Method for producing L-amino acids in Corynebacteria using a glycine cleavage system

The present invention relates to a method for producing L-amino acids in Corynebacteria in which a glycine cleavage system is used.

Methods for producing L-amino acids that use bacteria from the genus Corynebacterium are known to those skilled in the art.

Although numerous Corynebacterium species are known, bacteria of the Corynebacterium glutamicum species are normally used in these methods, since this species has been found to be particularly advantageous for producing L-amino acids.

It has also been found that the yield of L-amino acid may be further increased by using a glycine cleavage system (GCV), since the formation of the undesired L-glycine by-product can be largely prevented by the glycine cleavage system. The suppression of the formation of L-glycine or of the degradation of excess L-glycine is particularly of particular significance in the production of L-methionine, since L-glycine is produced here as equimolar by-product.

A glycine cleavage system is composed of two or more subunits, namely the subunits GcvP, GcvT and GcvH. It takes the form of a multi-enzyme complex, which catalyses the oxidative decarboxylation and deamination of glycine to carbon dioxide, ammonium ions and N^{5-10}-methylenetetrahydrofolate.

The glycine dehydrogenase GcvP is a pyridoxal phosphate-containing decarboxylase which liberates carbon dioxide and leaves the aminomethyl compound bound to pyridoxal phosphate.

The H-protein GcvH is a lipoamide-containing aminomethyltransferase.

The enzyme GcvT catalyses the nucleophilic attack on the aminomethyllipoamide by tetrahydrofolate forming N^{5-10}-methylenetetrahydrofolate and liberating ammonium ions, wherein fully reduced lipoamide remains bound to GcvH.

Glycine cleavage systems are not present in all Corynebacteria, but to date only very few Corynebacteria have been decribed. For instance, the production strain C. glutamicum particularly preferred for amino acid production, for example, has no inherent glycine

cleavage system. In order to utilise the advantages of a glycine cleavage system for C. glutamicum, such a system had to be incorporated into C. glutamicum from another Corynebacterium and be expressed heterologously. The glycine cleavage system from C. jeikeium (WO 2008/101857) has been used to date for this purpose. A serious disadvantage in this case is that C. jeikeium is a pathogenic organism. A further disadvantage is that, for the purpose of degradation of the undesired glycine by-product, a heterologous construct had to be prepared.

It was a primary object of the present invention, therefore, to provide a novel glycine cleavage system, preferably a glycine cleavage system that does not originate from a pathogenic organism, wherein the glycine cleavage system is preferably suitable for incorporation into other Corynebacteria, in particular, C. glutamicum.

A further object of the present invention was to provide a Corynebacterium that is intrinsically capable of producing L-amino acids and furthermore has an inherent glycine cleavage system such that the preparation of a heterologous construct - as in the case of C. glutamicum - is not necessary.

It has now been found in accordance with the invention, surprisingly, that the species Corynebacterium humireducens, which is non-pathogenic, has an inherent glycine cleavage system which is structurally significantly different from the glycine cleavage systems described to date.

It has further been found, surprisingly, that the glycine cleavage system of Corynebacterium humireducens is very effective, such that glycine, which is an undesirable by-product in amino acid synthesis, only accumulates in the cell in relatively low amounts, if at all, in the wild-type strain. By amplification of a glycine cleavage system according to the invention, particularly by overexpression, the suppression of glycine by-product formation can be correspondingly further improved. In particular, the glycine by-product formation can also be effectively suppressed by overexpression of a glycine cleavage system according to the invention in other microorganisms, particularly in C. glutamicum.

It has furthermore been found, surprisingly, that C. humireducens is even intrinsically capable of producing L-amino acids, particularly L-alanine, L-valine and L-glutamic acid, via the inherent requirement thereof, such that C. humireducens is an L-amino acid-producing strain having a homologous glycine cleavage system which may be employed particularly as

a starting point for the development of further production strains having a host glycine cleavage system.

The C. humireducens strain is described for the first time by Wu et al. (International Journal of Systematic and Evolutionary Microbiology (2011), 61, 882-887). Said strain was deposited in the DSMZ under the deposition number DSM 45392 and its 16S rRNA was deposited in the EMBL and has the accession number GQ421281. The parent strain is a halotolerant, alkaliphilic, humic acid-reducing bacterium.

Further information regarding C. humireducens are to be found in the following publications: Wu et al. (Microb. Biotechnol. (2013), 6(2), 141-149), Lin et al. (Bioresour. Technol. (2013), 136, 302-308).

A first object of the present invention therefore relates to the enzymes of a glycine cleavage system selected from the group consisting of:

a) an enzyme GcvP having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 40,

b) an enzyme GcvT having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 42,

c) an enzyme GcvH having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 38.

The present invention therefore further relates to a glycine cleavage system comprising the enzymes GcvP, GcvT and GcvH, characterized in that said system comprises at least one of the following polypeptides:

a) an enzyme GcvP having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 40,

b) an enzyme GcvT having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 42,

c) an enzyme GcvH having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 38.

In this case, a glycine cleavage system according to the invention preferably comprises at least two, preferably all three, of the polypeptides (a) to (c) mentioned above.

Particular preference is given here to a glycine cleavage system comprising the following three polypeptides:

a) an enzyme GcvP having a sequence identity of at least 95 or 98% to the sequence according to SEQ ID NO: 40,

b) an enzyme GcvT having a sequence identity of at least 95 or 98% to the sequence according to SEQ ID NO: 42,

c) an enzyme GcvH having a sequence identity of at least 95 or 98% to the sequence according to SEQ ID NO: 38.

In a broader sense, the enzymes LpdA, LplA, LipA, LipB and GcvH also belong to the glycine cleavage system.

The dihydrolipoamide dehydrogenase(LpdA) reoxidises the lipoamide bound to GcvH.

The lipoate-protein ligase A (LplA) catalyses the lipoylation of GcvH.

The lipoic acid synthase (LipA) catalyses the synthesis of lipoic acid.

The lipoyl-[acyl carrier protein]-protein N-lipoyltransferase (LipB) catalyses the transfer of lipoic acid to the GcvH.

GcvL is a dihydrolipoyl dehydrogenase.

In a preferred embodiment, a glycine cleavage system according to the invention therefore further comprises at least one further enzyme selected from the group consisting of:

a) an enzyme LipA, preferably an enzyme LipA having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 48,

b) an enzyme LipB, preferably an enzyme LipB having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 50,

c) an enzyme Lpd, preferably an enzyme Lpd having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 52,

d) an enzyme LplA, preferably an enzyme LplA having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 94,

e) an enzyme GcvL, preferably an enzyme GcvL having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 96.

In a particularly preferred embodiment in accordance with the invention, a glycine cleavage system according to the invention in this case comprises at least two, three or four, preferably all five, of the polypeptides mentioned above.

The present invention therefore further relates also to enzymes selected from the group consisting of:

a) an enzyme LipA, preferably an enzyme LipA having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 48,

b) an enzyme LipB, preferably an enzyme LipB having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 50,

c) an enzyme Lpd, preferably an enzyme Lpd having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 52,

d) an enzyme LplA, preferably an enzyme LplA having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 94,

e) an enzyme GcvL, preferably an enzyme GcvL having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 96.

As an alternative to or in addition to the use of the appropriate enzymes which ensure an adequate synthesis of lipoic acid and/or lipoamide, these compounds may also be added to the reaction medium, for example, in amounts of up to 15 mM.

The present invention further relates also to polynucleotides coding for enzymes according to the invention and/or a glycine cleavage system according to the invention. These polynucleotides are preferably selected from the group consisting of:

a) a polynucleotide (gcvP), which codes for the enzyme GcvP and has a sequence identity of at least 70 or 75%, preferably at least 80 or 85%, particularly at least 90 or 95%, especially at least 98 or 100%, to the sequence of position 301 to 3162 according to SEQ ID NO: 39 and/or hybridizes under stringent conditions with a polynucleotide of which the sequence is complementary to the sequence of position 301 to 3162 according to SEQ ID NO: 39;

b) a polynucleotide (gcvT), which codes for the enzyme GcvT and has a sequence identity of at least 70 or 75%, preferably at least 80 or 85%, particularly at least 90 or 95%, especially at least 98 or 100%, to the sequence of position 301 to 1404 according to SEQ ID NO: 41 and/or hybridizes under stringent conditions with a polynucleotide of which the sequence is complementary to the sequence of position 301 to 1404 according to SEQ ID NO: 41;

c) a polynucleotide (gcvH), which codes for the enzyme GcvH and has a sequence identity of at least 70 or 75%, preferably at least 80 or 85%, particularly at least 90 or 95%, especially at least 98 or 100%, to the sequence of position 301 to 699 according to SEQ ID NO: 37 and/or hybridizes under stringent conditions with a polynucleotide of which the sequence is complementary to the sequence of position 301 to 699 according to SEQ ID NO: 37;

d) a polynucleotide (lipA), which codes for an enzyme LipA and has a sequence identity of at least 70%, preferably at least 80 or 85%, particularly at least 90 or 95%, especially at least 98 or 100%, to the sequence of position 301 to 1344 according to SEQ ID NO: 47 and/or hybridizes under stringent conditions with a

polynucleotide of which the sequence is complementary to the sequence of position 301 to 1344 according to SEQ ID NO: 47;

e) a polynucleotide (lipB), which codes for an enzyme LipB and has a sequence identity of at least 70%, preferably at least 80 or 85%, particularly at least 90 or 95%, especially at least 98 or 100%, to the sequence of position 301 to 1089 according to SEQ ID NO: 49 and/or hybridizes under stringent conditions with a polynucleotide of which the sequence is complementary to the sequence of position 301 to 1089 according to SEQ ID NO: 49;

f) a polynucleotide (lpd), which codes for an enzyme Lpd and has a sequence identity of at least 70%, preferably at least 80 or 85%, particularly at least 90 or 95%, especially at least 98 or 100%, to the sequence of position 301 to 1710 according to SEQ ID NO: 51 and/or hybridizes under stringent conditions with a polynucleotide of which the sequence is complementary to the sequence of position 301 to 1710 according to SEQ ID NO: 51;

g) a polynucleotide (lplA), which codes for an enzyme LplA and has a sequence identity of at least 70%, preferably at least 80 or 85%, particularly at least 90 or 95%, especially at least 98 or 100%, to the sequence of position 301 to 1089 according to SEQ ID NO: 93 and/or hybridizes under stringent conditions with a polynucleotide of which the sequence is complementary to the sequence of position 301 to 1089 according to SEQ ID NO: 93;

h) a polynucleotide (gcvL), which codes for an enzyme GcvL and has a sequence identity of at least 70%, preferably at least 80 or 85%, particularly at least 90 or 95%, especially at least 98 or 100%, to the sequence of position 301 to 1710 according to SEQ ID NO: 95 and/or hybridizes under stringent conditions with a polynucleotide of which the sequence is complementary to the sequence of position 301 to 1710 according to SEQ ID NO: 95.

In accordance with the invention, "stringent conditions" is understood to mean washing at a salt concentration of 1 x SSC and 0.1% by weight SDS at a temperature of 80°C.

The present invention further relates likewise to polynucleotides which are complementary to the coding polynucleotides mentioned above.

The present invention further relates to appropriate vectors, particularly cloning and expression vectors, comprising at least one polynucleotide according to the invention. These vectors can be appropriately incorporated into microorganisms, particularly in coryneform bacteria, especially from the genus Corynbebacterium, or Enterobacteriaceae, especially from the genus Escherichia.

Vectors according to the invention may comprise one or more polynucleotides in accordance with the invention. A preferred vector in accordance with the invention comprises at least one polynucleotide coding for an enzyme according to the invention selected from GcvP, GcvT and GcvH. A particularly preferred vector comprises polynucleotides which code for all three enzymes GcvP, GcvT and GcvH in accordance with the invention.

Vectors according to the invention preferably have a suitable promoter and/or suitable promoters and optionally further regulatory elements which enable the expression of the inventive polynucleotides in the recombinant bacterium, preferably the recombinant Corynebacterium.

Furthermore, polynucleotides according to the invention may also, for the purpose of expression of the coded genes, be incorporated into the genome of microorganisms, particularly into the genome of coryneform bacteria, particularly those of the genus Corynebacterium, or into the genome of Enterobacteriaceae, especially of the genus Escherichia.

The present invention further relates also to corresponding recombinant microorganisms, preferably bacteria, particularly coryneform bacteria, especially those of the genus Corynebacterium, particularly preferably of the species C. humireducens or C. glutamicum, and also Enterobacteriaceae, especially those of the genus Escherichia, comprising at least one enzyme according to the invention and/or at least one polynucleotide according to the invention and/or at least one vector according to the invention and/or one glycine cleavage system according to the invention and/or a polynucleotide coding for a glycine cleavage system according to the invention.

A preferred object is, in this context, recombinant Corynebacteria, particularly of the species C. humireducens and the species C. glutamicum, comprising at least one enzyme according to the invention, preferably all enzymes according to the invention, selected from GcvP, GcvT and GcvH, and/or polynucleotides coding for said enzymes and/or at least one vector comprising said polynucleotides.

The present invention particularly relates also to, in particular, recombinant microorganisms, preferably bacteria, particularly coryneform bacteria, especially those of the genus Corynebacterium with the exception of the species C. humireducens, particularly those of the species C. glutamicum, comprising at least one enzyme according to the invention and/or at least one polynucleotide according to the invention and/or at least one vector according to the invention and/or one glycine cleavage system according to the invention and/or a polynucleotide coding for a glycine cleavage system according to the invention.

A preferred object is, in this context, recombinant Corynebacteria, with the exception of the species C. humireducens, particularly of the species C. glutamicum, comprising at least one enzyme according to the invention, preferably all enzymes according to the invention, selected from GcvP, GcvT and GcvH, and/or polynucleotides coding for said enzymes and/or at least one vector comprising said polynucleotides.

In accordance with the invention, "recombinant microorganism" or "recombinant bacterium" is understood to mean a microorganism or bacterium that has been subjected to at least one genetic engineering measure. The genetic engineering measure may be, in this context, in particular a targeted or random mutation, the incorporation of a foreign gene and/or the overexpression or attenuation of a host gene or foreign gene. A recombinant microorganism according to the invention or a recombinant bacterium according to the invention is preferably characterized by the overexpression or attenuation of at least one gene. In a particularly preferred embodiment, a recombinant microorganism according to the invention or a recombinant bacterium according to the invention is characterized by the overexpression of at least one enzyme according to the invention and/or polynucleotide coding for said enzyme and/or the overexpression of a glycine cleavage system according to the invention or polynucleotide coding for said system.

"Relatively low amount", with respect to glycine formation, is understood to mean an amount of at most 0.3 g/l, preferably at most 0.2 or 0.1 g/l, particularly preferably at most 0.05 or at most 0.03 g/l, based in each case on the accumulated glycine content in the cell and/or in the fermentation medium after completion of the fermentation.

Within the genus Corynebacterium, preference is given to strains according to the invention based on the following species: Corynebacterium efficiens, such as type strain DSM44549, Corynebacterium glutamicum, such as type strain ATCC13032 or the strain R, Corynebacterium ammoniagenes, such as type strain ATCC6871, Corynebacterium

humireducens, such as the strain DSM 45392, and Corynebacterium pekinese, such as the strain CGMCC No. 5361.

Particular preference is given to the species Corynebacterium glutamicum and Corynebacterium humireducens. If, in the context of this application, the strain Corynebacterium humireducens is mentioned, said strain is preferably strain DSM 45392 or a strain derived therefrom.

Some representatives of the species Corynebacterium glutamicum are also known in the prior art under other names. These include for example: Corynebacterium acetoacidophilum ATCC13870, Corynebacterium lilium DSM20137, Corynebacterium melassecola ATCC17965, Brevibacterium flavum ATCC14067, Brevibacterium lactofermentum ATCC13869 and Brevibacterium divaricatum ATCC14020. The term "Micrococcus glutamicus" for Corynebacterium glutamicum has likewise been in use. Some representatives of the species Corynebacterium efficiens have also been referred to in the prior art as Corynebacterium thermoaminogenes, for example the strain FERM BP-1539.

Information on the taxonomic classification of strains of the group of the coryneform bacteria can be found, inter alia, in Seiler (Journal of General Microbiology 129, 1433-1477 (1983)), Kinoshita (1985, Glutamic Acid Bacteria, p 115-142. In: Demain and Solomon (ed), Biology of Industrial Microorganisms. The Benjamin/Cummins Publishing Co., London, UK), Kämpfer and Kroppenstedt (Canadian Journal of Microbiology 42, 989-1005 (1996)), Liebl et al (International Journal of Systematic Bacteriology 41, 255-260 (1991)), Fudou et al (International Journal of Systematic and Evolutionary Microbiology 52, 1127-1131 (2002)) and in US-A-5,250,434.

Strains with the designation "ATCC" may be obtained from the American Type Culture Collection (Manassas, VA, USA). Strains with the designation "DSM" may be obtained from the Deutschen Sammlung von Mikroorganismen und Zellkulturen (German Microorganism and Cell Culture Collection) (DSMZ, Braunschweig, Germany). Strains with the designation "NRRL" may be obtained from the Agricultural Research Service Patent Culture Collection (ARS, Peoria, Illinois, US). Strains with the designation "FERM" may be obtained from the National Institute of Advanced Industrial Science and Technology (AIST Tsukuba Central 6, 1-1-1 Higashi, Tsukuba Ibaraki, Japan). Strains with the designation "CGMCC" may be obtained from the China General Microbiological Culture Collection Center (CGMCC, Beijing, China).

The present invention further relates also to a method for overproducing an L-amino acid, characterized in that at least one enzyme according to the invention and/or a polynucleotide coding for said enzyme and/or a glycine cleavage system according to the invention and/or polynucleotides coding for said system and/or a recombinant microorganism according to the invention, preferably a recombinant bacterium according to the invention, particularly a recombinant coryneform bacterium according to the invention, particularly preferably a recombinant Corynebacterium according to the invention, especially a Corynebacterium of the species C. humireducens or C. glutamicum, is used in said method. In a preferred embodiment according to the invention, the at least one polynucleotide according to the invention is used in this case in overexpressed form.

The present invention in this case preferably relates to a method for overproducing an L-amino acid, characterized in that a glycine cleavage system comprising the enzymes GcvP, GcvT and GcvH is used in said method, wherein the glycine cleavage system comprises at least one of the enzymes GcvP, GcvT and GcvH in accordance with the invention, and/or polynucleotides coding for the GcvP, GcvT and GcvH enzymes of a glycine cleavage system are used in said method, wherein said polynucleotides comprise at least one of the polynucleotides gcvP, gcvT and gcvH in accordance with the invention, and/or a recombinant Corynebacterium is used, preferably of the species C. humireducens or C. glutamicum, which comprises at least one enzyme according to the invention, preferably all three enzymes according to the invention, selected from GcvP, GcvT and GcvH and/or at least one polynucleotide according to the invention, preferably all three polynucleotides according to the invention, selected from gcvP, gcvT and gcvH.

The present invention in this case particularly preferably relates to a method for overproducing an L-amino acid, characterized in that a glycine cleavage system is used in said method, which comprises the enzymes GcvP, GcvT and GcvH in accordance with the invention and/or polynucleotides coding for said enzymes, and/or a recombinant Corynebacterium is used in said method, preferably of the species C. humireducens or C. glutamicum, which comprises such a glycine cleavage system and/or polynucleotides coding for said system.

"L-amino acid" in accordance with the invention is understood to mean, in particular, the proteinogenic L-amino acids.

The L-amino acid is in this case preferably selected from L-alanine, L-valine, L-amino acids of the glutamate family, particularly L-glutamate, L-glutamine, L-proline and L-arginine, and

L-amino acids of the aspartate family, particularly L-aspartate, L-asparagine, L-methionine, L-lysine, L-isoleucine and L-threonine, particularly preferably selected from L-alanine, L-valine, L-glutamate, L-methionine, L-lysine and L-threonine. Particular preference is given to L-methionine.

The overproduction of the L-amino acids is preferably effected, in accordance with the invention, in C. humireducens or C. glutamicum.

Methods according to the invention are preferably characterized in that only low amounts of glycine occur as by-product. In the method according to the invention, glycine occurs preferably in an amount of less than 0.2 g/l, particularly in an amount of less than 0.1 g/l, particularly preferably in an amount of less than 0.05 g/l.

"Overproduce" or "overproduction" in relation to the L-amino acids is understood to mean, in accordance with the invention, that the microorganisms produce the L-amino acids according to their own requirement thereof, which either enrich in the cell or are secreted into the surrounding nutrient medium where they accumulate. In this case, the microorganisms preferably have the ability to enrich or accumulate in the cell or in the nutrient medium ≥ (at least) 0.25 g/l, ≥ 0.5 g/l, ≥ 1.0 g/l, ≥ 1.5 g/l, ≥ 2.0 g/l, ≥ 4 g/l or ≥ 10 g/l of the relevant L-amino acids in ≤ (at most) 120 hours, ≤ 96 hours, ≤ 48 hours, ≤ 36 hours, ≤ 24 hours or ≤ 12 hours.

Recombinant microorganisms according to the invention, in which polynucleotides according to the invention and/or vectors according to the invention have been incorporated, already have the capability, in a preferred embodiment, to overproduce an L-amino acid before the incorporation of the polynucleotides and/or vectors according to the invention. The starting strains are preferably strains which have been produced by mutagenesis and selection, by recombinant DNA techniques or by a combination of both methods.

It is obvious and requires no further explanation, that a recombinant microorganism in accordance with the invention can also be thus produced, in which a wild strain, in which a polynucleotide according to the invention and/or a vector according to the invention is present or has been incorporated and by subsequent suitable further genetic engineering measures, causes the L-amino acid to be produced or the L-amino acid production to be increased.

The present invention further relates also to other polynucleotides from C. humireducens and also the polypeptides encoded by said polynucleotides. By means of overexpression of the

relevant polynucleotides or polypeptides, the amino acid production of certain L-amino acids can be positively influenced.

The present invention therefore likewise relates to:

a) a threonine dehydratase (IlvA, EC 4.3.1.19) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 106 and polynucleotides coding for the same,

b) the subunit of an acetolactate synthase (IlvB) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 98 and polynucleotides coding for the same,

c) an isomeroreductase (IlvC, EC 1.1.1.86) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 100 and polynucleotides coding for the same,

d) a dihydroxyacid dehydratase (IlvD, EC 4.2.1.9) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 102 and polynucleotides coding for the same,

e) a transaminase (IlvE, EC 2.6.1.42) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 104 and polynucleotides coding for the same,

f) an acetolactate synthase (IlvH, EC 2.2.1.6) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 122 and polynucleotides coding for the same,

g) a 3-methyl-2-oxobutanoate hydroxymethyltransferase (PanB, EC 2.1.2.11) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 118 and polynucleotides coding for the same,

h) a pantothenate synthase (PanC, EC 6.3.2.1) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 120 and polynucleotides coding for the same,

i) a glutamate dehydrogenase (Gdh) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 124 and polynucleotides coding for the same,

j) a glutamine synthetase (glutamine synthetase 1) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 126 and polynucleotides coding for the same,

k) a glutamine synthetase (glutamine synthetase 2) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 128 and polynucleotides coding for the same,

l) a glutamate synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 130 and polynucleotides coding for the same,

m) an isocitrate dehydrogenase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 132 and polynucleotides coding for the same,

n) an aconitate hydrase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 134 and polynucleotides coding for the same,

o) a citrate synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 136 and polynucleotides coding for the same,

p) an aminopeptidase C (PepC) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 138 and polynucleotides coding for the same,

q) a pyruvate dehydrogenase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 140 and polynucleotides coding for the same,

r) a pyruvate kinase (pyruvate kinase 1) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 142 and polynucleotides coding for the same,

s) a pyruvate kinase (pyruvate kinase 2) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 144 and polynucleotides coding for the same,

t) an enolase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 146 and polynucleotides coding for the same,

u) a 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (GpmA) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 148 and polynucleotides coding for the same,

v) a phosphoglycerate kinase (Pgk) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 150 and polynucleotides coding for the same,

w) a glyceraldehyde-3-phosphate dehydrogenase (glycerol-3-phosphate dehydrogenase 1) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 152 and polynucleotides coding for the same,

x) a glyceraldehyde-3-phosphate dehydrogenase (glycerol-3-phosphate dehydrogenase 2) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 154 and polynucleotides coding for the same,

y) a triosephosphate isomerase (TpiA) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 156 and polynucleotides coding for the same,

z) a fructose bisphosphate aldolase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 158 and polynucleotides coding for the same,

aa) a 1-phosphofructokinase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 160 and polynucleotides coding for the same,

bb) a 6-phosphofructokinase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 162 and polynucleotides coding for the same,

cc) a homoserine kinase (ThrB, EC 2.7.1.39) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 4 and polynucleotides coding for the same,

dd) a cysteine synthase (CBS, CysK) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 22 and polynucleotides coding for the same,

ee) a cystathionine beta-lyase (AecD) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 26 and polynucleotides coding for the same,

ff) an aspartate semialdehyde dehydrogenase (Asd, EC 1.2.1.11) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 28 and polynucleotides coding for the same,

gg) the smaller subunit of a transporter for branched-chain amino acids (BrnE) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 30 and polynucleotides coding for the same,

hh) the larger subunit of a transporter for branched-chain amino acids (BrnF) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 32 and polynucleotides coding for the same,

ii) a serine acetyltransferase (CysE) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 34 and polynucleotides coding for the same,

jj) a cysteine synthase (CysK) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 36 and polynucleotides coding for the same,

kk) a serine hydroxymethyltransferase (GlyA) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 44 and polynucleotides coding for the same,

ll) an optionally feedback-resistant homoserine dehydrogenase (Hom, EC 1.2.1.11) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 46 and polynucleotides coding for the same,

mm) an optionally feedback-resistant aspartate kinase (LysC, EC 2.7.2.4) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 54 and polynucleotides coding for the same,

nn) a cystathionine gamma-synthase (MetB) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 56 and polynucleotides coding for the same,

oo) a 5,10-methylenetetrahydrofolate reductase (MetF) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 58 and polynucleotides coding for the same,

pp) a homoserine O-acetyltransferase (MetX) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 60 and polynucleotides coding for the same,

qq) an O-acetylhomoserine lyase (MetY) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 62 and polynucleotides coding for the same,

rr) an optionally feedback-resistant pyruvate carboxylase (Pyc, EC 6.4.1.1) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 64 and polynucleotides coding for the same,

ss) an optionally feedback-resistant D-3-phosphoglycerate dehydrogenase (SerA) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 66 and polynucleotides coding for the same,

tt) a phosphoserine phosphatase (SerB) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 68 and polynucleotides coding for the same,

uu) a phosphoserine aminotransferase (SerC) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 70 and polynucleotides coding for the same,

vv) the subunit of a sulphate adenylyltransferase (CysD) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 74 and polynucleotides coding for the same,

ww) an adenosine phosphosulphate reductase (CysH) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 76 and polynucleotides coding for the same,

xx) a sulphite reductase (CysI) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 78 and polynucleotides coding for the same,

yy) an NADPH-dependent glutamate synthase beta chain (CysJ) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 80 and polynucleotides coding for the same,

zz) the large subunit of a sulphate adenylyltransferase (CysN) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 82 and polynucleotides coding for the same,

aaa) a cystathionine beta-synthase (CysY) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 84 and polynucleotides coding for the same,

bbb) a sulphate transporter (CysZ) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 86 and polynucleotides coding for the same,

ccc) a 5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase (MetE) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 88 and polynucleotides coding for the same,

ddd) a peptidyl-tRNA hydrolase 1 (PtH1) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 90 and polynucleotides coding for the same,

eee) a peptidyl-tRNA hydrolase 2 (PtH2) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 92 and polynucleotides coding for the same,

fff) a diaminopimelate dehydrogenase (Ddh, EC 1.4.1.16) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 202 and polynucleotides coding for the same,

ggg) a diaminopimelate decarboxylase (LysA, EC 4.1.1.20) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 164 and polynucleotides coding for the same,

hhh) an aspartate aminotransferase (AaT, EC 2.6.1.1) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 166 and polynucleotides coding for the same,

iii) an L-lysine exporter (LysE, lysine efflux permease) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 168 and polynucleotides coding for the same,

jjj) a dihydropicolinate reductase (DapB, EC 1.3.1.26) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 170 and polynucleotides coding for the same,

kkk) a glucose-6-phosphate dehydrogenase (EC 1.1.1.49) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 172 and polynucleotides coding for the same,

lll) the Zwf subunit of a glucose-6-phosphate dehydrogenase (Zwf, EC 1.1.1.49) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 186 and polynucleotides coding for the same,

mmm) the OpcA subunit of a glucose-6-phosphate dehydrogenase (OpcA, EC 1.1.1.49) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 188 and polynucleotides coding for the same,

nnn) a phosphogluconic acid dehydrogenase (Gnd, EC 1.1.1.44) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 174 and polynucleotides coding for the same.

The present invention further relates also to vectors comprising the polynucleotides mentioned above and also recombinant microorganisms comprising the enzymes and/or

polynucleotides and/or vectors mentioned above. In a preferred embodiment, the relevant polypeptide and/or polynucleotide is present in this case in the microorganism in overexpressed form. The recombinant microorganisms are preferably in this case coryneform bacteria, especially Corynebacteria, particularly those of the species C. humireducens or C. glutamicum.

The present invention therefore further relates also to a method for overproducing an L-amino acid, preferably selected from L-alanine, L-valine, L-amino acids of the glutamate family, particularly L-glutamate, L-glutamine, L-proline and L-arginine, and L-amino acids of the aspartate family, particularly L-aspartate, L-asparagine, L-methionine, L-lysine, L-isoleucine and L-threonine, particularly preferably selected from L-alanine, L-valine, L-glutamate, L-methionine, L-lysine and L-threonine, especially for overproducing L-methionine, in which at least one, preferably at least two, three or four, of the polynucleotides mentioned are present in overexpressed form, wherein the method is preferably carried out in Corynebacteria, particularly those of the species C. humireducens or C. glutamicum.

The present invention further relates also to other polynucleotides from C. humireducens and also the polypeptides encoded by said polynucleotides. By means of deactivation or attenuation of the relevant polynucleotides or polypeptides, the amino acid production of certain L-amino acids can be positively influenced.

