



(86) Date de dépôt PCT/PCT Filing Date: 2000/06/23
(87) Date publication PCT/PCT Publication Date: 2001/01/04
(85) Entrée phase nationale/National Entry: 2001/12/20
(86) N° demande PCT/PCT Application No.: IB 2000/000923
(87) N° publication PCT/PCT Publication No.: 2001/000843
(30) Priorités/Priorities: 1999/06/25 (60/141,031) US;
1999/07/01 (199 30 476.9) DE;
1999/07/02 (60/142,101) US;
1999/07/08 (199 31 415.2) DE;
1999/07/08 (199 31 419.5) DE;
1999/07/08 (199 31 418.7) DE;
1999/07/08 (199 31 636.8) DE;
1999/07/08 (199 31 634.1) DE; ...

(51) Cl.Int.⁷/Int.Cl.⁷ C12N 15/31, C12N 9/90, C12Q 1/68,
C12N 15/61, C07K 14/34, C12N 1/21, C12P 13/08

(71) Demandeur/Applicant:
BASF AKTIENGESELLSCHAFT, DE

(72) Inventeurs/Inventors:
POMPEJUS, MARKUS, DE;
KROGER, BURKHARD, DE;
SCHRODER, HARTWIG, DE;
ZELDER, OSKAR, DE;
HABERHAUER, GREGOR, DE

(74) Agent: BORDEN LADNER GERVAIS LLP

(54) Titre : GENES DE CORYNEBACTERUM GLUTAMICUM CODANT POUR DES PROTEINES DE VOIE
METABOLIQUE

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

(57) **Abrégé/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.

(30) **Priorités(suite)/Priorities(continued):** 1999/07/08 (199 31 632.5) DE; 1999/07/08 (199 31 592.2) DE;
1999/07/08 (199 31 573.6) DE; 1999/07/08 (199 31 541.8) DE; 1999/07/08 (199 31 510.8) DE;
1999/07/08 (199 31 478.0) DE; 1999/07/08 (199 31 465.9) DE; 1999/07/08 (199 31 457.8) DE;
1999/07/08 (199 31 453.5) DE; 1999/07/08 (199 31 443.8) DE; 1999/07/08 (199 31 435.7) DE;
1999/07/08 (199 31 434.9) DE; 1999/07/08 (199 31 428.4) DE; 1999/07/08 (199 31 424.1) DE;
1999/07/08 (199 31 420.9) DE; 1999/07/09 (199 32 125.6) DE; 1999/07/09 (199 32 130.2) DE;
1999/07/09 (199 32 126.4) DE; 1999/07/09 (199 32 228.7) DE; 1999/07/09 (199 32 227.9) DE;
1999/07/09 (199 32 206.6) DE; 1999/07/09 (199 32 186.8) DE; 1999/07/09 (199 32 230.9) DE;
1999/07/09 (199 32 229.5) DE; 1999/07/14 (199 32 926.5) DE; 1999/07/14 (199 32 922.2) DE;
1999/07/14 (199 33 006.9) DE; 1999/07/14 (199 33 005.0) DE; 1999/07/14 (199 33 004.2) DE;
1999/07/14 (199 32 928.1) DE; 1999/08/12 (60/148,613) US; 1999/08/27 (199 40 764.9) DE;
1999/08/27 (199 40 766.5) DE; 1999/08/27 (199 40 765.7) DE; 1999/08/27 (199 40 832.7) DE;
1999/08/31 (199 41 378.9) DE; 1999/08/31 (199 41 394.0) DE; 1999/08/31 (199 41 379.7) DE;
1999/08/31 (199 41 380.0) DE; 1999/08/31 (199 41 396.7) DE; 1999/09/03 (199 42 129.3) DE;
1999/09/03 (199 42 077.7) DE; 1999/09/03 (199 42 087.4) DE; 1999/09/03 (199 42 086.6) DE;
1999/09/03 (199 42 079.3) DE; 1999/09/03 (199 42 076.9) DE; 1999/09/03 (199 42 124.2) DE;
1999/09/03 (199 42 095.5) DE; 1999/09/03 (199 42 088.2) DE; 2000/03/09 (60/187,970) US

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
4 January 2001 (04.01.2001)

(10) International Publication Number
WO 01/00843 A3

PCT

(51) International Patent Classification⁷: C12N 15/31, 15/61, 1/21, 9/90, C07K 14/34, C12P 13/08, C12Q 1/68 // (C12N 15/61, C12R 1:15)			199 33 004.2	14 July 1999 (14.07.1999)	DE
			199 33 005.0	14 July 1999 (14.07.1999)	DE
			199 33 006.9	14 July 1999 (14.07.1999)	DE
			60/148,613	12 August 1999 (12.08.1999)	US
(21) International Application Number: PCT/IB00/00923			199 40 764.9	27 August 1999 (27.08.1999)	DE
			199 40 765.7	27 August 1999 (27.08.1999)	DE
(22) International Filing Date: 23 June 2000 (23.06.2000)			199 40 766.5	27 August 1999 (27.08.1999)	DE
			199 40 832.7	27 August 1999 (27.08.1999)	DE
(25) Filing Language: English			199 41 378.9	31 August 1999 (31.08.1999)	DE
			199 41 379.7	31 August 1999 (31.08.1999)	DE
(26) Publication Language: English			199 41 394.0	31 August 1999 (31.08.1999)	DE
			199 41 396.7	31 August 1999 (31.08.1999)	DE
(30) Priority Data:			199 41 380.0	31 August 1999 (31.08.1999)	DE
60/141,031	25 June 1999 (25.06.1999)	US	199 42 077.7	3 September 1999 (03.09.1999)	DE
199 30 476.9	1 July 1999 (01.07.1999)	DE	199 42 129.3	3 September 1999 (03.09.1999)	DE
60/142,101	2 July 1999 (02.07.1999)	US	199 42 076.9	3 September 1999 (03.09.1999)	DE
199 31 415.2	8 July 1999 (08.07.1999)	DE	199 42 079.3	3 September 1999 (03.09.1999)	DE
199 31 418.7	8 July 1999 (08.07.1999)	DE	199 42 086.6	3 September 1999 (03.09.1999)	DE
199 31 419.5	8 July 1999 (08.07.1999)	DE	199 42 087.4	3 September 1999 (03.09.1999)	DE
199 31 420.9	8 July 1999 (08.07.1999)	DE	199 42 088.2	3 September 1999 (03.09.1999)	DE
199 31 424.1	8 July 1999 (08.07.1999)	DE	199 42 095.5	3 September 1999 (03.09.1999)	DE
199 31 428.4	8 July 1999 (08.07.1999)	DE	199 42 124.2	3 September 1999 (03.09.1999)	DE
199 31 434.9	8 July 1999 (08.07.1999)	DE	60/187,970	9 March 2000 (09.03.2000)	US
199 31 435.7	8 July 1999 (08.07.1999)	DE	(71) Applicant: BASF AKTIENGESELLSCHAFT [DE/DE]; D-67056 Ludwigshafen (DE).		
199 31 443.8	8 July 1999 (08.07.1999)	DE	(72) Inventors: POMPEJUS, Markus; Wenjenstr. 21, D-67251 Freinsheim (DE). KRÖGER, Burkhard; Im Waldhof 1, D-67117 Limburgerhof (DE). SCHRÖDER, Hartwig; Goethestr. 5, D-69226 Nussloch (DE). ZELDER, Oskar; Rossmarktstr. 27, D-67346 Speyer (DE). HABERHAUER, Gregor; Moselstr. 42, D-67117 Limburgerhof (DE).		
199 31 453.5	8 July 1999 (08.07.1999)	DE	(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.		
199 31 457.8	8 July 1999 (08.07.1999)	DE	(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE		
199 31 465.9	8 July 1999 (08.07.1999)	DE			
199 31 478.0	8 July 1999 (08.07.1999)	DE			
199 31 510.8	8 July 1999 (08.07.1999)	DE			
199 31 541.8	8 July 1999 (08.07.1999)	DE			
199 31 573.6	8 July 1999 (08.07.1999)	DE			
199 31 592.2	8 July 1999 (08.07.1999)	DE			
199 31 632.5	8 July 1999 (08.07.1999)	DE			
199 31 634.1	8 July 1999 (08.07.1999)	DE			
199 31 636.8	8 July 1999 (08.07.1999)	DE			
199 32 125.6	9 July 1999 (09.07.1999)	DE			
199 32 126.4	9 July 1999 (09.07.1999)	DE			
199 32 130.2	9 July 1999 (09.07.1999)	DE			
199 32 186.8	9 July 1999 (09.07.1999)	DE			

[Continued on next page]

(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.



WO 01/00843 A3

WO 01/00843 A3



IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

(88) Date of publication of the international search report:
29 March 2001

Published:

— *With international search report.*

— *Before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments.*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

DEMANDES OU BREVETS VOLUMINEUX

**LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVETS
COMPREND PLUS D'UN TOME.**

CECI EST LE TOME __1__ DE __4__

NOTE: Pour les tomes additionels, veuillez contacter le Bureau Canadien des Brevets.

JUMBO APPLICATIONS / PATENTS

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

THIS IS VOLUME __1__ OF __4__

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

- 1 -

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

Related Applications

The present application claims priority to prior filed U.S. Provisional Patent
5 Application Serial No. 60/141031, filed June 25 , 1999, U.S. Provisional Patent
Application Serial No. 60/142101, filed July 2, 1999, U.S. Provisional Patent
Application Serial No. 60/148613, filed August 12, 1999, and also to U.S. Provisional
Patent Application Serial No. 60/187970, filed March 9, 2000. The present application
also claims priority to prior filed German Patent Application No. 19930476.9, filed July
10 1, 1999, German Patent Application No. 19931415.2, filed July 8, 1999, German Patent
Application No. 19931418.7, filed July 8, 1999, German Patent Application No.
19931419.5, filed July 8, 1999, German Patent Application No. 19931420.9, filed July
8, 1999, German Patent Application No. 19931424.1, filed July 8, 1999, German Patent
Application No. 19931428.4, filed July 8, 1999, German Patent Application No.
15 19931434.9, filed July 8, 1999, German Patent Application No. 19931435.7, filed July
8, 1999, German Patent Application No. 19931443.8, filed July 8, 1999, German Patent
Application No. 19931453.5, filed July 8, 1999, German Patent Application No.
19931457.8, filed July 8, 1999, German Patent Application No. 19931465.9, filed July
8, 1999, German Patent Application No. 19931478.0, filed July 8, 1999, German Patent
20 Application No. 19931510.8, filed July 8, 1999, German Patent Application No.
19931541.8, filed July 8, 1999, German Patent Application No. 19931573.6, filed July
8, 1999, German Patent Application No. 19931592.2, filed July 8, 1999, German Patent
Application No. 19931632.5, filed July 8, 1999, German Patent Application No.
19931634.1, filed July 8, 1999, German Patent Application No. 19931636.8, filed July
25 8, 1999, German Patent Application No. 19932125.6, filed July 9, 1999, German Patent
Application No. 19932126.4, filed July 9, 1999, German Patent Application No.
19932130.2, filed July 9, 1999, German Patent Application No. 19932186.8, filed July
9, 1999, German Patent Application No. 19932206.6, filed July 9, 1999, German Patent
Application No. 19932227.9, filed July 9, 1999, German Patent Application No.
30 19932228.7, filed July 9, 1999, German Patent Application No. 19932229.5, filed July
9, 1999, German Patent Application No. 19932230.9, filed July 9, 1999, German Patent
Application No. 19932922.2, filed July 14, 1999, German Patent Application No.

- 2 -

19932926.5, filed July 14, 1999, German Patent Application No. 19932928.1, filed July 14, 1999, German Patent Application No. 19933004.2, filed July 14, 1999, German Patent Application No. 19933005.0, filed July 14, 1999, German Patent Application No. 19933006.9, filed July 14, 1999, German Patent Application No. 19940764.9, filed
5 August 27, 1999, German Patent Application No. 19940765.7, filed August 27, 1999, German Patent Application No. 19940766.5, filed August 27, 1999, German Patent Application No. 19940832.7, filed August 27, 1999, German Patent Application No. 19941378.9, filed August 31, 1999, German Patent Application No. 19941379.7, filed August 31, 1999, German Patent Application No. 19941380.0, filed August 31, 1999,
10 German Patent Application No. 19941394.0, filed August 31, 1999, German Patent Application No. 19941396.7, filed August 31, 1999, German Patent Application No. 19942076.9, filed September 3, 1999, German Patent Application No. 19942077.7, filed September 3, 1999, German Patent Application No. 19942079.3, filed September 3, 1999, German Patent Application No. 19942086.6, filed September 3, 1999, German
15 Patent Application No. 19942087.4, filed September 3, 1999, German Patent Application No. 19942088.2, filed September 3, 1999, German Patent Application No. 19942095.5, filed September 3, 1999, German Patent Application No. 19942124.2, filed September 3, 1999, and German Patent Application No. 19942129.3, filed September 3, 1999. The entire contents of all of the aforementioned applications are hereby expressly
20 incorporated herein by this reference.

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
25 pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through large-scale culture of bacteria developed to produce
30 and secrete large quantities of a particular desired molecule. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have

- 3 -

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.

5 Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related
10 bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as 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
15 degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of 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
20 invention, can be used to modulate the production of one or more fine chemicals from a microorganism (*e.g.*, to improve the yield or production of one or more fine chemicals from a *Corynebacterium* or *Brevibacterium* species).

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
25 presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain
30 whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium*

- 4 -

diphtheriae (the causative agent of diphtheria); the detection of such organisms is of 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.

5 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, vitamins, cofactors, nutraceuticals,

10 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

15 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
20 indirect effect of such manipulation. Specifically, alterations in *C. glutamicum* metabolic pathways for amino acids, 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 biosynthetic pathway protein or decreasing the activity of a lysine degradative pathway
25 protein may result in an increase in the yield or efficiency of production of lysine 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
30 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, a vitamin, or a nucleotide may increase the overall

- 5 -

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 may be utilized to
5 directly improve the production or efficiency of production of one or more desired fine chemicals from *Corynebacterium glutamicum*. Using recombinant genetic techniques well known in the art, one or more of the biosynthetic or degradative enzymes of the invention for amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, or trehalose may be manipulated such that its function is modulated. For example, a
10 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
15 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, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose through indirect mechanisms. Metabolism of any one compound is necessarily
20 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
25 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
30 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.

- 6 -

This invention provides novel nucleic acid molecules which encode proteins, referred to herein as metabolic pathway proteins (MP), 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, vitamins, cofactors, nucleotides and nucleosides, or trehalose. Nucleic acid molecules encoding an MP protein are referred to herein as MP nucleic acid molecules. In a preferred embodiment, the MP protein performs an enzymatic step related to the metabolism of one or more of the following: amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an 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, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth as the odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth as an odd-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth as an even-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8....). The preferred MP 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

- 7 -

sequence having an even-numbered SEQ ID NO: in the Sequence Listing), *e.g.*, sufficiently homologous to an amino acid sequence of the invention such that the protein or portion thereof maintains an 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, 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%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an 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). 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 NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....)).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an 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) and is able to catalyze a reaction in a metabolic pathway for an amino acid, 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). 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 portion thereof.

- 8 -

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

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

In another aspect, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of
25 one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in the Sequence Listing as SEQ ID NOs 1 through 1156) 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 a
30 portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated MP protein or portion thereof can catalyze an enzymatic reaction involved in one or more pathways for the metabolism of an amino acid, a vitamin, a cofactor, a

- 9 -

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 that the protein or portion thereof maintains the ability to
5 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
10 invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) (encoded by an open reading frame set forth in a corresponding odd-numbered SEQ ID NO: of the
15 Sequence Listing). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In other embodiments, the isolated MP protein
20 comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and is able to 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.

25 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%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98,%, or 99% or more homologous to a nucleotide sequence of one of
30 the even-numbered 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.

- 10 -

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 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 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 a vector directing the expression of an MP nucleic acid molecule of the invention, 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 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.

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

- 11 -

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.

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

15

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, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and
20 trehalose. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (*e.g.*, where modulation of the activity of a lysine biosynthesis protein has a direct impact on the production or efficiency of production of lysine from that organism), or may have an indirect impact which nonetheless results in an increase of
25 yield or efficiency of production of the 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). Aspects of the invention are further explicated below.

30

- 12 -

I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include

5 organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty

10 acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids,

15 Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) Chemicals by Fermentation, Noyes Data Corporation, ISBN:

20 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

A. Amino Acid Metabolism and Uses

Amino acids comprise the basic structural units of all proteins, and as such are

25 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 Ullmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH:

30 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

- 13 -

have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

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

- 14 -

step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain β -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

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

- 15 -

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

- 16 -

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.

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

- 17 -

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.

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

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
10 structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a 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
15 their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA 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).

20 Several publications have described the use of these chemicals for these medical 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
25 development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) “Enzymes in nucleotide synthesis.” *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine,
30 folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) Nucleotides and

- 18 -

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.

- 5 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,
10 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
15 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).
20 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.

25 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.
30 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

- 19 -

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

5 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, 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, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic
10 pathways. In a preferred embodiment, the activity of the MP molecules of the present invention 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
15 *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*.

 The language, “MP protein” or “MP polypeptide” includes proteins which play
20 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
25 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
30 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

- 20 -

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.

In another embodiment, the MP molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. Using recombinant genetic techniques, one or more of the biosynthetic or degradative enzymes of the invention for amino acids, 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

- 21 -

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.

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 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

The MP protein or a biologically active portion or fragment thereof of the invention can catalyze an enzymatic reaction in one or more amino acid, vitamin,

- 22 -

cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways, or have one or more of the activities set forth in Table 1.

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

5

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.

30

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

- 23 -

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., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.*, an odd-numbered SEQ ID NO:) can be isolated by 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

- 24 -

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 each of the nucleic acid and amino acid sequences set forth in the Sequence Listing has an identifying RXA, RXN, RXS, or RXC number having the designation "RXA", "RXN", "RXS", or "RXC" followed by 5 digits (*i.e.*, RXA00007, RXN00023, RXS00116, or RXC00128). 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 RXA02229 is set forth in SEQ ID NO:1, while the amino acid sequence which it encodes is set forth as SEQ ID NO:2. The 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 RXA02229, RX00351, RXS02970, and RXC02390 are translations of the coding regions of the nucleotide sequences of nucleic acid molecules RXA02229, RX00351, RXS02970, and RXC02390, 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:5, designated, as indicated on Table 1, as "F RXA01009", is an F-designated gene, as are SEQ ID NOs: 73, 75, and 77 (designated on Table 1 as "F RXA00007", "F RXA00364", and "F RXA00367", respectively).

- 25 -

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

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

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of the sequence of one of the odd-numbered SEQ ID NOs

- 26 -

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 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, 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. 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.

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, 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 Listing) amino acid residues to an amino acid sequence of the invention such that the

- 27 -

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, 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 forth in Table 1.

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

Portions of proteins encoded by the 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.

- 28 -

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 Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (*e.g.*, a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 40% identical to the nucleotide sequence designated RXA00115 (SEQ ID NO:185), a nucleotide sequence which is greater than and/or at least % identical to the nucleotide sequence designated RXA00131 (SEQ ID NO:991), and a nucleotide sequence which is greater than and/or at least 39% identical to the nucleotide sequence designated RXA00219 (SEQ ID NO:345). 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 acid sequences having percent identities greater than the lower threshold so calculated (*e.g.*, at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%,

- 29 -

74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more 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 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 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* 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 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 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.

- 30 -

A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by 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.*, encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* MP protein.

10 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 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-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.

15 20 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

25 30

- 31 -

acid molecule is at least about 50-60% homologous to the amino acid sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, more preferably at least about 60-70% homologous to one of these sequences, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of these sequences, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the amino acid sequences of the invention.

To determine the percent homology of two amino acid sequences (*e.g.*, one of the amino acid sequences of the invention and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence (*e.g.*, one of the amino acid sequences 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

- 32 -

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).

15 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 (RXA02229) comprises nucleotides 1 to 825). In another 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 sequences set forth as odd-numbered SEQ ID NOs in the Sequence Listing), antisense

- 33 -

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 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 antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-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 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).

- 34 -

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an MCT protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by
5 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 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
10 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 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.

15 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 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
20 chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they
25 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
30 (RXA02229). 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.*

- 35 -

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 RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

5 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 Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and
10 Maher, L.J. (1992) *Bioassays* 14(12):807-15.

B. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an MP protein (or a portion thereof). As
15 used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of
20 autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to
25 which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors,
30 such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

- 36 -

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

5 operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory

10 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 Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990).

15 Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as *cos*-, *tac*-, *trp*-, *tet*-, *trp-tet*-, *lpp*-, *lac*-, *lpp-lac*-, *lacI^q*-, *T7*-, *T5*-, *T3*-, *gal*-, *trc*-, *ara*-, *SP6*-, *arny*, *SPO2*, λ -*P_R*- or λ *P_L*, which are used preferably in bacteria.

20 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 ordinary skill in the art that the design of the expression vector can depend on such

25 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, fusion proteins, etc.).

30 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

- 37 -

expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* -mediated transformation of *Arabidopsis 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.

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 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 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 (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

- 38 -

the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant MP protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

5 Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315) pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1, λ gt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and
10 Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 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
15 host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming *Streptomyces*, while plasmids pUB110, pC194, or pBD214 are suited for transformation
20 of *Bacillus* species. Several plasmids of use in the transfer of genetic information into *Corynebacterium* include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York 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
25 recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in 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*
30 (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

- 39 -

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

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both

- 40 -

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.

- 5 In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* 10 (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), 15 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) 20 *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 25 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.
- 30 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

- 41 -

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

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these

- 42 -

integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be
5 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 marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which
10 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 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
15 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
20 endogenous MP protein). In the homologous recombination vector, the altered portion 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
25 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
30 endogenous MP gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene.

- 43 -

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.

In another embodiment, an endogenous MP gene in a host cell is disrupted (*e.g.*,
5 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 embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or
10 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 produced using the methods of the invention, and are meant to be included in the present
15 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
20 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.

25

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
30 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

- 44 -

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
5 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
10 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
15 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
20 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*.

An isolated MP protein or a portion thereof of the invention can catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide,
25 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 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
30 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

- 45 -

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 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 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of the invention, or a portion thereof. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred 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.

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 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%,

- 46 -

78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to 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 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 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 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

- 47 -

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
5 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
10 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
15 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
20 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
25 undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric
30 gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An MP-

- 48 -

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" 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 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 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 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).

- 49 -

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

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.*

- 50 -

glutamicum sequences of interest; evolutionary studies; determination of MP protein 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.

5 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 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
10 extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is not pathogenic to humans, it is related to species which are human pathogens, such as *Corynebacterium diphtheriae*.
15 *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the
20 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 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
25 least 5,000 deaths since 1990.

 In one embodiment, the invention provides a method of identifying the presence or activity of *Cornyebacterium 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
30 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*

- 51 -

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.

- 52 -

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
5 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
10 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
15 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
20 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
25 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
30 compounds, the modulation of activity of one of the proteins of the invention may still 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

- 53 -

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 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 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 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 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 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

- 54 -

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
5 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.

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

TABLE 1: 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>
1	2	RXA02229	GR00653	2793	3617	DIAMINOPELATE EPIMERASE (EC 5.1.1.7)
3	4	RXS02970				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
5	6	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
7	8	RXC02390				MEMBRANE SPANNING PROTEIN INVOLVED IN LYSINE METABOLISM
9	10	RXC01796				MEMBRANE ASSOCIATED PROTEIN INVOLVED IN LYSINE METABOLISM
11	12	RXC01207				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF LYSINE AND THREONINE
13	14	RXC00657				TRANSCRIPTIONAL REGULATOR INVOLVED IN LYSINE METABOLISM
15	16	RXC00552				CYTOSOLIC PROTEIN INVOLVED IN LYSINE METABOLISM

Trehalose

<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>
17	18	RXN00351	VV0135	37078	38532	ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 56 KD SUBUNIT (EC 2.4.1.15)
19	20	F RXA00351	GR00066	1486	2931	ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 56 KD SUBUNIT (EC 2.4.1.15)
21	22	RXA00873	GR00241	3	758	trehalose synthase (EC 2.4.1.-)
23	24	RXA00891	GR00243	1005	4	trehalose synthase (EC 2.4.1.-)

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>
25	26	RXA00534	GR00137	4758	3496	ASPARTOKINASE ALPHA AND BETA SUBUNITS (EC 2.7.2.4)
27	28	RXA00533	GR00137	3469	2438	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE (EC 1.2.1.11)
29	30	RXA02843	GR00842	543	4	2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
31	32	RXA02022	GR00613	2063	3169	SUCCINYL-DIAMINOPELATE DESUCCINYLASE (EC 3.5.1.18)
33	34	RXA00044	GR00007	3458	4393	DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52)
35	36	RXA00863	GR00236	896	1639	DIHYDRODIPICOLINATE REDUCTASE (EC 1.3.1.26)
37	38	RXA00864	GR00236	1694	2443	probable 2,3-dihydrodipicolinate N-C6-lyase (cyclizing) (EC 4.3.3.-) - Corynebacterium glutamicum
39	40	RXA02843	GR00842	543	4	2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
41	42	RXN00355	VV0135	31980	30961	MESO-DIAMINOPELATE D-DEHYDROGENASE
43	44	F RXA00352	GR00068	861	4	MESO-DIAMINOPELATE D-DEHYDROGENASE (EC 1.4.1.16)

Table 1 (continued)

<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>
45	46	RXA00972	GR00274	3	1379	DIAMINOPELMATE DECARBOXYLASE (EC 4.1.1.20)
47	48	RXA02653	GR00752	5237	7234	DIAMINOPELMATE DECARBOXYLASE (EC 4.1.1.20)
49	50	RXA01393	GR00408	4249	3380	LYSINE EXPORT REGULATOR PROTEIN
51	52	RXA00241	GR00036	5443	6945	L-LYSINE TRANSPORT PROTEIN
53	54	RXA01394	GR00408	4320	5018	LYSINE EXPORTER PROTEIN
55	56	RXA00865	GR00236	2647	3549	DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52)
57	58	RXS02021				2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
59	60	RXS02157				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
61	62	RXC00733				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN LYSINE METABOLISM
63	64	RXC00861				PROTEIN INVOLVED IN LYSINE METABOLISM
65	66	RXC00866				ZN-DEPENDENT HYDROLASE INVOLVED IN LYSINE METABOLISM
67	68	RXC02095				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN LYSINE METABOLISM
69	70	RXC03185				PROTEIN INVOLVED IN LYSINE METABOLISM

Glutamate and glutamine metabolism

<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>
71	72	RXN00367	VV0196	9744	14273	GLUTAMATE SYNTHASE [NADH] PRECURSOR (EC 1.4.1.14)
73	74	F RXA00007	GR00001	7107	8912	GLUTAMATE SYNTHASE (NADPH) LARGE CHAIN PRECURSOR (EC 1.4.1.13)
75	76	F RXA00364	GR00074	1296	4	GLUTAMATE SYNTHASE (NADPH) LARGE CHAIN PRECURSOR (EC 1.4.1.13)
77	78	F RXA00367	GR00075	1806	964	GLUTAMATE SYNTHASE (NADPH) LARGE CHAIN PRECURSOR (EC 1.4.1.13)
79	80	RXN00076	VV0154	2752	4122	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
81	82	F RXA00075	GR00012	2757	3419	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
83	84	RXN00198	VV0181	7916	7368	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
85	86	F RXA00198	GR00031	2	283	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
87	88	RXN00365	VV0196	14607	15233	GLUTAMATE SYNTHASE [NADPH] SMALL CHAIN (EC 1.4.1.13)
89	90	F RXA00365	GR00075	630	4	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
91	92	RXA00366	GR00075	961	605	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
93	94	RXA02072	GR00628	1259	2599	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
95	96	RXA00323	GR00057	3855	5192	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
97	98	RXA00335	GR00057	19180	17750	NADP-SPECIFIC GLUTAMATE DEHYDROGENASE (EC 1.4.1.4)
99	100	RXA00324	GR00057	5262	8396	GLUTAMINE SYNTHETASE (EC 6.3.1.2)
101	102	RXN03176	VV0332	2	862	GLUTAMINE SYNTHETASE (EC 6.3.1.2)
103	104	F RXA02879	GR10017	2	862	GLUTAMINE SYNTHETASE (EC 6.3.1.2)
105	106	RXA00278	GR00043	2612	1581	GLUTAMINE-BINDING PROTEIN PRECURSOR
107	108	RXA00727	GR00193	614	1525	GLUTAMINE-BINDING PERIPLASMIC PROTEIN PRECURSOR

Table 1 (continued)
Alanine and Aspartate and Asparagine metabolism

<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>
109	110	RXA02139	GR00639	6739	4901	ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING) (EC 6.3.5.4)
111	112	RXN00116	VV0100	26974	25814	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
113	114	F RXA00116	GR00018	510	4	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
115	116	RXN00618	VV0135	10288	9182	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
117	118	F RXA00618	GR00163	213	746	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
119	120	F RXA00627	GR00164	854	1138	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
121	122	RXA02550	GR00729	1585	275	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
123	124	RXA02193	GR00645	1942	365	ASPARTATE AMMONIA-LYASE (EC 4.3.1.1)
125	126	RXA02432	GR00708	2669	1695	L-ASPARAGINASE (EC 3.5.1.1)
127	128	RXN03003	VV0138	680	6	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
129	130	RXN00508	VV0086	4701	5783	ALANINE RACEMASE (EC 5.1.1.1)
131	132	RXN00636	VV0135	20972	19944	ALANINE RACEMASE, BIOSYNTHETIC (EC 5.1.1.1)

beta-Alanine metabolism

<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>
133	134	RXA02536	GR00726	8581	7826	BETA-UREIDOPROPIONASE (EC 3.5.1.6)
135	136	RXS00870				METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE (ACYLATING) (EC 1.2.1.27)
137	138	RXS02299				ASPARTATE 1-DECARBOXYLASE PRECURSOR (EC 4.1.1.11)

Glycine and serine metabolism

<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>
139	140	RXA01561	GR00435	1113	2042	L-SERINE DEHYDRATASE (EC 4.2.1.13)
141	142	RXA01850	GR00525	481	1827	L-SERINE DEHYDRATASE (EC 4.2.1.13)
143	144	RXA00580	GR00156	7343	6042	SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1)
145	146	RXA01821	GR00515	10253	9876	SARCOSINE OXIDASE (EC 1.5.3.1)
147	148	RXN02263	VV0202	11783	12160	SARCOSINE OXIDASE (EC 1.5.3.1)
149	150	F RXA02263	GR00654	33454	33813	SARCOSINE OXIDASE (EC 1.5.3.1)
151	152	RXA02176	GR00641	11454	12581	PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52)
153	154	RXN02758	GR00766	5082	4648	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
155	156	F RXA02479	GR00717	393	4	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
157	158	F RXA02758	GR00766	5082	4648	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
159	160	F RXA02759	GR00766	5330	5220	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
161	162	RXA02501	GR00720	15041	13977	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
163	164	RXN03105	VV0074	15857	15423	SARCOSINE OXIDASE (EC 1.5.3.1)
165	166	RXS01130				D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
167	168	RXS03112				D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)

Table 1 (continued)

Threonine metabolism

<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>
169	170	RXN00969	VV0149	12053	13387	HOMOSERINE DEHYDROGENASE (EC 1.1.1.3)
171	172	F RXA00974	GR00274	2623	3015	HOMOSERINE DEHYDROGENASE (EC 1.1.1.3)
173	174	RXA00970	GR00273	161	1087	HOMOSERINE KINASE (EC 2.7.1.39)
175	176	RXA00330	GR00057	12968	14410	THREONINE SYNTHASE (EC 4.2.99.2)
177	178	RXN00403	VV0086	70041	68911	HOMOSERINE O-ACETYLTRANSFERASE
179	180	F RXA00403	GR00088	723	1832	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.11)
181	182	RXC01207				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF LYSINE AND THREONINE
183	184	RXC00152				MEMBRANE ASSOCIATED PROTEIN INVOLVED IN THREONINE 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>
185	186	RXA00115	GR00017	5359	4313	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.31)
187	188	RXN00403	VV0086	70041	68911	HOMOSERINE O-ACETYLTRANSFERASE
189	190	F RXA00403	GR00088	723	1832	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.11)
191	192	RXS03158				CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
193	194	F RXA00254	GR00038	2404	1811	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
195	196	RXA02532	GR00726	3085	2039	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
197	198	RXS03159				CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
199	200	F RXA02768	GR00770	1919	2521	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
201	202	RXA00216	GR00032	16286	15297	5-methyltetrahydrofolate-homocysteine methyltransferase (methionine synthetase)
203	204	RXN00402	VV0086	70787	70188	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
205	206	F RXA00402	GR00088	1	576	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
207	208	RXA00405	GR00089	3289	3801	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
209	210	RXA02197	GR00645	4552	4025	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
211	212	RXN02198	VV0302	9228	11726	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
213	214	F RXA02198	GR00646	2483	6	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
215	216	RXN03074	VV0042	2238	1741	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
217	218	F RXA02906	GR10044	1142	645	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
219	220	RXN00132	VV0124	3612	5045	ADENOSYLMOCYSTEINASE (EC 3.3.1.1)
221	222	F RXA00132	GR00020	7728	7624	ADENOSYLMOCYSTEINASE (EC 3.3.1.1)

Table 1 (continued)

<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>
223	224	F RXA01371 RXN02085	GR00398	2339	3634	ADENOSYLHOMOCYSTEINASE (EC 3.3.1.1)
225	226					5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
227	228	F RXA02085	GR00629	3496	5295	METHYLTRANSFERASE (EC 2.1.1.14)
229	230	F RXA02086	GR00629	5252	5731	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
231	232	RXN02648				METHYLTRANSFERASE (EC 2.1.1.14)
233	234	F RXA02648	GR00751	5254	4730	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
235	236	F RXA02658	GR00752	14764	15447	METHYLTRANSFERASE (EC 2.1.1.14)
237	238	RXC02238				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
239	240	RXC00128				METHYLTRANSFERASE (EC 2.1.1.14) PROTEIN INVOLVED IN METABOLISM OF S-ADENOSYLMETHIONINE, PURINES AND PANTOTHENATE EXPORTED PROTEIN INVOLVED IN METABOLISM OF PYRIDIMES AND ADENOSYLHOMOCYSTEINE

S-adenosyl 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>
241	242	RXA02240	GR00654	7160	8380	S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6)

Cysteine metabolism

<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>
243	244	RXA00780	GR00206	1689	2234	SERINE ACETYLTRANSFERASE (EC 2.3.1.30)
245	246	RXA00779	GR00206	550	1482	CYSTEINE SYNTHASE (EC 4.2.99.8)
247	248	RXN00402	VV0086	70787	70188	O-ACETYLMOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
249	250	F RXA00402	GR00088	1	576	O-ACETYLMOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
251	252	RXS00405				O-ACETYLMOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
253	254	RXC00164				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN CYSTEINE METABOLISM
255	256	RXC01191				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN CYSTEINE METABOLISM

Table 1 (continued)

Valine, leucine and isoleucine

<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>
257	258	RXA02646	GR00751	3856	2588	THREONINE DEHYDRATASE BIOSYNTHETIC (EC 4.2.1.16)
259	260	RXA00766	GR00204	5091	4249	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
261	262	RXN01690	VV0246	1296	196	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
263	264	F RXA01690	GR00473	1248	196	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
265	266	RXN01026	VV0143	9171	7513	3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (EC 4.2.1.33)
267	268	F RXA01026	GR00294	1	1602	3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (EC 4.2.1.33)
269	270	RXN01127	VV0157	4491	3472	3-ISOPROPYLMALATE DEHYDROGENASE (EC 1.1.1.85)
271	272	F RXA01132	GR00315	1349	1651	3-ISOPROPYLMALATE DEHYDROGENASE (EC 1.1.1.85)
273	274	RXN00536	VV0219	6128	7498	2-ISOPROPYLMALATE SYNTHASE (EC 4.1.3.12)
275	276	F RXA00536	GR00137	6128	7360	2-ISOPROPYLMALATE SYNTHASE (EC 4.1.3.1)
277	278	RXN02965	VV0143	7711	7121	3-ISOPROPYLMALATE DEHYDRATASE SMALL SUBUNIT (EC 4.2.1.33)
279	280	RXN01929	VV0127	47590	48402	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11) / DECARBOXYLASE (EC 4.1.1.44)
281	282	F RXA01929	GR00555	2766	1960	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11)
283	284	RXN01420	VV0122	15584	14643	4"-MYCAROSYL ISOVALERYL-COA TRANSFERASE (EC 2.-.-.-)
285	286	RXS01145				KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)
287	288	F RXA01145	GR00321	1075	1530	KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)

Arginine and proline metabolism

Enzymes of proline 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>
289	290	RXA02375	GR00689	1449	223	GLUTAMATE 5-KINASE (EC 2.7.2.11)
291	292	RXN02382	VV0213	5162	3867	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41)
293	294	F RXA02378	GR00690	624	16	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41)
295	296	F RXA02382	GR00691	2493	1894	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41)
297	298	RXA02499	GR00720	11883	12692	PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2)
299	300	RXS02157				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
301	302	RXS02262				ORNITHINE CYCLODEAMINASE (EC 4.3.1.12)
303	304	RXS02970				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
305	306	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)

Table 1 (continued)

Enzymes of proline degradation:

<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>
307	308	RXN00023	VV0127	68158	64703	PROLINE DEHYDROGENASE (EC 1.5.99.8) / DELTA-1- PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (EC 1.5.1.12)
309	310	F RXA00023	GR00003	2	454	PROLINE DEHYDROGENASE (EC 1.5.99.8) / DELTA-1- PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (EC 1.5.1.12)
311	312	F RXA02284	GR00660	3028	5	PROLINE DEHYDROGENASE (EC 1.5.99.8) / DELTA-1- PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (EC 1.5.1.12)
313	314	RXC02498				PROTEIN INVOLVED IN PROLINE METABOLISM

Synthesis of 3-Hydroxy-proline:

<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>
315	316	RXA01491	GR00423	5337	4687	DNA FOR L-PROLINE 3-HYDROXYLASE, COMPLETE CDS

Enzymes of ornithine, arginine and spermidine metabolism:

<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>
317	318	RXA02155	GR00640	1913	3076	GLUTAMATE N-ACETYLTRANSFERASE (EC 2.3.1.35) / AMINO-ACID ACETYLTRANSFERASE (EC 2.3.1.1)
319	320	RXA02156	GR00640	3125	4075	ACETYLGLUTAMATE KINASE (EC 2.7.2.8)
321	322	RXN02153	VV0122	14106	13327	N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE (EC 1.2.1.38)
323	324	F RXA02153	GR00640	757	1536	N-ACETYLGLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE
325	326	RXA02154	GR00640	1536	1826	N-ACETYLGLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE
327	328	RXA02157	GR00640	4079	5251	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
329	330	RXS02970				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
331	332	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
333	334	RXA02158	GR00640	5268	6224	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
335	336	RXA02160	GR00640	6914	8116	ORNITHINE CARBAMOYLTRANSFERASE (EC 2.1.3.3)
337	338	RXN02162	VV0122	6683	5253	ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5)
339	340	F RXA02161	GR00640	8180	8962	ARGININOSUCCINATE LYASE (EC 4.3.2.1)
341	342	F RXA02162	GR00640	8949	9611	ARGININOSUCCINATE LYASE (EC 4.3.2.1)
343	344	RXA02262	GR00654	32291	33436	ARGININOSUCCINATE LYASE (EC 4.3.2.1)
345	346	RXA00219	GR00032	19289	20230	ORNITHINE CYCLODEAMINASE (EC 4.3.1.12)
347	348	RXA01508	GR00424	12652	14190	SPERMIDINE SYNTHASE (EC 2.5.1.16)
349	350	RXA01757	GR00498	2942	2142	SPERMIDINE SYNTHASE (EC 2.5.1.16)
351	352	RXA02159	GR00640	6231	6743	PUTRESCINE OXIDASE (EC 1.4.3.10)
353	354	RXN02154	VV0122	13327	13037	ARGININE HYDROXIMATE RESISTANCE PROTEIN
355	356	RXS00147				N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE (EC 1.2.1.38)
357	358	RXS00905				CARBAMOYL-PHOSPHATE SYNTHASE SMALL CHAIN (EC 6.3.5.5)
359	360	RXS00906				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
						N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)

Table 1 (continued)

<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>
361	362	RXS00907				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
363	364	RXS02001				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
365	366	RXS02101				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
367	368	RXS02234				CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
369	370	F RXA02234	GR00654	1	3198	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
371	372	RXS02565				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
373	374	RXS02937				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)

Histidine metabolism

<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>
375	376	RXA02194	GR00645	2897	2055	ATP PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.17)
377	378	RXA02195	GR00645	3186	2917	PHOSPHORIBOSYL-ATP PYROPHOSPHOHYDROLASE (EC 3.6.1.31)
379	380	RXA01097	GR00306	4726	4373	PHOSPHORIBOSYL-AMP CYCLOHYDROLASE (EC 3.5.4.19)
381	382	RXA01100	GR00306	7072	6335	PHOSPHORIBOSYLFORMIMINO-5-AMINOIMIDAZOLE CARBOXAMIDE RIBOTIDE ISOMERASE (EC 5.3.1.16)
383	384	RXA01101	GR00306	7726	7094	AMIDOTRANSFERASE HISH (EC 2.4.2.-)
385	386	RXN01657	VV0010	39950	39351	AMIDOTRANSFERASE HISH (EC 2.4.2.-)
387	388	F RXA01657	GR00460	2444	2944	AMIDOTRANSFERASE HISH (EC 2.4.2.-)
389	390	RXA01098	GR00306	5499	4726	HISF PROTEIN
391	392	RXN01104	VV0059	7037	6432	IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (EC 4.2.1.19)
393	394	F RXA01104	GR00306	10927	10322	IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (EC 4.2.1.19) / HISTIDINOL-PHOSPHATASE (EC 3.1.3.15)
395	396	RXN00446	VV0112	24181	23318	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
397	398	F RXA00446	GR00108	4	525	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
399	400	RXA01105	GR00306	12044	10947	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
401	402	RXA01106	GR00306	13378	12053	HISTIDINOL DEHYDROGENASE (EC 1.1.1.23)
403	404	RXC00930				PROTEIN INVOLVED IN HISTIDINE METABOLISM
405	406	RXC01096				PROTEIN INVOLVED IN HISTIDINE METABOLISM
407	408	RXC01656				PROTEIN INVOLVED IN HISTIDINE METABOLISM
409	410	RXC01158				MEMBRANE SPANNING PROTEIN INVOLVED IN HISTIDINE METABOLISM

Metabolism of aromatic amino acids

<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>
411	412	RXA02458	GR00712	3056	4345	3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE (EC 2.5.1.19)
413	414	RXA02790	GR00777	5806	6948	4-AMINO-4-DEOXYCHORISMATE LYASE (EC 4.-.-.-)
415	416	RXN00954	VV0247	3197	2577	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.18)
417	418	F RXA00954	GR00263	3	590	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.18)
419	420	RXN00957	VV0208	1211	2764	ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27)
421	422	F RXA00957	GR00264	3	1130	ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start		NT Stop		Function
423	424	RXA02687	GR00754	11306	12250			CHORISMATE MUTASE (EC 5.4.99.5) / PREPHENATE DEHYDRATASE (EC 4.2.1.51)
425	426	RXN01698	VV0134	11507	12736			CHORISMATE SYNTHASE (EC 4.6.1.4)
427	428	F RXA01698	GR00477	2	991			CHORISMATE SYNTHASE (EC 4.6.1.4)
429	430	RXA01095	GR00306	3603	2821			INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE (EC 4.1.1.48)
431	432	RXA00955	GR00263	586	2007			INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE (EC 4.1.1.48) / N-(5'-PHOSPHO-RIBOSYL)ANTHRANILATE ISOMERASE (EC 5.3.1.24)
433	434	RXA02814	GR00795	598	128			ISOCHORISMATE MUTASE
435	436	RXA00229	GR00033	1715	936			SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.25)
437	438	RXA02093	GR00629	12444	13247			SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.25)
439	440	RXA02791	GR00777	6968	7795			SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.25)
441	442	RXA01699	GR00477	984	1553			SHIKIMATE KINASE (EC 2.7.1.71)
443	444	RXA00952	GR00262	97	936			TRYPTOPHAN SYNTHASE ALPHA CHAIN (EC 4.2.1.20)
445	446	RXN00956	VV0247	1140	4			TRYPTOPHAN SYNTHASE BETA CHAIN (EC 4.2.1.20)
447	448	F RXA00956	GR00263	2027	3157			TRYPTOPHAN SYNTHASE BETA CHAIN (EC 4.2.1.20)
449	450	RXA00064	GR00010	2499	3776			TYROSINE AMINOTRANSFERASE (EC 2.6.1.5)
451	452	RXN00448	VV0112	33959	32940			PREPHENATE DEHYDROGENASE (EC 1.3.1.12)
453	454	F RXA00448	GR00109	3	668			PREPHENATE DEHYDROGENASE (EC 1.3.1.12)
455	456	F RXA00452	GR00110	854	1099			PREPHENATE DEHYDROGENASE (EC 1.3.1.12)
457	458	RXA00584	GR00156	11384	10260			PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)
459	460	RXA00579	GR00156	5946	4087			PARA-AMINOBENZOATE SYNTHASE COMPONENT I (EC 4.1.3.-)
461	462	RXA00958	GR00264	1130	1753			PARA-AMINOBENZOATE SYNTHASE GLUTAMINE AMIDOTRANSFERASE COMPONENT II (EC 4.1.3.-) / ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27)
463	464	RXN03007	VV0208	3410	3778			ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27)
465	466	RXN02918	VV0086	25447	25887			TRYPTOPHAN SYNTHASE BETA CHAIN (EC 4.2.1.20)
467	468	RXN01116	VV0182	7497	6886			3-OXOADIPATE COA-TRANSFERASE SUBUNIT B (EC 2.8.3.6)
469	470	RXN01115	VV0182	10347	11099			3-OXOADIPATE ENOL-LACTONE HYDROLASE (EC 3.1.1.24) / 4-CARBOXYMUCONOLACTONE
471	472	RXS00116						ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
473	474	F RXA00116	GR00018	510	4			ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
475	476	RXS00391						O-SUCCINYLBENZOIC ACID--COA LIGASE (EC 6.2.1.26)
477	478	RXS00393						1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.-)
479	480	F RXA00393	GR00086	4030	4911			1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.-)
481	482	RXS00446						HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
483	484	F RXA00446	GR00108	4	525			HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
485	486	RXS00618						ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
487	488	F RXA00618	GR00163	213	746			ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
489	490	F RXA00627	GR00164	854	1138			ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
491	492	RXS01105						HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
493	494	RXS02315						2-SUCCINYL-6-HYDROXY-2,4-CYCLOHEXADIENE-1-CARBOXYLATE SYNTHASE / 2-OXOGLUTARATE DECARBOXYLASE (EC 4.1.1.71)
495	496	RXS02550						ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
497	498	RXS02319						NAPHTHOATE SYNTHASE (EC 4.1.3.36)
499	500	RXS02908						O-SUCCINYLBENZOIC ACID--COA LIGASE (EC 6.2.1.26)
501	502	RXS03003						ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
503	504	RXS03026						3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10)

Table 1 (continued)

<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>
505	506	RXS03074				S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
507	508	RXC01434				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS AND RIBOFLAVIN
509	510	RXC02080				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS
511	512	RXC02789				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS
513	514	RXC02295				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS

Aminobutyrate metabolism

<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>
515	516	RXN03063	VV0035	666	1697	4-aminobutyrate aminotransferase (EC 2.6.1.19)
517	518	RXN02970	VV0021	4714	6081	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
519	520	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)

Vitamins, vitamin-like substances (cofactors), nutraceuticals

Thiamine metabolism

<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>
521	522	RXA01551	GR00431	2945	4819	THIAMIN BIOSYNTHESIS PROTEIN THIC
523	524	RXA01019	GR00291	6	995	THIAMIN-MONOPHOSPHATE KINASE (EC 2.7.4.16)
525	526	RXA01352	GR00393	609	4	THIAMIN-PHOSPHATE PYROPHOSPHORYLASE (EC 2.5.1.3)
527	528	RXA01381	GR00403	3206	2286	THIF PROTEIN
529	530	RXA01360	GR00394	162	4	THIG PROTEIN
531	532	RXA01361	GR00394	983	378	THIG PROTEIN
533	534	RXA01208	GR00348	229	1032	HYDROXYETHYLTHIAZOLE KINASE (EC 2.7.1.50)
535	536	RXA00838	GR00227	1532	633	APBA PROTEIN
537	538	RXA02400	GR00699	1988	2557	THIAMIN BIOSYNTHESIS PROTEIN X
539	540	RXN01209	VV0270	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
541	542	F RXA01209	GR00348	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
543	544	RXN01413	VV0050	27306	27905	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
545	546	RXN01617	VV0050	22187	22858	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
547	548	F RXA01617	GR00451	2	616	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
549	550	RXS01807				PYRIDOXINE KINASE (EC 2.7.1.35)
551	552	RXC01021				CYTOSOLIC KINASE INVOLVED IN METABOLISM OF SUGARS AND THIAMIN

Table 1 (continued)

