cgt gtg ggc aac ccc acc atc gtg gca tta gag cag acc gtc gca gca 307
 Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala
 55 60 65

ctc gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg gct gca 355
 Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala
 70 75 80 85

acc gac atc ctg ttc cgc atc atc ctc aag ccg ggc gat cac atc gtc 403
 Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val
 90 95 100

ctc ggc aac gat gct tac ggc gga acc tac cgc ctg atc gac acc gta 451
 Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val
 105 110 115

ttc acc gca tgg ggc gtc gaa tac acc gtt gtt gat acc tcc gtc gtg 499

Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val
 120 125 130
 gaa gag gtc aag gca gcg atc aag gac aac acc aag gct gat ctt ggt 547
 Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Ala Asp Leu Gly
 135 140 145
 gga aac ccc aac caa ccc agc act ttg gca tta ccc gac atc gaa gca 595
 Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu Pro Asp Ile Glu Ala
 150 155 160 165
 gtn tgc aaa act tca ccc gaa agg cac caa ccc caa gct tgt tgt ttg 643
 Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro Gln Ala Cys Cys Leu
 170 175 180
 aca aca cct tcg cat tcc cca tac ctg cag can cca ctt aaa ant tnn 691
 Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa Pro Leu Lys Xaa Xaa
 185 190 195
 gng cac acg cag 703
 Xaa His Thr Gln
 200

<210> 84

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<220>

<223> All occurrences of Xaa = any amino acid

<400> 84

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 20 25 30
 Tyr Ala Ser Thr Thr Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys
 35 40 45
 Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu
 50 55 60
 Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser
 65 70 75 80
 Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro
 85 90 95
 Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg
 100 105 110
 Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val
 115 120 125
 Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr
 130 135 140
 Lys Ala Asp Leu Gly Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu

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145                      150                      155                      160
Pro Asp Ile Glu Ala Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro
                      165                      170                      175

Gln Ala Cys Cys Leu Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa
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Pro Leu Lys Xaa Xaa Xaa His Thr Gln
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<222> (101)..(1090)
<223> RXA00216

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                      Leu Gly Ala Tyr Gly
                      1                      5

tta ggt gag ctt cct gga aaa tcc gcc gcg gaa gcc gcc gac att att 163
Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu Ala Ala Asp Ile Ile
                      10                      15                      20

cag ggt gaa acg ggc gat ctt ctc cat att cct cag ctt ccg gcg cga 211
Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro Gln Leu Pro Ala Arg
                      25                      30                      35

ggg ttg ggt gct gat ctg atc ggt cga acc gtc ggt ctg ctg gac atg 259
Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val Gly Leu Leu Asp Met
                      40                      45                      50

atc aac gtt gat cgc ggg gcc cga tot tgg gtg atg agc aca cgc ccc 307
Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val Met Ser Thr Arg Pro
                      55                      60                      65

agc aga ttg acg cac ctg acc ggc gat ttc ctt gac atg gat ttg gat 355
Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu Asp Met Asp Leu Asp
                      70                      75                      80                      85

gcg tgc gag gaa acc tgg gga acg ggc gtc gac aag cta aaa atc caa 403
Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp Lys Leu Lys Ile Gln
                      90                      95                      100

gtt gct ggt ccc tgg act tta ggt gcg cgc att gag ttg gcc aat ggc 451
Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile Glu Leu Ala Asn Gly
                      105                      110                      115

cat cgc gtt ttg tct gat cgc ggt gcg atg cgt gat ctc acg cag gcg 499
His Arg Val Leu Ser Asp Arg Gly Ala Met Arg Asp Leu Thr Gln Ala
                      120                      125                      130

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ctg atc gcc ggc atc gat gcg cat gca cgc aag gtt gct ggg cga ttt 547
Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys Val Ala Gly Arg Phe
135 140 145

cgc gcc gaa gtg cag gtg caa att gat gag ccg gag ctg aaa tcg ctt 595
Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro Glu Leu Lys Ser Leu
150 155 160 165

atc gac ggc tcc ctc cct ggc act tcc acc ttt gac att att cct gcg 643
Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe Asp Ile Ile Pro Ala
170 175 180

gtg aat gtc gct gat gcc agt gaa cgt ttg cag cag gtc ttt agc tcg 691
Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln Gln Val Phe Ser Ser
185 190 195

att gag ggg ccg aca tat ctc aac ctc acc ggc cag att cct act tgg 739
Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly Gln Ile Pro Thr Trp
200 205 210

gat gtg gct cgg ggt gcg ggc gcc gat act gtg cag att tcc atg gat 787
Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val Gln Ile Ser Met Asp
215 220 225

caa gtc cgt gga aat gaa cat ttg gat ggt ttt ggt gaa acc atc acc 835
Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe Gly Glu Thr Ile Thr
230 235 240 245

agt gga att cgt ctt ggt ttg ggc att acg aca gga aaa gat gtc gta 883
Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr Gly Lys Asp Val Val
250 255 260

gat gaa ctg ctc gag cga ccg cgg caa aag gcc gtt gag gta gca cgc 931
Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala Val Glu Val Ala Arg
265 270 275

ttt ttt gat cgt tta ggt gtg ggc cga aac tat ctc gtg gat gct gtt 979
Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr Leu Val Asp Ala Val
280 285 290

gat att cat ccg ggt gag gat ttg gtg cag ggg acc atc acc gag gcc 1027
Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly Thr Ile Thr Glu Ala
295 300 305

gcg cag gct tat cgc atg gcc cgg gtg atg tcg gag atg ttg tcg aag 1075
Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser Glu Met Leu Ser Lys
310 315 320 325

gat tca tgc gac ctt taaggcttta ccggcgctgg gtg 1113
Asp Ser Cys Asp Leu
330

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<210> 86

<211> 330

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 86

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			20					25					30		
Gln	Leu	Pro	Ala	Arg	Gly	Leu	Gly	Ala	Asp	Leu	Ile	Gly	Arg	Thr	Val
		35					40					45			
Gly	Leu	Leu	Asp	Met	Ile	Asn	Val	Asp	Arg	Gly	Ala	Arg	Ser	Trp	Val
	50					55					60				
Met	Ser	Thr	Arg	Pro	Ser	Arg	Leu	Thr	His	Leu	Thr	Gly	Asp	Phe	Leu
65					70					75					80
Asp	Met	Asp	Leu	Asp	Ala	Cys	Glu	Glu	Thr	Trp	Gly	Thr	Gly	Val	Asp
				85					90					95	
Lys	Leu	Lys	Ile	Gln	Val	Ala	Gly	Pro	Trp	Thr	Leu	Gly	Ala	Arg	Ile
			100					105					110		
Glu	Leu	Ala	Asn	Gly	His	Arg	Val	Leu	Ser	Asp	Arg	Gly	Ala	Met	Arg
		115					120					125			
Asp	Leu	Thr	Gln	Ala	Leu	Ile	Ala	Gly	Ile	Asp	Ala	His	Ala	Arg	Lys
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Val	Ala	Gly	Arg	Phe	Arg	Ala	Glu	Val	Gln	Val	Gln	Ile	Asp	Glu	Pro
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Gly	Glu	Thr	Ile	Thr	Ser	Gly	Ile	Arg	Leu	Gly	Leu	Gly	Ile	Thr	Thr
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Gly	Lys	Asp	Val	Val	Asp	Glu	Leu	Leu	Glu	Arg	Pro	Arg	Gln	Lys	Ala
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Leu	Val	Asp	Ala	Val	Asp	Ile	His	Pro	Gly	Glu	Asp	Leu	Val	Gln	Gly
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Thr	Ile	Thr	Glu	Ala	Ala	Gln	Ala	Tyr	Arg	Met	Ala	Arg	Val	Met	Ser
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 Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp
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 Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
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 Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
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 tac ttg gaa gtt cac ggc atc ggc gtg cag ctg acc gaa gca ttg gcc 240
 Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
 65 70 75 80
 gag tac tgg cac tcc cga gtg cgc agc gaa ctg aag ctg aac gac ggt 288
 Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
 85 90 95
 gga tct gtc gct gat ttt gat cca gaa gac aag acc aag ttc ttc gac 336
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
 100 105 110
 ctg gat tac cgc ggc gcc cgc ttc tcc ttt ggt tac ggt tct tgc cct 384
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
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 gat ctg gaa gac cgc gca aag ctg gtg gaa ttg ctg gag cca ggc cgt 432
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg
 130 135 140
 atc ggc gtg gag ttg tcc gag gaa ctg cag ctg cac cca gag cag tcc 480
 Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
 145 150 155 160
 aca gac gcg ttt gtg ctg tac cac cca gag gca aag tac ttt aac gtc 528
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Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
 50 55 60

Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
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Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
 85 90 95

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

gaa tac cca ctt gag gct gag gat ttg gcg cag gcg ctg gct gga ttc	979
Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe	
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Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr	
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Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu	
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Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln	
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Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr	
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Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg	
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Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly	
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Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr	
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Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu	
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cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt	1459
Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu	
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Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp	
455 460 465	
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Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys	
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Gln His Gly Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln	
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Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp	
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gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac	1699
Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp	
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Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp	
535 540 545	
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Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro	
550 555 560 565	
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Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn	
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cct gct gca cgc cag gtt ctt aac tct gtg ttc ctc aat gag tgc att	1891
Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile	
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Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro	
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Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val	
615 620 625	
tat gat cgc cgc acc gag gat tac gat ccg ctg cag gaa ttc atg cag	2035
Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln	
630 635 640 645	
ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa	2083
Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu	
650 655 660	
cag ctg gcc gct atg cct ttg ttt gag cgt ttg gca cag cgc atc atc	2131
Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile	
665 670 675	
gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag	2179
Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys	
680 685 690	
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Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met	
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Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe	
710 715 720 725	
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Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu	
730 735 740	
ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag	2371
Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu	
745 750 755	
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Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp
 760 765 770
 atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac 2467
 Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp
 775 780 785
 gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca 2515
 Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala
 790 795 800 805
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 Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val
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 35 40 45
 Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp
 50 55 60
 Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu
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 Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr
 85 90 95
 Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val
 100 105 110
 Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg
 115 120 125
 Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu
 130 135 140
 Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala
 145 150 155 160
 Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala
 165 170 175
 Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala
 180 185 190

Met	Ala	Glu	Leu	Asp	Thr	Phe	Leu	Pro	Ile	Ile	Cys	His	Val	Thr	Val	195	200	205
Glu	Thr	Thr	Gly	Thr	Met	Leu	Met	Gly	Ser	Glu	Ile	Gly	Ala	Ala	Leu	210	215	220
Thr	Ala	Leu	Gln	Pro	Leu	Gly	Ile	Asp	Met	Ile	Gly	Leu	Asn	Cys	Ala	225	230	235
Thr	Gly	Pro	Asp	Glu	Met	Ser	Glu	His	Leu	Arg	Tyr	Leu	Ser	Lys	His	245	250	255
Ala	Asp	Ile	Pro	Val	Ser	Val	Met	Pro	Asn	Ala	Gly	Leu	Pro	Val	Leu	260	265	270
Gly	Lys	Asn	Gly	Ala	Glu	Tyr	Pro	Leu	Glu	Ala	Glu	Asp	Leu	Ala	Gln	275	280	285
Ala	Leu	Ala	Gly	Phe	Val	Ser	Glu	Tyr	Gly	Leu	Ser	Met	Val	Gly	Gly	290	295	300
Cys	Cys	Gly	Thr	Thr	Pro	Glu	His	Ile	Arg	Ala	Val	Arg	Asp	Ala	Val	305	310	315
Val	Gly	Val	Pro	Glu	Gln	Glu	Thr	Ser	Thr	Leu	Thr	Lys	Ile	Pro	Ala	325	330	335
Gly	Pro	Val	Glu	Gln	Ala	Ser	Arg	Glu	Val	Glu	Lys	Glu	Asp	Ser	Val	340	345	350
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Ala	Met	Leu	Ser	Gly	Asp	Trp	Glu	Lys	Cys	Val	Asp	Ile	Ala	Lys	Gln	385	390	395
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Val	Asn	Phe	Glu	Asp	Gly	Asp	Gly	Pro	Glu	Ser	Arg	Tyr	Gln	Arg	Ile	465	470	475
Met	Lys	Leu	Val	Lys	Gln	His	Gly	Ala	Ala	Val	Val	Ala	Leu	Thr	Ile	485	490	495
Asp	Glu	Glu	Gly	Gln	Ala	Arg	Thr	Ala	Glu	His	Lys	Val	Arg	Ile	Ala	500	505	510

Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys
 515 520 525
 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu
 530 535 540
 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu
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 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile
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 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe
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 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser
 595 600 605
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
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 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu
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 645 650 655
 Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu
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 Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu
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 690 695 700
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 705 710 715 720
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 Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly
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 Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser
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Pro	Ile	Met	Ile	Asp	Ser	Thr	Glu	Pro	Glu	Val	Ile	Arg	Thr	Gly	Leu					
		440					445					450								
gag	cac	ttg	ggg	gga	cga	agc	atc	gtt	aac	tcc	gtc	aac	ttt	gaa	gac	1507				
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	455					460					465									
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Gly	Asp	Gly	Pro	Glu	Ser	Arg	Tyr	Gln	Arg	Ile	Met	Lys	Leu	Val	Lys					
470					475					480					485					
cag	cac	ggg	gcg	gcc	gtg	gtt	gcg	ctg	acc	att	gat	gag	gaa	ggc	cag	1603				
Gln	His	Gly	Ala	Ala	Val	Val	Ala	Leu	Thr	Ile	Asp	Glu	Glu	Gly	Gln					
			490					495						500						
gca	cgt	acc	gct	gag	cac	aag	gtg	cgc	att	gct	aaa	cga	ctg	att	gac	1651				
Ala	Arg	Thr	Ala	Glu	His	Lys	Val	Arg	Ile	Ala	Lys	Arg	Leu	Ile	Asp					
			505					510					515							
gat	atc	acc	ggc	agc	tac	ggc	ctg	gat	atc	aaa	gac	atc	gtt	gtg	gac	1699				
Asp	Ile	Thr	Gly	Ser	Tyr	Gly	Leu	Asp	Ile	Lys	Asp	Ile	Val	Val	Asp					
		520					525					530								
tgc	ctg	acc	ttc	ccg	atc	tct	act	ggc	cag	gaa	gaa	acc	agg	cga	gat	1747				
Cys	Leu	Thr	Phe	Pro	Ile	Ser	Thr	Gly	Gln	Glu	Glu	Thr	Arg	Arg	Asp					
	535					540					545									
ggc	att	gaa	acc	atc	gaa	gcc	atc	cgc	gag	ctg	aag	aag	ctc	tac	cca	1795				
Gly	Ile	Glu	Thr	Ile	Glu	Ala	Ile	Arg	Glu	Leu	Lys	Lys	Leu	Tyr	Pro					
550					555				560						565					
gaa	atc	cac	acc	acc	ctg	ggg	ctg	tcc	aat	att	tcc	ttc	ggc	ctg	aac	1843				
Glu	Ile	His	Thr	Thr	Leu	Gly	Leu	Ser	Asn	Ile	Ser	Phe	Gly	Leu	Asn					
			570					575						580						
cct	gct	gca	cgc	cag	gtt	ctt	aac	tct	gtg	ttc	ctc	aat	gag	tgc	att	1891				
Pro	Ala	Ala	Arg	Gln	Val	Leu	Asn	Ser	Val	Phe	Leu	Asn	Glu	Cys	Ile					
			585					590					595							
gag	gct	ggg	ctg	gac	tct	gcg	att	gcg	cac	agc	tcc	aag	att	ttg	ccg	1939				
Glu	Ala	Gly	Leu	Asp	Ser	Ala	Ile	Ala	His	Ser	Ser	Lys	Ile	Leu	Pro					
		600					605					610								
atg	aac	cgc	att	gat	gat	cgc	cag	cgc	gaa	gtg	gcg	ttg	gat	atg	gtc	1987				
Met	Asn	Arg	Ile	Asp	Asp	Arg	Gln	Arg	Glu	Val	Ala	Leu	Asp	Met	Val					
	615					620					625									
tat	gat	cgc	cgc	acc	gag	gat	tac	gat	ccg	ctg	cag	gaa	ttc	atg	cag	2035				
Tyr	Asp	Arg	Arg	Thr	Glu	Asp	Tyr	Asp	Pro	Leu	Gln	Glu	Phe	Met	Gln					
630					635					640					645					
ctg	ttt	gag	ggc	gtt	tct	gct	gcc	gat	gcc	aag	gat	gct	cgc	gct	gaa	2083				
Leu	Phe	Glu	Gly	Val	Ser	Ala	Ala	Asp	Ala	Lys	Asp	Ala	Arg	Ala	Glu					
			650					655						660						

cag ctg gcc gct atg cct ttg ttt gag cgt ttg gca cag cgc atc atc 2131
 Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile
 665 670 675
 gag ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag 2179
 Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys
 680 685 690
 gag aag tct cct att gcg atc atc aac gag gac ctt ctc aac ggc atg 2227
 Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met
 695 700 705
 aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc 2275
 Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe
 710 715 720 725
 gtg ctg caa tcg gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa 2323
 Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu
 730 735 740
 ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag 2371
 Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu
 745 750 755
 ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat 2419
 Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp
 760 765 770
 atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac 2467
 Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp
 775 780 785
 gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca 2515
 Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala
 790 795 800 805
 gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg 2563
 Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val
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 aag tcc acc gtg gtg 2578
 Lys Ser Thr Val Val
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<211> 826

<212> PRT

<213> Corynebacterium glutamicum

<400> 92

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 20 25 30

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 35 40 45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp
 50 55 60
 Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu
 65 70 75 80
 Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr
 85 90 95
 Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val
 100 105 110
 Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg
 115 120 125
 Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu
 130 135 140
 Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala
 145 150 155 160
 Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala
 165 170 175
 Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala
 180 185 190
 Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val
 195 200 205
 Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu
 210 215 220
 Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala
 225 230 235 240
 Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His
 245 250 255
 Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu
 260 265 270
 Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln
 275 280 285
 Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly
 290 295 300
 Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val
 305 310 315 320
 Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala
 325 330 335
 Gly Pro Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val
 340 345 350
 Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser
 355 360 365
 Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu

370					375					380					
Ala	Met	Leu	Ser	Gly	Asp	Trp	Glu	Lys	Cys	Val	Asp	Ile	Ala	Lys	Gln
385					390					395					400
Gln	Thr	Arg	Asp	Gly	Ala	His	Met	Leu	Asp	Leu	Cys	Val	Asp	Tyr	Val
				405					410					415	
Gly	Arg	Asp	Gly	Thr	Ala	Asp	Met	Ala	Thr	Leu	Ala	Ala	Leu	Leu	Ala
			420					425					430		
Thr	Ser	Ser	Thr	Leu	Pro	Ile	Met	Ile	Asp	Ser	Thr	Glu	Pro	Glu	Val
		435					440					445			
Ile	Arg	Thr	Gly	Leu	Glu	His	Leu	Gly	Gly	Arg	Ser	Ile	Val	Asn	Ser
	450					455					460				
Val	Asn	Phe	Glu	Asp	Gly	Asp	Gly	Pro	Glu	Ser	Arg	Tyr	Gln	Arg	Ile
465					470					475					480
Met	Lys	Leu	Val	Lys	Gln	His	Gly	Ala	Ala	Val	Val	Ala	Leu	Thr	Ile
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Asp	Glu	Glu	Gly	Gln	Ala	Arg	Thr	Ala	Glu	His	Lys	Val	Arg	Ile	Ala
			500					505					510		
Lys	Arg	Leu	Ile	Asp	Asp	Ile	Thr	Gly	Ser	Tyr	Gly	Leu	Asp	Ile	Lys
		515					520					525			
Asp	Ile	Val	Val	Asp	Cys	Leu	Thr	Phe	Pro	Ile	Ser	Thr	Gly	Gln	Glu
	530					535					540				
Glu	Thr	Arg	Arg	Asp	Gly	Ile	Glu	Thr	Ile	Glu	Ala	Ile	Arg	Glu	Leu
545					550					555					560
Lys	Lys	Leu	Tyr	Pro	Glu	Ile	His	Thr	Thr	Leu	Gly	Leu	Ser	Asn	Ile
				565					570					575	
Ser	Phe	Gly	Leu	Asn	Pro	Ala	Ala	Arg	Gln	Val	Leu	Asn	Ser	Val	Phe
			580					585					590		
Leu	Asn	Glu	Cys	Ile	Glu	Ala	Gly	Leu	Asp	Ser	Ala	Ile	Ala	His	Ser
		595					600					605			
Ser	Lys	Ile	Leu	Pro	Met	Asn	Arg	Ile	Asp	Asp	Arg	Gln	Arg	Glu	Val
	610					615					620				
Ala	Leu	Asp	Met	Val	Tyr	Asp	Arg	Arg	Thr	Glu	Asp	Tyr	Asp	Pro	Leu
625					630					635					640
Gln	Glu	Phe	Met	Gln	Leu	Phe	Glu	Gly	Val	Ser	Ala	Ala	Asp	Ala	Lys
				645					650					655	
Asp	Ala	Arg	Ala	Glu	Gln	Leu	Ala	Ala	Met	Pro	Leu	Phe	Glu	Arg	Leu
			660					665					670		
Ala	Gln	Arg	Ile	Ile	Asp	Gly	Asp	Lys	Asn	Gly	Leu	Glu	Asp	Asp	Leu
		675					680					685			
Glu	Ala	Gly	Met	Lys	Glu	Lys	Ser	Pro	Ile	Ala	Ile	Ile	Asn	Glu	Asp
	690					695					700				

Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln
 705 710 715 720
 Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala
 725 730 735
 Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly
 740 745 750
 Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys
 755 760 765
 Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser
 770 775 780
 Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser
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 <222> (101)..(598)
 <223> RXN03074

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 Met Thr Gln Ser Ala
 1 5
 cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
 10 15 20
 gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
 25 30 35
 ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50
 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65
 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala

70	75	80	85	
gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca				403
Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala	90	95	100	
att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc				451
Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala	105	110	115	
ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga				499
Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg	120	125	130	
gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac				547
Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr	135	140	145	
gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag				595
Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys	150	155	160	165
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Gln				

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<213> Corynebacterium glutamicum

<400> 94

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			20					25									30		
Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe																			
			35				40										45		
Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly																			
			50				55					60							
Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val																			
			65				70					75							80
Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val																			
							85					90							95
Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr																			
			100						105								110		
Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr																			
			115						120								125		
Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe																			
			130						135								140		
Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr																			

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Glu Ala Pro Ile Lys Gln																				165																			
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																				Met Thr Gln Ser Ala 5																			
																				1																			
cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163																																							
Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn 20																																							
																				10 15																			
gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211																																							
Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu 35																																							
																				25 30																			
ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259																																							
Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu 50																																							
																				40 45																			
ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307																																							
Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile 65																																							
																				55 60																			
gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355																																							
Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala 85																																							
																				70 75 80																			
gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403																																							
Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala 100																																							
																				90 95																			
att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451																																							
Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala 115																																							
																				105 110																			
ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499																																							
Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg 130																																							
																				120 125																			
gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547																																							
Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr 145																																							
																				135 140																			
gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595																																							
Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys																																							

150 155 160 165
 cag taatttgttt tgacgacgca gta 621
 Gln

<210> 96
 <211> 166
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 96
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 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95
 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110
 Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125
 Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140
 Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
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 Glu Ala Pro Ile Lys Gln
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 <212> DNA
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 <222> (101)..(1534)
 <223> RXN00132

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															1				5	
gac	ttc	aag	gtt	gcc	gat	ctt	tca	cta	gca	gag	gca	gga	cgt	cac	cag	163				
Asp	Phe	Lys	Val	Ala	Asp	Leu	Ser	Leu	Ala	Glu	Ala	Gly	Arg	His	Gln					
				10					15					20						
att	cgt	ctt	gca	gag	tat	gag	atg	cca	ggt	ctc	atg	cag	ttg	cgc	aag	211				
Ile	Arg	Leu	Ala	Glu	Tyr	Glu	Met	Pro	Gly	Leu	Met	Gln	Leu	Arg	Lys					
				25					30					35						
gaa	ttc	gca	gac	gag	cag	cct	ttg	aag	ggc	gcc	cga	att	gct	ggt	tct	259				
Glu	Phe	Ala	Asp	Glu	Gln	Pro	Leu	Lys	Gly	Ala	Arg	Ile	Ala	Gly	Ser					
				40					45					50						
atc	cac	atg	acg	gtc	cag	acc	gcc	gtg	ctt	att	gag	acc	ctc	act	gct	307				
Ile	His	Met	Thr	Val	Gln	Thr	Ala	Val	Leu	Ile	Glu	Thr	Leu	Thr	Ala					
				55					60					65						
ttg	ggc	gct	gag	gtt	cgt	tgg	gct	tcc	tgc	aac	att	ttc	tcc	acc	cag	355				
Leu	Gly	Ala	Glu	Val	Arg	Trp	Ala	Ser	Cys	Asn	Ile	Phe	Ser	Thr	Gln					
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gat	gag	gct	gca	gcg	gct	atc	gtt	gtc	ggc	tcc	ggc	acc	gtc	gaa	gag	403				
Asp	Glu	Ala	Ala	Ala	Ala	Ile	Val	Val	Gly	Ser	Gly	Thr	Val	Glu	Glu					
				90					95					100						
cca	gct	ggt	gtt	cca	gta	ttc	gcg	tgg	aag	ggt	gag	tca	ctg	gag	gag	451				
Pro	Ala	Gly	Val	Pro	Val	Phe	Ala	Trp	Lys	Gly	Glu	Ser	Leu	Glu	Glu					
				105					110					115						
tac	tgg	tgg	tgc	atc	aac	cag	atc	ttc	agc	tgg	ggc	gat	gag	ctg	cca	499				
Tyr	Trp	Trp	Cys	Ile	Asn	Gln	Ile	Phe	Ser	Trp	Gly	Asp	Glu	Leu	Pro					
				120					125					130						
aac	atg	atc	ctc	gac	gac	ggc	ggt	gac	gcc	acc	atg	gct	gtt	att	cgc	547				
Asn	Met	Ile	Leu	Asp	Asp	Gly	Gly	Asp	Ala	Thr	Met	Ala	Val	Ile	Arg					
				135					140					145						
ggt	cgc	gaa	tac	gag	cag	gct	ggt	ctg	gtt	cca	cca	gca	gag	gcc	aac	595				
Gly	Arg	Glu	Tyr	Glu	Gln	Ala	Gly	Leu	Val	Pro	Pro	Ala	Glu	Ala	Asn					
				150					155					160						
gat	tcc	gat	gag	tac	atc	gca	ttc	ttg	ggc	atg	ctg	cgt	gag	gtt	ctt	643				
Asp	Ser	Asp	Glu	Tyr	Ile	Ala	Phe	Leu	Gly	Met	Leu	Arg	Glu	Val	Leu					
				170					175					180						
gct	gca	gag	cct	ggc	aag	tgg	ggc	aag	atc	gct	gag	gcc	gtt	aag	ggt	691				
Ala	Ala	Glu	Pro	Gly	Lys	Trp	Gly	Lys	Ile	Ala	Glu	Ala	Val	Lys	Gly					
				185					190					195						
gtc	acc	gag	gaa	acc	acc	acc	ggt	gtg	cac	cgc	ctg	tac	cac	ttc	gct	739				
Val	Thr	Glu	Glu	Thr	Thr	Thr	Gly	Val	His	Arg	Leu	Tyr	His	Phe	Ala					
				200					205					210						
gaa	gaa	ggc	gtg	ctg	cct	ttc	cca	gcg	atg	aac	gtc	aac	gac	gct	gtc	787				
Glu	Glu	Gly	Val	Leu	Pro	Phe	Pro	Ala	Met	Asn	Val	Asn	Asp	Ala	Val					
				215					220					225						
acc	aag	tcc	aag	ttt	gat	aac	aag	tac	ggc	acc	cgc	cac	tcc	ctg	atc	835				
Thr	Lys	Ser	Lys	Phe	Asp	Asn	Lys	Tyr	Gly	Thr	Arg	His	Ser	Leu	Ile					