The present invention therefore also relates to polypeptides selected from the following list:

a) a threonine synthase (ThrC, EC 4.2.3.1) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 108 and polynucleotides coding for the same,
b) an isopropylmalate synthase (LeuA, EC 2.3.3.13) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 110 and polynucleotides coding for the same,
c) an isopropylmalate dehydrogenase (LeuB, EC 1.1.1.85) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 112 and polynucleotides coding for the same,
d) the subunits of an isopropylmalate isomerase (LeuCD, EC 4.2.1.33) having sequence identities of at least 90, 95 or 98%, preferably 100%, to the sequences according to SEQ ID NO: 114 or SEQ ID NO: 116 and polynucleotides coding for the same,

e) the subunits of a succinyl-CoA ligase (SucCD, EC 6.2.1.5) each having sequence identities of at least 90, 95 or 98%, preferably 100%, to the sequences according to SEQ ID NO: 198 or SEQ ID NO: 200 and polynucleotides coding for the same,

f) a DNA binding domain of type HTH tetR (McbR) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 2 and polynucleotides coding for the same,

g) a homoserine kinase (ThrB, EC 2.7.1.39) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 4 and polynucleotides coding for the same,

h) a glucose-6-phosphate isomerase (Pgi, EC 5.3.1.9) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 6 and polynucleotides coding for the same,

i) a phosphoenolpyruvate carboxykinase (Pck, EC 4.1.1.32) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 8 and polynucleotides coding for the same,

j) a D-methionine-binding lipoprotein (MetQ) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 10 and polynucleotides coding for the same,

k) a methionine transporter (MetP) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 12 and polynucleotides coding for the same,

l) an ATP-dependent methionine transporter (MetN) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 14 and polynucleotides coding for the same,

m) an S-adenosylmethionine synthase (MetK) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 16 and polynucleotides coding for the same,

n) a methionine import system permease (MetI) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 18 and polynucleotides coding for the same,

o) a 4-hydroxy-tetrahydrodipicolinate synthase (DapA, EC 4.3.3.7) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 20 and polynucleotides coding for the same,

p) a carboxylate-amine ligase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 24 and polynucleotides coding for the same,

q) a malate:quinone oxidoreductase (Mqo, EC 1.1.99.16) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 176 and polynucleotides coding for the same,

r) the E1p subunit of a pyruvate dehydrogenase complex (AceE, EC 1.2.4.1) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 178 and polynucleotides coding for the same,

s) a citrate synthase (GltA, EC 4.1.3.7) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 180 and polynucleotides coding for the same,

t) a malate dehydrogenase (Mdh, EC 1.1.1.37) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 182 and polynucleotides coding for the same,

u) a UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase (MurE, EC 6.3.2.13) having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 184, and polynucleotides coding for the same,

The present invention further relates also to vectors comprising the polynucleotides mentioned above and also recombinant microorganisms comprising the enzymes and/or polynucleotides and/or vectors mentioned above. In a preferred embodiment, the relevant polypeptide and/or polynucleotide is present in this case in the microorganism in deactivated or attenuated form. The recombinant microorganisms are preferably in this case coryneform bacteria, especially Corynebacteria, particularly those of the species C. humireducens or C. glutamicum, especially of the species C. humireducens.

The present invention therefore further relates also to a method for overproducing an L-amino acid, preferably selected from L-alanine, L-valine, L-amino acids of the glutamate family, particularly L-glutamate, L-glutamine, L-proline and L-arginine, and L-amino acids of the aspartate family, particularly L-aspartate, L-asparagine, L-methionine, L-lysine, L-isoleucine and L-threonine, particularly preferably selected from L-alanine, L-valine, L-glutamate, L-methionine, L-lysine and L-threonine, especially for overproducing L-methionine, in which at least one, preferably at least two, three or four, of the polynucleotides mentioned are present in deactivated or attenuated form, wherein the method is preferably

carried out in Corynebacteria, particularly those of the species C. humireducens or C. glutamicum. In a preferred embodiment, at least one, preferably at least two, three or four of the polynucleotides mentioned in the detailed list above is present in this case at the same time in overexpressed form.

In a further preferred embodiment according to the invention, microorganisms or bacteria according to the invention, particularly Corynebacteria according to the invention, especially Corynebacteria according to the invention of the species C. humireducens or C. glutamicum, particularly L-methionine-overproducing strains according to the invention, in addition to an inventive, preferably overexpressed glycine cleavage system or polynucleotides coding for said system, have at least one, preferably at least two or three, particularly preferably at least four or five, of the following features:

a) an attenuated polynucleotide (mcbR), which codes for a DNA binding domain of the type HTH tetR (McbR), preferably for a DNA binding domain having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 2,
b) an attenuated polynucleotide (thrB gene), which codes for a homoserine kinase (ThrB, EC 2.7.1.39), preferably for a homoserine kinase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 4,
c) an attenuated polynucleotide (pgi), which codes for a glucose-6-phosphate isomerase (Pgi, EC 5.3.1.9), preferably for a glucose-6-phosphate isomerase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 6,
d) an attenuated polynucleotide (pck), which codes for a phosphoenolpyruvate carboxykinase (Pck, EC 4.1.1.32), preferably for a phosphoenolpyruvate carboxykinase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 8,
e) an attenuated polynucleotide (metQ), which codes for a D-methionine-binding lipoprotein (MetQ), preferably for a D-methionine-binding lipoprotein having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 10,
f) an attenuated polynucleotide (metP), which codes for a methionine transporter (MetP), preferably for a methionine transporter having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 12,

g) an attenuated polynucleotide (metN), which codes for an ATP-dependent methionine transporter (MetN), preferably for an ATP-dependent methionine transporter having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 14,

h) an attenuated polynucleotide (metK), which codes for an S-adenosylmethionine synthase (MetK), preferably for an S-adenosylmethionine synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 16,

i) an attenuated polynucleotide (metI), which codes for a methionine import system permease (MetI), preferably for a methionine import system permease having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 18,

j) an attenuated polynucleotide (dapA), which codes for a 4-hydroxy-tetrahydrodipicolinate synthase (DapA), preferably for a 4-hydroxy-tetrahydrodipicolinate synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 20,

k) an overexpressed polynucleotide (CBS), which codes for a cysteine synthase (CBS), preferably for a cysteine synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 22,

l) an attenuated polynucleotide, which codes for a cg3031 homologue, preferably for a cg3031 homologue having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 24,

m) an overexpressed polynucleotide (aecD), which codes for a cystathionine beta-lyase (AecD), preferably for a cystathionine beta-lyase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 26,

n) an overexpressed polynucleotide (asd), which codes for an aspartate semialdehyde dehydrogenase (Asd), preferably for an aspartate semialdehyde dehydrogenase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 28,

o) an overexpressed polynucleotide (metH), which codes for a 5-methyltetrahydrofolate homocysteine methyltransferase (MetH, EC 2.1.1.13),

p) an overexpressed polynucleotide (brnE), which codes for the smaller subunit of a transporter for branched-chain amino acids (BrnE), preferably for a subunit having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 30,

q) an overexpressed polynucleotide (brnF), which codes for the larger subunit of a transporter for branched-chain amino acids (BrnF), preferably for a subunit having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 32,

r) an overexpressed polynucleotide (cysE), which codes for a serine acetyltransferase (CysE), preferably for a serine acetyltransferase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 34,

s) an overexpressed polynucleotide (cysK), which codes for a cysteine synthase (CysK), preferably for a cysteine synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 36,

t) an overexpressed polynucleotide (glyA), which codes for a serine hydroxymethyltransferase (GlyA), preferably for a serine hydroxymethyltransferase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 44,

u) an overexpressed polynucleotide (hom), which codes for an optionally feedback-resistant homoserine dehydrogenase (Hom), preferably for a homoserine dehydrogenase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 46,

v) an overexpressed polynucleotide (lysC), which codes for an optionally feedback-resistant aspartate kinase (LysC), preferably for an aspartate kinase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 54,

w) an overexpressed polynucleotide (metB), which codes for a cystathionine gamma-synthase (MetB), preferably for a cystathionine gamma-synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 56,

x) an overexpressed polynucleotide (metF), which codes for a 5,10-methylenetetrahydrofolate reductase (MetF), preferably for a 5,10-methylenetetrahydrofolate reductase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 58,

y) an overexpressed polynucleotide (metX), which codes for a homoserine O-acetyltransferase (MetX), preferably for a homoserine O-acetyltransferase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 60,

z) an overexpressed polynucleotide (metY), which codes for an O-acetylhomoserine lyase (MetY), preferably for an O-acetylhomoserine lyase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 62,

aa) an overexpressed polynucleotide (pyc), which codes for a pyruvate carboxylase (Pyc), preferably for a pyruvate carboxylase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 64,

bb) an overexpressed polynucleotide (serA), which codes for an optionally feedback-resistant D-3-phosphoglycerate dehydrogenase (SerA), preferably for a D-3-phosphoglycerate dehydrogenase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 66,

cc) an overexpressed polynucleotide (serB), which codes for a phosphoserine phosphatase (SerB), preferably for a phosphoserine phosphatase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 68,

dd) an overexpressed polynucleotide (serC), which codes for a phosphoserine aminotransferase (SerC), preferably for a phosphoserine aminotransferase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 70,

ee) an overexpressed polynucleotide (ald), which codes for an alanine dehydrogenase (Ald), preferably for an alanine dehydrogenase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 72,

ff) an overexpressed polynucleotide (cysD), which codes for the subunit of a sulphate adenylyltransferase (CysD), preferably for a subunit having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 74,

gg) an overexpressed polynucleotide (cysH), which codes for an adenosine phosphosulphate reductase (CysH), preferably for an adenosine phosphosulphate reductase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 76,

hh) an overexpressed polynucleotide (cysI), which codes for a sulphite reductase (CysI), preferably for a sulphite reductase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 78,

ii) an overexpressed polynucleotide (cysJ), which codes for (CysJ), preferably for one having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 80,

jj) an overexpressed polynucleotide (cysN), which codes for the subunit of a sulphate adenylyltransferase (CysN), preferably for a subunit having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 82,

kk) an overexpressed polynucleotide (cysY), which codes for a cystathionine beta-synthase (CysY), preferably for a cystathionine beta-synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 84,

ll) an overexpressed polynucleotide (cysZ), which codes for a putative sulphate transporter (CysZ), preferably for a sulphate transporter having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 86,

mm) an overexpressed polynucleotide (metE), which codes for a 5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase (MetE), preferably for a protein having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 88,

nn) an overexpressed polynucleotide (ptH1), which codes for a peptidyl-tRNA hydrolase 1 (PtH1), preferably for a peptidyl-tRNA hydrolase 1 having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 90,

oo) an overexpressed polynucleotide (ptH2), which codes for a peptidyl-tRNA hydrolase 2 (PtH2), preferably for a peptidyl-tRNA hydrolase 2 having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 92.

The present invention further relates also to a corresponding method for overproducing an L-amino acid, particularly L-methionine, in which such a microorganism or such a bacterium is used.

In a further preferred embodiment according to the invention, microorganisms or bacteria according to the invention, particularly Corynebacteria according to the invention, especially Corynebacteria according to the invention of the species C. humireducens or C. glutamicum, particularly L-valine-overproducing strains according to the invention, in addition to an inventive, preferably overexpressed glycine cleavage system or polynucleotides coding for said system, have at least one, preferably at least 2 or 3, particularly preferably at least 4 or 5, of the following features:

a) an overexpressed polynucleotide (ilvA gene), which codes for a threonine dehydratase (IlvA EC 4.3.1.19), preferably for a threonine dehydratase having a

sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 106,

b) an overexpressed polynucleotide (ilvB gene), which codes for the subunit of an acetolactate synthase (IlvB), preferably for the subunit of an acetolactate synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 98,

c) an overexpressed polynucleotide (ilvN gene), which codes for the optionally feedback-resistant subunit of an acetolactate synthase (IlvN),

d) an overexpressed polynucleotide (ilvC gene), which codes for an isomeroreductase (IlvC, EC 1.1.1.86), preferably for an isomeroreductase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 100,

e) an overexpressed polynucleotide (ilvD gene), which codes for a dihydroxyacid dehydratase (IlvD, EC 4.2.1.9), preferably for a dihydroxyacid dehydratase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 102,

f) an overexpressed polynucleotide (ilvE gene), which codes for a transaminase (IlvE, EC 2.6.1.42), preferably for a transaminase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 104,

g) an overexpressed polynucleotide (ilvH gene), which codes for an acetolactate synthase (IlvH, EC 2.2.1.6), preferably for an acetolactate synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 122,

h) an attenuated polynucleotide (thrB gene), which codes for a homoserine kinase (ThrB, EC 2.7.1.39), preferably for a homoserine kinase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 4,

i) an attenuated polynucleotide (thrC gene), which codes for a threonine synthase (ThrC, EC 4.2.3.1), preferably for a threonine synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 108,

j) an overexpressed polynucleotide (hom gene), which codes for an optionally feedback-resistant homoserine dehydrogenase (Hom, EC 1.2.1.11), preferably for a homoserine dehydrogenase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 46,

k) an attenuated polynucleotide (leuA gene), which codes for an optionally feedback-resistant isopropylmalate synthase (LeuA, EC 2.3.3.13), preferably for an isopropylmalate synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 110,

l) an attenuated polynucleotide (leuB gene), which codes for an isopropylmalate dehydrogenase (LeuB, EC 1.1.1.85), preferably for an isopropylmalate dehydrogenase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 112,

m) attenuated polynucleotides (leuCD gene), which code for the subunits of an isopropylmalate isomerase (LeuCD, EC 4.2.1.33), preferably for the subunits of an isopropylmalate isomerase having sequence identities of at least 90, 95 or 98 %, preferably 100 %, to the sequences according to SEQ ID NO: 114 and SEQ ID NO: 116,

n) an overexpressed polynucleotide (panB gene), which codes for a 3-methyl-2-oxobutanoate hydroxymethyltransferase (PanB, EC 2.1.2.11), preferably for a 3-methyl-2-oxobutanoate hydroxymethyltransferase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 118,

o) an overexpressed polynucleotide (panC gene), which codes for a pantothenate synthase (PanC, EC 6.3.2.1), preferably for a pantothenate synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 120.

The present invention further relates accordingly also to a method for overproducing an L-amino acid, particularly L-valine, in which such a microorganism or such a bacterium is used.

In a further preferred embodiment according to the invention, microorganisms or bacteria according to the invention, particularly Corynebacteria according to the invention, especially Corynebacteria according to the invention of the species C. humireducens or C. glutamicum, particularly L-glutamate-overproducing strains according to the invention, in addition to an inventive, preferably overexpressed glycine cleavage system or polynucleotides coding for said system, have at least one, preferably at least two or three, particularly preferably at least four or five, of the following features:

a) an overexpressed polynucleotide (gdh), which codes for a glutamate dehydrogenase (Gdh), preferably for a glutamate dehydrogenase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 124,

b) an overexpressed polynucleotide, which codes for a glutamine synthetase (glutamine synthetase 1), preferably for a glutamine synthetase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 126,

c) an overexpressed polynucleotide, which codes for a glutamine synthetase (glutamine synthetase 2), preferably for a glutamine synthetase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 128,

d) an overexpressed polynucleotide, which codes for a glutamate synthase, preferably for a glutamate synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 130,

e) an overexpressed polynucleotide, which codes for an isocitrate dehydrogenase, preferably for an isocitrate dehydrogenase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 132,

f) an overexpressed polynucleotide, which codes for an aconitate hydrase, preferably for an aconitate hydrase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 134,

g) an overexpressed polynucleotide, which codes for a citrate synthase, preferably for a citrate synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 136,

h) an overexpressed polynucleotide (pepC), which codes for an aminopeptidase C (PepC), preferably for an aminopeptidase C having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 138,

i) an overexpressed polynucleotide, which codes for a pyruvate dehydrogenase, preferably for a pyruvate dehydrogenase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 140,

j) an overexpressed polynucleotide, which codes for a pyruvate kinase (pyruvate kinase 1), preferably for a pyruvate kinase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 142,

k) an overexpressed polynucleotide, which codes for a pyruvate kinase (pyruvate kinase 2), preferably for a pyruvate kinase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 144,

l) an overexpressed polynucleotide, which codes for an enolase, preferably for an enolase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 146,

m) an overexpressed polynucleotide (gpmA), which codes for a 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (GpmA), preferably for a phosphoglycerate mutase

having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 148,

n) an overexpressed polynucleotide (pgk), which codes for a phosphoglycerate kinase (Pgk), preferably for a phosphoglycerate kinase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 150,

o) an overexpressed polynucleotide, which codes for a glyceraldehyde-3-phosphate dehydrogenase (glycerol-3-phosphate dehydrogenase 1), preferably for a glyceraldehyde-3-phosphate dehydrogenase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 152,

p) an overexpressed polynucleotide, which codes for a glyceraldehyde-3-phosphate dehydrogenase (glycerol-3-phosphate dehydrogenase 2), preferably for a glyceraldehyde-3-phosphate dehydrogenase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 154,

q) an overexpressed polynucleotide (tpiA), which codes for a triosephosphate isomerase (TpiA), preferably for a triosephosphate isomerase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 156,

r) an overexpressed polynucleotide, which codes for a fructose bisphosphate aldolase, preferably for a fructose bisphosphate aldolase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 158,

s) an overexpressed polynucleotide, which codes for a 1-phosphofructokinase, preferably for a 1-phosphofructokinase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 160,

t) an overexpressed polynucleotide, which codes for a 6-phosphofructokinase, preferably for a 6-phosphofructokinase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 162,

u) an overexpressed polynucleotide (pgi), which codes for a glucose-6-phosphate isomerase, preferably for a glucose-6-phosphate isomerase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 6,

v) attenuated polynucleotides (sucCD), which code for the subunits of a succinyl-CoA ligase (SucCD, EC 6.2.1.5), preferably for the subunits of a succinyl-CoA ligase having sequence identities of at least 90, 95 or 98 %, preferably 100 %, to the sequences according to SEQ ID NO: 198 or SEQ ID NO: 200.

The present invention further relates accordingly also to a method for overproducing an L-amino acid, particularly L-glutamate, in which such a microorganism or such a bacterium is used.

In a further preferred embodiment according to the invention, microorganisms or bacteria according to the invention, particularly Corynebacteria according to the invention, especially Corynebacteria according to the invention of the species C. humireducens or C. glutamicum, particularly L-alanine-overproducing strains according to the invention, in addition to an inventive, preferably overexpressed glycine cleavage system or polynucleotides coding for said system, have at least one, preferably at least two or three, particularly preferably at least four or five, of the following features:

a) an overexpressed polynucleotide (alaD), which codes for an alanine dehydrogenase (AlaD), preferably for an alanine dehydrogenase from Corynebacteria,
b) an overexpressed polynucleotide (gapA), which codes for a glyceraldehyde-3-phosphate dehydrogenase (GapA), preferably for a glyceraldehyde-3-phosphate dehydrogenase from Corynebacteria,
c) a deactivated or attenuated polynucleotide (ldhA), which codes for an L-lactate dehydrogenase (LdhA), preferably for an L-lactate dehydrogenase from Corynebacteria,
d) a deactivated or attenuated polynucleotide (ppc), which codes for a phosphoenolpyruvate carboxylase (Ppc), preferably for a phosphoenolpyruvate carboxylase from Corynebacteria,
e) a deactivated or attenuated polynucleotide (alr), which codes for an alanine racemase (Alr), preferably for an alanine racemase from Corynebacteria.

The present invention further relates accordingly also to a method for overproducing an L-amino acid, particularly L-alanine, in which such a microorganism or such a bacterium is used.

In a further preferred embodiment according to the invention, microorganisms or bacteria according to the invention, particularly Corynebacteria according to the invention, especially Corynebacteria according to the invention of the species C. humireducens or C. glutamicum, particularly L-lysine-overproducing strains according to the invention, in addition to an inventive, preferably overexpressed glycine cleavage system or polynucleotides coding for said system, have at least one, preferably at least 2 or 3, particularly preferably at least 4 or 5, of the following features:

a) an overexpressed polynucleotide (dapA gene), which codes for a dihydrodipicolinate synthase (DapA, EC 4.2.1.52), preferably for a dihydrodipicolinate synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 20,

b) an overexpressed polynucleotide (lysC), which codes for a preferably feedback-resistant aspartate kinase (LysC, EC 2.7.2.4), preferably for an aspartate kinase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 54,

c) an overexpressed polynucleotide (ddh), which codes for a diaminopimelate dehydrogenase (Ddh, EC 1.4.1.16), preferably for a diaminopimelate dehydrogenase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 202,

d) an overexpressed polynucleotide (asd gene), which codes for an aspartate semialdehyde dehydrogenase (Asd, EC 1.2.1.11), preferably for an aspartate semialdehyde dehydrogenase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 28,

e) an overexpressed polynucleotide (lysA gene), which codes for a diaminopimelate decarboxylase (LysA, EC 4.1.1.20), preferably for a diaminopimelate decarboxylase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 164,

f) an overexpressed polynucleotide (aat gene), which codes for an aspartate aminotransferase (AaT, EC 2.6.1.1), preferably for an aspartate aminotransferase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 166,

g) an overexpressed polynucleotide (lysE gene), which codes for an L-lysine exporter (LysE, lysine efflux permease), preferably for an L-lysine exporter having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 168,

h) an overexpressed polynucleotide (pyc gene), which codes for a pyruvate carboxylase (Pyc, EC 6.4.1.1), preferably for a pyruvate carboxylase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 64,

i) an overexpressed polynucleotide (dapF gene), which codes for a diaminopimelate epimerase (DapF, EC 5.1.1.7),

j) an overexpressed polynucleotide (dapB gene), which codes for a dihydropicolinate reductase (DapB, EC 1.3.1.26), preferably for a dihydropicolinate reductase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 172,

k) an overexpressed polynucleotide, which codes for a glucose-6-phosphate dehydrogenase (EC 1.1.1.49), preferably for a glucose-6-phosphate dehydrogenase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 174,

l) an overexpressed polynucleotide (zwf gene), which codes for a Zwf subunit of a glucose-6-phosphate dehydrogenase (Zwf, EC 1.1.1.49), preferably for a Zwf subunit having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 188,

m) an overexpressed polynucleotide (opcA gene), which codes for the OpcA subunit of a glucose-6-phosphate dehydrogenase (OpcA, EC 1.1.1.49), preferably for an OpcA subunit having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 190,

n) an overexpressed polynucleotide (gnd gene), which codes for a phosphogluconic acid dehydrogenase (Gnd, EC 1.1.1.44), preferably for a phosphogluconic acid dehydrogenase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 176,

o) a deactivated or attenuated polynucleotide (mqo), which codes for a malate:quinone oxidoreductase (Mqo, EC 1.1.99.16), preferably for a malate:quinone oxidoreductase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 178,

p) a deactivated or attenuated polynucleotide (aceE), which codes for the E1p subunit of a pyruvate dehydrogenase complex (AceE, EC 1.2.4.1), preferably for an E1p subunit having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 180,

q) a deactivated or attenuated polynucleotide (gltA), which codes for a citrate synthase (GltA, EC 4.1.3.7), preferably for a citrate synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 182,

r) a deactivated or attenuated polynucleotide (mdh), which codes for a malate dehydrogenase (Mdh, EC 1.1.1.37), preferably for a malate dehydrogenase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 184,

s) a deactivated or attenuated polynucleotide (murE), which codes for a UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase (MurE, EC 6.3.2.13), preferably for an enzyme having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 186.

The present invention further relates accordingly also to a method for overproducing an L-amino acid, particularly L-lysine, in which such a microorganism or such a bacterium is used.

The polynucleotides and polypeptides used or to be used in the method according to the invention mentioned above preferably originate from Corynebacteria, particularly from C. glutamicum or C. humireducens, particularly preferably from C. humireducens.

"Overexpression" in accordance with the invention is generally understood to mean an increase in the intracellular concentration or activity of a ribonucleic acid, a protein (polypeptide) or an enzyme, which are encoded by a corresponding DNA, in a microorganism, compared to the starting strain (parent strain) or wild-type strain. A starting strain (parent strain) means the strain on which the measure leading to overexpression has been carried out.

The increase in the concentration or activity can be achieved, for example, by increasing the copy number of the corresponding coding polynucleotides, chromosomally or extrachromosomally, by at least one copy.

A widespread method for increasing the copy number consists of incorporating the corresponding coding polynucleotide into a vector, preferably a plasmid, which is replicated from a microorganism, particularly a coryneform bacteria. Furthermore, transposons, insertion elements (IS elements) or phages can be used as vectors. An abundance of suitable vectors is described in the prior art.

Another widespread method for achieving overexpression is the method of chromosomal gene amplification. In this method, at least one additional copy of the polynucleotide of interest is inserted into the chromosome of a coryneform bacterium. Such amplification methods are described for example in WO 03/014330 or WO 03/040373.

A further method for achieving overexpression consists of linking the corresponding gene or allele in a functional manner (operably linked) to a promoter or an expression cassette. Suitable promoters for Corynebacterium glutamicum are described, for example, in Fig. 1 of the review article of Patek et al. (Journal of Biotechnology 104(1-3), 311-323 (2003)) and in comprehensive reviews such as the "Handbook of Corynebacterium glutamicum" (Eds.: Lothar Eggeling and Michael Bott, CRC Press, Boca Raton, US (2005)) or the book "Corynebacteria, Genomics and Molecular Biology" (Ed.: Andreas Burkovski, Caister Academic Press, Norfolk, UK (2008)). In the same way, variants of the dapA promoter, the

promoter A25 for example, described in Vasicova et al (Journal of Bacteriology 181, 6188-6191 (1999)), may be used. Furthermore, the gap promoter of Corynebacterium glutamicum (EP 06007373) may be used. Finally, the well known promoters T3, T7, SP6, M13, lac, tac and trc, described by Amann et al. (Gene 69(2), 301-315 (1988)) and Amann and Brosius (Gene 40(2-3), 183-190 (1985)), may be used. Such a promoter can be inserted, for example, upstream of the relevant gene, typically at a distance of about 1-500 nucleobases from the start codon.

The measures of overexpression increase the activity or concentration of the corresponding polypeptide preferably by at least 10%, 25%, 50%, 75%, 100%, 150%, 200%, 300%, 400% or 500%, preferably at most by 1000% or 2000%, based on the activity or concentration of said polypeptide in the strain prior to the measure resulting in overexpression.

The concentration of a protein may be determined via 1- and 2-dimensional protein gel fractionation and subsequent optical identification of the protein concentration by appropriate evaluation software in the gel. A customary method of preparing protein gels for coryneform bacteria and of identifying said proteins is the procedure described by Hermann et al. (Electrophoresis, 22:1712-23 (2001)). The protein concentration may likewise be determined by Western blot hybridization using an antibody specific for the protein to be detected (Sambrook et al., Molecular Cloning: a laboratory manual, 2nd Ed. 2nd Ed. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989) and subsequent optical evaluation using corresponding software for concentration determination (Lohaus and Meyer (1998) Biospektrum 5:32-39; Lottspeich, Angewandte Chemie 38: 2630-2647 (1999)). The activity may be determined by means of a suitable enzyme assay.

"Attenuation" in accordance with the invention refers to a decrease in the intracellular concentration or activity of a ribonucleic acid, a protein (polypeptide) or an enzyme, which are encoded by a corresponding DNA, in a microorganism, compared to the starting strain (parent strain) or wild-type strain. The starting strain (parent strain) refers to the strain on which the measure for the attenuation was carried out.

The attenuation can be achieved by reducing the expression of a polypeptide, for example, by using a weak promoter or by using an allele coding for a polypeptide having a lower activity and optionally these measures may be combined. The attenuation can also be achieved by completely preventing the expression of the polypeptide, for example, by deactivating the coding gene.

The measure of attenuation decreases the activity or concentration of the corresponding polypeptide preferably by at least 10%, 25%, 50% or 75%, at most 100%, based on the activity or concentration of said polypeptide in the strain prior to the measure resulting in attenuation. In a preferred embodiment, the attenuation consists of completely deactivating the expression of the relevant polypeptide.

Feedback-resistant enzymes in connection with amino acid production is generally understood to mean enzymes which, compared to the wild form, have a lower sensitivity to inhibition by the L-amino acids and/or analogues thereof produced.

In particular, feedback-resistant aspartate kinases ($LysC^{FBR}$) mean aspartate kinases which, by comparison with the wild form, show less sensitivity to inhibition by mixtures of lysine and threonine or mixtures of AEC (aminoethylcysteine) and threonine or lysine alone or AEC alone. For lysine production, corresponding strains are preferably used which comprise such feedback-resistant or desensitised aspartate kinases.

For example, the following feedback-resistant aspartate kinases from C. glutamicum are known from the literature: A279T, A279V, S301F, S301Y, T308I, T311I, R320G, G345D, S381F. With respect to feedback-resistant aspartate kinases from C. glutamicum, reference is also made to the following publications: JP1993184366-A, JP1994062866-A, JP1994261766-A, JP1997070291-A, JP1997322774-A, JP1998165180-A, JP1998215883-A, US5688671-A, EP0387527, WO00/63388, US3732144, JP6261766, Jetten et al. (1995; Applied Microbiology Biotechnology 43: 76-82). Feedback-resistant aspartate kinases from C. glutamicum are deposited in the NCBI GenBank under the following accession numbers: E05108, E06825, E06826, E06827, E08177, E08178, E08179, E08180, E08181, E08182, E12770, E14514, E16352, E16745, E16746, I74588, I74589, I74590, I74591, I74592, I74593, I74594, I74595, I74596, I74597, X57226, L16848, L27125.

The following feedback-resistant aspartate kinases from C. humireducens according to the invention are preferably used: D274Y, A279E, S301Y, T308I, T311I, G359D.

For threonine production, preference is likewise given to using strains comprising a corresponding feedback-resistant homoserine dehydrogenase (Hom^{FBR}).

For isoleucine production and valine production, preference is likewise given to using strains comprising a corresponding feedback-resistant acetolactate synthase.

For leucine production, preference is likewise given to using strains comprising a corresponding feedback-resistant isopropylmalate synthase ($LeuA^{FBR}$).

For proline production, preference is likewise given to using strains comprising a corresponding feedback-resistant glutamate-5-kinase ($ProB^{FBR}$) .

For arginine production, preference is likewise given to using strains comprising a corresponding feedback-resistant ornithine carbamoyltransferase ($ArgF^{FBR}$).

For serine production, preference is likewise given to using strains comprising a corresponding feedback-resistant D-3-phosphoglycerate dehydrogenase ($SerA^{FBR}$) .

For methionine production, preference is likewise given to using strains comprising a corresponding feedback-resistant D-3-phosphoglycerate dehydrogenase ($SerA^{FBR}$) and/or feedback-resistant pyruvate carboxylases (Pyc^{FBR}) .

For tryptophan production, preference is likewise given to using strains comprising a corresponding feedback-resistant phospho-2-dehydro-3-deoxyheptonate aldolase ($AroG^{FBR}$ or $AroH^{FBR}$) .