Riboflavin metabolism

<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>
553	554	RXN02246	VV0130	4388	5371	diaminohydroxyphosphoribosylaminopyrimidine deaminase (EC 3.5.4.26) / 5-amino-6-(5-phosphoribosylamino)uracil reductase (EC 1.1.1.193)
555	556	F RXA02246	GR00654	14299	15282	RIBG PROTEIN riboflavin-specific deaminase [EC:3.5.4.-]
557	558	RXA02247	GR00654	15286	15918	RIBOFLAVIN SYNTHASE ALPHA CHAIN (EC 2.5.1.9)
559	560	RXN02248	VV0130	6021	7286	GTP CYCLOHYDROLASE II (EC 3.5.4.25) / 3,4-DIHYDROXY-2-BUTANONE 4-PHOSPHATE SYNTHASE
561	562	F RXA02248	GR00654	15932	17197	RIBA PROTEIN - GTP cyclohydrolase II [EC:3.5.4.25]
563	564	RXN02249	VV0130	7301	7777	6,7-DIMETHYL-8-RIBITYLLUMAZINE SYNTHASE (EC 2.5.1.9)
565	566	F RXA02249	GR00654	17212	17688	RIBH PROTEIN - 6,7-dimethyl-8-ribityllumazine synthase (dmrl synthase, lumazine synthase, riboflavin synthase beta chain) [EC:2.5.1.9]
567	568	RXA02250	GR00654	17778	18356	RIBX PROTEIN
569	570	RXA01489	GR00423	3410	2388	RIBOFLAVIN KINASE (EC 2.7.1.26) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2)
571	572	RXA02135	GR00639	2809	1736	NICOTINATE-NUCLEOTIDE--DIMETHYLBENZIMIDAZOLE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.21)
573	574	RXA01489	GR00423	3410	2388	RIBOFLAVIN KINASE (EC 2.7.1.26) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2)
575	576	RXN01712	VV0191	8993	8298	RIBOFLAVIN-SPECIFIC DEAMINASE (EC 3.5.4.-)
577	578	F RXA01712	GR00484	2652	2152	RIBOFLAVIN-SPECIFIC DEAMINASE (EC 3.5.4.-)
579	580	RXN02384	VV0213	1386	679	ALPHA-RIBAZOLE-5'-PHOSPHATE PHOSPHATASE (EC 3.1.3.-)
581	582	RXN01560	VV0319	767	438	RIBOFLAVIN-SPECIFIC DEAMINASE (EC 3.5.4.-)
583	584	RXN00667	VV0109	1363	350	DRAP DEAMINASE
585	586	RXC01711				MEMBRANE SPANNING PROTEIN INVOLVED IN RIBOFLAVIN METABOLISM
587	588	RXC02380				PROTEIN INVOLVED IN RIBOFLAVIN METABOLISM
589	590	F RXA02380		709	56	Predicted nucleotidyltransferases
591	592	RXC02921	GR00691			CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF RIBOFLAVIN AND LIPIDS
593	594	RXC01434				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS AND RIBOFLAVIN

Vitamin B6 metabolism

<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>
595	596	RXA01807	GR00509	7868	7077	PYRIDOXINE KINASE (EC 2.7.1.35), pyridoxal/pyridoxine/pyridoxamine kinase

Table 1 (continued)
Nicotinate (nicotinic acid), nicotinamide, NAD and NADP

<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>
597	598	RXN02754	VV0084	22564	23901	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)
599	600	F RXA02405	GR00701	774	4	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)
601	602	F RXA02754	GR00766	3	488	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)
603	604	RXA02112	GR00632	5600	6436	NICOTINATE-NUCLEOTIDE PYROPHOSPHORYLASE (CARBOXYLATING) (EC 2.4.2.19)
605	606	RXA02111	GR00632	4310	5593	QUINOLINATE SYNTHETASE A

NAD 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>
607	608	RXA01073	GR00300	1274	2104	NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1)
609	610	RXN02754	VV0084	22564	23901	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)

Pantothenate and Coenzyme A (CoA) 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>
611	612	RXA02299	GR00662	10452	10859	ASPARTATE 1-DECARBOXYLASE PRECURSOR (EC 4.1.1.11)
613	614	RXA01928	GR00555	1957	1121	PANTOATE--BETA-ALANINE LIGASE (EC 6.3.2.1)
615	616	RXN01929	VV0127	47590	48402	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11) / DECARBOXYLASE (EC 4.1.1.44)
617	618	F RXA01929	GR00555	2766	1960	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11)
619	620	RXA01521	GR00424	25167	25964	PANTOATE--BETA-ALANINE LIGASE (EC 6.3.2.1)
621	622	RXS01145				KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)
623	624	F RXA01145	GR00321	1075	1530	KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)
625	626	RXA02239	GR00654	5784	7049	DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN
627	628	RXA00581	GR00156	7572	8540	PANTOTHENATE KINASE (EC 2.7.1.33)
629	630	RXS00838				2-DEHYDROPANTOATE 2-REDUCTASE (EC 1.1.1.169)
631	632	RXC02238				PROTEIN INVOLVED IN METABOLISM OF S-ADENOSYLMETHIONINE, PURINES AND PANTOTHENATE

Biotin metabolism

<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>
633	634	RXN03058	VV0028	8272	8754	BIOTIN SYNTHESIS PROTEIN BIOC

Table 1 (continued)

<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>
635	636	F RXA02903	GR10040	11532	12014	BIOTIN SYNTHESIS PROTEIN BIOC
637	638	RXA00166	GR00025	3650	4309	BIOTIN SYNTHESIS PROTEIN BIOC
639	640	RXA00633	GR00166	3556	2288	ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (EC 2.6.1.62)
641	642	RXA00632	GR00166	2281	1610	DETHIOBIOTIN SYNTHETASE (EC 6.3.3.3)
643	644	RXA00295	GR00047	3407	4408	BIOTIN SYNTHASE (EC 2.8.1.6)
645	646	RXA00223	GR00032	23967	22879	NIFS PROTEIN
647	648	RXN00262	VV0123	16681	15608	NIFS PROTEIN
649	650	F RXA00262	GR00040	79	897	NIFS PROTEIN
651	652	RXN00435	VV0112	10037	11209	NIFS PROTEIN
653	654	F RXA00435	GR00100	3563	2949	NIFS PROTEIN
655	656	F RXA02801	GR00782	438	4	NIFS PROTEIN
657	658	RXA02516	GR00723	1724	2986	NIFS PROTEIN
659	660	RXA02517	GR00723	2989	3435	NIFU PROTEIN

Lipoic Acid

<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>
661	662	RXA01747	GR00495	2506	3549	LIPIC ACID SYNTHETASE
663	664	RXA01746	GR00495	1614	2366	LIPOATE-PROTEIN LIGASE B (EC 6.-.-.-)
665	666	RXA02106	GR00632	472	1527	LIPOATE-PROTEIN LIGASE A (EC 6.-.-.-)
667	668	RXS01183				DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2- OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
669	670	RXS01260				LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)
671	672	RXS01261				LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)

Folate 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>
673	674	RXA02717	GR00758	18281	17400	5,10-METHYLENETETRAHYDROFOLATE REDUCTASE (EC 1.7.99.5)
675	676	RXN02027	VV0296	503	1003	5-FORMYLTETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.3.2)
677	678	F RXA02027	GR00616	500	6	5-FORMYLTETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.3.2)
679	680	RXA00106	GR00014	17469	17924	DIHYDROFOLATE REDUCTASE (EC 1.5.1.3)
681	682	RXN01321	VV0082	8868	9788	FORMYLTETRAHYDROFOLATE DEFORMYLASE (EC 3.5.1.10)
683	684	F RXA01321	GR00384	23	559	FORMYLTETRAHYDROFOLATE DEFORMYLASE (EC 3.5.1.10)
685	686	RXA00461	GR00116	428	1279	METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9)
687	688	RXA01514	GR00424	20922	21509	GTP CYCLOHYDROLASE I (EC 3.5.4.16)
689	690	RXA01516	GR00424	22360	22749	DIHYDRONEOPTERIN ALDOLASE (EC 4.1.2.25)

Table 1 (continued)

<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>
691	692	RXA01515	GR00424	21513	22364	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
693	694	RXA02024	GR00613	4026	4784	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
695	696	RXA00106	GR00014	17469	17924	DIHYDROFOLATE REDUCTASE (EC 1.5.1.3)
697	698	RXA00989	GR00280	2903	1371	FOLYLPOLYGLUTAMATE SYNTHASE (EC 6.3.2.17)
699	700	RXA01517	GR00424	22752	23228	2-AMINO-4-HYDROXY-6-HYDROXYMETHYLDIHYDROPTERIDINE PYROPHOSPHOKINASE (EC 2.7.6.3)
701	702	RXA00579	GR00156	5946	4087	PARA-AMINOBENZOATE SYNTHASE COMPONENT I (EC 4.1.3.-)
703	704	RXA00958	GR00264	1130	1753	PARA-AMINOBENZOATE SYNTHASE GLUTAMINE AMIDOTRANSFERASE COMPONENT II (EC 4.1.3.-) / ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27)
705	706	RXA02790	GR00777	5806	6948	4-AMINO-4-DEOXYCHORISMATE LYASE (EC 4.-.-.-)
707	708	RXA00106	GR00014	17469	17924	DIHYDROFOLATE REDUCTASE (EC 1.5.1.3)
709	710	RXN02198	VV0302	9228	11726	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
711	712	F RXA02198	GR00646	2483	6	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
713	714	RXN02085	VV0126	8483	10717	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE
715	716	F RXA02085	GR00629	3496	5295	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
717	718	F RXA02086	GR00629	5252	5731	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
719	720	RXN02648				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
721	722	F RXA02648	GR00751	5254	4730	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
723	724	F RXA02658	GR00752	14764	15447	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
725	726	RXS02197				5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
727	728	RXC00988				PROTEIN INVOLVED IN FOLATE METABOLISM
729	730	RXC01518				MEMBRANE SPANNING PROTEIN INVOLVED IN FOLATE METABOLISM
731	732	RXC01942				ATP-BINDING PROTEIN INVOLVED IN FOLATE METABOLISM

Molybdopterin Metabolism

<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>
733	734	RXN02802	VV0112	17369	16299	MOLYBDOPTERIN BIOSYNTHESIS MOEB PROTEIN
735	736	F RXA02802	GR00783	7	474	MOLYBDOPTERIN BIOSYNTHESIS MOEB PROTEIN
737	738	F RXA00438	GR00103	362	796	MOLYBDOPTERIN BIOSYNTHESIS MOEB PROTEIN
739	740	RXN00437	VV0112	17824	17369	MOLYBDOPTERIN (MPT) CONVERTING FACTOR, SUBUNIT 2
741	742	F RXA00437	GR00103	3	362	MOLYBDOPTERIN (MPT) CONVERTING FACTOR, SUBUNIT 2
743	744	RXN00439	VV0112	18742	18275	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
745	746	F RXA00439	GR00104	2	196	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
747	748	F RXA00442	GR00105	830	1087	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN

Table 1 (continued)

<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>
749	750	RXA00440	GR00104	196	654	MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN CB
751	752	RXN00441	VV0112	19942	18779	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
753	754	F RXA00441	GR00105	2	793	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
755	756	RXN02085				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
757	758	F RXA02085	GR00629	3496	5295	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
759	760	F RXA02086	GR00629	5252	5731	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
761	762	RXN02648				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
763	764	F RXA02648	GR00751	5254	4730	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
765	766	F RXA02658	GR00752	14764	15447	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
767	768	RXA01516	GR00424	22360	22749	DIHYDRONEOPTERIN ALDOLASE (EC 4.1.2.25)
769	770	RXA01515	GR00424	21513	22364	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
771	772	RXA02024	GR00613	4026	4784	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
773	774	RXA01719	GR00488	1264	704	MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN A
775	776	RXA01720	GR00488	2476	1268	MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN
777	778	RXS03223				MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN
779	780	F RXA01970	GR00568	2	1207	MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN
781	782	RXA02629	GR00748	1274	690	MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN
783	784	RXA02318	GR00665	9684	9962	MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN
785	786	RXA01517	GR00424	22752	23228	(D90909) pterin-4a-carbinolamine dehydratase [Synecocystis sp.]
						2-AMINO-4-HYDROXY-6-HYDROXYMETHYLDIHYDROPTERIDINE
						PYROPHOSPHOKINASE (EC 2.7.6.3)
787	788	RXN01304	VV0148	4449	4934	MOLYBDOPTERIN BIOSYNTHESIS MOG PROTEIN
789	790	RXS02556				FLAVOHEMOPROTEIN / DIHYDROPTERIDINE REDUCTASE (EC 1.6.99.7)
791	792	RXS02560				OXYGEN-INSENSITIVE NAD(P)H NITROREDUCTASE (EC 1.-.-.-) /
						DIHYDROPTERIDINE REDUCTASE (EC1.6.99.7)

Vitamin B₁₂, porphyrins and heme metabolism

<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>
793	794	RXA00382	GR00082	2752	1451	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE (EC 5.4.3.8)
795	796	RXA00156	GR00023	10509	9400	FERROCHELATASE (EC 4.99.1.1)
797	798	RXA00624	GR00163	7910	8596	FERROCHELATASE (EC 4.99.1.1)
799	800	RXA00306	GR00051	2206	1274	HEMK PROTEIN
801	802	RXA00884	GR00242	10137	11276	OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.-)
803	804	RXN02503	VV0007	22456	22854	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)
805	806	F RXA02503	GR00720	16906	17340	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)
807	808	RXA00377	GR00081	1427	306	UROPORPHYRINOGEN DECARBOXYLASE (EC 4.1.1.37)
809	810	RXN02504	VV0007	22805	23362	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)
811	812	F RXA02504	GR00720	17379	17816	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)

Table 1 (continued)

<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>
813	814	RXN01162	VV0088	1849	524	PRECORRIN-6Y METHYLASE (EC 2.1.1.-)
815	816	F RXA01162	GR00330	1248	4	PRECORRIN-6Y METHYLASE (EC 2.1.1.-)
817	818	RXA01692	GR00474	1498	749	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107)
819	820	RXN00371	VV0226	4180	5973	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) / UROPORPHYRINOGEN-III SYNTHASE (EC 4.2.1.75)
821	822	F RXA00371	GR00078	929	6	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) / UROPORPHYRINOGEN-III SYNTHASE (EC 4.2.1.75)
823	824	F RXA00374	GR00079	1102	371	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) / UROPORPHYRINOGEN-III SYNTHASE (EC 4.2.1.75)
825	826	RXN00383	VV0223	4206	2863	PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4)
827	828	F RXA00376	GR00081	287	6	PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4)
829	830	F RXA00383	GR00082	3876	2863	PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4)
831	832	RXA01253	GR00365	2536	1787	COBYRIC ACID SYNTHASE
833	834	RXA02134	GR00639	1721	801	COBALAMIN (5'-PHOSPHATE) SYNTHASE
835	836	RXA02135	GR00639	2809	1736	NICOTINATE-NUCLEOTIDE--DIMETHYLBENZIMIDAZOLE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.21)
837	838	RXA02136	GR00639	3362	2841	COBINAMIDE KINASE / COBINAMIDE PHOSPHATE GUANYLYLTRANSFERASE
839	840	RXN03114	VV0088	1	552	COBG PROTEIN (EC 1.-.-.-)
841	842	RXN01810	VV0082	1739	663	HEMIN-BINDING PERIPLASMIC PROTEIN HMUT PRECURSOR
843	844	RXS03205				HEMK PROTEIN
845	846	F RXA00306				HEMK PROTEIN
847	848	RXC01715				CYTOSOLIC PROTEIN INVOLVED IN PORPHYRIN METABOLISM

Vitamin C precursors

<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>
849	850	RXN00420	VV0112	2511	1048	L-GULONOLACTONE OXIDASE (EC 1.1.3.8)
851	852	F RXA00420	GR00096	2	541	L-GULONOLACTONE OXIDASE (EC 1.1.3.8)
853	854	F RXA00426	GR00097	1737	2258	L-GULONOLACTONE OXIDASE (EC 1.1.3.8)
855	856	RXN00708	VV0005	4678	3872	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE (EC 1.1.1.-)
857	858	F RXA00708	GR00185	2030	1359	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE (EC 1.1.1.-)
859	860	RXA02373	GR00688	1540	626	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE (EC 1.1.1.-) oxoglutarate semialdehyde dehydrogenase (EC 1.2.1.-)
861	862	RXS00389				ACETOACETYL-COA REDUCTASE (EC 1.1.1.36)
863	864	RXS00419				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF VITAMIN C PRECURSORS
865	866	RXC00416				OXIDOREDUCTASE INVOLVED IN METABOLISM OF VITAMIN C PRECURSORS
867	868	RXC02206				

Vitamin K2

<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>
869	870	RXS03074				S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)

Table 1 (continued)

<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>
871	872	F RXA02906	GR10044	1142	645	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
873	874	RXA02315	GR00665	8011	6383	2-SUCCINYL-6-HYDROXY-2,4-CYCLOHEXADIENE-1-CARBOXYLATE SYNTHASE /2-OXOGLUTARATE DECARBOXYLASE (EC 4.1.1.71)
875	876	RXA02319	GR00665	9977	10933	NAPHTHOATE SYNTHASE (EC 4.1.3.36)
877	878	RXS00393				1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.-)
879	880	F RXA00393	GR00086	4030	4911	1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.-)
881	882	RXA00391	GR00086	2031	2750	O-SUCCINYL BENZOIC ACID--COA LIGASE (EC 6.2.1.26)
883	884	RXS02908				O-SUCCINYL BENZOIC ACID--COA LIGASE (EC 6.2.1.26)

Ubiquinone 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>
885	886	RXA00997	GR00283	2389	1808	3-DEMETHYLBUBIQUINONE-9 3-METHYLTRANSFERASE (EC 2.1.1.64)
887	888	RXA02189	GR00642	986	249	3-DEMETHYLBUBIQUINONE-9 3-METHYLTRANSFERASE (EC 2.1.1.64)
889	890	RXA02311	GR00665	3073	2384	3-DEMETHYLBUBIQUINONE-9 3-METHYLTRANSFERASE (EC 2.1.1.64)
891	892	RXN02912	VV0135	13299	12547	UBIQUINONE/MENAQUINONE BIOSYNTHESIS METHYLTRANSFERASE UBIE (EC 2.1.1.-)
893	894	RXS00998				COMA OPERON PROTEIN 2

Purines and Pyrimidines and other Nucleotides

Regulation of purine and pyrimidine biosynthesis pathways

Purine metabolism

Purine 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>
895	896	RXA01215	GR00352	1187	213	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE, PRPP synthetase (EC 2.7.6.1)
897	898	RXN00558	VV0103	8235	9581	AMIDOPHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.14)
899	900	F RXA00558	GR00148	61	501	AMIDOPHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.14)
901	902	RXN00626	VV0135	11624	10362	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13)
903	904	F RXA00629	GR00165	1450	1713	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13)
905	906	F RXA00626	GR00164	1	780	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE, GARS (EC 6.3.4.13)
907	908	RXA02623	GR00746	4875	4285	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13) / PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1) / PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE (EC 2.1.2.2)
909	910	RXA01442	GR00418	10277	9054	PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE 2 (EC 2.1.2.-)

Table 1 (continued)

<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>
911	912	RXN00537	VV0103	3351	5636	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
913	914	F RXA02805	GR00786	54	638	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
915	916	F RXA00537	GR00138	23	697	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
917	918	F RXA00561	GR00150	2	280	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
919	920	RXA00541	GR00139	2269	2937	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
921	922	RXA00620	GR00163	3049	3939	PHOSPHORIBOSYLAMIDOIMIDAZOLE-SUCCINOCARBOXAMIDE SYNTHASE (EC 6.3.2.6)
923	924	RXN00770	VV0103	9614	10783	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1)
925	926	F RXA00557	GR00147	15	818	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1)
927	928	F RXA00770	GR00204	7809	7495	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1)
929	930	RXN02345	VV0078	4788	5984	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE ATPASE SUBUNIT (EC 4.1.1.21)
931	932	F RXA02345	GR00676	1534	725	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE ATPASE SUBUNIT (EC 4.1.1.21)
933	934	RXN02350	VV0078	8369	8863	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE CATALYTIC SUBUNIT (EC 4.1.1.21)
935	936	F RXA02346	GR00677	127	5	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE CATALYTIC SUBUNIT (EC 4.1.1.21)
937	938	F RXA02350	GR00678	1120	911	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE CATALYTIC SUBUNIT (EC 4.1.1.21)
939	940	RXA01087	GR00304	498	1373	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE (EC 4.1.1.21)
941	942	RXA00619	GR00163	793	2220	ADENYLOSUCCINATE LYASE (EC 4.3.2.2)
943	944	RXA02622	GR00746	4274	2715	PHOSPHORIBOSYLAMINOIMIDAZOLECARBOXAMIDE FORMYLTRANSFERASE (EC 2.1.2.3) / IMP CYCLOHYDROLASE (EC 3.5.4.10)

GMP, GDP, AMP and ADP synthesis, from inosine-5'-monophosphate (IMP)

<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>
945	946	RXN00488	VV0086	19066	20583	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
947	948	F RXA00492	GR00122	1171	1644	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
949	950	F RXA00488	GR00121	1	534	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
951	952	RXA02469	GR00715	1927	497	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
953	954	RXN00487	VV0086	23734	25302	GMP SYNTHASE [GLUTAMINE-HYDROLYZING] (EC 6.3.5.2)
955	956	F RXA00487	GR00120	712	2097	GMP SYNTHASE (EC 6.3.4.1)
957	958	RXA02237	GR00654	4577	5146	GUANYLATE KINASE (EC 2.7.4.8)
959	960	RXA01446	GR00418	17765	16476	ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4)
961	962	RXA00619	GR00163	793	2220	ADENYLOSUCCINATE LYASE (EC 4.3.2.2)
963	964	RXA00688	GR00179	10443	10985	ADENYLATE KINASE (EC 2.7.4.3)
965	966	RXA00266	GR00040	3769	3362	NUCLEOSIDE DIPHOSPHATE KINASE (EC 2.7.4.6)

Table 1 (continued)

GMP/AMP degrading activities

<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>
967	968	RXA00489	GR00121	654	1775	GMP REDUCTASE (EC 1.6.6.8)
969	970	RXN02281	VV0152	1893	3323	AMP NUCLEOSIDASE (EC 3.2.2.4)
971	972	F RXA02281	GR00659	1101	34	AMP NUCLEOSIDASE (EC 3.2.2.4)

Pyrimidine metabolism

Pyrimidine biosynthesis de novo:

<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>
973	974	RXA00147	GR00022	9722	10900	CARBAMOYL-PHOSPHATE SYNTHASE SMALL CHAIN (EC 6.3.5.5)
975	976	RXA00145	GR00022	7258	8193	ASPARTATE CARBAMOYLTRANSFERASE CATALYTIC CHAIN (EC 2.1.3.2)
977	978	RXA00146	GR00022	8249	9589	DIHYDROOROTASE (EC 3.5.2.3)
979	980	RXA02208	GR00647	2	1003	DIHYDROOROTATE DEHYDROGENASE (EC 1.3.3.1)
981	982	RXA01660	GR00462	591	1142	OROTATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.10)
983	984	RXA02235	GR00654	3207	4040	OROTIDINE 5'-PHOSPHATE DECARBOXYLASE (EC 4.1.1.23)
985	986	RXN01892	VV0150	3020	3748	URIDYLATE KINASE (EC 2.7.4.-)
987	988	F RXA01892	GR00542	47	775	URIDYLATE KINASE (EC 2.7.4.-)
989	990	RXA00105	GR00014	16672	17346	THYMIDYLATE SYNTHASE (EC 2.1.1.45)
991	992	RXA00131	GR00020	7621	7013	THYMIDYLATE KINASE (EC 2.7.4.9)
993	994	RXA00266	GR00040	3769	3362	NUCLEOSIDE DIPHOSPHATE KINASE (EC 2.7.4.6)
995	996	RXA00718	GR00188	4576	5283	CYTIDYLATE KINASE (EC 2.7.4.14)
997	998	RXA01599	GR00447	8780	10441	CTP SYNTHASE (EC 6.3.4.2)
999	1000	RXN02234	VV0134	24708	28046	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
1001	1002	F RXA02234	GR00654	1	3198	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
1003	1004	RXN00450	VV0112	34491	34814	CYTOSINE DEAMINASE (EC 3.5.4.1)
1005	1006	F RXA00450	GR00110	322	5	CYTOSINE DEAMINASE (EC 3.5.4.1)
1007	1008	RXN02272	VV0020	15566	16810	CYTOSINE DEAMINASE (EC 3.5.4.1)
1009	1010	F RXA02272	GR00655	6691	7935	CREATININE DEAMINASE (EC 3.5.4.21)
1011	1012	RXN03004	VV0237	1862	2341	DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13)
1013	1014	RXN03137	VV0129	9680	9579	THYMIDYLATE SYNTHASE (EC 2.1.1.45)
1015	1016	RXN03171	VV0328	568	1080	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)
1017	1018	F RXA02857	GR10003	570	1082	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)

Table 1 (continued)
Purine and pyrimidine base, nucleoside and nucleotide salvage, interconversion, reduction and degradation:
Purines:

<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>
1019	1020	RXA02771	GR00772	1329	1883	ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7)
1021	1022	RXA01512	GR00424	17633	18232	HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8)
1023	1024	RXA02031	GR00618	3820	3347	XANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.22)
1025	1026	RXA00981	GR00276	3388	4017	GTP PYROPHOSPHOKINASE (EC 2.7.6.5)
1027	1028	RXN02772	VV0171	2045	1011	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1029	1030	F RXA02772	GR00772	1962	2741	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1031	1032	F RXA02773	GR00772	2741	2902	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1033	1034	RXA01835	GR00517	3147	3677	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1035	1036	RXA01483	GR00422	19511	18240	DEOXYGUANOSINETRIPHOSPHATE TRIPHOSPHOHYDROLASE (EC 3.1.5.1)
1037	1038	RXN01027	VV0143	5761	6768	DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1039	1040	F RXA01024	GR00293	661	5	DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1041	1042	F RXA01027	GR00294	2580	2347	DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1043	1044	RXA01528	GR00425	5653	5126	DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1045	1046	RXA00072	GR00012	446	6	PHOSPHOADENOSINE PHOSPHOSULFATE REDUCTASE (EC 1.8.99.4)
1047	1048	RXA01878	GR00537	1239	2117	DIMETHYLADENOSINE TRANSFERASE (EC 2.1.1.-)
1049	1050	RXN02281	VV0152	1893	3323	AMP NUCLEOSIDASE (EC 3.2.2.4)
1051	1052	F RXA02281	GR00659	1101	34	AMP NUCLEOSIDASE (EC 3.2.2.4)
1053	1054	RXN01240	VV0090	30442	29420	GTP PYROPHOSPHOKINASE (EC 2.7.6.5)
1055	1056	RXN02008	VV0171	1138	5	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)

Pyrimidine and purine metabolism:

<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>
1057	1058	RXN01940	VV0120	10268	9333	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1059	1060	F RXA01940	GR00557	3	581	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1061	1062	RXA02559	GR00731	5418	6320	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1063	1064	RXA02497	GR00720	10059	10985	EXOPOLYPHOSPHATASE (EC 3.6.1.11)
1065	1066	RXN01079	VV0084	38084	35982	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
1067	1068	F RXA01079	GR00301	693	4	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
1069	1070	F RXA01084	GR00302	3402	2062	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
1071	1072	RXN01920	VV0084	32843	31842	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
1073	1074	F RXA01920	GR00550	1321	908	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 2 BETA CHAIN (EC 1.17.4.1)
1075	1076	RXA01080	GR00301	1240	797	RIBONUCLEOTIDE REDUCTASE SUBUNIT R2F
1077	1078	RXA00867	GR00237	1	627	NRDI PROTEIN
1079	1080	RXA01416	GR00413	2	631	POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8)
1081	1082	RXA01486	GR00423	660	4	POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8)

Table 1 (continued)

<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>
1083	1084	RXA01678	GR00467	7162	7689	2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE (EC 3.1.4.16)
1085	1086	RXA01679	GR00467	7729	8964	2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE (EC 3.1.4.16)
1087	1088	RXN01488	VV0139	39842	40789	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1089	1090	RXC00540				CYTOSOLIC PROTEIN INVOLVED IN PURINE METABOLISM
1091	1092	RXC00560				PROTEIN INVOLVED IN PURINE METABOLISM
1093	1094	RXC01088				CYTOSOLIC PROTEIN INVOLVED IN PURINE METABOLISM
1095	1096	RXC02624				MEMBRANE SPANNING PROTEIN INVOLVED IN PURINE METABOLISM
1097	1098	RXC02665				PROTEIN INVOLVED IN PURINE METABOLISM
1099	1100	RXC02770				LIPOPROTEIN INVOLVED IN PURINE METABOLISM
1101	1102	RXC02238				PROTEIN INVOLVED IN METABOLISM OF S-ADENOSYLMETHIONINE, PURINES AND PANTOTHENATE
1103	1104	RXC01946				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN PURINE METABOLISM

Pyrimidines:

<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>
1105	1106	RXN03171	VV0328	568	1080	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)
1107	1108	F RXA02857	GR10003	570	1082	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)
1109	1110	RXN00450	VV0112	34491	34814	CYTOSINE DEAMINASE (EC 3.5.4.1)
1111	1112	F RXA00450	GR00110	322	5	CYTOSINE DEAMINASE (EC 3.5.4.1)
1113	1114	RXA00465	GR00117	337	828	CYTOSINE DEAMINASE (EC 3.5.4.1)
1115	1116	RXA00717	GR00188	3617	4576	RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70)
1117	1118	RXA01894	GR00542	1622	2476	PHOSPHATIDATE CYTIDYLTRANSFERASE (EC 2.7.7.41)
1119	1120	RXA02536	GR00726	8581	7826	BETA-UREIDOPROPIONASE (EC 3.5.1.6)
1121	1122	RXN01209	VV0270	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1123	1124	F RXA01209	GR00348	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1125	1126	RXN01617	VV0050	22187	22858	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1127	1128	F RXA01617	GR00451	2	616	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1129	1130	RXC01600				CYTOSOLIC PROTEIN INVOLVED IN PYRIMIDINE METABOLISM
1131	1132	RXC01622				CYTOSOLIC PROTEIN INVOLVED IN PYRIMIDINE METABOLISM
1133	1134	RXC00128				EXPORTED PROTEIN INVOLVED IN METABOLISM OF PYRIDINES AND ADENOSYLMOCYSTEINE
1135	1136	RXC01709				CYTOSOLIC PROTEIN INVOLVED IN PYRIMIDINE METABOLISM
1137	1138	RXC02207				EXPORTED PROTEIN INVOLVED IN PYRIMIDINE METABOLISM

Table 1 (continued)

Sugars
Trehalose

<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>
1139	1140	RXA00347	GR00065	246	1013	TREHALOSE-PHOSPHATASE (EC 3.1.3.12)
1141	1142	RXN01239	VV0090	32921	30489	maltooligosyltrehalose synthase
1143	1144	F RXA01239	GR00358	5147	7579	maltooligosyltrehalose synthase
1145	1146	RXA02645	GR00751	714	2543	maltooligosyltrehalose trehalohydrolase
1147	1148	RXN02355	VV0051	735	4	TREHALOSE/MALTOSE BINDING PROTEIN
1149	1150	RXN02909	VV0135	38532	39017	Hypothetical Trehalose-Binding Protein
1151	1152	RXS00349				Hypothetical Trehalose Transport Protein
1153	1154	RXS03183				TREHALOSE/MALTOSE BINDING PROTEIN
1155	1156	RXC00874				TRANSMEBRANE PROTEIN INVOLVED IN TREHALOSE METABOLISM

TABLE 2 – Excluded Genes

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for 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	gltB; 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 carbamolytransferase	
AF036932	aroD	3-dehydroquinate dehydratase	
AF038548	pyc	Pyruvate carboxylase	

Table 2 (continued)

AF038651	dcIAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the <i>Corynebacterium glutamicum</i> 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 <i>Corynebacterium glutamicum</i> ," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinase synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the <i>Corynebacterium glutamicum</i> panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in <i>Escherichia coli</i> ," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		

Table 2 (continued)

AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> ; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol acetyl transferase	
AJ224946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from <i>Corynebacterium glutamicum</i> ," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> : The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the <i>Corynebacterium glutamicum</i> (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87

Table 2 (continued)

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

Table 2 (continued)

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

Table 2 (continued)

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 <i>Corynebacterium glutamicum</i> ," <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 <i>Corynebacterium glutamicum</i> 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	ilvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in <i>Corynebacterium glutamicum</i> : molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A. et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in <i>Escherichia coli</i> 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 <i>Corynebacterium glutamicum</i> mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in <i>Corynebacterium glutamicum</i> ," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from <i>Corynebacterium glutamicum</i> ," <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 <i>Corynebacterium diphtheriae</i> dtxR from <i>Brevibacterium lactofermentum</i> ," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the <i>Corynebacterium glutamicum</i> 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 <i>Brevibacterium lactofermentum</i> , 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 <i>Brevibacterium lactofermentum</i> , a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)

Table 2 (continued)

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

Table 2 (continued)

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

Table 2 (continued)

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

Table 2 (continued)

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

Table 2 (continued)

	16S rDNA	16S ribosomal RNA	
X82061		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)
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in <i>Corynebacterium glutamicum</i> : enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting 'Arthrobacter aureus C70,'" <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

Table 2 (continued)

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

Table 2 (continued)

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

Table 2 (continued)

Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of <i>Corynebacterium glutamicum</i> glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site Corynebacterium 304L	
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Moreau, S. et al. "Analysis of the integration functions of ϕ 304L: An integrase module among corynephages," <i>Virology</i> , 255(1):150-159 (1999)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	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)
Z29563	thrC	Threonine synthase	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)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	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)
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
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

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

FERM: Fermentation Research Institute, Chiba, Japan

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

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

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

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

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

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

Table 4: Alignment Results

ID #	length (NT)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rxa00023	3579	GB_EST33:AI776129	483	AI776129	EST257217 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLER17D3, mRNA sequence.	Lycopersicon esculentum	40,956	29-Jun-99
		GB_EST33:AI776129	483	AI776129	EST257217 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLER17D3, mRNA sequence.	Lycopersicon esculentum	40,956	29-Jun-99
rxa00044	1059	EM_PAT:E11760	6911	E11760	Base sequence of sucrose gene.	Corynebacterium glutamicum	42,979	08-OCT-1997 (Rel. 52, Created) 07-OCT-1996
		GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	42,979	07-OCT-1996
		GB_BA2:ECOUIW89	176195	U00006	E. coli chromosomal region from 89.2 to 92.8 minutes.	Escherichia coli	39,097	17-DEC-1993
rxa00064	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 02.O.3 map 99B-99B strain y; cn bw sp, *** SEQUENCING IN PROGRESS	Drosophila melanogaster	31,111	2-Aug-99
		GB_HTG2:AC007892	134257	AC007892	Drosophila melanogaster chromosome 3 clone BACR02O03 (D797) RPCI-98 02.O.3 map 99B-99B strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 113 unordered pieces.	Drosophila melanogaster	31,111	2-Aug-99
rxa00072								
rxa00105	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
rxa00106	579	GB_BA2:AE000366	10405	AE000366	Escherichia coli K-12 MG-1655 section 256 of 400 of the complete genome.	Escherichia coli	35,669	12-Nov-98
		GB_EST15:AA494237	367	AA494237	ng83f04.s1 NCI_CGAP_Pr6 Homo sapiens cDNA clone IMAGE:941407 similar to SW:DYR_LACCA P00381 DIHYDROFOLATE REDUCTASE ;, mRNA sequence.	Homo sapiens	42,896	20-Aug-97
rxa00115	1170	GB_BA2:AF161327	2021	AF161327	Corynebacterium diphtheriae histidine kinase ChrS (chrS) and response regulator ChrA (chrA) genes, complete cds.	Corynebacterium diphtheriae	40,210	9-Sep-99
		GB_PAT:AR041189	654	AR041189	Sequence 4 from patent US 5811286.	Unknown.	41,176	29-Sep-99
		GB_PR4:AC007110	148336	AC007110	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 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 IN PROGRESS *** , 93 unordered pieces.	Homo sapiens	40,296	2-Sep-99

Table 4 (continued)

rxa00116	1284	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 mannosyltransferase (lpsD), putative mannosyltransferase (lpsE), outer membrane protein (rsaF), and putative perosamine transferase (lpsE) genes, complete cds. Sequence 6 from patent US 5500353.	Caulobacter crescentus	36,235	19-OCT-1999
		GB_PAT:118647	3300	118647		Unknown.	36,821	07-OCT-1996
		GB_GSS13:AQ446197	751	AQ446197	nbxb0062D16r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0062D16r, genomic survey sequence.	Oryza sativa	38,124	8-Apr-99
rxa00131	732	GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	43,571	17-Jun-98
		GB_BA1:SAR7932	15176	AJ007932	Streptomyces argillaceus mithramycin biosynthetic genes.	Streptomyces argillaceus	41,116	15-Jun-99
		GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	39,726	17-Jun-98
rxa00132	1557	GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	36,788	17-Jun-98
		GB_IN2:TVU40872	1882	U40872	Trichomonas vaginalis S-adenosyl-L-homocysteine hydrolase gene, complete cds.	Trichomonas vaginalis	61,914	31-OCT-1996
		GB_HTG6:AC010706	169265	AC010706	Drosophila melanogaster chromosome X clone BACR36D15 (D887) RPC1-98 36.D.15 map 13C-13E strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 74 unordered pieces.	Drosophila melanogaster	51,325	22-Nov-99
rxa00145	1059	GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	63,365	18-Jun-98
		GB_BA1:PSEPYRBX	2273	L19649	Pseudomonas aeruginosa aspartate transcarbamoylase (pyrB) and dihydroorotase-like (pyrX) genes, complete cds's.	Pseudomonas aeruginosa	56,080	26-Jul-93
		GB_BA1:LLPYRBDNA	1468	X84262	L.leichmannii pyrB gene.	Lactobacillus leichmannii	47,514	29-Apr-97
rxa00146	1464	GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	60,714	18-Jun-98
		GB_BA1:MTCY154	13935	Z98209	Mycobacterium tuberculosis H37Rv complete genome; segment 121/162.	Mycobacterium tuberculosis	39,229	17-Jun-98
		GB_BA1:MSGY154	40221	AD000002	Mycobacterium tuberculosis sequence from clone y154.	Mycobacterium tuberculosis	36,618	03-DEC-1996
rxa00147	1302	GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	61,527	18-Jun-98
		GB_BA1:MSGB937C	38914	L78820	Mycobacterium leprae cosmid B937 DNA sequence.	Mycobacterium leprae	59,538	15-Jun-96
		GB_BA1:PAU81259	7285	U81259	Pseudomonas aeruginosa dihydrodipicolinate 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.	Pseudomonas aeruginosa	55,396	23-DEC-1996
rxa00156	1233	GB_BA1:SC9B10	33320	AL009204	Streptomyces coelicolor cosmid 9B10.	Streptomyces coelicolor	52,666	10-Feb-99

Table 4 (continued)

	GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.	Mycobacterium avium	54,191	26-MAR-1998
	GB_BA1:D85417	7984	D85417	Propionibacterium freudenreichii hemY, hemH, hemB, hemX, hemR and hemL genes, complete cds.	Propionibacterium freudenreichii	46,667	6-Feb-99
rxa00166	783	GB_HTG3:AC008167	174223	AC008167	Homo sapiens clone NH0172013, *** SEQUENCING IN PROGRESS *** , 7 unordered pieces.	37,451	21-Aug-99
	GB_HTG3:AC008167	174223	AC008167	Homo sapiens clone NH0172013, *** SEQUENCING IN PROGRESS *** , 7 unordered pieces.	Homo sapiens	37,451	21-Aug-99
	GB_HTG4:AC010118	80605	AC010118	Drosophila melanogaster chromosome 3L/62B1 clone RPC198-10D15, *** SEQUENCING IN PROGRESS *** , 51 unordered pieces.	Drosophila melanogaster	38,627	16-OCT-1999
rxa00198	672	GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	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
rxa00216	1113	GB_HTG2:HSDJ850E	117353	AL121758	Homo sapiens chromosome 20 clone RP5-850E9, *** SEQUENCING IN PROGRESS *** , in unordered pieces.	37,965	03-DEC-1999
	GB_HTG2:HSDJ850E	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
rxa00219	1065	GB_HTG2:AC005079	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS *** , 3 unordered pieces.	38,227	22-Nov-98
	GB_HTG2:AC005079	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS *** , 3 unordered pieces.	Homo sapiens	38,227	22-Nov-98
	GB_HTG2:AC005079	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS *** , 3 unordered pieces.	Homo sapiens	38,227	22-Nov-98
rxa00223	1212	GB_BA1:PPEA3NIF	19771	X99694	Plasmid pEA3 nitrogen fixation genes.	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 RPC198-9B18, *** SEQUENCING IN PROGRESS *** , 64 unordered pieces.	Drosophila melanogaster	39,527	16-OCT-1999
rxa00229	803	GB_BA2:AF124518	1758	AF124518	Corynebacterium glutamicum 3-dehydroquinase (aroD) and shikimate dehydrogenase (aroE) genes, complete cds.	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
rxa00241	1626	GB_BA1:CGLYSI	4232	X60312	C.glutamicum lysI gene for L-lysine permease.	100,000	30-Jan-92

Table 4 (continued)

rxa00262	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
		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)
rxa00278	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
		GB_RO:RNU30789	3510	U30789	Rattus norvegicus clone N27 mRNA.	Rattus norvegicus	38,190	20-Aug-96
rxa00295	1125	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.	glutamicum	98,207	29-Sep-97
		GB_BA1:MTCY427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	glutamicum	35,615	24-Jun-99
rxa00323	1461	GB_BA1:MSGB32CS	36404	L78818	Mycobacterium leprae cosmid B32 DNA sequence.	Mykobacterium tuberculosis	60,917	15-Jun-96
		GB_BA1:MTCY427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mykobacterium tuberculosis	44,606	24-Jun-99
		GB_BA1:MSGB32CS	36404	L78818	Mycobacterium leprae cosmid B32 DNA sequence.	Mykobacterium leprae	52,516	15-Jun-96
		GB_BA1:MTCY427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mykobacterium tuberculosis	38,079	24-Jun-99
rxa00330	1566	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:I09078	3146	I09078	Sequence 4 from Patent WO 8809819.	Unknown.	99,617	02-DEC-1994
		GB_BA1:BLTHRESY	1892	Z29563	Brevibacterium lactofermentum; ATCC 13869;; DNA (genomic);.	Corynebacterium glutamicum	99,170	20-Sep-95
rxa00335	1554	GB_BA1:CGGLNA	3686	Y13221	Corynebacterium glutamicum glnA gene.	Corynebacterium glutamicum	100,000	28-Aug-97

Table 4 (continued)

	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
rxa00347	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 I 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
	GB_BA1:MLU15187	36138	U15187	Mycobacterium leprae cosmid L296.	Mycobacterium leprae	52,972	09-MAR-1995
rxa00351	GB_IN2:AC004373	72722	AC004373	Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.	Drosophila melanogaster	46,341	17-Jul-98
	GB_IN2:AF145653	3197	AF145653	Drosophila melanogaster clone GH08860 BcDNA.GH08860 (BcDNA.GH08860) mRNA, complete cds.	Drosophila melanogaster	49,471	14-Jun-99
rxa00365	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
	GB_BA1:SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	37,946	16-Aug-99
rxa00366	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
rxa00367	GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	99,312	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
rxa00371	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	Ljirnp03-215-c10 Ljirnp Lambda HybriZap two-hybrid library Lotus japonicus cDNA clone LP215-03-c10 5' similar to 60S ribosomal protein L39, mRNA sequence.	Lotus japonicus	42,593	24-Aug-99
	GB_IN1:CELK09H9	37881	AF043700	Caenorhabditis elegans cosmid K09H9.	Caenorhabditis elegans	34,295	22-Jan-98

Table 4 (continued)

rxa00377	1245	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_T7A 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
rxa00382	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
rxa00383	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
rxa00391	843	GB_EST38:AW017053	613	AW017053	Schistosoma mansoni male, Phil LoVerde/Joe Merrick	Schistosoma mansoni	40,472	10-Sep-99
		GB_PAT:AR065852	32207	AR065852	Schistosoma mansoni cDNA clone SMMAS14 5' end, mRNA sequence.	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
rxa00393	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
rxa00402	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
rxa00403	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.	Onchocerca volvulus	37,565	31-Aug-98

Table 4 (continued)

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-523A23 (Genome Systems Human BAC library) complete sequence.	Homo sapiens	34,179	08-DEC-1998
		GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	40,169	23-Jun-99
rx00420	1587	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:MSGB971C	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	46,538	17-Aug-99
		GB_HTG3:AC009120	269445	AC009120	Homo sapiens chromosome 16 clone RPCI-11_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:HSDJ719K	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:HSDJ719K	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 RPCI98-48B15, *** SEQUENCING IN PROGRESS ***, 44 unordered pieces.	Drosophila melanogaster	34,959	16-OCT-1999
		GB_HTG4:AC009367	226055	AC009367	Drosophila melanogaster chromosome 3L/76A2 clone RPCI98-48B15, *** SEQUENCING IN PROGRESS ***, 44 unordered pieces.	Drosophila melanogaster	34,959	16-OCT-1999

Table 4 (continued)

rx00448	1143	GB_PR3:AC003670	88945	AC003670	Homo sapiens 12q13.1 PAC RPCI1-130F5 (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 RPCI-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 RPCI-1 130F5 map 12q13.1, *** SEQUENCING IN PROGRESS ***, 156 unordered pieces.	Homo sapiens	31,373	18-OCT-1997
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:AI818057	412	AI818057	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:AQ64032	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.ammoniagenes guaA gene.	Corynebacterium ammoniagenes	74,259	8-Jan-98
		GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	37,248	01-MAR-1994
		GB_BA1:MTCY78	33818	Z77165	Mycobacterium tuberculosis H37Rv complete genome; segment 145/162.	Mycobacterium tuberculosis	39,725	17-Jun-98
rx00488	1641	GB_BA1:MTCY78	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
rx00489	1245	GB_BA1:SCAJ10601	4692	AJ010601	Streptomyces coelicolor A3(2) DNA for whiD and whiK loci.	Streptomyces coelicolor	60,835	17-Sep-98
		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

Table 4 (continued)

	GB_BA1:CGCYSCAS D	1591	X82928	C.glutamicum aspartate-semialdehyde dehydrogenase gene.				Corynebacterium glutamicum	99,221	17-Feb-97
rxa00534	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
rxa00536	GB_PAT:E14514	1643	E14514	DNA encoding Brevibacterium aspartokinase.				Corynebacterium glutamicum	98,773	28-Jul-99
	GB_BA1:CGLEUA	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
rxa00537	GB_BA1:MTU88526	2412	U88526	Mycobacterium tuberculosis putative alpha-isopropyl malate synthase (leuA) gene, complete cds.				Mycobacterium tuberculosis	68,185	26-Feb-97
	GB_BA2:SCD25	41622	AL118514	Streptomyces coelicolor cosmid D25.				Streptomyces coelicolor A3(2)	63,187	21-Sep-99
	GB_BA1:MTCY7H7A	10451	Z95618	Mycobacterium tuberculosis H37Rv complete genome; segment 39/162.				Mycobacterium tuberculosis	62,401	17-Jun-98
rxa00541	GB_BA1:MTU34956	2462	U34956	Mycobacterium tuberculosis phosphoribosylformylglycinamide synthase (purL) gene, complete cds.				Mycobacterium tuberculosis	62,205	28-Jan-97
	GB_PAT:I92052	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
rxa00558	GB_BA1:MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome; segment 36/162.				Mycobacterium tuberculosis	60,814	17-Jun-98
	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
rxa00579	GB_BA1:MTCY7H7A	10451	Z95618	Mycobacterium tuberculosis H37Rv complete genome; segment 39/162.				Mycobacterium tuberculosis	64,863	17-Jun-98
	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)
rxa00580	GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.				Corynebacterium glutamicum	98,810	24-Jun-98
	GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.				Corynebacterium glutamicum	99,368	24-Jun-98

Table 4 (continued)

rxa00581	1092	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) 24-Jun-98
		GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	37,071	08-OCT-1997 (Rel. 52, Created) 05-DEC-1998
		EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	37,071	08-OCT-1997 (Rel. 52, Created) 05-DEC-1998
		GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	37,071	05-DEC-1998
rxa00584	1248	GB_BA1:CORAHP5	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
rxa00618	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
		GB_IN1:DMANILLIN	4029	X89858	D.melanogaster mRNA for anillin protein.	Drosophila melanogaster	34,398	8-Nov-95
rxa00619	1551	GB_BA1:MTCY369	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
rxa00620	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
		GB_HTG3:AC008763	214575	AC008763	Homo sapiens chromosome 19 clone CITB-E1_3214H19, *** SEQUENCING IN PROGRESS ***, 21 unordered pieces.	Homo sapiens	40,020	3-Aug-99
rxa00624	810	GB_IN1:CEY41E3	150641	Z95559	Caenorhabditis elegans cosmid Y41E3, complete sequence.	Caenorhabditis elegans	36,986	2-Sep-99
		GB_EST13:AA362167	372	AA362167	EST71561 Macrophage I Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	38,378	21-Apr-97
		GB_IN1:CEY41E3	150641	Z95559	Caenorhabditis elegans cosmid Y41E3, complete sequence.	Caenorhabditis elegans	37,694	2-Sep-99
rxa00626	1386	GB_BA1:MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome; segment 36/162.	Mycobacterium tuberculosis	57,971	17-Jun-98
		GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	58,806	24-Jun-97
		GB_BA1:MLU15187	36138	U15187	Mycobacterium leprae cosmid L296.	Mycobacterium leprae	38,007	09-MAR-1995