230	235	240	245	
gac ggc atc aac cgc gcc act gac atg ctc atg ggc ggc aag aac gtg Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met Gly Gly Lys Asn Val	250	255	260	883
ctt gtc tgc ggt tac ggc gat gtc ggc aag ggc tgc gct gag gct ttc Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe	265	270	275	931
gac ggc cag ggc gct cgc gtc aag gtc acc gaa gct gac cca atc aac Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn	280	285	290	979
gct ctt cag gct ctg atg gat ggc tac tct gtg gtc acc gtt gat gag Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu	295	300	305	1027
gcc atc gag gac gcc gac atc gtg atc acc gcg acc ggc aac aag gac Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp	310	315	320	1075
atc att tcc ttc gag cag atg ctc aag atg aag gat cac gct ctg ctg Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu	330	335	340	1123
ggc aac atc ggt cac ttt gat aat gag atc gat atg cat tcc ctg ttg Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu	345	350	355	1171
cac cgc gac gac gtc acc cgc acc acg atc aag cca cag gtc gac gag His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu	360	365	370	1219
ttc acc ttc tcc acc ggt cgc tcc atc atc gtc ctg tcc gaa ggt cgc Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg	375	380	385	1267
ctg ttg aac ctt ggc aac gcc acc gga cac cca tca ttt gtc atg tcc Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser	390	395	400	1315
aac tct ttc gcc gat cag acc att gcg cag atc gaa ctg ttc caa aac Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn	410	415	420	1363
gaa gga cag tac gag aac gag gtc tac cgt ctg cct aag gtt ctc gac Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu Pro Lys Val Leu Asp	425	430	435	1411
gaa aag gtg gca cgc atc cac gtt gag gct ctc ggc ggt cag ctc acc Glu Lys Val Ala Arg Ile His Val Glu Ala Leu Gly Gly Gln Leu Thr	440	445	450	1459
gaa ctg acc aag gag cag gct gag tac atc gcg gtt gac gtt gca gcc Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly Val Asp Val Ala Gly	455	460	465	1507
cca ttc aag ccg gag cac tac cgc tac taatgattgt cagcattgag gga Pro Phe Lys Pro Glu His Tyr Arg Tyr	470	475		1557

<210> 98

<211> 478

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 98

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

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

Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala
 305 310 315 320

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

Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp
 340 345 350

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

Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val
 370 375 380

Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro
 385 390 395 400

Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile
 405 410 415

Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu
 420 425 430

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

Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly
 450 455 460

Val Asp Val Ala Gly Pro Phe Lys Pro Glu His Tyr Arg Tyr
 465 470 475

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 <211> 128
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(105)
 <223> FRXA00132

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 His Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln
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gct gag tac atc ggc gtt gac gtt gca ggc cca ttc aag ccg gag cac 96
 Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His
 20 25 30

tac cgc tac taatgattgt cagcattgag gga 128
 Tyr Arg Tyr
 35

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<400> 100
His Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln
  1                      5                      10                      15

Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His
      20                      25                      30

Tyr Arg Tyr
      35

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<220>
<221> CDS
<222> (101)..(1396)
<223> FRXA01371
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140

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Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp Gly Asp Glu Leu Pro	
120 125 130	
aac atg atc ctc gac gac ggc ggt gac gcc acc atg gct gtt att cgc	547
Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr Met Ala Val Ile Arg	
135 140 145	
ggt cgc gaa tac gag cag gct ggt ctg gtt cca cca gca gag gcc aac	595
Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro Pro Ala Glu Ala Asn	
150 155 160 165	
gat tcc gat gag tac atc gca ttc ttg ggc atg ctg cgt gag gtt ctt	643
Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met Leu Arg Glu Val Leu	
170 175 180	
gct gca gag cct ggc aag tgg ggc aag atc gct gag gcc gtt aag ggt	691
Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala Glu Ala Val Lys Gly	
185 190 195	
gtc acc gag gaa acc acc acc ggt gtg cac cgc ctg tac cac ttc gct	739
Val Thr Glu Glu Thr Thr Thr Gly Val His Arg Leu Tyr His Phe Ala	
200 205 210	
gaa gaa ggc gtg ctg cct ttc cca gcg atg aac gtc aac gac gct gtc	787
Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn Val Asn Asp Ala Val	
215 220 225	
acc aag tcc aag ttt gat aac aag tac ggc acc cgc cac tcc ctg atc	835
Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr Arg His Ser Leu Ile	
230 235 240 245	
gac ggc atc aac cgc gcc act gac atg ctc atg ggc ggc aag aac gtg	883
Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met Gly Gly Lys Asn Val	
250 255 260	
ctt gtc tgc ggt tac ggc gat gtc ggc aag ggc tgc gct gag gct ttc	931
Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe	
265 270 275	
gac ggc cag ggc gct cgc gtc aag gtc acc gaa gct gac cca atc aac	979
Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn	
280 285 290	
gct ctt cag gct ctg atg gat ggc tac tct gtg gtc acc gtt gat gag	1027
Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu	
295 300 305	
gcc atc gag gac gcc gac atc gtg atc acc gcg acc ggc aac aag gac	1075
Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp	
310 315 320 325	
atc att tcc ttc gag cag atg ctc aag atg aag gat cac gct ctg ctg	1123
Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu	
330 335 340	
ggc aac atc ggt cac ttt gat aat gag atc gat atg cat tcc ctg ttg	1171
Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu	
345 350 355	

cac cgc gac gac gtc acc cgc acc acg atc aag cca cag gtc gac gag 1219
 His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu
 360 365 370
 ttc acc ttc tcc acc ggt cgc tcc atc atc gtc ctg tcc gaa ggt cgc 1267
 Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg
 375 380 385
 ctg ttg aac ctt ggc aac gcc acc gga cac cca tca ttt gtc atg tcc 1315
 Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser
 390 395 400 405
 aac tct ttc gcc gat cag acc att gcg cag atc gaa ctg ttc caa aac 1363
 Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn
 410 415 420
 gaa gga cag tac gag aac gag gtc tac cgt ctg 1396
 Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu
 425 430

<210> 102

<211> 432

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 102

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

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

<210> 103

<211> 2358

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2335)

<223> RXN02085

<400> 103

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gatccgcacg ttcgggtcaa gcagaaagtc tttaactcac	atg act tcc aac ttt	115
	Met Thr Ser Asn Phe	
	1 5	
tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg	163	
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu		
10 15 20		
aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa	211	
Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu		
25 30 35		
ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg	259	
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu		
40 45 50		
tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca	307	
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala		
55 60 65		
atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat	355	
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp		
70 75 80 85		
gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc	403	
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg		
90 95 100		
tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg	451	
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met		
105 110 115		
acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct	499	
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser		
120 125 130		
gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc	547	
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu		
135 140 145		
cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt	595	
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly		
150 155 160 165		
cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct	643	
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro		
170 175 180		
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag	691	
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys		
185 190 195		
tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc	739	
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr		
200 205 210		
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	787	
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr		
215 220 225		
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc	835	