With regard to further more preferable properties of the L-amino acid-overproducing C. humireducens strain to be used in accordance with the invention, reference is made to the publication of Wu et al. (2011) cited above and the other publications mentioned above.

Microorganisms according to the invention, particularly bacteria of the genus Corynebacterium, may be cultured continuously – as described for example in WO 05/021772- or discontinuously in a batch process (batch cultivation or batch method) or in a fed batch or repeated fed batch process for the purpose of producing L-lysine. A general review of known cultivation methods is available in the textbook by Chmiel (Bioprozesstechnik 1. Einführung in die Bioverfahrenstechnik [Bioprocess Technology 1. Introduction to Bioprocess Technology] (Gustav Fischer Verlag, Stuttgart, 1991)) or in the textbook by Storhas (Bioreaktoren und periphere Einrichtungen [Bioreactors and Peripheral Devices] (Vieweg Verlag, Braunschweig/ Wiesbaden, 1994)).

The culture medium or fermentation medium to be used has to satisfy the demands of the particular strains in a suitable manner. Descriptions of culture media of different microorganisms are present in the handbook "Manual of Methods for General Bacteriology",

of the American Society for Bacteriology (Washington D. C., USA, 1981). The terms culture medium and fermentation medium or medium are mutually interchangeable.

The carbon sources used may be sugars and carbohydrates such as glucose, sucrose, lactose, fructose, maltose, molasses, sucrose-containing solutions from sugarbeet or sugarcane production, starch, starch hydrolysate and cellulose, oils and fats such as soybean oil, sunflower oil, groundnut oil and coconut fat, fatty acids such as palmitic acid, stearic acid and linoleic acid, alcohols such as glycerol, methanol and ethanol and organic acids such as acetic acid or lactic acid.

It is possible to use, as nitrogen source, organic nitrogen-containing compounds such as peptones, yeast extract, meat extract, malt extract, corn steep liquor, soybean flour and urea, or inorganic compounds such as ammonium sulphate, ammonium chloride, ammonium phosphate, ammonium carbonate and ammonium nitrate. The nitrogen sources may be used individually or as a mixture.

The phosphorus sources used may be phosphoric acid, potassium dihydrogen phosphate or dipotassium hydrogen phosphate or the corresponding sodium-containing salts.

The culture medium must additionally contain salts, for example in the form of chlorides or sulphates of metals such as sodium, potassium, magnesium, calcium and iron, for example magnesium sulphate or iron sulphate, which are needed for growth. Finally, essential growth factors such as amino acids, for example homoserine, and vitamins, for example thiamine, biotin or pantothenic acid, may be used in addition to the substances mentioned above.

The feedstocks mentioned may be added to the culture in the form of a single mixture or may be fed in during the cultivation in a suitable manner.

The pH of the culture can be controlled by employing basic compounds such as sodium hydroxide, potassium hydroxide, ammonia or aqueous ammonia, or acidic compounds such as phosphoric acid or sulphuric acid in a suitable manner. The pH is generally adjusted to a value of 6.0 to 9.0, preferably 6.5 to 8. To control the evolution of foam, it is possible to use antifoams, for example fatty acid polyglycol esters. To maintain the stability of plasmids, it is possible to add to the medium suitable selective substances such as, for example, antibiotics. In order to maintain aerobic conditions, oxygen or oxygenous gas mixtures, for example air, are introduced into the culture. The use of liquids enriched with hydrogen peroxide is likewise possible. If appropriate, the fermentation is conducted at elevated

pressure, for example at a pressure of 0.03 to 0.2 MPa. The temperature of the culture is normally 20°C to 45°C and preferably 25°C to 40°C. In batch processes, the cultivation is continued until a maximum of the desired L-amino acid has formed. This aim is normally achieved within 10 hours to 160 hours. In continuous processes, longer cultivation times are possible. The activity of the bacteria results in a concentration (accumulation) of the L-amino acid in the fermentation medium and/or in the bacterial cells.

Examples of suitable fermentation media are found, inter alia, in the patent specifications 5,770,409, US 5,840,551 and US 5,990,350 or US 5,275,940.

Analysis of L-amino acids to determine the concentration at one or more time(s) during the fermentation can take place by separating the L-amino acids by means of ion exchange chromatography, preferably cation exchange chromatography, with subsequent post-column derivatization using ninhydrin, as described in Spackman et al. (Analytical Chemistry 30: 1190-1206 (1958)). It is also possible to employ ortho-phthalaldehyde rather than ninhydrin for post-column derivatization. An overview article on ion exchange chromatography can be found in Pickering (LC·GC (Magazine of Chromatographic Science) 7(6), 484-487 (1989)).

It is likewise possible to carry out a pre-column derivatization, for example using ortho-phthalaldehyde or phenyl isothiocyanate, and to fractionate the resulting amino acid derivates by reversed-phase chromatography (RP), preferably in the form of high-performance liquid chromatography (HPLC). A method of this type is described, for example, in Lindroth et al. (Analytical Chemistry 51: 1167 - 1174 (1979)).

Detection is carried out photometrically (absorption, fluorescence).

A review regarding amino acid analysis can be found inter alia in the textbook "Bioanalytik" from Lottspeich and Zorbas (Spektrum Akademischer Verlag, Heidelberg, Germany 1998).

Accordingly, the invention relates also to a method for producing an L-amino acid, characterized in that the following steps are carried out:

a) fermentation of the microorganisms according to the invention, particularly coryneform bacteria, preferably of the genus Corynebacterium, particularly preferably of the species Corynebacterium glutamicum or Corynebacterium humireducens, in a suitable nutrient medium, and

b) accumulation of the L-amino acids in the nutrient medium and/or in the cells of the bacteria mentioned.

A product containing L-amino acid is then provided or produced or recovered in liquid or solid form.

The fermentation measures result in a fermentation broth which comprises the relevant L-amino acid.

A fermentation broth means a fermentation medium or nutrient medium in which a microorganism has been cultivated for a certain time and at a certain temperature. The fermentation medium or the media used during the fermentation comprises/comprise all of the substances or components which ensure propagation of the microorganism and formation of the desired L-amino acid.

When the fermentation is complete, the resulting fermentation broth accordingly comprises

a) the biomass (cell mass) of the microorganism, said biomass having been produced due to propagation of the cells of said microorganism,

b) the L-amino acid formed during the fermentation,

c) the organic by-products formed during the fermentation, and

d) the constituents of the fermentation medium employed or of the starting materials, such as, for example, vitamins such as biotin or salts such as magnesium sulphate, which have not been consumed in the fermentation.

The organic by-products include substances which are produced by the microorganisms employed in the fermentation in addition to the desired L-amino acid and are optionally secreted. These also include sugars such as, for example, trehalose.

The fermentation broth is removed from the culture vessel or fermentation tank, collected where appropriate, and used for providing an L-amino acid-containing product, in liquid or solid form. The expression "recovering the L-amino acid-containing product" is also used for this. In the simplest case, the L-amino acid-containing fermentation broth itself constitutes the recovered product.

One or more of the measures selected from the group consisting of

a) partial (> 0% to < 80%) to complete (100%) or virtually complete (≥ 80%, ≥ 90%, ≥ 95%, ≥ 96%, ≥ 97%, ≥ 98%, ≥ 99%) removal of the water,

b) partial (> 0% to < 80%) to complete (100%) or virtually complete (≥ 80%, ≥ 90%, ≥ 95%, ≥ 96%, ≥ 97%, ≥ 98%, ≥ 99%) removal of the biomass, the latter being optionally inactivated before removal,

c) partial (> 0% to < 80%) to complete (100%) or virtually complete (≥ 80%, ≥ 90%, ≥ 95%, ≥ 96%, ≥ 97%, ≥ 98%, ≥ 99%, ≥ 99.3%, ≥ 99.7%) removal of the organic by - products formed during fermentation, and

d) partial (> 0%) to complete (100%) or virtually complete (≥ 80%, ≥ 90%, ≥ 95%, ≥ 96%, ≥ 97%, ≥ 98%, ≥ 99%, ≥ 99.3%, ≥ 99.7%) removal of the constituents of the fermentation medium employed or of the starting materials, which have not been consumed in the fermentation,

from the fermentation broth achieves concentration or purification of the L-amino acid. Products having a desired content of L-amino acid are isolated in this way.

The partial (> 0% to < 80%) to complete (100%) or virtually complete (≥ 80% to < 100%) removal of the water (measure a)) is also referred to as drying.

Complete or virtually complete removal of the water, of the biomass, of the organic by-products and of the unconsumed constituents of the fermentation medium employed results in pure (≥ 80% by weight, ≥ 90% by weight) or high-purity (≥ 95% by weight, ≥ 97% by weight, ≥ 99% by weight) product forms of the L-amino acid. An abundance of technical instructions for measures a), b), c) and d) are available in the prior art.

Working examples

Example 1: Alanine and valine production by C. humireducens

To assess alanine and valine production, the strain *C. humireducens* (DSM 45392) was cultured in a shaking flask batch. For this purpose, the *C. humireducens* strain was incubated in 10 ml of BHI liquid medium (Brain Heart Infusion; Merck) (37 g/l H_2O) at 37°C at 200 rpm for 24 h as preculture. 10 ml of shaking flask medium were then inoculated to an OD_{660} of 0.2 and cultured at 37°C at 200 rpm for 48 h. To prepare said medium, 20 g of ammonium sulphate, 0.4 g of $MgSO_4*7H_2O$, 0.6 g of KH_2PO_4 and 10 g of yeast extract were dissolved in

750 ml of H_2O. The pH of the solution was adjusted to 7.8 with 20% NH_4OH and the solution was then autoclaved. 4 ml of a vitamin solution (pH 7 with NH_4OH), consisting of 0.25 g/l of thiamine, 50 mg/l of cyanocobalamin, 25 mg/l of biotin and 1.25 g/l of pyridoxine, were then added. In addition, 140 ml of a sterile-filtered 50% glucose solution and 50 g of dry autoclaved $CaCO_3$ were added and the medium subsequently made up to one litre. After culturing, the supernatant of four parallel cultures was in each case analysed by HPLC to determine the alanine, glycine and valine content with a detection limit of ≥0.01 g/l.

The strain *C. humireducens* after culturing for 48 h in shaking flask medium at 37°C, 200 rpm at a shaking flask scale produces around 0.81 g/l of alanine (net yield: 0.011 $g_{alanine}/g_{glucose}$) and 1.6 g/l of valine (net yield: 0.022 $g_{valine}/g_{glucose}$) (Tab. 1). Glycine was only produced in small amounts as by-product.

Tab. 1: Analytical data from a shaking flask experiment with the strain *C. humireducens*. The values measured after culturing with cells and with the blank medium are shown.

	Alanine (g/l)	**Valine (g/l)**
C. humireducens	1.27	1.9
Blank medium without cells	0.46	0.3

Example 3: Glutamate performance assay

For the L-glutamate performance assay, the strain *C. humireducens* (DSM 45392) was cultured in a shaking flask batch. For this purpose, the *C. humireducens* strain was incubated in 10 ml of BHI liquid medium (Brain Heart Infusion; Merck) (37 g/l H_2O) at 37°C at 200 rpm for 24 h as preculture. 10 ml of shaking flask medium were then inoculated to an OD_{660} of 0.2 and cultured at 37°C at 200 rpm for 48 h. To prepare said medium, 20 g of ammonium sulphate, 0.4 g of $MgSO_4*7H_2O$, 0.6 g of KH_2PO_4 and 10 g of yeast extract were dissolved in 750 ml of H_2O. The pH of the solution was adjusted to 7.8 with 20% NH_4OH and the solution was then autoclaved. 4 ml of a vitamin solution (pH 7 with NH_4OH), consisting of 0.25 g/l of thiamine, 50 mg/l of cyanocobalamin, 25 mg/l of biotin and 1.25 g/l of pyridoxine, were then added. In addition, 140 ml of a sterile-filtered 50% glucose solution and 50 g of dry

autoclaved $CaCO_3$ were added. 5 ml of a 400 mM sterile-filtered threonine stock solution were then added and the medium was subsequently made up to one litre.
After culturing, the supernatant of four parallel cultures was in each case analysed by HPLC to determine the glutamate content with a detection limit of ≥0.01 g/l.

The strain *C. humireducens* after culturing for 48 h in shaking flask medium at 37°C, 200 rpm at a shaking flask scale produced 1.8 (+/-0.6) g/l of L-glutamate. The initial concentration of L-glutamate in the medium was 0.78 (+/-0.1) g/l. Glycine was only produced in small amounts as by-product.

Claims

1. Glycine cleavage system comprising the enzymes GcvP, GcvT and GcvH, characterized in that said system comprises at least one of the following polypeptides:
   a) an enzyme GcvP having a sequence identity of at least 80% to the sequence according to SEQ ID NO: 40,
   b) an enzyme GcvT having a sequence identity of at least 80% to the sequence according to SEQ ID NO: 42,
   c) an enzyme GcvH having a sequence identity of at least 80% to the sequence according to SEQ ID NO: 38.

2. Glycine cleavage system according to Claim 1, characterized in that said system comprises two, preferably all three of the polypeptides mentioned above.

3. Glycine cleavage system according to Claim 2, characterized in that said system comprises the following polypeptides:
   a) an enzyme GcvP having a sequence identity of at least 95 or 98% to the sequence according to SEQ ID NO: 40,
   b) an enzyme GcvT having a sequence identity of at least 95 or 98% to the sequence according to SEQ ID NO: 42,
   c) an enzyme GcvH having a sequence identity of at least 95 or 98% to the sequence according to SEQ ID NO: 38.

4. Glycine cleavage system according to any of the preceding claims, characterized in that said system comprises at least one further polypeptide selected from the group consisting of:
   a) an enzyme LipA having a sequence identity of at least 80% to the sequence according to SEQ ID NO: 48,
   b) an enzyme LipB having a sequence identity of at least 80% to the sequence according to SEQ ID NO: 50,
   c) an enzyme Lpd having a sequence identity of at least 80% to the sequence according to SEQ ID NO: 52,

d) an enzyme LplA having a sequence identity of at least 80% to the sequence according to SEQ ID NO: 94,

e) an enzyme GcvL having a sequence identity of at least 80% to the sequence according to SEQ ID NO: 96.

5. Polypeptides, which constitute enzymes of a glycine cleavage system, selected from the group consisting of:

a) an enzyme GcvP having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 40,

b) an enzyme GcvT having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 42,

c) an enzyme GcvH having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 38,

d) an enzyme LipA, preferably an enzyme LipA having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 48,

e) an enzyme LipB, preferably an enzyme LipB having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 50,

f) an enzyme Lpd, preferably an enzyme Lpd having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 52,

g) an enzyme LplA, preferably an enzyme LplA having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%, especially 100%, to the sequence according to SEQ ID NO: 94,

h) an enzyme GcvL, preferably an enzyme GcvL having a sequence identity of at least 80%, preferably at least 85 or 90%, particularly at least 92, 94, 96 or 98%,

especially 100%, to the sequence according to SEQ ID NO: 96.

6. Polynucleotides, which code for enzymes of a glycine cleavage system, selected from the group consisting of:

a) a polynucleotide (gcvP), which codes for the enzyme GcvP and has a sequence identity of at least 70 or 75%, preferably at least 80 or 85%, particularly at least 90 or 95%, especially at least 98 or 100%, to the sequence of position 301 to 3162 according to SEQ ID NO: 39 and/or hybridizes under stringent conditions with a polynucleotide of which the sequence is complementary to the sequence of position 301 to 3162 according to SEQ ID NO: 39;

b) a polynucleotide (gcvT), which codes for the enzyme GcvT and has a sequence identity
of at least 70 or 75%, preferably at least 80 or 85%, particularly at least 90 or 95%, especially at least 98 or 100%, to the sequence of position 301 to 1404 according to SEQ ID NO: 41 and/or hybridizes under stringent conditions with a polynucleotide of which the sequence is complementary to the sequence of position 301 to 1404 according to SEQ ID NO: 41;

c) a polynucleotide (gcvH), which codes for the enzyme GcvH and has a sequence identity of at least 70 or 75%, preferably at least 80 or 85%, particularly at least 90 or 95%, especially at least 98 or 100%, to the sequence of position 301 to 699 according to SEQ ID NO: 37 and/or hybridizes under stringent conditions with a polynucleotide of which the sequence is complementary to the sequence of position 301 to 699 according to SEQ ID NO: 37;

d) a polynucleotide (lipA), which codes for an enzyme LipA and has a sequence identity of at least 70%, preferably at least 80 or 85%, particularly at least 90 or 95%, especially at least 98 or 100%, to the sequence of position 301 to 1344 according to SEQ ID NO: 47 and/or hybridizes under stringent conditions with a polynucleotide of which the sequence is complementary to the sequence of position 301 to 1344 according to SEQ ID NO: 47;

e) a polynucleotide (lipB), which codes for an enzyme LipB and has a sequence identity of at least 70%, preferably at least 80 or 85%, particularly at least 90 or 95%, especially at least 98 or 100%, to the sequence of position 301 to 1089 according to SEQ ID NO: 49 and/or hybridizes under stringent conditions with a polynucleotide of which the sequence is complementary to the sequence of position 301 to 1089 according to SEQ ID NO: 49;

f) a polynucleotide (lpd), which codes for an enzyme Lpd and has a sequence identity of at least 70%, preferably at least 80 or 85%, particularly at least 90 or 95%, especially at least 98 or 100%, to the sequence of position 301 to 1710 according to SEQ ID NO: 51 and/or hybridizes under stringent conditions with a polynucleotide of which the sequence is complementary to the sequence of position 301 to 1710 according to SEQ ID NO: 51;

g) a polynucleotide (lplA), which codes for an enzyme LplA and has a sequence identity of at least 70%, preferably at least 80 or 85%, particularly at least 90 or 95%, especially at least 98 or 100%, to the sequence of position 301 to 1089 according to SEQ ID NO: 93 and/or hybridizes under stringent conditions with a polynucleotide of which the sequence is complementary to the sequence of position 301 to 1089 according to SEQ ID NO: 93;

h) a polynucleotide (gcvL), which codes for an enzyme GcvL and has a sequence identity of at least 70%, preferably at least 80 or 85%, particularly at least 90 or 95%, especially at least 98 or 100%, to the sequence of position 301 to 1710 according to SEQ ID NO: 95 and/or hybridizes under stringent conditions with a polynucleotide of which the sequence is complementary to the sequence of position 301 to 1710 according to SEQ ID NO: 95.

7. Vector, characterized in that said vector comprises at least one polynucleotide, preferably at least two or three polynucleotides, according to Claim 6.

8. Recombinant microorganism, characterized in that said microorganism comprises at least one glycine cleavage system according to any of Claims 1 to 4 and/or polynucleotides coding for such a glycine cleavage system and/or at least one polypeptide according to Claim 5 and/or a polynucleotide coding for such a polypeptide or polynucleotides coding for such polypeptides and/or at least one polynucleotide according to Claim 6 and/or a vector according to Claim 7.

9. Recombinant microorganism according to Claim 8, characterized in that the glycine cleavage system and/or polynucleotides coding for such a system are present in overexpressed form.

10. Recombinant microorganism according to Claim 8 or 9, characterized in that said microorganism is an L-methionine-overproducing strain having at least one,

preferably at least two or three, particularly preferably at least four or five, of the following features:

a) an attenuated polynucleotide (mcbR), which codes for a DNA binding domain of the type HTH tetR (McbR), preferably for a DNA binding domain having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 2,

b) an attenuated polynucleotide (thrB gene), which codes for a homoserine kinase (ThrB, EC 2.7.1.39), preferably for a homoserine kinase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 4,

c) an attenuated polynucleotide (pgi), which codes for a glucose-6-phosphate isomerase (Pgi, EC 5.3.1.9), preferably for a glucose-6-phosphate isomerase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 6,

d) an attenuated polynucleotide (pck), which codes for a phosphoenolpyruvate carboxykinase (Pck, EC 4.1.1.32), preferably for a phosphoenolpyruvate carboxykinase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 8,

e) an attenuated polynucleotide (metQ), which codes for a D-methionine-binding lipoprotein (MetQ), preferably for a D-methionine-binding lipoprotein having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 10,

f) an attenuated polynucleotide (metP), which codes for a methionine transporter (MetP), preferably for a methionine transporter having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 12,

g) an attenuated polynucleotide (metN), which codes for an ATP-dependent methionine transporter (MetN), preferably for an ATP-dependent methionine transporter having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 14,

h) an attenuated polynucleotide (metK), which codes for an S-adenosylmethionine synthase (MetK), preferably for an S-adenosylmethionine synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 16,

i) an attenuated polynucleotide (metI), which codes for a methionine import system permease (MetI), preferably for a methionine import system permease having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 18,

j) an attenuated polynucleotide (dapA), which codes for a 4-hydroxy-tetrahydrodipicolinate synthase (DapA), preferably for a 4-hydroxy-tetrahydrodipicolinate synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 20,

k) an overexpressed polynucleotide (CBS), which codes for a cysteine synthase (CBS), preferably for a cysteine synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 22,

l) an attenuated polynucleotide, which codes for a cg3031 homologue, preferably for a cg3031 homologue having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 24,

m) an overexpressed polynucleotide (aecD), which codes for a cystathionine beta-lyase (AecD), preferably for a cystathionine beta-lyase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 26,

n) an overexpressed polynucleotide (asd), which codes for an aspartate semialdehyde dehydrogenase (Asd), preferably for an aspartate semialdehyde dehydrogenase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 28,

o) an overexpressed polynucleotide (metH), which codes for a 5-methyltetrahydrofolate homocysteine methyltransferase (MetH, EC 2.1.1.13),

p) an overexpressed polynucleotide (brnE), which codes for the smaller subunit of a transporter for branched-chain amino acids (BrnE), preferably for a subunit having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 30,

q) an overexpressed polynucleotide (brnF), which codes for the larger subunit of a transporter for branched-chain amino acids (BrnF), preferably for a subunit having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 32,

r) an overexpressed polynucleotide (cysE), which codes for a serine acetyltransferase (CysE), preferably for a serine acetyltransferase having a

sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 34,

s) an overexpressed polynucleotide (cysK), which codes for a cysteine synthase (CysK), preferably for a cysteine synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 36,

t) an overexpressed polynucleotide (glyA), which codes for a serine hydroxymethyltransferase (GlyA), preferably for a serine hydroxymethyltransferase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 44,

u) an overexpressed polynucleotide (hom), which codes for an optionally feedback-resistant homoserine dehydrogenase (Hom), preferably for a homoserine dehydrogenase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 46,

v) an overexpressed polynucleotide (lysC), which codes for an optionally feedback-resistant aspartate kinase (LysC), preferably for an aspartate kinase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 54,

w) an overexpressed polynucleotide (metB), which codes for a cystathionine gamma-synthase (MetB), preferably for a cystathionine gamma-synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 56,

x) an overexpressed polynucleotide (metF), which codes for a 5,10-methylenetetrahydrofolate reductase (MetF), preferably for a 5,10-methylenetetrahydrofolate reductase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 58,

y) an overexpressed polynucleotide (metX), which codes for a homoserine O-acetyltransferase (MetX), preferably for a homoserine O-acetyltransferase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 60,

z) an overexpressed polynucleotide (metY), which codes for an O-acetylhomoserine lyase (MetY), preferably for an O-acetylhomoserine lyase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 62,

aa) an overexpressed polynucleotide (pyc), which codes for a pyruvate carboxylase (Pyc), preferably for a pyruvate carboxylase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 64,

bb) an overexpressed polynucleotide (serA), which codes for an optionally feedback-resistant D-3-phosphoglycerate dehydrogenase (SerA), preferably for a D-3-phosphoglycerate dehydrogenase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 66,

cc) an overexpressed polynucleotide (serB), which codes for a phosphoserine phosphatase (SerB), preferably for a phosphoserine phosphatase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 68,

dd) an overexpressed polynucleotide (serC), which codes for a phosphoserine aminotransferase (SerC), preferably for a phosphoserine aminotransferase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 70,

ee) an overexpressed polynucleotide (ald), which codes for an alanine dehydrogenase (Ald), preferably for an alanine dehydrogenase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 72,

ff) an overexpressed polynucleotide (cysD), which codes for the subunit of a sulphate adenylyltransferase (CysD), preferably for a subunit having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 74,

gg) an overexpressed polynucleotide (cysH), which codes for an adenosine phosphosulphate reductase (CysH), preferably for an adenosine phosphosulphate reductase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 76,

hh) an overexpressed polynucleotide (cysI), which codes for a sulphite reductase (CysI), preferably for a sulphite reductase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 78,

ii) an overexpressed polynucleotide (cysJ), which codes for (CysJ), preferably for one having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 80,

jj) an overexpressed polynucleotide (cysN), which codes for the subunit of a sulphate adenylyltransferase (CysN), preferably for a subunit having a sequence

identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 82,

kk) an overexpressed polynucleotide (cysY), which codes for a cystathionine beta-synthase (CysY), preferably for a cystathionine beta-synthase having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 84,

ll) an overexpressed polynucleotide (cysZ), which codes for a putative sulphate transporter (CysZ), preferably for a sulphate transporter having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 86,

mm) an overexpressed polynucleotide (metE), which codes for a 5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase (MetE), preferably for a protein having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 88,

nn) an overexpressed polynucleotide (ptH1), which codes for a peptidyl-tRNA hydrolase 1 (PtH1), preferably for a peptidyl-tRNA hydrolase 1 having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 90,

oo) an overexpressed polynucleotide (ptH2), which codes for a peptidyl-tRNA hydrolase 2 (PtH2), preferably for a peptidyl-tRNA hydrolase 2 having a sequence identity of at least 90, 95 or 98%, preferably 100%, to the sequence according to SEQ ID NO: 92.

11. Recombinant microorganism according to any of Claims 8 to 10, characterized in that said microorganism is a coryneform bacterium, particularly a Corynebacterium, preferably C. glutamicum or C. humireducens.

12. Method for overproducing an L-amino acid, characterized in that a glycine cleavage system according to any of Claims 1 to 4 and/or at least one polypeptide according to Claim 5 and/or at least one polynucleotide according to Claim 6 and/or a vector according to Claim 7 and/or a recombinant microorganism according to any of Claims 8 to 11 is used in said method.

13. Method according to the preceding claim, characterized in that the overproduced L-amino acid is selected from L-alanine, L-valine, L-amino acids of the glutamate

family, particularly L-glutamate, L-glutamine, L-proline and L-arginine, and L-amino acids of the aspartate family, particularly L-aspartate, L-asparagine, L-methionine, L-lysine, L-isoleucine and L-threonine.

14. Method according to Claim 13, characterized in that the overproduced L-amino acid is L-methionine.

15. Method according to any of the preceding claims, characterized in that only low amounts of glycine occur as by-product.