Table 4 (continued)

rxa00632	795	GB_BA1:BRLBIOAD	2272	D14083	Brevibacterium flavum genes for 7,8-diaminopelargonic acid aminotransferase and dethiobiotin synthetase, complete cds.	Corynebacterium glutamicum	97,358	3-Feb-99
		GB_PAT:E04041	675	E04041	DNA sequence coding for desthiobiotinsynthetase.	Corynebacterium glutamicum	98,074	29-Sep-97
		GB_PAT:E04040	1272	E04040	DNA sequence coding for diamino pelargonic acid aminotransferase.	Corynebacterium glutamicum	93,814	29-Sep-97
rxa00633	1392	GB_BA1:BRLBIOAD	2272	D14083	Brevibacterium flavum genes for 7,8-diaminopelargonic acid aminotransferase and dethiobiotin synthetase, complete cds.	Corynebacterium glutamicum	95,690	3-Feb-99
		GB_PAT:E04040	1272	E04040	DNA sequence coding for diamino pelargonic acid aminotransferase.	Corynebacterium glutamicum	95,755	29-Sep-97
		GB_BA2:EHU38519	1290	U38519	Erwinia herbicola adenosylmethionine-8-amino-7-oxononanoate transaminase (bioA) gene, complete cds.	Erwinia herbicola	55,564	4-Nov-96
rxa00688	666	GB_BA1:MTV041	28826	AL021958	Mycobacterium tuberculosis H37Rv complete genome; segment 35/162.	Mycobacterium tuberculosis	60,030	17-Jun-98
		GB_BA1:BRLSECY	1516	D14162	Brevibacterium flavum gene for SecY protein (complete cds) and gene or adenylate kinase (partial cds).	Corynebacterium glutamicum	99,563	3-Feb-99
		GB_BA2:MBU77912	7163	U77912	Mycobacterium bovis MBE50a gene, partial cds; and MBE50b, MBE50c, preprotein translocase SecY subunit (secY), adenylate kinase (adk), methionine aminopeptidase (map), RNA polymerase ECF sigma factor (sigE50), MBE50d, and MBE50e genes, complete cds.	Mycobacterium bovis	60,030	27-Jan-99
rxa00708	930	GB_BA2:AF157493	25454	AF157493	Zymomonas mobilis ZM4 fosmid clone 42D7, complete sequence.	Zymomonas mobilis	39,116	5-Jul-99
		GB_PAT:I00836	1853	I00836	Sequence 1 from Patent US 4758514.	Unknown.	47,419	21-MAY-1993
		GB_PAT:E00311	1853	E00311	DNA coding of 2,5-diketogluconic acid reductase.	unidentified	47,419	29-Sep-97
rxa00717	1083	GB_PAT:I78753	1187	I78753	Sequence 9 from patent US 5693781.	Unknown.	37,814	3-Apr-98
		GB_PAT:I92042	1187	I92042	Sequence 9 from patent US 5726299.	Unknown.	37,814	01-DEC-1998
		GB_BA1:MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	50,647	17-Jun-98
rxa00718	831	GB_BA1:MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	55,228	17-Jun-98
		GB_BA1:MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	40,300	17-Jun-98
		GB_GSS12:AQ42075	671	AQ420755	RPCI-11-168G18.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-168G18, genomic survey sequence.	Homo sapiens	35,750	23-MAR-1999
rxa00727	1035	GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPCI-98 48.D.10 map 34A-34A strain y; cn bw sp, *** SEQUENCING IN PROGRESS	Drosophila melanogaster	40,634	6-Aug-99
		GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPCI-98 48.D.10 map 34A-34A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 78 unordered pieces.	Drosophila melanogaster	40,634	6-Aug-99

Table 4 (continued)

966	966	GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPCI-98 48.D.10 map 34A-34A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 78 unordered pieces.	Drosophila melanogaster	33,888	6-Aug-99
		GB_HTG2:AC006789	83823	AC006789	Caenorhabditis elegans clone Y49F6, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.	Caenorhabditis elegans	36,737	25-Feb-99
		GB_HTG2:AC006789	83823	AC006789	Caenorhabditis elegans clone Y49F6, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.	Caenorhabditis elegans	36,737	25-Feb-99
		GB_BA1:D90810	20476	D90810	E.coli genomic DNA, Kohara clone #319(37.4-37.8 min.).	Escherichia coli	36,526	29-MAY-1997
	1293	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
	1056	GB_HTG1:CER08A5	51920	Z82281	Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	64,896	14-OCT-1998
		GB_HTG1:CER08A5	51920	Z82281	Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	64,896	14-OCT-1998
		GB_PL2:AF078693	1492	AF078693	Chlamydomonas reinhardtii putative O-acetylserine(thiol)lyase precursor (Crcys-1A) mRNA, nuclear gene encoding organellar protein, complete cds.	Chlamydomonas reinhardtii	57,970	3-Nov-99
	669	GB_BA1:MTCY98	31225	Z83860	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162.	Mycobacterium tuberculosis	54,410	17-Jun-98
		GB_BA1:AVINIFREG	7099	M60090	Azotobacter chroococcum nifU, nifS, nifV, nifP, nifW, nifZ and nifM genes, complete cds.	Azotobacter chroococcum	51,729	26-Apr-93
		GB_BA2:AF001780	6701	AF001780	Cyanothece PCC 8801 NifP (nifP), nitrogenase (nifB), FdxN (fdxN), NifS (nifS) and NifU (nifU) genes, complete cds, and NifH (nifH) gene, partial cds.	Cyanothece PCC8801	36,309	08-MAR-1999
	1023	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:AI998439	455	AI998439	701545695 A. thaliana, Columbia Col-0, rosette-2 Arabidopsis thaliana cDNA clone 701545695, mRNA sequence.	Arabidopsis thaliana	36,044	8-Sep-99
	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
	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

Table 4 (continued)

rxa00865	1026	GB_PAT:E14520	2001	E14520	DNA encoding Brevibacterium dihydrodipicolinic acid synthase.	Corynebacterium glutamicum	100,000	28-Jul-99
		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
rxa00867	650	GB_PAT:AR038113	1411	AR038113	Sequence 18 from patent US 5804414.	Unknown.	99,805	29-Sep-99
		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 (gpsI) gene, complete cds.	Streptomyces antibioticus	69,706	25-OCT-1996
rxa00873	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
		GB_BA1:D78198	2304	D78198	Pimelobacter sp. DNA for trehalose synthase, complete cds.	Pimelobacter sp.	60,594	5-Feb-99
rxa00884	1263	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:AQ65460	468	AQ654600	Sheared DNA-1O14.TF Sheared DNA Trypanosoma brucei genomic clone 0	Trypanosoma brucei	33,974	22-Jun-99
rxa00891	1102	GB_BA1:MTCI418B	11700	Z96071	Sheared DNA-1O14, genomic survey sequence.	Mycobacterium tuberculosis	63,297	18-Jun-98
		GB_BA1:SCO001206	9184	AJ001206	Streptomyces coelicolor A3(2), glycogen metabolism cluster II.	Streptomyces coelicolor	61,965	29-MAR-1999
		GB_BA1:SCO001205	9589	AJ001205	Streptomyces coelicolor A3(2) glycogen metabolism clusterI.	Streptomyces coelicolor	61,727	29-MAR-1999
rxa00952	963	EM_PAT:E10963	3118	E10963	gDNA encoding tryptophan synthase.	Corynebacterium glutamicum	99,688	08-OCT-1997 (Rel. 52, Created)
		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 prepibacterium latophelmentamn.	unidentified	98,428	29-Sep-97
rxa00954	644	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 prepibacterium latophelmentamn.	unidentified	98,758	29-Sep-97
		GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	98,758	10-Feb-99
rxa00955	1545	GB_PAT:E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,372	29-Sep-97

Table 4 (continued)

	GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	98,372	10-Feb-99
rxa00956	GB_PAT:E01688	7725	E01688	Genomic DNA of trp operon of prepibacterium latophelmentamn. gDNA encoding tryptophan synthase.	unidentified	98,242	29-Sep-97
	EM_PAT:E10963	3118	E10963		Corynebacterium glutamicum	98,949	08-OCT-1997 (Rel. 52, Created)
							10-Feb-99
rxa00957	GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	99,107	29-Sep-97
	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
rxa00958	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 prepibacterium latophelmentamn. Brevibacterium lactofermentum tryptophan operon.	unidentified	98,867	29-Sep-97
	GB_BA1:BLTRP	7725	X04960		Corynebacterium glutamicum	98,792	10-Feb-99
rxa00970	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 prepibacterium latophelmentamn. Corynebacterium glutamicum hom-thrB genes for homoserine dehydrogenase and homoserine kinase. Sequence 1 from Patent WO 8809819.	unidentified	98,658	29-Sep-97
	GB_BA1:CGHOMTHR	3685	Y00546		Corynebacterium glutamicum	99,905	12-Sep-93
rxa00972	GB_PAT:I09077	3685	I09077		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
	GB_PAT:E16755	3579	E16755	gDNA encoding diaminopimelate decarboxylase (DDC) and arginyl-tRNA synthase.	Corynebacterium glutamicum	99,931	28-Jul-99
rxa00981	GB_PAT:AR038110	3579	AR038110	Sequence 15 from patent US 5804414. DNA encoding Brevibacterium diaminopimelic acid decarboxylase and arginyl-tRNA synthase. Gallus gallus partial mRNA for ATP-citrate lyase (ACL gene). Genomic sequence for Arabidopsis thaliana BAC F15O4 from chromosome I, complete sequence. Arabidopsis thaliana genome survey sequence T7 end of BAC F14D7 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.	Unknown.	99,931	29-Sep-99
	GB_PAT:E14508	3579	E14508		Corynebacterium glutamicum	99,931	28-Jul-99
	GB_OV:GGA245664	512	AJ245664		Gallus gallus	37,538	28-Sep-99
rxa00989	GB_PL2:AC007887	159434	AC007887	Genomic sequence for Arabidopsis thaliana BAC F15O4 from chromosome I, complete sequence. Arabidopsis thaliana genome survey sequence T7 end of BAC F14D7 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.	Arabidopsis thaliana	37,600	04-OCT-1999
	GB_GSS1:CNS00RN	542	AL087338		Arabidopsis thaliana	41,264	28-Jun-99
	GB_BA1:MTV008	63033	AL021246		Mycobacterium tuberculosis	40,773	17-Jun-98
rxa00972	GB_BA1:SCVALSFP	3619	Y13070	S.coelicolor valS, fpgs, ndk genes. Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Streptomyces coelicolor	58,119	03-MAR-1998
	GB_BA1:MTV008	63033	AL021246		Mycobacterium tuberculosis	38,167	17-Jun-98

Table 4 (continued)

rxa00997	705	GB_BA2:CGU31225	1817	U31225	Corynebacterium glutamicum L-proline:NADP+ 5-oxidoreductase (proC) gene, complete cds.	40,841	2-Aug-96
rxa01019	1110	GB_HTG1:CEY39C12	282838	AL009026	Caenorhabditis elegans chromosome IV clone Y39C12, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	36,416	26-OCT-1999
		GB_IN1:CEB0001	39416	Z69634	Caenorhabditis elegans cosmid B0001, complete sequence.	36,416	2-Sep-99
		GB_HTG2:AC005052	144734	AC005052	Homo sapiens clone RG038K21, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	39,172	12-Jun-98
		GB_HTG2:AC005052	144734	AC005052	Homo sapiens clone RG038K21, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	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.	34,661	17-OCT-1998
rxa01026	1782	GB_BA1:SC1C2	42210	AL031124	Streptomyces coelicolor cosmid 1C2.	68,275	15-Jan-99
		GB_BA1:ATLEUCD	2982	X84647	A.teichomyceticus leuC and leuD genes.	65,935	04-OCT-1995
rxa01027	1131	GB_BA1:MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	40,454	23-Jun-99
		GB_BA1:MLCB637	44882	Z99263	Mycobacterium leprae cosmid B637.	38,636	17-Sep-97
		GB_BA1:MTCY349	43523	Z83018	Mycobacterium tuberculosis H37Rv complete genome; segment 131/162.	51,989	17-Jun-98
		GB_BA1:SPUNGMUT X	1172	Z21702	S.pneumoniae ung gene and mutX genes encoding uracil-DNA glycosylase and 8-oxodGTP nucleoside triphosphatase.	38,088	15-Jun-94
rxa01073	954	GB_BA1:BACOUTB	1004	M15811	Bacillus subtilis outB gene encoding a sporulation protein, complete cds.	53,723	26-Apr-93
		GB_PR4:AC007938	167237	AC007938	Homo sapiens clone UWGC:djs201 from 7q31, complete sequence.	34,322	1-Jul-99
		GB_PL2:ATAC006282	92577	AC006282	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence.	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.	99,820	5-Aug-99
rxa01080	567	GB_BA1:CANRDFGE N	6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	75,966	18-Apr-98
		GB_BA1:MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	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.	100,000	5-Aug-99
		GB_BA1:CANRDFGE N	6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	65,511	18-Apr-98
rxa01087	999	GB_BA1:STNRD	4894	X73226	S.typhimurium nrdEF operon.	52,477	03-MAR-1997
		GB_IN2:AF063412	1093	AF063412	Limnadia lenticularis elongation factor 1-alpha mRNA, partial cds.	43,750	29-MAR-1999
		GB_PR3:HS24M15	134539	Z94055	Human DNA sequence from PAC 24M15 on chromosome 1. Contains tenascin-R (restrictin), EST.	37,475	23-Nov-99
		GB_IN2:ARU85702	1240	U85702	Anathix ralla elongation factor-1 alpha (EF-1a) gene, partial cds.	37,319	16-Jul-97

Table 4 (continued)

rxa01095	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
rxa01097	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
rxa01098	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
rxa01100	861	GB_BA1:MLCB1610	40055	AL049913	Mycobacterium leprae cosmid B1610.	Mycobacterium leprae	61,366	27-Aug-99
		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
rxa01101	756	GB_BA2:AF060558	636	AF060558	Corynebacterium glutamicum glutamine amidotransferase (hisH) gene, complete cds.	Corynebacterium glutamicum	95,455	29-Apr-98
		GB_BA1:SC4G6	36917	AL096884	Streptomyces coelicolor cosmid 4G6.	Streptomyces coelicolor A3(2)	38,378	23-Jul-99
rxa01104	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:STMHISOPA	3981	M31628	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:SC4G6	36917	AL096884	Streptomyces coelicolor cosmid 4G6.	Streptomyces coelicolor A3(2)	39,045	23-Jul-99
rxa01105	1221	GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	60,364	24-Jun-99
		GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	60,931	24-Jun-99
		GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	36,851	10-DEC-1996
rxa01106	1449	GB_BA1:MLCB1610	40055	AL049913	Mycobacterium leprae cosmid B1610.	Mycobacterium leprae	60,902	27-Aug-99
		GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	37,233	10-DEC-1996

Table 4 (continued)

	GB_BA1:MSHISCD	2298	X65542	M.smegmatis genes hisD and hisC for histidinol dehydrogenase and histidinol-Mycobacterium smegmatis phosphate aminotransferase, respectively.	60,111	30-Jun-93
	GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	58,420	24-Jun-99
rx01145	GB_BA1:CORAIA	4705	L09232	Corynebacterium glutamicum acetohydroxy acid synthase (ilvB) and (ilvN) genes, and acetohydroxy acid isomeroreductase (ilvC) gene, complete cds.	100,000	23-Feb-95
	GB_BA1:BRLILVCA	1364	D14551	Brevibacterium flavum ilvC gene for acetohydroxy acid isomeroreductase, complete cds.	99,560	3-Feb-99
	GB_PAT:E08232	1017	E08232	DNA encoding acetohydroxy-acid isomeroreductase.	99,803	29-Sep-97
	GB_PAT:A60299	2869	A60299	Sequence 18 from Patent WO9706261.	38,675	06-MAR-1998
rx01162	GB_PR3:HS24E5	35506	Z82185	Human DNA sequence from Fosmid 24E5 on chromosome 22q11.2-qter contains parvalbumin, ESTs, STS.	36,204	23-Nov-99
rx01208	GB_PR3:AC005265	43900	AC005265	Homo sapiens chromosome 19, cosmid F19750, complete sequence.	38,363	6-Jul-98
	GB_HTG2:AC004965	323792	AC004965	Homo sapiens clone DJ1106H14, *** SEQUENCING IN PROGRESS ***, 42 unordered pieces.	36,058	12-Jun-98
	GB_HTG2:AC004965	323792	AC004965	Homo sapiens clone DJ1106H14, *** SEQUENCING IN PROGRESS ***, 42 unordered pieces.	36,058	12-Jun-98
rx01209	GB_PL2:TAU55859	2397	U55859	Triticum aestivum heat shock protein 80 mRNA, complete cds.	37,269	1-Feb-99
	GB_HTG3:AC011469	113436	AC011469	Homo sapiens chromosome 19 clone CIT-HSPC_475D23, *** SEQUENCING IN PROGRESS ***, 31 unordered pieces.	40,000	07-OCT-1999
	GB_HTG3:AC011469	113436	AC011469	Homo sapiens chromosome 19 clone CIT-HSPC_475D23, *** SEQUENCING IN PROGRESS ***, 31 unordered pieces.	40,000	07-OCT-1999
rx01215	GB_PL1:AB010077	77380	AB010077	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence.	36,803	20-Nov-99
	GB_BA1:MTCY10G2	38970	Z92539	Mycobacterium tuberculosis H37Rv complete genome; segment 47/162.	37,047	17-Jun-98
	GB_IN1:LEIPRPP	1887	M76553	Leishmania donovani phosphoribosylpyrophosphate synthetase gene, complete cds.	50,738	7-Jun-93
rx01239	GB_HTG2:HSJ799D1	130149	AL050344	Homo sapiens chromosome 1 clone RP4-799D16 map p34.3-36.1, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	38,135	29-Nov-99
	GB_BA1:MTCY48	35377	Z74020	Mycobacterium tuberculosis H37Rv complete genome; segment 69/162.	38,139	17-Jun-98
	GB_PR2:AB029032	6377	AB029032	Homo sapiens mRNA for KIAA1109 protein, partial cds.	39,394	4-Aug-99
rx01253	GB_GSS9:AQ107201	355	AQ107201	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.	41,408	28-Aug-98
	GB_PL2:F5O8	99923	AC005990	Arabidopsis thaliana chromosome 1 BAC F5O8 sequence, complete sequence.	36,118	23-DEC-1998
	GB_PL2:F5O8	99923	AC005990	Arabidopsis thaliana chromosome 1 BAC F5O8 sequence, complete sequence.	35,574	23-DEC-1998
	GB_IN1:CELC06G1	31205	U41014	Caenorhabditis elegans cosmid C06G1.	38,560	30-Nov-95

Table 4 (continued)

rxa01321	1044	GB_GSS14:AQ51884 3	441	AQ518843	HS_5106_A1_D10_SP6E RPCI-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) RPCI-98 38.D.12 map 48A-48B strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 60 unordered pieces.	Drosophila melanogaster	40,634	2-Aug-99
		GB_HTG4:AC011696	115847	AC011696	Drosophila melanogaster chromosome 2 clone BACR35F01 (D1156) RPCI-98 35.F.1 map 48A-48C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 108 unordered pieces.	Drosophila melanogaster	38,290	26-OCT-1999
rxa01352	706	GB_PL2:ATAC005167	83260	AC005167	Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence.	Arabidopsis thaliana	34,311	15-OCT-1998
		GB_PL2:ATAC005825	97380	AC005825	Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence.	Arabidopsis thaliana	34,311	12-Apr-99
		GB_HTG3:AC011150	127222	AC011150	Homo sapiens clone 4_K_17, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	37,722	01-OCT-1999
rxa01360	259	GB_EST32:AI725583	728	AI725583	BNLGH112371 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (U86081) root hair defective 3 [Arabidopsis thaliana], mRNA sequence.	Gossypium hirsutum	38,492	11-Jun-99
		GB_PR2:HS227P17	82951	Z81007	Human DNA sequence from PAC 227P17, between markers DXS6791 andDXS8038 on chromosome X contains CpG island, EST.	Homo sapiens	39,738	23-Nov-99
		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
rxa01361	629	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 mkia Mus musculus cDNA clone IMAGE:1432243 5' similar to TR:O35120 O35120 MGPI1P.; mRNA sequence.	Mus musculus	44,097	9-Jul-98
rxa01381	944	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
rxa01393	993	GB_BA1:MTV043	68848	AL022004	Mycobacterium tuberculosis H37Rv complete genome; segment 40/162.	Mycobacterium tuberculosis	37,419	24-Jun-99
		GB_BA1:CGLYSEG	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
rxa01394	822	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

Table 4 (continued)

		GB_BA1:CGLYSEG	2374	X96471	C.glutamicum lysE and lysG genes.	Corynebacterium glutamicum	33,665	24-Feb-97
rx01416	630	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
rx01442	1347	GB_BA1:D90828	14590	D90828	E.coli genomic DNA, Kohara clone #336gap(41.6-41.9 min.).	Escherichia coli	56,151	21-MAR-1997
rx01446	1413	GB_BA2:AE000279	10855	AE000279	Escherichia coli K-12 MG1655 section 169 of 400 of the complete genome.	Escherichia coli	56,021	12-Nov-98
		GB_BA1:SCH10	39524	AL049754	Streptomyces coelicolor cosmid H10.	Streptomyces coelicolor	39,037	04-MAY-1999
rx01483	1395	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
rx01486	757	GB_BA1:MTCY98	31225	Z83860	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162.	Mycobacterium tuberculosis	39,057	17-Jun-98
		GB_BA1:MSGB1229C	30670	L78812	Mycobacterium leprae cosmid B1229 DNA sequence.	Mycobacterium leprae	54,382	15-Jun-96
rx01489	1146	GB_BA2:AF027507	5168	AF027507	Mycobacterium smegmatis dGTPase (dgt), and primase (dnaG) genes, complete cds; tRNA-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
rx01491	774	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
rx01508	1662	GB_BA1:CORFADS	1547	D37967	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
rx01512	723	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
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:OMDNAPROI	7327	X92380	O.mossambicus prolactin I gene.	Tilapia mossambica	38,289	19-OCT-1995
rx01512	723	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

Table 4 (continued)

rxa01514	711	GB_BA1:MTY15C10	33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome; segment 154/162.	Mycobacterium tuberculosis	40,086	17-Jun-98
		GB_BA1:MTCY7H7B	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
rxa01515	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
rxa01516	513	GB_IN1:DME238847	5419	AJ238847	Drosophila melanogaster mRNA for drosophila dodeca-satellite protein 1 (DDP-1).	Drosophila melanogaster	36,346	13-Aug-99
		GB_HTG3:AC009210	103814	AC009210	Drosophila melanogaster chromosome 2 clone BACR01106 (D1054) RPCI-98 01.1.6 map 55D-55D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 86 unordered pieces.	Drosophila melanogaster	37,897	20-Aug-99
rxa01517	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 saponariae internal transcribed spacer 1, 5.8S ribosomal RNA gene; and internal transcribed spacer 2, complete sequence.	Sorosporium saponariae	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
rxa01521	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 RG204116 from 7q31, complete sequence.	Homo sapiens	36,623	20-Aug-97
		GB_PR2:AC002461	197273	AC002461	Human BAC clone RG204116 from 7q31, complete sequence.	Homo sapiens	34,719	20-Aug-97
rxa01528	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
rxa01551	1998	GB_BA1:MTCY22G10	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
rxa01561	1053	GB_BA1:SCQ11	15441	AL096823	Streptomyces coelicolor cosmid Q11.	Streptomyces coelicolor	60,775	8-Jul-99
		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
rxa01599	1785	GB_OM:PIGDAO1	395	M18444	Pig D-amino acid oxidase (DAO) gene, exon 1.	Sus scrofa	39,340	27-Apr-93
		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

Table 4 (continued)

rxa01617	795	GB_BA1:MLCB1351 GB_PR2:HSMTM0	38936 217657	Z95117 AL034384	Mycobacterium leprae cosmid B1351. Human chromosome Xq28, cosmid clones 7H3, 14D7, C1230, 11E7, F1096, A12197, 12G8, A09100; complete sequence bases 1. .217657.	Mycobacterium leprae Homo sapiens	36,756 40,811	24-Jun-97 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
		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
rxa01657	723	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+ (TFujiwara) Homo sapiens cDNA clone GEN-213D06 5', mRNA sequence.	Homo sapiens	44,262	9-Feb-96
		GB_BA2:AF129925	10243	AF129925	Thiobacillus ferrooxidans carboxysome operon, complete cds.	Thiobacillus ferrooxidans	40,709	17-MAY-1999
rxa01660	675	GB_BA1:MTV013	11364	AL021309	Mycobacterium tuberculosis H37Rv complete genome; segment 134/162.	Mycobacterium tuberculosis	40,986	17-Jun-98
		GB_RO:MMFV1 GB_PAT:A67508	6480 6480	X97719 A67508	M.musculus retrovirus restriction gene Fv1. Sequence 1 from Patent WO9743410.	Mus musculus Mus musculus	35,364 35,364	29-Aug-96 05-MAY-1999
rxa01678	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
rxa01679	1359	GB_EST5:H91843	362	H91843	ys81e01.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:221208 3' similar to gb.X63749_rna1 GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-1 (HUMAN);, mRNA sequence.	Homo sapiens	39,157	29-Nov-95
		GB_STS:G26925 GB_PL2:AF139451	362 1202	G26925 AF139451	human STS SHGC-30023, sequence tagged site. Gossypium robinsonii CclA2 pseudogene, partial sequence.	Homo sapiens Gossypium robinsonii	39,157 38,910	14-Jun-96 1-Jun-99
rxa01690	1224	GB_BA1:SC1C2 GB_EST22:A1064232	42210 493	AL031124 A1064232	Streptomyces coelicolor cosmid 1C2. GH04563.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH04563 5prime, mRNA sequence.	Streptomyces coelicolor Drosophila melanogaster	60,644 38,037	15-Jan-99 24-Nov-98
		GB_IN2:AF117896 GB_BA2:AF067123	1020 1034	AF117896 AF067123	Drosophila melanogaster neuropeptide F (npf) gene, complete cds. Lactobacillus reuteri cobalamin biosynthesis protein J (cbiJ) gene, partial cds; and uroporphyrin-III C-methyltransferase (sumT) gene, complete cds.	Drosophila melanogaster Lactobacillus reuteri	36,122 48,079	2-Jul-99 3-Jun-98
rxa01692	873	GB_RO:RATNFHPEP	3085	M37227	Rat heavy neurofilament (NF-H) polypeptide, partial cds.	Rattus norvegicus	37,093	27-Apr-93
		GB_RO:RSNFH GB_BA2:AF124600	3085 4115	X13804 AF124600	Rat mRNA for heavy neurofilament polypeptide NF-H C-terminus. Corynebacterium glutamicum chorismate synthase (aroC), shikimate kinase (aroK), and 3-dehydroquinase synthase (aroB) genes, complete cds; and putative cytoplasmic peptidase (pepQ) gene, partial cds.	Rattus sp. Corynebacterium glutamicum	37,093 100,000	14-Jul-95 04-MAY-1999
rxa01698	1353	GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	36,323	17-Jun-98

Table 4 (continued)

rxa01699	693	GB_BA1:MSGB937C	38914	L78820	Mycobacterium leprae cosmid B937 DNA sequence.	Mycobacterium leprae	62,780	15-Jun-96
		GB_BA2:AF124600	4115	AF124600	Corynebacterium glutamicum chorismate synthase (aroC), shikimate kinase (aroK), and 3-dehydroquinase 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
rxa01712	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
		GB_EST21:AA952466	278	AA952466	TENS1404 T. cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 1404 5', mRNA sequence.	Trypanosoma cruzi	41,367	29-OCT-1998
rxa01719	684	GB_HTG1:HSDJ534K	154416	AL109925	Homo sapiens chromosome 1 clone RP4-534K7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	35,651	23-Nov-99
		GB_HTG1:HSDJ534K	154416	AL109925	Homo sapiens chromosome 1 clone RP4-534K7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	35,651	23-Nov-99
		GB_EST27:AI447108	431	AI447108	m91e08.x1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:586118 3', mRNA sequence.	Mus musculus	39,671	09-MAR-1999
rxa01720	1332	GB_PR4:AC006322	179640	AC006322	Homo sapiens PAC clone DJ1060B11 from 7q11.23-q21.1, complete sequence.	Homo sapiens	35,817	18-MAR-1999
		GB_PL2:TM018A10	106184	AF013294	Arabidopsis thaliana BAC TM018A10.	Arabidopsis thaliana	35,698	12-Jul-97
		GB_PR4:AC006322	179640	AC006322	Homo sapiens PAC clone DJ1060B11 from 7q11.23-q21.1, complete sequence.	Homo sapiens	37,243	18-MAR-1999
rxa01746	876	GB_EST3:R46227	443	R46227	y952a03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36000 3', mRNA sequence.	Homo sapiens	42,812	22-MAY-1995
		GB_EST3:R46227	443	R46227	y952a03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36000 3', mRNA sequence.	Homo sapiens	42,655	22-MAY-1995
rxa01747	1167	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	59,294	17-Jun-98
		GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	57,584	22-Aug-97
		GB_BA1:SC5F7	40024	AL096872	Streptomyces coelicolor cosmid 5F7.	Streptomyces coelicolor A3(2)	61,810	22-Jul-99
rxa01757	924	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.	Homo sapiens	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.	Rattus sp.	35,942	2-Apr-98
		GB_EST20:AA899038	450	AA899038	NCP6G8T7 Perithecial Neurospora crassa cDNA clone NP6G8 3' end, mRNA sequence.	Neurospora crassa	40,000	12-Apr-98

Table 4 (continued)

rx01807	915	GB_BA1:AP000063 GB_HTG4:AC010694	185300 115857	AP000063 AC010694	Aeropyrum pernix Drosophila melanogaster	40,067 35,450	22-Jun-99 16-OCT-1999
		GB_HTG4:AC010694	115857	AC010694	PROGRESS ***, 75 unordered pieces.		
		GB_HTG4:AC010694	115857	AC010694	Drosophila melanogaster clone RPCI98-6H2, *** SEQUENCING IN PROGRESS ***, 75 unordered pieces.	35,450	16-OCT-1999
rx01821	401	GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, amt 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
rx01835	654	GB_OV:APIGY2 GB_EST30:A1629479	1381 353	X78272 A1629479	Anas platyrhynchos (Super M) IgY upsilon heavy chain gene, exon 2. 486101D10.x1 486 - leaf primordia cDNA library from Hake lab Zea mays cDNA, mRNA sequence.	36,962 38,109	15-Feb-99 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	RPCI11-4I12.TV RPCI-11 Homo sapiens genomic clone RPCI-11-4I12, genomic survey sequence.	37,021	8-Apr-99
rx01850	1470	GB_BA2:ECOUW67_0	110000	U18997	Escherichia coli K-12 chromosomal region from 67.4 to 76.0 minutes.	37,196	U18997
		GB_BA2:AE000392 GB_BA2:U32715	10345 13136	AE000392 U32715	Escherichia coli K-12 MG1655 section 282 of 400 of the complete genome. Haemophilus influenzae Rd section 30 of 163 of the complete genome.	38,021 39,860	12-Nov-98 29-MAY-1998
rx01878	1002	GB_HTG1:CEY64F11	177748	Z99776	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	37,564	14-OCT-1998
		GB_HTG1:CEY64F11	177748	Z99776	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	37,564	14-OCT-1998
		GB_HTG1:CEY64F11	177748	Z99776	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	37,576	14-OCT-1998
rx01892	852	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	35,910	19-Jun-98
		GB_BA1:MLCB250 GB_BA1:MSG1529C	40603 36985	Z97369 L78824	Mycobacterium leprae cosmid B250. Mycobacterium leprae cosmid B1529 DNA sequence.	64,260 64,260	27-Aug-99 15-Jun-96
rx01894	978	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	37,229	19-Jun-98
		GB_IN1:CELF46H5 GB_HTG3:AC009204	38886 115633	U41543 AC009204	Caenorhabditis elegans cosmid F46H5. Drosophila melanogaster chromosome 2 clone BACR03E19 (D1033) RPCI-98 03.E.19 map 36E-37C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 94 unordered pieces.	38,525 31,579	29-Nov-96 18-Aug-99
rx01920	1125	GB_BA2:AF112536	1798	AF112536	Corynebacterium glutamicum ribonucleotide reductase beta-chain (nrdF) gene, complete cds.	99,733	5-Aug-99
		GB_BA1:CANRDFGE	6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	70,321	18-Apr-98

Table 4 (continued)

rx01928	960	GB_BA2:AF050168	1228	AF050168	Corynebacterium ammoniagenes ribonucleoside diphosphate reductase small subunit (nrdF) gene, complete cds.	Corynebacterium ammoniagenes	72,082	23-Apr-98
		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-96
		GB_BA1:XANHRRPB6	1329	M99174	Xanthomonas campestris hrpB6 gene, complete cds.	Xanthomonas campestris	39,305	14-Sep-93
		GB_IN2:CFU43371	1060	U43371	Crithidia fasciculata inosine-uridine preferring nucleoside hydrolase (IUNH) gene, complete cds.	Crithidia fasciculata	61,417	18-Jun-96
rx02022	1230	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
		GB_BA1:CGDAPE	1966	X81379	C.glutamicum dapE gene and orf2.	Corynebacterium glutamicum	100,000	8-Aug-95
		GB_BA1:CGDNAARO	2612	X85965	C.glutamicum ORF3 and aroP gene.	Corynebacterium glutamicum	38,889	30-Nov-97
rx02024	859	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
		GB_BA1:MTC1364	29540	Z93777	Mycobacterium tuberculosis H37Rv complete genome; segment 52/162.	Mycobacterium tuberculosis	59,415	17-Jun-98
		GB_BA1:MSGB1912C	38503	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
rx02027								
rx02031								
rx02072	1464	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	62,247	6-Feb-99

Table 4 (continued)

rxa02085	2358	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
rxa02093	927	GB_EST14:AA448146	452	AA448146	zw82h01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782737	Homo sapiens	34,163	4-Jun-97
		GB_EST17:AA641937	444	AA641937	5', mRNA sequence.	Homo sapiens	35,586	27-OCT-1997
		GB_PR3:AC003074	143029	AC003074	Human PAC clone DJ0596O09 from 7p15, complete sequence.	Homo sapiens	31,917	6-Nov-97
rxa02106	1179	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	Homo sapiens	41,162	18-MAY-1995
rxa02111	1407	GB_BA1:SC6G10	36734	AL049497	PRECURSOR (HUMAN);, mRNA sequence.	Streptomyces coelicolor	50,791	24-MAR-1999
		GB_BA1:U00010	41171	U00010	Streptomyces coelicolor cosmid 6G10.	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
rxa02112	960	GB_HTG3:AC010579	157658	AC010579	Drosophila melanogaster chromosome 3 clone BACR09D08 (D1101) RPCI-98	Drosophila melanogaster	37,909	24-Sep-99
		GB_GSS3:B09839	1191	B09839	09.D.8 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 121 unordered pieces.	Arabidopsis thaliana	37,843	14-MAY-1997
		GB_HTG3:AC010579	157658	AC010579	T12A12-Sp6 TAMU Arabidopsis thaliana genomic clone T12A12, genomic survey sequence.	Drosophila melanogaster	37,909	24-Sep-99
rxa02134	1044	GB_BA1:SCSECYDN A	6154	X83011	Drosophila melanogaster chromosome 3 clone BACR09D08 (D1101) RPCI-98	Streptomyces coelicolor	36,533	02-MAR-1998
		GB_EST32:AI731596	568	AI731596	09.D.8 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 121 unordered pieces.	Gossypium hirsutum	33,451	11-Jun-99
		GB_BA1:SCSECYDN A	6154	X83011	S.coelicolor secY locus DNA.	Streptomyces coelicolor	36,756	02-MAR-1998
rxa02135	1197	GB_PR3:HS525L6	168111	AL023807	BNLGHj10185 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AC004005) putative ribosomal protein L7 [Arabidopsis thaliana], mRNA sequence.	Homo sapiens	34,365	23-Nov-99
		GB_PL2:ATF21P8	85785	AL022347	Human DNA sequence from clone RP3-525L6 on chromosome 6p22.3-23 Contains CA repeat, STSs, GSSs and a CpG Island, complete sequence.	Arabidopsis thaliana	34,325	9-Jun-99
		GB_PL2:U89959	106973	U89959	Arabidopsis thaliana DNA chromosome 4, BAC clone F21P8 (ESSA project).	Arabidopsis thaliana	33,874	26-Jun-98

Table 4 (continued)

rxa02136	645	GB_PL2:ATAC005819	57752	AC005819	Arabidopsis thaliana chromosome II BAC T3A4 genomic sequence, complete sequence.	Arabidopsis thaliana	34,123	3-Nov-98
rxa02139	1962	GB_PL2:F15K9	71097	AC005278	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence.	Arabidopsis thaliana	31,260	7-Nov-98
		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:MSGB1554C	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	36,648	15-Jun-96
rxa02153	903	GB_BA1:MSGB1551C	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	36,648	15-Jun-96
		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	99,104	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:CGARGCJB	4355	X86157	C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
rxa02154	414	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	98,551	1-Jul-98
rxa02155	1287	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:CGARGCJB	4355	X86157	C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
		GB_BA1:CGARGCJB	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-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	99,378	1-Jul-98
rxa02156	1074	GB_BA1:MSGB1133C	42106	L78811	Mycobacterium leprae cosmid B1133 DNA sequence.	Mycobacterium leprae	55,504	15-Jun-96
		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

Table 4 (continued)

	GB_BA2:AF048764	1437	AF048764	Corynebacterium glutamicum argininosuccinate lyase (argH) gene, complete cds.	Corynebacterium glutamicum	87,561	1-Jul-98
	GB_BA1:MTCY06H11	38000	Z85982	Mycobacterium tuberculosis H37Rv complete genome; segment 73/162.	Mycobacterium tuberculosis	64,732	17-Jun-98
rxa02176	GB_BA1:MTCY31	37630	Z73101	Mycobacterium tuberculosis H37Rv complete genome; segment 41/162.	Mycobacterium tuberculosis	36,998	17-Jun-98
	GB_BA1:CGGLTG	3013	X66112	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
rxa02189	GB_PR3:AC002468	115888	AC002468	Human Chromosome 15q26.1 PAC clone pDJ417d7, complete sequence.	Homo sapiens	35,941	16-Sep-98
	GB_BA1:MSGB1970C	39399	L78815	Mycobacterium leprae cosmid B1970 DNA sequence.	Mycobacterium leprae	40,286	15-Jun-96
	GB_PR3:AC002468	115888	AC002468	Human Chromosome 15q26.1 PAC clone pDJ417d7, complete sequence.	Homo sapiens	33,689	16-Sep-98
rxa02193	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
rxa02194	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
	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
rxa02195	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
rxa02197	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
rxa02198	GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	36,770	01-MAR-1994
	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
rxa02208	GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	59,823	01-MAR-1994
	GB_BA1:AP0000063	185300	AP0000063	Aeropyrum pernix genomic DNA, section 6/7.	Aeropyrum pernix	39,442	22-Jun-99

Table 4 (continued)

rxa02229	948	GB_PR4:AC006236	127593	AC006236	Homo sapiens chromosome 17, clone hCIT.162_E_12, complete sequence.	Homo sapiens	37,191	29-DEC-1998
		GB_BA1:MSGY154	40221	AD0000002	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
rxa02234	3462	GB_BA1:MSGB937C	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
rxa02235	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 ***	Homo sapiens	37,994	1-Sep-99
		GB_HTG3:AC009364	192791	AC009364	unordered pieces.	Homo sapiens	37,994	1-Sep-99
		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
rxa02239	1389	GB_BA1:MTCY21B4	39150	Z80108	Mycobacterium tuberculosis H37Rv complete genome; segment 62/162.	Mycobacterium tuberculosis	56,282	23-Jun-98
		GB_HTG3:AC010745	193862	AC010745	Homo sapiens clone NH0549D18, *** SEQUENCING IN PROGRESS ***	Homo sapiens	36,772	21-Sep-99
		GB_HTG3:AC010745	193862	AC010745	unordered pieces.	Homo sapiens	36,772	21-Sep-99
		GB_HTG3:AC010745	193862	AC010745	Homo sapiens clone NH0549D18, *** SEQUENCING IN PROGRESS ***	Homo sapiens	36,772	21-Sep-99
rxa02240	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 Streptomyces spectabilis S-adenosylmethionine synthetase (metK) gene, complete cds.	Streptomyces spectabilis	65,000	31-MAR-1999
rxa02246	1107	EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	52,909	03-OCT-1997 (Rel. 52, Created)

Table 4 (continued)

	GB_EST23:AI128623	363	AI128623	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
rx022299	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 genomic clone Plate=2171 Col=2 Row=I, genomic survey sequence.	Homo sapiens	37,278	16-OCT-1998
rx02311	GB_VI:MH68TKH	4557	X93468	Murine herpesvirus type 68 thymidine kinase and glycoprotein H genes.	murine herpesvirus 68	40,288	3-Sep-96
	GB_HTG4:AC006091	176878	AC006091	Drosophila melanogaster chromosome 3 clone BACR48G05 (D475) RPCI-98 48.G.5 map 91F1-91F13 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Drosophila melanogaster	36,454	27-OCT-1999
	GB_HTG4:AC006091	176878	AC006091	Drosophila melanogaster chromosome 3 clone BACR48G05 (D475) RPCI-98 48.G.5 map 91F1-91F13 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Drosophila melanogaster	36,454	27-OCT-1999
	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	GB_BA1:MSGY224	40051	AD0000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	49,418	03-DEC-1996
	GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	49,360	17-Jun-98
	GB_BA1:MSGY224	40051	AD0000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	38,150	03-DEC-1996
rx02318	GB_HTG3:AC011348	111083	AC011348	Homo sapiens chromosome 5 clone CIT-HSPC_303E13, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.	Homo sapiens	35,821	06-OCT-1999
	GB_HTG3:AC011348	111083	AC011348	Homo sapiens chromosome 5 clone CIT-HSPC_303E13, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.	Homo sapiens	35,821	06-OCT-1999
	GB_HTG3:AC011412	89234	AC011412	Homo sapiens chromosome 5 clone CIT978SKB_81K21, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.	Homo sapiens	36,181	06-OCT-1999
rx02319	GB_BA1:MSGY224	40051	AD0000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	37,792	03-DEC-1996
	GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	37,792	17-Jun-98
	GB_EST23:AI117213	476	AI117213	ub83h02.r1 Soares 2NbMT Mus musculus cDNA clone IMAGE:1395123 5', mRNA sequence.	Mus musculus	35,084	2-Sep-98

Table 4 (continued)

rx02345	1320	GB_BA1:BAPURKE	2582	X91189	B.ammoniagenes purK and purE genes.	Corynebacterium ammoniagenes	61,731	14-Jan-97
		GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	39,624	10-Feb-99
		GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	39,847	10-Feb-99
rx02350	618	GB_BA1:BAPURKE	2582	X91189	B.ammoniagenes purK and purE genes.	Corynebacterium ammoniagenes	64,286	14-Jan-97
		GB_PL1:SC130KBXV	129528	X94335	S.cerevisiae 130kb DNA fragment from chromosome XV.	Saccharomyces cerevisiae	36,617	15-Jul-97
		GB_PL1:SCXVORFS	50984	X90518	S.cerevisiae DNA of 51 Kb from chromosome XV right arm.	Saccharomyces cerevisiae	36,617	1-Nov-95
rx02373	1038	GB_PAT:E00311	1853	E00311	DNA coding of 2,5-diketogluconic acid reductase.	unidentified	56,123	29-Sep-97
		GB_PAT:I06030	1853	I06030	Sequence 4 from Patent EP 0305608.	Unknown.	56,220	02-DEC-1994
		GB_PAT:I00836	1853	I00836	Sequence 1 from Patent US 4758514.	Unknown.	56,220	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.	Corynebacterium glutamicum	99,332	2-Aug-96
		GB_HTG3:AC009946	169072	AC009946	Homo sapiens clone NH0012C17, *** SEQUENCING IN PROGRESS ***	Homo sapiens	36,115	8-Sep-99
		GB_HTG3:AC009946	169072	AC009946	Homo sapiens clone NH0012C17, *** SEQUENCING IN PROGRESS ***	Homo sapiens	36,115	8-Sep-99
rx02380	777	GB_BA1:MTCY253	41230	Z81368	Mycobacterium tuberculosis H37Rv complete genome; segment 106/162.	Mycobacterium tuberculosis	38,088	17-Jun-98
		GB_HTG4:AC010658	120754	AC010658	Drosophila melanogaster chromosome 3L/75C1 clone RPCI98-3B20, *** SEQUENCING IN PROGRESS ***	Drosophila melanogaster	35,817	16-OCT-1999
		GB_HTG4:AC010658	120754	AC010658	Drosophila melanogaster chromosome 3L/75C1 clone RPCI98-3B20, *** SEQUENCING IN PROGRESS ***	Drosophila melanogaster	35,817	16-OCT-1999
rx02382	1419	GB_BA1:CGPROAGE	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 Obg 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:AQ60684	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

Table 4 (continued)

rx02517	570	GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	61,335	17-Jun-98
		GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	37,018	04-DEC-1998
		GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	37,018	01-MAR-1994
rx02532	1170	GB_BA1:SCC22	22115	AL096839	Streptomyces coelicolor cosmid C22.	Streptomyces coelicolor	37,071	12-Jul-99
		GB_OV:AF137219	831	AF137219	Amia calva mixed lineage leukemia-like protein (Mll) gene, partial cds.	Amia calva	36,853	7-Sep-99
		GB_EST30:AI645057	301	AI645057	vs52a10.y1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1149882 5', mRNA sequence.	Mus musculus	41,860	29-Apr-99
		GB_EST20:AA822595	429	AA822595	vs52a10.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1149882 5', mRNA sequence.	Mus musculus	42,353	17-Feb-98
rx02536	879	GB_HTG2:AF130866	118874	AF130866	Homo sapiens chromosome 8 clone PAC 172N13 map 8q24, *** SEQUENCING IN PROGRESS *** , in unordered pieces.	Homo sapiens	40,754	21-MAR-1999
		GB_HTG2:AF130866	118874	AF130866	Homo sapiens chromosome 8 clone PAC 172N13 map 8q24, *** SEQUENCING IN PROGRESS *** , in unordered pieces.	Homo sapiens	40,754	21-MAR-1999
		GB_PL1:ATT12J5	84499	AL035522	Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5 (ESSAII project).	Arabidopsis thaliana	35,063	24-Feb-99
rx02550	1434	GB_BA1:MTCY279	9150	Z97991	Mycobacterium tuberculosis H37Rv complete genome; segment 17/162.	Mycobacterium tuberculosis	37,773	17-Jun-98
		GB_BA1:MSGB1970C	39399	L78815	Mycobacterium leprae cosmid B1970 DNA sequence.	Mycobacterium leprae	39,024	15-Jun-96
rx02559	1026	GB_BA2:SC2H4	25970	AL031514	Streptomyces coelicolor cosmid 2H4.	Streptomyces coelicolor A3(2)	37,906	19-OCT-1999
		GB_BA1:MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162.	Mycobacterium tuberculosis	47,358	18-Jun-98
		GB_PAT:128684	5100	I28684	Sequence 1 from patent US 5573915.	Unknown.	39,138	6-Feb-97
		GB_BA1:MTU27357	5100	U27357	Mycobacterium tuberculosis cyclopropane mycolic acid synthase (cma1) gene, complete cds.	Mycobacterium tuberculosis	39,138	26-Sep-95
rx02622	1683	GB_BA2:AE001780	11997	AE001780	Thermotoga maritima section 92 of 136 of the complete genome.	Thermotoga maritima	44,914	2-Jun-99
		GB_OV:AF064564	49254	AF064564	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds.	Fugu rubripes	39,732	17-Aug-99
		GB_OV:AF064564	49254	AF064564	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds.	Fugu rubripes	36,703	17-Aug-99
rx02623	714	GB_GSS5:AQ818728	444	AQ818728	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	38,801	26-Aug-99
		GB_HTG5:AC011083	198586	AC011083	Homo sapiens chromosome 9 clone RP11-111M7 map 9, WORKING DRAFT SEQUENCE, 51 unordered pieces.	Homo sapiens	35,714	19-Nov-99
		GB_GSS6:AQ826948	544	AQ826948	HS_5014_A2_C12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=590 Col=24 Row=E, genomic survey sequence.	Homo sapiens	39,146	27-Aug-99

Table 4 (continued)

rxa02629	708	GB_VI:BRSMGP	462	M86652	Bovine respiratory syncytial virus membrane glycoprotein mRNA, complete cds.	Bovine respiratory syncytial virus	28-Apr-93
		GB_VI:BRSMGP	462	M86652	Bovine respiratory syncytial virus membrane glycoprotein mRNA, complete cds.	Bovine respiratory syncytial virus	28-Apr-93
rxa02645	1953	GB_PAT:A45577	1925	A45577	Sequence 1 from Patent WO9519442.	Corynebacterium glutamicum	07-MAR-1997
		GB_PAT:A45581	1925	A45581	Sequence 5 from Patent WO9519442.	Corynebacterium glutamicum	07-MAR-1997
		GB_BA1:CORILVA	1925	L01508	Corynebacterium glutamicum threonine dehydratase (ilvA) gene, complete cds.	Corynebacterium glutamicum	26-Apr-93
rxa02646	1392	GB_BA1:CORILVA	1925	L01508	Corynebacterium glutamicum threonine dehydratase (ilvA) gene, complete cds.	Corynebacterium glutamicum	26-Apr-93
		GB_PAT:A45585	1925	A45585	Sequence 9 from Patent WO9519442.	Corynebacterium glutamicum	07-MAR-1997
		GB_PAT:A45583	1925	A45583	Sequence 7 from Patent WO9519442.	Corynebacterium glutamicum	07-MAR-1997
rxa02648	1326	GB_OV:ICTCNC	2049	M83111	Ictalurus punctatus cyclic nucleotide-gated channel RNA sequence.	Ictalurus punctatus	24-MAY-1993
		GB_EST11:AA265464	345	AA265464	mx91c06.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:693706 5' mRNA sequence.	Mus musculus	20-MAR-1997
		GB_GSS8:AQ006950	480	AQ006950	CIT-HSP-2294E14.TR CIT-HSP Homo sapiens genomic clone 2294E14, genomic survey sequence.	Homo sapiens	27-Jun-98
rxa02653							
rxa02687	1068	GB_BA1:CORPHEA	1088	M13774	C.glutamicum pheA gene encoding prephenate dehydratase, complete cds.	Corynebacterium glutamicum	26-Apr-93
		GB_PAT:E04483	948	E04483	DNA encoding prephenate dehydratase.	Corynebacterium glutamicum	29-Sep-97
		GB_PAT:E06110	948	E06110	DNA encoding prephenate dehydratase.	Corynebacterium glutamicum	29-Sep-97
rxa02717	1005	GB_PL1:HVCH4H	59748	Y14573	Hordeum vulgare DNA for chromosome 4H.	Hordeum vulgare	25-MAR-1999
		GB_PR2:HS310H5	29718	Z69705	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.	Homo sapiens	22-Nov-99
		GB_PR3:AC004754	39188	AC004754	Homo sapiens chromosome 16, cosmid clone RT286 (LANL), complete sequence.	Homo sapiens	28-MAY-1998
rxa02754	1461	GB_HTG2:AC008223	130212	AC008223	Drosophila melanogaster chromosome 3 clone BACR16118 (D815) RPCI-98 16.l.18 map 95A-95A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Drosophila melanogaster	2-Aug-99

Table 4 (continued)

	GB_HTG2:AC008223	130212	AC008223	Drosophila melanogaster chromosome 3 clone BACR16118 (D815) RPCI-98 16.L.18 map 95A-95A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 101 unordered pieces.	Drosophila melanogaster	32,757	2-Aug-99
	GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	37,838	10-Feb-99
rx02758	GB_HTG5:AC011678	171967	AC011678	Homo sapiens clone 14_B_7, *** SEQUENCING IN PROGRESS *** , 20 unordered pieces.	Homo sapiens	35,331	5-Nov-99
	GB_HTG5:AC011678	171967	AC011678	Homo sapiens clone 14_B_7, *** SEQUENCING IN PROGRESS *** , 20 unordered pieces.	Homo sapiens	33,807	5-Nov-99
	GB_BA2:AF064070	23183	AF064070	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.	Burkholderia pseudomallei	36,929	20-Jan-99
rx02771	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
rx02772	GB_EST36:AV193572	360	AV193572	AV193572 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk618h8 5', mRNA sequence.	Caenorhabditis elegans	48,588	22-Jul-99
	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	99,914	14-Sep-98
	GB_BA1:MTCY227	35946	Z77724	Mycobacterium tuberculosis H37Rv complete genome; segment 114/162.	Mycobacterium tuberculosis	38,339	17-Jun-98
	GB_BA1:U00011	40429	U00011	Mycobacterium leprae cosmid B1177.	Mycobacterium leprae	38,996	01-MAR-1994
rx02790	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 RPCI11-259O18 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	37,906	3-Jun-99
	GB_PR4:AC006581	172931	AC006581	Homo sapiens 12p21 BAC RPCI11-259O18 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	35,280	3-Jun-99
rx02791	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	GB_EST24:A1223401	169	A1223401	qg48g01.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

Table 4 (continued)

		GB_EST24:AI223401	169	AI223401	qg48g01.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
rxa02814	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
rxs02843	608	GB_BA1:CGAJ4934	1160	AJ004934	Corynebacterium glutamicum dapD 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 B1756.	Mycobacterium leprae	39,626	09-MAR-1995
rxs03205	963	GB_BA1:BLSIGBGN	2906	Z49824	B.lactofermentum orf1 gene and sigB gene.	Corynebacterium glutamicum	8,854	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
rxs03223	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
		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	34,634	17-DEC-1999

Exemplification

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

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

- 133 -

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

5

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

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

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

20

Example 3: DNA Sequencing and Computational Functional Analysis

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

25

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

30

- 134 -

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

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

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

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

- 135 -

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

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

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

Example 6: Assessment of the Expression of the Mutant Protein

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

- 136 -

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

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

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

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The 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 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

- 137 -

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

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

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

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

- 138 -

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

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

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

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

25

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

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

30

- 139 -

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

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

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

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

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

- 140 -

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 5 469-714, 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, 10 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 15 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 20 measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

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

25 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 30 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*

- 141 -

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 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 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 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) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotekhnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley and Sons; Fallon, A. *et al.* (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 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*

- 142 -

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 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 parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

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

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

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

- 143 -

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

Example 12: Construction and Operation of DNA Microarrays

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

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

- 144 -

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

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

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

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

- 145 -

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:

- 146 -

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 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 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 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 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) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

- 147 -

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

5 following claims.