Leu	Ala	Lys	Arg	Asp	Gly	Val	Phe	Val	Asn	Thr	Tyr	Phe	Gly	Ser	Gly		
230					235					240					245		
gat	cag	gcg	ctg	aac	act	ctt	gcg	ggc	atc	ggc	ctt	ggc	gcg	att	ggc	883	
Asp	Gln	Ala	Leu	Asn	Thr	Leu	Ala	Gly	Ile	Gly	Leu	Gly	Ala	Ile	Gly		
				250					255					260			
gtt	gac	ttg	gtc	acc	cat	ggc	gtc	act	gag	ctt	gct	gcg	tgg	aag	ggt	931	
Val	Asp	Leu	Val	Thr	His	Gly	Val	Thr	Glu	Leu	Ala	Ala	Trp	Lys	Gly		
				265					270					275			
gag	gag	ctg	ctg	gtt	gcg	ggc	atc	gtt	gat	ggt	cgt	aac	att	tgg	cgc	979	
Glu	Glu	Leu	Leu	Val	Ala	Gly	Ile	Val	Asp	Gly	Arg	Asn	Ile	Trp	Arg		
				280					285					290			
acc	gac	ctg	tgt	gct	gct	ctt	gct	tcc	ctg	aag	cgc	ctg	gca	gct	cgc	1027	
Thr	Asp	Leu	Cys	Ala	Ala	Leu	Ala	Ser	Leu	Lys	Arg	Leu	Ala	Ala	Arg		
						300					305						
ggc	cca	atc	gca	gtg	tct	acc	tct	tgt	tca	ctg	ctg	cac	gtt	cct	tac	1075	
Gly	Pro	Ile	Ala	Val	Ser	Thr	Ser	Cys	Ser	Leu	Leu	His	Val	Pro	Tyr		
					315						320				325		
acc	ctc	gag	gct	gag	aac	att	gag	cct	gag	gtc	cgc	gac	tgg	ctt	gcc	1123	
Thr	Leu	Glu	Ala	Glu	Asn	Ile	Glu	Pro	Glu	Val	Arg	Asp	Trp	Leu	Ala		
					330				335						340		
ttc	ggc	tcg	gag	aag	atc	acc	gag	gtc	aag	ctg	ctt	gcc	gac	gcc	cta	1171	
Phe	Gly	Ser	Glu	Lys	Ile	Thr	Glu	Val	Lys	Leu	Leu	Ala	Asp	Ala	Leu		
				345					350					355			
gcc	ggc	aac	atc	gac	gcg	gct	gcg	ttc	gat	gcg	gcg	tcc	gca	gca	att	1219	
Ala	Gly	Asn	Ile	Asp	Ala	Ala	Ala	Phe	Asp	Ala	Ala	Ser	Ala	Ala	Ile		
				360					365					370			
gct	tct	cga	cgc	acc	tcc	cca	cgc	acc	gca	cca	atc	acg	cag	gaa	ctc	1267	
Ala	Ser	Arg	Arg	Thr	Ser	Pro	Arg	Thr	Ala	Pro	Ile	Thr	Gln	Glu	Leu		
						380						385					
cct	ggc	cgt	agc	cgt	gga	tcc	ttc	gac	act	cgt	gtt	acg	ctg	cag	gag	1315	
Pro	Gly	Arg	Ser	Arg	Gly	Ser	Phe	Asp	Thr	Arg	Val	Thr	Leu	Gln	Glu		
					395					400					405		
aag	tca	ctg	gag	ctt	cca	gct	ctg	cca	acc	acc	acc	att	ggt	tct	ttc	1363	
Lys	Ser	Leu	Glu	Leu	Pro	Ala	Leu	Pro	Thr	Thr	Thr	Ile	Gly	Ser	Phe		
					410				415					420			
cca	cag	acc	cca	tcc	att	cgt	tct	gct	cgc	gct	cgt	ctg	cgc	aag	gaa	1411	
Pro	Gln	Thr	Pro	Ser	Ile	Arg	Ser	Ala	Arg	Ala	Arg	Leu	Arg	Lys	Glu		
					425				430					435			
tcc	atc	act	ttg	gag	cag	tac	gaa	gag	gca	atg	cgc	gaa	gaa	atc	gat	1459	
Ser	Ile	Thr	Leu	Glu	Gln	Tyr	Glu	Glu	Ala	Met	Arg	Glu	Glu	Ile	Asp		
					440				445					450			
ctg	gtc	atc	gcc	aag	cag	gaa	gaa	ctt	ggt	ctt	gat	gtg	ttg	gtt	cac	1507	
Leu	Val	Ile	Ala	Lys	Gln	Glu	Glu	Leu	Gly	Leu	Asp	Val	Leu	Val	His		
					455				460					465			
ggt	gag	cca	gag	cgc	aac	gac	atg	gtt	cag	tac	ttc	tct	gaa	ctt	ctc	1555	
Gly	Glu	Pro	Glu	Arg	Asn	Asp	Met	Val	Gln	Tyr	Phe	Ser	Glu	Leu	Leu		

470	475	480	485	
gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser	490	495	500	1603
cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala	505	510	515	1651
cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys	520	525	530	1699
cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser	535	540	545	1747
ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala	550	555	560	1795
ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys	570	575	580	1843
atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccg cta cga Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Leu Arg	585	590	595	1891
gac gtc gat aag cct gcc tac ctg cag tgg tcc gtg gac tcc ttc cgc Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg	600	605	610	1939
ctg gcg act gcc ggc gca ccc gac gac gtc caa atc cac acc cac atg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met	615	620	625	1987
tgc tac tcc gag ttc aac gaa gtg atc tcc tcg gtc atc gcg ttg gat Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp	630	635	640	2035
gcc gat gtc acc acc atc gaa gca gca cgt tcc gac atg cag gtc ctc Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu	650	655	660	2083
gct gct ctg aaa tct tcc ggc ttc gag ctc ggc gtc gga cct ggt gtg Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val	665	670	675	2131
tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly	680	685	690	2179
ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val	695	700	705	2227
aac cca gac tgt ggt ctg aag acc cgt gga tgg cca gaa gtg gaa gct Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala	710	715	720	2275
			725	

tcc cta aag gtt ctc gtt gag tcc gct aag cag gct cgt gag aaa atc 2323
 Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile
 730 735 740

gga gca act atc taaattgggt taccgctagg aac 2358
 Gly Ala Thr Ile
 745

<210> 104

<211> 745

<212> PRT

<213> Corynebacterium glutamicum

<400> 104

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

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
 35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
 50 55 60

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

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
 85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
 100 105 110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
 115 120 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
 130 135 140

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

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
 165 170 175

Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
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Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
 195 200 205

Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
 210 215 220

Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
 225 230 235 240

Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
 245 250 255
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
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 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
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 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
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 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
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 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
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 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
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 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
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 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
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 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
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 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
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 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile

565										570					575				
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Leu	Leu	Pro	Leu	Arg	Asp	Val	Asp	Lys	Pro	Ala	Tyr	Leu	Gln	Trp	Ser				
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Ile	His	Thr	His	Met	Cys	Tyr	Ser	Glu	Phe	Asn	Glu	Val	Ile	Ser	Ser				
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Val	Gly	Pro	Gly	Val	Trp	Asp	Ile	His	Ser	Pro	Arg	Val	Pro	Ser	Ala				
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Gln	Lys	Val	Asp	Gly	Leu	Leu	Glu	Ala	Ala	Leu	Gln	Ser	Val	Asp	Pro				
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Pro	Glu	Val	Glu	Ala	Ser	Leu	Lys	Val	Leu	Val	Glu	Ser	Ala	Lys	Gln				
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<211> 1923

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1900)

<223> FRXA02085

<400> 105

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tct	tcc	act	gtc	gct	ggt	ctt	cct	cgc	atc	gga	gcg	aag	cgt	gaa	ctg	163
Ser	Ser	Thr	Val	Ala	Gly	Leu	Pro	Arg	Ile	Gly	Ala	Lys	Arg	Glu	Leu	
			10					15						20		

aag	ttc	gcg	ctc	gaa	ggc	tac	tgg	aat	gga	tca	att	gaa	ggt	cgc	gaa	211
Lys	Phe	Ala	Leu	Glu	Gly	Tyr	Trp	Asn	Gly	Ser	Ile	Glu	Gly	Arg	Glu	
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ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg	259
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu	
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Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala	
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Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp	
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Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg	
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Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met	
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acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct	499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser	
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gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc	547
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu	
135 140 145	
cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt	595
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly	
150 155 160 165	
cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct	643
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro	
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Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
185 190 195	
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Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
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gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
215 220 225	
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Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
230 235 240 245	
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Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
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gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt	931
Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
265 270 275	
gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc	979