SEQUENCE LISTING

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<120> Method for producing L-amino acids in Corynebacteria using a glycine cleavage system

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            20                  25                  30

gtg ggc atc tac gac acc gtc gag gtc gag gtc atc gag tcg ggc ctc         444
Val Gly Ile Tyr Asp Thr Val Glu Val Glu Val Ile Glu Ser Gly Leu
        35                  40                  45

gag gtc gag gtc ttc ggc gag ggc gag gac gac ctg ccc cgc gac ggt         492
Glu Val Glu Val Phe Gly Glu Gly Glu Asp Asp Leu Pro Arg Asp Gly
    50                  55                  60

tcc cac ctg gtg gtc aag gcc atc cgg tcg ggc ctc aac gcc gcc cac         540
Ser His Leu Val Val Lys Ala Ile Arg Ser Gly Leu Asn Ala Ala His
65                  70                  75                  80

gcc gag gcc ccg ggc ctg cgc gtg gtg tgc acc aac gcc atc ccg cag         588
Ala Glu Ala Pro Gly Leu Arg Val Val Cys Thr Asn Ala Ile Pro Gln
                85                  90                  95

tcc cgt ggc ctg ggc tcc tcc gcc gcc gca gcc gtc gcg gga gtt ctg         636
Ser Arg Gly Leu Gly Ser Ser Ala Ala Ala Ala Val Ala Gly Val Leu
            100                 105                 110

gcc gcc aac ggt ctg gcg ggc aac ccg ctg acc acc gac cag gtg gtc         684
Ala Ala Asn Gly Leu Ala Gly Asn Pro Leu Thr Thr Asp Gln Val Val
        115                 120                 125

cag ctg tcc tcc gcc ttc gag ggg cac ccc gac aac gcc gcg gcc tcc         732
Gln Leu Ser Ser Ala Phe Glu Gly His Pro Asp Asn Ala Ala Ala Ser
    130                 135                 140

gtc ctc ggt tcc gcc gtg gtc tcc tgg acc acg acc ccg gtc gac ggc         780
Val Leu Gly Ser Ala Val Val Ser Trp Thr Thr Thr Pro Val Asp Gly
145                 150                 155                 160

tcg cag ccg ggg tac cgg gcg gtg gcg gtg gac gtc gac aag cgc atc         828
Ser Gln Pro Gly Tyr Arg Ala Val Ala Val Asp Val Asp Lys Arg Ile
                165                 170                 175

cgg gcg acg gct ctc gtg ccg gac ttc cac gcc tcc acc cag gcg gtg         876
Arg Ala Thr Ala Leu Val Pro Asp Phe His Ala Ser Thr Gln Ala Val
            180                 185                 190

cgt cgc gtg ctg ccg agc cac gtc acc cac acg gac gcg cgt ttc aac         924
Arg Arg Val Leu Pro Ser His Val Thr His Thr Asp Ala Arg Phe Asn
        195                 200                 205

gtc tcg cgc acc gcg gtg atg acc gtg gcg ctg cag aac cac ccg gag         972
Val Ser Arg Thr Ala Val Met Thr Val Ala Leu Gln Asn His Pro Glu
    210                 215                 220
```

```
ctg ctg tgg gag ggc acc cgt gac cgc ctg cac cag ccc tac cgc gcc      1020
Leu Leu Trp Glu Gly Thr Arg Asp Arg Leu His Gln Pro Tyr Arg Ala
225                 230                 235                 240

gac gtg ctg ccg gtg acc gcc gag tgg gtc aac cgt ctg cgc aac cgc      1068
Asp Val Leu Pro Val Thr Ala Glu Trp Val Asn Arg Leu Arg Asn Arg
                245                 250                 255

ggt tac gcc gcg tac ctc tcc ggc gcc ggc ccg acc tgc atg gtc ctg      1116
Gly Tyr Ala Ala Tyr Leu Ser Gly Ala Gly Pro Thr Cys Met Val Leu
            260                 265                 270

tcg gtc gac ccg atc gag gag gcc atc ctc gag gag gcc cgc gcc gcc      1164
Ser Val Asp Pro Ile Glu Glu Ala Ile Leu Glu Glu Ala Arg Ala Ala
        275                 280                 285

ggt ctg cgc gtc ctc gag ctg gag gtc gcc ggt ccg gcg acc gtc gag      1212
Gly Leu Arg Val Leu Glu Leu Glu Val Ala Gly Pro Ala Thr Val Glu
    290                 295                 300

gtc agc cgg gtc tga cctaccggtc gtcggcgggg gtccccctgt cggcgaccac      1267
Val Ser Arg Val
305

cgagcacgcg cccgagggct ggaaggggcg caggctcagc cggacggggg cggagccgac    1327

ggactcctgc aggaaaccct cgtggatggc gcagatcatg agcgagggtc ggtgcccctc    1387

ggcgacgaag gggcacgcct gcagctcgat gtcgaccgac tccgcgtcgg tgcccccgtc    1447

gccctgctcc ctgcgcatgg tcgggtcgaa acccagctca cggagggtgt ggtggagacg    1507

gtcgagcgcc gtgtccatgg                                               1527
```

<210> 4
<211> 308
<212> PRT
<213> Corynebacterium humireducens

<400> 4

```
Val Ser Ile Gln Leu Glu Val Gly Thr Arg Ala Thr Val Thr Val Pro
1               5                   10                  15

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

Val Gly Ile Tyr Asp Thr Val Glu Val Glu Val Ile Glu Ser Gly Leu
        35                  40                  45

Glu Val Glu Val Phe Gly Glu Gly Glu Asp Asp Leu Pro Arg Asp Gly
    50                  55                  60
```

```
Ser His Leu Val Val Lys Ala Ile Arg Ser Gly Leu Asn Ala Ala His
65                  70                  75                  80

Ala Glu Ala Pro Gly Leu Arg Val Val Cys Thr Asn Ala Ile Pro Gln
                85                  90                  95

Ser Arg Gly Leu Gly Ser Ser Ala Ala Ala Ala Val Ala Gly Val Leu
            100                 105                 110

Ala Ala Asn Gly Leu Ala Gly Asn Pro Leu Thr Thr Asp Gln Val Val
        115                 120                 125

Gln Leu Ser Ser Ala Phe Glu Gly His Pro Asp Asn Ala Ala Ala Ser
    130                 135                 140

Val Leu Gly Ser Ala Val Val Ser Trp Thr Thr Thr Pro Val Asp Gly
145                 150                 155                 160

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

Arg Ala Thr Ala Leu Val Pro Asp Phe His Ala Ser Thr Gln Ala Val
            180                 185                 190

Arg Arg Val Leu Pro Ser His Val Thr His Thr Asp Ala Arg Phe Asn
        195                 200                 205

Val Ser Arg Thr Ala Val Met Thr Val Ala Leu Gln Asn His Pro Glu
    210                 215                 220

Leu Leu Trp Glu Gly Thr Arg Asp Arg Leu His Gln Pro Tyr Arg Ala
225                 230                 235                 240

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

Gly Tyr Ala Ala Tyr Leu Ser Gly Ala Gly Pro Thr Cys Met Val Leu
            260                 265                 270

Ser Val Asp Pro Ile Glu Glu Ala Ile Leu Glu Glu Ala Arg Ala Ala
        275                 280                 285

Gly Leu Arg Val Leu Glu Leu Glu Val Ala Gly Pro Ala Thr Val Glu
    290                 295                 300
```

Val Ser Arg Val
305

<210> 5
<211> 2238
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1938)
<223> gene pgi

<400> 5
caggcgatgt aggactcctc gtcggcccag cgggtgacca cgaagtagcg gttctccccg 60

gccacggggc ggagaagctg gaaaccctcg aagccgggtg cctggtcgac ggcgttcttc 120

cgggcggcga agcgctcctc cagctgcggg ccggcgccct cggggacggt gatggcgttg 180

attttcacga tgctcatgcc ccccattgtg cccaaccggc cgcttccccg gcggacaccc 240

gggaaagtca ctagattcgt gagtgtcccg aacatatccc cgcattgagg agcccgaccc 300

atg gcc gac atc acc acc tcc gct gaa tgg aag aac ctg gag tcc gag 348
Met Ala Asp Ile Thr Thr Ser Ala Glu Trp Lys Asn Leu Glu Ser Glu
1 5 10 15

ttc gag cgc acc cag ggt cag acc ctg cgg gag ctg ttc gcc gcg gat 396
Phe Glu Arg Thr Gln Gly Gln Thr Leu Arg Glu Leu Phe Ala Ala Asp
20 25 30

ccg cag cgt gcg gag aag ctg acc ttc gat gcg gcc ggt ctc cac gtc 444
Pro Gln Arg Ala Glu Lys Leu Thr Phe Asp Ala Ala Gly Leu His Val
35 40 45

gac ctc tcc aag aac ctg ctt gac gac gcc acc gtg gcc tcc ctc gtc 492
Asp Leu Ser Lys Asn Leu Leu Asp Asp Ala Thr Val Ala Ser Leu Val
50 55 60

gcc ctc gcc aag gag gcg cag ctc acc gag gcc atc gag gcg atg ttc 540
Ala Leu Ala Lys Glu Ala Gln Leu Thr Glu Ala Ile Glu Ala Met Phe
65 70 75 80

agc ggc gtg cac atc aac aac acc gag gac cgc gcc gtg ctg cac acc 588
Ser Gly Val His Ile Asn Asn Thr Glu Asp Arg Ala Val Leu His Thr
85 90 95

gcc ctg cgt ctg ccg gtc gag gag gac ctc gag gtc gac ggc cag gac 636
Ala Leu Arg Leu Pro Val Glu Glu Asp Leu Glu Val Asp Gly Gln Asp
100 105 110

gtc gcc gcc gac gtc cac gag gtg ctc ggc cgc atg cgc gac ttc gcc 684
Val Ala Ala Asp Val His Glu Val Leu Gly Arg Met Arg Asp Phe Ala
115 120 125

```
tcc tcc ctg cgt gcg ggc acc tgg ctc ggc cac acc ggc cgc acc atc        732
Ser Ser Leu Arg Ala Gly Thr Trp Leu Gly His Thr Gly Arg Thr Ile
    130                 135                 140

aag aag gtc gtc aac atc ggc atc ggc ggc tcc gac ctg ggc ccg gcc        780
Lys Lys Val Val Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Pro Ala
145                 150                 155                 160

atg gcc gcc cgg gcg ctg cgc tcc tac gcc acc gcc ggc atc acc gcc        828
Met Ala Ala Arg Ala Leu Arg Ser Tyr Ala Thr Ala Gly Ile Thr Ala
                165                 170                 175

gag ttc gtc tcc aac gtc gac ccg gcc gac atg tcc gcc acc ctc gac        876
Glu Phe Val Ser Asn Val Asp Pro Ala Asp Met Ser Ala Thr Leu Asp
            180                 185                 190

gag ctc gac ccc gag tcg acc ctg ttc atc atc gcc tcc aag acc ttc        924
Glu Leu Asp Pro Glu Ser Thr Leu Phe Ile Ile Ala Ser Lys Thr Phe
        195                 200                 205

acc acc cag gag acc ctc gcc aac gcg cac gcc gcg aag cgc tgg ctg        972
Thr Thr Gln Glu Thr Leu Ala Asn Ala His Ala Ala Lys Arg Trp Leu
    210                 215                 220

ctg cag gcc ttc gac ggg gac gag tcg gcc gtc gcg aag cac ttc gtg       1020
Leu Gln Ala Phe Asp Gly Asp Glu Ser Ala Val Ala Lys His Phe Val
225                 230                 235                 240

gcg gtg tcc acc aac gcc cag aag gtc gcc gag ttc ggc atc gac acc       1068
Ala Val Ser Thr Asn Ala Gln Lys Val Ala Glu Phe Gly Ile Asp Thr
                245                 250                 255

gac aac atg ttc ggc ttc tgg gac tgg gta ggc ggc cgc tac tcc gtc       1116
Asp Asn Met Phe Gly Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser Val
            260                 265                 270

gac tcc gcc atc ggc ctg tcc ctc atg gcc gtc atc ggc ccg ctg gac       1164
Asp Ser Ala Ile Gly Leu Ser Leu Met Ala Val Ile Gly Pro Leu Asp
        275                 280                 285

ttc atg cgc ttc ctc gag ggc ttc cgc gcc atg gac gag cac ttc cgc       1212
Phe Met Arg Phe Leu Glu Gly Phe Arg Ala Met Asp Glu His Phe Arg
    290                 295                 300

gcg acc ccc ttc gag aag aac gtg ccc gtc ctc atg gcg ctg ctg ggc       1260
Ala Thr Pro Phe Glu Lys Asn Val Pro Val Leu Met Ala Leu Leu Gly
305                 310                 315                 320

atc tgg tac gtc aac ttc cac ggc ttc gag acc cac gcg gtc ctc ccc       1308
Ile Trp Tyr Val Asn Phe His Gly Phe Glu Thr His Ala Val Leu Pro
                325                 330                 335

tac tct cag gac ctc tcc cgt ttc gcc gcc tac ctg cag cag ctg acc       1356
Tyr Ser Gln Asp Leu Ser Arg Phe Ala Ala Tyr Leu Gln Gln Leu Thr
            340                 345                 350

atg gag tcc aac ggc aag tcc gtc cga cac gac ggc acc gcc gtc gac       1404
Met Glu Ser Asn Gly Lys Ser Val Arg His Asp Gly Thr Ala Val Asp
        355                 360                 365
```

```
tac gcc acc ggt gag atc tac tgg ggc gag ccg ggc acc aac ggc cag      1452
Tyr Ala Thr Gly Glu Ile Tyr Trp Gly Glu Pro Gly Thr Asn Gly Gln
    370                 375                 380

cac gcc ttc tac cag ctc atg cac cag ggc acc cgc gtc gtc ccg gcc      1500
His Ala Phe Tyr Gln Leu Met His Gln Gly Thr Arg Val Val Pro Ala
385                 390                 395                 400

gac ttc atc ggc ttc gcc cgc ccg aag aac gac ctg ccg acc gcc acc      1548
Asp Phe Ile Gly Phe Ala Arg Pro Lys Asn Asp Leu Pro Thr Ala Thr
                405                 410                 415

ggc gag ggc tcc atg cac gac ctg ctc atg ggc aac ctc ttc gcc cag      1596
Gly Glu Gly Ser Met His Asp Leu Leu Met Gly Asn Leu Phe Ala Gln
            420                 425                 430

agc aag gtg ctg gcc ttc ggc aag acc gcc gag gag atc gcc gcc gag      1644
Ser Lys Val Leu Ala Phe Gly Lys Thr Ala Glu Glu Ile Ala Ala Glu
        435                 440                 445

gga gtg tcc gcg gac ctc gtc gcc cac aag gtc atg ccg ggc aac cgc      1692
Gly Val Ser Ala Asp Leu Val Ala His Lys Val Met Pro Gly Asn Arg
    450                 455                 460

ccg tcc acg acc atc ctc gcg gag gag ctc acc ccg gcg gtg ctc ggc      1740
Pro Ser Thr Thr Ile Leu Ala Glu Glu Leu Thr Pro Ala Val Leu Gly
465                 470                 475                 480

gcg ctc atc gcc ctc tac gag cac atc acc ttc gtc cag ggc gtc atc      1788
Ala Leu Ile Ala Leu Tyr Glu His Ile Thr Phe Val Gln Gly Val Ile
                485                 490                 495

tgg gac atc aac tcc ttc gac cag tgg ggc gtg gag ctg ggc aag cag      1836
Trp Asp Ile Asn Ser Phe Asp Gln Trp Gly Val Glu Leu Gly Lys Gln
            500                 505                 510

cag gcc aac cag ctg gcc gcc gcc gtc tcc ggc gcc gag gag gtc gac      1884
Gln Ala Asn Gln Leu Ala Ala Ala Val Ser Gly Ala Glu Glu Val Asp
        515                 520                 525

tcc ggc gac tcc tcc acc gac gcg ctc gtg cgc tgg tac cgc gcg aac      1932
Ser Gly Asp Ser Ser Thr Asp Ala Leu Val Arg Trp Tyr Arg Ala Asn
    530                 535                 540

cgc tag ttcggcaggg ccggcatccc gaggggggtg ccggccctct gcttctcgac      1988
Arg
545

gtcgccccgt tccccgtaac tgaaccggaa ctcgtggaac ggcaggttca cggtctccag    2048

gtggtagaag gcgttccggg cgtgcttgga gtagtggtac tcgcgggccc ggagggtggt    2108

caccgacagc aggttgccgt agccgggcag cagcaggtgc gcgtactgcc ggaggaaggg    2168

caccaggtcg aggctccatc cctcccccgt gcgggtcagt tccgccgggt acaggtcgac    2228

ggtggccacg                                                          2238
```

<210> 6
<211> 545
<212> PRT
<213> Corynebacterium humireducens

<400> 6

Met Ala Asp Ile Thr Thr Ser Ala Glu Trp Lys Asn Leu Glu Ser Glu
1 5 10 15

Phe Glu Arg Thr Gln Gly Gln Thr Leu Arg Glu Leu Phe Ala Ala Asp
20 25 30

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

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

Ala Leu Ala Lys Glu Ala Gln Leu Thr Glu Ala Ile Glu Ala Met Phe
65 70 75 80

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

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

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

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

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

Met Ala Ala Arg Ala Leu Arg Ser Tyr Ala Thr Ala Gly Ile Thr Ala
165 170 175

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

Glu Leu Asp Pro Glu Ser Thr Leu Phe Ile Ile Ala Ser Lys Thr Phe
195 200 205

```
Thr Thr Gln Glu Thr Leu Ala Asn Ala His Ala Ala Lys Arg Trp Leu
    210                 215                 220

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

Ala Val Ser Thr Asn Ala Gln Lys Val Ala Glu Phe Gly Ile Asp Thr
                245                 250                 255

Asp Asn Met Phe Gly Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser Val
            260                 265                 270

Asp Ser Ala Ile Gly Leu Ser Leu Met Ala Val Ile Gly Pro Leu Asp
        275                 280                 285

Phe Met Arg Phe Leu Glu Gly Phe Arg Ala Met Asp Glu His Phe Arg
    290                 295                 300

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

Ile Trp Tyr Val Asn Phe His Gly Phe Glu Thr His Ala Val Leu Pro
                325                 330                 335

Tyr Ser Gln Asp Leu Ser Arg Phe Ala Ala Tyr Leu Gln Gln Leu Thr
            340                 345                 350

Met Glu Ser Asn Gly Lys Ser Val Arg His Asp Gly Thr Ala Val Asp
        355                 360                 365

Tyr Ala Thr Gly Glu Ile Tyr Trp Gly Glu Pro Gly Thr Asn Gly Gln
    370                 375                 380

His Ala Phe Tyr Gln Leu Met His Gln Gly Thr Arg Val Val Pro Ala
385                 390                 395                 400

Asp Phe Ile Gly Phe Ala Arg Pro Lys Asn Asp Leu Pro Thr Ala Thr
                405                 410                 415

Gly Glu Gly Ser Met His Asp Leu Leu Met Gly Asn Leu Phe Ala Gln
            420                 425                 430

Ser Lys Val Leu Ala Phe Gly Lys Thr Ala Glu Glu Ile Ala Ala Glu
        435                 440                 445
```

Gly Val Ser Ala Asp Leu Val Ala His Lys Val Met Pro Gly Asn Arg
450 455 460

Pro Ser Thr Thr Ile Leu Ala Glu Glu Leu Thr Pro Ala Val Leu Gly
465 470 475 480

Ala Leu Ile Ala Leu Tyr Glu His Ile Thr Phe Val Gln Gly Val Ile
485 490 495

Trp Asp Ile Asn Ser Phe Asp Gln Trp Gly Val Glu Leu Gly Lys Gln
500 505 510

Gln Ala Asn Gln Leu Ala Ala Ala Val Ser Gly Ala Glu Glu Val Asp
515 520 525

Ser Gly Asp Ser Ser Thr Asp Ala Leu Val Arg Trp Tyr Arg Ala Asn
530 535 540

Arg
545

<210> 7
<211> 2430
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(2130)
<223> gene pck

<400> 7
cgctatgaca tctggactac agacccgcac cgcgcggcct ggggtctggc ggtcccggaa 60

cctgtgaaac ctcagtcaga ggggcccctg gcgtggggtt tagccggtat ggtcaccccc 120

gaaagtgtgg cctccaacca gggcatttcc ggggaaaagg cacggtggcg gcggatcgac 180

ggcggataaa cccgctggat atgacctgtg acccgtacct catgtcctgt gagaccgtca 240

caaccgcgat ttaatggata ccctgtatag agagaactgc cgcaaacgtc aggagaacac 300

atg acc act gcc atc aag ggc ctc gtc ggc ccc gca ccg acc gat aac 348
Met Thr Thr Ala Ile Lys Gly Leu Val Gly Pro Ala Pro Thr Asp Asn
1 5 10 15

gag aag ctc ctc acc tgg atc gcc gag gca gtg gag ctg atg cag ccg 396
Glu Lys Leu Leu Thr Trp Ile Ala Glu Ala Val Glu Leu Met Gln Pro
20 25 30

```
gag aag gtc gtc ttc gcc gac ggc tcc cag gag gag tgg gac cgc ctc        444
Glu Lys Val Val Phe Ala Asp Gly Ser Gln Glu Glu Trp Asp Arg Leu
        35                  40                  45

tcc gcc gag ctc gtg gag gca ggc acc ttc atc cgc ctc aac gag gag        492
Ser Ala Glu Leu Val Glu Ala Gly Thr Phe Ile Arg Leu Asn Glu Glu
    50                  55                  60

aag cgc ccg aac agc ttc ctg gcc cgc tcc aac ccg gac gat gtc gcc        540
Lys Arg Pro Asn Ser Phe Leu Ala Arg Ser Asn Pro Asp Asp Val Ala
65                  70                  75                  80

cgc gtc gag tcc cgc acc ttc atc tgc tcc gag aag gag gag gac gcc        588
Arg Val Glu Ser Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp Ala
                85                  90                  95

ggc ccg acc aac aac tgg gcg gac ccg gtc gag atg aag aag gag atg        636
Gly Pro Thr Asn Asn Trp Ala Asp Pro Val Glu Met Lys Lys Glu Met
            100                 105                 110

acc gag gta tac cgc ggc tcc atg aag ggc cgc acc atg tac gtc gtg        684
Thr Glu Val Tyr Arg Gly Ser Met Lys Gly Arg Thr Met Tyr Val Val
        115                 120                 125

ccg ttc tgc atg ggc ccg atc acc gac ccg gag ccg aag ctc ggt gtc        732
Pro Phe Cys Met Gly Pro Ile Thr Asp Pro Glu Pro Lys Leu Gly Val
    130                 135                 140

cag ctc acc gac tcc gcc tac gtc gtc ctc tcc atg cgc atc atg acc        780
Gln Leu Thr Asp Ser Ala Tyr Val Val Leu Ser Met Arg Ile Met Thr
145                 150                 155                 160

cgt atg ggc tcc gag gcg ctc gag aag atc ggc acc gac ggc gat ttc        828
Arg Met Gly Ser Glu Ala Leu Glu Lys Ile Gly Thr Asp Gly Asp Phe
                165                 170                 175

gtc cgc gca ctc cac tcc gtc ggc gcc ccg ctg gag ccg ggc cag gag        876
Val Arg Ala Leu His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln Glu
            180                 185                 190

gac gtc atc tgg ccg tgc aac gac acc aag tac atc acc cag ttc ccg        924
Asp Val Ile Trp Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe Pro
        195                 200                 205

gag acc aag gag atc tgg tcc tac ggc tcc ggt tac ggc ggc aac gcc        972
Glu Thr Lys Glu Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn Ala
    210                 215                 220

atc ctg gcc aag aag tgc tac gcc ctg cgc atc gcc tcc gtc atg gcc       1020
Ile Leu Ala Lys Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met Ala
225                 230                 235                 240

aag gag gag ggc tgg atg gct gag cac atg ctc atc ctg aag ctc aac       1068
Lys Glu Glu Gly Trp Met Ala Glu His Met Leu Ile Leu Lys Leu Asn
                245                 250                 255

tcc ccg gag ggc aag agc tac cac atc gcg gca gct ttc ccg tcc gcc       1116
Ser Pro Glu Gly Lys Ser Tyr His Ile Ala Ala Ala Phe Pro Ser Ala
```

```
                260                 265                 270

tgc ggc aag acc aac ctc gcc atg atc acc ccg acc atc gag ggc tgg      1164
Cys Gly Lys Thr Asn Leu Ala Met Ile Thr Pro Thr Ile Glu Gly Trp
        275                 280                 285

acc gcc gag gtc gtc ggc gac gac atc gcc tgg ctc aag ctg cgc gag      1212
Thr Ala Glu Val Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg Glu
    290                 295                 300

gac ggc ctc tac gcc gtc aac ccg gag aac ggc ttc ttc ggc gtc gca      1260
Asp Gly Leu Tyr Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val Ala
305                 310                 315                 320

ccg ggc acc aac tac gcc tcc aac ccg atc gcc atg gag acc atg gag      1308
Pro Gly Thr Asn Tyr Ala Ser Asn Pro Ile Ala Met Glu Thr Met Glu
                325                 330                 335

ccg ggc aac acc ctg ttc acc aac gtc gca ctg acc gac gac ggt gac      1356
Pro Gly Asn Thr Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly Asp
            340                 345                 350

gtc tgg tgg gag ggc atg gac ggc gag aag ccg gag cac ctc atc gac      1404
Val Trp Trp Glu Gly Met Asp Gly Glu Lys Pro Glu His Leu Ile Asp
        355                 360                 365

tgg ctg ggc aac gac tgg acc ccg gag tcc ggc acc aac gcc gca cac      1452
Trp Leu Gly Asn Asp Trp Thr Pro Glu Ser Gly Thr Asn Ala Ala His
    370                 375                 380

ccg aac tcc cgc tac tgc gtg gcc atc gag cag tgc ccg gtc gcc gca      1500
Pro Asn Ser Arg Tyr Cys Val Ala Ile Glu Gln Cys Pro Val Ala Ala
385                 390                 395                 400

ccg gag ttc aac gac ccg aag ggc gtc aag atc gac gcc atc ctc ttc      1548
Pro Glu Phe Asn Asp Pro Lys Gly Val Lys Ile Asp Ala Ile Leu Phe
                405                 410                 415

ggt ggc cgt cgt gcc gac acc gtc ccg ctg gtc acc cag tcc tac gac      1596
Gly Gly Arg Arg Ala Asp Thr Val Pro Leu Val Thr Gln Ser Tyr Asp
            420                 425                 430

tgg gag cac ggc acc ttc atc ggt gcg acc ctg gcc tcc ggc cag acc      1644
Trp Glu His Gly Thr Phe Ile Gly Ala Thr Leu Ala Ser Gly Gln Thr
        435                 440                 445

gcc gca tcc gct gag gcg aag gtc ggc tcc ctg cgc cac gac ccg atg      1692
Ala Ala Ser Ala Glu Ala Lys Val Gly Ser Leu Arg His Asp Pro Met
    450                 455                 460

gcc atg ctg ccg ttc atg ggc tac aac gcc ggt gac tac ctg cag cac      1740
Ala Met Leu Pro Phe Met Gly Tyr Asn Ala Gly Asp Tyr Leu Gln His
465                 470                 475                 480

tgg atc gac atg ggc aag aag ggc ggc gac cgt atg ccg gcc atc ttc      1788
Trp Ile Asp Met Gly Lys Lys Gly Gly Asp Arg Met Pro Ala Ile Phe
                485                 490                 495

ctg gtc aac tgg ttc cgc cgt ggc gag gac ggc cgc ttc ctg tgg ccg      1836
```

```
Leu Val Asn Trp Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp Pro
            500                 505                 510

ggc ttc ggt gac aac tcc cgt gtc ctg aag tgg atc att gac cgc atc      1884
Gly Phe Gly Asp Asn Ser Arg Val Leu Lys Trp Ile Ile Asp Arg Ile
        515                 520                 525

gag ggc aag gtc gac gcc gag gag acc gtc gtg ggc cac acc gcc cgc      1932
Glu Gly Lys Val Asp Ala Glu Glu Thr Val Val Gly His Thr Ala Arg
    530                 535                 540

gcc gag gac ctc gac ctg acc ggc ctg gac acc ccg ctc gag gac gtc      1980
Ala Glu Asp Leu Asp Leu Thr Gly Leu Asp Thr Pro Leu Glu Asp Val
545                 550                 555                 560

aag gag gcc ctg act gcg ccg gcc gca gac tgg gag cgc gac gtc gcc      2028
Lys Glu Ala Leu Thr Ala Pro Ala Ala Asp Trp Glu Arg Asp Val Ala
                565                 570                 575

gac aac gag gag tac ctg gca ttc ctc ggc ccg cgt gtc ccg aac gag      2076
Asp Asn Glu Glu Tyr Leu Ala Phe Leu Gly Pro Arg Val Pro Asn Glu
            580                 585                 590

gtc cac gag cag ctg ggc aag ctc aag gag cgc atc gag gcg aac aag      2124
Val His Glu Gln Leu Gly Lys Leu Lys Glu Arg Ile Glu Ala Asn Lys
        595                 600                 605

aac tag ttcgtctccc ctcagaactt ccaccctcca ggttgactca gtccctgggg      2180
Asn

ggtgggattt tttctgcccc ggtcgcaccg taagtccgag agaggatgtt cgagaggaga  2240

gtcctctcga acgtgcggga cccccgcggg actcctctcg acgatgtgat ctcgacgtca  2300

gggaagaggg gggaagggga acgccgtcag tgcttccgca gcacgaccac caggttcgac  2360

acgaggaact cccgcagcag cggcacccgc accatccacc acgcccacga ggggtggtag  2420

cgggggaagg                                                         2430
```

<210> 8
<211> 609
<212> PRT
<213> Corynebacterium humireducens

<400> 8

```
Met Thr Thr Ala Ile Lys Gly Leu Val Gly Pro Ala Pro Thr Asp Asn
1               5                   10                  15

Glu Lys Leu Leu Thr Trp Ile Ala Glu Ala Val Glu Leu Met Gln Pro
            20                  25                  30

Glu Lys Val Val Phe Ala Asp Gly Ser Gln Glu Glu Trp Asp Arg Leu
        35                  40                  45
```

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

Lys Arg Pro Asn Ser Phe Leu Ala Arg Ser Asn Pro Asp Asp Val Ala
65 70 75 80

Arg Val Glu Ser Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp Ala
85 90 95

Gly Pro Thr Asn Asn Trp Ala Asp Pro Val Glu Met Lys Lys Glu Met
100 105 110

Thr Glu Val Tyr Arg Gly Ser Met Lys Gly Arg Thr Met Tyr Val Val
115 120 125

Pro Phe Cys Met Gly Pro Ile Thr Asp Pro Glu Pro Lys Leu Gly Val
130 135 140

Gln Leu Thr Asp Ser Ala Tyr Val Val Leu Ser Met Arg Ile Met Thr
145 150 155 160

Arg Met Gly Ser Glu Ala Leu Glu Lys Ile Gly Thr Asp Gly Asp Phe
165 170 175

Val Arg Ala Leu His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln Glu
180 185 190

Asp Val Ile Trp Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe Pro
195 200 205

Glu Thr Lys Glu Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn Ala
210 215 220

Ile Leu Ala Lys Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met Ala
225 230 235 240

Lys Glu Glu Gly Trp Met Ala Glu His Met Leu Ile Leu Lys Leu Asn
245 250 255

Ser Pro Glu Gly Lys Ser Tyr His Ile Ala Ala Ala Phe Pro Ser Ala
260 265 270

Cys Gly Lys Thr Asn Leu Ala Met Ile Thr Pro Thr Ile Glu Gly Trp

```
          275                 280                 285

Thr Ala Glu Val Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg Glu
    290                 295                 300

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

Pro Gly Thr Asn Tyr Ala Ser Asn Pro Ile Ala Met Glu Thr Met Glu
                325                 330                 335

Pro Gly Asn Thr Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly Asp
            340                 345                 350

Val Trp Trp Glu Gly Met Asp Gly Glu Lys Pro Glu His Leu Ile Asp
        355                 360                 365

Trp Leu Gly Asn Asp Trp Thr Pro Glu Ser Gly Thr Asn Ala Ala His
    370                 375                 380

Pro Asn Ser Arg Tyr Cys Val Ala Ile Glu Gln Cys Pro Val Ala Ala
385                 390                 395                 400

Pro Glu Phe Asn Asp Pro Lys Gly Val Lys Ile Asp Ala Ile Leu Phe
                405                 410                 415

Gly Gly Arg Arg Ala Asp Thr Val Pro Leu Val Thr Gln Ser Tyr Asp
            420                 425                 430

Trp Glu His Gly Thr Phe Ile Gly Ala Thr Leu Ala Ser Gly Gln Thr
        435                 440                 445

Ala Ala Ser Ala Glu Ala Lys Val Gly Ser Leu Arg His Asp Pro Met
    450                 455                 460

Ala Met Leu Pro Phe Met Gly Tyr Asn Ala Gly Asp Tyr Leu Gln His
465                 470                 475                 480

Trp Ile Asp Met Gly Lys Lys Gly Gly Asp Arg Met Pro Ala Ile Phe
                485                 490                 495

Leu Val Asn Trp Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp Pro
            500                 505                 510
```

```
Gly Phe Gly Asp Asn Ser Arg Val Leu Lys Trp Ile Ile Asp Arg Ile
        515                 520                 525

Glu Gly Lys Val Asp Ala Glu Glu Thr Val Val Gly His Thr Ala Arg
    530                 535                 540

Ala Glu Asp Leu Asp Leu Thr Gly Leu Asp Thr Pro Leu Glu Asp Val
545                 550                 555                 560

Lys Glu Ala Leu Thr Ala Pro Ala Ala Asp Trp Glu Arg Asp Val Ala
                565                 570                 575

Asp Asn Glu Glu Tyr Leu Ala Phe Leu Gly Pro Arg Val Pro Asn Glu
            580                 585                 590

Val His Glu Gln Leu Gly Lys Leu Lys Glu Arg Ile Glu Ala Asn Lys
        595                 600                 605

Asn
```

<210> 9
<211> 1461
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1161)
<223> gene metQ

<400> 9