SEQUENCE LISTING

<110> BASF Aktiengesellschaft

<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
METABOLIC PATHWAY PROTEINS

<130> BGI-121CPPC

<140>

<141>

<160> 1156

<210> 1

<211> 948

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(925)

<223> RXA02229

<400> 1

gctgggttcaa cagagaccac cgcgtgtcct gggtcgacgc ctctggcgat cccaccgcac 60

aagccttgga gattttgggt ctacaatagc gaggggtgaat ttg acc atc ccc ttt 115
Leu Thr Ile Pro Phe
1 5gcc 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 15 20gat 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 30 35cgc 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 45 50gca 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 60 65tac 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 75 80 85cgc 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 100agc 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 115cag 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 130gac 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	165
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			
	230	235	240
cca cgt ggg gaa gta gaa gtc cag atc ttt gac gac ggc tcc aca ctc			883
Pro Arg Gly Glu Val Glu Val Gln Ile Phe Asp Asp Gly Ser Thr Leu			
	250	255	260
acc ggc cca agc gcc atc atc gca ctc ggt gag gtg cag atc			925
Thr Gly Pro Ser Ala Ile Ile Ala Leu Gly Glu Val Gln Ile			
	265	270	275
taagattcgc gattgtagtt cgg			948

<210> 2

<211> 275

<212> PRT

<213> Corynebacterium glutamicum

<400> 2

Leu Thr Ile Pro Phe Ala Lys Gly His Ala Thr Glu Asn Asp Phe Ile	
1 5 10 15	
Ile Ile Pro Asp Glu Asp Ala Arg Leu Asp Leu Thr Pro Glu Met Val	
20 25 30	
Val Thr Leu Cys Asp Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu	
35 40 45	
Arg Val Val Lys Ala Ala Asp Val Glu Gly Ser Thr Val Asp Pro Ser	
50 55 60	
Leu Trp Phe Met Asp Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met	
65 70 75 80	
Cys Gly Asn Gly Val Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly	
85 90 95	

WO 01/00843

PCT/IB00/00923

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

<210> 3
 <211> 1491
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1468)
 <223> RXS02970

<400> 3
 aaccgacaaa acagccgttc acgtgctaaa gcagctcggc ttgatctagg gtgaggtgag 60
 ttattttaaag acttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115
 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	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	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
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 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

gcg ttg ttc taagttttct agataacaag gcc
 1491
 Ala Leu Phe
 455

<210> 4

WO 01/00843

PCT/IB00/00923

<211> 456

<212> PRT

<213> Corynebacterium glutamicum

<400> 4

Leu	Ala	Leu	Lys	Gly	Tyr	Thr	Asn	Phe	Asp	Gly	Glu	Phe	Ile	Glu	Phe	1	5	10	15
Gly	Ser	Val	Gln	Ala	Lys	Glu	Glu	Glu	Lys	Arg	Ala	Phe	Asp	Asn	Asp	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
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
 435 440 445
 Leu Thr Phe Ala Gly Ala Leu Phe
 450 455

<210> 5
 <211> 1330
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1330)
 <223> FRXA01009

<400> 5
 aaccgacaaa acagccgttc acgtgctaaa gcagctcggc ttgatctagg gtgaggtgag 60
 ttattttaag acttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115
 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	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	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
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
410

<210> 6

<211> 410

<212> PRT

<213> Corynebacterium glutamicum

<400> 6

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe
1 5 10 15

Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
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			
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
 405 410

<210> 7
 <211> 792
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(769)
 <223> RXC02390

<400> 7
 gctggtggtg ctgacccata cgctggaact ccaactgctg ttgataccgc caagatgttt 60
 ggccgcgagg atctcgtagc tcgcttcgag tcataggccg gtg gag tgg acc gct 115
 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
 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

WO 01/00843

PCT/IB00/00923

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> 8

<211> 223

<212> PRT

<213> Corynebacterium glutamicum

<400> 8

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
 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

WO 01/00843

PCT/IB00/00923

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
 210 215 220

<210> 9

<211> 897

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(874)

<223> RXC01796

<400> 9

atgtaactcg atcaggtgga aatgccccgca aaagtggcgg cggtggccga gggatggccg 60

ttggtgcggc atcgggtggcc 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

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

WO 01/00843

PCT/IB00/00923

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

 <210> 10
 <211> 258
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 10
 Leu Leu Leu Gly Gly Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly
 1 5 10 15
 Asp Gln Thr Gln Ile Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe
 20 25 30
 Asp His Cys Gln Thr Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg
 35 40 45
 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

WO 01/00843

PCT/IB00/00923

130		135		140
Gly Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn				
145		150		155
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
Thr Gly Gln Met Ser Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn				
	245		250	255

Asp Ala

<210> 11
 <211> 771
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(748)
 <223> RXC01207

<400> 11
 cttcatgatc tcaccggcag agcgcgtttt gttacagcgc gtaaactgtg actttgaaaa 60
 atttttgaac aatccgtaca ccaacttcag gagaaaaaca gtg agc aga atc tat 115
 Val Ser Arg Ile Tyr
 1 5
 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

WO 01/00843

PCT/IB00/00923

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	ggc	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	ggc	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	taa	atg	ggg	ag	tcg	gtt	tcgc	ggg						771
Ser	Leu	Arg														
		215														

<210> 12

<211> 216

<212> PRT

<213> Corynebacterium glutamicum

<400> 12

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> 13
<211> 1026
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1003)  
<223> RXC00657
```

```

<400> 13
gtgcg gatcg ggtatccgcg ctacacttag aggtgttaga gatcatgagt ttccacgaac 60
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 tcg 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
cgg tgg 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

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

```


WO 01/00843

PCT/IB00/00923

<210> 14

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 14

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	
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	

WO 01/00843

PCT/IB00/00923

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

<210> 15
 <211> 1059
 <212> DNA
 <213> Corynebacterium glutamicum

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

<400> 15
 ccgccaacaa ggcagcaaag ctcgatccaa ttgacgcctt gcgttatgag taaaagcctc 60
 gttttttaagg 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
 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

WO 01/00843

PCT/IB00/00923

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 taaaaagggt atggtggctg ggt
 1059
 Val Thr Ser
 310

<210> 16
 <211> 312
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 16
 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

WO 01/00843

PCT/IB00/00923

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

<210> 17

<211> 1578

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1555)

<223> RXN00351

<400> 17

gaaggctgct gctaagaaaa cgaccaagaa gaccactaag aaaactacta aaaagaccac 60

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

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

gtg gca gct gtc cat gat ttg aag cac aat ccg gaa tct gcg gca acg
1459

Val Ala Ala Val His Asp Leu Lys His Asn Pro Glu Ser Ala Ala Thr
440 445 450

cga atg aaa acg aac agc gag cag gtc tat acc cac gac gtc aac gtg
1507

Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr His Asp Val Asn Val
455 460 465

tgg gct aat agt ttc ctg gat tgt ttg gca cag tcg gga gaa aac tca
1555

Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln Ser Gly Glu Asn Ser
470 475 480 485

tgaaccgcgc acgaatcgcg acc
1578

<210> 18

<211> 485

<212> PRT

<213> Corynebacterium glutamicum

<400> 18

Met Asp Asp Ser Asn Ser Phe Val Val Val Ala Asn Arg Leu Pro Val
1 5 10 15

Asp Met Thr Val His Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro
20 25 30

Gly Gly Leu Val Thr Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly
35 40 45

Cys Trp Val Gly Trp Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe
50 55 60

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

Asp Tyr Glu Gly Phe Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro
85 90 95

Leu Phe His Asp Leu Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp
100 105 110

His Ala Phe Arg Glu Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln
115 120 125

Val Ala Ala His Gly Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu
130 135 140

Leu Val Pro Gly Ile Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly
145 150 155 160

Phe Phe Leu His Ile Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu
165 170 175

Pro Trp Arg Glu Glu Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val
180 185 190

WO 01/00843

PCT/IB00/00923

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

<210> 19
 <211> 1546
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1546)

<223> FRXA00351

<400> 19

gaaggctgct gctaagaaaa cgaccaagaa gaccactaag aaaactacta aaaagaccac 60

cgcaaagaag	accacaaaga	agtcttaagc	cggatcttat	atg	gat	gät	tcc	aat	115
				Met	Asp	Asp	Ser	Asn	
				1				5	

agc	ttt	gta	ggt	ggt	gct	aac	cgt	ctg	cca	gtg	gat	atg	act	gtc	cac	163
Ser	Phe	Val	Val	Val	Ala	Asn	Arg	Leu	Pro	Val	Asp	Met	Thr	Val	His	
				10					15					20		

cca	gat	ggt	agc	tat	agc	atc	tcc	ccc	agc	ccc	ggt	ggc	ctt	gtc	acg	211
Pro	Asp	Gly	Ser	Tyr	Ser	Ile	Ser	Pro	Ser	Pro	Gly	Gly	Leu	Val	Thr	
			25					30					35			

ggg	ctt	tcc	ccc	ggt	ctg	gaa	caa	cat	cgt	gga	tgt	tgg	gtc	gga	tgg	259
Gly	Leu	Ser	Pro	Val	Leu	Glu	Gln	His	Arg	Gly	Cys	Trp	Val	Gly	Trp	
		40					45					50				

cct	gga	act	gta	gat	ggt	gca	ccc	gaa	cca	ttt	cga	aca	gat	acg	ggt	307
Pro	Gly	Thr	Val	Asp	Val	Ala	Pro	Glu	Pro	Phe	Arg	Thr	Asp	Thr	Gly	
	55					60					65					

ggt	ttg	ctg	cac	cct	ggt	gtc	ctc	act	gca	agt	gac	tat	gaa	ggc	ttc	355
Val	Leu	Leu	His	Pro	Val	Val	Leu	Thr	Ala	Ser	Asp	Tyr	Glu	Gly	Phe	
	70				75					80					85	

tac	gag	ggc	ttt	tca	aac	gca	acg	ctg	tgg	cct	ctt	ttc	cac	gat	ctg	403
Tyr	Glu	Gly	Phe	Ser	Asn	Ala	Thr	Leu	Trp	Pro	Leu	Phe	His	Asp	Leu	
				90					95					100		

att	ggt	act	ccg	gtg	tac	aac	acc	gat	tgg	tgg	cat	gcg	ttt	cgg	gag	451
Ile	Val	Thr	Pro	Val	Tyr	Asn	Thr	Asp	Trp	Trp	His	Ala	Phe	Arg	Glu	
			105					110					115			

gta	aac	ctc	aag	ttc	gct	gaa	gcc	gtg	agc	caa	gtg	gcg	gca	cac	ggt	499
Val	Asn	Leu	Lys	Phe	Ala	Glu	Ala	Val	Ser	Gln	Val	Ala	Ala	His	Gly	
		120					125					130				

gcc	act	gtg	tgg	gtg	cag	gac	tat	cag	ctg	ttg	ctg	ggt	cct	ggc	att	547
Ala	Thr	Val	Trp	Val	Gln	Asp	Tyr	Gln	Leu	Leu	Leu	Val	Pro	Gly	Ile	
	135				140						145					

ttg	cgc	cag	atg	cgc	cct	gat	ttg	aag	atc	ggg	ttc	ttc	ctc	cac	att	595
Leu	Arg	Gln	Met	Arg	Pro	Asp	Leu	Lys	Ile	Gly	Phe	Phe	Leu	His	Ile	
	150				155					160					165	

ccc	ttc	cct	tcc	cct	gat	ctg	ttc	cgt	cag	ctg	ccg	tgg	cgt	gaa	gag	643
Pro	Phe	Pro	Ser	Pro	Asp	Leu	Phe	Arg	Gln	Leu	Pro	Trp	Arg	Glu	Glu	
				170					175					180		

att	ggt	cga	ggc	atg	ctg	ggc	gca	gat	ttg	gtg	gga	ttc	cat	ttg	ggt	691
Ile	Val	Arg	Gly	Met	Leu	Gly	Ala	Asp	Leu	Val	Gly	Phe	His	Leu	Val	
			185					190					195			

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

WO 01/00843

PCT/IB00/00923

gct ttg gtg ctg tcc gaa ttt gcc ggc gcg gcc act gag ctg acc ggt
1363

Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala Thr Glu Leu Thr Gly
410 415 420

gcg tat tta tgc aac cca ttt gat gtg gaa tcc atc aaa cgg caa atg
1411

Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser Ile Lys Arg Gln Met
425 430 435

gtg gca gct gtc cat gat ttg aag cac aat ccg gaa tct gcg gca acg
1459

Val Ala Ala Val His Asp Leu Lys His Asn Pro Glu Ser Ala Ala Thr
440 445 450

cga atg aaa acg aac agc gag cag gtc tat acc cac gac gtc aac gtg
1507

Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr His Asp Val Asn Val
455 460 465

tgg gct aat agt ttc ctg gat tgt ttg gca cag tcg gga
1546

Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln Ser Gly
470 475 480

<210> 20

<211> 482

<212> PRT

<213> Corynebacterium glutamicum

<400> 20

Met Asp Asp Ser Asn Ser Phe Val Val Val Ala Asn Arg Leu Pro Val
1 5 10 15

Asp Met Thr Val His Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro
20 25 30

Gly Gly Leu Val Thr Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly
35 40 45

Cys Trp Val Gly Trp Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe
50 55 60

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

Asp Tyr Glu Gly Phe Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro
85 90 95

Leu Phe His Asp Leu Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp
100 105 110

His Ala Phe Arg Glu Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln
115 120 125

Val Ala Ala His Gly Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu
130 135 140

Leu Val Pro Gly Ile Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly
145 150 155 160

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

WO 01/00843

PCT/IB00/00923

Ser Gly

<210> 21

<211> 779

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(756)

<223> RXA00873

<400> 21

act gcc caa tgg ggt att ttc ctg cgt aat cat gat gag ctc acc ctt	48
Thr Ala Gln Trp Gly Ile Phe Leu Arg Asn His Asp Glu Leu Thr Leu	
1 5 10 15	
gaa atg gtc tcc gat gag gaa cgc agc tac atg tac tcc caa ttc gcc	96
Glu Met Val Ser Asp Glu Glu Arg Ser Tyr Met Tyr Ser Gln Phe Ala	
20 25 30	
tcc gaa cct cgc atg cgc gcc aac gta gga atc cgc agg cgc ctt tcc	144
Ser Glu Pro Arg Met Arg Ala Asn Val Gly Ile Arg Arg Arg Leu Ser	
35 40 45	
cca ctg ctt gaa ggc gac cgc aac cag ctg gaa ctc ctt cac ggt ttg	192
Pro Leu Leu Glu Gly Asp Arg Asn Gln Leu Glu Leu Leu His Gly Leu	
50 55 60	
ttg ctg tct cta cct ggc tca ccc gtg ttg tat tac ggt gat gaa att	240
Leu Leu Ser Leu Pro Gly Ser Pro Val Leu Tyr Tyr Gly Asp Glu Ile	
65 70 75 80	
ggc atg ggc gac aat atc tgg ctc cac gac cgc gac gga gtg cgc acc	288
Gly Met Gly Asp Asn Ile Trp Leu His Asp Arg Asp Gly Val Arg Thr	
85 90 95	
ccc atg cag tgg tcc aac gac cgc aac ggt ggt ttc tcc aaa gct gat	336
Pro Met Gln Trp Ser Asn Asp Arg Asn Gly Gly Phe Ser Lys Ala Asp	
100 105 110	
cct gaa cgc ctg tac ctt cca gcg atc caa aat gat caa tac ggc tac	384
Pro Glu Arg Leu Tyr Leu Pro Ala Ile Gln Asn Asp Gln Tyr Gly Tyr	
115 120 125	
gcc caa gta aac gtg gaa agc caa ctc aac cgc gaa aac tcc ctg ctg	432
Ala Gln Val Asn Val Glu Ser Gln Leu Asn Arg Glu Asn Ser Leu Leu	
130 135 140	
cgc tgg ctc cga aac caa atc ctt atc cgc aag cag tac cgc gca ttt	480
Arg Trp Leu Arg Asn Gln Ile Leu Ile Arg Lys Gln Tyr Arg Ala Phe	
145 150 155 160	
ggt gcc gga acc tac cgt gaa gtg tcc tcc acc aat gag tca gtg ttg	528
Gly Ala Gly Thr Tyr Arg Glu Val Ser Ser Thr Asn Glu Ser Val Leu	
165 170 175	
aca ttt tta cga gaa cac aag ggc caa acc att ttg tgt gtc aac aac	576
Thr Phe Leu Arg Glu His Lys Gly Gln Thr Ile Leu Cys Val Asn Asn	

WO 01/00843

PCT/IB00/00923

180					185					190						
atg	agc	aaa	tat	cct	cag	gca	gtc	tcg	ctt	gat	ttg	cgt	gaa	ttt	gca	624
Met	Ser	Lys	Tyr	Pro	Gln	Ala	Val	Ser	Leu	Asp	Leu	Arg	Glu	Phe	Ala	
		195					200					205				
gga	cac	acc	cct	cga	gag	atg	tcg	ggc	ggg	cag	ctg	ttc	cct	acc	att	672
Gly	His	Thr	Pro	Arg	Glu	Met	Ser	Gly	Gly	Gln	Leu	Phe	Pro	Thr	Ile	
	210					215					220					
gct	gaa	cgg	gag	tgg	att	gtc	act	tta	gcc	cct	cac	gga	ttc	ttc	tgg	720
Ala	Glu	Arg	Glu	Trp	Ile	Val	Thr	Leu	Ala	Pro	His	Gly	Phe	Phe	Trp	
225					230				235						240	
ttt	gat	ctc	acc	gcc	gat	gaa	aag	gac	gat	atg	gaa	tgagcattgg				766
Phe	Asp	Leu	Thr	Ala	Asp	Glu	Lys	Asp	Asp	Met	Glu					
				245				250								
ccaacacatc	atc															779
<210> 22																
<211> 252																
<212> PRT																
<213> Corynebacterium glutamicum																
<400> 22																
Thr	Ala	Gln	Trp	Gly	Ile	Phe	Leu	Arg	Asn	His	Asp	Glu	Leu	Thr	Leu	
1				5				10					15			
Glu	Met	Val	Ser	Asp	Glu	Glu	Arg	Ser	Tyr	Met	Tyr	Ser	Gln	Phe	Ala	
		20					25						30			
Ser	Glu	Pro	Arg	Met	Arg	Ala	Asn	Val	Gly	Ile	Arg	Arg	Arg	Leu	Ser	
		35				40						45				
Pro	Leu	Leu	Glu	Gly	Asp	Arg	Asn	Gln	Leu	Glu	Leu	Leu	His	Gly	Leu	
	50				55						60					
Leu	Leu	Ser	Leu	Pro	Gly	Ser	Pro	Val	Leu	Tyr	Tyr	Gly	Asp	Glu	Ile	
65				70				75							80	
Gly	Met	Gly	Asp	Asn	Ile	Trp	Leu	His	Asp	Arg	Asp	Gly	Val	Arg	Thr	
			85				90						95			
Pro	Met	Gln	Trp	Ser	Asn	Asp	Arg	Asn	Gly	Gly	Phe	Ser	Lys	Ala	Asp	
		100					105						110			
Pro	Glu	Arg	Leu	Tyr	Leu	Pro	Ala	Ile	Gln	Asn	Asp	Gln	Tyr	Gly	Tyr	
		115				120						125				
Ala	Gln	Val	Asn	Val	Glu	Ser	Gln	Leu	Asn	Arg	Glu	Asn	Ser	Leu	Leu	
	130				135						140					
Arg	Trp	Leu	Arg	Asn	Gln	Ile	Leu	Ile	Arg	Lys	Gln	Tyr	Arg	Ala	Phe	
145				150					155						160	
Gly	Ala	Gly	Thr	Tyr	Arg	Glu	Val	Ser	Ser	Thr	Asn	Glu	Ser	Val	Leu	
			165					170						175		
Thr	Phe	Leu	Arg	Glu	His	Lys	Gly	Gln	Thr	Ile	Leu	Cys	Val	Asn	Asn	

WO 01/00843

PCT/IB00/00923

	180		185		190										
Met	Ser	Lys	Tyr	Pro	Gln	Ala	Val	Ser	Leu	Asp	Leu	Arg	Glu	Phe	Ala
		195					200					205			
Gly	His	Thr	Pro	Arg	Glu	Met	Ser	Gly	Gly	Gln	Leu	Phe	Pro	Thr	Ile
	210					215					220				
Ala	Glu	Arg	Glu	Trp	Ile	Val	Thr	Leu	Ala	Pro	His	Gly	Phe	Phe	Trp
225					230					235					240
Phe	Asp	Leu	Thr	Ala	Asp	Glu	Lys	Asp	Asp	Met	Glu				
				245					250						

<210> 23
 <211> 1102
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1102)
 <223> RXA00891

<400> 23
 tcaatattcc gaagaaaacc gcgcagctct ctactagtc tcaggtgagg cgaaagtggg 60
 gaaagaccgc ctacgcatgg tgcgcctggc tttttagaat gtg ctg caa acc tcc 115
 Val Leu Gln Thr Ser
 1 5
 tgg cat ttc tct atc ctg gca ggc atg act gat acc tct ccg ttg aat 163
 Trp His Phe Ser Ile Leu Ala Gly Met Thr Asp Thr Ser Pro Leu Asn
 10 15 20
 tct cag ccg agt gca gat cac cac cct gat cac gcg gct cgc cca gtt 211
 Ser Gln Pro Ser Ala Asp His His Pro Asp His Ala Ala Arg Pro Val
 25 30 35
 ctt gat gcc cac ggc ttg atc gtt gag cac gaa tcg gaa gag ttt cca 259
 Leu Asp Ala His Gly Leu Ile Val Glu His Glu Ser Glu Glu Phe Pro
 40 45 50
 gtc ccc gca ccc gct ccc ggt gaa cag ccc tgg gag aag aaa aac cgc 307
 Val Pro Ala Pro Ala Pro Gly Glu Gln Pro Trp Glu Lys Lys Asn Arg
 55 60 65
 gag tgg tac aaa gac gcc gtt ttc tac gaa gtg ctg gtt cgt gcc ttc 355
 Glu Trp Tyr Lys Asp Ala Val Phe Tyr Glu Val Leu Val Arg Ala Phe
 70 75 80 85
 tac gat cca gaa ggc aac gga gtc gga tcg ttg aaa ggc ctg acc gaa 403
 Tyr Asp Pro Glu Gly Asn Gly Val Gly Ser Leu Lys Gly Leu Thr Glu
 90 95 100
 aaa ctg gat tac atc cag tgg ctc ggc gtg gat tgc att tgg atc cca 451
 Lys Leu Asp Tyr Ile Gln Trp Leu Gly Val Asp Cys Ile Trp Ile Pro
 105 110 115
 ccg ttt tat gat tcc cca ctg cgc gac ggc ggt tac gat atc cgc aac 499

WO 01/00843

PCT/IB00/00923

Pro	Phe	Tyr	Asp	Ser	Pro	Leu	Arg	Asp	Gly	Gly	Tyr	Asp	Ile	Arg	Asn		
		120					125					130					
ttc	cgt	gaa	atc	ctg	ccc	gaa	ttc	ggc	acc	gtc	gat	gac	ttc	gtg	gaa	547	
Phe	Arg	Glu	Ile	Leu	Pro	Glu	Phe	Gly	Thr	Val	Asp	Asp	Phe	Val	Glu		
	135					140					145						
ctc	gtt	gac	cac	gcc	cac	cgc	cgt	ggc	ctg	cgt	gtt	atc	acc	gac	ttg	595	
Leu	Val	Asp	His	Ala	His	Arg	Arg	Gly	Leu	Arg	Val	Ile	Thr	Asp	Leu		
150					155					160					165		
gtc	atg	aat	cac	acc	tcc	gac	cag	cac	gca	tgg	ttc	caa	gaa	tcc	cgg	643	
Val	Met	Asn	His	Thr	Ser	Asp	Gln	His	Ala	Trp	Phe	Gln	Glu	Ser	Arg		
				170					175					180			
cgc	gac	cca	acc	ggc	ccc	tac	gga	gat	ttc	tat	gtg	tgg	agc	gat	gat	691	
Arg	Asp	Pro	Thr	Gly	Pro	Tyr	Gly	Asp	Phe	Tyr	Val	Trp	Ser	Asp	Asp		
			185					190					195				
ccc	acc	ctg	tac	aac	gaa	gcc	cgc	atc	atc	ttt	gta	gat	aca	gaa	gaa	739	
Pro	Thr	Leu	Tyr	Asn	Glu	Ala	Arg	Ile	Ile	Phe	Val	Asp	Thr	Glu	Glu		
		200					205					210					
tcc	aac	tgg	acc	tat	gat	ccg	gtg	cgt	ggc	cag	tac	ttc	tgg	cac	cgc	787	
Ser	Asn	Trp	Thr	Tyr	Asp	Pro	Val	Arg	Gly	Gln	Tyr	Phe	Trp	His	Arg		
	215					220					225						
ttc	ttc	tcc	cac	caa	cca	gac	ctc	aac	tac	gac	aac	ccc	gca	gtc	caa	835	
Phe	Phe	Ser	His	Gln	Pro	Asp	Leu	Asn	Tyr	Asp	Asn	Pro	Ala	Val	Gln		
230					235				240						245		
gag	gcc	atg	cta	gat	gtc	ttg	cgt	ttc	tgg	ctg	gac	ctg	gga	ctt	gat	883	
Glu	Ala	Met	Leu	Asp	Val	Leu	Arg	Phe	Trp	Leu	Asp	Leu	Gly	Leu	Asp		
				250					255					260			
ggt	ttc	cga	cta	gat	gcc	gtt	cct	tat	ctt	ttt	gaa	cgc	gaa	ggc	acc	931	
Gly	Phe	Arg	Leu	Asp	Ala	Val	Pro	Tyr	Leu	Phe	Glu	Arg	Glu	Gly	Thr		
			265				270						275				
aac	ggc	gaa	aac	ctc	aaa	gaa	acc	cac	gat	ttc	ctc	aaa	ctg	tgt	cgc	979	
Asn	Gly	Glu	Asn	Leu	Lys	Glu	Thr	His	Asp	Phe	Leu	Lys	Leu	Cys	Arg		
		280					285					290					
tct	gtc	att	gag	aag	gaa	tac	ccc	ggc	cga	atc	ctg	ctc	gca	gaa	gcc		
1027																	
Ser	Val	Ile	Glu	Lys	Glu	Tyr	Pro	Gly	Arg	Ile	Leu	Leu	Ala	Glu	Ala		
	295					300					305						
aac	caa	tgg	ccc	caa	gat	gtg	gtc	gaa	tac	ttc	ggt	gaa	aaa	gac	aaa		
1075																	
Asn	Gln	Trp	Pro	Gln	Asp	Val	Val	Glu	Tyr	Phe	Gly	Glu	Lys	Asp	Lys		
310					315				320						325		
ggc	gat	gaa	tgc	cac	atg	gcc	ttc	cac									
1102																	
Gly	Asp	Glu	Cys	His	Met	Ala	Phe	His									
				330													

<210> 24

<211> 334

WO 01/00843

PCT/IB00/00923

Leu Leu Ala Glu Ala Asn Gln Trp Pro Gln Asp Val Val Glu Tyr Phe
305 310 315 320

Gly Glu Lys Asp Lys Gly Asp Glu Cys His Met Ala Phe His
325 330

<210> 25

<211> 1386

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1363)

<223> RXA00534

<400> 25

ctgtgcagaa agaaaacact cctctggcta ggtagacaca gtttataaag gtagagttga 60

gcgggtaact gtcagcacgt agatcgaaag gtgcacaaag gtg gcc ctg gtc gta 115
Val Ala Leu Val Val
1 5

cag aaa tat ggc ggt tcc tcg ctt gag agt gcg gaa cgc att aga aac 163
Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala Glu Arg Ile Arg Asn
10 15 20

gtc gct gaa cgg atc gtt gcc acc aag aag gct gga aat gat gtc gtg 211
Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala Gly Asn Asp Val Val
25 30 35

gtt gtc tgc tcc gca atg gga gac acc acg gat gaa ctt cta gaa ctt 259
Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp Glu Leu Leu Glu Leu
40 45 50

gca gcg gca gtg aat ccc gtt ccg cca gct cgt gaa atg gat atg ctc 307
Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg Glu Met Asp Met Leu
55 60 65

ctg act gct ggt gag cgt att tct aac gct ctc gtc gcc atg gct att 355
Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala Ile
70 75 80 85

gag tcc ctt ggc gca gaa gcc caa tct ttc acg ggc tct cag gct ggt 403
Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr Gly Ser Gln Ala Gly
90 95 100

gtg ctc acc acc gag cgc cac gga aac gca cgc att gtt gat gtc act 451
Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg Ile Val Asp Val Thr
105 110 115

cca ggt cgt gtg cgt gaa gca ctc gat gag ggc aag atc tgc att gtt 499
Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly Lys Ile Cys Ile Val
120 125 130

gct ggt ttc cag ggt gtt aat aaa gaa acc cgc gat gtc acc acg ttg 547
Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg Asp Val Thr Thr Leu
135 140 145

ggc cgt ggt ggt tct gac acc act gca gtt gcg ttg gca gct gct ttg 595

WO 01/00843

PCT/IB00/00923

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

aac atc gaa ttg att tcc acc tct gag att cgt att tcc gtg ctg atc
1267

Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg Ile Ser Val Leu Ile
375 380 385

cgt gaa gat gat ctg gat gct gct gca cgt gca ttg cat gag cag ttc
1315

Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala Leu His Glu Gln Phe
390 395 400 405

cag ctg ggc ggc gaa gac gaa gcc gtc gtt tat gca ggc acc gga cgc
1363

Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr Ala Gly Thr Gly Arg
410 415 420

taaagtttta aaggagtagt ttt
1386

<210> 26

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 26

Val Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala
1 5 10 15

Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
20 25 30

Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
50 55 60

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

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

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

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

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
130 135 140

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

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
180 185 190

WO 01/00843

PCT/IB00/00923

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

<210> 27
 <211> 1155
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1132)
 <223> RXA00533

<400> 27
 ctgcacgtgc attgcatgag cagttccagc tgggcggcga agacgaagcc gtcgtttatg 60
 caggcaccgg acgctaaagt tttaaaggag tagttttaca atg acc acc atc gca 115
 Met Thr Thr Ile Ala

1															5	
gtt	gtt	ggt	gca	acc	ggc	cag	gtc	ggc	cag	gtt	atg	cgc	acc	ctt	ttg	163
Val	Val	Gly	Ala	Thr	Gly	Gln	Val	Gly	Gln	Val	Met	Arg	Thr	Leu	Leu	
				10					15					20		
gaa	gag	cgc	aat	ttc	cca	gct	gac	act	gtt	cgt	ttc	ttt	gct	tcc	cca	211
Glu	Glu	Arg	Asn	Phe	Pro	Ala	Asp	Thr	Val	Arg	Phe	Phe	Ala	Ser	Pro	
			25					30					35			
cgt	tcc	gca	ggc	cgt	aag	att	gaa	ttc	cgt	ggc	acg	gaa	atc	gag	gta	259
Arg	Ser	Ala	Gly	Arg	Lys	Ile	Glu	Phe	Arg	Gly	Thr	Glu	Ile	Glu	Val	
		40					45					50				
gaa	gac	att	act	cag	gca	acc	gag	gag	tcc	ctc	aag	gac	atc	gac	gtt	307
Glu	Asp	Ile	Thr	Gln	Ala	Thr	Glu	Glu	Ser	Leu	Lys	Asp	Ile	Asp	Val	
	55					60					65					
gcg	ttg	ttc	tcc	gct	gga	ggc	acc	gct	tcc	aag	cag	tac	gct	cca	ctg	355
Ala	Leu	Phe	Ser	Ala	Gly	Gly	Thr	Ala	Ser	Lys	Gln	Tyr	Ala	Pro	Leu	
70					75					80					85	
ttc	gct	gct	gca	ggc	gcg	act	gtt	gtg	gat	aac	tct	tct	gct	tgg	cgc	403
Phe	Ala	Ala	Ala	Gly	Ala	Thr	Val	Val	Asp	Asn	Ser	Ser	Ala	Trp	Arg	
				90					95					100		
aag	gac	gac	gag	gtt	cca	cta	atc	gtc	tct	gag	gtg	aac	cct	tcc	gac	451
Lys	Asp	Asp	Glu	Val	Pro	Leu	Ile	Val	Ser	Glu	Val	Asn	Pro	Ser	Asp	
			105					110					115			
aag	gat	tcc	ctg	gtc	aag	ggc	att	att	gcg	aac	cct	aac	tgc	acc	acc	499
Lys	Asp	Ser	Leu	Val	Lys	Gly	Ile	Ile	Ala	Asn	Pro	Asn	Cys	Thr	Thr	
		120					125					130				
atg	gct	gcg	atg	cca	gtg	ctg	aag	cca	ctt	cac	gat	gcc	gct	ggt	ctt	547
Met	Ala	Ala	Met	Pro	Val	Leu	Lys	Pro	Leu	His	Asp	Ala	Ala	Gly	Leu	
	135					140					145					
gta	aag	ctt	cac	gtt	tcc	tct	tac	cag	gct	gtt	tcc	ggt	tct	ggt	ctt	595
Val	Lys	Leu	His	Val	Ser	Ser	Tyr	Gln	Ala	Val	Ser	Gly	Ser	Gly	Leu	
150					155					160					165	
gca	ggt	gtg	gaa	acc	ttg	gca	aag	cag	gtt	gct	gca	gtt	gga	gac	cac	643
Ala	Gly	Val	Glu	Thr	Leu	Ala	Lys	Gln	Val	Ala	Ala	Val	Gly	Asp	His	
				170					175					180		
aac	gtt	gag	ttc	gtc	cat	gat	gga	cag	gct	gct	gac	gca	ggc	gat	gtc	691
Asn	Val	Glu	Phe	Val	His	Asp	Gly	Gln	Ala	Ala	Asp	Ala	Gly	Asp	Val	
			185					190					195			
gga	cct	tat	gtt	tca	cca	atc	gct	tac	aac	gtg	ctg	cca	ttc	gcc	gga	739
Gly	Pro	Tyr	Val	Ser	Pro	Ile	Ala	Tyr	Asn	Val	Leu	Pro	Phe	Ala	Gly	
		200					205					210				
aac	ctc	gtc	gat	gac	ggc	acc	ttc	gaa	acc	gat	gaa	gag	cag	aag	ctg	787
Asn	Leu	Val	Asp	Asp	Gly	Thr	Phe	Glu	Thr	Asp	Glu	Glu	Gln	Lys	Leu	
	215					220					225					
cgc	aac	gaa	tcc	cgc	aag	att	ctc	ggt	ctc	cca	gac	ctc	aag	gtc	tca	835
Arg	Asn	Glu	Ser	Arg	Lys	Ile	Leu	Gly	Leu	Pro	Asp	Leu	Lys	Val	Ser	
230					235					240					245	

ggc acc tgc gtc cgc gtg ccg gtt ttc acc ggc cac acg ctg acc att 883
 Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly His Thr Leu Thr Ile
 250 255 260

cac gcc gaa ttc gac aag gca atc acc gtg gac cag gcg cag gag atc 931
 His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp Gln Ala Gln Glu Ile
 265 270 275

ttg ggt gcc gct tca ggc gtc aag ctt gtc gac gtc cca acc cca ctt 979
 Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp Val Pro Thr Pro Leu
 280 285 290

gca gct gcc ggc att gac gaa tcc ctc gtt gga cgc atc cgt cag gac
 1027
 Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly Arg Ile Arg Gln Asp
 295 300 305

tcc act gtc gac gat aac cgc ggt ctg gtt ctc gtc gta tct ggc gac
 1075
 Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu Val Val Ser Gly Asp
 310 315 320 325

aac ctc cgc aag ggt gct gcg cta aac acc atc cag atc gct gag ctg
 1123
 Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile Gln Ile Ala Glu Leu
 330 335 340

ctg gtt aag taaaaacccg ccattaaaaa ctc
 1155
 Leu Val Lys

<210> 28
 <211> 344
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 28
 Met Thr Thr Ile Ala Val Val Gly Ala Thr Gly Gln Val Gly Gln Val
 1 5 10 15
 Met Arg Thr Leu Leu Glu Glu Arg Asn Phe Pro Ala Asp Thr Val Arg
 20 25 30
 Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly
 35 40 45
 Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu
 50 55 60
 Lys Asp Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys
 65 70 75 80
 Gln Tyr Ala Pro Leu Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn
 85 90 95
 Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu
 100 105 110

WO 01/00843

PCT/IB00/00923

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

<210> 29

<211> 608

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (69) .. (608)

<223> RXA02843

<400> 29

cccattgcgc ggaggtcgca ccccttccga cttgaactga taggccgata gaaattattc 60

tggacgtcatg act act gct tcc gca acc gga att gca aca ctg acc tcc 110
 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
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> 30

<211> 180

<212> PRT

<213> Corynebacterium glutamicum

<400> 30

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

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

Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val Thr Arg
35 40 45

Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr
 50 55 60
 Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg
 65 70 75 80
 Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val
 85 90 95
 Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr
 100 105 110
 Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp
 115 120 125
 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> 31
 <211> 1230
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1207)
 <223> RXA02022

<400> 31
 tattttgcgat tccaactgct tgggctccgc gaatgttttc actcattttt taatcgaccg 60
 cttccatcat gttttaacta aggtttgtag gcttaaacct gtg aac tct gaa ctc 115
 Val Asn Ser Glu Leu
 1 5
 aaa cca gga tta gat ctc ctc ggc gac cca att gtc ctt act caa cgt 163
 Lys Pro Gly Leu Asp Leu Leu Gly Asp Pro Ile Val Leu Thr Gln Arg
 10 15 20
 ttg gta gat ata ccg agt ccg tcg ggt cag gaa aag cag att gct gat 211
 Leu Val Asp Ile Pro Ser Pro Ser Gly Gln Glu Lys Gln Ile Ala Asp
 25 30 35
 gaa att gaa gat gcc ctt cgg aac ctt aat cta cct ggt gta gag gtc 259
 Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu Pro Gly Val Glu Val
 40 45 50
 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 tcg 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	595
Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu Ala Leu Leu Gly Glu	
150 155 160 165	
cct act ggc ggc tgg att gag gcg ggc tgc cag ggc aat ctg cgc atc	643
Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln Gly Asn Leu Arg Ile	
170 175 180	
aag gtg acg gcg cat ggt gtg cgt gcc cat tcg gcg aga agc tgg ttg	691
Lys Val Thr Ala His Gly Val Arg Ala His Ser Ala Arg Ser Trp Leu	
185 190 195	
ggt gat aat gcg atg cat aag ttg tcg ccg atc att tcg aag gtt gct	739
Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile Ile Ser Lys Val Ala	
200 205 210	
gcg tat aag gcc gca gaa gtc aac att gat ggc ttg acc tac cgt gaa	787
Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly Leu Thr Tyr Arg Glu	
215 220 225	
ggc ctc aac atc gtt ttc tgc gaa tcg ggc gtg gca aac aac gtc att	835
Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val Ala Asn Asn Val Ile	
230 235 240 245	
cca gac ctc gcg tgg atg aac ctc aac ttc cgt ttc gcg ccg aat cgc	883
Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg Phe Ala Pro Asn Arg	
250 255 260	
gat ctc aac gag gcg atc gag cat gtc gtc gaa acg ctt gag ctt gac	931
Asp Leu Asn Glu Ala Ile Glu His Val Val Glu Thr Leu Glu Leu Asp	
265 270 275	
ggt caa gac ggc atc gaa tgg gcc gta gaa gac ggg gca ggc ggt gcc	979
Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp Gly Ala Gly Gly Ala	
280 285 290	
ctt cca ggc ttg ggg cag cag gtg aca agc ggg ctt atc gac gcc gtc	
1027	
Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly Leu Ile Asp Ala Val	
295 300 305	

ggc cgc gaa aaa atc cgc gca aaa ttc ggc tgg acc gat gtc tca cgt
1075

Gly Arg Glu Lys Ile Arg Ala Lys Phe Gly Trp Thr Asp Val Ser Arg
310 315 320 325

ttt tca gcc atg gga att cca gcc cta aac ttt ggc gct ggt gat cca
1123

Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe Gly Ala Gly Asp Pro
330 335 340

agt ttc gcg cat aaa cgc gac gag cag tgc cca gtg gag caa atc acg
1171

Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro Val Glu Gln Ile Thr
345 350 355

gat gtg gca gca att ttg aag cag tac ctg agc gag taaccgcatt
1217

Asp Val Ala Ala Ile Leu Lys Gln Tyr Leu Ser Glu
360 365

cgggggttatc gtg
1230

<210> 32

<211> 369

<212> PRT

<213> Corynebacterium glutamicum

<400> 32

Val Asn Ser Glu Leu Lys Pro Gly Leu Asp Leu Leu Gly Asp Pro Ile
1 5 10 15

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

WO 01/00843

PCT/IB00/00923

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

<210> 33
<211> 1059
<212> DNA
<213> Corynebacterium glutamicum

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

<400> 33
attacctcag ccttccaagc tgatgatgca ttacttaaaa actgcagaca cttgaaaaac 60

ttctcaccgc cactcgttcc 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	ggc	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	ggc	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	499
Glu	Ile	Glu	Glu	His	Phe	Arg	Lys	Ile	His	Ala	Ala	Ala	Pro	Glu	Leu	
		120					125					130				
cca	ctg	ttt	gcc	tac	aac	atc	cca	gtg	tcg	gtg	cac	tcc	aac	ctc	aac	547
Pro	Leu	Phe	Ala	Tyr	Asn	Ile	Pro	Val	Ser	Val	His	Ser	Asn	Leu	Asn	
		135				140					145					
cca	gtc	atg	ctt	ttg	acg	ctg	gcc	aag	gat	ggc	gtt	ctt	gca	ggc	acc	595
Pro	Val	Met	Leu	Leu	Thr	Leu	Ala	Lys	Asp	Gly	Val	Leu	Ala	Gly	Thr	
					155					160					165	
aag	gat	tcc	agt	ggc	aat	gat	ggc	gca	atc	cgc	tca	ctg	atc	gaa	gct	643
Lys	Asp	Ser	Ser	Gly	Asn	Asp	Gly	Ala	Ile	Arg	Ser	Leu	Ile	Glu	Ala	
				170				175						180		
cgt	gat	gat	gct	gga	ctc	act	gag	cag	ttc	aag	atc	ctc	acc	ggc	agc	691
Arg	Asp	Asp	Ala	Gly	Leu	Thr	Glu	Gln	Phe	Lys	Ile	Leu	Thr	Gly	Ser	
			185					190					195			
gaa	acc	acc	gtt	gat	ttc	gcc	tac	ctt	gca	ggc	ggt	gca	gct	gga	gtt	739
Glu	Thr	Thr	Val	Asp	Phe	Ala	Tyr	Leu	Ala	Gly	Ala	Asp	Gly	Val	Val	
			200				205					210				
cca	ggc	ctg	ggc	aat	gtt	gat	cct	gca	gca	tac	gca	gct	tta	gca	aaa	787
Pro	Gly	Leu	Gly	Asn	Val	Asp	Pro	Ala	Ala	Tyr	Ala	Ala	Leu	Ala	Lys	
		215				220					225					
ctc	tgc	ctc	gat	gga	aag	tgg	gca	gaa	gct	gct	gct	ttg	cag	aag	cgc	835
Leu	Cys	Leu	Asp	Gly	Lys	Trp	Ala	Glu	Ala	Ala	Ala	Leu	Gln	Lys	Arg	
	230				235				240						245	
atc	aac	cac	ctc	ttc	cac	atc	gtc	ttc	gtg	gga	gac	acc	tcc	cat	atg	883
Ile	Asn	His	Leu	Phe	His	Ile	Val	Phe	Val	Gly	Asp	Thr	Ser	His	Met	

WO 01/00843

PCT/IB00/00923

250 255 260
 tcc gga tcc agc gct ggt ttg ggc ggt ttc aag aca gca ctc gca cac 931
 Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys Thr Ala Leu Ala His
 265 270 275
 ctt ggc att att gaa tcc aat gcg atg gca gtt cct cac cag agc ctc 979
 Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val Pro His Gln Ser Leu
 280 285 290
 agc gac gaa gaa act gct cgc att cac gcc att gtt gat gaa ttc ctg
 1027
 Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile Val Asp Glu Phe Leu
 295 300 305
 tac acc gct taaggccac acctcatgac tga
 1059
 Tyr Thr Ala
 310
 <210> 34
 <211> 312
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 34
 Met Ala Ser Ala Thr Phe Thr Gly Val Ile Pro Pro Val Met Thr Pro
 1 5 10 15
 Leu His Ala Asp Gly Ser Val Asp Val Glu Ser Leu Arg Lys Leu Val
 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		
		290				295					300						
Val	Asp	Glu	Phe	Leu	Tyr	Thr	Ala										
305					310												

<210> 35
 <211> 867
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(844)
 <223> RXA00863

<400> 35
 aacgggtcagt taggtatgga tatcagcacc ttctgaacgg gtacgtctag actggtgggc 60
 gtttgaaaaa ctcttcgccc cacgaaaatg aaggagcata atg gga atc aag gtt 115
 Met Gly Ile Lys Val
 1 5
 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

WO 01/00843

PCT/IB00/00923

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> 36

<211> 248

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

Met	Gly	Ile	Lys	Val	Gly	Val	Leu	Gly	Ala	Lys	Gly	Arg	Val	Gly	Gln	
1				5					10					15		

Thr	Ile	Val	Ala	Ala	Val	Asn	Glu	Ser	Asp	Asp	Leu	Glu	Leu	Val	Ala	
			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
Phe Asp Asp Ala Arg Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys		
	85	90
Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val		
	100	105
Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala		
	115	120
Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly		
	130	135
Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala		
145	150	155
Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser		
	165	170
Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser		
	180	185
Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr		
	195	200
Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly		
	210	215
Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val		
225	230	235
Gly Leu Glu His Tyr Leu Gly Leu		
	245	

<210> 37
 <211> 873
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(850)
 <223> RXA00864

<400> 37
 acagcaccca ggcctagtcg taggacttga gcattaccta ggcctgtaaa ggctcatttc 60
 agcagcgggt ggaatttttt aaaaggagcg tttaaaggct gtg gcc gaa caa gtt 115
 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
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	ggg	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	tcg	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												
				250												

WO 01/00843

PCT/IB00/00923

<210> 38
 <211> 250
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 38
 Val Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser
 1 5 10 15
 Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala
 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
 145 150 155 160
 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
 225 230 235 240
 Met Ala Thr Ser Pro Tyr Val Met Asp Phe
 245 250

<210> 39
 <211> 608
 <212> DNA
 <213> Corynebacterium glutamicum

WO 01/00843

PCT/IB00/00923

<220>

<221> CDS

<222> (69)..(608)

<223> RXA02843

<400> 39