Glu	Glu	Leu	Leu	Val	Ala	Gly	Ile	Val	Asp	Gly	Arg	Asn	Ile	Trp	Arg		
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Thr	Asp	Leu	Cys	Ala	Ala	Leu	Ala	Ser	Leu	Lys	Arg	Leu	Ala	Ala	Arg		
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ggc	cca	atc	gca	gtg	tct	acc	tct	tgt	tca	ctg	ctg	cac	gtt	cct	tac	1075	
Gly	Pro	Ile	Ala	Val	Ser	Thr	Ser	Cys	Ser	Leu	Leu	His	Val	Pro	Tyr		
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Thr	Leu	Glu	Ala	Glu	Asn	Ile	Glu	Pro	Glu	Val	Arg	Asp	Trp	Leu	Ala		
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ttc	ggc	tgc	gag	aag	atc	acc	gag	gtc	aag	ctg	ctt	gcc	gac	gcc	cta	1171	
Phe	Gly	Ser	Glu	Lys	Ile	Thr	Glu	Val	Lys	Leu	Leu	Ala	Asp	Ala	Leu		
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Ala	Ser	Arg	Arg	Thr	Ser	Pro	Arg	Thr	Ala	Pro	Ile	Thr	Gln	Glu	Leu		
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Pro	Gly	Arg	Ser	Arg	Gly	Ser	Phe	Asp	Thr	Arg	Val	Thr	Leu	Gln	Glu		
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Lys	Ser	Leu	Glu	Leu	Pro	Ala	Leu	Pro	Thr	Thr	Thr	Ile	Gly	Ser	Phe		
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Pro	Gln	Thr	Pro	Ser	Ile	Arg	Ser	Ala	Arg	Ala	Arg	Leu	Arg	Lys	Glu		
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tcc	atc	act	ttg	gag	cag	tac	gaa	gag	gca	atg	cgc	gaa	gaa	atc	gat	1459	
Ser	Ile	Thr	Leu	Glu	Gln	Tyr	Glu	Glu	Ala	Met	Arg	Glu	Glu	Ile	Asp		
		440					445					450					
ctg	gtc	atc	gcc	aag	cag	gaa	gaa	ctt	ggt	ctt	gat	gtg	ttg	gtt	cac	1507	
Leu	Val	Ile	Ala	Lys	Gln	Glu	Glu	Leu	Gly	Leu	Asp	Val	Leu	Val	His		
	455					460					465						
ggt	gag	cca	gag	cgc	aac	gac	atg	gtt	cag	tac	ttc	tct	gaa	ctt	ctc	1555	
Gly	Glu	Pro	Glu	Arg	Asn	Asp	Met	Val	Gln	Tyr	Phe	Ser	Glu	Leu	Leu		
	470				475					480					485		
gac	ggt	ttc	ctc	tca	acc	gcc	aac	ggc	tgg	gtc	caa	agc	tac	ggc	tcc	1603	
Asp	Gly	Phe	Leu	Ser	Thr	Ala	Asn	Gly	Trp	Val	Gln	Ser	Tyr	Gly	Ser		
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cgc	tgt	gtt	cgt	cct	cca	gtg	ttg	ttc	gga	aac	gtt	tcc	cgc	cca	gcg	1651	
Arg	Cys	Val	Arg	Pro	Pro	Val	Leu	Phe	Gly	Asn	Val	Ser	Arg	Pro	Ala		
			505					510					515				
cca	atg	act	gtc	aag	tgg	ttc	cag	tac	gca	cag	agc	ctg	acc	cag	aag	1699	
Pro	Met	Thr	Val	Lys	Trp	Phe	Gln	Tyr	Ala	Gln	Ser	Leu	Thr	Gln	Lys		


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      520              525              530
cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc 1747
His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
535              540              545

ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca 1795
Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
550              555              560              565

ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag 1843
Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys
570              575              580

atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccc gct acg 1891
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Arg Arg Arg
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<210> 106
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<213> Corynebacterium glutamicum

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Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
50 55 60

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

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
100 105 110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
115 120 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
130 135 140

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

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
165 170 175

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Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
 180 185 190
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
 195 200 205
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
 210 215 220
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
 225 230 235 240
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
 245 250 255
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
 290 295 300
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
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 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala
 355 360 365
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro
 370 375 380
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
 385 390 395 400
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
 405 410 415
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
 420 425 430
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
 435 440 445
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
 450 455 460
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
 465 470 475 480
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
 485 490 495

Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
 500 505 510

Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
 515 520 525

Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
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Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
 545 550 555 560

Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
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Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
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Leu Leu Pro Ala Thr Arg Arg Arg
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> FRXA02086

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 Met Ser Leu Arg Phe
 1 5

gtg aac tgt tgc ccg cta cga gac gtc gat aag cct gcc tac ctg cag 163
 Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln
 10 15 20

tgg tcc gtg gac tcc ttc cgc ctg gcg act gcc ggc gca ccc gac gac 211
 Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp
 25 30 35

gtc caa atc cac acc cac atg tgc tac tcc gag ttc aac gaa gtg atc 259
 Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile
 40 45 50

tcc tcg gtc atc gcg ttg gat gcc gat gtc acc acc atc gaa gca gca 307
 Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala
 55 60 65

cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc ggc ttc gag 355
 Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu
 70 75 80 85

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 Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro

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Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val
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gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag acc cgt 499
Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg
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gga tgg cca gaa gtg gaa gct tcc cta aag gtt ctc gtt gag tcc gct 547
Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala
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aag cag gct cgt gag aaa atc gga gca act atc taaattgggt taccgctagg 600
Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
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aac 603

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Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
          35              40              45

Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
          50              55              60

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

Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His
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Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala
          100              105              110

Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys
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Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val
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<222> (101)..(1303)

<223> RXN02648

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Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
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Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
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Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
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Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
                        55 60 65
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Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
                        70 75 80 85
ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
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Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
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Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
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Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
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cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
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Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
                        170 175 180
gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
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Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala Pro
      215                      220                      225

gac ttg gca gaa gca tgg gat cag atc aac cca gag cca agc gtg aag 835
Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro Ser Val Lys
      230                      235                      240                      245

gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca 883
Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala
      250                      255                      260

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Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly
      265                      270                      275

tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att 979
Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile
      280                      285                      290

ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca 1027
Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala
      295                      300                      305

tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa aac aag ctt 1075
Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu
      310                      315                      320                      325

cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac 1123
Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn
      330                      335                      340

gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc 1171
Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala
      345                      350                      355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg 1219
Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu
      360                      365                      370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta 1267
Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu
      375                      380                      385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac 1313
Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
      390                      395                      400

aacgagggtt gct 1326

<210> 110
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<212> PRT
<213> Corynebacterium glutamicum

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<400> 110

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Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
      20           25           30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
      35           40           45

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

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65           70           75           80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
      85           90           95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
      100           105           110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
      115           120           125

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

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
      145           150           155           160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
      165           170           175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
      180           185           190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
      195           200           205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
      210           215           220

Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro
      225           230           235           240

Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp
      245           250           255