```
aagctgtagg agctcacggc gtggagctcc gcgaagggga gggcggaggg ggcgacgggg        60

cggcgtcggc aagcaccctc cccgagatgg ccgaccggga cgggcgtggg gcccgggcgg       120

ccggagagga tgcgctccag ccgcgaccag ccgaggtgtg ccccaccgtg gaatcccatg       180

ccccgcaatc taccctgat cgaacagatg tgccacactg cccgcggcaa ggactagaca       240

gagcggtacg cccggtgcta ggtttcagaa ccaacgaacc gaacacgtaa ggacaccacc       300

atg act ttc cgt cgc ctc ctg gcc ggc acc gcc gcc gcc gtc atc gcc         348
Met Thr Phe Arg Arg Leu Leu Ala Gly Thr Ala Ala Ala Val Ile Ala
1               5                   10                  15

tcc gtg ggc ctc gtc gcc tgc ggc tcc ggc tcc tcc ggg gag acc gtc         396
Ser Val Gly Leu Val Ala Cys Gly Ser Gly Ser Ser Gly Glu Thr Val
            20                  25                  30

cgc atc ggc acc acc gac gcc cag ctc aag gag tgg gac gtc ttc gcc         444
```

```
Arg Ile Gly Thr Thr Asp Ala Gln Leu Lys Glu Trp Asp Val Phe Ala
        35                  40                  45

gac atc gtc gag gcg gag ggc atc gac atc gag atc gtg ccg ttc tcc      492
Asp Ile Val Glu Ala Glu Gly Ile Asp Ile Glu Ile Val Pro Phe Ser
    50                  55                  60

gac tac aac acc ccg aac gac gcg ctc gtg cag ggt gag atc gac gtc      540
Asp Tyr Asn Thr Pro Asn Asp Ala Leu Val Gln Gly Glu Ile Asp Val
65                  70                  75                  80

aac aag ttc cag cac ctg gac ttc ctc gcc tcc tac aac aaa ggc gcc      588
Asn Lys Phe Gln His Leu Asp Phe Leu Ala Ser Tyr Asn Lys Gly Ala
                85                  90                  95

aac gcc gac ctc gtg ccg tac gcc gcc acc gag atc aac ccg ctg tcc      636
Asn Ala Asp Leu Val Pro Tyr Ala Ala Thr Glu Ile Asn Pro Leu Ser
            100                 105                 110

ctg ttc tgg aag gac cac gac tcc ctc gac ggc atc gag ggc gag ggc      684
Leu Phe Trp Lys Asp His Asp Ser Leu Asp Gly Ile Glu Gly Glu Gly
        115                 120                 125

gtc gtc atc ccc aac gac gac acc aac cag ggc cgc gcc atc aac gtc      732
Val Val Ile Pro Asn Asp Asp Thr Asn Gln Gly Arg Ala Ile Asn Val
    130                 135                 140

ctc gcc cag gcc ggt ctg gtg acc ctg cgc gac gac agc gtc tac aac      780
Leu Ala Gln Ala Gly Leu Val Thr Leu Arg Asp Asp Ser Val Tyr Asn
145                 150                 155                 160

ccg acc ccg gcc gac gtc gac acc gag aag tcc aag gtc tcc atc gtc      828
Pro Thr Pro Ala Asp Val Asp Thr Glu Lys Ser Lys Val Ser Ile Val
                165                 170                 175

acc gtc gac gcc gcc cag acc acc acc gcc tac cac gag ggt cgc ccg      876
Thr Val Asp Ala Ala Gln Thr Thr Thr Ala Tyr His Glu Gly Arg Pro
            180                 185                 190

gcc atc atc aac aac tcc ttc ctg gag cgc gcc agc atc gac ccg tcc      924
Ala Ile Ile Asn Asn Ser Phe Leu Glu Arg Ala Ser Ile Asp Pro Ser
        195                 200                 205

ctc gcc atc ttc cag gat gac ccg agc acc gag cag gcc gag ccg tac      972
Leu Ala Ile Phe Gln Asp Asp Pro Ser Thr Glu Gln Ala Glu Pro Tyr
    210                 215                 220

atc aac gcc tgg gtg acc acc cgc gac aag gcc gac gac gag acc ctc     1020
Ile Asn Ala Trp Val Thr Thr Arg Asp Lys Ala Asp Asp Glu Thr Leu
225                 230                 235                 240

atc cgt ctc gcc gag ctg tgg aag gac ccg gcc gtc acc gcc gcc gtc     1068
Ile Arg Leu Ala Glu Leu Trp Lys Asp Pro Ala Val Thr Ala Ala Val
                245                 250                 255

ctg gag acc tcc ggc aac acc gcc gtc acc gtc gag cgc tcg ccc gag     1116
Leu Glu Thr Ser Gly Asn Thr Ala Val Thr Val Glu Arg Ser Pro Glu
            260                 265                 270
```

gag ctc gcc gcg atc atg gag cgc ctc gcg gcc cgc gag cag tag 1161
Glu Leu Ala Ala Ile Met Glu Arg Leu Ala Ala Arg Glu Gln
275 280 285

gccgcactcc gcccacctgc cccgtcgcgt tcccgcggcg gggtttagca tttacctgac 1221

cagtcccccc cccagaacgg cccccagaac accgtgaccg aacctgtgac cgcaccaccc 1281

acccggccgc gtaccggtac ccgcatcgag ttccgcgatg tgaccaaggt cttcaccaac 1341

cagcggaaga ccgagacccg cgccgtcgac ggcgtcaccc tgaccgtcga acccggcgag 1401

atcctcggcg tcatcggcta ctccggcgcc ggcaagtcga cgctcgtccg cctcatcaac 1461

<210> 10
<211> 286
<212> PRT
<213> Corynebacterium humireducens

<400> 10

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

Ser Val Gly Leu Val Ala Cys Gly Ser Gly Ser Ser Gly Glu Thr Val
20 25 30

Arg Ile Gly Thr Thr Asp Ala Gln Leu Lys Glu Trp Asp Val Phe Ala
35 40 45

Asp Ile Val Glu Ala Glu Gly Ile Asp Ile Glu Ile Val Pro Phe Ser
50 55 60

Asp Tyr Asn Thr Pro Asn Asp Ala Leu Val Gln Gly Glu Ile Asp Val
65 70 75 80

Asn Lys Phe Gln His Leu Asp Phe Leu Ala Ser Tyr Asn Lys Gly Ala
85 90 95

Asn Ala Asp Leu Val Pro Tyr Ala Ala Thr Glu Ile Asn Pro Leu Ser
100 105 110

Leu Phe Trp Lys Asp His Asp Ser Leu Asp Gly Ile Glu Gly Glu Gly
115 120 125

Val Val Ile Pro Asn Asp Asp Thr Asn Gln Gly Arg Ala Ile Asn Val
130 135 140

Leu Ala Gln Ala Gly Leu Val Thr Leu Arg Asp Asp Ser Val Tyr Asn

```
145                 150                 155                 160

Pro Thr Pro Ala Asp Val Asp Thr Glu Lys Ser Lys Val Ser Ile Val
                165                 170                 175

Thr Val Asp Ala Ala Gln Thr Thr Thr Ala Tyr His Glu Gly Arg Pro
            180                 185                 190

Ala Ile Ile Asn Asn Ser Phe Leu Glu Arg Ala Ser Ile Asp Pro Ser
        195                 200                 205

Leu Ala Ile Phe Gln Asp Asp Pro Ser Thr Glu Gln Ala Glu Pro Tyr
    210                 215                 220

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

Ile Arg Leu Ala Glu Leu Trp Lys Asp Pro Ala Val Thr Ala Ala Val
                245                 250                 255

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

Glu Leu Ala Ala Ile Met Glu Arg Leu Ala Ala Arg Glu Gln
        275                 280                 285
```

<210> 11
<211> 2259
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1959)
<223> gene metP

<400> 11

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tcaatcgtcg cgaaggggta gttcgcggcg agaacatcgt ttcgggtcag ggcattgaag       60

agggtggact tgccgacgtt gggcagaccg acgattccaa gagtaaggct cacgggcgta      120

gatcctagca gccagcggtt ttgcctctcc ggtcagcgcc cgtacctgtg ttgcgggatg      180

atacggacgt cattatatga tcaggccact tcaacgataa atacgtcgca ccctggacgt      240

tttcctctcc ctaaccatcg ggagccaact acacatcctc cacctcagac aggtatacac      300

atg tct tcg acc acc ccg cag ccc gcg ccg tcg ggc cag gag cag ggc         348
Met Ser Ser Thr Thr Pro Gln Pro Ala Pro Ser Gly Gln Glu Gln Gly
```

```
1               5                   10                  15

gag cgg cgc gag atc ttc tcg tcc cgt tgg gcg ttc ctg ctg gcc gcc        396
Glu Arg Arg Glu Ile Phe Ser Ser Arg Trp Ala Phe Leu Leu Ala Ala
            20                  25                  30

atc ggc tcc gcc gtc ggc ctg ggc aac atc tgg cgc ttc ccc tac gtc        444
Ile Gly Ser Ala Val Gly Leu Gly Asn Ile Trp Arg Phe Pro Tyr Val
        35                  40                  45

gct tac gac aac ggc ggc ggc gcc ttc ctc atc ccc tac ctc gtg gca        492
Ala Tyr Asp Asn Gly Gly Gly Ala Phe Leu Ile Pro Tyr Leu Val Ala
    50                  55                  60

ctg ctg tcc gct ggt atc ccg ctg ctc ttc ctc gac tac gcc ctg ggc        540
Leu Leu Ser Ala Gly Ile Pro Leu Leu Phe Leu Asp Tyr Ala Leu Gly
65                  70                  75                  80

cac cgc tac cgt ggt tcc gcc ccg ctg gtg ttc cgt cgc atc aag tcc        588
His Arg Tyr Arg Gly Ser Ala Pro Leu Val Phe Arg Arg Ile Lys Ser
                85                  90                  95

tgg gct gag ccg gtc ggc tgg gtc cag gtc ggt gtg tcc ttt ttc atc        636
Trp Ala Glu Pro Val Gly Trp Val Gln Val Gly Val Ser Phe Phe Ile
            100                 105                 110

act atc tac tac gcc gcg atc atc ggc tgg gcc gcg ctc tac gcg gtc        684
Thr Ile Tyr Tyr Ala Ala Ile Ile Gly Trp Ala Ala Leu Tyr Ala Val
        115                 120                 125

aag tcc ttc aac aag gcg tgg ggc acc gac ccg aac agc tac ttc ttc        732
Lys Ser Phe Asn Lys Ala Trp Gly Thr Asp Pro Asn Ser Tyr Phe Phe
    130                 135                 140

ggc gat ttc ctc cag ttc gac gag acc gcc acc ttc tcc acc gac ttc        780
Gly Asp Phe Leu Gln Phe Asp Glu Thr Ala Thr Phe Ser Thr Asp Phe
145                 150                 155                 160

gtc ccg cag atc gcc ctg gcc ctg gcc ggc gtg tgg atc gcc gcg atc        828
Val Pro Gln Ile Ala Leu Ala Leu Ala Gly Val Trp Ile Ala Ala Ile
                165                 170                 175

atc gtg ctg gcg atc ggc gtg gac aag ggc atc ggc aag gtc tcc aag        876
Ile Val Leu Ala Ile Gly Val Asp Lys Gly Ile Gly Lys Val Ser Lys
            180                 185                 190

atc ttc atc ccc ctg ctg gcg gtc ctc ttc ctc atc gtc gta gtc cag        924
Ile Phe Ile Pro Leu Leu Ala Val Leu Phe Leu Ile Val Val Val Gln
        195                 200                 205

gcg ctc atg ctg ccg ggt gcc gcc acg ggt ctc gac gcc ctg ttc acc        972
Ala Leu Met Leu Pro Gly Ala Ala Thr Gly Leu Asp Ala Leu Phe Thr
    210                 215                 220

ccg gac tgg aac gcc ctg acc aac ggc act gtg tgg atc gcc gcc tac       1020
Pro Asp Trp Asn Ala Leu Thr Asn Gly Thr Val Trp Ile Ala Ala Tyr
225                 230                 235                 240

ggc cag atc ttc ttc tcc ctg tcc gtg agc ttc ggc atc atg ctc acc       1068
```

```
Gly Gln Ile Phe Phe Ser Leu Ser Val Ser Phe Gly Ile Met Leu Thr
                245                 250                 255

tac tcc tcc tac ctg cgt ccg cgc acc aac ctg acg ggc acc ggc ctg      1116
Tyr Ser Ser Tyr Leu Arg Pro Arg Thr Asn Leu Thr Gly Thr Gly Leu
            260                 265                 270

acc acc gcc ttc gcg aac tcc tcc ttc gag gtc ctc gcc ggc gtc ggt      1164
Thr Thr Ala Phe Ala Asn Ser Ser Phe Glu Val Leu Ala Gly Val Gly
        275                 280                 285

gtc ttc gcc gcc ctg ggc ttc atg gcc gtg cag cag tcg gtc gcc gtc      1212
Val Phe Ala Ala Leu Gly Phe Met Ala Val Gln Gln Ser Val Ala Val
    290                 295                 300

gac gag gtc gcg acc tcg ggc atc ggt ctg gcc ttc gtg gcc ttc ccg      1260
Asp Glu Val Ala Thr Ser Gly Ile Gly Leu Ala Phe Val Ala Phe Pro
305                 310                 315                 320

gcg atc atc aac gag atg gcc ttc ggc ccg atc ttc ggc gtc ctg ttc      1308
Ala Ile Ile Asn Glu Met Ala Phe Gly Pro Ile Phe Gly Val Leu Phe
                325                 330                 335

ttc ggc tcc ctc acc atc gcc ggc ttc acc tcg ctg ttc tcc ctg ctc      1356
Phe Gly Ser Leu Thr Ile Ala Gly Phe Thr Ser Leu Phe Ser Leu Leu
            340                 345                 350

gag gtc gtc gtc tcc gcc gtc aag gac aag ctg aac ctg ccg cgc aag      1404
Glu Val Val Val Ser Ala Val Lys Asp Lys Leu Asn Leu Pro Arg Lys
        355                 360                 365

acc gtc gcc atc ggc atc ggc acc ttc atg gcg ctg atc tcc ctg gcg      1452
Thr Val Ala Ile Gly Ile Gly Thr Phe Met Ala Leu Ile Ser Leu Ala
    370                 375                 380

ctg ttc tcc acg acg tcc ggc ctc atg gcc ctg gac atc atg gac aag      1500
Leu Phe Ser Thr Thr Ser Gly Leu Met Ala Leu Asp Ile Met Asp Lys
385                 390                 395                 400

ttc acc aac aac atc ggc atc gtc gcc atc gcc ctg atc gcg gtc atc      1548
Phe Thr Asn Asn Ile Gly Ile Val Ala Ile Ala Leu Ile Ala Val Ile
                405                 410                 415

atc ctc gat tgg gtc ctg cgc cgg atc gac gag ttc tcg ctc cac atc      1596
Ile Leu Asp Trp Val Leu Arg Arg Ile Asp Glu Phe Ser Leu His Ile
            420                 425                 430

aac gcc gtg tcc tcc ttc aag gtg ggc acg ctg tgg cgc atc ttc gtg      1644
Asn Ala Val Ser Ser Phe Lys Val Gly Thr Leu Trp Arg Ile Phe Val
        435                 440                 445

gtc aac gtc acc acc ctg gtg ctg gga ttc acc ctg gcg cag gag ctc      1692
Val Asn Val Thr Thr Leu Val Leu Gly Phe Thr Leu Ala Gln Glu Leu
    450                 455                 460

atc tcc ctg atc cag gag ccc tac ggc ggc tac acg acg acg cag atc      1740
Ile Ser Leu Ile Gln Glu Pro Tyr Gly Gly Tyr Thr Thr Thr Gln Ile
465                 470                 475                 480
```

```
gcc atc tac ggc tgg gcc gtc ctg gcg ctc atc ggt atc aac gcc ctc       1788
Ala Ile Tyr Gly Trp Ala Val Leu Ala Leu Ile Gly Ile Asn Ala Leu
                485                 490                 495

gtc ttc tcc ctg gtg ccg tgg cgc ggc aac ctg ccg ctc aac ggt ccg       1836
Val Phe Ser Leu Val Pro Trp Arg Gly Asn Leu Pro Leu Asn Gly Pro
            500                 505                 510

ccg ggc tcc gac ttc ggt gtt gac ccg gag gtc cac cgc gag ctc cac       1884
Pro Gly Ser Asp Phe Gly Val Asp Pro Glu Val His Arg Glu Leu His
        515                 520                 525

gcg ccg cgc aag tac aac ggt gac cac cgg gtg ggc gtc gac aag cac       1932
Ala Pro Arg Lys Tyr Asn Gly Asp His Arg Val Gly Val Asp Lys His
    530                 535                 540

acc acc gag gaa gga acg atc cga tga gcggtctcgc aatcatgatg            1979
Thr Thr Glu Glu Gly Thr Ile Arg
545                 550

atggtcctgt tcatggtcgt catctggggt ggtttcatcg ccagcgccct gcacctgcgg     2039

gcgaaccccg atgacacctc cggcgccctg ggcgtcgcgg accatgcgcg cgacgagcac     2099

ctcgccgcgc aggaactcca ctagtcacac cacaccggga tgtcaggcaa tatggagtct     2159

gtgactgacc agccgacctc ccgcatcccc ggggacgaga ctcccccgac cggctcctcc     2219

ggcgacgccg ggtccaccgc cttcggcagc atggacctgg                           2259
```

<210> 12
<211> 552
<212> PRT
<213> Corynebacterium humireducens

<400> 12

```
Met Ser Ser Thr Thr Pro Gln Pro Ala Pro Ser Gly Gln Glu Gln Gly
1               5                   10                  15

Glu Arg Arg Glu Ile Phe Ser Ser Arg Trp Ala Phe Leu Leu Ala Ala
            20                  25                  30

Ile Gly Ser Ala Val Gly Leu Gly Asn Ile Trp Arg Phe Pro Tyr Val
        35                  40                  45

Ala Tyr Asp Asn Gly Gly Gly Ala Phe Leu Ile Pro Tyr Leu Val Ala
    50                  55                  60

Leu Leu Ser Ala Gly Ile Pro Leu Leu Phe Leu Asp Tyr Ala Leu Gly
65                  70                  75                  80

His Arg Tyr Arg Gly Ser Ala Pro Leu Val Phe Arg Arg Ile Lys Ser
```

```
                  85                  90                  95

Trp Ala Glu Pro Val Gly Trp Val Gln Val Gly Val Ser Phe Phe Ile
            100                 105                 110

Thr Ile Tyr Tyr Ala Ala Ile Ile Gly Trp Ala Ala Leu Tyr Ala Val
        115                 120                 125

Lys Ser Phe Asn Lys Ala Trp Gly Thr Asp Pro Asn Ser Tyr Phe Phe
    130                 135                 140

Gly Asp Phe Leu Gln Phe Asp Glu Thr Ala Thr Phe Ser Thr Asp Phe
145                 150                 155                 160

Val Pro Gln Ile Ala Leu Ala Leu Ala Gly Val Trp Ile Ala Ala Ile
                165                 170                 175

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

Ile Phe Ile Pro Leu Leu Ala Val Leu Phe Leu Ile Val Val Val Gln
        195                 200                 205

Ala Leu Met Leu Pro Gly Ala Ala Thr Gly Leu Asp Ala Leu Phe Thr
    210                 215                 220

Pro Asp Trp Asn Ala Leu Thr Asn Gly Thr Val Trp Ile Ala Ala Tyr
225                 230                 235                 240

Gly Gln Ile Phe Phe Ser Leu Ser Val Ser Phe Gly Ile Met Leu Thr
                245                 250                 255

Tyr Ser Ser Tyr Leu Arg Pro Arg Thr Asn Leu Thr Gly Thr Gly Leu
            260                 265                 270

Thr Thr Ala Phe Ala Asn Ser Ser Phe Glu Val Leu Ala Gly Val Gly
        275                 280                 285

Val Phe Ala Ala Leu Gly Phe Met Ala Val Gln Gln Ser Val Ala Val
    290                 295                 300

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

```
Ala Ile Ile Asn Glu Met Ala Phe Gly Pro Ile Phe Gly Val Leu Phe
                325                 330                 335

Phe Gly Ser Leu Thr Ile Ala Gly Phe Thr Ser Leu Phe Ser Leu Leu
            340                 345                 350

Glu Val Val Val Ser Ala Val Lys Asp Lys Leu Asn Leu Pro Arg Lys
        355                 360                 365

Thr Val Ala Ile Gly Ile Gly Thr Phe Met Ala Leu Ile Ser Leu Ala
    370                 375                 380

Leu Phe Ser Thr Thr Ser Gly Leu Met Ala Leu Asp Ile Met Asp Lys
385                 390                 395                 400

Phe Thr Asn Asn Ile Gly Ile Val Ala Ile Ala Leu Ile Ala Val Ile
                405                 410                 415

Ile Leu Asp Trp Val Leu Arg Arg Ile Asp Glu Phe Ser Leu His Ile
            420                 425                 430

Asn Ala Val Ser Ser Phe Lys Val Gly Thr Leu Trp Arg Ile Phe Val
        435                 440                 445

Val Asn Val Thr Thr Leu Val Leu Gly Phe Thr Leu Ala Gln Glu Leu
    450                 455                 460

Ile Ser Leu Ile Gln Glu Pro Tyr Gly Gly Tyr Thr Thr Thr Gln Ile
465                 470                 475                 480

Ala Ile Tyr Gly Trp Ala Val Leu Ala Leu Ile Gly Ile Asn Ala Leu
                485                 490                 495

Val Phe Ser Leu Val Pro Trp Arg Gly Asn Leu Pro Leu Asn Gly Pro
            500                 505                 510

Pro Gly Ser Asp Phe Gly Val Asp Pro Glu Val His Arg Glu Leu His
        515                 520                 525

Ala Pro Arg Lys Tyr Asn Gly Asp His Arg Val Gly Val Asp Lys His
    530                 535                 540

Thr Thr Glu Glu Gly Thr Ile Arg
545                 550
```

<210> 13
<211> 1650
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1350)
<223> gene metN

<400> 13
ccgtacatca acgcctgggt gaccacccgc gacaaggccg acgacgagac cctcatccgt 60

ctcgccgagc tgtggaagga cccggccgtc accgccgccg tcctggagac ctccggcaac 120

accgccgtca ccgtcgagcg ctcgcccgag gagctcgccg cgatcatgga gcgcctcgcg 180

gcccgcgagc agtaggccgc actccgccca cctgccccgt cgcgttcccg cggcggggtt 240

tagcatttac ctgaccagtc cccctcccag aacggccccc agaacaccgt gaccgaacct 300

gtg acc gca cca ccc acc cgg ccg cgt acc ggt acc cgc atc gag ttc 348
Val Thr Ala Pro Pro Thr Arg Pro Arg Thr Gly Thr Arg Ile Glu Phe
1 5 10 15

cgc gat gtg acc aag gtc ttc acc aac cag cgg aag acc gag acc cgc 396
Arg Asp Val Thr Lys Val Phe Thr Asn Gln Arg Lys Thr Glu Thr Arg
20 25 30

gcc gtc gac ggc gtc acc ctg acc gtc gaa ccc ggc gag atc ctc ggc 444
Ala Val Asp Gly Val Thr Leu Thr Val Glu Pro Gly Glu Ile Leu Gly
35 40 45

gtc atc ggc tac tcc ggc gcc ggc aag tcg acg ctc gtc cgc ctc atc 492
Val Ile Gly Tyr Ser Gly Ala Gly Lys Ser Thr Leu Val Arg Leu Ile
50 55 60

aac ggg ctg gac tcc aca acc tcc ggc cag ctg ctt ctc gac ggc acc 540
Asn Gly Leu Asp Ser Thr Thr Ser Gly Gln Leu Leu Leu Asp Gly Thr
65 70 75 80

gac atc gtc gga ctc ccc gag tcc aag ctg cgc tcg atc cgc cgg ggc 588
Asp Ile Val Gly Leu Pro Glu Ser Lys Leu Arg Ser Ile Arg Arg Gly
85 90 95

atc ggc atg atc ttc cag cag ttc aac ctc ttc cag tcc cgc acg gcc 636
Ile Gly Met Ile Phe Gln Gln Phe Asn Leu Phe Gln Ser Arg Thr Ala
100 105 110

gcc ggc aac atc gcc tac ccg ctg gag ctg gcc ggc atg ccg cgc gcg 684
Ala Gly Asn Ile Ala Tyr Pro Leu Glu Leu Ala Gly Met Pro Arg Ala
115 120 125

gag cgg cgg cgg cgc gtc gcc gag ctc ctc gac ttc gtc ggc ctg ggc 732
Glu Arg Arg Arg Arg Val Ala Glu Leu Leu Asp Phe Val Gly Leu Gly
130 135 140

```
gac aag ggc gac aac tac ccg gag cag ctg tcg ggc ggc cag aag cag        780
Asp Lys Gly Asp Asn Tyr Pro Glu Gln Leu Ser Gly Gly Gln Lys Gln
145                 150                 155                 160

cgc gtc ggc atc gcc cgc gcc ctg gcc acc aac ccg cgg ctc ctg ctc        828
Arg Val Gly Ile Ala Arg Ala Leu Ala Thr Asn Pro Arg Leu Leu Leu
                165                 170                 175

gcc gac gag gcc acc tcg gcc ctc gac ccg gag acc acc cag gac gtg        876
Ala Asp Glu Ala Thr Ser Ala Leu Asp Pro Glu Thr Thr Gln Asp Val
            180                 185                 190

ctc gac ctg ctc cgg gag atc aac cgc gag ctg ggc atc acc atc gtc        924
Leu Asp Leu Leu Arg Glu Ile Asn Arg Glu Leu Gly Ile Thr Ile Val
        195                 200                 205

gta atc acc cat gag atg gac gtc gtg cgt tcc atc gcc gac aag gtc        972
Val Ile Thr His Glu Met Asp Val Val Arg Ser Ile Ala Asp Lys Val
    210                 215                 220

gcc gtc atg gag gcc ggc cgg gtg gtc gag cac ggc agc gtc tac gag       1020
Ala Val Met Glu Ala Gly Arg Val Val Glu His Gly Ser Val Tyr Glu
225                 230                 235                 240

gtg ttc tcc cgc ccg cag act gcg gtg gcg cgg cgc ttc gtg tcc acc       1068
Val Phe Ser Arg Pro Gln Thr Ala Val Ala Arg Arg Phe Val Ser Thr
                245                 250                 255

tcg ctg cgc aac acc ccc gac cag gtc gag gcg gag gac ctg ctg gcc       1116
Ser Leu Arg Asn Thr Pro Asp Gln Val Glu Ala Glu Asp Leu Leu Ala
            260                 265                 270

cac gag ggc cgc ctg ttc acc atc acc ctc acg gag gac tcc ggg ttc       1164
His Glu Gly Arg Leu Phe Thr Ile Thr Leu Thr Glu Asp Ser Gly Phe
        275                 280                 285

ttc gcc gcg gcc gcc gcc ggc cgt gag gag ggg atg ctc atc aac atc       1212
Phe Ala Ala Ala Ala Ala Gly Arg Glu Glu Gly Met Leu Ile Asn Ile
    290                 295                 300

gtc cac ggc ggc gtc acc acg ctg cag cgg cag tcc ttc ggc aag atg       1260
Val His Gly Gly Val Thr Thr Leu Gln Arg Gln Ser Phe Gly Lys Met
305                 310                 315                 320

acc gtc cgg gtg acg ggg ccg gac gcg gcc gtc gag aag ttc cgt gac       1308
Thr Val Arg Val Thr Gly Pro Asp Ala Ala Val Glu Lys Phe Arg Asp
                325                 330                 335

acg ctg tcc cgc acc acc gac atc cag gag atc acg cga tga               1350
Thr Leu Ser Arg Thr Thr Asp Ile Gln Glu Ile Thr Arg
            340                 345

acgagaccct cctcgccgca gactggaacc gtctcggccc gaccttcatc gacgccatcg     1410

gcgacaccct cgtcatggtg tccctcacga tggtgctcgg cggcctcggc ggcctgctca     1470

tcggcctgct gctgtacacg tcccgcgcgg gcggcatcct gcagtcgaag ccgctgtact     1530

ggacgctcaa catcctggtg aacttcgtcc gcccgatccc cttcatcgtg ctcatcgcca     1590
```

tgctggcgcc ggtgacggtc caggtcgtgg gcaccaccat cggccggtcc gcggcgatct 1650

<210> 14
<211> 349
<212> PRT
<213> Corynebacterium humireducens

<400> 14

Val Thr Ala Pro Pro Thr Arg Pro Arg Thr Gly Thr Arg Ile Glu Phe
1 5 10 15

Arg Asp Val Thr Lys Val Phe Thr Asn Gln Arg Lys Thr Glu Thr Arg
20 25 30

Ala Val Asp Gly Val Thr Leu Thr Val Glu Pro Gly Glu Ile Leu Gly
35 40 45

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

Asn Gly Leu Asp Ser Thr Thr Ser Gly Gln Leu Leu Leu Asp Gly Thr
65 70 75 80

Asp Ile Val Gly Leu Pro Glu Ser Lys Leu Arg Ser Ile Arg Arg Gly
85 90 95

Ile Gly Met Ile Phe Gln Gln Phe Asn Leu Phe Gln Ser Arg Thr Ala
100 105 110

Ala Gly Asn Ile Ala Tyr Pro Leu Glu Leu Ala Gly Met Pro Arg Ala
115 120 125

Glu Arg Arg Arg Arg Val Ala Glu Leu Leu Asp Phe Val Gly Leu Gly
130 135 140

Asp Lys Gly Asp Asn Tyr Pro Glu Gln Leu Ser Gly Gly Gln Lys Gln
145 150 155 160

Arg Val Gly Ile Ala Arg Ala Leu Ala Thr Asn Pro Arg Leu Leu Leu
165 170 175

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

```
Leu Asp Leu Leu Arg Glu Ile Asn Arg Glu Leu Gly Ile Thr Ile Val
        195                 200                 205

Val Ile Thr His Glu Met Asp Val Val Arg Ser Ile Ala Asp Lys Val
    210                 215                 220

Ala Val Met Glu Ala Gly Arg Val Val Glu His Gly Ser Val Tyr Glu
225                 230                 235                 240

Val Phe Ser Arg Pro Gln Thr Ala Val Ala Arg Arg Phe Val Ser Thr
                245                 250                 255

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

His Glu Gly Arg Leu Phe Thr Ile Thr Leu Thr Glu Asp Ser Gly Phe
        275                 280                 285

Phe Ala Ala Ala Ala Ala Gly Arg Glu Glu Gly Met Leu Ile Asn Ile
    290                 295                 300