```

cccattgcgc ggaggtcgca ccccttccga cttgaactga taggccgata gaaattattc 60

tggacgtcatg act act gct tcc gca acc gga att gca aca ctg acc tcc 110
      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
Leu Gly Ala Ser Met Val
175              180

```

<210> 40

<211> 180

<212> PRT

WO 01/00843

PCT/IB00/00923

<213> Corynebacterium glutamicum

<400> 40

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

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

Ala	Leu	Thr	Pro	Leu	Glu	Gly	Val	Asp	Glu	Asp	Arg	Asn	Val	Thr	Arg
		35					40					45			

Lys	Ile	Val	Thr	Thr	Thr	Ile	Asp	Thr	Asp	Ala	Ala	Pro	Thr	Asp	Thr
	50					55					60				

Tyr	Asp	Ala	Trp	Leu	Arg	Leu	His	Leu	Leu	Ser	His	Arg	Val	Phe	Arg
65					70					75					80

Pro	His	Thr	Ile	Asn	Leu	Asp	Gly	Ile	Phe	Gly	Leu	Leu	Asn	Asn	Val
				85					90					95	

Val	Trp	Thr	Asn	Phe	Gly	Pro	Cys	Ala	Val	Asp	Gly	Phe	Ala	Leu	Thr
			100					105					110		

Arg	Ala	Arg	Leu	Ser	Arg	Arg	Gly	Gln	Val	Thr	Val	Tyr	Ser	Val	Asp
		115					120					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> 41

<211> 1143

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1120)

<223> RXN00355

<400> 41

aatagatcag cgcattccgtg gtggaaccaa aaggctcaac aatacgaaac gttcgctttc 60

ggtcctgatg	aaagagatgt	ccctgaatca	tcattctaagt	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		

WO 01/00843

PCT/IB00/00923

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	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	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

WO 01/00843

PCT/IB00/00923

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

<210> 42
 <211> 340
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 42
 Met His Leu Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu
 1 5 10 15

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
 Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile
 325 330 335
 Ala Arg Asp Val
 340

<210> 43
 <211> 958
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(958)
 <223> FRXA00352

<400> 43
 aatagatcag cgcattccgtg gtggaaccaa aaggctcaac aatacgaaac gttcgctttc 60
 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	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	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
 Asn His Thr Val Glu Tyr Ile Leu Lys
 280 285

958

<210> 44
 <211> 286
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 44
 Met His Leu Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu
 1 5 10 15
 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> 45			
<211> 1400			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (1)..(1377)			
<223> RXA00972			
<400> 45			
cct gca cct ggt tgg cgt ttc cgc acc gga gaa gat gta aca atg gct			48
Pro Ala Pro Gly Trp Arg Phe Arg Thr Gly Glu Asp Val Thr Met Ala			
1	5	10	15
aca gtt gaa aat ttc aat gaa ctt ccc gca cac gta tgg cca 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			240
Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly			
65	70	75	80
cca ggc aat gtg cac tac gca tct aaa gcg ttc ctg acc aag acc att			288
Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile			
85	90	95	
gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gca tcc atc			336
Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile			
100	105	110	
aac gaa ctg ggc att gcc ctg gcc gct ggt ttc ccc gcc agc cgt atc			384
Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile			
115	120	125	
acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg ttg gtt			432
Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val			
130	135	140	
caa aac ggt gtg gga cac gtg gtg ctg gac tcc gca cag gaa cta gaa			480
Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu			
145	150	155	160
ctg ttg gat tac gtt gcc gct ggt gaa ggc aag att cag gac gtg ttg			528
Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu			
165	170	175	

atc cgc gta aag cca ggc atc gaa gca cac acc cac gag ttc atc gcc	576
Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe Ile Ala	
180 185 190	
act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc ggt tcc	624
Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser	
195 200 205	
gca ttc gaa gca gca aaa gcc gcc aac aac gca gaa aac ctg aac ctg	672
Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu	
210 215 220	
gtt ggc ctg cac tgc cac gtt ggt tcc cag gtg ttc gac gcc gaa ggc	720
Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Glu Gly	
225 230 235 240	
ttc aag ctg gca gca gaa cgc gtg ttg ggc ctg tac tca cag atc cac	768
Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His	
245 250 255	
agc gaa ctg ggc gtt gcc ctt cct gaa ctg gat ctc ggt ggc gga tac	816
Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr	
260 265 270	
ggc att gcc tat acc gca gct gaa gaa cca ctc aac gtc gca gaa gtt	864
Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val	
275 280 285	
gcc tcc gac ctg ctc acc gca gtc gga aaa atg gca gcg gaa cta ggc	912
Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly	
290 295 300	
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	

WO 01/00843

PCT/IB00/00923

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> 46

<211> 459

<212> PRT

<213> Corynebacterium glutamicum

<400> 46

Pro Ala Pro Gly Trp Arg Phe Arg Thr Gly Glu Asp Val Thr Met Ala
1 5 10 15

Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro Arg Asn
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

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

WO 01/00843

PCT/IB00/00923

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				
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
			420					425					430		
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> 47

<211> 2121

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2098)

<223> RXA02653

<400> 47

agacagagtg ttagtgcggtg gggcagctct cactttcatc gacatcactc gagtatgctc 60

accggccgta ttcattccaa taacccgcac agggaaacta atg ata ccg aag ccc 115
 Met Ile Pro Lys Pro
 1 5

gac gtg acc gac tta tat tta gag gac ctc tta aat gag ggt tcg 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
 410 415 420
 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

WO 01/00843

PCT/IB00/00923

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
 <210> 48
 <211> 666
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 48
 Met Ile Pro Lys Pro Asp Val Thr Asp Leu Tyr Leu Glu Asp Leu Leu
 1 5 10 15
 Asn Glu Gly Ser Glu Lys Ile Arg Ser Ala Lys Asp Leu Ser Glu Leu
 20 25 30
 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

WO 01/00843

PCT/IB00/00923

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			
						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
 545 550 555 560
 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
 625 630 635 640
 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

<210> 49
 <211> 993
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(970)
 <223> RXA01393

<400> 49
 caaaagcaga cctgtaatga agatttccat gatcaccatc gtgacctatg gaagtactta 60
 agtaaaatga ttggttctta acatgggttta 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	ggg	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					165	
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	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					245	
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	tag	ttact	ttc	980
Asp	Ala	Val	Val	Asp	Ala	Ala	Ile	Glu	Gly	Leu	Arg	Pro				
		280					285					290				

tgaaaagggtt cag

993

<210> 50

<211> 290

<212> PRT

<213> Corynebacterium glutamicum

<400> 50

Met	Asn	Pro	Ile	Gln	Leu	Asp	Thr	Leu	Leu	Ser	Ile	Ile	Asp	Glu	Gly
1				5				10						15	

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		

WO 01/00843

PCT/IB00/00923

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

Arg Pro
 290

<210> 51
 <211> 1626
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1603)
 <223> RXA00241

<400> 51
 ggtctccagc ctttctaaac aattcatctg cacttgatta attggcccca agattacgcg 60
 aagtttagcg acttcgccgt acgtcaacta cgttaaata gtg aat act caa tca 115
 Val Asn Thr Gln Ser
 1 5
 gat tct gcg ggg tct caa ggt gca gcg gcc aca agt cgt act gta tct 163
 Asp Ser Ala Gly Ser Gln Gly Ala Ala Ala Thr Ser Arg Thr Val Ser
 10 15 20
 att aga acc ctc atc gcg ctg atc atc gga tcg acc gtc ggc gcg gga 211
 Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser Thr Val Gly Ala Gly
 25 30 35
 att ttc tcc atc cct caa aac atc ggc tca gtc gca ggt ccc ggc gcg 259
 Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val Ala Gly Pro Gly Ala
 40 45 50
 atg ctc atc ggc tgg ctg atc gcc ggt gtg ggc atg ttg tcc gta gcg 307
 Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly Met Leu Ser Val Ala
 55 60 65
 ttc gtg ttc cat gtt ctt gcc cgc cgt aaa cct cac ctc gat tct ggc 355
 Phe Val Phe His Val Leu Ala Arg Arg Lys Pro His Leu Asp Ser Gly
 70 75 80 85
 gtc tac gca tat gcg cgt gtt gga ttg ggc gat tat gta ggt ttc tcc 403
 Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp Tyr Val Gly Phe Ser
 90 95 100
 tcc gct tgg ggt tat tgg ctg ggt tca gtc atc gcc caa gtt ggc tac 451
 Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile Ala Gln Val Gly Tyr
 105 110 115
 gca acg tta ttt ttc tcc acg ttg ggc cac tac gta ccg ctg ttt tcc 499
 Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr Val Pro Leu Phe Ser
 120 125 130
 caa gat cat cca ttt gtg tca gcg ttg gca gtt agc gct ttg acc tgg 547
 Gln Asp His Pro Phe Val Ser Ala Leu Ala Val Ser Ala Leu Thr Trp
 135 140 145
 ctg gtg ttt gga gtt gtt tcc cga gga att agc caa gct gct ttc ttg 595

WO 01/00843

PCT/IB00/00923

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

WO 01/00843

PCT/IB00/00923

gct acc aac cta tac ttg gtg cct tac ctg ttc tct gcc ttt tat ctg
1267

Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe Ser Ala Phe Tyr Leu
375 380 385

gtc atg ctg gca aca cgt gga aaa gga atc acc cac cca cat gcc ggc
1315

Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr His Pro His Ala Gly
390 395 400 405

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
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
490 495 500

taaacaccga aaccttcctg cta
1626

<210> 52

<211> 501

<212> PRT

<213> Corynebacterium glutamicum

<400> 52

Val Asn Thr Gln Ser Asp Ser Ala Gly Ser Gln Gly Ala Ala Ala Thr
1 5 10 15

Ser Arg Thr Val Ser Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser
20 25 30

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
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
 465 470 475 480
 Val Val Leu Val Val Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn
 485 490 495
 Gly Ser Leu Ser Leu
 500

<210> 53
 <211> 822
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(799)
 <223> RXA01394

<400> 53
 gagcaaagtg tccagttgaa tggggttcat gaagctatat taaacatgt taagaaccaa 60
 tcattttact taagtacttc cataggtcac gatgggtgatc atg gaa atc ttc att 115
 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 ggc 595
 Thr Trp Leu Asn Pro Asn Ala Tyr Leu Asp Ala Phe Val Phe Ile Gly
 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 gggtttttgga atc 822
 Met Leu Met Gly
 230

<210> 54

<211> 233

<212> PRT

<213> Corynebacterium glutamicum

<400> 54

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	
Trp	Ile	Phe	Ala	Ala	Gly	Ala	Phe	Ala	Ala	Ser	Leu	Ile	Trp	Phe	Pro
			180					185					190		
Leu	Val	Gly	Phe	Gly	Ala	Ala	Ala	Leu	Ser	Arg	Pro	Leu	Ser	Ser	Pro
		195					200					205			
Lys	Val	Trp	Arg	Trp	Ile	Asn	Val	Val	Val	Ala	Val	Val	Met	Thr	Ala
	210					215					220				
Leu	Ala	Ile	Lys	Leu	Met	Leu	Met	Gly							
225					230										

<210> 55

<211> 1026

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1003)

<223> RXA00865

<400> 55

ttatcgggaat gtggcttggg cgattgttat gcaaaagttg ttaggttttt tgccggggttg 60

tttaaccccc	aatgagggga	agaaggtaac	cttgaactct	atg	agc	aca	ggt	tta	115
				Met	Ser	Thr	Gly	Leu	
				1				5	

aca	gct	aag	acc	gga	gta	gag	cac	ttc	ggc	acc	ggt	gga	gta	gca	atg	163
Thr	Ala	Lys	Thr	Gly	Val	Glu	His	Phe	Gly	Thr	Val	Gly	Val	Ala	Met	
				10					15					20		

ggt	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	gcg	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	
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	
150 155 160 165	
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	
230 235 240 245	
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	

WO 01/00843

PCT/IB00/00923

gac atg aaa aaa gct gga gtt cta taaatatgaa tgattcccga aat
1026

Asp Met Lys Lys Ala Gly Val Leu
295 300

<210> 56

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 56

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

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

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

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> 57
 <211> 1071
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1048)
 <223> RXS02021

<400> 57
 ttgggtcgcc gaggagatct aatcctgggt tgagttcaga gttcacaggt ttaagcctac 60
 aaaccttagt taaaacatga tggaagcggc 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

WO 01/00843

PCT/IB00/00923

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

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> 58

<211> 316

<212> PRT

<213> Corynebacterium glutamicum

<400> 58

Met Ser Glu Asn Ile Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile
 1 5 10 15

Ala Met Asp Gly Thr Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile
 20 25 30

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

WO 01/00843

PCT/IB00/00923

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				
305					310					315					

<210> 59

<211> 1296

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

WO 01/00843

PCT/IB00/00923

<222> (101)..(1273)

<223> RXS02157

<400> 59

gggtggaatt ggcacgatgg tgctgccgga tgtttttgat cgggagaatt atcctgaagg 60

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
390

```

```

<210> 60
<211> 391
<212> PRT
<213> Corynebacterium glutamicum

```


WO 01/00843

PCT/IB00/00923

<400> 60
Met Ser Thr Leu Glu Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly
1 5 10 15
Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp
20 25 30
Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
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

<400> 61																	
acggcgaggt	tgtcggtatt	ggaacgcaca	cgaattttgct	gaacacgtgc	ggtacctacc	60											
gtgaaattgt	tgaatcccaa	gagactgcgc	aggcgcaatc	atg	agt	aat	act	gca	115								
				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	ggc	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	ggc	gca	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	ggc	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	ggc	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 tgc ttg ttc cag gcg cgg 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> 62
 <211> 295
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 62
 Met Ser Asn Thr Ala Gly Pro Arg Gly Arg Ser His Gln Ala Asp Ala
 1 5 10 15

Ala Pro Asn Gln Lys Ala Gln Asn Phe Gly Pro Ser Ala Lys Arg Leu

WO 01/00843

PCT/IB00/00923

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> 63

<211> 426

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

WO 01/00843

PCT/IB00/00923

<222> (1)..(426)

<223> RXC00861

<400> 63

```

atg gct cct cac aag gtc atg ctg att acc act ggt act cag ggt gag 48
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

ggg 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

ggg 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
          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

```

<210> 64

<211> 142

<212> PRT

<213> Corynebacterium glutamicum

<400> 64

```

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

```


<400> 65																					
gcatcaacgt aggagatcct cgacttccaa ttatggctcc aaatgagcag gaacttgagg																60					
ctctccgaga agacatgaaa aaagctggag ttctataaat																					
																atg	aat	gat	tcc	cga	115
																Met	Asn	Asp	Ser	Arg	
																1				5	
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																					

WO 01/00843

PCT/IB00/00923

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> 66

<211> 322

<212> PRT

<213> Corynebacterium glutamicum

<400> 66

Met	Asn	Asp	Ser	Arg	Asn	Arg	Gly	Arg	Lys	Val	Thr	Arg	Lys	Ala	Gly
1					5				10					15	

WO 01/00843

PCT/IB00/00923

Pro Pro Glu Ala Gly Gln Glu Asn His Leu Asp Thr Pro Val Phe Gln
 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> 67
 <211> 1527
 <212> DNA
 <213> Corynebacterium glutamicum

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

<400> 67
 ctctcttgggt cctctcccca cccatttttta agtactcaag acccttccaa cagaaaggat 60
 tactcccca acagggtcaa aaatactgaa aggctcacgc 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 355
 Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg Phe Thr Pro Ser Gly
 70 75 80 85
 tta agc gtg ttg acc agc gtc att gcc ctt atc gtg ctt ctc gcg ttg 403
 Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile Val Leu Leu Ala Leu
 90 95 100
 ctt cgc tat gcc agt caa ttt gga cgg cga tac acc gca ggc aag ctc 451
 Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr Thr Ala Gly Lys Leu
 105 110 115
 agc atg ggg gta cag cat gat gtc cgg ctt aaa acg atg cgc tca ttg 499
 Ser Met Gly Val Gln His Asp Val Arg Leu Lys Thr Met Arg Ser Leu
 120 125 130
 cag aac ctc gat ggg cca ggt cag gac tct att cgc aca ggc caa gta 547
 Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile Arg Thr Gly Gln Val
 135 140 145
 gtc agt cgg tcc att tcg gat atc aac atg gtg caa agc ctt gtg gcg 595
 Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val Gln Ser Leu Val Ala
 150 155 160 165
 atg ttg ccg atg ttg atc gga aat gtg gtc aag ctt gtg ctc act ttg 643
 Met Leu Pro Met Leu Ile Gly Asn Val Val Lys Leu Val Leu Thr Leu
 170 175 180

gtg atc atg ctg gct att tcc ccg ccg ctg acc atc atc gct gca gtg	691
Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr Ile Ile Ala Ala Val	
185 190 195	
ttg gtg cct ttg ctg ttg tgg gcc gtg gcc tat tcg cga aaa gcg ctt	739
Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr Ser Arg Lys Ala Leu	
200 205 210	
ttt gcg tcc acg tgg tcg gcc cag caa aag gct gcg gat ctg acc act	787
Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala Ala Asp Leu Thr Thr	
215 220 225	
cat gtg gaa gaa act gtc acg ggt atc cgc gtg gtc aag gca ttt gcg	835
His Val Glu Glu Thr Val Thr Gly Ile Arg Val Val Lys Ala Phe Ala	
230 235 240 245	
cag gaa gac cgc gag acc gac aaa ttg gat ctc acc gca cgt gag tta	883
Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu Thr Ala Arg Glu Leu	
250 255 260	
ttt gcc cag cgc atg cgc act gca cgt ctg acg gca aag ttc atc ccc	931
Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr Ala Lys Phe Ile Pro	
265 270 275	
atg gtt gag cag ctt ccg cag ctt gct ttg gtg gtc aac att gtt ggc	979
Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val Val Asn Ile Val Gly	
280 285 290	
ggt ggc tat ttg gcc atg act ggt cac atc acg gtg ggc acg ttt gtg	
1027 Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr Val Gly Thr Phe Val	
295 300 305	
gcg ttt tct tcc tat ctc act agc ttg tcg 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 tcg 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	

WO 01/00843

PCT/IB00/00923

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> 68

<211> 468

<212> PRT

<213> Corynebacterium glutamicum

<400> 68

Met Lys Thr Glu Gln Ser Gln Lys Ala Gln Leu Ala Pro Lys Lys Ala
1 5 10 15

Pro Glu Lys Pro Gln Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln
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

WO 01/00843

PCT/IB00/00923

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												
465															

WO 01/00843

PCT/IB00/00923

<221> CDS

<222> (101)..(4630)

<223> RXN00367

<400> 71

```

atcgaaagta acccttttgt tacttgcggt gcaggtagtg tccctgattt tcttattatc 60

gaacgattga tagaaacagg attaaagtga ggtatcccgc atg aaa cca caa gga 115
                                         Met Lys Pro Gln Gly
                                         1 5

ctc tac aac cct gcg cat gaa cat gac gcc tgc ggt gtg gcg ttt att 163
Leu Tyr Asn Pro Ala His Glu His Asp Ala Cys Gly Val Ala Phe Ile
                        10 15 20

gcg gat atc cac ggt cga ccc agc cgc agc att gtt gat cgt gca ctt 211
Ala Asp Ile His Gly Arg Pro Ser Arg Ser Ile Val Asp Arg Ala Leu
                        25 30 35

gag gcg ctt cgc aac att gac cac cga ggt gcc gcc ggt gca gag aag 259
Glu Ala Leu Arg Asn Ile Asp His Arg Gly Ala Ala Gly Ala Glu Lys
                        40 45 50

aac act ggc gat ggt gcg ggc atc ctc atg cag att ccg gac ggc ttt 307
Asn Thr Gly Asp Gly Ala Gly Ile Leu Met Gln Ile Pro Asp Gly Phe
                        55 60 65

tat cgt gaa gta tct ggc att gag ctt cct gag gca ggg gag tat gcc 355
Tyr Arg Glu Val Ser Gly Ile Glu Leu Pro Glu Ala Gly Glu Tyr Ala
                        70 75 80 85

act ggt att gcg ttc ttg cct cgc ggt cgc atg gcg atg atg gat gct 403
Thr Gly Ile Ala Phe Leu Pro Arg Gly Arg Met Ala Met Met Asp Ala
                        90 95 100

cag aag gaa att gag cgc atc gca aag caa gaa ggt gcc gat gtg ctt 451
Gln Lys Glu Ile Glu Arg Ile Ala Lys Gln Glu Gly Ala Asp Val Leu
                        105 110 115

ggt tgg cgc atg gtt cct ttt gat tct cgt gat ttg ggt tcc atg gct 499
Gly Trp Arg Met Val Pro Phe Asp Ser Arg Asp Leu Gly Ser Met Ala
                        120 125 130

gag gag gcg atg cct agt ttc gcg cag att ttc ctt act gtg cct gga 547
Glu Glu Ala Met Pro Ser Phe Ala Gln Ile Phe Leu Thr Val Pro Gly
                        135 140 145

aaa tct ggt gaa gat ctt gac cgt gtg atg ttc ttt atc cgt aag cgt 595
Lys Ser Gly Glu Asp Leu Asp Arg Val Met Phe Phe Ile Arg Lys Arg
150 155 160 165

tgt gag cgt gag ctg ggc acc acc aat ggt cgc gat acg gtg tat ttc 643
Cys Glu Arg Glu Leu Gly Thr Thr Asn Gly Arg Asp Thr Val Tyr Phe
                        170 175 180

ccg tcg cta tct tca cgc acc atc att tac aaa ggc atg ttg acc act 691
Pro Ser Leu Ser Ser Arg Thr Ile Ile Tyr Lys Gly Met Leu Thr Thr
                        185 190 195

ctg cag ctt gag ggc ttc ttt gag gat ctg ggt gat gct cgc ctg gag 739
Leu Gln Leu Glu Gly Phe Phe Glu Asp Leu Gly Asp Ala Arg Leu Glu

```


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

agc gaa gcg cag cca tat ggt gag tgg att cgc gat aat ttt gtg cat
1411

Ser Glu Ala Gln Pro Tyr Gly Glu Trp Ile Arg Asp Asn Phe Val His
425 430 435

ctg gat cgt ctg cct cag aca cgc tac aac tac atg gcg cac tct cgt
1459

Leu Asp Arg Leu Pro Gln Thr Arg Tyr Asn Tyr Met Ala His Ser Arg
440 445 450

gct gtg ttg cgt cag cgt gtt ttc gga atc act gaa gaa gat gtg gat
1507

Ala Val Leu Arg Gln Arg Val Phe Gly Ile Thr Glu Glu Asp Val Asp
455 460 465

ttg ttg ctg ctg ccg atg gcc cgc cag ggt gct gag gcg att ggt tcc
1555

Leu Leu Leu Leu Pro Met Ala Arg Gln Gly Ala Glu Ala Ile Gly Ser
470 475 480 485

atg ggt tcg gat acg cca att gcg gcg cta tcc cag cga cca cgc atg
1603

Met Gly Ser Asp Thr Pro Ile Ala Ala Leu Ser Gln Arg Pro Arg Met
490 495 500

ctt tat gat ttc ttc gcg cag cgc ttt gct cag gtg aca aac cca ccg
1651

Leu Tyr Asp Phe Phe Ala Gln Arg Phe Ala Gln Val Thr Asn Pro Pro
505 510 515

ttg gac tct atc cgc gaa aag cct gtg acc agc atg ttc act ttg ttg
1699

Leu Asp Ser Ile Arg Glu Lys Pro Val Thr Ser Met Phe Thr Leu Leu
520 525 530

ggt gcg cag tct gac gtg ctc aat ccg ggt cct gat gcg gcg cga cgt
1747

Gly Ala Gln Ser Asp Val Leu Asn Pro Gly Pro Asp Ala Ala Arg Arg
535 540 545

atc cgt ttg gaa tcg ccg atc att gat aac cat gag ctg gcc acc ttg
1795

Ile Arg Leu Glu Ser Pro Ile Ile Asp Asn His Glu Leu Ala Thr Leu
550 555 560 565

atc aat gcc aac gcg cat ggt gag tgg gat tcc ttt ggt gct gct gta
1843

Ile Asn Ala Asn Ala His Gly Glu Trp Asp Ser Phe Gly Ala Ala Val
570 575 580

att tct ggt ttg tac cca gtg gct cac cat ggt gcc ggc atg aag gct
1891

Ile Ser Gly Leu Tyr Pro Val Ala His His Gly Ala Gly Met Lys Ala
585 590 595

gcg att gct cgt gtg cgc cgc gag gtt tct gaa gca atc cgc aat ggc
1939

Ala Ile Ala Arg Val Arg Arg Glu Val Ser Glu Ala Ile Arg Asn Gly
600 605 610

aag acg ttg atc gtg ctg tcg gat cgt gaa tct gat gag cgc atg gca
1987

Lys Thr Leu Ile Val Leu Ser Asp Arg Glu Ser Asp Glu Arg Met Ala
615 620 625

cct atc cct gcg ctg ctg ctg act tcc gct gtg cat cag tac ttg gtg
2035

Pro Ile Pro Ala Leu Leu Leu Thr Ser Ala Val His Gln Tyr Leu Val
630 635 640 645

cag caa cgt acc cgt acc cag tgc tcc ctg gtg gtg gaa tcc ggc gat
2083

Gln Gln Arg Thr Arg Thr Gln Cys Ser Leu Val Val Glu Ser Gly Asp
650 655 660

gcc cgc gag gtt cat cac ctg gcg atg ctc att ggt ttt ggt gcc gat
2131

Ala Arg Glu Val His His Leu Ala Met Leu Ile Gly Phe Gly Ala Asp
665 670 675

gcg atc aac ccg tac atg gca ttt gaa acc atc gat gag ctg cgc atg
2179

Ala Ile Asn Pro Tyr Met Ala Phe Glu Thr Ile Asp Glu Leu Arg Met
680 685 690

aag ggt cag ttg ggt gat ctt tct ttg gat gag gca tcc cga aac tac
2227

Lys Gly Gln Leu Gly Asp Leu Ser Leu Asp Glu Ala Ser Arg Asn Tyr
695 700 705

atc aag gca gcc acc act ggt gtg ctg aag gtg atg tcc aag atg ggc
2275

Ile Lys Ala Ala Thr Thr Gly Val Leu Lys Val Met Ser Lys Met Gly
710 715 720 725

att gca acg gtg tct tcg tac cgt ggc gcg cag ctt gcc gat gtc act
2323

Ile Ala Thr Val Ser Ser Tyr Arg Gly Ala Gln Leu Ala Asp Val Thr
730 735 740

ggt ctg cac cag gat ctc ctg gac aac tac ttc ggt ggt att gct tca
2371

Gly Leu His Gln Asp Leu Leu Asp Asn Tyr Phe Gly Gly Ile Ala Ser
745 750 755

cca att tct ggc atc ggt ctg gat gaa gtt gca gct gac gta gaa gct
2419

Pro Ile Ser Gly Ile Gly Leu Asp Glu Val Ala Ala Asp Val Glu Ala
760 765 770

cgt cac cgc agc gca ttt ttg cca cgc cct gaa gag cac gct cac cgt
2467

Arg His Arg Ser Ala Phe Leu Pro Arg Pro Glu Glu His Ala His Arg
775 780 785

gaa ttg gat ttg ggt ggt gaa tac aag tgg cgc cgc gaa ggt gaa tac
2515

Glu Leu Asp Leu Gly Gly Glu Tyr Lys Trp Arg Arg Glu Gly Glu Tyr
790 795 800 805

WO 01/00843

PCT/IB00/00923

cac ctg ttc aac cca gaa acc atc ttc aag ctg cag cat gca acg cgt
 2563
 His Leu Phe Asn Pro Glu Thr Ile Phe Lys Leu Gln His Ala Thr Arg
 810 815 820

tct ggc agc tac gag att ttc aag gat tac acc cgc aag gtt gat gat
 2611
 Ser Gly Ser Tyr Glu Ile Phe Lys Asp Tyr Thr Arg Lys Val Asp Asp
 825 830 835

caa tcc act cgc ttg ggt act att cgt gga ctg ttt gag ttc agc acg
 2659
 Gln Ser Thr Arg Leu Gly Thr Ile Arg Gly Leu Phe Glu Phe Ser Thr
 840 845 850

gac cgc aag cca att tcg gtg tct gag gtg gag ccg gtc agt gag atc
 2707
 Asp Arg Lys Pro Ile Ser Val Ser Glu Val Glu Pro Val Ser Glu Ile
 855 860 865

gtg aag cgt ttc tcc act ggt gcg atg tct tat ggc tcg att tct gct
 2755
 Val Lys Arg Phe Ser Thr Gly Ala Met Ser Tyr Gly Ser Ile Ser Ala
 870 875 880 885

gaa gcc cat gag gtc ttg gcc atc gcc atg aac cga ctg ggc ggt atg
 2803
 Glu Ala His Glu Val Leu Ala Ile Ala Met Asn Arg Leu Gly Gly Met
 890 895 900

tcc aac tcc ggc gaa ggt ggc gag gac gcc cgc cga ttt gat gtg gaa
 2851
 Ser Asn Ser Gly Glu Gly Gly Glu Asp Ala Arg Arg Phe Asp Val Glu
 905 910 915

ccc aac ggt gac tgg aag cgc tct gcc att aag cag gtg gcc tcg gga
 2899
 Pro Asn Gly Asp Trp Lys Arg Ser Ala Ile Lys Gln Val Ala Ser Gly
 920 925 930

cgt ttc ggc gtg acc agc cac tac ttg aac aac tgc acc gat att cag
 2947
 Arg Phe Gly Val Thr Ser His Tyr Leu Asn Asn Cys Thr Asp Ile Gln
 935 940 945

atc aag atg gca cag ggc gca aag ccc ggt gaa ggt ggc cag ctg cca
 2995
 Ile Lys Met Ala Gln Gly Ala Lys Pro Gly Glu Gly Gly Gln Leu Pro
 950 955 960 965

cca aac aag gtg tac cca tgg gtt gca gaa gtc cgc atc acc acc cca
 3043
 Pro Asn Lys Val Tyr Pro Trp Val Ala Glu Val Arg Ile Thr Thr Pro
 970 975 980

ggc gtt ggt ctg att tcc cct cca cca cac cac gat att tac tcc att
 3091
 Gly Val Gly Leu Ile Ser Pro Pro Pro His His Asp Ile Tyr Ser Ile
 985 990 995

gag gat ctg gct cag ctg atc cac gac ctg aag aac gct aac cca cgc
 3139
 Glu Asp Leu Ala Gln Leu Ile His Asp Leu Lys Asn Ala Asn Pro Arg
 1000 1005 1010

gca cga atc cac gtg aag cta gtg gca gaa caa ggc gtg ggc acc gtt
 3187
 Ala Arg Ile His Val Lys Leu Val Ala Glu Gln Gly Val Gly Thr Val
 1015 1020 1025

gcc gca ggt gtg tcc aaa gca cac gct gat gtg gtg ctt att tcc ggc
 3235
 Ala Ala Gly Val Ser Lys Ala His Ala Asp Val Val Leu Ile Ser Gly
 1030 1035 1040 1045

cac gat ggc gga act ggc gca tct cct ttg acc tcc ctg aag cat gcc
 3283
 His Asp Gly Gly Thr Gly Ala Ser Pro Leu Thr Ser Leu Lys His Ala
 1050 1055 1060

ggt ggt cca tgg gag ttg ggc ttg gct gaa acc cag caa acg ttg ctg
 3331
 Gly Gly Pro Trp Glu Leu Gly Leu Ala Glu Thr Gln Gln Thr Leu Leu
 1065 1070 1075

ctc aac ggc ctg cgc gat cgt att cgc gtg cag tgc gat ggt cag ctg
 3379
 Leu Asn Gly Leu Arg Asp Arg Ile Arg Val Gln Cys Asp Gly Gln Leu
 1080 1085 1090

aaa act ggc cga gac gtg gtt atc gca gct ctt ctc ggt gcc gaa gaa
 3427
 Lys Thr Gly Arg Asp Val Val Ile Ala Ala Leu Leu Gly Ala Glu Glu
 1095 1100 1105

ttc ggt ttt gcc acc gca ccg ctg gtg gtt gaa ggc tgc atc atg atg
 3475
 Phe Gly Phe Ala Thr Ala Pro Leu Val Val Glu Gly Cys Ile Met Met
 1110 1115 1120 1125

cgc gtc tgc cac ctg gac acc tgc ccg gtg ggt atc gct acc cag aac
 3523
 Arg Val Cys His Leu Asp Thr Cys Pro Val Gly Ile Ala Thr Gln Asn
 1130 1135 1140

ccg gat ttg cgt tcc aag ttc acc ggc aag gct gaa cac gtg gtc aac
 3571
 Pro Asp Leu Arg Ser Lys Phe Thr Gly Lys Ala Glu His Val Val Asn
 1145 1150 1155

ttc ttc acc ttc atc gcc cag gaa gtc cgt gag tac ttg gca cag ctt
 3619
 Phe Phe Thr Phe Ile Ala Gln Glu Val Arg Glu Tyr Leu Ala Gln Leu
 1160 1165 1170

ggt ttc cgc tct att gat gaa gcc gtc gga caa gcc cag gtg ctg cgc
 3667
 Gly Phe Arg Ser Ile Asp Glu Ala Val Gly Gln Ala Gln Val Leu Arg
 1175 1180 1185

aag cgt tcc gga atc cca gct gat tcc cgc gca gca cac ctg gat ttg
3715
Lys Arg Ser Gly Ile Pro Ala Asp Ser Arg Ala Ala His Leu Asp Leu
1190 1195 1200 1205

agc cca att ttc cat cgc cca gaa act cca cac ttc cca act cag gat
3763
Ser Pro Ile Phe His Arg Pro Glu Thr Pro His Phe Pro Thr Gln Asp
1210 1215 1220

gtg cgt tgc acc aag acc cag gaa cac agc cta gaa aaa gcc ctg gac
3811
Val Arg Cys Thr Lys Thr Gln Glu His Ser Leu Glu Lys Ala Leu Asp
1225 1230 1235

aac gca ttt att gat aag gct tcg gac acg atc acc cgt gcc gca gcg
3859
Asn Ala Phe Ile Asp Lys Ala Ser Asp Thr Ile Thr Arg Ala Ala Ala
1240 1245 1250

ggc gtg gaa acc agc att gtt att gat agc tcc atc agc aac gtc aac
3907
Gly Val Glu Thr Ser Ile Val Ile Asp Ser Ser Ile Ser Asn Val Asn
1255 1260 1265

cgt tca gtt ggc acg atg ctg ggt tct gca gtc agc cgc gtg gct ggt
3955
Arg Ser Val Gly Thr Met Leu Gly Ser Ala Val Ser Arg Val Ala Gly
1270 1275 1280 1285

gcc caa ggt ttg cca gac ggc acc atc acc ttg aat ctt caa ggc tgc
4003
Ala Gln Gly Leu Pro Asp Gly Thr Ile Thr Leu Asn Leu Gln Gly Cys
1290 1295 1300

gcc ggt aac tcc ttt ggc gcg ttc atc cca cga ggc atc acc atc aac
4051
Ala Gly Asn Ser Phe Gly Ala Phe Ile Pro Arg Gly Ile Thr Ile Asn
1305 1310 1315

ctc acc ggc gat gcc aat gac ttt gtg ggc aag gga tta tct ggc gga
4099
Leu Thr Gly Asp Ala Asn Asp Phe Val Gly Lys Gly Leu Ser Gly Gly
1320 1325 1330

aag att gtg atc aag cct tcc gct cag gct ccg aag cag ctg aag aac
4147
Lys Ile Val Ile Lys Pro Ser Ala Gln Ala Pro Lys Gln Leu Lys Asn
1335 1340 1345

aat cca aat atc att gcc gga aac gtg ctt gga tac ggc gca acc agt
4195
Asn Pro Asn Ile Ile Ala Gly Asn Val Leu Gly Tyr Gly Ala Thr Ser
1350 1355 1360 1365

ggc gaa ttg ttc att cgt ggc cag gtc ggc gaa cgt ttc tgc gtc cgt
4243
Gly Glu Leu Phe Ile Arg Gly Gln Val Gly Glu Arg Phe Cys Val Arg
1370 1375 1380

WO 01/00843

PCT/IB00/00923

aac tct ggc gcc acc gca gtg gtt gaa ggt atc gga aac cac ggt tgt
4291

Asn Ser Gly Ala Thr Ala Val Val Glu Gly Ile Gly Asn His Gly Cys
1385 1390 1395

gag tac atg act ggc ggc cga gtc ctg gtt ttg ggc ccg gtt ggt gag
4339

Glu Tyr Met Thr Gly Gly Arg Val Leu Val Leu Gly Pro Val Gly Glu
1400 1405 1410

aac ttt ggt gcc ggc atg tct ggt ggc att gca tac ctg gct aat tcc
4387

Asn Phe Gly Ala Gly Met Ser Gly Gly Ile Ala Tyr Leu Ala Asn Ser
1415 1420 1425

ccg gac cta aac cag aag atc aat ggc gaa ttg gtg gat gtt gtt cca
4435

Pro Asp Leu Asn Gln Lys Ile Asn Gly Glu Leu Val Asp Val Val Pro
1430 1435 1440 1445

ctg agc gct gac gat ctg acg tgg gct gat gag ctc att gct cgc cac
4483

Leu Ser Ala Asp Asp Leu Thr Trp Ala Asp Glu Leu Ile Ala Arg His
1450 1455 1460

cgc gaa ctc acc gga tcc gag acc aag ctg cgt gca caa gat ttg gtg
4531

Arg Glu Leu Thr Gly Ser Glu Thr Lys Leu Arg Ala Gln Asp Leu Val
1465 1470 1475

aaa atc atg ccg cgc gat ttc caa aaa gta ctc aac atc atc gaa acg
4579

Lys Ile Met Pro Arg Asp Phe Gln Lys Val Leu Asn Ile Ile Glu Thr
1480 1485 1490

gcc cac gct gag ggc caa gac cca gca atc aag atc atg gag gca gtg
4627

Ala His Ala Glu Gly Gln Asp Pro Ala Ile Lys Ile Met Glu Ala Val
1495 1500 1505

agc taatggccga cccacaagga ttc
4653

Ser
1510

<210> 72

<211> 1510

<212> PRT

<213> Corynebacterium glutamicum

<400> 72

Met Lys Pro Gln Gly Leu Tyr Asn Pro Ala His Glu His Asp Ala Cys
1 5 10 15

Gly Val Ala Phe Ile Ala Asp Ile His Gly Arg Pro Ser Arg Ser Ile
20 25 30

Val Asp Arg Ala Leu Glu Ala Leu Arg Asn Ile Asp His Arg Gly Ala
35 40 45

Ala	Gly	Ala	Glu	Lys	Asn	Thr	Gly	Asp	Gly	Ala	Gly	Ile	Leu	Met	Gln
50						55					60				
Ile	Pro	Asp	Gly	Phe	Tyr	Arg	Glu	Val	Ser	Gly	Ile	Glu	Leu	Pro	Glu
65					70					75					80
Ala	Gly	Glu	Tyr	Ala	Thr	Gly	Ile	Ala	Phe	Leu	Pro	Arg	Gly	Arg	Met
				85					90					95	
Ala	Met	Met	Asp	Ala	Gln	Lys	Glu	Ile	Glu	Arg	Ile	Ala	Lys	Gln	Glu
			100					105					110		
Gly	Ala	Asp	Val	Leu	Gly	Trp	Arg	Met	Val	Pro	Phe	Asp	Ser	Arg	Asp
		115					120					125			
Leu	Gly	Ser	Met	Ala	Glu	Glu	Ala	Met	Pro	Ser	Phe	Ala	Gln	Ile	Phe
	130					135					140				
Leu	Thr	Val	Pro	Gly	Lys	Ser	Gly	Glu	Asp	Leu	Asp	Arg	Val	Met	Phe
145					150					155					160
Phe	Ile	Arg	Lys	Arg	Cys	Glu	Arg	Glu	Leu	Gly	Thr	Thr	Asn	Gly	Arg
				165					170					175	
Asp	Thr	Val	Tyr	Phe	Pro	Ser	Leu	Ser	Ser	Arg	Thr	Ile	Ile	Tyr	Lys
			180					185					190		
Gly	Met	Leu	Thr	Thr	Leu	Gln	Leu	Glu	Gly	Phe	Phe	Glu	Asp	Leu	Gly
		195					200					205			
Asp	Ala	Arg	Leu	Glu	Ser	Ala	Ile	Ala	Ile	Val	His	Ser	Arg	Phe	Ser
	210					215					220				
Thr	Asn	Thr	Phe	Pro	Ser	Trp	Pro	Leu	Ala	His	Pro	Tyr	Arg	Phe	Val
225					230					235					240
Ala	His	Asn	Gly	Glu	Ile	Asn	Thr	Val	Arg	Gly	Asn	Glu	Asn	Trp	Met
				245					250					255	
Arg	Ala	Arg	Glu	Ala	Leu	Ile	Lys	Asn	Asp	Lys	Leu	Gly	Asn	Leu	Ser
			260					265					270		
Ser	Val	Leu	Pro	Ile	Cys	Thr	Pro	Glu	Gly	Ser	Asp	Thr	Ala	Arg	Phe
		275					280					285			
Asp	Glu	Ala	Leu	Glu	Leu	Leu	His	Leu	Gly	Gly	Tyr	Ser	Leu	Pro	His
	290					295					300				
Ala	Val	Ala	Met	Met	Ile	Pro	Gln	Ala	Trp	Glu	His	Asn	Lys	Thr	Leu
305					310					315					320
Ser	Pro	Glu	Leu	Arg	Asp	Phe	Tyr	Glu	Tyr	His	Ser	Cys	Leu	Met	Glu
				325					330					335	
Pro	Trp	Asp	Gly	Pro	Ala	Ala	Leu	Ala	Phe	Thr	Asp	Gly	Arg	Phe	Val
			340					345					350		
Gly	Ala	Val	Leu	Asp	Arg	Asn	Gly	Leu	Arg	Pro	Gly	Arg	Ile	Thr	Ile
		355					360					365			
Thr	Asp	Ser	Gly	Leu	Val	Val	Met	Ala	Ser	Glu	Ser	Gly	Val	Leu	Asp

370		375		380
Leu Arg Glu Glu Ser Val Val Lys Arg Thr Arg Val Gln Pro Gly Arg				
385		390		400
Met Phe Leu Val Asp Thr Ala Glu Gly Arg Ile Val Glu Asp Glu Glu				
	405		410	415
Ile Lys Gln Lys Leu Ser Glu Ala Gln Pro Tyr Gly Glu Trp Ile Arg				
	420		425	430
Asp Asn Phe Val His Leu Asp Arg Leu Pro Gln Thr Arg Tyr Asn Tyr				
	435		440	445
Met Ala His Ser Arg Ala Val Leu Arg Gln Arg Val Phe Gly Ile Thr				
	450		455	460
Glu Glu Asp Val Asp Leu Leu Leu Leu Pro Met Ala Arg Gln Gly Ala				
465		470		480
Glu Ala Ile Gly Ser Met Gly Ser Asp Thr Pro Ile Ala Ala Leu Ser				
	485		490	495
Gln Arg Pro Arg Met Leu Tyr Asp Phe Phe Ala Gln Arg Phe Ala Gln				
	500		505	510
Val Thr Asn Pro Pro Leu Asp Ser Ile Arg Glu Lys Pro Val Thr Ser				
	515		520	525
Met Phe Thr Leu Leu Gly Ala Gln Ser Asp Val Leu Asn Pro Gly Pro				
	530		535	540
Asp Ala Ala Arg Arg Ile Arg Leu Glu Ser Pro Ile Ile Asp Asn His				
545		550		560
Glu Leu Ala Thr Leu Ile Asn Ala Asn Ala His Gly Glu Trp Asp Ser				
	565		570	575
Phe Gly Ala Ala Val Ile Ser Gly Leu Tyr Pro Val Ala His His Gly				
	580		585	590
Ala Gly Met Lys Ala Ala Ile Ala Arg Val Arg Arg Glu Val Ser Glu				
	595		600	605
Ala Ile Arg Asn Gly Lys Thr Leu Ile Val Leu Ser Asp Arg Glu Ser				
	610		615	620
Asp Glu Arg Met Ala Pro Ile Pro Ala Leu Leu Leu Thr Ser Ala Val				
625		630		640
His Gln Tyr Leu Val Gln Gln Arg Thr Arg Thr Gln Cys Ser Leu Val				
	645		650	655
Val Glu Ser Gly Asp Ala Arg Glu Val His His Leu Ala Met Leu Ile				
	660		665	670
Gly Phe Gly Ala Asp Ala Ile Asn Pro Tyr Met Ala Phe Glu Thr Ile				
	675		680	685
Asp Glu Leu Arg Met Lys Gly Gln Leu Gly Asp Leu Ser Leu Asp Glu				
	690		695	700

Ala	Ser	Arg	Asn	Tyr	Ile	Lys	Ala	Ala	Thr	Thr	Gly	Val	Leu	Lys	Val	705	710	715	720
Met	Ser	Lys	Met	Gly	Ile	Ala	Thr	Val	Ser	Ser	Tyr	Arg	Gly	Ala	Gln	725	730	735	
Leu	Ala	Asp	Val	Thr	Gly	Leu	His	Gln	Asp	Leu	Leu	Asp	Asn	Tyr	Phe	740	745	750	
Gly	Gly	Ile	Ala	Ser	Pro	Ile	Ser	Gly	Ile	Gly	Leu	Asp	Glu	Val	Ala	755	760	765	
Ala	Asp	Val	Glu	Ala	Arg	His	Arg	Ser	Ala	Phe	Leu	Pro	Arg	Pro	Glu	770	775	780	
Glu	His	Ala	His	Arg	Glu	Leu	Asp	Leu	Gly	Gly	Glu	Tyr	Lys	Trp	Arg	785	790	795	800
Arg	Glu	Gly	Glu	Tyr	His	Leu	Phe	Asn	Pro	Glu	Thr	Ile	Phe	Lys	Leu	805	810	815	
Gln	His	Ala	Thr	Arg	Ser	Gly	Ser	Tyr	Glu	Ile	Phe	Lys	Asp	Tyr	Thr	820	825	830	
Arg	Lys	Val	Asp	Asp	Gln	Ser	Thr	Arg	Leu	Gly	Thr	Ile	Arg	Gly	Leu	835	840	845	
Phe	Glu	Phe	Ser	Thr	Asp	Arg	Lys	Pro	Ile	Ser	Val	Ser	Glu	Val	Glu	850	855	860	
Pro	Val	Ser	Glu	Ile	Val	Lys	Arg	Phe	Ser	Thr	Gly	Ala	Met	Ser	Tyr	865	870	875	880
Gly	Ser	Ile	Ser	Ala	Glu	Ala	His	Glu	Val	Leu	Ala	Ile	Ala	Met	Asn	885	890	895	
Arg	Leu	Gly	Gly	Met	Ser	Asn	Ser	Gly	Glu	Gly	Gly	Glu	Asp	Ala	Arg	900	905	910	
Arg	Phe	Asp	Val	Glu	Pro	Asn	Gly	Asp	Trp	Lys	Arg	Ser	Ala	Ile	Lys	915	920	925	
Gln	Val	Ala	Ser	Gly	Arg	Phe	Gly	Val	Thr	Ser	His	Tyr	Leu	Asn	Asn	930	935	940	
Cys	Thr	Asp	Ile	Gln	Ile	Lys	Met	Ala	Gln	Gly	Ala	Lys	Pro	Gly	Glu	945	950	955	960
Gly	Gly	Gln	Leu	Pro	Pro	Asn	Lys	Val	Tyr	Pro	Trp	Val	Ala	Glu	Val	965	970	975	
Arg	Ile	Thr	Thr	Pro	Gly	Val	Gly	Leu	Ile	Ser	Pro	Pro	Pro	His	His	980	985	990	
Asp	Ile	Tyr	Ser	Ile	Glu	Asp	Leu	Ala	Gln	Leu	Ile	His	Asp	Leu	Lys	995	1000	1005	
Asn	Ala	Asn	Pro	Arg	Ala	Arg	Ile	His	Val	Lys	Leu	Val	Ala	Glu	Gln	1010	1015	1020	