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

His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro
      275           280           285

Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe
      290           295           300

Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp
      305           310           315           320

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Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val
 325 330 335

Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg
 340 345 350

Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser
 355 360 365

Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala
 370 375 380

Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu
 385 390 395 400

Phe

<210> 111
 <211> 548
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(525)
 <223> FRXA02648

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agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc 96
 Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
 20 25 30

aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc 144
 Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
 35 40 45

tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt 192
 Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
 50 55 60

gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc 240
 Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65 70 75 80

gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa 288
 Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
 85 90 95

aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac 336
 Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
 100 105 110

tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt 384
 Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
 115 120 125

cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac 432
 Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
 130 135 140
 tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480
 Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
 145 150 155 160
 gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525
 Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 165 170 175
 taagctagac aacgagggtt gct 548

<210> 112
 <211> 175
 <212> PRT
 <213> *Corynebacterium glutamicum*

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

<210> 113
 <211> 784
 <212> DNA
 <213> *Corynebacterium glutamicum*

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<222> (101)..(784)
<223> FRXA02658

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gagtttgata ctttcttttcg acttttagat tggattttca atg agc cag aac cgc 115
Met Ser Gln Asn Arg
1 5

atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
10 15 20

gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
25 30 35

ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
40 45 50

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr ..
55 60 65

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
70 75 80 85

ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
90 95 100

gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
105 110 115

cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
120 125 130

ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
135 140 145

cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
150 155 160 165

ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
170 175 180

gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
185 190 195

act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739

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Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
 200 205 210

tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784
 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala
 215 220 225

<210> 114

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 114

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 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45

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

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125

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

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220

Gln Leu Asp Ala
 225

<210> 115

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 <213> Corynebacterium glutamicum

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 <223> RXC02238

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 Val Thr Asn Val Ser
 1 5
 aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
 10 15 20
 acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
 25 30 35
 gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
 40 45 50
 tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
 Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
 55 60 65
 act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
 Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
 70 75 80 85
 aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405
 Asn Ala Gly Leu Leu Asp His Glu Glu Gly
 90 95
 cac 408

<210> 116
 <211> 95
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 116
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 Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys
 20 25 30
 Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
 35 40 45
 Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
 50 55 60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
 65 70 75 80
 Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly
 85 90 95

<210> 117
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1804)
 <223> RXC00128

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 Val Ser Lys Ile Ser
 1 5
 acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg 163
 Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val
 10 15 20
 gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc 211
 Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg
 25 30 35
 tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg 259
 Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro
 40 45 50
 aat caa gat ccg gat ttg ttg atc cgc gcc ttc ttc agc gca ggt gcg 307
 Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala
 55 60 65
 tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg 355
 Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly
 70 75 80 85
 acg cgc agc acg tgg aat ccg gct gcg tgc act cgt att ttg gat cgc 403
 Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg
 90 95 100
 att gat ctg aac act ctg cca ggt tgc acg aat gcg gaa cga acg att 451
 Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile
 105 110 115
 gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt gcc gtg tat 499
 Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr
 120 125 130
 cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt ccg gaa 547
 Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu
 135 140 145
 gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag 595

Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu 150 155 160 165	
aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe 170 175 180	643
gat cct tct ggc cag gtg ttg gtg ggg gat cgg cgt tgg ttg ttc aat Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn 185 190 195	691
gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly 200 205 210	739
cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp 215 220 225	787
gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu 230 235 240 245	835
gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg Gly Asn Leu Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val 250 255 260	883
tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala 265 270 275	931
gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp 280 285 290	979
ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu 295 300 305	1027
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agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala 330 335 340	1123
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gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala 360 365 370	1219
ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser 375 380 385	1267
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390          395          400          405
tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg 1363
Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu
          410          415          420

cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act 1411
Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr
          425          430          435

ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc 1459
Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val
          440          445          450

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag 1507
Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu
          455          460          465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca 1555
Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro
          470          475          480          485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg 1603
Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp
          490          495          500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat 1651
Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Ser Met Pro Ser Gly Asn
          505          510          515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac 1699
Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr
          520          525          530

gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat 1747
Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp
          535          540          545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg 1795
Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val
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Val Ala Tyr

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<210> 118

<211> 568

<212> PRT

<213> Corynebacterium glutamicum

<400> 118

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Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp
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Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile
          35          40          45

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Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
 50 55 60
 Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala
 65 70 75 80
 Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr
 85 90 95
 Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn
 100 105 110
 Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu
 115 120 125
 Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile
 130 135 140
 Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp
 145 150 155 160
 Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His
 165 170 175
 Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg
 180 185 190
 Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala
 195 200 205
 Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
 210 215 220
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
 225 230 235 240
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe
 245 250 255
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
 260 265 270
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr
 275 280 285
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn
 290 295 300
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val
 305 310 315 320
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp
 325 330 335
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val
 340 345 350
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly
 355 360 365

Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe
 370 375 380
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro
 385 390 395 400
 Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu
 405 410 415
 Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe
 420 425 430
 Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys
 435 440 445
 Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val
 450 455 460
 Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser
 465 470 475 480
 Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro
 485 490 495
 Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser
 500 505 510
 Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser
 515 520 525
 Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro
 530 535 540
 Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr
 545 550 555 560
 Arg Ala Ala Pro Val Val Ala Tyr
 565

<210> 119
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <221> CDS
 <222> (101)..(1321)
 <223> RXA02240

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 Val Ala Gln Pro Thr
 1 5
 gcc gtc cgt ttg ttc acc agt gaa tct gta act gag gga cat cca gac 163
 Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr Glu Gly His Pro Asp
 10 15 20

aaa ata tgt gat gct att tcc gat acc att ttg gac gcg ctg ctc gaa	211
Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu Asp Ala Leu Leu Glu	
25 30 35	
aaa gat ccg cag tcc cgc gtc gca gtg gaa act gtg gtc acc acc gga	259
Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr Val Val Thr Thr Gly	
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Ile Val His Val Val Gly Glu Val Arg Thr Ser Ala Tyr Val Glu Ile	
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Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val Ser Val Ser Ile Gly	
90 95 100	
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Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp Asn Ser Asp Glu Ala	
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Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg Ala Gly Ala Gly Asp	
120 125 130	
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Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu Thr Glu Glu Tyr Met	
135 140 145	
cct ctt cct atc gcg ttg gcg cac cga ctg tca cgt cgt ctg acc cag	595
Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser Arg Arg Leu Thr Gln	
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Val Arg Lys Glu Gly Ile Val Pro His Leu Arg Pro Asp Gly Lys Thr	
170 175 180	
cag gtc acc ttc gca tac gat gcg caa gac cgc cct agc cac ctg gat	691
Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg Pro Ser His Leu Asp	
185 190 195	
acc gtt gtc atc tcc acc cag cac gac cca gaa gtt gac cgt gca tgg	739
Thr Val Val Ile Ser Thr Gln His Asp Pro Glu Val Asp Arg Ala Trp	
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Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp Trp Val Ile Lys Asp	
215 220 225	
gca ggc att gag gat ctg gca acc ggt gag atc acc gtg ttg atc aac	835
Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile Thr Val Leu Ile Asn	
230 235 240 245	
cct tca ggt tcc ttc att ctg ggt ggc ccc atg ggt gat gcg ggt ctg	883
Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met Gly Asp Ala Gly Leu	
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Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala Arg His
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 Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp Thr Asn Lys Glu Gly
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 Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg Thr Asp Leu Asp Leu
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