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

Thr Val Arg Val Thr Gly Pro Asp Ala Ala Val Glu Lys Phe Arg Asp
                325                 330                 335

Thr Leu Ser Arg Thr Thr Asp Ile Gln Glu Ile Thr Arg
            340                 345
```

<210> 15
<211> 1854
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1554)
<223> gene metK

<400> 15

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gacggacaga ccagcgcgct cgagtacgcg caggccaagc tcacccgcaa gggctgcgac       60

ctgctcatgg ccaacgaggt gggggagggc cgggtcttcg gccagacccg caacagcggc      120

tggctgctca ccgccgacgg cgctgtcacg gaggttccgg acggttccaa gcacgtggtg      180

gcggcggcga tcctcagcgc cgtcgacgac ctgcgcaatt gacgctttta gaccgcttgg      240
```

```
tctatattgg gcgggacgct cagtcatatc attaatttga cccccgaaaa ggacccgccc      300

gtg tca gag aac ccc gcc acc acc acg gtg gcc ttc gac aag ccc gcc      348
Val Ser Glu Asn Pro Ala Thr Thr Thr Val Ala Phe Asp Lys Pro Ala
1               5                  10                  15

acg atc cgc ctg ttc acc agc gag tcc gtc acc gag ggc cac ccg gac      396
Thr Ile Arg Leu Phe Thr Ser Glu Ser Val Thr Glu Gly His Pro Asp
            20                  25                  30

aag atc tgc gac gcc atc tcg gac acc atc ctc gac gcc atg ctc gag      444
Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu Asp Ala Met Leu Glu
        35                  40                  45

cag gac ccg acc gcg cgc gtg gcc gtc gag acg ctc gtg acc acc ggc      492
Gln Asp Pro Thr Ala Arg Val Ala Val Glu Thr Leu Val Thr Thr Gly
    50                  55                  60

cag gtc cac gtc gtc ggt gag gtc cgc acc acc ggc tac gtc gag atc      540
Gln Val His Val Val Gly Glu Val Arg Thr Thr Gly Tyr Val Glu Ile
65                  70                  75                  80

ccg cag ctc gtg cgc aag acc ctc gtg gac atc ggc ttc atc tcc tcc      588
Pro Gln Leu Val Arg Lys Thr Leu Val Asp Ile Gly Phe Ile Ser Ser
                85                  90                  95

gag gtc ggc ttc gac ggc acc acc tgc ggc gtc aac atc gcc atc ggc      636
Glu Val Gly Phe Asp Gly Thr Thr Cys Gly Val Asn Ile Ala Ile Gly
            100                 105                 110

gag cag tcc cag gag atc gcc gac ggc gtc gac tcc tcc cac gag gag      684
Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp Ser Ser His Glu Glu
        115                 120                 125

cgt tcc ggc gtc gag atc gac gag gac gac cgc gcc ggc gcc ggc gac      732
Arg Ser Gly Val Glu Ile Asp Glu Asp Asp Arg Ala Gly Ala Gly Asp
    130                 135                 140

cag ggc ctc atg ttc ggc tac gcc agc aac gag acc ccc gag tac atg      780
Gln Gly Leu Met Phe Gly Tyr Ala Ser Asn Glu Thr Pro Glu Tyr Met
145                 150                 155                 160

ccg ctg ccc atc gcc ctg gcc cac cgc ctg gcc cgc cgc ctc acc gag      828
Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ala Arg Arg Leu Thr Glu
                165                 170                 175

gtg cgc aac cag ggc atc gtc ccg cac ctg cgt ccc gac ggc aag acc      876
Val Arg Asn Gln Gly Ile Val Pro His Leu Arg Pro Asp Gly Lys Thr
            180                 185                 190

cag gtc acc ttc gcc tac gac gag cag gac cgc ccg gtc cgc ctc gac      924
Gln Val Thr Phe Ala Tyr Asp Glu Gln Asp Arg Pro Val Arg Leu Asp
        195                 200                 205

acc gtg gtc atc tcc acg cag cac gac ccg gag gtc acc cag gac tgg      972
Thr Val Val Ile Ser Thr Gln His Asp Pro Glu Val Thr Gln Asp Trp
    210                 215                 220
```

```
ctg cac gag cag ctg cgc gag cac gtc ctc gac tgg gtc atc gcc gac      1020
Leu His Glu Gln Leu Arg Glu His Val Leu Asp Trp Val Ile Ala Asp
225                 230                 235                 240

gcc ggc ctg atc ggc atg gtc gac gag gag ctc acc ctc ctg gtc aac      1068
Ala Gly Leu Ile Gly Met Val Asp Glu Glu Leu Thr Leu Leu Val Asn
                245                 250                 255

ccg tcc ggc tcc ttc atc ctc ggc ggc ccg atg ggc gac gct ggc ctg      1116
Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met Gly Asp Ala Gly Leu
            260                 265                 270

acg ggc cgc aag atc atc gtc gac acc tac ggc ggc atg gcc cgc cac      1164
Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala Arg His
        275                 280                 285

ggc ggc ggc gcc ttc tcc ggc aag gac ccg tcc aag gtg gac cgt tcc      1212
Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp Arg Ser
    290                 295                 300

gcc gcg tac gcc atg cgc tgg gtg gcc aag aac atc gtc gcc gcc ggc      1260
Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn Ile Val Ala Ala Gly
305                 310                 315                 320

ctg gcc gag cgc gtc gag gtc cag gtg gcc tac gcc atc ggc cgc gcg      1308
Leu Ala Glu Arg Val Glu Val Gln Val Ala Tyr Ala Ile Gly Arg Ala
                325                 330                 335

aag ccg gtc ggc ctc tac gtg gag tcc ttc ggc acc gcc gcc gcg ggc      1356
Lys Pro Val Gly Leu Tyr Val Glu Ser Phe Gly Thr Ala Ala Ala Gly
            340                 345                 350

ctc agt gac gcg gac atc cag ggc gcc gtc gag aag gtc ttc gac ctg      1404
Leu Ser Asp Ala Asp Ile Gln Gly Ala Val Glu Lys Val Phe Asp Leu
        355                 360                 365

cgg ccc gcc gcc atc atc cgc gag ctc gac ctg ctg cgc ccg atc tac      1452
Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu Leu Arg Pro Ile Tyr
    370                 375                 380

gcg cag acc tcc gcc tac ggc cac ttc ggc cgc ctc gac ctg gat ctg      1500
Ala Gln Thr Ser Ala Tyr Gly His Phe Gly Arg Leu Asp Leu Asp Leu
385                 390                 395                 400

ccc tgg gag cgg ctc aac cgg gtg gac gag ctc aag gcg gct ctg ggc      1548
Pro Trp Glu Arg Leu Asn Arg Val Asp Glu Leu Lys Ala Ala Leu Gly
                405                 410                 415

cgc tag agtattcggc atggcctccc cccgcgtccc cgcagaacac ctgccggtgg      1604
Arg
```

cgcgggttct gcctctcctg ggcctggccc acctcgaccg gcccttcgac taccaggtgc 1664

cgtcgacgct ggatgacgac gcccagcccg gcgtccgcgt ccgcatccgc ttcgccgggc 1724

ggcttgtcga cgccgtcctc ctcgaacgcc gcgccgacac cgagcacgag ggcgggctga 1784

gctggatcga gcgggtgatc tccccgcacg tcgtgtaccc gccgcgcacc gcccggctca 1844

tcgaggcgct 1854

<210> 16
<211> 417
<212> PRT
<213> Corynebacterium humireducens

<400> 16

```
Val Ser Glu Asn Pro Ala Thr Thr Thr Val Ala Phe Asp Lys Pro Ala
1               5                  10                  15

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

Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu Asp Ala Met Leu Glu
        35                  40                  45

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

Gln Val His Val Val Gly Glu Val Arg Thr Thr Gly Tyr Val Glu Ile
65                  70                  75                  80

Pro Gln Leu Val Arg Lys Thr Leu Val Asp Ile Gly Phe Ile Ser Ser
                85                  90                  95

Glu Val Gly Phe Asp Gly Thr Thr Cys Gly Val Asn Ile Ala Ile Gly
            100                 105                 110

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

Arg Ser Gly Val Glu Ile Asp Glu Asp Asp Arg Ala Gly Ala Gly Asp
    130                 135                 140

Gln Gly Leu Met Phe Gly Tyr Ala Ser Asn Glu Thr Pro Glu Tyr Met
145                 150                 155                 160

Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ala Arg Arg Leu Thr Glu
                165                 170                 175

Val Arg Asn Gln Gly Ile Val Pro His Leu Arg Pro Asp Gly Lys Thr
            180                 185                 190
```

```
Gln Val Thr Phe Ala Tyr Asp Glu Gln Asp Arg Pro Val Arg Leu Asp
        195                 200                 205

Thr Val Val Ile Ser Thr Gln His Asp Pro Glu Val Thr Gln Asp Trp
    210                 215                 220

Leu His Glu Gln Leu Arg Glu His Val Leu Asp Trp Val Ile Ala Asp
225                 230                 235                 240

Ala Gly Leu Ile Gly Met Val Asp Glu Glu Leu Thr Leu Leu Val Asn
                245                 250                 255

Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met Gly Asp Ala Gly Leu
            260                 265                 270

Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala Arg His
        275                 280                 285

Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp Arg Ser
    290                 295                 300

Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn Ile Val Ala Ala Gly
305                 310                 315                 320

Leu Ala Glu Arg Val Glu Val Gln Val Ala Tyr Ala Ile Gly Arg Ala
                325                 330                 335

Lys Pro Val Gly Leu Tyr Val Glu Ser Phe Gly Thr Ala Ala Ala Gly
            340                 345                 350

Leu Ser Asp Ala Asp Ile Gln Gly Ala Val Glu Lys Val Phe Asp Leu
        355                 360                 365

Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu Leu Arg Pro Ile Tyr
    370                 375                 380

Ala Gln Thr Ser Ala Tyr Gly His Phe Gly Arg Leu Asp Leu Asp Leu
385                 390                 395                 400

Pro Trp Glu Arg Leu Asn Arg Val Asp Glu Leu Lys Ala Ala Leu Gly
                405                 410                 415

Arg
```

<210> 17
<211> 1278
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(978)
<223> gene metI

<400> 17
ggcgcggcgc ttcgtgtcca cctcgctgcg caacaccccc gaccaggtcg aggcggagga 60

cctgctggcc cacgagggcc gcctgttcac catcaccctc acggaggact ccgggttctt 120

cgccgcggcc gccgccggcc gtgaggaggg gatgctcatc aacatcgtcc acggcggcgt 180

caccacgctg cagcggcagt ccttcggcaa gatgaccgtc cgggtgacgg ggccggacgc 240

ggccgtcgag aagttccgtg acacgctgtc ccgcaccacc gacatccagg agatcacgcg 300

atg aac gag acc ctc ctc gcc gca gac tgg aac cgt ctc ggc ccg acc 348
Met Asn Glu Thr Leu Leu Ala Ala Asp Trp Asn Arg Leu Gly Pro Thr
1 5 10 15

ttc atc gac gcc atc ggc gac acc ctc gtc atg gtg tcc ctc acg atg 396
Phe Ile Asp Ala Ile Gly Asp Thr Leu Val Met Val Ser Leu Thr Met
20 25 30

gtg ctc ggc ggc ctc ggc ggc ctg ctc atc ggc ctg ctg ctg tac acg 444
Val Leu Gly Gly Leu Gly Gly Leu Leu Ile Gly Leu Leu Leu Tyr Thr
35 40 45

tcc cgc gcg ggc ggc atc ctg cag tcg aag ccg ctg tac tgg acg ctc 492
Ser Arg Ala Gly Gly Ile Leu Gln Ser Lys Pro Leu Tyr Trp Thr Leu
50 55 60

aac atc ctg gtg aac ttc gtc cgc ccg atc ccc ttc atc gtg ctc atc 540
Asn Ile Leu Val Asn Phe Val Arg Pro Ile Pro Phe Ile Val Leu Ile
65 70 75 80

gcc atg ctg gcg ccg gtg acg gtc cag gtc gtg ggc acc acc atc ggc 588
Ala Met Leu Ala Pro Val Thr Val Gln Val Val Gly Thr Thr Ile Gly
85 90 95

cgg tcc gcg gcg atc ttc gtc atg tgc atc gcc gcc gcc ttc gcc gtg 636
Arg Ser Ala Ala Ile Phe Val Met Cys Ile Ala Ala Ala Phe Ala Val
100 105 110

gcc cgc atc gtc gag cag aac ctc gtg gcc atc gac ccc ggc gtc atc 684
Ala Arg Ile Val Glu Gln Asn Leu Val Ala Ile Asp Pro Gly Val Ile
115 120 125

gag gcc gcc cgc gcc atg ggg gcg ggg ccg tgg cgg atc atc cgc acg 732
Glu Ala Ala Arg Ala Met Gly Ala Gly Pro Trp Arg Ile Ile Arg Thr
130 135 140

```
gtg atc atc ccg gag gcc ctc ggc ccg ctg gtc ctc ggc tac acg ttc        780
Val Ile Ile Pro Glu Ala Leu Gly Pro Leu Val Leu Gly Tyr Thr Phe
145                 150                 155                 160

atc ttc atc gcg gtg gtc gac atg tcc gcg atg gcc ggc tac atc ggc        828
Ile Phe Ile Ala Val Val Asp Met Ser Ala Met Ala Gly Tyr Ile Gly
                165                 170                 175

ggt ggt ggc ctg ggt gac ttc gcc atc gtc tac ggc tac cgc gcc tac        876
Gly Gly Gly Leu Gly Asp Phe Ala Ile Val Tyr Gly Tyr Arg Ala Tyr
            180                 185                 190

gac ctg gag gtc acg tac gcg gcg gtc atc gtc atc gtc atc atc gtg        924
Asp Leu Glu Val Thr Tyr Ala Ala Val Ile Val Ile Val Ile Ile Val
        195                 200                 205

cag atc gcg cag ctg ctg ggc aac tgg ctc tcg cga aag ctc atg cgg        972
Gln Ile Ala Gln Leu Leu Gly Asn Trp Leu Ser Arg Lys Leu Met Arg
    210                 215                 220

cgt tag cgtcgcccgc cgttcacacc cccgaccccg tgtcgggggt tttgcgtacc       1028
Arg
225

cggagccgaa acgggggctc ccgatcgaga acacgtcggg gcgacgacct gccgtgcgga    1088

agtacccttc tgcccgctcg accgcactgt ttccccagga cacaacctgg cctgcagaca    1148

cagacgggta cctcagaacg cagctagcct ggatgtcatg aagatcgccg ccttcgacat    1208

cgacgacacc ctgctgttcc cccacggcat cgccgaggag gacatccgcg ccatccgcgc    1268

ctggcaggag                                                          1278
```

<210> 18
<211> 225
<212> PRT
<213> Corynebacterium humireducens

<400> 18

```
Met Asn Glu Thr Leu Leu Ala Ala Asp Trp Asn Arg Leu Gly Pro Thr
1               5                   10                  15

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

Val Leu Gly Gly Leu Gly Gly Leu Leu Ile Gly Leu Leu Leu Tyr Thr
        35                  40                  45

Ser Arg Ala Gly Gly Ile Leu Gln Ser Lys Pro Leu Tyr Trp Thr Leu
    50                  55                  60

Asn Ile Leu Val Asn Phe Val Arg Pro Ile Pro Phe Ile Val Leu Ile
```

65 70 75 80

Ala Met Leu Ala Pro Val Thr Val Gln Val Val Gly Thr Thr Ile Gly
85 90 95

Arg Ser Ala Ala Ile Phe Val Met Cys Ile Ala Ala Ala Phe Ala Val
100 105 110

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

Glu Ala Ala Arg Ala Met Gly Ala Gly Pro Trp Arg Ile Ile Arg Thr
130 135 140

Val Ile Ile Pro Glu Ala Leu Gly Pro Leu Val Leu Gly Tyr Thr Phe
145 150 155 160

Ile Phe Ile Ala Val Val Asp Met Ser Ala Met Ala Gly Tyr Ile Gly
165 170 175

Gly Gly Gly Leu Gly Asp Phe Ala Ile Val Tyr Gly Tyr Arg Ala Tyr
180 185 190

Asp Leu Glu Val Thr Tyr Ala Ala Val Ile Val Ile Val Ile Ile Val
195 200 205

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

Arg
225

<210> 19
<211> 1509
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1209)
<223> gene dapA

<400> 19
ggcaggccgc ccgcgcggtg ctgccgaacg ccacggagtc acgcatcgtc gtcaccggca 60

actaccgggc gtggcgccac ttcatcggcg cccgggccac cgagcacgcg gacgtcgaga 120

```
tccgggcact ggcggtggcg tgcctccgcc tcctcgcgca gcagtccccg gtgctcttcg      180

ccgatttcca gatctccact ctctccgacg gcacagagat ggccgtcagt ccctacgcca      240

ccgacttctg accagcgagg gattccccag cggaaaggta aacaggtaac cttgaacacc      300

atg agt aca ggt atg act tcg aag acc gga gtc gag gac ttc ggt acc        348
Met Ser Thr Gly Met Thr Ser Lys Thr Gly Val Glu Asp Phe Gly Thr
1               5                  10                  15

gtc tgc gtc gcc atg gtc acg ccc ttc gac cgg gac ggc gcc ctg gac        396
Val Cys Val Ala Met Val Thr Pro Phe Asp Arg Asp Gly Ala Leu Asp
            20                  25                  30

ctc gag gcc ggt cgc cgc atc gcg gcc cac ctc gtc gac aac ggt ctg        444
Leu Glu Ala Gly Arg Arg Ile Ala Ala His Leu Val Asp Asn Gly Leu
        35                  40                  45

gac gcc ctc gtg ctc gca ggc acg acc ggt gag tcc ccg acc acc acg        492
Asp Ala Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr
    50                  55                  60

ctc gac gag aag atc agc ctg ctc aag gcg gtg aag gag gag gtc ggc        540
Leu Asp Glu Lys Ile Ser Leu Leu Lys Ala Val Lys Glu Glu Val Gly
65                  70                  75                  80

gac cgc tgc aag ctc atc gcg ggt gcc ggc acc aac gac acc gcc tcc        588
Asp Arg Cys Lys Leu Ile Ala Gly Ala Gly Thr Asn Asp Thr Ala Ser
                85                  90                  95

tcc atc gag ctc gcc cgc gcc tcc gcc gag gcc ggc gcc gac gcc ctg        636
Ser Ile Glu Leu Ala Arg Ala Ser Ala Glu Ala Gly Ala Asp Ala Leu
            100                 105                 110

ctc gtg gtc acc ccc tac tac tcg aag ccg agc cag gag ggt gtc tac        684
Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Val Tyr
        115                 120                 125

cag cac ttc aag gcc gtc gcc ggg gcc acc gac ctg ccc atc atg ctc        732
Gln His Phe Lys Ala Val Ala Gly Ala Thr Asp Leu Pro Ile Met Leu
    130                 135                 140

tac gac atc ccg ccg cgc tcc tcg atc ccg atc gag ggg gac acc atc        780
Tyr Asp Ile Pro Pro Arg Ser Ser Ile Pro Ile Glu Gly Asp Thr Ile
145                 150                 155                 160

cgc cga ctc gcg gag ctg ccc acc att cgt gcg gtg aag gat gca aag        828
Arg Arg Leu Ala Glu Leu Pro Thr Ile Arg Ala Val Lys Asp Ala Lys
                165                 170                 175

ggt aac atg gct gag tct gca ccg ctc atg cat gag acc ggt ctc gcc        876
Gly Asn Met Ala Glu Ser Ala Pro Leu Met His Glu Thr Gly Leu Ala
            180                 185                 190

tgg tac tcg ggc gat gat ccg ctc aac gtc ccg tgg ctg tcg ctc ggc        924
Trp Tyr Ser Gly Asp Asp Pro Leu Asn Val Pro Trp Leu Ser Leu Gly
        195                 200                 205

gcc tcg gga ttc gtt tcc gtg gtc ggc cat gcc gca ccc cag gca ctg        972
```

```
Ala Ser Gly Phe Val Ser Val Val Gly His Ala Ala Pro Gln Ala Leu
    210                 215                 220

cgt gag ctg tac aca agt ttc gag gaa ggc gac ctc gcc cgt gcg cgg      1020
Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Ala Arg Ala Arg
225                 230                 235                 240

gaa atc aac gcc act gtt ctt tca ccg ctg atc gcc gct cag ggt cgc      1068
Glu Ile Asn Ala Thr Val Leu Ser Pro Leu Ile Ala Ala Gln Gly Arg
                245                 250                 255

ctg ggt ggt gtc agc atg gcc aag gct gcc ctg cgt ctg cag ggc att      1116
Leu Gly Gly Val Ser Met Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile
            260                 265                 270

gag gtg ggg gac ccg cgt ctg cct gtc gtc gct ccc gac gag cag gag      1164
Glu Val Gly Asp Pro Arg Leu Pro Val Val Ala Pro Asp Glu Gln Glu
        275                 280                 285

atc gag gcc ctc cgc cgt gac atg gaa aag gct gga gtc ctt taa          1209
Ile Glu Ala Leu Arg Arg Asp Met Glu Lys Ala Gly Val Leu
    290                 295                 300

atatgactga atcccgtagt cgtgcccgga aggtcacccg caaggcgggc ccgccggaga    1269

ccgagagcac tggtgcatcc ccggttttcc aggcaccgac cccggaaacg aacggaaacg    1329

gcgcatccgc cgagaagaag accaccgaaa ggaagtccgc ggacaccgac aacgccccgc    1389

ggggcggcgg caaccgctcc cggaacggtg gcggccgcgc ccgcggcggc cgtggtggcc    1449

gcggcggtca gggtggccag ggccagggcg gtcagggtgg tcagcagggg ggacggggac    1509
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<210> 20
<211> 302
<212> PRT
<213> Corynebacterium humireducens

<400> 20

```
Met Ser Thr Gly Met Thr Ser Lys Thr Gly Val Glu Asp Phe Gly Thr
1               5                   10                  15

Val Cys Val Ala Met Val Thr Pro Phe Asp Arg Asp Gly Ala Leu Asp
            20                  25                  30

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

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

Leu Asp Glu Lys Ile Ser Leu Leu Lys Ala Val Lys Glu Glu Val Gly
65                  70                  75                  80
```

```
Asp Arg Cys Lys Leu Ile Ala Gly Ala Gly Thr Asn Asp Thr Ala Ser
                85                  90                  95

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

Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Val Tyr
        115                 120                 125

Gln His Phe Lys Ala Val Ala Gly Ala Thr Asp Leu Pro Ile Met Leu
    130                 135                 140

Tyr Asp Ile Pro Pro Arg Ser Ser Ile Pro Ile Glu Gly Asp Thr Ile
145                 150                 155                 160

Arg Arg Leu Ala Glu Leu Pro Thr Ile Arg Ala Val Lys Asp Ala Lys
                165                 170                 175

Gly Asn Met Ala Glu Ser Ala Pro Leu Met His Glu Thr Gly Leu Ala
            180                 185                 190

Trp Tyr Ser Gly Asp Asp Pro Leu Asn Val Pro Trp Leu Ser Leu Gly
        195                 200                 205

Ala Ser Gly Phe Val Ser Val Val Gly His Ala Ala Pro Gln Ala Leu
    210                 215                 220

Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Ala Arg Ala Arg
225                 230                 235                 240

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

Leu Gly Gly Val Ser Met Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile
            260                 265                 270

Glu Val Gly Asp Pro Arg Leu Pro Val Val Ala Pro Asp Glu Gln Glu
        275                 280                 285

Ile Glu Ala Leu Arg Arg Asp Met Glu Lys Ala Gly Val Leu
    290                 295                 300
```

<210> 21

<211> 1515
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1215)
<223> CBS

<400> 21
gggcctccgc gacgggagcg ctggaaccac cgcgccaggg gccctgtgcc tcggccacct 60

gagtggcgga cagggtgagg gcgacggcca gggcggccgc gctgatctga cggtgtcggc 120

gggtgaaagc catgttcatc atctcctatg agctctattg gcgtaagggt ggatgatagg 180

gcagaaaatg caggttagat accctgccgg gtatgggata tctcacgggc tgcgacggga 240

acttcgcggt ccggaaaaag ttcccgcctt cccttgactt tgcggcgtaa gatgtcattt 300

atg agt ctc gag ccc ggg aac acc ccg ctc gta cgt ctg gac cgg ctc 348
Met Ser Leu Glu Pro Gly Asn Thr Pro Leu Val Arg Leu Asp Arg Leu
1 5 10 15

ccc ggc cgg ccc ggt gtc acc ctg tgg gcg aag ctg gag ggc cac aac 396
Pro Gly Arg Pro Gly Val Thr Leu Trp Ala Lys Leu Glu Gly His Asn
20 25 30

ccc agc ggc agt gcc aag gac cgg acc gcg cac gcc atc ctc gcg gcg 444
Pro Ser Gly Ser Ala Lys Asp Arg Thr Ala His Ala Ile Leu Ala Ala
35 40 45

gcg gat ctg cgg ccc ggc gcg gtc atc gtc gag tcg agc tcg ggc aac 492
Ala Asp Leu Arg Pro Gly Ala Val Ile Val Glu Ser Ser Ser Gly Asn
50 55 60

ctc ggc gtc gcc ctg gcc cgg gag gcg gtc ctc ggc ggc tgg acc ttc 540
Leu Gly Val Ala Leu Ala Arg Glu Ala Val Leu Gly Gly Trp Thr Phe
65 70 75 80

cac tgt gtc gtc gat ccg aag gcg aat cgc tcg acc atc gcc acc atg 588
His Cys Val Val Asp Pro Lys Ala Asn Arg Ser Thr Ile Ala Thr Met
85 90 95

cgc gcg ttc ggg gcg gtc gtc cac gag gtc acc gca ccc gat ccg gcc 636
Arg Ala Phe Gly Ala Val Val His Glu Val Thr Ala Pro Asp Pro Ala
100 105 110

acc ggt gac tgg ctc gcc gcc cgg cgc gcg cgg gtc gcg gaa ctg ctc 684
Thr Gly Asp Trp Leu Ala Ala Arg Arg Ala Arg Val Ala Glu Leu Leu
115 120 125

acc gag atc ccc ggg gcc gtc tgc ctc gac cag tac tcc aac cgg gcg 732
Thr Glu Ile Pro Gly Ala Val Cys Leu Asp Gln Tyr Ser Asn Arg Ala
130 135 140

gcc ttc acg gcc cac gac gag ggc acg atg gcc gag atc gtc gcg cag 780
Ala Phe Thr Ala His Asp Glu Gly Thr Met Ala Glu Ile Val Ala Gln

```
145                 150                 155                 160

ctc ggc cac acc ccc gcg cac ctg ttc gtg gcg gtg agc acc acc ggc        828
Leu Gly His Thr Pro Ala His Leu Phe Val Ala Val Ser Thr Thr Gly
                165                 170                 175

acg atc ggc ggc tgc ctg cgc cgc atc gcc cgg gag ggg tgg gac acg        876
Thr Ile Gly Gly Cys Leu Arg Arg Ile Ala Arg Glu Gly Trp Asp Thr
            180                 185                 190

gag gtc acc gcc gtc gac gcc gag ggt tcc gtg ctt ttc gac ggc gcc        924
Glu Val Thr Ala Val Asp Ala Glu Gly Ser Val Leu Phe Asp Gly Ala
        195                 200                 205

cgt ggc cgc cgc cac ctt ccc ggc ttc ggc gcc ggc atc gtc ccg gac        972
Arg Gly Arg Arg His Leu Pro Gly Phe Gly Ala Gly Ile Val Pro Asp
    210                 215                 220

ctg gcc gcc gag gtg acc ccg gac cgc atc gtc cgg gtc ggc gac cgt       1020
Leu Ala Ala Glu Val Thr Pro Asp Arg Ile Val Arg Val Gly Asp Arg
225                 230                 235                 240

gac tcc gtc gcc gcc gcg cgg cag ctg gcc cgc acg gaa ggg gtg ttg       1068
Asp Ser Val Ala Ala Ala Arg Gln Leu Ala Arg Thr Glu Gly Val Leu
                245                 250                 255

tgc ggt gcc tcg ggt ggg gcg gtg gtg gcg gcc gtc ggg aag ctc ctg       1116
Cys Gly Ala Ser Gly Gly Ala Val Val Ala Ala Val Gly Lys Leu Leu
            260                 265                 270

ccg gag ctg cac ggg gac gtc gtc ctc gtg ctc cac gac ggt ggc acc       1164
Pro Glu Leu His Gly Asp Val Val Leu Val Leu His Asp Gly Gly Thr
        275                 280                 285

cac tac ctg gac acc gtg tac aac gac gac tgg gtg gag gag aac ctg       1212
His Tyr Leu Asp Thr Val Tyr Asn Asp Asp Trp Val Glu Glu Asn Leu
    290                 295                 300

tga caaccgtggt gatcatcggc ggcggcccgc gcggactgtg ggcggcggag            1265

gaactgctgg gcctggcacg cgagaggggc gcggccctcg acgtccacgt catcgacgac     1325

ggcggaccgc aggcctacga cccggggcag ccggaggagt ggctcatcaa cgtgcgggcc     1385

tccgtgatcc gcacggggct gggctccttc gacgagtggc gcggggccgc cgacccttc      1445

ccgccgcgac gcgaggtggc ccgtttcctc gccgcctcct gggaggagct cgcacagcac     1505

gtgtcgccgc                                                           1515
```

<210> 22
<211> 304
<212> PRT
<213> Corynebacterium humireducens

<400> 22

```
Met Ser Leu Glu Pro Gly Asn Thr Pro Leu Val Arg Leu Asp Arg Leu
```

```
1               5                   10                  15

Pro Gly Arg Pro Gly Val Thr Leu Trp Ala Lys Leu Glu Gly His Asn
            20                  25                  30

Pro Ser Gly Ser Ala Lys Asp Arg Thr Ala His Ala Ile Leu Ala Ala
        35                  40                  45

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

Leu Gly Val Ala Leu Ala Arg Glu Ala Val Leu Gly Gly Trp Thr Phe
65                  70                  75                  80

His Cys Val Val Asp Pro Lys Ala Asn Arg Ser Thr Ile Ala Thr Met
                85                  90                  95

Arg Ala Phe Gly Ala Val Val His Glu Val Thr Ala Pro Asp Pro Ala
            100                 105                 110

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

Thr Glu Ile Pro Gly Ala Val Cys Leu Asp Gln Tyr Ser Asn Arg Ala
    130                 135                 140