Gly Val Gly Thr Val Ala Ala Gly Val Ser Lys Ala His Ala Asp Val
 1025 1030 1035 1040
 Val Leu Ile Ser Gly His Asp Gly Gly Thr Gly Ala Ser Pro Leu Thr
 1045 1050 1055
 Ser Leu Lys His Ala Gly Gly Pro Trp Glu Leu Gly Leu Ala Glu Thr
 1060 1065 1070
 Gln Gln Thr Leu Leu Leu Asn Gly Leu Arg Asp Arg Ile Arg Val Gln
 1075 1080 1085
 Cys Asp Gly Gln Leu Lys Thr Gly Arg Asp Val Val Ile Ala Ala Leu
 1090 1095 1100
 Leu Gly Ala Glu Glu Phe Gly Phe Ala Thr Ala Pro Leu Val Val Glu
 1105 1110 1115 1120
 Gly Cys Ile Met Met Arg Val Cys His Leu Asp Thr Cys Pro Val Gly
 1125 1130 1135
 Ile Ala Thr Gln Asn Pro Asp Leu Arg Ser Lys Phe Thr Gly Lys Ala
 1140 1145 1150
 Glu His Val Val Asn Phe Phe Thr Phe Ile Ala Gln Glu Val Arg Glu
 1155 1160 1165
 Tyr Leu Ala Gln Leu Gly Phe Arg Ser Ile Asp Glu Ala Val Gly Gln
 1170 1175 1180
 Ala Gln Val Leu Arg Lys Arg Ser Gly Ile Pro Ala Asp Ser Arg Ala
 1185 1190 1195 1200
 Ala His Leu Asp Leu Ser Pro Ile Phe His Arg Pro Glu Thr Pro His
 1205 1210 1215
 Phe Pro Thr Gln Asp Val Arg Cys Thr Lys Thr Gln Glu His Ser Leu
 1220 1225 1230
 Glu Lys Ala Leu Asp Asn Ala Phe Ile Asp Lys Ala Ser Asp Thr Ile
 1235 1240 1245
 Thr Arg Ala Ala Ala Gly Val Glu Thr Ser Ile Val Ile Asp Ser Ser
 1250 1255 1260
 Ile Ser Asn Val Asn Arg Ser Val Gly Thr Met Leu Gly Ser Ala Val
 1265 1270 1275 1280
 Ser Arg Val Ala Gly Ala Gln Gly Leu Pro Asp Gly Thr Ile Thr Leu
 1285 1290 1295
 Asn Leu Gln Gly Cys Ala Gly Asn Ser Phe Gly Ala Phe Ile Pro Arg
 1300 1305 1310
 Gly Ile Thr Ile Asn Leu Thr Gly Asp Ala Asn Asp Phe Val Gly Lys
 1315 1320 1325
 Gly Leu Ser Gly Gly Lys Ile Val Ile Lys Pro Ser Ala Gln Ala Pro
 1330 1335 1340
 Lys Gln Leu Lys Asn Asn Pro Asn Ile Ile Ala Gly Asn Val Leu Gly

1345	1350	1355	1360
Tyr Gly Ala Thr Ser Gly Glu Leu Phe Ile Arg Gly Gln Val Gly Glu			
	1365	1370	1375
Arg Phe Cys Val Arg Asn Ser Gly Ala Thr Ala Val Val Glu Gly Ile			
	1380	1385	1390
Gly Asn His Gly Cys Glu Tyr Met Thr Gly Gly Arg Val Leu Val Leu			
	1395	1400	1405
Gly Pro Val Gly Glu Asn Phe Gly Ala Gly Met Ser Gly Gly Ile Ala			
	1410	1415	1420
Tyr Leu Ala Asn Ser Pro Asp Leu Asn Gln Lys Ile Asn Gly Glu Leu			
	1425	1430	1435
Val Asp Val Val Pro Leu Ser Ala Asp Asp Leu Thr Trp Ala Asp Glu			
	1445	1450	1455
Leu Ile Ala Arg His Arg Glu Leu Thr Gly Ser Glu Thr Lys Leu Arg			
	1460	1465	1470
Ala Gln Asp Leu Val Lys Ile Met Pro Arg Asp Phe Gln Lys Val Leu			
	1475	1480	1485
Asn Ile Ile Glu Thr Ala His Ala Glu Gly Gln Asp Pro Ala Ile Lys			
	1490	1495	1500
Ile Met Glu Ala Val Ser			
1505	1510		

<210> 73
 <211> 1906
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1906)
 <223> FRXA00007

<400> 73
 atcgaaagta acccttttgt tacttgcggt gcaggtagtg tccctgattt tcttattatc 60
 gaacgattga tagaaacagg attaaagtga ggtatcccg atg aaa cca caa gga 115
 Met Lys Pro Gln Gly
 1 5
 ctc tac aac cct gcg cat gaa cat gac gcc tgc ggt gtg gcg ttt att 163
 Leu Tyr Asn Pro Ala His Glu His Asp Ala Cys Gly Val Ala Phe Ile
 10 15 20
 gcg gat atc cac ggt cga ccc agc cgc agc att gtt gat cgt gca ctt 211
 Ala Asp Ile His Gly Arg Pro Ser Arg Ser Ile Val Asp Arg Ala Leu
 25 30 35
 gag gcg ctt cgc aac att gac cac cga ggt gcc gcc ggt gca gag aag 259
 Glu Ala Leu Arg Asn Ile Asp His Arg Gly Ala Ala Gly Ala Glu Lys
 40 45 50

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

ctt ttg cac ctg ggc gga tac tca ctt ccg cat gct gtt gcg atg atg
 1027
 Leu Leu His Leu Gly Gly Tyr Ser Leu Pro His Ala Val Ala Met Met
 295 300 305

atc cct cag gcg tgg gaa cac aac aag acg ctg agc cct gag ctg cgt
 1075
 Ile Pro Gln Ala Trp Glu His Asn Lys Thr Leu Ser Pro Glu Leu Arg
 310 315 320 325

gat ttc tac gaa tac cac tct tgt ctg atg gag cca tgg gat ggt cct
 1123
 Asp Phe Tyr Glu Tyr His Ser Cys Leu Met Glu Pro Trp Asp Gly Pro
 330 335 340

gca gcg ctg gca ttt act gac ggt cgt ttt gtg ggt gcc gtg ctg gac
 1171
 Ala Ala Leu Ala Phe Thr Asp Gly Arg Phe Val Gly Ala Val Leu Asp
 345 350 355

cgt aat ggc ctg cga cct ggg cga atc acc att act gat tcg ggt ttg
 1219
 Arg Asn Gly Leu Arg Pro Gly Arg Ile Thr Ile Thr Asp Ser Gly Leu
 360 365 370

gtt gtg atg gct tct gaa tcg gga gtg ttg gac ttg agg gag gag agc
 1267
 Val Val Met Ala Ser Glu Ser Gly Val Leu Asp Leu Arg Glu Glu Ser
 375 380 385

gtc gta aag cgt act cgc gta cag cct gga cgc atg ttc ctt gtt gac
 1315
 Val Val Lys Arg Thr Arg Val Gln Pro Gly Arg Met Phe Leu Val Asp
 390 395 400 405

act gcc gag ggc cgc atc gtt gaa gac gag gaa atc aag cag aaa tta
 1363
 Thr Ala Glu Gly Arg Ile Val Glu Asp Glu Glu Ile Lys Gln Lys Leu
 410 415 420

agc gaa gcg cag cca tat ggt gag tgg att cgc gat aat ttt gtg cat
 1411
 Ser Glu Ala Gln Pro Tyr Gly Glu Trp Ile Arg Asp Asn Phe Val His
 425 430 435

ctg gat cgt ctg cct cag aca cgc tac aac tac atg gcg cac tct cgt
 1459
 Leu Asp Arg Leu Pro Gln Thr Arg Tyr Asn Tyr Met Ala His Ser Arg
 440 445 450

gct gtg ttg cgt cag cgt gtt ttc gga atc act gaa gaa gat gtg gat
 1507
 Ala Val Leu Arg Gln Arg Val Phe Gly Ile Thr Glu Glu Asp Val Asp
 455 460 465

ttg ttg ctg ctg ccg atg gcc cgc cag ggt gct gag gcg att ggt tcc
 1555
 Leu Leu Leu Leu Pro Met Ala Arg Gln Gly Ala Glu Ala Ile Gly Ser
 470 475 480 485

WO 01/00843

PCT/IB00/00923

atg ggt tcg gat acg cca att gcg gcg cta tcc cag cga cca cgc atg
 1603
 Met Gly Ser Asp Thr Pro Ile Ala Ala Leu Ser Gln Arg Pro Arg Met
 490 495 500

ctt tat gat ttc ttc gcg cag cgc ttt gct cag gtg aca aac cca ccg
 1651
 Leu Tyr Asp Phe Phe Ala Gln Arg Phe Ala Gln Val Thr Asn Pro Pro
 505 510 515

ttg gac tct atc cgc gaa aag cct gtg acc agc atg ttc act ttg ttg
 1699
 Leu Asp Ser Ile Arg Glu Lys Pro Val Thr Ser Met Phe Thr Leu Leu
 520 525 530

ggt gcg cag tct gac gtg ctc aat ccg ggt cct gat gcg gcg cga cgt
 1747
 Gly Ala Gln Ser Asp Val Leu Asn Pro Gly Pro Asp Ala Ala Arg Arg
 535 540 545

att cgt ttg gaa tcg ccg atc att gat aac cat gag ctg gcc acc ttg
 1795
 Ile Arg Leu Glu Ser Pro Ile Ile Asp Asn His Glu Leu Ala Thr Leu
 550 555 560 565

atc aat gcc aac gcg cat ggt gag tgg gat tcc ttt ggt gct gct gta
 1843
 Ile Asn Ala Asn Ala His Gly Glu Trp Asp Ser Phe Gly Ala Ala Val
 570 575 580

att tct ggt ttg tac cca gtg gct cac cat ggt gcc ggc atg aag gct
 1891
 Ile Ser Gly Leu Tyr Pro Val Ala His His Gly Ala Gly Met Lys Ala
 585 590 595

gcg att gct cgt gtg
 1906
 Ala Ile Ala Arg Val
 600

<210> 74
 <211> 602
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 74
 Met Lys Pro Gln Gly Leu Tyr Asn Pro Ala His Glu His Asp Ala Cys
 1 5 10 15
 Gly Val Ala Phe Ile Ala Asp Ile His Gly Arg Pro Ser Arg Ser Ile
 20 25 30
 Val Asp Arg Ala Leu Glu Ala Leu Arg Asn Ile Asp His Arg Gly Ala
 35 40 45
 Ala Gly Ala Glu Lys Asn Thr Gly Asp Gly Ala Gly Ile Leu Met Gln
 50 55 60
 Ile Pro Asp Gly Phe Tyr Arg Glu Val Ser Gly Ile Glu Leu Pro Glu
 65 70 75 80

Ala	Gly	Glu	Tyr	Ala	Thr	Gly	Ile	Ala	Phe	Leu	Pro	Arg	Gly	Arg	Met	
				85					90						95	
Ala	Met	Met	Asp	Ala	Gln	Lys	Glu	Ile	Glu	Arg	Ile	Ala	Lys	Gln	Glu	
			100					105					110			
Gly	Ala	Asp	Val	Leu	Gly	Trp	Arg	Met	Val	Pro	Phe	Asp	Ser	Arg	Asp	
		115					120					125				
Leu	Gly	Ser	Met	Ala	Glu	Glu	Ala	Met	Pro	Ser	Phe	Ala	Gln	Ile	Phe	
	130					135					140					
Leu	Thr	Val	Pro	Gly	Lys	Ser	Gly	Glu	Asp	Leu	Asp	Arg	Val	Met	Phe	
145					150					155					160	
Phe	Ile	Arg	Lys	Arg	Cys	Glu	Arg	Glu	Leu	Gly	Thr	Thr	Asn	Gly	Arg	
				165					170					175		
Asp	Thr	Val	Tyr	Phe	Pro	Ser	Leu	Ser	Ser	Arg	Thr	Ile	Ile	Tyr	Lys	
			180					185					190			
Gly	Met	Leu	Thr	Thr	Leu	Gln	Leu	Glu	Gly	Phe	Phe	Glu	Asp	Leu	Gly	
		195					200					205				
Asp	Ala	Arg	Leu	Glu	Ser	Ala	Ile	Ala	Ile	Val	His	Ser	Arg	Phe	Ser	
	210					215					220					
Thr	Asn	Thr	Phe	Pro	Ser	Trp	Pro	Leu	Ala	His	Pro	Tyr	Arg	Phe	Val	
225					230					235					240	
Ala	His	Asn	Gly	Glu	Ile	Asn	Thr	Val	Arg	Gly	Asn	Glu	Asn	Trp	Met	
				245					250					255		
Arg	Ala	Arg	Glu	Ala	Leu	Ile	Lys	Asn	Asp	Lys	Leu	Gly	Asn	Leu	Ser	
			260					265					270			
Ser	Val	Leu	Pro	Ile	Cys	Thr	Pro	Glu	Gly	Ser	Asp	Thr	Ala	Arg	Phe	
		275					280					285				
Asp	Glu	Ala	Leu	Glu	Leu	Leu	His	Leu	Gly	Gly	Tyr	Ser	Leu	Pro	His	
	290					295					300					
Ala	Val	Ala	Met	Met	Ile	Pro	Gln	Ala	Trp	Glu	His	Asn	Lys	Thr	Leu	
305					310					315					320	
Ser	Pro	Glu	Leu	Arg	Asp	Phe	Tyr	Glu	Tyr	His	Ser	Cys	Leu	Met	Glu	
				325					330					335		
Pro	Trp	Asp	Gly	Pro	Ala	Ala	Leu	Ala	Phe	Thr	Asp	Gly	Arg	Phe	Val	
			340					345					350			
Gly	Ala	Val	Leu	Asp	Arg	Asn	Gly	Leu	Arg	Pro	Gly	Arg	Ile	Thr	Ile	
		355					360					365				
Thr	Asp	Ser	Gly	Leu	Val	Val	Met	Ala	Ser	Glu	Ser	Gly	Val	Leu	Asp	
	370					375					380					
Leu	Arg	Glu	Glu	Ser	Val	Val	Lys	Arg	Thr	Arg	Val	Gln	Pro	Gly	Arg	
385					390					395					400	

WO 01/00843

PCT/IB00/00923

Met Phe Leu Val Asp Thr Ala Glu Gly Arg Ile Val Glu Asp Glu Glu
 405 410 415
 Ile Lys Gln Lys Leu Ser Glu Ala Gln Pro Tyr Gly Glu Trp Ile Arg
 420 425 430
 Asp Asn Phe Val His Leu Asp Arg Leu Pro Gln Thr Arg Tyr Asn Tyr
 435 440 445
 Met Ala His Ser Arg Ala Val Leu Arg Gln Arg Val Phe Gly Ile Thr
 450 455 460
 Glu Glu Asp Val Asp Leu Leu Leu Leu Pro Met Ala Arg Gln Gly Ala
 465 470 475 480
 Glu Ala Ile Gly Ser Met Gly Ser Asp Thr Pro Ile Ala Ala Leu Ser
 485 490 495
 Gln Arg Pro Arg Met Leu Tyr Asp Phe Phe Ala Gln Arg Phe Ala Gln
 500 505 510
 Val Thr Asn Pro Pro Leu Asp Ser Ile Arg Glu Lys Pro Val Thr Ser
 515 520 525
 Met Phe Thr Leu Leu Gly Ala Gln Ser Asp Val Leu Asn Pro Gly Pro
 530 535 540
 Asp Ala Ala Arg Arg Ile Arg Leu Glu Ser Pro Ile Ile Asp Asn His
 545 550 555 560
 Glu Leu Ala Thr Leu Ile Asn Ala Asn Ala His Gly Glu Trp Asp Ser
 565 570 575
 Phe Gly Ala Ala Val Ile Ser Gly Leu Tyr Pro Val Ala His His Gly
 580 585 590
 Ala Gly Met Lys Ala Ala Ile Ala Arg Val
 595 600

<210> 75
 <211> 1362
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (70)..(1362)
 <223> FRXA00364

<400> 75
 accaatttct ggcattcggtc tggatgaagt tgcagctgac gtagaaagct cgtcaccgca 60

gcgcattttttg cca cgc cct gaa gag cac gct cac cgt gaa ttg gat ttg 111
 Leu Pro Arg Pro Glu Glu His Ala His Arg Glu Leu Asp Leu
 1 5 10

ggt ggt gaa tac aag tgg cgc cgc gaa ggt gaa tac cac ctg ttc aac 159
 Gly Gly Glu Tyr Lys Trp Arg Arg Glu Gly Glu Tyr His Leu Phe Asn
 15 20 25 30

WO 01/00843

PCT/IB00/00923

cca gaa acc atc ttc aag ctg cag cat gca acg cgt tct ggc agc tac	207
Pro Glu Thr Ile Phe Lys Leu Gln His Ala Thr Arg Ser Gly Ser Tyr	
35 40 45	
gag att ttc aag gat tac acc cgc aag gtt gat gat caa tcc act cgc	255
Glu Ile Phe Lys Asp Tyr Thr Arg Lys Val Asp Asp Gln Ser Thr Arg	
50 55 60	
ttg ggt act att cgt gga ctg ttt gag ttc agc acg gac cgc aag cca	303
Leu Gly Thr Ile Arg Gly Leu Phe Glu Phe Ser Thr Asp Arg Lys Pro	
65 70 75	
att tcg gtg tct gag gtg gag ccg gtc agt gag atc gtg aag cgt ttc	351
Ile Ser Val Ser Glu Val Glu Pro Val Ser Glu Ile Val Lys Arg Phe	
80 85 90	
tcc act ggt gcg atg tct tat ggc tcg att tct gct gaa gcc cat gag	399
Ser Thr Gly Ala Met Ser Tyr Gly Ser Ile Ser Ala Glu Ala His Glu	
95 100 105 110	
gtc ttg gcc atc gcc atg aac cga ctg ggc ggt atg tcc aac tcc ggc	447
Val Leu Ala Ile Ala Met Asn Arg Leu Gly Gly Met Ser Asn Ser Gly	
115 120 125	
gaa ggt ggc gag gac gcc cgc cga ttt gat gtg gaa ccc aac ggt gac	495
Glu Gly Gly Glu Asp Ala Arg Arg Phe Asp Val Glu Pro Asn Gly Asp	
130 135 140	
tgg aag cgc tct gcc att aag cag gtg gcc tcg gga cgt ttc ggc gtg	543
Trp Lys Arg Ser Ala Ile Lys Gln Val Ala Ser Gly Arg Phe Gly Val	
145 150 155	
acc agc cac tac ttg aac aac tgc acc gat att cag atc aag atg gca	591
Thr Ser His Tyr Leu Asn Asn Cys Thr Asp Ile Gln Ile Lys Met Ala	
160 165 170	
cag ggc gca aag ccc ggt gaa ggt ggc cag ctg cca cca aac aag gtg	639
Gln Gly Ala Lys Pro Gly Glu Gly Gly Gln Leu Pro Pro Asn Lys Val	
175 180 185 190	
tac cca tgg gtt gca gaa gtc cgc atc acc acc cca ggc gtt ggt ctg	687
Tyr Pro Trp Val Ala Glu Val Arg Ile Thr Thr Pro Gly Val Gly Leu	
195 200 205	
att tcc cct cca cca cac cac gat att tac tcc att gag gat ctg gct	735
Ile Ser Pro Pro Pro His His Asp Ile Tyr Ser Ile Glu Asp Leu Ala	
210 215 220	
cag ctg atc cac gac ctg aag aac gct aac cca cgc gca cga atc cac	783
Gln Leu Ile His Asp Leu Lys Asn Ala Asn Pro Arg Ala Arg Ile His	
225 230 235	
gtg aag cta gtg gca gaa caa ggc gtg ggc acc gtt gcc gca ggt gtg	831
Val Lys Leu Val Ala Glu Gln Gly Val Gly Thr Val Ala Ala Gly Val	
240 245 250	
tcc aaa gca cac gct gat gtg gtg ctt att tcc ggc cac gat ggc gga	879
Ser Lys Ala His Ala Asp Val Val Leu Ile Ser Gly His Asp Gly Gly	
255 260 265 270	
act ggc gca tct cct ttg acc tcc ctg aag cat gcc ggt ggt cca tgg	927

WO 01/00843

PCT/IB00/00923

Thr Gly Ala Ser Pro Leu Thr Ser Leu Lys His Ala Gly Gly Pro Trp
 275 280 285
 gag ttg ggc ttg gct gaa acc cag caa acg ttg ctg ctc aac ggc ctg 975
 Glu Leu Gly Leu Ala Glu Thr Gln Gln Thr Leu Leu Leu Asn Gly Leu
 290 295 300
 cgc gat cgt att cgc gtg cag tgc gat ggt cag ctg aaa act ggc cga
 1023
 Arg Asp Arg Ile Arg Val Gln Cys Asp Gly Gln Leu Lys Thr Gly Arg
 305 310 315
 gac gtg gtt atc gca gct ctt ctc ggt gcc gaa gaa ttc ggt ttt gcc
 1071
 Asp Val Val Ile Ala Ala Leu Leu Gly Ala Glu Glu Phe Gly Phe Ala
 320 325 330
 acc gca ccg ctg gtg gtt gaa ggc tgc atc atg atg cgc gtc tgc cac
 1119
 Thr Ala Pro Leu Val Val Glu Gly Cys Ile Met Met Arg Val Cys His
 335 340 345 350
 ctg gac acc tgc ccg gtg ggt atc gct acc cag aac ccg gat ttg cgt
 1167
 Leu Asp Thr Cys Pro Val Gly Ile Ala Thr Gln Asn Pro Asp Leu Arg
 355 360 365
 tcc aag ttc acc ggc aag gct gaa cac gtg gtc aac ttc ttc acc ttc
 1215
 Ser Lys Phe Thr Gly Lys Ala Glu His Val Val Asn Phe Phe Thr Phe
 370 375 380
 atc gcc cag gaa gtc cgt gag tac ttg gca cag ctt ggt ttc cgc tct
 1263
 Ile Ala Gln Glu Val Arg Glu Tyr Leu Ala Gln Leu Gly Phe Arg Ser
 385 390 395
 att gat gaa gcc gtc gga caa gcc cag gtg ctg cgc aag cgt tcc gga
 1311
 Ile Asp Glu Ala Val Gly Gln Ala Gln Val Leu Arg Lys Arg Ser Gly
 400 405 410
 atc cca gct gat tcc cgc gca gca cac ctg gat ttg agc cca att ttc
 1359
 Ile Pro Ala Asp Ser Arg Ala Ala His Leu Asp Leu Ser Pro Ile Phe
 415 420 425 430
 atc
 1362
 Ile

<210> 76
 <211> 431
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 76
 Leu Pro Arg Pro Glu Glu His Ala His Arg Glu Leu Asp Leu Gly Gly
 1 5 10 15

Glu Tyr Lys Trp Arg Arg Glu Gly Glu Tyr His Leu Phe Asn Pro Glu
 20 25 30
 Thr Ile Phe Lys Leu Gln His Ala Thr Arg Ser Gly Ser Tyr Glu Ile
 35 40 45
 Phe Lys Asp Tyr Thr Arg Lys Val Asp Asp Gln Ser Thr Arg Leu Gly
 50 55 60
 Thr Ile Arg Gly Leu Phe Glu Phe Ser Thr Asp Arg Lys Pro Ile Ser
 65 70 75 80
 Val Ser Glu Val Glu Pro Val Ser Glu Ile Val Lys Arg Phe Ser Thr
 85 90 95
 Gly Ala Met Ser Tyr Gly Ser Ile Ser Ala Glu Ala His Glu Val Leu
 100 105 110
 Ala Ile Ala Met Asn Arg Leu Gly Gly Met Ser Asn Ser Gly Glu Gly
 115 120 125
 Gly Glu Asp Ala Arg Arg Phe Asp Val Glu Pro Asn Gly Asp Trp Lys
 130 135 140
 Arg Ser Ala Ile Lys Gln Val Ala Ser Gly Arg Phe Gly Val Thr Ser
 145 150 155 160
 His Tyr Leu Asn Asn Cys Thr Asp Ile Gln Ile Lys Met Ala Gln Gly
 165 170 175
 Ala Lys Pro Gly Glu Gly Gly Gln Leu Pro Pro Asn Lys Val Tyr Pro
 180 185 190
 Trp Val Ala Glu Val Arg Ile Thr Thr Pro Gly Val Gly Leu Ile Ser
 195 200 205
 Pro Pro Pro His His Asp Ile Tyr Ser Ile Glu Asp Leu Ala Gln Leu
 210 215 220
 Ile His Asp Leu Lys Asn Ala Asn Pro Arg Ala Arg Ile His Val Lys
 225 230 235 240
 Leu Val Ala Glu Gln Gly Val Gly Thr Val Ala Ala Gly Val Ser Lys
 245 250 255
 Ala His Ala Asp Val Val Leu Ile Ser Gly His Asp Gly Gly Thr Gly
 260 265 270
 Ala Ser Pro Leu Thr Ser Leu Lys His Ala Gly Gly Pro Trp Glu Leu
 275 280 285
 Gly Leu Ala Glu Thr Gln Gln Thr Leu Leu Leu Asn Gly Leu Arg Asp
 290 295 300
 Arg Ile Arg Val Gln Cys Asp Gly Gln Leu Lys Thr Gly Arg Asp Val
 305 310 315 320
 Val Ile Ala Ala Leu Leu Gly Ala Glu Glu Phe Gly Phe Ala Thr Ala
 325 330 335

Pro Leu Val Val Glu Gly Cys Ile Met Met Arg Val Cys His Leu Asp
 340 345 350

Thr Cys Pro Val Gly Ile Ala Thr Gln Asn Pro Asp Leu Arg Ser Lys
 355 360 365

Phe Thr Gly Lys Ala Glu His Val Val Asn Phe Phe Thr Phe Ile Ala
 370 375 380

Gln Glu Val Arg Glu Tyr Leu Ala Gln Leu Gly Phe Arg Ser Ile Asp
 385 390 395 400

Glu Ala Val Gly Gln Ala Gln Val Leu Arg Lys Arg Ser Gly Ile Pro
 405 410 415

Ala Asp Ser Arg Ala Ala His Leu Asp Leu Ser Pro Ile Phe Ile
 420 425 430

<210> 77
 <211> 866
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(843)
 <223> FRXA00367

<400> 77
 cac agc cta gaa aaa gcc ctg gac aac gca ttt att gat aag gct tcg 48
 His Ser Leu Glu Lys Ala Leu Asp Asn Ala Phe Ile Asp Lys Ala Ser
 1 5 10 15

gac acg atc acc cgt gcc gca gcg ggt gtg gaa acc agc att gtt att 96
 Asp Thr Ile Thr Arg Ala Ala Ala Gly Val Glu Thr Ser Ile Val Ile
 20 25 30

gat agc tcc atc agc aac gtc aac cgt tca gtt ggc acg atg ctg ggt 144
 Asp Ser Ser Ile Ser Asn Val Asn Arg Ser Val Gly Thr Met Leu Gly
 35 40 45

tct gca gtc agc cgc gtg gct ggt gcc caa ggt ttg cca gac ggc acc 192
 Ser Ala Val Ser Arg Val Ala Gly Ala Gln Gly Leu Pro Asp Gly Thr
 50 55 60

atc acc ttg aat ctt caa ggc tgc gcc ggt aac tcc ttt ggc gcg ttc 240
 Ile Thr Leu Asn Leu Gln Gly Cys Ala Gly Asn Ser Phe Gly Ala Phe
 65 70 75 80

atc cca cga ggc atc acc atc aac ctc acc ggc gat gcc aat gac ttt 288
 Ile Pro Arg Gly Ile Thr Ile Asn Leu Thr Gly Asp Ala Asn Asp Phe
 85 90 95

gtg ggc aag gga tta tct ggc gga aag att gtg atc aag cct tcc gct 336
 Val Gly Lys Gly Leu Ser Gly Gly Lys Ile Val Ile Lys Pro Ser Ala
 100 105 110

cag gct ccg aag cag ctg aag aac aat cca aat atc att gcc gga aac 384
 Gln Ala Pro Lys Gln Leu Lys Asn Asn Pro Asn Ile Ile Ala Gly Asn
 115 120 125

gtg ctt gga tac ggc gca acc agt ggt gaa ttg ttc att cgt ggc cag 432
 Val Leu Gly Tyr Gly Ala Thr Ser Gly Glu Leu Phe Ile Arg Gly Gln
 130 135 140

gtc ggc gaa cgt ttc tgc gtc cgt aac tct ggc gcc acc gca gtg gtt 480
 Val Gly Glu Arg Phe Cys Val Arg Asn Ser Gly Ala Thr Ala Val Val
 145 150 155 160

gaa ggt atc gga aac cac ggt tgt gag tac atg act ggc ggc cga gtc 528
 Glu Gly Ile Gly Asn His Gly Cys Glu Tyr Met Thr Gly Gly Arg Val
 165 170 175

ctg gtt ttg ggc ccg gtt ggt gag aac ttt ggt gcc ggc atg tct ggt 576
 Leu Val Leu Gly Pro Val Gly Glu Asn Phe Gly Ala Gly Met Ser Gly
 180 185 190

ggc att gca tac ctg gct aat tcc ccg gac cta aac cag aag atc aat 624
 Gly Ile Ala Tyr Leu Ala Asn Ser Pro Asp Leu Asn Gln Lys Ile Asn
 195 200 205

ggc gaa ttg gtg gat gtt gtt cca ctg agc gct gac gat ctg acg tgg 672
 Gly Glu Leu Val Asp Val Val Pro Leu Ser Ala Asp Asp Leu Thr Trp
 210 215 220

gct gat gag ctc att gct cgc cac cgc gaa ctc acc gga tcc gag acc 720
 Ala Asp Glu Leu Ile Ala Arg His Arg Glu Leu Thr Gly Ser Glu Thr
 225 230 235 240

aag ctg cgt gca caa gat ttg gtg aaa atc atg ccg cgc gat ttc caa 768
 Lys Leu Arg Ala Gln Asp Leu Val Lys Ile Met Pro Arg Asp Phe Gln
 245 250 255

aaa gta ctc aac atc atc gaa acg gcc cac gct gag ggc caa gac cca 816
 Lys Val Leu Asn Ile Ile Glu Thr Ala His Ala Glu Gly Gln Asp Pro
 260 265 270

gca atc aag atc atg gag gca gtg agc taatggccga cccacaagga 863
 Ala Ile Lys Ile Met Glu Ala Val Ser
 275 280

ttc 866

<210> 78

<211> 281

<212> PRT

<213> Corynebacterium glutamicum

<400> 78

His Ser Leu Glu Lys Ala Leu Asp Asn Ala Phe Ile Asp Lys Ala Ser
 1 5 10 15

Asp Thr Ile Thr Arg Ala Ala Ala Gly Val Glu Thr Ser Ile Val Ile
 20 25 30

Asp Ser Ser Ile Ser Asn Val Asn Arg Ser Val Gly Thr Met Leu Gly
 35 40 45

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

Ile Thr Leu Asn Leu Gln Gly Cys Ala Gly Asn Ser Phe Gly Ala Phe
65 70 75 80

Ile Pro Arg Gly Ile Thr Ile Asn Leu Thr Gly Asp Ala Asn Asp Phe
85 90 95

Val Gly Lys Gly Leu Ser Gly Gly Lys Ile Val Ile Lys Pro Ser Ala
100 105 110

Gln Ala Pro Lys Gln Leu Lys Asn Asn Pro Asn Ile Ile Ala Gly Asn
115 120 125

Val Leu Gly Tyr Gly Ala Thr Ser Gly Glu Leu Phe Ile Arg Gly Gln
130 135 140

Val Gly Glu Arg Phe Cys Val Arg Asn Ser Gly Ala Thr Ala Val Val
145 150 155 160

Glu Gly Ile Gly Asn His Gly Cys Glu Tyr Met Thr Gly Gly Arg Val
165 170 175

Leu Val Leu Gly Pro Val Gly Glu Asn Phe Gly Ala Gly Met Ser Gly
180 185 190

Gly Ile Ala Tyr Leu Ala Asn Ser Pro Asp Leu Asn Gln Lys Ile Asn
195 200 205

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

Ala Asp Glu Leu Ile Ala Arg His Arg Glu Leu Thr Gly Ser Glu Thr
225 230 235 240

Lys Leu Arg Ala Gln Asp Leu Val Lys Ile Met Pro Arg Asp Phe Gln
245 250 255

Lys Val Leu Asn Ile Ile Glu Thr Ala His Ala Glu Gly Gln Asp Pro
260 265 270

Ala Ile Lys Ile Met Glu Ala Val Ser
275 280

<210> 79

<211> 1494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (1471)

<223> RXN00076

<400> 79

tctaggagtg ttaaacagcc tggacttgaa acacctttaa ctacttgatt ttcacaccct 60

tgtttccata aaagggctca cgaaaggcaa cttcaaacac atg aca act ccc ctg 115
Met Thr Thr Pro Leu
1 5

WO 01/00843

PCT/IB00/00923

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

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

WO 01/00843

PCT/IB00/00923

cca gca att gtc taaattgttt taacgcgtga agc

1494

Pro Ala Ile Val

455

<210> 80

<211> 457

<212> PRT

<213> Corynebacterium glutamicum

<400> 80

Met	Thr	Thr	Pro	Leu	Arg	Val	Ala	Val	Ile	Gly	Ala	Gly	Pro	Ala	Gly
1				5					10					15	

Ile	Tyr	Ala	Ser	Asp	Leu	Leu	Ile	Arg	Asn	Glu	Glu	Arg	Glu	Val	Phe
			20					25					30		

Val	Asp	Leu	Phe	Glu	Gln	Met	Pro	Ala	Pro	Phe	Gly	Leu	Ile	Arg	Tyr
		35					40					45			

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

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

Ile	Gly	Lys	Asp	Ile	Thr	Val	Glu	Glu	Leu	Arg	Asp	Tyr	Tyr	Asp	Ala
				85					90					95	

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

Gly	Ile	Glu	Ala	Glu	Gly	Ser	Phe	Gly	Ala	Gly	Glu	Phe	Val	Gly	Phe
		115					120					125			

Tyr	Asp	Gly	Asn	Pro	Arg	Phe	Glu	Arg	Ser	Trp	Asp	Leu	Ser	Ala	Gln
	130					135					140				

Ser	Val	Ala	Val	Ile	Gly	Val	Gly	Asn	Val	Gly	Leu	Asp	Val	Ala	Arg
145					150					155					160

Ile	Leu	Ala	Lys	Thr	Gly	Asp	Glu	Leu	Lys	Val	Thr	Glu	Ile	Ser	Asp
				165					170					175	

Asn	Val	Tyr	Asp	Ser	Leu	Lys	Glu	Asn	Lys	Ala	Thr	Glu	Val	His	Val
			180					185					190		

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

Lys	Glu	Leu	Asp	His	Ser	Pro	Thr	Ile	Asn	Val	Val	Val	Asp	Pro	Glu
	210					215					220				

Asp	Ile	Asp	Tyr	Asp	Gly	Ala	Ser	Glu	Glu	Ala	Arg	Arg	Ala	Ser	Lys
225					230					235					240

Ser	Gln	Asp	Leu	Val	Cys	Gln	Ile	Leu	Glu	Gln	Tyr	Ala	Ile	Arg	Glu
				245					250					255	

Pro	Lys	Asp	Ala	Pro	His	Thr	Leu	Gln	Ile	His	Leu	Phe	Glu	Asn	Pro


```

<400> 81
tctaggagtg ttaaacagcc tggacttgaa acacctttaa ctacttgatt ttcacaccct 60

tgtttccata aaagggctca cgaaaggcaa cttcaaacac atg aca act ccc ctg 115
                                         Met Thr Thr Pro Leu
                                           1                               5

cgc gta gcc gtc atc gga gct ggc cct gct ggc att tac gca tcc gac 163
Arg Val Ala Val Ile Gly Ala Gly Pro Ala Gly Ile Tyr Ala Ser Asp
                    10                               15                               20

ctc ctc atc cgc aat gaa gag cgc gaa gtg ttc gtt gac ctt ttc gag 211

```


Leu	Leu	Ile	Arg	Asn	Glu	Glu	Arg	Glu	Val	Phe	Val	Asp	Leu	Phe	Glu		
			25					30					35				
caa	atg	cct	gca	ccg	ttc	gga	ctc	atc	cgt	tac	ggc	gtt	gct	cca	gac	259	
Gln	Met	Pro	Ala	Pro	Phe	Gly	Leu	Ile	Arg	Tyr	Gly	Val	Ala	Pro	Asp		
		40					45					50					
cac	cca	cgc	atc	aag	ggc	atc	gtt	aag	tcc	ctg	cac	aac	gtg	ttg	gac	307	
His	Pro	Arg	Ile	Lys	Gly	Ile	Val	Lys	Ser	Leu	His	Asn	Val	Leu	Asp		
		55				60					65						
aag	cca	cgc	ctg	cgc	ctg	ctc	ggc	aac	att	gaa	atc	ggc	aaa	gac	atc	355	
Lys	Pro	Arg	Leu	Arg	Leu	Leu	Gly	Asn	Ile	Glu	Ile	Gly	Lys	Asp	Ile		
	70				75					80					85		
acc	gtc	gaa	gaa	ctc	cgc	gac	tac	tac	gat	gca	gtc	gtg	ttc	tcc	acc	403	
Thr	Val	Glu	Glu	Leu	Arg	Asp	Tyr	Tyr	Asp	Ala	Val	Val	Phe	Ser	Thr		
				90				95						100			
ggc	gca	gtt	gca	gac	cgc	gac	ctc	aac	atc	ccc	gga	att	gaa	gca	gaa	451	
Gly	Ala	Val	Ala	Asp	Arg	Asp	Leu	Asn	Ile	Pro	Gly	Ile	Glu	Ala	Glu		
			105					110					115				
ggc	tcc	ttc	ggc	gcc	ggc	gag	ttc	gtt	ggc	ttc	tac	gac	ggc	aac	cca	499	
Gly	Ser	Phe	Gly	Ala	Gly	Glu	Phe	Val	Gly	Phe	Tyr	Asp	Gly	Asn	Pro		
		120					125					130					
cgc	ttc	gag	cgc	tcc	tgg	gat	ctg	tct	gca	cag	tcc	gtc	gct	gtt	atc	547	
Arg	Phe	Glu	Arg	Ser	Trp	Asp	Leu	Ser	Ala	Gln	Ser	Val	Ala	Val	Ile		
	135					140					145						
ggc	gtt	ggc	aac	gtc	ggc	ctc	gac	gta	gcc	cgc	atc	ctg	gct	aag	aca	595	
Gly	Val	Gly	Asn	Val	Gly	Leu	Asp	Val	Ala	Arg	Ile	Leu	Ala	Lys	Thr		
	150				155					160					165		
ggc	gac	gag	ctc	aaa	gtc	acc	gaa	att	tcc	gac	aac	gtc	tac	gac	tcc	643	
Gly	Asp	Glu	Leu	Lys	Val	Thr	Glu	Ile	Ser	Asp	Asn	Val	Tyr	Asp	Ser		
				170				175						180			
ctc	aaa	gaa	aac	aag	gyc	wct	gaa	gtg	cac	gtt	ttc	gga	cgt	cgg	tgg	691	
Leu	Lys	Glu	Asn	Lys	Xaa	Xaa	Glu	Val	His	Val	Phe	Gly	Arg	Arg	Trp		
			185					190					195				
ccc	agc	aca	ggc	caa	gtt	cac	ccc	aca	gga	act	maa	aga	act	cgr	cca	739	
Pro	Ser	Thr	Gly	Gln	Val	His	Pro	Thr	Gly	Thr	Xaa	Arg	Thr	Xaa	Pro		
		200					205					210					
ctc	ccc	cac	cat	caa	cgt	ggc	tgt	tgatccagaa	gacatcgact	acg						786	
Leu	Pro	His	His	Gln	Arg	Gly	Cys										
	215					220											

<210> 82

<211> 221

<212> PRT

<213> Corynebacterium glutamicum

<400> 82

Met	Thr	Thr	Pro	Leu	Arg	Val	Ala	Val	Ile	Gly	Ala	Gly	Pro	Ala	Gly
1				5					10					15	


```
<400> 83
atgcaggatt agagcagcag caacggagcc agaatacagtc tccaatttg atatccagcc 60

ccgcgctcct ttccagcgcg ccgattccac tccatggccg atg tac ccc aac ctc      115
                                         Met Tyr Pro Asn Leu
                                              1           5

ttc cgc acc gca acg gct cac gaa gaa ggc gaa tac atc atc act ggc      163
Phe Arg Thr Ala Thr Ala His Glu Glu Gly Glu Tyr Ile Ile Thr Gly
                     10                          15                      20
```


WO 01/00843

PCT/IB00/00923

gat gaa tca gcc gat gaa atc gca gcc ctg ggc ctc gcc gaa cgt gcc 211
Asp Glu Ser Ala Asp Glu Ile Ala Ala Leu Gly Leu Ala Glu Arg Ala
25 30 35

gca ggc tcc acg ctt ggt gaa cgt aaa ttt gct gtc aac acc gtg gaa 259
Ala Gly Ser Thr Leu Gly Glu Arg Lys Phe Ala Val Asn Thr Val Glu
40 45 50

ttc cac ggc aac aac ggc cac gtc acc gga ctc acc ggc aac caa atc 307
Phe His Gly Asn Asn Gly His Val Thr Gly Leu Thr Gly Asn Gln Ile
55 60 65

cga gtt gtc aac ggc aaa cgt gaa cca atc gaa ggc acc gaa ttc ccc 355
Arg Val Val Asn Gly Lys Arg Glu Pro Ile Glu Gly Thr Glu Phe Pro
70 75 80 85

ttc gaa gca gac ctc gtt ctt gtt gca ctt ggc ttc acc ggc gca gaa 403
Phe Glu Ala Asp Leu Val Leu Val Ala Leu Gly Phe Thr Gly Ala Glu
90 95 100

caa ggc gga ttg gca cac gaa cta ggc gta ggt ttc gac gac cgg ggc 451
Gln Gly Gly Leu Ala His Glu Leu Gly Val Gly Phe Asp Asp Arg Gly
105 110 115

cgc atc ctc cgc gat tcc gaa tac cgc agc ccc acc aac tcc cgc gtt 499
Arg Ile Leu Arg Asp Ser Glu Tyr Arg Ser Pro Thr Asn Ser Arg Val
120 125 130

tac atc gca ggc gac aac ggc cgt ggc cag tcc ctg atc gtg tgg gca 547
Tyr Ile Ala Gly Asp Asn Gly Arg Gly Gln Ser Leu Ile Val Trp Ala
135 140 145

atc gcc gaa ggc cgc gca tgc gcc gca gct atc gac gcc gat ctc atg 595
Ile Ala Glu Gly Arg Ala Cys Ala Ala Ala Ile Asp Ala Asp Leu Met
150 155 160 165

ggt gaa act gca ctc cct gta gca gtt gca cca cag gac gtg ccg ctg 643
Gly Glu Thr Ala Leu Pro Val Ala Val Ala Pro Gln Asp Val Pro Leu
170 175 180

gct gtc tagcttgggt agaaaatgct aga 672
Ala Val

<210> 84

<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 84

Met Tyr Pro Asn Leu Phe Arg Thr Ala Thr Ala His Glu Glu Gly Glu
1 5 10 15

Tyr Ile Ile Thr Gly Asp Glu Ser Ala Asp Glu Ile Ala Ala Leu Gly
20 25 30

Leu Ala Glu Arg Ala Ala Gly Ser Thr Leu Gly Glu Arg Lys Phe Ala
35 40 45

Val Asn Thr Val Glu Phe His Gly Asn Asn Gly His Val Thr Gly Leu

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

<210> 85
 <211> 305
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(282)
 <223> FRXA00198

<400> 85	
ctc gtt ctt gtt gca ctt ggc ttc acc ggc gca gaa caa ggc gga ttg	48
Leu Val Leu Val Ala Leu Gly Phe Thr Gly Ala Glu Gln Gly Gly Leu	
1 5 10 15	
gca cac gaa cta ggc gta ggt ttc gac gac cgg ggc cgc atc ctc cgc	96
Ala His Glu Leu Gly Val Gly Phe Asp Asp Arg Gly Arg Ile Leu Arg	
20 25 30	
gat tcc gaa tac cgc agc ccc acc aac tcc cgc gtt tac atc gca ggc	144
Asp Ser Glu Tyr Arg Ser Pro Thr Asn Ser Arg Val Tyr Ile Ala Gly	
35 40 45	
gac aac ggc cgt ggc cag tcc ctg atc gtg tgg gca atc gcc gaa ggc	192
Asp Asn Gly Arg Gly Gln Ser Leu Ile Val Trp Ala Ile Ala Glu Gly	
50 55 60	
cgc gca tgc gcc gca gct atc gac gcc gat ctc atg ggt gaa act gca	240
Arg Ala Cys Ala Ala Ala Ile Asp Ala Asp Leu Met Gly Glu Thr Ala	
65 70 75 80	
ctc cct gta gca gtt gca cca cag gac gtg ccg ctg gct gtc	282
Leu Pro Val Ala Val Ala Pro Gln Asp Val Pro Leu Ala Val	
85 90	

tagcttgggt agaaaatgct aga

305

<210> 86

<211> 94

<212> PRT

<213> Corynebacterium glutamicum

<400> 86

Leu Val Leu Val Ala Leu Gly Phe Thr Gly Ala Glu Gln Gly Gly Leu
 1 5 10 15

Ala His Glu Leu Gly Val Gly Phe Asp Asp Arg Gly Arg Ile Leu Arg
 20 25 30

Asp Ser Glu Tyr Arg Ser Pro Thr Asn Ser Arg Val Tyr Ile Ala Gly
 35 40 45

Asp Asn Gly Arg Gly Gln Ser Leu Ile Val Trp Ala Ile Ala Glu Gly
 50 55 60

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

Leu Pro Val Ala Val Ala Pro Gln Asp Val Pro Leu Ala Val
 85 90

<210> 87

<211> 727

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(727)

<223> RXN00365

<400> 87

gaagcctacg atcgcttgca cgcgaccaac aatttccccg agttcaccgg ccgtttgtgc 60

cccgccaccct gcgaaggcgc ctgcgtgctc ggtatcaacg atg att ctg tca cca 115
 Met Ile Leu Ser Pro
 1 5

tca aaa acg ttt gag ctg gaa atc gtc gaa aaa gca ttc cgc gaa ggc 163
 Ser Lys Thr Phe Glu Leu Glu Ile Val Glu Lys Ala Phe Arg Glu Gly
 10 15 20

tgg gtg caa cca gta atc cca tcc atg tct acc ggg ctg tca gtc gcc 211
 Trp Val Gln Pro Val Ile Pro Ser Met Ser Thr Gly Leu Ser Val Ala
 25 30 35

gtc gtc ggt tcc ggc ccc gct ggc ctt gcc gcc gcg cag cag ctc acc 259
 Val Val Gly Ser Gly Pro Ala Gly Leu Ala Ala Ala Gln Gln Leu Thr
 40 45 50

cgc gca ggc cac agc gtt acc gtc ttt gaa cgc gac gac cgc ctc ggc 307
 Arg Ala Gly His Ser Val Thr Val Phe Glu Arg Asp Asp Arg Leu Gly
 55 60 65


```

ggc ctc atg cgc tac ggc gtg cca gaa tac aaa atg gag aac cgc tgg 355
Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys Met Glu Asn Arg Trp
70 75 80 85

atc gac cgc cgc atc gag caa atg gaa gca gag ggc aca act ttc cag 403
Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu Gly Thr Thr Phe Gln
90 95 100

gta ggc acc tcg ccg cgc gcc gct gaa cta gcg ctt ttc gac gcg atc 451
Val Gly Thr Ser Pro Arg Ala Ala Glu Leu Ala Leu Phe Asp Ala Ile
105 110 115

ctc ctc gca acc ggc acc cca gtg gcc cgc gaa ctc tca gtt cca ggc 499
Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu Leu Ser Val Pro Gly
120 125 130

cac gat ctc aac ggc atc cat gcg gca atg gat tac ctc acc gcc caa 547
His Asp Leu Asn Gly Ile His Ala Ala Met Asp Tyr Leu Thr Ala Gln
135 140 145

aac cgc atc aac gaa ggc gac ggt gaa gtc tct cca atc aac gcc aaa 595
Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser Pro Ile Asn Ala Lys
150 155 160 165

ggc aag aaa gtt gtc atc atc ggt ggc ggc gac acc ggc acc gac tgc 643
Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp Thr Gly Thr Asp Cys
170 175 180

ttc ggc acc gca ctg cgc caa gga gca gaa tca gtc acc caa ttt gat 691
Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser Val Thr Gln Phe Asp
185 190 195

atc cgc ccc cgc gct cct ttc cag cgc gcc gat tcc 727
Ile Arg Pro Arg Ala Pro Phe Gln Arg Ala Asp Ser
200 205

```

<210> 88

<211> 209

<212> PRT

<213> Corynebacterium glutamicum

<400> 88

```

Met Ile Leu Ser Pro Ser Lys Thr Phe Glu Leu Glu Ile Val Glu Lys
1 5 10 15

Ala Phe Arg Glu Gly Trp Val Gln Pro Val Ile Pro Ser Met Ser Thr
20 25 30

Gly Leu Ser Val Ala Val Val Gly Ser Gly Pro Ala Gly Leu Ala Ala
35 40 45

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

Asp Asp Arg Leu Gly Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys
65 70 75 80

Met Glu Asn Arg Trp Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu
85 90 95

```


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

Ser

<210> 89
 <211> 727
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(727)
 <223> FRXA00365

<400> 89
 gaagcctacg atcgcttgca cgcgaccaac aatttccccg agttcaccgg ccgtttgtgc 60
 cccgcaccct gcgaaggcgc ctgctgtgctc ggtatcaacg atg att ctg tca cca 115
 Met Ile Leu Ser Pro
 1 5
 tca aaa acg ttt gag ctg gaa atc gtc gaa aaa gca ttc cgc gaa ggc 163
 Ser Lys Thr Phe Glu Leu Glu Ile Val Glu Lys Ala Phe Arg Glu Gly
 10 15 20
 tgg gtg caa cca gta atc cca tcc atg tct acc ggg ctg tca gtc gcc 211
 Trp Val Gln Pro Val Ile Pro Ser Met Ser Thr Gly Leu Ser Val Ala
 25 30 35
 gtc gtc ggt tcc ggc ccc gct ggc ctt gcc gcc gcg cag cag ctc acc 259
 Val Val Gly Ser Gly Pro Ala Gly Leu Ala Ala Ala Gln Gln Leu Thr
 40 45 50
 cgc gca ggc cac agc gtt acc gtc ttt gaa cgc gac gac cgc ctc ggc 307
 Arg Ala Gly His Ser Val Thr Val Phe Glu Arg Asp Asp Arg Leu Gly
 55 60 65
 ggc ctc atg cgc tac ggc gtg cca gaa tac aaa atg gag aac cgc tgg 355
 Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys Met Glu Asn Arg Trp

WO 01/00843

PCT/IB00/00923

70	75	80	85	
atc gac cgc cgc atc gag caa atg gaa gca gag ggc aca act ttc cag				403
Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu Gly Thr Thr Phe Gln	90	95	100	
gta ggc acc tcg ccg cgc gcc gct gaa cta gcg ctt ttc gac gcg atc				451
Val Gly Thr Ser Pro Arg Ala Ala Glu Leu Ala Leu Phe Asp Ala Ile	105	110	115	
ctc ctc gca acc ggc acc cca gtg gcc cgc gaa ctc tca gtt cca ggc				499
Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu Leu Ser Val Pro Gly	120	125	130	
cac gat ctc aac ggc atc cat gcg gca atg gat tac ctc acc gcc caa				547
His Asp Leu Asn Gly Ile His Ala Ala Met Asp Tyr Leu Thr Ala Gln	135	140	145	
aac cgc atc aac gaa ggc gac ggt gaa gtc tct cca atc aac gcc aaa				595
Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser Pro Ile Asn Ala Lys	150	155	160	165
ggc aag aaa gtt gtc atc atc ggt ggc ggc gac acc ggc acc gac tgc				643
Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp Thr Gly Thr Asp Cys	170	175	180	
ttc ggc acc gca ctg cgc caa gga gca gaa tca gtc acc caa ttt gat				691
Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser Val Thr Gln Phe Asp	185	190	195	
atc cgc ccc cgc gct cct ttc cag cgc gcc gat tcc				727
Ile Arg Pro Arg Ala Pro Phe Gln Arg Ala Asp Ser	200	205		

<210> 90

<211> 209

<212> PRT

<213> Corynebacterium glutamicum

<400> 90

Met Ile Leu Ser Pro Ser Lys Thr Phe Glu Leu Glu Ile Val Glu Lys	1	5	10	15
Ala Phe Arg Glu Gly Trp Val Gln Pro Val Ile Pro Ser Met Ser Thr	20	25	30	
Gly Leu Ser Val Ala Val Val Gly Ser Gly Pro Ala Gly Leu Ala Ala	35	40	45	
Ala Gln Gln Leu Thr Arg Ala Gly His Ser Val Thr Val Phe Glu Arg	50	55	60	
Asp Asp Arg Leu Gly Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys	65	70	75	80
Met Glu Asn Arg Trp Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu	85	90	95	
Gly Thr Thr Phe Gln Val Gly Thr Ser Pro Arg Ala Ala Glu Leu Ala	100	105	110	

Leu Phe Asp Ala Ile Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu
 115 120 125
 Leu Ser Val Pro Gly His Asp Leu Asn Gly Ile His Ala Ala Met Asp
 130 135 140
 Tyr Leu Thr Ala Gln Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser
 145 150 155 160
 Pro Ile Asn Ala Lys Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp
 165 170 175
 Thr Gly Thr Asp Cys Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser
 180 185 190
 Val Thr Gln Phe Asp Ile Arg Pro Arg Ala Pro Phe Gln Arg Ala Asp
 195 200 205
 Ser

<210> 91
 <211> 480
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(457)
 <223> RXA00366

<400> 91
 aaatcatgcc gcgcgatttc caaaaagttac tcaacatcat cgaaacggcc cacgctgagg 60
 gccaaagaccc agcaatcaag atcatggagg cagtgagcta atg gcc gac cca caa 115
 Met Ala Asp Pro Gln
 1 5
 gga ttc atc aaa tac tcc cga cgc gag cct gca cac cgc ccg gtc ccg 163
 Gly Phe Ile Lys Tyr Ser Arg Arg Glu Pro Ala His Arg Pro Val Pro
 10 15 20
 ctg cgc ctc atg gac cac tcc gag gtc tac gaa aag gca ccg gca ggt 211
 Leu Arg Leu Met Asp His Ser Glu Val Tyr Glu Lys Ala Pro Ala Gly
 25 30 35
 cag atc gag gaa cag gct gcc cgc tgc atg gat tgc ggt gtc ccg ttc 259
 Gln Ile Glu Glu Gln Ala Ala Arg Cys Met Asp Cys Gly Val Pro Phe
 40 45 50
 tgc cac gaa ggc tgc cca ctg ggc aac atc atc cct gag tgg aat gat 307
 Cys His Glu Gly Cys Pro Leu Gly Asn Ile Ile Pro Glu Trp Asn Asp
 55 60 65
 ctg gta cgc caa ggt cgg tgg aag gaa gcc tac gat cgc ttg cac gcg 355
 Leu Val Arg Gln Gly Arg Trp Lys Glu Ala Tyr Asp Arg Leu His Ala
 70 75 80 85
 acc aac aat ttc ccc gag ttc acc ggc cgt ttg tgc ccc gca ccc tgc 403

WO 01/00843

PCT/IB00/00923

Thr Asn Asn Phe Pro Glu Phe Thr Gly Arg Leu Cys Pro Ala Pro Cys
 90 95 100

gaa ggc gcc tgc gtg ctc ggt atc aac gat gat tct gtc acc atc aaa 451
 Glu Gly Ala Cys Val Leu Gly Ile Asn Asp Asp Ser Val Thr Ile Lys
 105 110 115

aac gtt tgagctggaa atcgctgaaa aag 480
 Asn Val

<210> 92
 <211> 119
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 92
 Met Ala Asp Pro Gln Gly Phe Ile Lys Tyr Ser Arg Arg Glu Pro Ala
 1 5 10 15

His Arg Pro Val Pro Leu Arg Leu Met Asp His Ser Glu Val Tyr Glu
 20 25 30

Lys Ala Pro Ala Gly Gln Ile Glu Glu Gln Ala Ala Arg Cys Met Asp
 35 40 45

Cys Gly Val Pro Phe Cys His Glu Gly Cys Pro Leu Gly Asn Ile Ile
 50 55 60

Pro Glu Trp Asn Asp Leu Val Arg Gln Gly Arg Trp Lys Glu Ala Tyr
 65 70 75 80

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

Cys Pro Ala Pro Cys Glu Gly Ala Cys Val Leu Gly Ile Asn Asp Asp
 100 105 110

Ser Val Thr Ile Lys Asn Val
 115

<210> 93
 <211> 1464
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1441)
 <223> RXA02072

<400> 93
 tacatggtgc cctcaatggg aaccaccaac atcactaaat ggcccaggta cacacttta 60

aatcgtgcgc gcatgcagcc gagatgggaa cgaggaaatc atg aca gtt gat gag 115
 Met Thr Val Asp Glu
 1 5

cag gtc tct aac tat tac gac atg ctt ctg aag cgc aat gct ggc gag 163

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

WO 01/00843

PCT/IB00/00923

	250		255		260	
ttc tcc gat tcc agc ggt tgg gtt cat acc cct aac ggc gtt gac gtg						931
Phe Ser Asp Ser Ser Gly Trp Val His Thr Pro Asn Gly Val Asp Val						
	265		270		275	
gct aag ctc cgc gaa atc aag gaa gtt cgt cgc gca cgc gta tcc gtg						979
Ala Lys Leu Arg Glu Ile Lys Glu Val Arg Arg Ala Arg Val Ser Val						
	280		285		290	
tac gcc gac gaa gtt gaa ggc gca acc tac cac acc gac ggt tcc atc						
1027						
Tyr Ala Asp Glu Val Glu Gly Ala Thr Tyr His Thr Asp Gly Ser Ile						
	295		300		305	
tgg gat ctc aag tgc gat atc gct ctt cct tgt gca act cag aac gag						
1075						
Trp Asp Leu Lys Cys Asp Ile Ala Leu Pro Cys Ala Thr Gln Asn Glu						
310		315		320		325
ctc aac ggc gag aac gct aag act ctt gca gac aac ggc tgc cgt ttc						
1123						
Leu Asn Gly Glu Asn Ala Lys Thr Leu Ala Asp Asn Gly Cys Arg Phe						
	330		335		340	
gtt gct gaa ggc gcg aac atg cct tcc acc cct gag gct gtt gag gtc						
1171						
Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro Glu Ala Val Glu Val						
	345		350		355	
ttc cgt gag cgc gac atc cgc ttc gga cca ggc aag gca gct aac gct						
1219						
Phe Arg Glu Arg Asp Ile Arg Phe Gly Pro Gly Lys Ala Ala Asn Ala						
	360		365		370	
ggt ggc gtt gca acc tcc gct ctg gag atg cag cag aac gct tcg cgc						
1267						
Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln Gln Asn Ala Ser Arg						
	375		380		385	
gat tcc tgg agc ttc gag tac acc gac gag cgc ctc cag gtg atc atg						
1315						
Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg Leu Gln Val Ile Met						
390		395		400		405
aag aac atc ttc aag acc tgt gca gag acc gca gca gag tat gga cac						
1363						
Lys Asn Ile Phe Lys Thr Cys Ala Glu Thr Ala Ala Glu Tyr Gly His						
	410		415		420	
gag aac gat tac gtt gtc ggc gct aac att gct ggc ttc aag aag gta						
1411						
Glu Asn Asp Tyr Val Val Gly Ala Asn Ile Ala Gly Phe Lys Lys Val						
	425		430		435	
gct gac gcg atg ctg gca cag ggc gtc atc taagaccct gcgctttact						
1461						
Ala Asp Ala Met Leu Ala Gln Gly Val Ile						
	440		445			

WO 01/00843

PCT/IB00/00923

taa
1464

<210> 94
<211> 447
<212> PRT
<213> Corynebacterium glutamicum

<400> 94

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

WO 01/00843

PCT/IB00/00923

Asn Gly Val Asp Val Ala Lys Leu Arg Glu Ile Lys Glu Val Arg Arg
 275 280 285
 Ala Arg Val Ser Val Tyr Ala Asp Glu Val Glu Gly Ala Thr Tyr His
 290 295 300
 Thr Asp Gly Ser Ile Trp Asp Leu Lys Cys Asp Ile Ala Leu Pro Cys
 305 310 315 320
 Ala Thr Gln Asn Glu Leu Asn Gly Glu Asn Ala Lys Thr Leu Ala Asp
 325 330 335
 Asn Gly Cys Arg Phe Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro
 340 345 350
 Glu Ala Val Glu Val Phe Arg Glu Arg Asp Ile Arg Phe Gly Pro Gly
 355 360 365
 Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln
 370 375 380
 Gln Asn Ala Ser Arg Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg
 385 390 395 400
 Leu Gln Val Ile Met Lys Asn Ile Phe Lys Thr Cys Ala Glu Thr Ala
 405 410 415
 Ala Glu Tyr Gly His Glu Asn Asp Tyr Val Val Gly Ala Asn Ile Ala
 420 425 430
 Gly Phe Lys Lys Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile
 435 440 445

<210> 95

<211> 1461

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1438)

<223> RXA00323

<400> 95

cgcgacatcc ttgagtaact ctgagaaaaa ctacccccga tgggagtata aaagtggcaa 60

atgcgcagtc gatgtcccat cgctgcgtag attagttttc atg aac agc gaa cag 115
 Met Asn Ser Glu Gln
 1 5

gaa ttt gta ctc agc gcc att gaa gaa cgc gac att aag ttt gtg cgt 163
 Glu Phe Val Leu Ser Ala Ile Glu Glu Arg Asp Ile Lys Phe Val Arg
 10 15 20

cta tgg ttc act gac att ctt ggc cac ttg aag tca gtg gtt gtg gct 211
 Leu Trp Phe Thr Asp Ile Leu Gly His Leu Lys Ser Val Val Val Ala
 25 30 35

cct gca gaa cta gag tct gcg ttg gaa gaa ggc atc gga ttc gat ggc 259
 Pro Ala Glu Leu Glu Ser Ala Leu Glu Glu Gly Ile Gly Phe Asp Gly

40				45				50								
tca	gcc	att	gag	ggc	tac	gcg	cgt	atc	tcg	gaa	gcg	gac	acc	att	gcc	307
Ser	Ala	Ile	Glu	Gly	Tyr	Ala	Arg	Ile	Ser	Glu	Ala	Asp	Thr	Ile	Ala	
	55					60					65					
cgc	cca	gat	cca	tcg	aca	ttc	cag	gtc	ctc	cca	cta	gaa	gcg	ggc	atc	355
Arg	Pro	Asp	Pro	Ser	Thr	Phe	Gln	Val	Leu	Pro	Leu	Glu	Ala	Gly	Ile	
	70				75					80					85	
tca	aaa	ctg	cag	gca	gca	cgc	ctg	ttt	tgc	gat	gtc	acg	atg	cca	gac	403
Ser	Lys	Leu	Gln	Ala	Ala	Arg	Leu	Phe	Cys	Asp	Val	Thr	Met	Pro	Asp	
				90					95					100		
gga	cag	cca	tct	ttt	tct	gac	ccg	cgc	caa	gtg	ctg	cgc	agg	cag	gtc	451
Gly	Gln	Pro	Ser	Phe	Ser	Asp	Pro	Arg	Gln	Val	Leu	Arg	Arg	Gln	Val	
			105					110					115			
caa	cta	gct	gca	gat	gaa	ggc	ttg	acc	tgc	atg	atc	tca	cca	gag	att	499
Gln	Leu	Ala	Ala	Asp	Glu	Gly	Leu	Thr	Cys	Met	Ile	Ser	Pro	Glu	Ile	
		120					125					130				
gag	ttc	tat	ttg	gtg	caa	agc	ctt	cgc	acc	aac	gga	ctg	cca	cct	gtg	547
Glu	Phe	Tyr	Leu	Val	Gln	Ser	Leu	Arg	Thr	Asn	Gly	Leu	Pro	Pro	Val	
	135					140					145					
ccc	act	gac	aac	ggc	gga	tat	ttc	gac	caa	gcc	aca	ttc	aat	gag	gcg	595
Pro	Thr	Asp	Asn	Gly	Gly	Tyr	Phe	Asp	Gln	Ala	Thr	Phe	Asn	Glu	Ala	
150				155						160					165	
ccg	aat	ttc	cgt	cga	aac	gcg	atg	gta	gcg	ctg	gag	gaa	ctc	ggc	atc	643
Pro	Asn	Phe	Arg	Arg	Asn	Ala	Met	Val	Ala	Leu	Glu	Glu	Leu	Gly	Ile	
				170					175					180		
cct	gtc	gag	ttc	tcc	cac	cat	gaa	act	gca	cct	ggc	cag	caa	gaa	atc	691
Pro	Val	Glu	Phe	Ser	His	His	Glu	Thr	Ala	Pro	Gly	Gln	Gln	Glu	Ile	
			185					190					195			
gat	tta	cgc	cat	gcg	gat	gcg	ctc	acc	atg	gcc	gac	aac	atc	atg	acc	739
Asp	Leu	Arg	His	Ala	Asp	Ala	Leu	Thr	Met	Ala	Asp	Asn	Ile	Met	Thr	
		200					205					210				
ttc	cgc	tac	atc	atg	aaa	cag	gtg	gca	agg	gac	caa	ggc	gtc	ggg	gca	787
Phe	Arg	Tyr	Ile	Met	Lys	Gln	Val	Ala	Arg	Asp	Gln	Gly	Val	Gly	Ala	
	215					220					225					
tca	ttt	atg	ccc	aag	cca	ttc	caa	gaa	cat	gca	ggc	tcc	gcc	atg	cac	835
Ser	Phe	Met	Pro	Lys	Pro	Phe	Gln	Glu	His	Ala	Gly	Ser	Ala	Met	His	
230				235						240					245	
acg	cac	atg	tcc	tta	ttt	gag	ggc	gat	acc	aac	gcg	ttc	cac	gat	cca	883
Thr	His	Met	Ser	Leu	Phe	Glu	Gly	Asp	Thr	Asn	Ala	Phe	His	Asp	Pro	
				250					255					260		
gac	gat	tct	tac	atg	ctg	tcc	aaa	acc	gca	aaa	cag	ttc	atc	gct	gga	931
Asp	Asp	Ser	Tyr	Met	Leu	Ser	Lys	Thr	Ala	Lys	Gln	Phe	Ile	Ala	Gly	
			265					270					275			
atc	ttg	cat	cac	gct	cca	gaa	ttc	acc	gct	gtg	acc	aac	cag	tgg	gtc	979
Ile	Leu	His	His	Ala	Pro	Glu	Phe	Thr	Ala	Val	Thr	Asn	Gln	Trp	Val	
		280					285					290				

aat tcc tac aaa cgc atc gtg tac gga aac gaa gct cca act gcg gca
1027

Asn Ser Tyr Lys Arg Ile Val Tyr Gly Asn Glu Ala Pro Thr Ala Ala
295 300 305

acc tgg ggt gta tct aat cgt tct gcg ctg gtt cgt gtt cct acc tac
1075

Thr Trp Gly Val Ser Asn Arg Ser Ala Leu Val Arg Val Pro Thr Tyr
310 315 320 325

cgt ttg aat aag gag gag tcg cgc cgg gtg gag gtg cgt ctt cct gat
1123

Arg Leu Asn Lys Glu Glu Ser Arg Arg Val Glu Val Arg Leu Pro Asp
330 335 340

acc gct tgt aac cca tat ttg gcg ttt tca gtg atg ctc ggc gct ggt
1171

Thr Ala Cys Asn Pro Tyr Leu Ala Phe Ser Val Met Leu Gly Ala Gly
345 350 355

ttg aaa ggc att aaa gaa ggt tat gag ctc gac gag cca gct gag gac
1219

Leu Lys Gly Ile Lys Glu Gly Tyr Glu Leu Asp Glu Pro Ala Glu Asp
360 365 370

gat atc tcc aac ttg agc ttc cgg gaa cgt cgc gcc atg ggc tac aac
1267

Asp Ile Ser Asn Leu Ser Phe Arg Glu Arg Arg Ala Met Gly Tyr Asn
375 380 385

gat ctg cca agc agc ctt gat cag gca ctg cgc caa atg gaa aag tca
1315

Asp Leu Pro Ser Ser Leu Asp Gln Ala Leu Arg Gln Met Glu Lys Ser
390 395 400 405

gag ctt gtt gct gac atc ctc ggt gag cac gtt ttt gag ttt ttc ttg
1363

Glu Leu Val Ala Asp Ile Leu Gly Glu His Val Phe Glu Phe Phe Leu
410 415 420

cgc aat aag tgg cgt gaa tgg cgt gac tac caa gag cag atc act ccg
1411

Arg Asn Lys Trp Arg Glu Trp Arg Asp Tyr Gln Glu Gln Ile Thr Pro
425 430 435

tgg gag ctc cga aac aat ctt gat tac tagacttttg cactccaatg
1458

Trp Glu Leu Arg Asn Asn Leu Asp Tyr
440 445

gaa
1461

<210> 96

<211> 446

<212> PRT

<213> Corynebacterium glutamicum

<400> 96

WO 01/00843

PCT/IB00/00923

Met	Asn	Ser	Glu	Gln	Glu	Phe	Val	Leu	Ser	Ala	Ile	Glu	Glu	Arg	Asp	1	5	10	15
Ile	Lys	Phe	Val	Arg	Leu	Trp	Phe	Thr	Asp	Ile	Leu	Gly	His	Leu	Lys	20	25	30	
Ser	Val	Val	Val	Ala	Pro	Ala	Glu	Leu	Glu	Ser	Ala	Leu	Glu	Glu	Gly	35	40	45	
Ile	Gly	Phe	Asp	Gly	Ser	Ala	Ile	Glu	Gly	Tyr	Ala	Arg	Ile	Ser	Glu	50	55	60	
Ala	Asp	Thr	Ile	Ala	Arg	Pro	Asp	Pro	Ser	Thr	Phe	Gln	Val	Leu	Pro	65	70	75	80
Leu	Glu	Ala	Gly	Ile	Ser	Lys	Leu	Gln	Ala	Ala	Arg	Leu	Phe	Cys	Asp	85	90	95	
Val	Thr	Met	Pro	Asp	Gly	Gln	Pro	Ser	Phe	Ser	Asp	Pro	Arg	Gln	Val	100	105	110	
Leu	Arg	Arg	Gln	Val	Gln	Leu	Ala	Ala	Asp	Glu	Gly	Leu	Thr	Cys	Met	115	120	125	
Ile	Ser	Pro	Glu	Ile	Glu	Phe	Tyr	Leu	Val	Gln	Ser	Leu	Arg	Thr	Asn	130	135	140	
Gly	Leu	Pro	Pro	Val	Pro	Thr	Asp	Asn	Gly	Gly	Tyr	Phe	Asp	Gln	Ala	145	150	155	160
Thr	Phe	Asn	Glu	Ala	Pro	Asn	Phe	Arg	Arg	Asn	Ala	Met	Val	Ala	Leu	165	170	175	
Glu	Glu	Leu	Gly	Ile	Pro	Val	Glu	Phe	Ser	His	His	Glu	Thr	Ala	Pro	180	185	190	
Gly	Gln	Gln	Glu	Ile	Asp	Leu	Arg	His	Ala	Asp	Ala	Leu	Thr	Met	Ala	195	200	205	
Asp	Asn	Ile	Met	Thr	Phe	Arg	Tyr	Ile	Met	Lys	Gln	Val	Ala	Arg	Asp	210	215	220	
Gln	Gly	Val	Gly	Ala	Ser	Phe	Met	Pro	Lys	Pro	Phe	Gln	Glu	His	Ala	225	230	235	240
Gly	Ser	Ala	Met	His	Thr	His	Met	Ser	Leu	Phe	Glu	Gly	Asp	Thr	Asn	245	250	255	
Ala	Phe	His	Asp	Pro	Asp	Asp	Ser	Tyr	Met	Leu	Ser	Lys	Thr	Ala	Lys	260	265	270	
Gln	Phe	Ile	Ala	Gly	Ile	Leu	His	His	Ala	Pro	Glu	Phe	Thr	Ala	Val	275	280	285	
Thr	Asn	Gln	Trp	Val	Asn	Ser	Tyr	Lys	Arg	Ile	Val	Tyr	Gly	Asn	Glu	290	295	300	
Ala	Pro	Thr	Ala	Ala	Thr	Trp	Gly	Val	Ser	Asn	Arg	Ser	Ala	Leu	Val	305	310	315	320
Arg	Val	Pro	Thr	Tyr	Arg	Leu	Asn	Lys	Glu	Glu	Ser	Arg	Arg	Val	Glu				

				325						330					335	
Val	Arg	Leu	Pro	Asp	Thr	Ala	Cys	Asn	Pro	Tyr	Leu	Ala	Phe	Ser	Val	
			340					345					350			
Met	Leu	Gly	Ala	Gly	Leu	Lys	Gly	Ile	Lys	Glu	Gly	Tyr	Glu	Leu	Asp	
		355					360					365				
Glu	Pro	Ala	Glu	Asp	Asp	Ile	Ser	Asn	Leu	Ser	Phe	Arg	Glu	Arg	Arg	
	370					375					380					
Ala	Met	Gly	Tyr	Asn	Asp	Leu	Pro	Ser	Ser	Leu	Asp	Gln	Ala	Leu	Arg	
385					390					395					400	
Gln	Met	Glu	Lys	Ser	Glu	Leu	Val	Ala	Asp	Ile	Leu	Gly	Glu	His	Val	
				405					410					415		
Phe	Glu	Phe	Phe	Leu	Arg	Asn	Lys	Trp	Arg	Glu	Trp	Arg	Asp	Tyr	Gln	
			420					425					430			
Glu	Gln	Ile	Thr	Pro	Trp	Glu	Leu	Arg	Asn	Asn	Leu	Asp	Tyr			
		435					440					445				

<210> 97

<211> 1554

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1531)

<223> RXA00335

<400> 97

actacatttg cagccaagtc tactacttga tcttcaaagg tcagcaattg tgaacaaagc 60

tacaaataaa	ccgttccgcc	catgtcaatg	aggagtcacc	gtg	gcg	ttt	gaa	acc	115
				Val	Ala	Phe	Glu	Thr	
				1				5	

ccg	gaa	gaa	att	gtc	aag	ttc	atc	aag	gat	gaa	aac	gtc	gag	ttc	gtt	163
Pro	Glu	Glu	Ile	Val	Lys	Phe	Ile	Lys	Asp	Glu	Asn	Val	Glu	Phe	Val	
			10					15					20			

gac	gtt	cga	ttc	acc	gac	ctt	ccc	ggc	acc	gag	cag	cac	ttc	agc	atc	211
Asp	Val	Arg	Phe	Thr	Asp	Leu	Pro	Gly	Thr	Glu	Gln	His	Phe	Ser	Ile	
			25					30					35			

cca	gct	gcc	agc	ttc	gat	gca	gat	aca	atc	gaa	gaa	ggt	ctc	gca	ttc	259
Pro	Ala	Ala	Ser	Phe	Asp	Ala	Asp	Thr	Ile	Glu	Glu	Gly	Leu	Ala	Phe	
		40					45					50				

gac	gga	tcc	tcg	atc	cgt	ggc	ttc	acc	acg	atc	gac	gaa	tct	gac	atg	307
Asp	Gly	Ser	Ser	Ile	Arg	Gly	Phe	Thr	Thr	Ile	Asp	Glu	Ser	Asp	Met	
	55					60					65					

aat	ctc	ctg	cca	gac	ctc	gga	acg	gcc	acc	ctt	gat	cca	ttc	cgc	aag	355
Asn	Leu	Leu	Pro	Asp	Leu	Gly	Thr	Ala	Thr	Leu	Asp	Pro	Phe	Arg	Lys	
70					75					80					85	

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

tac cac cgt ctg gtt cca ggc ttc gag gct cca atc aac ctg gtg tac
1123

Tyr His Arg Leu Val Pro Gly Phe Glu Ala Pro Ile Asn Leu Val Tyr
330 335 340

tca cag cgc aac cgt tcc gct gct gtc cgt atc cca atc acc gga tcc
1171

Ser Gln Arg Asn Arg Ser Ala Ala Val Arg Ile Pro Ile Thr Gly Ser
345 350 355

aac ccg aag gca aag cgc atc gaa ttc cgc gct cca gac cca tca ggc
1219

Asn Pro Lys Ala Lys Arg Ile Glu Phe Arg Ala Pro Asp Pro Ser Gly
360 365 370

aac cca tac ctg ggc ttt gca gcg atg atg atg gcc ggc ctc gac ggc
1267

Asn Pro Tyr Leu Gly Phe Ala Ala Met Met Met Ala Gly Leu Asp Gly
375 380 385

atc aag aac cgc atc gag cca cac gct cca gtg gac aag gac ctc tac
1315

Ile Lys Asn Arg Ile Glu Pro His Ala Pro Val Asp Lys Asp Leu Tyr
390 395 400 405

gaa cta cca cca gag gaa gct gca tcc att cca cag gca cca acc tcc
1363

Glu Leu Pro Pro Glu Glu Ala Ala Ser Ile Pro Gln Ala Pro Thr Ser
410 415 420

ctg gaa gca tcc ctg aag gca ctg cag gaa gac acc gac ttc ctc acc
1411

Leu Glu Ala Ser Leu Lys Ala Leu Gln Glu Asp Thr Asp Phe Leu Thr
425 430 435

gag tct gac gtc ttc acc gag gat ctc atc gag gcg tac atc cag tac
1459

Glu Ser Asp Val Phe Thr Glu Asp Leu Ile Glu Ala Tyr Ile Gln Tyr
440 445 450

aag tac gac aac gag atc tcc cca gtt cgc ctg cgc cca acc ccg cag
1507

Lys Tyr Asp Asn Glu Ile Ser Pro Val Arg Leu Arg Pro Thr Pro Gln
455 460 465

gaa ttc gaa ttg tac ttc gac tgc taattcactt agctagccga tag
1554

Glu Phe Glu Leu Tyr Phe Asp Cys
470 475

<210> 98

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 98

Val Ala Phe Glu Thr Pro Glu Glu Ile Val Lys Phe Ile Lys Asp Glu
1 5 10 15

149

WO 01/00843

PCT/IB00/00923

340	345	350
Pro Ile Thr Gly Ser Asn Pro Lys Ala Lys Arg Ile Glu Phe Arg Ala		
355	360	365
Pro Asp Pro Ser Gly Asn Pro Tyr Leu Gly Phe Ala Ala Met Met Met		
370	375	380
Ala Gly Leu Asp Gly Ile Lys Asn Arg Ile Glu Pro His Ala Pro Val		
385	390	395
Asp Lys Asp Leu Tyr Glu Leu Pro Pro Glu Glu Ala Ala Ser Ile Pro		
	405	410
Gln Ala Pro Thr Ser Leu Glu Ala Ser Leu Lys Ala Leu Gln Glu Asp		
	420	425
Thr Asp Phe Leu Thr Glu Ser Asp Val Phe Thr Glu Asp Leu Ile Glu		
	435	440
Ala Tyr Ile Gln Tyr Lys Tyr Asp Asn Glu Ile Ser Pro Val Arg Leu		
450	455	460
Arg Pro Thr Pro Gln Glu Phe Glu Leu Tyr Phe Asp Cys		
465	470	475

<210> 99

<211> 3258

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(3235)

<223> RXA00324

<400> 99

tccgtgggag ctccgaaaca atcttgatta ctagactttt gcactccaat ggaaacccta 60

cggcgaccca attgcgaccc gatgaaggag gggagaagct	atg tca gga ccg tta	115
	Met Ser Gly Pro Leu	
	1 5	

aga agt gaa cgt aaa gtc gtt ggc ttt gtc aga gac cca ctg cca aaa	163
Arg Ser Glu Arg Lys Val Val Gly Phe Val Arg Asp Pro Leu Pro Lys	
10 15 20	

gtt ggt tct tta tcg ctg aaa tct gag cat gcc caa gca gat cta gag	211
Val Gly Ser Leu Ser Leu Lys Ser Glu His Ala Gln Ala Asp Leu Glu	
25 30 35	

cat ttg ggt tgg cgc aat gtt gag tct ttg gat ttg ttg tgg ggc ttg	259
His Leu Gly Trp Arg Asn Val Glu Ser Leu Asp Leu Leu Trp Gly Leu	
40 45 50	

tca ggt gca ggc gat ccc gat gtc gcg ctg aac ctt ctt att cgg ctg	307
Ser Gly Ala Gly Asp Pro Asp Val Ala Leu Asn Leu Leu Ile Arg Leu	
55 60 65	

tat cag gca ctt gaa gca atc ggc gag gat gct cga aac gag ctt gat	355

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

ggt aaa agt ggc gct ctt gtg cgc tct ttg gat tcc cat atg gcg tat
1075

Gly Lys Ser Gly Ala Leu Val Arg Ser Leu Asp Ser His Met Ala Tyr
310 315 320 325

tac aag cgc tgg gcg gaa acc tgg gag ttt cag gca ctg ctg aaa gct
1123

Tyr Lys Arg Trp Ala Glu Thr Trp Glu Phe Gln Ala Leu Leu Lys Ala
330 335 340

cgt ccc atg acg ggt gat att aac ctt ggg cag tcc tat gtg gat gct
1171

Arg Pro Met Thr Gly Asp Ile Asn Leu Gly Gln Ser Tyr Val Asp Ala
345 350 355

ctt tca ccg ttg att tgg acg gct agc cag cgg gaa tca ttt gtc aca
1219

Leu Ser Pro Leu Ile Trp Thr Ala Ser Gln Arg Glu Ser Phe Val Thr
360 365 370

gat gtc caa gct atg cgc cgt cga gtg ttg gac aat gtt ccg gaa gac
1267

Asp Val Gln Ala Met Arg Arg Arg Val Leu Asp Asn Val Pro Glu Asp
375 380 385

ttg cgt gat cgt gag ctg aag ctt ggt cgc ggt ggt ttg agg gat gtg
1315

Leu Arg Asp Arg Glu Leu Lys Leu Gly Arg Gly Gly Leu Arg Asp Val
390 395 400 405

gag ttt gct gtc cag ctc ctt cag atg gtg cat ggt cgc att gat gag
1363

Glu Phe Ala Val Gln Leu Leu Gln Met Val His Gly Arg Ile Asp Glu
410 415 420

acg ttg cgg gtt cgg tca acg gta aat gct ttg cat gtg ttg gtt gat
1411

Thr Leu Arg Val Arg Ser Thr Val Asn Ala Leu His Val Leu Val Asp
425 430 435

cag gga tat gtg ggt cgt gaa gac ggg cat aat ctc att gag tcg tat
1459

Gln Gly Tyr Val Gly Arg Glu Asp Gly His Asn Leu Ile Glu Ser Tyr
440 445 450

gag ttt ttg cgt ctg ttg gag cat cgc ctt caa ttg gag cgg atc aag
1507

Glu Phe Leu Arg Leu Leu Glu His Arg Leu Gln Leu Glu Arg Ile Lys
455 460 465

cgc act cac ttg tta ccg aaa cct gat gac cga atg aat atg cgc tgg
1555

Arg Thr His Leu Leu Pro Lys Pro Asp Asp Arg Met Asn Met Arg Trp
470 475 480 485

ttg gcg cgc gct tct ggg ttt act ggt tcg atg gag caa agt tcg gcc
1603

Leu Ala Arg Ala Ser Gly Phe Thr Gly Ser Met Glu Gln Ser Ser Ala
490 495 500

aaa gct atg gaa cgg cat ttg cgt aag gtt cgt ttg cag att cag tcg
 1651
 Lys Ala Met Glu Arg His Leu Arg Lys Val Arg Leu Gln Ile Gln Ser
 505 510 515

ttg cat agt cag ctg ttt tat cgg cca ctg ctg aac tct gtg gtc aac
 1699
 Leu His Ser Gln Leu Phe Tyr Arg Pro Leu Leu Asn Ser Val Val Asn
 520 525 530

ttg agc gcg gat gcc atc agg ttg tct ccg gat gct gca aag cta caa
 1747
 Leu Ser Ala Asp Ala Ile Arg Leu Ser Pro Asp Ala Ala Lys Leu Gln
 535 540 545

ttg gcg gca ttg gga tac ctg cat cca tca cgt gct tat gaa cac ctg
 1795
 Leu Ala Ala Leu Gly Tyr Leu His Pro Ser Arg Ala Tyr Glu His Leu
 550 555 560 565

act gct ctt gca tca gga gct agc cgt aaa gcc aag att cag gcg atg
 1843
 Thr Ala Leu Ala Ser Gly Ala Ser Arg Lys Ala Lys Ile Gln Ala Met
 570 575 580

ttg ctg ccc acg ttg atg gag tgg ctg tct caa aca gct gaa cca gat
 1891
 Leu Leu Pro Thr Leu Met Glu Trp Leu Ser Gln Thr Ala Glu Pro Asp
 585 590 595

gcg gga ttg ctg aat tac cgc aag ctt tct gat gct tcc tat gat cgc
 1939
 Ala Gly Leu Leu Asn Tyr Arg Lys Leu Ser Asp Ala Ser Tyr Asp Arg
 600 605 610

agc tgg ttt ttg cgc atg ctg cgt gat gag ggc gta gtg ggg cag cgg
 1987
 Ser Trp Phe Leu Arg Met Leu Arg Asp Glu Gly Val Val Gly Gln Arg
 615 620 625

ttg atg cgt att ttg gga aat tct ccc tat att tct gaa ctg att atc
 2035
 Leu Met Arg Ile Leu Gly Asn Ser Pro Tyr Ile Ser Glu Leu Ile Ile
 630 635 640 645

tcc act ccg gac ttt atg aaa cag ctg ggt gat gcg gcg tct ggt cct
 2083
 Ser Thr Pro Asp Phe Met Lys Gln Leu Gly Asp Ala Ala Ser Gly Pro
 650 655 660

aaa ttg ctt gct act gca ccg act cag gtt gtg aaa gca atc aag gca
 2131
 Lys Leu Leu Ala Thr Ala Pro Thr Gln Val Val Lys Ala Ile Lys Ala
 665 670 675

acg gtg tcg cgt cat gag tca cct gat cgg gcg atc cag gct gca cga
 2179
 Thr Val Ser Arg His Glu Ser Pro Asp Arg Ala Ile Gln Ala Ala Arg
 680 685 690

tcg ctg agg agg cag gag ctg gca cgc att gcc tct gct gat ttg ctc
 2227
 Ser Leu Arg Arg Gln Glu Leu Ala Arg Ile Ala Ser Ala Asp Leu Leu
 695 700 705

aac atg ctc act gtt cag gaa gta tgc caa agc ttg tca cta gtc tgg
 2275
 Asn Met Leu Thr Val Gln Glu Val Cys Gln Ser Leu Ser Leu Val Trp
 710 715 720 725

gat gcg gtg ttg gat gct gcc ttg gat gcg gaa atc cgt gct gca ctt
 2323
 Asp Ala Val Leu Asp Ala Ala Leu Asp Ala Glu Ile Arg Ala Ala Leu
 730 735 740

aac gat cca cag aaa cca gat cag cct ctg gcc aat att tct gtg atc
 2371
 Asn Asp Pro Gln Lys Pro Asp Gln Pro Leu Ala Asn Ile Ser Val Ile
 745 750 755

ggc atg ggc cgt ttg ggt gga gca gaa ctt gga tac ggt tct gat gcc
 2419
 Gly Met Gly Arg Leu Gly Gly Ala Glu Leu Gly Tyr Gly Ser Asp Ala
 760 765 770

gat gtg atg ttt gta tgc gag ccg gta gcc ggt gtg gaa gag cat gag
 2467
 Asp Val Met Phe Val Cys Glu Pro Val Ala Gly Val Glu Glu His Glu
 775 780 785

gcc gtc aca tgg tct att gct atc tgt gat tcc atg cgg tcg agg ctt
 2515
 Ala Val Thr Trp Ser Ile Ala Ile Cys Asp Ser Met Arg Ser Arg Leu
 790 795 800 805

gcg cag cct tcc ggt gat cca cct ttg gag gtg gat ctg ggg ctg cgt
 2563
 Ala Gln Pro Ser Gly Asp Pro Pro Leu Glu Val Asp Leu Gly Leu Arg
 810 815 820

cct gaa ggg aga tct ggt gcg att gtg cgc acc gtt gat tcc tat gtg
 2611
 Pro Glu Gly Arg Ser Gly Ala Ile Val Arg Thr Val Asp Ser Tyr Val
 825 830 835

aag tac tac gaa aag tgg ggt gaa act tgg gag att cag gcg ctg ctg
 2659
 Lys Tyr Tyr Glu Lys Trp Gly Glu Thr Trp Glu Ile Gln Ala Leu Leu
 840 845 850

agg gct gcg tgg gtt gct ggt gat cgt gag ctg ggt att aag ttc ttg
 2707
 Arg Ala Ala Trp Val Ala Gly Asp Arg Glu Leu Gly Ile Lys Phe Leu
 855 860 865

gag tcg att gat cgt ttc cgc tac cca gtt gac ggg gca acg cag gcg
 2755
 Glu Ser Ile Asp Arg Phe Arg Tyr Pro Val Asp Gly Ala Thr Gln Ala
 870 875 880 885

WO 01/00843

PCT/IB00/00923

cag ctt cgt gaa gtt cgt cga att aag gcg agg gtg gat aat gag agg
 2803
 Gln Leu Arg Glu Val Arg Arg Ile Lys Ala Arg Val Asp Asn Glu Arg
 890 895 900

ctt ccg cgc ggg gct gat cga aat acc cat acc aag ctg ggt cgg gga
 2851
 Leu Pro Arg Gly Ala Asp Arg Asn Thr His Thr Lys Leu Gly Arg Gly
 905 910 915

gcg tta act gac atc gag tgg act gtg cag ttg ttg acc atg atg cat
 2899
 Ala Leu Thr Asp Ile Glu Trp Thr Val Gln Leu Leu Thr Met Met His
 920 925 930

gct cat gag att ccg gag ctg cac aat acg tcg acg ttg gaa gtt ctt
 2947
 Ala His Glu Ile Pro Glu Leu His Asn Thr Ser Thr Leu Glu Val Leu
 935 940 945

gaa gtg ctg gaa aag cat cag att att aac cct gtg cag gtg cag acg
 2995
 Glu Val Leu Glu Lys His Gln Ile Ile Asn Pro Val Gln Val Gln Thr
 950 955 960 965

ctt cgg gaa gcg tgg ctg acg gca acg gct gct agg aat gcg ctt gtg
 3043
 Leu Arg Glu Ala Trp Leu Thr Ala Thr Ala Ala Arg Asn Ala Leu Val
 970 975 980

ctg gtc agg ggt aag aga tta gat cag tta cct act cct ggt ccg cac
 3091
 Leu Val Arg Gly Lys Arg Leu Asp Gln Leu Pro Thr Pro Gly Pro His
 985 990 995

ctt gcg cag gtg gct ggt gcg tct ggt tgg gat cca aat gag tac cag
 3139
 Leu Ala Gln Val Ala Gly Ala Ser Gly Trp Asp Pro Asn Glu Tyr Gln
 1000 1005 1010

gag tat ttg gaa aac tat ctg aaa gtg acc agg aag agt cgt cag gtt
 3187
 Glu Tyr Leu Glu Asn Tyr Leu Lys Val Thr Arg Lys Ser Arg Gln Val
 1015 1020 1025

gtt gat gaa gtc ttc tgg ggt gtg gac tct atg gag caa cgt gag ttt
 3235
 Val Asp Glu Val Phe Trp Gly Val Asp Ser Met Glu Gln Arg Glu Phe
 1030 1035 1040 1045

taggtaggtg gtgggagccc caa
 3258

<210> 100

<211> 1045

<212> PRT

<213> Corynebacterium glutamicum

<400> 100

Met Ser Gly Pro Leu Arg Ser Glu Arg Lys Val Val Gly Phe Val Arg

WO 01/00843

PCT/IB00/00923

1	5	10	15
Asp Pro Leu Pro Lys Val Gly Ser Leu Ser Leu Lys Ser Glu His Ala	20	25	30
Gln Ala Asp Leu Glu His Leu Gly Trp Arg Asn Val Glu Ser Leu Asp	35	40	45
Leu Leu Trp Gly Leu Ser Gly Ala Gly Asp Pro Asp Val Ala Leu Asn	50	55	60
Leu Leu Ile Arg Leu Tyr Gln Ala Leu Glu Ala Ile Gly Glu Asp Ala	65	70	75
Arg Asn Glu Leu Asp Gln Glu Ile Arg Gln Asp Glu Lys Leu Arg Val	85	90	95
Arg Leu Phe Ala Leu Leu Gly Gly Ser Ser Ala Val Gly Asp His Leu	100	105	110
Val Ala Asn Pro Leu Gln Trp Lys Leu Leu Lys Leu Asp Ala Pro Ser	115	120	125
Arg Glu Glu Met Phe Gln Ala Leu Leu Glu Ser Val Lys Ala Gln Pro	130	135	140
Ala Val Leu Glu Val Glu Asp Phe Ser Asp Ala His Asn Ile Ala Arg	145	150	155
Asp Asp Leu Ser Thr Pro Gly Phe Tyr Thr Ala Ser Val Thr Gly Pro	165	170	175
Glu Ala Glu Arg Val Leu Lys Trp Thr Tyr Arg Thr Leu Leu Thr Arg	180	185	190
Ile Ala Ala His Asp Leu Ala Gly Thr Tyr Pro Thr Asp Met Arg Arg	195	200	205
Lys Gly Gly Asp Pro Val Pro Phe Ser Thr Val Thr Met Gln Leu Ser	210	215	220
Asp Leu Ala Asp Ala Ala Leu Thr Ala Ala Leu Ala Val Ala Ile Ala	225	230	235
Asn Val Tyr Gly Glu Lys Pro Val Asp Ser Ala Leu Ser Val Ile Ala	245	250	255
Met Gly Lys Cys Gly Ala Gln Glu Leu Asn Tyr Ile Ser Asp Val Asp	260	265	270
Val Val Phe Val Ala Glu Pro Ala Asn Ser Lys Ser Thr Arg Thr Ala	275	280	285
Ala Glu Leu Ile Arg Ile Gly Ser Asn Ser Phe Phe Glu Val Asp Ala	290	295	300
Ala Leu Arg Pro Glu Gly Lys Ser Gly Ala Leu Val Arg Ser Leu Asp	305	310	315
Ser His Met Ala Tyr Tyr Lys Arg Trp Ala Glu Thr Trp Glu Phe Gln	325	330	335

Ala Leu Leu Lys Ala Arg Pro Met Thr Gly Asp Ile Asn Leu Gly Gln
 340 345 350
 Ser Tyr Val Asp Ala Leu Ser Pro Leu Ile Trp Thr Ala Ser Gln Arg
 355 360 365
 Glu Ser Phe Val Thr Asp Val Gln Ala Met Arg Arg Arg Val Leu Asp
 370 375 380
 Asn Val Pro Glu Asp Leu Arg Asp Arg Glu Leu Lys Leu Gly Arg Gly
 385 390 395 400
 Gly Leu Arg Asp Val Glu Phe Ala Val Gln Leu Leu Gln Met Val His
 405 410 415
 Gly Arg Ile Asp Glu Thr Leu Arg Val Arg Ser Thr Val Asn Ala Leu
 420 425 430
 His Val Leu Val Asp Gln Gly Tyr Val Gly Arg Glu Asp Gly His Asn
 435 440 445
 Leu Ile Glu Ser Tyr Glu Phe Leu Arg Leu Leu Glu His Arg Leu Gln
 450 455 460
 Leu Glu Arg Ile Lys Arg Thr His Leu Leu Pro Lys Pro Asp Asp Arg
 465 470 475 480
 Met Asn Met Arg Trp Leu Ala Arg Ala Ser Gly Phe Thr Gly Ser Met
 485 490 495
 Glu Gln Ser Ser Ala Lys Ala Met Glu Arg His Leu Arg Lys Val Arg
 500 505 510
 Leu Gln Ile Gln Ser Leu His Ser Gln Leu Phe Tyr Arg Pro Leu Leu
 515 520 525
 Asn Ser Val Val Asn Leu Ser Ala Asp Ala Ile Arg Leu Ser Pro Asp
 530 535 540
 Ala Ala Lys Leu Gln Leu Ala Ala Leu Gly Tyr Leu His Pro Ser Arg
 545 550 555 560
 Ala Tyr Glu His Leu Thr Ala Leu Ala Ser Gly Ala Ser Arg Lys Ala
 565 570 575
 Lys Ile Gln Ala Met Leu Leu Pro Thr Leu Met Glu Trp Leu Ser Gln
 580 585 590
 Thr Ala Glu Pro Asp Ala Gly Leu Leu Asn Tyr Arg Lys Leu Ser Asp
 595 600 605
 Ala Ser Tyr Asp Arg Ser Trp Phe Leu Arg Met Leu Arg Asp Glu Gly
 610 615 620
 Val Val Gly Gln Arg Leu Met Arg Ile Leu Gly Asn Ser Pro Tyr Ile
 625 630 635 640
 Ser Glu Leu Ile Ile Ser Thr Pro Asp Phe Met Lys Gln Leu Gly Asp
 645 650 655