Ala Phe Thr Ala His Asp Glu Gly Thr Met Ala Glu Ile Val Ala Gln
145                 150                 155                 160

Leu Gly His Thr Pro Ala His Leu Phe Val Ala Val Ser Thr Thr Gly
                165                 170                 175

Thr Ile Gly Gly Cys Leu Arg Arg Ile Ala Arg Glu Gly Trp Asp Thr
            180                 185                 190

Glu Val Thr Ala Val Asp Ala Glu Gly Ser Val Leu Phe Asp Gly Ala
        195                 200                 205

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

Leu Ala Ala Glu Val Thr Pro Asp Arg Ile Val Arg Val Gly Asp Arg
225                 230                 235                 240
```

```
Asp Ser Val Ala Ala Ala Arg Gln Leu Ala Arg Thr Glu Gly Val Leu
                245                 250                 255

Cys Gly Ala Ser Gly Gly Ala Val Val Ala Ala Val Gly Lys Leu Leu
            260                 265                 270

Pro Glu Leu His Gly Asp Val Val Leu Val Leu His Asp Gly Gly Thr
        275                 280                 285

His Tyr Leu Asp Thr Val Tyr Asn Asp Asp Trp Val Glu Glu Asn Leu
    290                 295                 300
```

<210> 23
<211> 1746
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1446)
<223> gene cg3031-homolog

<400> 23

```
cccggagccg gagcgcctca acgtgctcaa caactcgacg gtgccgaacc tggccgcgca       60

ggtcgcggac cgcctgcggg aggacggttt cgaggtcggg gaggtcggca acctggcgga      120

ccacatcctc ccggagacca ccgtcttctt ccagcccggc aacgccgccg cggagcagcg      180

ggcgcgggag ctcgccgacc gcctcggcgg cgtcgcccgc gagtacgagg gcttcctccc      240

ggagaacacc gccggtcgca acgacctgac tctggtgctg gtgaaccagg tggcgctctg      300

atg ggc ccg ggg acc ggc atc gag ccg atc ccg ttc cgc cgc tcc ccg        348
Met Gly Pro Gly Thr Gly Ile Glu Pro Ile Pro Phe Arg Arg Ser Pro
1               5                   10                  15

cgg ccg acg ctc ggc gtc gag tgg gag atc gcg ctc atc gac ccc gag        396
Arg Pro Thr Leu Gly Val Glu Trp Glu Ile Ala Leu Ile Asp Pro Glu
            20                  25                  30

acc cgc gac ctg gcg ccc aag gcc gtc gag gtc atc gac ctc gtc cgg        444
Thr Arg Asp Leu Ala Pro Lys Ala Val Glu Val Ile Asp Leu Val Arg
        35                  40                  45

tcc cgc cac ccg gag gtg cac ctg gag aag gag ttc ctg cag aac acc        492
Ser Arg His Pro Glu Val His Leu Glu Lys Glu Phe Leu Gln Asn Thr
    50                  55                  60

gtc gaa ctg gtc acc ggc atc cac gaa acc gtg ccg gag gcg gtc gcg        540
Val Glu Leu Val Thr Gly Ile His Glu Thr Val Pro Glu Ala Val Ala
65                  70                  75                  80

gaa ctc gcc cgc gac ctg gcc gcc gtg aag gag gcc gcc gcc gac ctc        588
```

```
Glu Leu Ala Arg Asp Leu Ala Ala Val Lys Glu Ala Ala Ala Asp Leu
                85                  90                  95

gga ctg tgc ctg tgg tcc tcc ggc tcg cac ccc ttc tcg gac tgg cgg        636
Gly Leu Cys Leu Trp Ser Ser Gly Ser His Pro Phe Ser Asp Trp Arg
            100                 105                 110

aag aac ccg gtc agc gcg aag atg gcc tac gcc gag atc atc gag cgc        684
Lys Asn Pro Val Ser Ala Lys Met Ala Tyr Ala Glu Ile Ile Glu Arg
        115                 120                 125

acc cgc tac tgg ggt tcg cag atg ctc atc tgg ggc atc cac gtg cac        732
Thr Arg Tyr Trp Gly Ser Gln Met Leu Ile Trp Gly Ile His Val His
    130                 135                 140

gtc ggg atc agc cac gag gac cgg gtg tgg ccg atc atc aac gcc ctg        780
Val Gly Ile Ser His Glu Asp Arg Val Trp Pro Ile Ile Asn Ala Leu
145                 150                 155                 160

atg acc cgc tac ccg cac ctg ctg gcg ctg acg gcg tcg tcg ccg ggc        828
Met Thr Arg Tyr Pro His Leu Leu Ala Leu Thr Ala Ser Ser Pro Gly
                165                 170                 175

tgg gac ggc atc gac acg ggc tac gcc tcc aac cgc acg atg ctc tac        876
Trp Asp Gly Ile Asp Thr Gly Tyr Ala Ser Asn Arg Thr Met Leu Tyr
            180                 185                 190

cag cag ctg ccc acc gcc ggc ctg ccc ttc cag ttc cgg aac tgg gcc        924
Gln Gln Leu Pro Thr Ala Gly Leu Pro Phe Gln Phe Arg Asn Trp Ala
        195                 200                 205

gag tgg gag tcc tac atg cac gac cag ggc atc tcg ggc gtg atc aac        972
Glu Trp Glu Ser Tyr Met His Asp Gln Gly Ile Ser Gly Val Ile Asn
    210                 215                 220

cac acc ggg tcg atg cac ttc gac atc cgt ccc gcc ccg aag tgg ggc       1020
His Thr Gly Ser Met His Phe Asp Ile Arg Pro Ala Pro Lys Trp Gly
225                 230                 235                 240

acg gtc gag gtg cgg gtc tcc gac gcc acc tcc aac ctg cgg gaa ctc       1068
Thr Val Glu Val Arg Val Ser Asp Ala Thr Ser Asn Leu Arg Glu Leu
                245                 250                 255

gcc gcc gtc gtg gcg ctc acg cac tgc ctg gtc gtc cac tac gac cgc       1116
Ala Ala Val Val Ala Leu Thr His Cys Leu Val Val His Tyr Asp Arg
            260                 265                 270

atg atc gac cgc ggt gag gaa ctg ccc gtc ctg cag ccc tgg cac gtc       1164
Met Ile Asp Arg Gly Glu Glu Leu Pro Val Leu Gln Pro Trp His Val
        275                 280                 285

gcc gag aac aag tgg cgg gcc gcc cgc tac ggg ctg gag gca ctc gtg       1212
Ala Glu Asn Lys Trp Arg Ala Ala Arg Tyr Gly Leu Glu Ala Leu Val
    290                 295                 300

atc acc agc cgt gac acc gac gag cgc tgg gtc acc cag gag ctc gcg       1260
Ile Thr Ser Arg Asp Thr Asp Glu Arg Trp Val Thr Gln Glu Leu Ala
305                 310                 315                 320
```

```
gag ctt gtc gac gaa ctc gcg ccc ctc gcc acc gaa ctc ggc tgc ctc       1308
Glu Leu Val Asp Glu Leu Ala Pro Leu Ala Thr Glu Leu Gly Cys Leu
                325                 330                 335

gcc gaa ctc cag ctg gtc tcc gag atc ctc gaa cgt ggc gcc ggc tac       1356
Ala Glu Leu Gln Leu Val Ser Glu Ile Leu Glu Arg Gly Ala Gly Tyr
            340                 345                 350

cag cgt cag cgt cgc atc cac gac gtc acc ggc agc tgg atc ccc gtc       1404
Gln Arg Gln Arg Arg Ile His Asp Val Thr Gly Ser Trp Ile Pro Val
        355                 360                 365

atc gac gcc gcc tgc cgg gag atg gag gag atg gtc ccg tga               1446
Ile Asp Ala Ala Cys Arg Glu Met Glu Glu Met Val Pro
    370                 375                 380

gcgacgtcgt cctcgtccac tccaccgggc acctgccgga cgtgtggacg gaggtggtgc     1506

gcgccttccc ggccgactgg aagccgtggc tgcccaatct gggcgtgcag tccctcgagc     1566

agtacctgga ccggcaggag ctgcgccggg tggtgctcgt cggtcacggc accggcgccc     1626

tggccgtggc acgcctggcc cgggagcagc cgcagcgggt cacccacgcg gtgctgtccg     1686

tgccggaggc gccccgcctc gtgccacgtt tcctgcggcg ccggcaggag gaggccctgg     1746
```

<210> 24
<211> 381
<212> PRT
<213> Corynebacterium humireducens

<400> 24

```
Met Gly Pro Gly Thr Gly Ile Glu Pro Ile Pro Phe Arg Arg Ser Pro
1               5                   10                  15

Arg Pro Thr Leu Gly Val Glu Trp Glu Ile Ala Leu Ile Asp Pro Glu
            20                  25                  30

Thr Arg Asp Leu Ala Pro Lys Ala Val Glu Val Ile Asp Leu Val Arg
        35                  40                  45

Ser Arg His Pro Glu Val His Leu Glu Lys Glu Phe Leu Gln Asn Thr
    50                  55                  60

Val Glu Leu Val Thr Gly Ile His Glu Thr Val Pro Glu Ala Val Ala
65                  70                  75                  80

Glu Leu Ala Arg Asp Leu Ala Ala Val Lys Glu Ala Ala Ala Asp Leu
                85                  90                  95

Gly Leu Cys Leu Trp Ser Ser Gly Ser His Pro Phe Ser Asp Trp Arg
```

```
                100                 105                 110

Lys Asn Pro Val Ser Ala Lys Met Ala Tyr Ala Glu Ile Ile Glu Arg
        115                 120                 125

Thr Arg Tyr Trp Gly Ser Gln Met Leu Ile Trp Gly Ile His Val His
    130                 135                 140

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

Met Thr Arg Tyr Pro His Leu Leu Ala Leu Thr Ala Ser Ser Pro Gly
                165                 170                 175

Trp Asp Gly Ile Asp Thr Gly Tyr Ala Ser Asn Arg Thr Met Leu Tyr
            180                 185                 190

Gln Gln Leu Pro Thr Ala Gly Leu Pro Phe Gln Phe Arg Asn Trp Ala
        195                 200                 205

Glu Trp Glu Ser Tyr Met His Asp Gln Gly Ile Ser Gly Val Ile Asn
    210                 215                 220

His Thr Gly Ser Met His Phe Asp Ile Arg Pro Ala Pro Lys Trp Gly
225                 230                 235                 240

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

Ala Ala Val Val Ala Leu Thr His Cys Leu Val Val His Tyr Asp Arg
            260                 265                 270

Met Ile Asp Arg Gly Glu Glu Leu Pro Val Leu Gln Pro Trp His Val
        275                 280                 285

Ala Glu Asn Lys Trp Arg Ala Ala Arg Tyr Gly Leu Glu Ala Leu Val
    290                 295                 300

Ile Thr Ser Arg Asp Thr Asp Glu Arg Trp Val Thr Gln Glu Leu Ala
305                 310                 315                 320

Glu Leu Val Asp Glu Leu Ala Pro Leu Ala Thr Glu Leu Gly Cys Leu
                325                 330                 335
```

```
Ala Glu Leu Gln Leu Val Ser Glu Ile Leu Glu Arg Gly Ala Gly Tyr
            340                 345                 350

Gln Arg Gln Arg Arg Ile His Asp Val Thr Gly Ser Trp Ile Pro Val
        355                 360                 365

Ile Asp Ala Ala Cys Arg Glu Met Glu Glu Met Val Pro
    370                 375                 380
```

<210> 25
<211> 1731
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1431)
<223> gene aecD

<400> 25

```
aggccgaacg cgccgtccag gccggcctgg acgagctgat gaaggaccgc accacgctca       60

tcatcgcgca ccgcctgtcg acgatcgcgg gtgtggacac catcgtcacc ctccgcgacg      120

gcatggtcga cgaaataggt tcaccggacc agctcgccgc ctcgggtggc atctacgccg      180

aactcctgca gctcacggcg tcctcctcgg ccgctgaccg ggcccgtctg aagaggtacg      240

ggctcgtcgt cgacggtcac ggcgacgagg aggacgagga agaggactag tctgtctggc      300

atg cag ttc ccc acc ctc gac cag ctc aag gac cgt cgc acc cgc aag        348
Met Gln Phe Pro Thr Leu Asp Gln Leu Lys Asp Arg Arg Thr Arg Lys
1               5                   10                  15

tgg acg gtc tac gcc gac gac gtc ctg ccc ctg tgg atc gcg gag agt        396
Trp Thr Val Tyr Ala Asp Asp Val Leu Pro Leu Trp Ile Ala Glu Ser
            20                  25                  30

gac ttc ttc acc tgc ccg ccg gtg aag cag gcg atc gcg gac gcc atc        444
Asp Phe Phe Thr Cys Pro Pro Val Lys Gln Ala Ile Ala Asp Ala Ile
        35                  40                  45

gac cgg gag tcc ttc ggg tac acc ccg gcg acc tcc gac ctg ccg cag        492
Asp Arg Glu Ser Phe Gly Tyr Thr Pro Ala Thr Ser Asp Leu Pro Gln
    50                  55                  60

gcg gtc tcc gac ttc tac gcc gca cgt tac ggc tgg cgc ccg gac ccg        540
Ala Val Ser Asp Phe Tyr Ala Ala Arg Tyr Gly Trp Arg Pro Asp Pro
65                  70                  75                  80

gcg ctc atc gtc gcg gtc ccc gac gtc gtc cgt ggc ctg gcc ctc gcc        588
Ala Leu Ile Val Ala Val Pro Asp Val Val Arg Gly Leu Ala Leu Ala
                85                  90                  95

atc gag tac atg acg cgc ccg gac tcg ggt gtc atc gtg ccg gtg ccg        636
```

```
Ile Glu Tyr Met Thr Arg Pro Asp Ser Gly Val Ile Val Pro Val Pro
            100                 105                 110

gcg tac ccg ccg ttc ctg gag ctg ccg gag gcg acc cgc cgt ccg atg      684
Ala Tyr Pro Pro Phe Leu Glu Leu Pro Glu Ala Thr Arg Arg Pro Met
        115                 120                 125

cac cag atc gac gcc tac ggc ggg atc gac ctg ggg gac gtc gag aag      732
His Gln Ile Asp Ala Tyr Gly Gly Ile Asp Leu Gly Asp Val Glu Lys
    130                 135                 140

cag ttc gcg gcc ggc gcc ggc tcg atc ctc ctg tgc gcc ccg aac aac      780
Gln Phe Ala Ala Gly Ala Gly Ser Ile Leu Leu Cys Ala Pro Asn Asn
145                 150                 155                 160

ccc ctg ggg tac acg ttc gac gcg gag ttc ctg cgg gag ctg tgc gac      828
Pro Leu Gly Tyr Thr Phe Asp Ala Glu Phe Leu Arg Glu Leu Cys Asp
                165                 170                 175

ctg gcg gac cgt tac gac gcc cgc gtg ctc gtc gac gag atc cac gcc      876
Leu Ala Asp Arg Tyr Asp Ala Arg Val Leu Val Asp Glu Ile His Ala
            180                 185                 190

ccg ctg gtg ttc gac ggc acc cat gtg tgc gcc gcc gcc gtc agc gag      924
Pro Leu Val Phe Asp Gly Thr His Val Cys Ala Ala Ala Val Ser Glu
        195                 200                 205

acc gcc gcg cgg gtg tgc gtc acc gtc acg gcg acg tcg aag gcg tgg      972
Thr Ala Ala Arg Val Cys Val Thr Val Thr Ala Thr Ser Lys Ala Trp
    210                 215                 220

aac atc gcg ggc ctc aag tgc gcg cag atg atc ttc tcc aac ccg gcg     1020
Asn Ile Ala Gly Leu Lys Cys Ala Gln Met Ile Phe Ser Asn Pro Ala
225                 230                 235                 240

gac atg gac acg tgg cgg tcg atg acc ggc gtg gcc aag gac ggc acc     1068
Asp Met Asp Thr Trp Arg Ser Met Thr Gly Val Ala Lys Asp Gly Thr
                245                 250                 255

tcc acc ctg ggc atc tgg gcg gcg atc gcc tgc tac cgg gag ggc ggc     1116
Ser Thr Leu Gly Ile Trp Ala Ala Ile Ala Cys Tyr Arg Glu Gly Gly
            260                 265                 270

gac tgc ctc gac gag cag gtc gcg tac ctg cgg gag aac cgc gac tgg     1164
Asp Cys Leu Asp Glu Gln Val Ala Tyr Leu Arg Glu Asn Arg Asp Trp
        275                 280                 285

ctg gcc gag gag ctg ccg cgc cgc gtg ccg ggg ctg cag gtg atc agc     1212
Leu Ala Glu Glu Leu Pro Arg Arg Val Pro Gly Leu Gln Val Ile Ser
    290                 295                 300

ccg gcg gcg acc tat ctc atg tgg atg gac ttc tcc ggc acc tcc atc     1260
Pro Ala Ala Thr Tyr Leu Met Trp Met Asp Phe Ser Gly Thr Ser Ile
305                 310                 315                 320

ggg cac ctg gag cgc ccg gcg gtg tgg ctg cgg gag aac gcg aag gtc     1308
Gly His Leu Glu Arg Pro Ala Val Trp Leu Arg Glu Asn Ala Lys Val
                325                 330                 335
```

```
gcc ctc aac gac ggc gtc gcc ttc ggc ccg gga ggc agc cac cac gcg       1356
Ala Leu Asn Asp Gly Val Ala Phe Gly Pro Gly Gly Ser His His Ala
            340                 345                 350

cgg ctg aac ttc gcc acg tcc cgg gag atc ctg gag gag gcc tgc gac       1404
Arg Leu Asn Phe Ala Thr Ser Arg Glu Ile Leu Glu Glu Ala Cys Asp
        355                 360                 365

cgg ctg ggg tct gca ttc gcc cgg tga tttccctacc ctggatttca             1451
Arg Leu Gly Ser Ala Phe Ala Arg
    370                 375

tgactgacga gcgatacgac gacccgtccg ccacgaccgg cccccagggt cccggactgt     1511

ccatgggtcc gctgggggtc ggcgccgaac cggagaagtc cccggtccgc ccccgtaccg     1571

acgccgaggg ctacctggtc gaaccggagt ccgagcagtt cgagaccccg accccggcgc     1631

ccggtgacgc cccctgggag cgccccgagc cggagtggta caaggaggcc gtgttctacg     1691

aggtcctggt gcgcgccttc tacgacccgg agggcaccgg                           1731
```

<210> 26
<211> 376
<212> PRT
<213> Corynebacterium humireducens

<400> 26

```
Met Gln Phe Pro Thr Leu Asp Gln Leu Lys Asp Arg Arg Thr Arg Lys
1               5                   10                  15

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

Asp Phe Phe Thr Cys Pro Pro Val Lys Gln Ala Ile Ala Asp Ala Ile
        35                  40                  45

Asp Arg Glu Ser Phe Gly Tyr Thr Pro Ala Thr Ser Asp Leu Pro Gln
    50                  55                  60

Ala Val Ser Asp Phe Tyr Ala Ala Arg Tyr Gly Trp Arg Pro Asp Pro
65                  70                  75                  80

Ala Leu Ile Val Ala Val Pro Asp Val Val Arg Gly Leu Ala Leu Ala
                85                  90                  95

Ile Glu Tyr Met Thr Arg Pro Asp Ser Gly Val Ile Val Pro Val Pro
            100                 105                 110

Ala Tyr Pro Pro Phe Leu Glu Leu Pro Glu Ala Thr Arg Arg Pro Met
```

```
          115                 120                 125

His Gln Ile Asp Ala Tyr Gly Gly Ile Asp Leu Gly Asp Val Glu Lys
    130                 135                 140

Gln Phe Ala Ala Gly Ala Gly Ser Ile Leu Leu Cys Ala Pro Asn Asn
145                 150                 155                 160

Pro Leu Gly Tyr Thr Phe Asp Ala Glu Phe Leu Arg Glu Leu Cys Asp
                165                 170                 175

Leu Ala Asp Arg Tyr Asp Ala Arg Val Leu Val Asp Glu Ile His Ala
            180                 185                 190

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

Thr Ala Ala Arg Val Cys Val Thr Val Thr Ala Thr Ser Lys Ala Trp
    210                 215                 220

Asn Ile Ala Gly Leu Lys Cys Ala Gln Met Ile Phe Ser Asn Pro Ala
225                 230                 235                 240

Asp Met Asp Thr Trp Arg Ser Met Thr Gly Val Ala Lys Asp Gly Thr
                245                 250                 255

Ser Thr Leu Gly Ile Trp Ala Ala Ile Ala Cys Tyr Arg Glu Gly Gly
            260                 265                 270

Asp Cys Leu Asp Glu Gln Val Ala Tyr Leu Arg Glu Asn Arg Asp Trp
        275                 280                 285

Leu Ala Glu Glu Leu Pro Arg Arg Val Pro Gly Leu Gln Val Ile Ser
    290                 295                 300

Pro Ala Ala Thr Tyr Leu Met Trp Met Asp Phe Ser Gly Thr Ser Ile
305                 310                 315                 320

Gly His Leu Glu Arg Pro Ala Val Trp Leu Arg Glu Asn Ala Lys Val
                325                 330                 335

Ala Leu Asn Asp Gly Val Ala Phe Gly Pro Gly Gly Ser His His Ala
            340                 345                 350
```

```
Arg Leu Asn Phe Ala Thr Ser Arg Glu Ile Leu Glu Glu Ala Cys Asp
        355                 360                 365

Arg Leu Gly Ser Ala Phe Ala Arg
    370                 375
```

<210> 27
<211> 1632
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1332)
<223> gene asd

<400> 27

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cggctggtcc aacgtgctct acgacgacca ggtgggcaag gtctccctcg tgggtgccgg        60

catgaagtcc cacccgggcg tcaccgccga cttcgccgag gcgctccgcg acgccggcgt       120

gaacatcgag ctaatctcca cctcggagat ccgcatctcg gtgctcaccc gcgaggccga       180

cctggacgcc gccgcccgtg ccctgcacga gaagttcgag ctcggcggcg acgccgaggc       240

caccgtctac gccggcaccg gccgctagac aatcccttcc acagaggagc tttcactctc       300

atg acc acc att gct gtc gtc ggt gcc acc ggc cag gtc ggc cgc gtg         348
Met Thr Thr Ile Ala Val Val Gly Ala Thr Gly Gln Val Gly Arg Val
1               5                   10                  15

atg cgc tcg atc ctg gag gag cgc aac ttc ccg gcc gac aag gtc cgt         396
Met Arg Ser Ile Leu Glu Glu Arg Asn Phe Pro Ala Asp Lys Val Arg
            20                  25                  30

ttc ttc gcg tcc ccg cgc tcc gcg ggc acc gtc atc gag ttc cgc ggt         444
Phe Phe Ala Ser Pro Arg Ser Ala Gly Thr Val Ile Glu Phe Arg Gly
        35                  40                  45

gag gac atc acc gtc gag gac ctc acc cag atc acc ccg gag tcc gtc         492
Glu Asp Ile Thr Val Glu Asp Leu Thr Gln Ile Thr Pro Glu Ser Val
    50                  55                  60

aag gac gtc gac atc gcc ctc ttc tcc gcc ggt ggt tcc acc tcc cgt         540
Lys Asp Val Asp Ile Ala Leu Phe Ser Ala Gly Gly Ser Thr Ser Arg
65                  70                  75                  80

gag tgg gcc ccg gtc ttc gcc gag gcc ggc gcg acc gtc atc gac aac         588
Glu Trp Ala Pro Val Phe Ala Glu Ala Gly Ala Thr Val Ile Asp Asn
                85                  90                  95

tcc tcc gcc tgg cgc aag gac gac gag gtc ccg ctc gtc gtc gcc gag         636
Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Val Val Ala Glu
            100                 105                 110

gtc aac ggc gag gag gcg aag aac ccg tcc aag ggc atc gtc gcc aac         684
```

```
Val Asn Gly Glu Glu Ala Lys Asn Pro Ser Lys Gly Ile Val Ala Asn
        115                 120                 125

ccg aac tgc acc acc atg gcc gcc atg ccg gtg ctc aag ccg ctg cac      732
Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His
    130                 135                 140

gac gcc gcc ggc ctc atc cgc ctg cat gtc tcc tcc tac cag gcc gtc      780
Asp Ala Ala Gly Leu Ile Arg Leu His Val Ser Ser Tyr Gln Ala Val
145                 150                 155                 160

tcc ggc tcc ggc ctc gcc ggt gtg gag acc ctg gcg aag cag acc gcc      828
Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Thr Ala
                165                 170                 175

gag ctc ggt gag gac aac gtc aag ctg gtc cat gac ggt tcc gtc gag      876
Glu Leu Gly Glu Asp Asn Val Lys Leu Val His Asp Gly Ser Val Glu
            180                 185                 190

gcc ccc gcc gac ctg ggt ccc tac gtc gcc ccc atc gcg ttc aac gcc      924
Ala Pro Ala Asp Leu Gly Pro Tyr Val Ala Pro Ile Ala Phe Asn Ala
        195                 200                 205

ctg ccg ctg gcc ggc gcg ctg gtc gat gac ggc tcc ctg gag acg gat      972
Leu Pro Leu Ala Gly Ala Leu Val Asp Asp Gly Ser Leu Glu Thr Asp
    210                 215                 220

gag gag cag aag ctg cgc aac gag tcc cgc aag atc ctg gac atc ccg     1020
Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Asp Ile Pro
225                 230                 235                 240

ggt ctg cgc gtc gcc ggc acc tgc gtc cgc gtg ccg gtg ttc acc ggt     1068
Gly Leu Arg Val Ala Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly
                245                 250                 255

cac acc ctg acc atc cac gcc gag ttc gag cgt ccg atc acc gtc gac     1116
His Thr Leu Thr Ile His Ala Glu Phe Glu Arg Pro Ile Thr Val Asp
            260                 265                 270

gag gcc aag gcc ctg ctc gcc gac gcc ccg ggt gtc gag ctt gtc gac     1164
Glu Ala Lys Ala Leu Leu Ala Asp Ala Pro Gly Val Glu Leu Val Asp
        275                 280                 285

gtc ccg acc ccg ctg gag gcc gcc ggc aag gac acc tcc ctg gtc ggc     1212
Val Pro Thr Pro Leu Glu Ala Ala Gly Lys Asp Thr Ser Leu Val Gly
    290                 295                 300

cgt atc cgc cag gac cag tcc gtc gac gac aac aag ggc ctc gtg ctc     1260
Arg Ile Arg Gln Asp Gln Ser Val Asp Asp Asn Lys Gly Leu Val Leu
305                 310                 315                 320

gtc gtc tcc ggt gac aac ctg cgc aag ggc gcg gcg ctg aac acg gtg     1308
Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Val
                325                 330                 335

cag atc gcg gag ctg ctg gtg tag tccaccgcct ccactgatat cgggcccctc     1362
Gln Ile Ala Glu Leu Leu Val
            340
```

accatgttgt ggtgaggggc ccgttcttgt cggtggtctg gtaggggagg ccttcattct 1422

gtccagacaa ttcttgtggt gtcctggggc gtcggcatgc ggcgtcgggc gggtatcggc 1482

gttcccgttc ctcgtttggc ggttcactgc cggacaatgg aggattttct caggaacagg 1542

gatccctgct gatctcgtat ttcgccccgg aactccgctg gacgctcagc ttgtccccag 1602

aattggggtc tttccgcagc gaattgtgag 1632

<210> 28
<211> 343
<212> PRT
<213> Corynebacterium humireducens

<400> 28

Met Thr Thr Ile Ala Val Val Gly Ala Thr Gly Gln Val Gly Arg Val
1 5 10 15

Met Arg Ser Ile Leu Glu Glu Arg Asn Phe Pro Ala Asp Lys Val Arg
20 25 30

Phe Phe Ala Ser Pro Arg Ser Ala Gly Thr Val Ile Glu Phe Arg Gly
35 40 45

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

Lys Asp Val Asp Ile Ala Leu Phe Ser Ala Gly Gly Ser Thr Ser Arg
65 70 75 80

Glu Trp Ala Pro Val Phe Ala Glu Ala Gly Ala Thr Val Ile Asp Asn
85 90 95

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

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

165 170 175

Glu Leu Gly Glu Asp Asn Val Lys Leu Val His Asp Gly Ser Val Glu
180 185 190

Ala Pro Ala Asp Leu Gly Pro Tyr Val Ala Pro Ile Ala Phe Asn Ala
195 200 205

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

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

Gly Leu Arg Val Ala Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly
245 250 255

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

Glu Ala Lys Ala Leu Leu Ala Asp Ala Pro Gly Val Glu Leu Val Asp
275 280 285

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

Arg Ile Arg Gln Asp Gln Ser Val Asp Asp Asn Lys Gly Leu Val Leu
305 310 315 320

Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Val
325 330 335

Gln Ile Ala Glu Leu Leu Val
340

<210> 29
<211> 1725
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1425)
<223> gene brnE