WO 01/00843

PCT/IB00/00923

Ala	Ala	Ser	Gly	Pro	Lys	Leu	Leu	Ala	Thr	Ala	Pro	Thr	Gln	Val	Val			
			660					665					670					
Lys	Ala	Ile	Lys	Ala	Thr	Val	Ser	Arg	His	Glu	Ser	Pro	Asp	Arg	Ala			
		675					680					685						
Ile	Gln	Ala	Ala	Arg	Ser	Leu	Arg	Arg	Gln	Glu	Leu	Ala	Arg	Ile	Ala			
	690					695					700							
Ser	Ala	Asp	Leu	Leu	Asn	Met	Leu	Thr	Val	Gln	Glu	Val	Cys	Gln	Ser			
705					710					715					720			
Leu	Ser	Leu	Val	Trp	Asp	Ala	Val	Leu	Asp	Ala	Ala	Leu	Asp	Ala	Glu			
				725					730					735				
Ile	Arg	Ala	Ala	Leu	Asn	Asp	Pro	Gln	Lys	Pro	Asp	Gln	Pro	Leu	Ala			
		740						745					750					
Asn	Ile	Ser	Val	Ile	Gly	Met	Gly	Arg	Leu	Gly	Gly	Ala	Glu	Leu	Gly			
		755					760					765						
Tyr	Gly	Ser	Asp	Ala	Asp	Val	Met	Phe	Val	Cys	Glu	Pro	Val	Ala	Gly			
	770					775					780							
Val	Glu	Glu	His	Glu	Ala	Val	Thr	Trp	Ser	Ile	Ala	Ile	Cys	Asp	Ser			
785					790					795					800			
Met	Arg	Ser	Arg	Leu	Ala	Gln	Pro	Ser	Gly	Asp	Pro	Pro	Leu	Glu	Val			
				805					810					815				
Asp	Leu	Gly	Leu	Arg	Pro	Glu	Gly	Arg	Ser	Gly	Ala	Ile	Val	Arg	Thr			
			820					825					830					
Val	Asp	Ser	Tyr	Val	Lys	Tyr	Tyr	Glu	Lys	Trp	Gly	Glu	Thr	Trp	Glu			
		835					840					845						
Ile	Gln	Ala	Leu	Leu	Arg	Ala	Ala	Trp	Val	Ala	Gly	Asp	Arg	Glu	Leu			
	850					855					860							
Gly	Ile	Lys	Phe	Leu	Glu	Ser	Ile	Asp	Arg	Phe	Arg	Tyr	Pro	Val	Asp			
865					870					875					880			
Gly	Ala	Thr	Gln	Ala	Gln	Leu	Arg	Glu	Val	Arg	Arg	Ile	Lys	Ala	Arg			
				885					890					895				
Val	Asp	Asn	Glu	Arg	Leu	Pro	Arg	Gly	Ala	Asp	Arg	Asn	Thr	His	Thr			
			900					905					910					
Lys	Leu	Gly	Arg	Gly	Ala	Leu	Thr	Asp	Ile	Glu	Trp	Thr	Val	Gln	Leu			
		915					920					925						
Leu	Thr	Met	Met	His	Ala	His	Glu	Ile	Pro	Glu	Leu	His	Asn	Thr	Ser			
	930					935					940							
Thr	Leu	Glu	Val	Leu	Glu	Val	Leu	Glu	Lys	His	Gln	Ile	Ile	Asn	Pro			
945					950					955					960			
Val	Gln	Val	Gln	Thr	Leu	Arg	Glu	Ala	Trp	Leu	Thr	Ala	Thr	Ala	Ala			
				965					970					975				
Arg	Asn	Ala	Leu	Val	Leu	Val	Arg	Gly	Lys	Arg	Leu	Asp	Gln	Leu	Pro			

980	985	990
Thr Pro Gly Pro His Leu Ala Gln Val Ala Gly Ala Ser Gly Trp Asp		
995	1000	1005
Pro Asn Glu Tyr Gln Glu Tyr Leu Glu Asn Tyr Leu Lys Val Thr Arg		
1010	1015	1020
Lys Ser Arg Gln Val Val Asp Glu Val Phe Trp Gly Val Asp Ser Met		
1025	1030	1035
		1040
Glu Gln Arg Glu Phe		
	1045	

<210> 101
 <211> 861
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(861)
 <223> RXN03176

<400> 101

gag ttg gcc gat tac atc ccg gaa cta aaa tct gcg gac cca aac ccg	48
Glu Leu Ala Asp Tyr Ile Pro Glu Leu Lys Ser Ala Asp Pro Asn Pro	
1 5 10 15	
ctg gca gta gcc ctg tgc acc gtt aac gga cac atc tac agc gca ggc	96
Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly	
20 25 30	
gat gac gac atc gaa ttc acc atg caa agt att tcc aag cca ttt gcc	144
Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala	
35 40 45	
tac gca ctc gca ctc caa gaa tgc ggc ttt gat gag gtc tct gca tcc	192
Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser	
50 55 60	
gtg gcc ttg gag ccc tcc ggt gag gcc ttc aac gaa ctt tcc ctc gac	240
Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp	
65 70 75 80	
ggc gaa aac cgc ccc atg aac ccc atg atc aac gcc ggc gcg atc gcc	288
Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala	
85 90 95	
atc aac cag ctg atc aac ggc tcc gat tcc acc gtg gaa gac cgc gtg	336
Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val	
100 105 110	
gaa aaa atc cga cac tac ttc tct gaa ctt gct gga cgc gaa ctc acc	384
Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr	
115 120 125	
atc gac cgc gtg ctt gcc gaa tcc gaa ctc gcc ggc gcc gac cgc aac	432
Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn	
130 135 140	


```

ctc tcc atc gcc cac atg ctg cgc aat tac ggc gtc atc gaa gac gaa 480
Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu
145                      150                      155                      160

gcc cac gac gcc gtc ctc agc tac acg ctg caa tgc gcc atc aaa gta 528
Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val
165                      170                      175

acc acg cgc gac ctc gca gtc atg acc gcc acg ctc gcc gcc ggc ggc 576
Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly
180                      185                      190

aca cac cca att acc ggc aag aag ctt ctc gac gcc cgc gtc tgc cgc 624
Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg
195                      200                      205

ctc acc ctc tcc gtc atg gct tca gca ggc atg tac gac gag gca ggg 672
Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly
210                      215                      220

cag tgg ctc tcc acc gta ggc atc ccc gcg aaa tca gga gtc gcc ggc 720
Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly
225                      230                      235

gga ctc atc ggc att ctg cca ggt cag ctg ggc atc gcc aca ttt tcc 768
Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser
245                      250                      255

cca cgc ctg aac ccc aaa ggc aac agc gtg cgc ggc gta aaa ata ttc 816
Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe
260                      265                      270

aaa cag ctt tcc gac gac atg ggc ctc cac ctc atg tcc acc gag 861
Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu
275                      280                      285

```

<210> 102

<211> 287

<212> PRT

<213> Corynebacterium glutamicum

<400> 102

```

Glu Leu Ala Asp Tyr Ile Pro Glu Leu Lys Ser Ala Asp Pro Asn Pro
 1                      5                      10                      15

Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly
20                      25                      30

Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala
35                      40                      45

Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser
50                      55                      60

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

Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala
85                      90                      95

```


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

<210> 103

<211> 861

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(861)

<223> FRXA02879

<400> 103

gag ttg gcc gat tac atc ccg gaa cta aaa tct gcg gac cca aac ccg 48
 Glu Leu Ala Asp Tyr Ile Pro Glu Leu Lys Ser Ala Asp Pro Asn Pro
 1 5 10 15

ctg gca gta gcc ctg tgc acc gtt aac gga cac atc tac agc gca ggc 96
 Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly
 20 25 30

gat gac gac atc gaa ttc acc atg caa agt att tcc aag cca ttt gcc 144
 Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala
 35 40 45

tac gca ctc gca ctc caa gaa tgc ggc ttt gat gag gtc tct gca tcc	192
Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser	
50 55 60	
gtg gcc ttg gag ccc tcc ggt gag gcc ttc aac gaa ctt tcc ctc gac	240
Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp	
65 70 75 80	
ggc gaa aac cgc ccc atg aac ccc atg atc aac gcc ggc gcg atc gcc	288
Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala	
85 90 95	
atc aac cag ctg atc aac ggc tcc gat tcc acc gtg gaa gac cgc gtg	336
Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val	
100 105 110	
gaa aaa atc cga cac tac ttc tct gaa ctt gct gga cgc gaa ctc acc	384
Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr	
115 120 125	
atc gac cgc gtg ctt gcc gaa tcc gaa ctc gcc ggc gcc gac cgc aac	432
Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn	
130 135 140	
ctc tcc atc gcc cac atg ctg cgc aat tac ggc gtc atc gaa gac gaa	480
Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu	
145 150 155 160	
gcc cac gac gcc gtc ctc agc tac acg ctg caa tgc gcc atc aaa gta	528
Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val	
165 170 175	
acc acg cgc gac ctc gca gtc atg acc gcc acg ctc gcc gcc ggc ggc	576
Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly	
180 185 190	
aca cac cca att acc ggc aag aag ctt ctc gac gcc cgc gtc tgc cgc	624
Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg	
195 200 205	
ctc acc ctc tcc gtc atg gct tca gca ggc atg tac gac gag gca ggg	672
Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly	
210 215 220	
cag tgg ctc tcc acc gta ggc atc ccc gcg aaa tca gga gtc gcc ggc	720
Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly	
225 230 235 240	
gga ctc atc ggc att ctg cca ggt cag ctg ggc atc gcc aca ttt tcc	768
Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser	
245 250 255	
cca cgc ctg aac ccc aaa ggc aac agc gtg cgc ggc gta aaa ata ttc	816
Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe	
260 265 270	
aaa cag ctt tcc gac gac atg ggc ctc cac ctc atg tcc acc gag	861
Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu	
275 280 285	

WO 01/00843

PCT/IB00/00923

<210> 104

<211> 287

<212> PRT

<213> Corynebacterium glutamicum

<400> 104

Glu Leu Ala Asp Tyr Ile Pro Glu Leu Lys Ser Ala Asp Pro Asn Pro
 1 5 10 15

Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly
 20 25 30

Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala
 35 40 45

Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser
 50 55 60

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

Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala
 85 90 95

Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val
 100 105 110

Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr
 115 120 125

Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn
 130 135 140

Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu
 145 150 155 160

Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val
 165 170 175

Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly
 180 185 190

Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg
 195 200 205

Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly
 210 215 220

Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly
 225 230 235 240

Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser
 245 250 255

Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe
 260 265 270

Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu
 275 280 285

<400> 105																
ggccacggag ttggtgtccg tcatggtgat gattctgtct gtcgtttctg tgttggcttt																60
gtgggtcggc atccgcccc gtttgcagga gtacttataa atg cac gct ttt cga																115
Met His Ala Phe Arg																
1 5																
cgc ccc cct cca ctc acc acg cga gtc ggc gct gca ttg ctg gcc gca																163
Arg Pro Pro Pro Leu Thr Thr Arg Val Gly Ala Ala Leu Leu Ala Ala																
10 15 20																
acg ctg ctt gct tcc tgc act cca aca cct gtg gaa ccg gca gaa acc																211
Thr Leu Leu Ala Ser Cys Thr Pro Thr Pro Val Glu Pro Ala Glu Thr																
25 30 35																
ttg act gct ttg gat ccc gat gcc ggt cca cca ctg cca ccg gat tct																259
Leu Thr Ala Leu Asp Pro Asp Ala Gly Pro Pro Leu Pro Pro Asp Ser																
40 45 50																
tcg att gaa gct ccc ggt gaa aaa gag ccc att gtg gaa gta ata gag																307
Ser Ile Glu Ala Pro Gly Glu Lys Glu Pro Ile Val Glu Val Ile Glu																
55 60 65																
aat tgg cca ggt tct tta cgc ccg gat gat ctg acc cct gag gag cgg																355
Asn Trp Pro Gly Ser Leu Arg Pro Asp Asp Leu Thr Pro Glu Glu Arg																
70 75 80 85																
gta cct ggc atc gtc aac cgg ggt cgc atc att gtg ggt gtg gat caa																403
Val Pro Gly Ile Val Asn Arg Gly Arg Ile Ile Val Gly Val Asp Gln																
90 95 100																
tcg caa aac ttg ctc agt ttc cgt gat ccg gtg act ggt gag ctg cgc																451
Ser Gln Asn Leu Leu Ser Phe Arg Asp Pro Val Thr Gly Glu Leu Arg																
105 110 115																
ggg ttt gaa gtg gaa tta gcg agg gaa att tcc cgc gac att ttc ggt																499
Gly Phe Glu Val Glu Leu Ala Arg Glu Ile Ser Arg Asp Ile Phe Gly																
120 125 130																
gac ccc aat aag gtg gat ttc cga ttc gtc ggc tcg tcc gac cgt ctg																547
Asp Pro Asn Lys Val Asp Phe Arg Phe Val Gly Ser Ser Asp Arg Leu																
135 140 145																
cgt tcc ctt gac caa ggt gat gta gat att gtg att cgt tcc gtc acg																595
Arg Ser Leu Asp Gln Gly Asp Val Asp Ile Val Ile Arg Ser Val Thr																
150 155 160 165																
atc acc gac gaa cgc gcc aaa ttg gtg gaa ttt tcc aca ccg tac ctg																643
Ile Thr Asp Glu Arg Ala Lys Leu Val Glu Phe Ser Thr Pro Tyr Leu																
170 175 180																

WO 01/00843

PCT/IB00/00923

cgc acc caa acc cgc atg ttg acc atg gaa tct tca gga atc acg tcc 691
 Arg Thr Gln Thr Arg Met Leu Thr Met Glu Ser Ser Gly Ile Thr Ser
 185 190 195

atc gca gat cta ccc ggc cac acc att tgt gtc acc gat ggc tcc act 739
 Ile Ala Asp Leu Pro Gly His Thr Ile Cys Val Thr Asp Gly Ser Thr
 200 205 210

tca ttg cag cga gcc cgc acc att gcg ccg gag gcc tca atc tta aaa 787
 Ser Leu Gln Arg Ala Arg Thr Ile Ala Pro Glu Ala Ser Ile Leu Lys
 215 220 225

act cgc aat tgg tcc gat tgt ctc atg gcg ttg cag cag cat cag gct 835
 Thr Arg Asn Trp Ser Asp Cys Leu Met Ala Leu Gln Gln His Gln Ala
 230 235 240 245

cag gtc att ttg ggc gat gat gtc att ttg tcc ggc atc gca gca cag 883
 Gln Val Ile Leu Gly Asp Asp Val Ile Leu Ser Gly Ile Ala Ala Gln
 250 255 260

gat ccc tac acc gag att ctt gat acc tcc ctc gat tcc cat tcc tat 931
 Asp Pro Tyr Thr Glu Ile Leu Asp Thr Ser Leu Asp Ser His Ser Tyr
 265 270 275

gga gtg gca gcg gca tcg acc act gct gaa aca gac tct tcg ggg ttg 979
 Gly Val Ala Ala Ala Ser Thr Thr Ala Glu Thr Asp Ser Ser Gly Leu
 280 285 290

att cgg cag gta aac tac aca att gaa cgg atc cgc aca gac cgc atg
 1027
 Ile Arg Gln Val Asn Tyr Thr Ile Glu Arg Ile Arg Thr Asp Arg Met
 295 300 305

tgg tgg aca atg ttc gac gat tgg ttc gga cct tat ctc tgg tcc tac
 1075
 Trp Trp Thr Met Phe Asp Asp Trp Phe Gly Pro Tyr Leu Trp Ser Tyr
 310 315 320 325

ggt cca cca cag ctg cag tac atg cca gag gaa gaa ggg aca gaa aac
 1123
 Gly Pro Pro Gln Leu Gln Tyr Met Pro Glu Glu Glu Gly Thr Glu Asn
 330 335 340

gat gaa gga taatgaagat ttcgatccag att
 1155
 Asp Glu Gly

<210> 106

<211> 344

<212> PRT

<213> Corynebacterium glutamicum

<400> 106

Met His Ala Phe Arg Arg Pro Pro Pro Leu Thr Thr Arg Val Gly Ala
 1 5 10 15

Ala Leu Leu Ala Ala Thr Leu Leu Ala Ser Cys Thr Pro Thr Pro Val
 20 25 30

WO 01/00843

PCT/IB00/00923

Glu Pro Ala Glu Thr Leu Thr Ala Leu Asp Pro Asp Ala Gly Pro Pro
 35 40 45
 Leu Pro Pro Asp Ser Ser Ile Glu Ala Pro Gly Glu Lys Glu Pro Ile
 50 55 60
 Val Glu Val Ile Glu Asn Trp Pro Gly Ser Leu Arg Pro Asp Asp Leu
 65 70 75 80
 Thr Pro Glu Glu Arg Val Pro Gly Ile Val Asn Arg Gly Arg Ile Ile
 85 90 95
 Val Gly Val Asp Gln Ser Gln Asn Leu Leu Ser Phe Arg Asp Pro Val
 100 105 110
 Thr Gly Glu Leu Arg Gly Phe Glu Val Glu Leu Ala Arg Glu Ile Ser
 115 120 125
 Arg Asp Ile Phe Gly Asp Pro Asn Lys Val Asp Phe Arg Phe Val Gly
 130 135 140
 Ser Ser Asp Arg Leu Arg Ser Leu Asp Gln Gly Asp Val Asp Ile Val
 145 150 155 160
 Ile Arg Ser Val Thr Ile Thr Asp Glu Arg Ala Lys Leu Val Glu Phe
 165 170 175
 Ser Thr Pro Tyr Leu Arg Thr Gln Thr Arg Met Leu Thr Met Glu Ser
 180 185 190
 Ser Gly Ile Thr Ser Ile Ala Asp Leu Pro Gly His Thr Ile Cys Val
 195 200 205
 Thr Asp Gly Ser Thr Ser Leu Gln Arg Ala Arg Thr Ile Ala Pro Glu
 210 215 220
 Ala Ser Ile Leu Lys Thr Arg Asn Trp Ser Asp Cys Leu Met Ala Leu
 225 230 235 240
 Gln Gln His Gln Ala Gln Val Ile Leu Gly Asp Asp Val Ile Leu Ser
 245 250 255
 Gly Ile Ala Ala Gln Asp Pro Tyr Thr Glu Ile Leu Asp Thr Ser Leu
 260 265 270
 Asp Ser His Ser Tyr Gly Val Ala Ala Ala Ser Thr Thr Ala Glu Thr
 275 280 285
 Asp Ser Ser Gly Leu Ile Arg Gln Val Asn Tyr Thr Ile Glu Arg Ile
 290 295 300
 Arg Thr Asp Arg Met Trp Trp Thr Met Phe Asp Asp Trp Phe Gly Pro
 305 310 315 320
 Tyr Leu Trp Ser Tyr Gly Pro Pro Gln Leu Gln Tyr Met Pro Glu Glu
 325 330 335
 Glu Gly Thr Glu Asn Asp Glu Gly
 340

<400> 107																
ttattgcacc	atggcaggta	gtatttttgcc	catgattgag	agtttcaccc	gattgcgaat											60
ttcgcagaca cgcctctga aacggctact gcatagcact																115
				ttg	cgt	ttc	ccc	aaa								
				Leu	Arg	Phe	Pro	Lys								
				1				5								
atc	ccc	aag	cgc	gct	gta	gcg	gcg	acc	gtc	ggc	atc	gtg	gca	acc	tca	163
Ile	Pro	Lys	Arg	Ala	Val	Ala	Ala	Thr	Val	Gly	Ile	Val	Ala	Thr	Ser	
				10					15					20		
ttc	acc	ttg	gct	tct	tgt	gtc	acc	aat	gag	gag	cag	ggc	aac	cca	gat	211
Phe	Thr	Leu	Ala	Ser	Cys	Val	Thr	Asn	Glu	Glu	Gln	Gly	Asn	Pro	Asp	
			25					30					35			
ggc	tgg	gag	cag	atc	gtt	cca	gat	cct	gta	ccg	gag	att	cag	gcg	atg	259
Gly	Trp	Glu	Gln	Ile	Val	Pro	Asp	Pro	Val	Pro	Glu	Ile	Gln	Ala	Met	
		40					45					50				
gtt	ccc	gaa	gct	ctg	gct	cag	cgc	ggt	gtg	ctc	acc	gcc	ggt	gcc	aac	307
Val	Pro	Glu	Ala	Leu	Ala	Gln	Arg	Gly	Val	Leu	Thr	Ala	Gly	Ala	Asn	
	55					60					65					
cca	cct	ttc	cca	ccg	ttt	gag	ttt	aaa	gat	tcc	gat	ggt	cag	att	atc	355
Pro	Pro	Phe	Pro	Pro	Phe	Glu	Phe	Lys	Asp	Ser	Asp	Gly	Gln	Ile	Ile	
70					75				80						85	
ggt	gtg	gaa	atg	gac	ctc	gtg	cgt	gca	atg	gcg	ggg	gtg	atg	ggc	ttg	403
Gly	Val	Glu	Met	Asp	Leu	Val	Arg	Ala	Met	Ala	Gly	Val	Met	Gly	Leu	
				90					95					100		
gag	ttc	agc	cct	cag	gag	cag	gat	ttc	tcc	ctc	atc	ctt	cca	tcg	gtt	451
Glu	Phe	Ser	Pro	Gln	Glu	Gln	Asp	Phe	Ser	Leu	Ile	Leu	Pro	Ser	Val	
			105					110					115			
caa	gct	ggc	acc	ctt	gat	atc	gga	gcc	tct	ggc	ttc	act	gac	aac	gag	499
Gln	Ala	Gly	Thr	Leu	Asp	Ile	Gly	Ala	Ser	Gly	Phe	Thr	Asp	Asn	Glu	
		120					125					130				
gaa	cgc	cgc	gag	aac	ttt	gat	ttc	atc	gat	ttc	ctc	ttc	gca	ggt	gtg	547
Glu	Arg	Arg	Glu	Asn	Phe	Asp	Phe	Ile	Asp	Phe	Leu	Phe	Ala	Gly	Val	
	135					140					145					
cag	tgg	gcg	cag	gca	act	gat	cgt	gaa	acc	cca	atc	gat	ccg	gaa	aac	595
Gln	Trp	Ala	Gln	Ala	Thr	Asp	Arg	Glu	Thr	Pro	Ile	Asp	Pro	Glu	Asn	
150					155					160					165	
gcc	tgt	ggt	ctc	acc	gtt	gct	gta	cag	cgc	aca	acc	gtg	gca	gag	acc	643
Ala	Cys	Gly	Leu	Thr	Val	Ala	Val	Gln	Arg	Thr	Thr	Val	Ala	Glu	Thr	
				170					175					180		

WO 01/00843

PCT/IB00/00923

gac gat gtc cgt cct cgc tca gct caa tgt gaa gcc gaa ggc aaa gag 691
 Asp Asp Val Arg Pro Arg Ser Ala Gln Cys Glu Ala Glu Gly Lys Glu
 185 190 195
 ccg atc acc att ttg tct tat gaa acc gca gat act gca gct acc gca 739
 Pro Ile Thr Ile Leu Ser Tyr Glu Thr Ala Asp Thr Ala Ala Thr Ala
 200 205 210
 ttg atc ctg gga cgc gca gac gca ctt gct gcg gac tcc cct gtt tca 787
 Leu Ile Leu Gly Arg Ala Asp Ala Leu Ala Ala Asp Ser Pro Val Ser
 215 220 225
 gct tgg gct gca gag cgc tcc gaa ggc cgc atc gaa gtt gtg ggc gat 835
 Ala Trp Ala Ala Glu Arg Ser Glu Gly Arg Ile Glu Val Val Gly Asp
 230 235 240 245
 atg tac ttg gct gcg cca ttt ggt ttc gca ttc ccg ttg gaa tct gac 883
 Met Tyr Leu Ala Ala Pro Phe Gly Phe Ala Phe Pro Leu Glu Ser Asp
 250 255 260
 ctc acc cca gca gca gct gcg gcg ttc caa cac ttg att gac acc ggc 931
 Leu Thr Pro Ala Ala Ala Ala Ala Phe Gln His Leu Ile Asp Thr Gly
 265 270 275
 gat tac cag cgc atc atg gcg caa tgg ggc att gaa gaa ggc ctt ctt 979
 Asp Tyr Gln Arg Ile Met Ala Gln Trp Gly Ile Glu Glu Gly Leu Leu
 280 285 290
 gat gag gcc ctg atc aac gaa cag cca ctc aac tagagccttc cagcaactaa
 1032
 Asp Glu Ala Leu Ile Asn Glu Gln Pro Leu Asn
 295 300

aaa
 1035

<210> 108
 <211> 304
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 108
 Leu Arg Phe Pro Lys Ile Pro Lys Arg Ala Val Ala Ala Thr Val Gly
 1 5 10 15
 Ile Val Ala Thr Ser Phe Thr Leu Ala Ser Cys Val Thr Asn Glu Glu
 20 25 30
 Gln Gly Asn Pro Asp Gly Trp Glu Gln Ile Val Pro Asp Pro Val Pro
 35 40 45
 Glu Ile Gln Ala Met Val Pro Glu Ala Leu Ala Gln Arg Gly Val Leu
 50 55 60
 Thr Ala Gly Ala Asn Pro Pro Phe Pro Pro Phe Glu Phe Lys Asp Ser
 65 70 75 80
 Asp Gly Gln Ile Ile Gly Val Glu Met Asp Leu Val Arg Ala Met Ala
 85 90 95

WO 01/00843

PCT/IB00/00923

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

<210> 109
 <211> 1962
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1939)
 <223> RXA02139

<400> 109
 tcaggaggat ttttcaatca tgtgcggcct tcttggcata ttgactgcaa atgggaacgc 60
 tgaagcattc gttcctgcac tcgagcgggc cttgccatgc atg cgc cac cgt ggt 115
 Met Arg His Arg Gly
 1 5
 cct gac gat gcc ggc act tgg cat gac gcc gat gca gcg ttt gga ttc 163

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

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

WO 01/00843

PCT/IB00/00923

gat ctg ttc acc tgg atg cgc ggc gac atc ctg gtc aag gct gac aag
1507

Asp Leu Phe Thr Trp Met Arg Gly Asp Ile Leu Val Lys Ala Asp Lys
455 460 465

atc aac atg gcg aac tcc ctt gag ctg cga gtt cca ttc ttg gat aag
1555

Ile Asn Met Ala Asn Ser Leu Glu Leu Arg Val Pro Phe Leu Asp Lys
470 475 480 485

gaa gtt ttc aag gtt gca gag acc att cct tac gac ctg aag att gcc
1603

Glu Val Phe Lys Val Ala Glu Thr Ile Pro Tyr Asp Leu Lys Ile Ala
490 495 500

aac ggt acc acc aag tac gcg ctg cgc agg gca ctc gag cag att gtt
1651

Asn Gly Thr Thr Lys Tyr Ala Leu Arg Arg Ala Leu Glu Gln Ile Val
505 510 515

ccg cct cac gtt ttg cac cgc aag aag ctg ggc ttc cct gtt ccc atg
1699

Pro Pro His Val Leu His Arg Lys Lys Leu Gly Phe Pro Val Pro Met
520 525 530

cgc cac tgg ctt gcc ggc gat gag ctg ttc ggt tgg gcg cag gac acc
1747

Arg His Trp Leu Ala Gly Asp Glu Leu Phe Gly Trp Ala Gln Asp Thr
535 540 545

atc aag gaa tcc ggt act gaa gat atc ttc aac aag cag gct gtg ctg
1795

Ile Lys Glu Ser Gly Thr Glu Asp Ile Phe Asn Lys Gln Ala Val Leu
550 555 560 565

gat atg ctg aac gag cac cgc gat ggc gtg tca gat cat tcc cgt cga
1843

Asp Met Leu Asn Glu His Arg Asp Gly Val Ser Asp His Ser Arg Arg
570 575 580

ctg tgg act gtt ctg tca ttt atg gtg tgg cac ggc att ttt gtg gaa
1891

Leu Trp Thr Val Leu Ser Phe Met Val Trp His Gly Ile Phe Val Glu
585 590 595

aac cgc att gat cca cag att gag gac cgc tcc tac cca gtc gag ctt
1939

Asn Arg Ile Asp Pro Gln Ile Glu Asp Arg Ser Tyr Pro Val Glu Leu
600 605 610

taagtcttaa agcctaaacc ccc
1962

<210> 110

<211> 613

<212> PRT

<213> Corynebacterium glutamicum

<400> 110

Met Arg His Arg Gly Pro Asp Asp Ala Gly Thr Trp His Asp Ala Asp

WO 01/00843

PCT/IB00/00923

1	5	10	15
Ala Ala Phe Gly Phe Asn Arg Leu Ser Ile Ile Asp Ile Ala His Ser	20	25	30
His Gln Pro Leu Arg Trp Gly Pro Ala Asp Glu Pro Asp Arg Tyr Ala	35	40	45
Met Thr Phe Asn Gly Glu Ile Tyr Asn Tyr Val Glu Leu Arg Lys Glu	50	55	60
Leu Ser Asp Leu Gly Tyr Ala Phe Asn Thr Ser Gly Asp Gly Glu Pro	65	70	75
Ile Val Val Gly Phe His His Trp Gly Glu Ser Val Val Glu His Leu	85	90	95
Arg Gly Met Phe Gly Ile Ala Ile Trp Asp Thr Lys Glu Lys Ser Leu	100	105	110
Phe Leu Ala Arg Asp Gln Phe Gly Ile Lys Pro Leu Phe Tyr Ala Thr	115	120	125
Thr Glu His Gly Thr Val Phe Ser Ser Glu Lys Lys Thr Ile Leu Glu	130	135	140
Met Ala Glu Glu Met Asn Leu Asp Leu Gly Leu Asp Lys Arg Thr Ile	145	150	155
Glu His Tyr Val Asp Leu Gln Tyr Val Pro Glu Pro Asp Thr Leu His	165	170	175
Ala Gln Ile Ser Arg Leu Glu Ser Gly Cys Thr Ala Thr Val Arg Pro	180	185	190
Gly Gly Lys Leu Glu Gln Lys Arg Tyr Phe Lys Pro Gln Phe Pro Val	195	200	205
Gln Lys Val Val Lys Gly Lys Glu Gln Asp Leu Phe Asp Arg Ile Ala	210	215	220
Gln Val Leu Glu Asp Ser Val Glu Lys His Met Arg Ala Asp Val Thr	225	230	235
Val Gly Ser Phe Leu Phe Gly Gly Ile Asp Ser Thr Ala Ile Ala Ala	245	250	255
Leu Ala Lys Arg His Asn Pro Asp Leu Leu Thr Phe Thr Thr Gly Phe	260	265	270
Glu Arg Glu Gly Tyr Ser Glu Val Asp Val Ala Ala Glu Ser Ala Ala	275	280	285
Ala Ile Gly Ala Glu His Ile Val Lys Ile Val Ser Pro Glu Glu Tyr	290	295	300
Ala Asn Ala Ile Pro Lys Ile Met Trp Tyr Leu Asp Asp Pro Val Ala	305	310	315
Asp Pro Ser Leu Val Pro Leu Tyr Phe Val Ala Ala Glu Ala Arg Lys	325	330	335

WO 01/00843

PCT/IB00/00923

His Val Lys Val Val Leu Ser Gly Glu Gly Ala Asp Glu Leu Phe Gly
 340 345 350
 Gly Tyr Thr Ile Tyr Lys Glu Pro Leu Ser Leu Ala Pro Phe Glu Lys
 355 360 365
 Ile Pro Ser Pro Leu Arg Lys Gly Leu Gly Lys Leu Ser Lys Val Leu
 370 375 380
 Pro Asp Gly Met Lys Gly Lys Ser Leu Leu Glu Arg Gly Ser Met Thr
 385 390 395 400
 Met Glu Glu Arg Tyr Tyr Gly Asn Ala Arg Ser Phe Asn Phe Glu Gln
 405 410 415
 Met Gln Arg Val Ile Pro Trp Ala Lys Arg Glu Trp Asp His Arg Glu
 420 425 430
 Val Thr Ala Pro Ile Tyr Ala Gln Ser Arg Asn Phe Asp Pro Val Ala
 435 440 445
 Arg Met Gln His Leu Asp Leu Phe Thr Trp Met Arg Gly Asp Ile Leu
 450 455 460
 Val Lys Ala Asp Lys Ile Asn Met Ala Asn Ser Leu Glu Leu Arg Val
 465 470 475 480
 Pro Phe Leu Asp Lys Glu Val Phe Lys Val Ala Glu Thr Ile Pro Tyr
 485 490 495
 Asp Leu Lys Ile Ala Asn Gly Thr Thr Lys Tyr Ala Leu Arg Arg Ala
 500 505 510
 Leu Glu Gln Ile Val Pro Pro His Val Leu His Arg Lys Lys Leu Gly
 515 520 525
 Phe Pro Val Pro Met Arg His Trp Leu Ala Gly Asp Glu Leu Phe Gly
 530 535 540
 Trp Ala Gln Asp Thr Ile Lys Glu Ser Gly Thr Glu Asp Ile Phe Asn
 545 550 555 560
 Lys Gln Ala Val Leu Asp Met Leu Asn Glu His Arg Asp Gly Val Ser
 565 570 575
 Asp His Ser Arg Arg Leu Trp Thr Val Leu Ser Phe Met Val Trp His
 580 585 590
 Gly Ile Phe Val Glu Asn Arg Ile Asp Pro Gln Ile Glu Asp Arg Ser
 595 600 605
 Tyr Pro Val Glu Leu
 610

<210> 111

<211> 1284

<212> DNA

<213> Corynebacterium glutamicum

WO 01/00843

PCT/IB00/00923

<220>

<221> CDS

<222> (101)..(1261)

<223> RXN00116

<400> 111

cgcggcacgc acgctggggg caagcgtcga caagcacaaa ctttttgctt aattgaatcc 60

tttgcgcacc	aatcaatggg	ggatcaaata	tagtagctgc	atg	agt	aat	gac	ttc		115
				Met	Ser	Asn	Asp	Phe		
				1				5		

gtc	gtt	tct	agg	ctt	aga	ccc	ttt	ggt	gaa	acg	att	ttt	gca	acc	atg	163
Val	Val	Ser	Arg	Leu	Arg	Pro	Phe	Gly	Glu	Thr	Ile	Phe	Ala	Thr	Met	
				10				15						20		

acc	cag	cga	gct	gtt	gag	gcg	ggt	gca	atc	aat	ctt	ggt	cag	ggc	ttt	211
Thr	Gln	Arg	Ala	Val	Glu	Ala	Gly	Ala	Ile	Asn	Leu	Gly	Gln	Gly	Phe	
			25				30						35			

cct	gat	gag	gat	ggt	cct	cgt	cgg	atg	tta	gag	atc	gcg	tcg	gag	cag	259
Pro	Asp	Glu	Asp	Gly	Pro	Arg	Arg	Met	Leu	Glu	Ile	Ala	Ser	Glu	Gln	
		40				45						50				

att	ctc	ggg	gga	aat	aat	cag	tat	tcg	gcg	ggg	cgt	ggg	gat	gct	tcg	307
Ile	Leu	Gly	Gly	Asn	Asn	Gln	Tyr	Ser	Ala	Gly	Arg	Gly	Asp	Ala	Ser	
	55					60					65					

ttg	agg	gca	gct	gtg	gct	cgt	gat	cat	ttg	gag	agg	ttt	gat	ctg	gag	355
Leu	Arg	Ala	Ala	Val	Ala	Arg	Asp	His	Leu	Glu	Arg	Phe	Asp	Leu	Glu	
70					75					80					85	

tac	aac	cct	gat	tcg	gag	gtg	ttg	atc	acg	gtg	ggg	gcc	act	gag	gcg	403
Tyr	Asn	Pro	Asp	Ser	Glu	Val	Leu	Ile	Thr	Val	Gly	Ala	Thr	Glu	Ala	
				90					95					100		

att	acg	gcg	act	gtg	ttg	ggt	ttg	gtg	gag	cct	ggg	gat	gaa	gtg	atc	451
Ile	Thr	Ala	Thr	Val	Leu	Gly	Leu	Val	Glu	Pro	Gly	Asp	Glu	Val	Ile	
			105					110					115			

gtt	ttg	gaa	ccg	tat	tac	gat	gcg	tat	gcg	gcg	gct	att	gcg	ttg	gcg	499
Val	Leu	Glu	Pro	Tyr	Tyr	Asp	Ala	Tyr	Ala	Ala	Ala	Ile	Ala	Leu	Ala	
		120					125						130			

ggg	gcg	acg	cgg	gtg	gcg	ggt	cct	ttg	cag	gag	gtg	gag	aac	tcg	tgg	547
Gly	Ala	Thr	Arg	Val	Ala	Val	Pro	Leu	Gln	Glu	Val	Glu	Asn	Ser	Trp	
	135					140					145					

gat	gtg	gat	gtc	gat	aag	ttg	cat	gcg	gcg	gtg	act	aag	aag	acg	cgg	595
Asp	Val	Asp	Val	Asp	Lys	Leu	His	Ala	Ala	Val	Thr	Lys	Lys	Thr	Arg	
150					155					160					165	

atg	att	atc	gtt	aat	tcg	ccg	cat	aat	ccg	acg	ggt	tcg	gtg	ttt	tct	643
Met	Ile	Ile	Val	Asn	Ser	Pro	His	Asn	Pro	Thr	Gly	Ser	Val	Phe	Ser	
				170					175					180		

aag	aag	gcg	ttg	aag	cag	ttg	gcg	ggt	gtt	gct	cgt	gcg	tat	gac	ttg	691
Lys	Lys	Ala	Leu	Lys	Gln	Leu	Ala	Gly	Val	Ala	Arg	Ala	Tyr	Asp	Leu	
			185					190					195			

ttg	gtg	ttg	tca	gat	gag	gtg	tat	gag	cat	ctt	gtt	ttt	gat	gat	cag	739

WO 01/00843

PCT/IB00/00923

Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu Val Phe Asp Asp Gln
 200 205 210
 aag cat gtg agt gtc gcg aag ctg ccc ggt atg tgg gat cgc acg gtg 787
 Lys His Val Ser Val Ala Lys Leu Pro Gly Met Trp Asp Arg Thr Val
 215 220 225
 acg gtg tcg tcg gcg gcg aaa acg ttc aat gtg act ggt tgg aag acg 835
 Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val Thr Gly Trp Lys Thr
 230 235 240 245
 ggg tgg gcg ttg gca ccg gag ccg ttg ttg gag gcg gtg ttg aag gcg 883
 Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu Ala Val Leu Lys Ala
 250 255 260
 aag cag ttt atg tct tat gtg ggg gct aca cct ttt cag ccg gct gtg 931
 Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro Phe Gln Pro Ala Val
 265 270 275
 gcg cat gcg att gaa cat gag cag aag tgg gtg tca aag atg tct aag 979
 Ala His Ala Ile Glu His Glu Gln Lys Trp Val Ser Lys Met Ser Lys
 280 285 290
 ggg ctt gag ctc aag cgg gat att ttg cgt act gcg tta gat aag gcg
 1027
 Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr Ala Leu Asp Lys Ala
 295 300 305
 ggg ctg aag act cat gac agt atg ggc acg tat ttc atc gtt gcg gat
 1075
 Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr Phe Ile Val Ala Asp
 310 315 320 325
 att ggg gat cgt gat ggt gcg gag ttc tgt ttt gag ttg att gag aag
 1123
 Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe Glu Leu Ile Glu Lys
 330 335 340
 gtt ggg gtg gcg gcg att ccg gtg cag gcg ttt gtg gat cat ccg aag
 1171
 Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe Val Asp His Pro Lys
 345 350 355
 aag tgg tcg tcg aag gtt cgt ttt gcg ttt tgc aaa aaa gaa gag acg
 1219
 Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys Lys Lys Glu Glu Thr
 360 365 370
 ctc cgc gaa gct gcg gag cgt ctc aag ggg att aag aaa cta
 1261
 Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile Lys Lys Leu
 375 380 385
 tagtttgaac aggttggttg ggg
 1284

<210> 112

<211> 387

<212> PRT

<213> Corynebacterium glutamicum

<400> 112

Met	Ser	Asn	Asp	Phe	Val	Val	Ser	Arg	Leu	Arg	Pro	Phe	Gly	Glu	Thr
1				5					10					15	
Ile	Phe	Ala	Thr	Met	Thr	Gln	Arg	Ala	Val	Glu	Ala	Gly	Ala	Ile	Asn
			20					25					30		
Leu	Gly	Gln	Gly	Phe	Pro	Asp	Glu	Asp	Gly	Pro	Arg	Arg	Met	Leu	Glu
		35					40					45			
Ile	Ala	Ser	Glu	Gln	Ile	Leu	Gly	Gly	Asn	Asn	Gln	Tyr	Ser	Ala	Gly
	50					55					60				
Arg	Gly	Asp	Ala	Ser	Leu	Arg	Ala	Ala	Val	Ala	Arg	Asp	His	Leu	Glu
65					70					75					80
Arg	Phe	Asp	Leu	Glu	Tyr	Asn	Pro	Asp	Ser	Glu	Val	Leu	Ile	Thr	Val
				85					90					95	
Gly	Ala	Thr	Glu	Ala	Ile	Thr	Ala	Thr	Val	Leu	Gly	Leu	Val	Glu	Pro
			100					105					110		
Gly	Asp	Glu	Val	Ile	Val	Leu	Glu	Pro	Tyr	Tyr	Asp	Ala	Tyr	Ala	Ala
		115					120					125			
Ala	Ile	Ala	Leu	Ala	Gly	Ala	Thr	Arg	Val	Ala	Val	Pro	Leu	Gln	Glu
	130					135					140				
Val	Glu	Asn	Ser	Trp	Asp	Val	Asp	Val	Asp	Lys	Leu	His	Ala	Ala	Val
145					150					155					160
Thr	Lys	Lys	Thr	Arg	Met	Ile	Ile	Val	Asn	Ser	Pro	His	Asn	Pro	Thr
				165					170					175	
Gly	Ser	Val	Phe	Ser	Lys	Lys	Ala	Leu	Lys	Gln	Leu	Ala	Gly	Val	Ala
			180					185					190		
Arg	Ala	Tyr	Asp	Leu	Leu	Val	Leu	Ser	Asp	Glu	Val	Tyr	Glu	His	Leu
		195					200					205			
Val	Phe	Asp	Asp	Gln	Lys	His	Val	Ser	Val	Ala	Lys	Leu	Pro	Gly	Met
	210					215					220				
Trp	Asp	Arg	Thr	Val	Thr	Val	Ser	Ser	Ala	Ala	Lys	Thr	Phe	Asn	Val
225					230					235					240
Thr	Gly	Trp	Lys	Thr	Gly	Trp	Ala	Leu	Ala	Pro	Glu	Pro	Leu	Leu	Glu
				245					250					255	
Ala	Val	Leu	Lys	Ala	Lys	Gln	Phe	Met	Ser	Tyr	Val	Gly	Ala	Thr	Pro
			260					265					270		
Phe	Gln	Pro	Ala	Val	Ala	His	Ala	Ile	Glu	His	Glu	Gln	Lys	Trp	Val
		275					280					285			
Ser	Lys	Met	Ser	Lys	Gly	Leu	Glu	Leu	Lys	Arg	Asp	Ile	Leu	Arg	Thr
	290					295					300				
Ala	Leu	Asp	Lys	Ala	Gly	Leu	Lys	Thr	His	Asp	Ser	Met	Gly	Thr	Tyr
305					310					315					320

Phe Ile Val Ala Asp Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe
 325 330 335

Glu Leu Ile Glu Lys Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe
 340 345 350

Val Asp His Pro Lys Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys
 355 360 365

Lys Lys Glu Glu Thr Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile
 370 375 380

Lys Lys Leu
 385

<210> 113
 <211> 607
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(607)
 <223> FRXA00116

<400> 113
 ttgcgccacc aatcaatggg ggatcaaata tagtagctgc atgagtaatg acttcgctcgt 60

ttctaggctt agaccctttg gtgaaacgat ttttgcaacc atg acc cag cga gct 115
 Met Thr Gln Arg Ala
 1 5

gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt cct gat gag gat 163
 Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe Pro Asp Glu Asp
 10 15 20

ggc cct cgt cgg atg tta gag atc gcg tcg gag cag att ctc ggg gga 211
 Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln Ile Leu Gly Gly
 25 30 35

aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg ttg agg gca gct 259
 Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser Leu Arg Ala Ala
 40 45 50

gtg gct cgt gat cat ttg gag agg ttt gat ctg gag tac aac cct gat 307
 Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu Tyr Asn Pro Asp
 55 60 65

tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg att acg gcg act 355
 Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala Ile Thr Ala Thr
 70 75 80 85

gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc gtt ttg gaa ccg 403
 Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile Val Leu Glu Pro
 90 95 100

tat tac gat gcg tat gcg gcg gct att gcg ttg gcg ggg gcg acg ccg 451
 Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala Gly Ala Thr Arg
 105 110 115

DEMANDES OU BREVETS VOLUMINEUX

**LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVETS
COMPREND PLUS D'UN TOME.**

CECI EST LE TOME __1__ DE __4__

NOTE: Pour les tomes additionels, veuillez contacter le Bureau Canadien des Brevets.

JUMBO APPLICATIONS / PATENTS

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

THIS IS VOLUME __1__ OF __4__

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

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding a
5 metabolic pathway protein, or a portion thereof, provided that the nucleic acid
molecule does not consist of any of the F-designated genes set forth in Table 1.
2. The isolated nucleic acid molecule of claim 1, wherein said metabolic pathway
protein is selected from the group consisting of proteins involved in the metabolism
10 of an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or
trehalose.
3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the
group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the
15 Sequence Listing, or a portion thereof, provided that the nucleic acid molecule does
not consist of any of the F-designated genes set forth in Table 1.
4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected
from the group consisting of those sequences set forth as even-numbered SEQ ID
20 NOs of the Sequence Listing, provided that the nucleic acid molecule does not
consist of any of the F-designated genes set forth in Table 1.
5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant
of a polypeptide selected from the group of amino acid sequences consisting of those
25 sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing,
provided that the nucleic acid molecule does not consist of any of the F-designated
genes set forth in Table 1.
6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least
30 50% homologous to a nucleotide sequence selected from the group consisting of
those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or

- 149 -

a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

- 5 7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
- 10 8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.
9. An isolated nucleic acid molecule comprising the nucleic acid molecule of any one of claims 1-8 or a portion thereof and a nucleotide sequence encoding a heterologous
15 polypeptide.
10. A vector comprising the nucleic acid molecule of any one of claims 1-9.
11. The vector of claim 10, which is an expression vector.
- 20 12. A host cell transfected with the expression vector of claim 11.
13. The host cell of claim 12, wherein said cell is a microorganism.
- 25 14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.
- 30 16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, nonproteinogenic amino acids, purine and pyrimidine

- 150 -

bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

17. A method of producing a polypeptide comprising culturing the host cell of claim 12
5 in an appropriate culture medium to, thereby, produce the polypeptide.
18. An isolated metabolic pathway polypeptide from *Corynebacterium glutamicum*, or a portion thereof.
- 10 19. The protein of claim 18, wherein said polypeptide is selected from the group of metabolic pathway proteins which participate in the metabolism of an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose.
- 15 20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 20 21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 25 22. The isolated polypeptide of any of claims 18-21, further comprising heterologous amino acid sequences.
- 30 23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.

- 151 -

24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing,
5 provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.
10
26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.
27. The method of claim 25, wherein said method further comprises the step of
15 transfecting said cell with the vector of claim 11 to result in a cell containing said vector.
28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
20
29. The method of claim 25, 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*,
25 *Brevibacterium butanicum*, *Brevibacterium divaricatum*, *Brevibacterium flavum*, *Brevibacterium healii*, *Brevibacterium ketoglutamicum*, *Brevibacterium ketosoreductum*, *Brevibacterium lactofermentum*, *Brevibacterium linens*, *Brevibacterium paraffinolyticum*, and those strains set forth in Table 3.
30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.
30

- 152 -

31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols,
5 carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.
32. The method of claim 25, wherein said fine chemical is an amino acid.
33. The method of claim 32, wherein said amino acid is drawn from the group consisting
10 of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, and tryptophan.
34. A method for producing a fine chemical, comprising culturing a cell whose genomic
15 DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.
35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more of SEQ ID NOs 1
20 through 1156 of the Sequence Listing in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1, thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.
- 25 36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the nucleic acid molecule is disrupted.
- 30 37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs in the Sequence Listing, wherein the nucleic acid molecule comprises one or more nucleic acid

- 153 -

modifications from the sequence set forth as odd-numbered SEQ ID NOs of the Sequence Listing s.

38. A host cell comprising a nucleic acid molecule selected from the group consisting of
5 the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing , wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.