<400> 29

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gatctcgttg gccttgcccg tggcaccgac ggcggtgagg gcgtcgagga cctcgcggga        60

ggcggcgtcg tcgagaagga cggaggccgg cagctccggg ccgtcctcac cgcagaggac       120

ggggacgagc agtgcgtcgg gggtcttcgg ggccttcttg gccagctcga cggcgggggt       180

ggtgccgcgg gcgggaaggg tgaaagtggg gttcgccatg gaaagtacct cctgagattg       240

acaagcgatg aacccagctt atagagatca cctctgggtc gtcggtgtag cgtgttcccc       300

atg acg tct ctc aat ttc acc gtg aac cgt acg agc acc ccg acg tcc          348
Met Thr Ser Leu Asn Phe Thr Val Asn Arg Thr Ser Thr Pro Thr Ser
1               5                  10                  15

gat gag gcg cgc gag gag att ctg cag aat ccg cgg ttc ggc aag aac         396
Asp Glu Ala Arg Glu Glu Ile Leu Gln Asn Pro Arg Phe Gly Lys Asn
            20                  25                  30

ttc acc gat cac atg gtc acc atc gag tgg tcc gag gac aag ggc tgg         444
Phe Thr Asp His Met Val Thr Ile Glu Trp Ser Glu Asp Lys Gly Trp
        35                  40                  45

cac gac gcc cgc gtg cgt ccc tac gag gcc atc ccg atg gat ccc gcg         492
His Asp Ala Arg Val Arg Pro Tyr Glu Ala Ile Pro Met Asp Pro Ala
    50                  55                  60

acc acg gtg ttc cac tac ggc cag gcg atc ttc gag ggc atc aag gcc         540
Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala
65                  70                  75                  80

tac cgt cag ccg gac ggc tcc atc gcc acc ttc cgc ccg gag cgc aac         588
Tyr Arg Gln Pro Asp Gly Ser Ile Ala Thr Phe Arg Pro Glu Arg Asn
                85                  90                  95

gcc gag cgc atg cag cgt tcc gcc gag cgc atg gcc atg ccg ccg ctg         636
Ala Glu Arg Met Gln Arg Ser Ala Glu Arg Met Ala Met Pro Pro Leu
            100                 105                 110

ccg acc gag gac ttc ctc gag acg ctc cgc ctg ctt gtc gac gtc gac         684
Pro Thr Glu Asp Phe Leu Glu Thr Leu Arg Leu Leu Val Asp Val Asp
        115                 120                 125

cgt gac tgg gtc ccc gcc gcc ggc ggc gag gcc agc ctc tac ctg cgt         732
Arg Asp Trp Val Pro Ala Ala Gly Gly Glu Ala Ser Leu Tyr Leu Arg
    130                 135                 140

ccc ttc atg atc tcc acc gag gtc tcc ctg ggc gtc agc ccg gcc aac         780
Pro Phe Met Ile Ser Thr Glu Val Ser Leu Gly Val Ser Pro Ala Asn
145                 150                 155                 160

cgg tac acc ttc ttc gtc atc gcc tcc ccg gtc ggg gcg tac ttc acc         828
Arg Tyr Thr Phe Phe Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
                165                 170                 175

ggt ggc gtc aag ccg gtc tcc gtg tgg ctg agc gag gac tac gtc cgt         876
Gly Gly Val Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
            180                 185                 190

gcc gcc ccg ggt ggc acc ggt gcc gcg aag ttc gcc ggc aac tac gcc         924
```

```
Ala Ala Pro Gly Gly Thr Gly Ala Ala Lys Phe Ala Gly Asn Tyr Ala
        195                 200                 205

gcc tcc ctg ctc gcg cag gcg cag gcg gag gag aag ggc tgc gac cag        972
Ala Ser Leu Leu Ala Gln Ala Gln Ala Glu Glu Lys Gly Cys Asp Gln
    210                 215                 220

gtc gtg tgg ctc gac gcc atc gag cac acc tac atc gag gag atg ggt       1020
Val Val Trp Leu Asp Ala Ile Glu His Thr Tyr Ile Glu Glu Met Gly
225                 230                 235                 240

ggc atg aac ctg ttc ttc gtg tac ggc tcg ggt gac gac gtc acc gtg       1068
Gly Met Asn Leu Phe Phe Val Tyr Gly Ser Gly Asp Asp Val Thr Val
                245                 250                 255

gcc acc ccc gag ctc tcc ggc tcc ctc ctg ccg ggc gtc acc cgc gac       1116
Ala Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Val Thr Arg Asp
            260                 265                 270

tcc ctc ctg cag gtc gcc cgc gat ctc ggc cac cgc acc gag gag cgg       1164
Ser Leu Leu Gln Val Ala Arg Asp Leu Gly His Arg Thr Glu Glu Arg
        275                 280                 285

agg atc tcc aag ttc gac tgg cgc gac gac gtc gcc tcc ggt gcg atg       1212
Arg Ile Ser Lys Phe Asp Trp Arg Asp Asp Val Ala Ser Gly Ala Met
    290                 295                 300

acc gag gcc atg gcc tgc ggc aca gcc gcc gtg atc acc ccg gtc ggc       1260
Thr Glu Ala Met Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly
305                 310                 315                 320

cgg gtc ctg tcc aac gac ggc gag ttc cag atc aat gac aac cag ccg       1308
Arg Val Leu Ser Asn Asp Gly Glu Phe Gln Ile Asn Asp Asn Gln Pro
                325                 330                 335

ggt gag gtc acc atg gcc atg cgc gag cgt ctc acc gac atc cag cgc       1356
Gly Glu Val Thr Met Ala Met Arg Glu Arg Leu Thr Asp Ile Gln Arg
            340                 345                 350

ggc ctg tac gag gac acc cac ggc tgg gtg cac acc ctc gtc ccg gct       1404
Gly Leu Tyr Glu Asp Thr His Gly Trp Val His Thr Leu Val Pro Ala
        355                 360                 365

gag gac cag ccg gcg gac tag tcggccagca gctcggcggc ggcccgcacc          1455
Glu Asp Gln Pro Ala Asp
    370

agcgggagcg ccgctagcgc gccggtgccc tggccggcgt tcatgtccag ggcgacgaga     1515

ggcgtgagtt cgagggcctg cagcgcgatg aggtgcgcgg gctccggggt cagctgccct     1575

gcctggcacc agggggcggt gccgggggag agacgttccg cgaggtaggc ggcgacggtg     1635

acgggggcgc cgtcgagaag cacgggggtg cggcgtgccg cggcctgcgc gatgaaggcc     1695

accagtgcca ccaggtccgg ggaggcgatc                                      1725
```

<210> 30

<211> 374
<212> PRT
<213> Corynebacterium humireducens

<400> 30

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

Asp Glu Ala Arg Glu Glu Ile Leu Gln Asn Pro Arg Phe Gly Lys Asn
20 25 30

Phe Thr Asp His Met Val Thr Ile Glu Trp Ser Glu Asp Lys Gly Trp
35 40 45

His Asp Ala Arg Val Arg Pro Tyr Glu Ala Ile Pro Met Asp Pro Ala
50 55 60

Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala
65 70 75 80

Tyr Arg Gln Pro Asp Gly Ser Ile Ala Thr Phe Arg Pro Glu Arg Asn
85 90 95

Ala Glu Arg Met Gln Arg Ser Ala Glu Arg Met Ala Met Pro Pro Leu
100 105 110

Pro Thr Glu Asp Phe Leu Glu Thr Leu Arg Leu Leu Val Asp Val Asp
115 120 125

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

Pro Phe Met Ile Ser Thr Glu Val Ser Leu Gly Val Ser Pro Ala Asn
145 150 155 160

Arg Tyr Thr Phe Phe Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
165 170 175

Gly Gly Val Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
180 185 190

Ala Ala Pro Gly Gly Thr Gly Ala Ala Lys Phe Ala Gly Asn Tyr Ala
195 200 205

Ala Ser Leu Leu Ala Gln Ala Gln Ala Glu Glu Lys Gly Cys Asp Gln

210 215 220

Val Val Trp Leu Asp Ala Ile Glu His Thr Tyr Ile Glu Glu Met Gly
225 230 235 240

Gly Met Asn Leu Phe Phe Val Tyr Gly Ser Gly Asp Asp Val Thr Val
245 250 255

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

Ser Leu Leu Gln Val Ala Arg Asp Leu Gly His Arg Thr Glu Glu Arg
275 280 285

Arg Ile Ser Lys Phe Asp Trp Arg Asp Asp Val Ala Ser Gly Ala Met
290 295 300

Thr Glu Ala Met Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly
305 310 315 320

Arg Val Leu Ser Asn Asp Gly Glu Phe Gln Ile Asn Asp Asn Gln Pro
325 330 335

Gly Glu Val Thr Met Ala Met Arg Glu Arg Leu Thr Asp Ile Gln Arg
340 345 350

Gly Leu Tyr Glu Asp Thr His Gly Trp Val His Thr Leu Val Pro Ala
355 360 365

Glu Asp Gln Pro Ala Asp
370

<210> 31
<211> 1296
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(996)
<223> gen brnF

<400> 31
cgacatggag acggccccgc agctcaaccg cctggccaac cgcctcgccc acgtcgacct 60

gcgcgccgat cccggtgaca tcgccgagct cgtcgagggc atgcgtctgt tcgccggtta 120

```
cgccgagtgg gcgcccggcc agctcgacgg ggagatcgac cgcggcgact ggttcgtcac      180

cccggcgctg cccaccgacg tcatcgtccc gggccgcacc gacctgtggg gcgacgtcat      240

gcgccgccag cagccgccgc tgccgctctt ctcgacgttc cccgccgacc tcatggacaa      300

ttg acc ccc gcg ttc cct gac gtc cgt gcc gga ctg cgg gac gcc tgg         348
Leu Thr Pro Ala Phe Pro Asp Val Arg Ala Gly Leu Arg Asp Ala Trp
1               5                  10                  15

gcc gtc gcg ctc ggg ctg gtc ccc ctg ggg ctg gcc ttc ggc ctg ctg      396
Ala Val Ala Leu Gly Leu Val Pro Leu Gly Leu Ala Phe Gly Leu Leu
            20                  25                  30

atg acg cag gtg ggt ttc gcc tgg tgg tgg acg ccg gtc ttc tcg gtg      444
Met Thr Gln Val Gly Phe Ala Trp Trp Trp Thr Pro Val Phe Ser Val
        35                  40                  45

ctc atc tac gcc ggg tcc atg gag ttc ctg gcg gtc aac ctg gtg ctc      492
Leu Ile Tyr Ala Gly Ser Met Glu Phe Leu Ala Val Asn Leu Val Leu
    50                  55                  60

gcc ggc gtc ggc ccc ctg tcg acg gcg ctg acc gcc ttc atg gtc aac      540
Ala Gly Val Gly Pro Leu Ser Thr Ala Leu Thr Ala Phe Met Val Asn
65                  70                  75                  80

ttc cgg cac atc ttc tac ggc ctc acc ttc ccc cgg cac ctc gtc cgg      588
Phe Arg His Ile Phe Tyr Gly Leu Thr Phe Pro Arg His Leu Val Arg
                85                  90                  95

ggc cgg gcc ggc cgt gct tac tcc acg tac tcg ctg acc gac gag tcc      636
Gly Arg Ala Gly Arg Ala Tyr Ser Thr Tyr Ser Leu Thr Asp Glu Ser
            100                 105                 110

tac gcc atc gcc tcc gcc cac cct ccg cgc tcc ggt acg cag gtg ctg      684
Tyr Ala Ile Ala Ser Ala His Pro Pro Arg Ser Gly Thr Gln Val Leu
        115                 120                 125

acg atc cag ctc ttc tgc cag gcg atg tgg gtg gtg ccc ggc atc atc      732
Thr Ile Gln Leu Phe Cys Gln Ala Met Trp Val Val Pro Gly Ile Ile
    130                 135                 140

ggg gcg ctc gtc ggt gag gtc atc ccg gcg ggc atc cag ggc atg gag      780
Gly Ala Leu Val Gly Glu Val Ile Pro Ala Gly Ile Gln Gly Met Glu
145                 150                 155                 160

ttc gca ctc gtc gca ctg ttc gtg gtg ctg gcg tgg gag acc ttc cgg      828
Phe Ala Leu Val Ala Leu Phe Val Val Leu Ala Trp Glu Thr Phe Arg
                165                 170                 175

ggc agc cgg gac ctc tcc ctg ccg ctg ctc gcc ggt ggc ctg gca ctc      876
Gly Ser Arg Asp Leu Ser Leu Pro Leu Leu Ala Gly Gly Leu Ala Leu
            180                 185                 190

gtt gcc ggc ctg gtg ctc ccg ggg cag atg ctc atg gtg gcg ctg agc      924
Val Ala Gly Leu Val Leu Pro Gly Gln Met Leu Met Val Ala Leu Ser
        195                 200                 205

gcc tac ttc ctc gtc ctc atc ggc cgg cac ctc tcc ccc gcc ctg gac      972
```

```
Ala Tyr Phe Leu Val Leu Ile Gly Arg His Leu Ser Pro Ala Leu Asp
    210                 215                 220

cgt cgc ctg gag tgg agg gtc tga tgtacgggct tcccgagggg gtcaccctca      1026
Arg Arg Leu Glu Trp Arg Val
225                 230

cccagacgtt ggcggtcctg ctgcccatcg gggtggtcac ggtggcgctg cgctggctgc      1086

ccttcgcctt tgtcagggcg ctgcgcgaca accagttctt cggtctgctc gcccggatga      1146

tgccggtggg agtgatgacc gtgctggtgg tgtacacgct cctcgggcag cgttcggcgc      1206

ccggtggcct ggcggcggcc ctcatcgggg tcgcggtgac cctggggctg cacgcctggc      1266

ggcgggactc tgggctctcg atcctcggag                                      1296
```

<210> 32
<211> 231
<212> PRT
<213> Corynebacterium humireducens

<400> 32

```
Leu Thr Pro Ala Phe Pro Asp Val Arg Ala Gly Leu Arg Asp Ala Trp
1               5                   10                  15

Ala Val Ala Leu Gly Leu Val Pro Leu Gly Leu Ala Phe Gly Leu Leu
            20                  25                  30

Met Thr Gln Val Gly Phe Ala Trp Trp Trp Thr Pro Val Phe Ser Val
        35                  40                  45

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

Ala Gly Val Gly Pro Leu Ser Thr Ala Leu Thr Ala Phe Met Val Asn
65                  70                  75                  80

Phe Arg His Ile Phe Tyr Gly Leu Thr Phe Pro Arg His Leu Val Arg
                85                  90                  95

Gly Arg Ala Gly Arg Ala Tyr Ser Thr Tyr Ser Leu Thr Asp Glu Ser
            100                 105                 110

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

Thr Ile Gln Leu Phe Cys Gln Ala Met Trp Val Val Pro Gly Ile Ile
    130                 135                 140
```

```
Gly Ala Leu Val Gly Glu Val Ile Pro Ala Gly Ile Gln Gly Met Glu
145                 150                 155                 160

Phe Ala Leu Val Ala Leu Phe Val Val Leu Ala Trp Glu Thr Phe Arg
                165                 170                 175

Gly Ser Arg Asp Leu Ser Leu Pro Leu Leu Ala Gly Gly Leu Ala Leu
            180                 185                 190

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

Ala Tyr Phe Leu Val Leu Ile Gly Arg His Leu Ser Pro Ala Leu Asp
    210                 215                 220

Arg Arg Leu Glu Trp Arg Val
225                 230
```

<210> 33
<211> 1200
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(900)
<223> gene cysE

<400> 33

```
tggaccgcaa ggtcctcgac gacgtcatca ccgtcaccaa cgaggacgcc atcgagacct       60

cccgtcagct ggcggtcaag gacggcatcc tgggcggtat ctcctccggc ggcaacgtct      120

gggccgcgct ggagctggcg aagaaggagg agaacgcggg caagaccatc gtcaccgtcg      180

tcaccgacta cggcgagcgt tacgtctcca ccgtcctgta cgaggacatt cgcgactagg      240

aaacggctta ggcccccgca gcgcccacca ggcgacgggc aagcaagtag actctgggcc      300

atg ctg ctg ttg aac atc gcg aag atg gtc cgg gag gac ctg cgc aac        348
Met Leu Leu Leu Asn Ile Ala Lys Met Val Arg Glu Asp Leu Arg Asn
1               5                   10                  15

gcc cgc gac cac gat ccc gcc gcc cgc ggc gac atc gag aac gcc gtc        396
Ala Arg Asp His Asp Pro Ala Ala Arg Gly Asp Ile Glu Asn Ala Val
            20                  25                  30

gtc tac tcg ggc ctg cac gcc atc tgg gca cac cgt gtc tcc cac tgg        444
Val Tyr Ser Gly Leu His Ala Ile Trp Ala His Arg Val Ser His Trp
        35                  40                  45
```

```
atg tgg gag cgc ggt ctc cgc ggc ccc gcg cga atc ctc gcg cag ctc        492
Met Trp Glu Arg Gly Leu Arg Gly Pro Ala Arg Ile Leu Ala Gln Leu
    50                  55                  60

aac cgg ttc ttc acg ggc atc gag atc cac ccc ggt gcc acc atc ggc        540
Asn Arg Phe Phe Thr Gly Ile Glu Ile His Pro Gly Ala Thr Ile Gly
65                  70                  75                  80

cgc cgt ttc ttc atc gac cac ggc atg ggc atc gtc atc ggc gag acc        588
Arg Arg Phe Phe Ile Asp His Gly Met Gly Ile Val Ile Gly Glu Thr
                85                  90                  95

acc gag atc ggc gac ggc gtc atg ctc tac cac ggc gtc acc ctg ggt        636
Thr Glu Ile Gly Asp Gly Val Met Leu Tyr His Gly Val Thr Leu Gly
            100                 105                 110

ggt cag gtg ctc acg cag acc aag cgc cac ccg acc atc gag gac aac        684
Gly Gln Val Leu Thr Gln Thr Lys Arg His Pro Thr Ile Glu Asp Asn
        115                 120                 125

gtc acc atc ggt gcc ggc gcc aag gtg ctc ggc ccg atc acc atc ggc        732
Val Thr Ile Gly Ala Gly Ala Lys Val Leu Gly Pro Ile Thr Ile Gly
    130                 135                 140

aag ggc tcc gcg atc ggc gcc aac gcc gtg gtg acc aag gac gtc ccg        780
Lys Gly Ser Ala Ile Gly Ala Asn Ala Val Val Thr Lys Asp Val Pro
145                 150                 155                 160

gcg gac cac atc gcc acg ggc atc ccg gcg aag aac cgc ccg cgc cgc        828
Ala Asp His Ile Ala Thr Gly Ile Pro Ala Lys Asn Arg Pro Arg Arg
                165                 170                 175

cag tcc gag cgc atc aag ctc gtc gat ccg gac tac tac acc tcc aac        876
Gln Ser Glu Arg Ile Lys Leu Val Asp Pro Asp Tyr Tyr Thr Ser Asn
            180                 185                 190

gat ccg gtc gac tac agc atc tag acacaaggaa ggccccggtt tcccggggcc        930
Asp Pro Val Asp Tyr Ser Ile
        195

tttttgtgct tcacgacgtc ggcgcgtgcc cgacgtcacc cgacgaggtc gcggtactcc       990

tcgttcttgc tgatgaagtg ctcgaccgcg gaacagctcg ggcgcacccg cgccccctcc      1050

tcccgggccc agtcgagggc ctcgcggatg agcggggtgg acagcgcacg tccgcggtag      1110

gcctggtcca ccacggtgtg gtggaagtcc agtaggccac cgtggcggac gtaggaggcg      1170

tagccgacct cccggtcgtc cacggagatg                                       1200
```

<210> 34
<211> 199
<212> PRT
<213> Corynebacterium humireducens

<400> 34

```
Met Leu Leu Leu Asn Ile Ala Lys Met Val Arg Glu Asp Leu Arg Asn
1               5                  10                  15

Ala Arg Asp His Asp Pro Ala Ala Arg Gly Asp Ile Glu Asn Ala Val
            20                  25                  30

Val Tyr Ser Gly Leu His Ala Ile Trp Ala His Arg Val Ser His Trp
        35                  40                  45

Met Trp Glu Arg Gly Leu Arg Gly Pro Ala Arg Ile Leu Ala Gln Leu
    50                  55                  60

Asn Arg Phe Phe Thr Gly Ile Glu Ile His Pro Gly Ala Thr Ile Gly
65                  70                  75                  80

Arg Arg Phe Phe Ile Asp His Gly Met Gly Ile Val Ile Gly Glu Thr
                85                  90                  95

Thr Glu Ile Gly Asp Gly Val Met Leu Tyr His Gly Val Thr Leu Gly
            100                 105                 110

Gly Gln Val Leu Thr Gln Thr Lys Arg His Pro Thr Ile Glu Asp Asn
        115                 120                 125

Val Thr Ile Gly Ala Gly Ala Lys Val Leu Gly Pro Ile Thr Ile Gly
    130                 135                 140

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

Ala Asp His Ile Ala Thr Gly Ile Pro Ala Lys Asn Arg Pro Arg Arg
                165                 170                 175

Gln Ser Glu Arg Ile Lys Leu Val Asp Pro Asp Tyr Tyr Thr Ser Asn
            180                 185                 190

Asp Pro Val Asp Tyr Ser Ile
        195
```

<210> 35
<211> 1536
<212> DNA
<213> Corynebacterium humireducens

<220>

<221> CDS
<222> (301)..(1236)
<223> gene cysK

<400> 35
cctccgggta cacccgtaca ggtgcacccg atgggcacat gaacgggggt aactttcctt 60

tacagatggg cattataacg cgacttcggg ggtaaacgga atcgaatccg ccgtaacttg 120

cgcattcaag accgttctga tcggaacaac ggcacccact gaaggggtga tatcccgcgc 180

cggagaccac ccccgcaacc ttggagaaac catgtggtct gccagggaca taccatcctg 240

tctactcaca tggtgtacgc tgacaccacc aacgtcagac gaagcaagga agcagtcacc 300

atg agc aag atc tac gac aac atc ctc gac acc atc gga aac acc ccg 348
Met Ser Lys Ile Tyr Asp Asn Ile Leu Asp Thr Ile Gly Asn Thr Pro
1 5 10 15

ctg gtg cgc ctc aac ggc ctc acc gag ggc ctc cag gcg gag gtg ctc 396
Leu Val Arg Leu Asn Gly Leu Thr Glu Gly Leu Gln Ala Glu Val Leu
20 25 30

gtg aag gtc gag tcc ttc aac ccg gcg aac tcc gtc aag gac cgc atc 444
Val Lys Val Glu Ser Phe Asn Pro Ala Asn Ser Val Lys Asp Arg Ile
35 40 45

ggc aag gcg atc atc gac gcc gcc gag gcc gac ggg tcc ctc cag ccg 492
Gly Lys Ala Ile Ile Asp Ala Ala Glu Ala Asp Gly Ser Leu Gln Pro
50 55 60

ggc ggc acc atc gtg gag gcc acc tcc ggc aac acc ggc atc gcc ctc 540
Gly Gly Thr Ile Val Glu Ala Thr Ser Gly Asn Thr Gly Ile Ala Leu
65 70 75 80

gcc ctc gtg ggc gcg gcc cgc ggc tac aac gtg atc ctc acc atg ccg 588
Ala Leu Val Gly Ala Ala Arg Gly Tyr Asn Val Ile Leu Thr Met Pro
85 90 95

gag acc atg tcc aac gag cgt cgc gtc atg ctc cgc gcc tac ggc gct 636
Glu Thr Met Ser Asn Glu Arg Arg Val Met Leu Arg Ala Tyr Gly Ala
100 105 110

cag atc gtc ctg acc ccg ggc gcg gcc ggc atg cag ggc gcc gtc gac 684
Gln Ile Val Leu Thr Pro Gly Ala Ala Gly Met Gln Gly Ala Val Asp
115 120 125

aag gcg aac gag atc gtc gcc gcc gag gac aac gcc atc ctc gcg aac 732
Lys Ala Asn Glu Ile Val Ala Ala Glu Asp Asn Ala Ile Leu Ala Asn
130 135 140

cag ttc gcg cac ccg gcg aac ctg cgg atc cac cgc gag acc acc gcc 780
Gln Phe Ala His Pro Ala Asn Leu Arg Ile His Arg Glu Thr Thr Ala
145 150 155 160

gag gag atc tgg aac gac acc gac ggc gag gtc gac atc ttc gtc gcg 828
Glu Glu Ile Trp Asn Asp Thr Asp Gly Glu Val Asp Ile Phe Val Ala
165 170 175

```
ggc atc ggc acg ggc ggc acc gtc tcc ggc gtc ggc cag gtg ctc aag        876
Gly Ile Gly Thr Gly Gly Thr Val Ser Gly Val Gly Gln Val Leu Lys
            180                 185                 190

gag cgc aag ccg gag gtc cag atc tac gcc gtc gag ccg gcc gcg tcc        924
Glu Arg Lys Pro Glu Val Gln Ile Tyr Ala Val Glu Pro Ala Ala Ser
        195                 200                 205

ccg ctg ctg tcc gcc ggc aag gcg ggc ccg cac aag atc cag ggc atc        972
Pro Leu Leu Ser Ala Gly Lys Ala Gly Pro His Lys Ile Gln Gly Ile
    210                 215                 220

ggc gcc aac ttc atc ccg gag gtc ctg gac cgc aag gtc ctc gac gac       1020
Gly Ala Asn Phe Ile Pro Glu Val Leu Asp Arg Lys Val Leu Asp Asp
225                 230                 235                 240

gtc atc acc gtc acc aac gag gac gcc atc gag acc tcc cgt cag ctg       1068
Val Ile Thr Val Thr Asn Glu Asp Ala Ile Glu Thr Ser Arg Gln Leu
                245                 250                 255

gcg gtc aag gac ggc atc ctg ggc ggt atc tcc tcc ggc ggc aac gtc       1116
Ala Val Lys Asp Gly Ile Leu Gly Gly Ile Ser Ser Gly Gly Asn Val
            260                 265                 270

tgg gcc gcg ctg gag ctg gcg aag aag gag gag aac gcg ggc aag acc       1164
Trp Ala Ala Leu Glu Leu Ala Lys Lys Glu Glu Asn Ala Gly Lys Thr
        275                 280                 285

atc gtc acc gtc gtc acc gac tac ggc gag cgt tac gtc tcc acc gtc       1212
Ile Val Thr Val Val Thr Asp Tyr Gly Glu Arg Tyr Val Ser Thr Val
    290                 295                 300

ctg tac gag gac att cgc gac tag gaaacggctt aggcccccgc agcgcccacc      1266
Leu Tyr Glu Asp Ile Arg Asp
305                 310

aggcgacggg caagcaagta gactctgggc catgctgctg ttgaacatcg cgaagatggt     1326

ccgggaggac ctgcgcaacg cccgcgacca cgatcccgcc gcccgcggcg acatcgagaa     1386

cgccgtcgtc tactcgggcc tgcacgccat ctgggcacac cgtgtctccc actggatgtg     1446

ggagcgcggt ctccgcggcc ccgcgcgaat cctcgcgcag ctcaaccggt tcttcacggg     1506

catcgagatc caccccggtg ccaccatcgg                                      1536
```

<210> 36
<211> 311
<212> PRT
<213> Corynebacterium humireducens

<400> 36

```
Met Ser Lys Ile Tyr Asp Asn Ile Leu Asp Thr Ile Gly Asn Thr Pro
1               5                   10                  15

Leu Val Arg Leu Asn Gly Leu Thr Glu Gly Leu Gln Ala Glu Val Leu
```

20 25 30

Val Lys Val Glu Ser Phe Asn Pro Ala Asn Ser Val Lys Asp Arg Ile
35 40 45

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

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

Ala Leu Val Gly Ala Ala Arg Gly Tyr Asn Val Ile Leu Thr Met Pro
85 90 95

Glu Thr Met Ser Asn Glu Arg Arg Val Met Leu Arg Ala Tyr Gly Ala
100 105 110

Gln Ile Val Leu Thr Pro Gly Ala Ala Gly Met Gln Gly Ala Val Asp
115 120 125

Lys Ala Asn Glu Ile Val Ala Ala Glu Asp Asn Ala Ile Leu Ala Asn
130 135 140

Gln Phe Ala His Pro Ala Asn Leu Arg Ile His Arg Glu Thr Thr Ala
145 150 155 160

Glu Glu Ile Trp Asn Asp Thr Asp Gly Glu Val Asp Ile Phe Val Ala
165 170 175

Gly Ile Gly Thr Gly Gly Thr Val Ser Gly Val Gly Gln Val Leu Lys
180 185 190

Glu Arg Lys Pro Glu Val Gln Ile Tyr Ala Val Glu Pro Ala Ala Ser
195 200 205

Pro Leu Leu Ser Ala Gly Lys Ala Gly Pro His Lys Ile Gln Gly Ile
210 215 220

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

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

```
Ala Val Lys Asp Gly Ile Leu Gly Gly Ile Ser Ser Gly Gly Asn Val
            260                 265                 270

Trp Ala Ala Leu Glu Leu Ala Lys Lys Glu Glu Asn Ala Gly Lys Thr
        275                 280                 285

Ile Val Thr Val Val Thr Asp Tyr Gly Glu Arg Tyr Val Ser Thr Val
    290                 295                 300

Leu Tyr Glu Asp Ile Arg Asp
305                 310
```

<210> 37
<211> 999
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(699)
<223> gene gcvH

<400> 37

```
cagggagccg accagcgcca tcgtcgggct ccggggtctg gggcgccgcg cggcccgcga        60

gggcgccgag gtctacctcg acggcgaaca ggtcggcgtg gtcacctccg ggcagccggc       120

gccggtgctc ggctacccga tcgcactcgc ccgcctgcgc cccgacgtca ccgcggccgg       180

cacggcactg gaggtggaca tccgtgggag gcggcacccc ttcgagatcg tcgacctgcc       240

cttctaccgc cgcgccgcac gataacctga acccaccacc aacggaaagg ctccccccacc      300

atg gcc acc gag cac tcc ctg ccc ggg aac tac tcc tac tcc gag gac          348
Met Ala Thr Glu His Ser Leu Pro Gly Asn Tyr Ser Tyr Ser Glu Asp
1               5                   10                  15

cac gag tgg atc gac gcg acg ccc gag gac gcc gtc ggc gcg acc gtg          396
His Glu Trp Ile Asp Ala Thr Pro Glu Asp Ala Val Gly Ala Thr Val
            20                  25                  30

aag gtc ggc atc acc tcc gtg gcc acc gaa cgc ctc ggc gag gtc gtc          444
Lys Val Gly Ile Thr Ser Val Ala Thr Glu Arg Leu Gly Glu Val Val
        35                  40                  45

tac gcg gag ctc ccg cag gtc ggt gac gcc gtc acc gcc ggt gaa ccg          492
Tyr Ala Glu Leu Pro Gln Val Gly Asp Ala Val Thr Ala Gly Glu Pro
    50                  55                  60

tgc ggc gag gtc gag tcc acg aag tcg gtc tcc gac ctc tac gcg ccg          540
Cys Gly Glu Val Glu Ser Thr Lys Ser Val Ser Asp Leu Tyr Ala Pro
65                  70                  75                  80

gtc acg ggc acc gtc acc gag gtc aac gac gcg gtc cac gac gac tac          588
```

```
Val Thr Gly Thr Val Thr Glu Val Asn Asp Ala Val His Asp Asp Tyr
                85                  90                  95

gcc gtg atc aac gac gac ccc ttc ggc gcg ggc tgg ctc ttc gcc gtc        636
Ala Val Ile Asn Asp Asp Pro Phe Gly Ala Gly Trp Leu Phe Ala Val
            100                 105                 110

gag gtc gac gag gtc gga ccg ctc atg acc gcc gcc gag tac gcg gag        684
Glu Val Asp Glu Val Gly Pro Leu Met Thr Ala Ala Glu Tyr Ala Glu
        115                 120                 125

gcc aac ggc gtg tga ccgcccggga ccggtaccct ggtcccatca tgactgcacc        739
Ala Asn Gly Val
    130

ccgtgagccc ttcttccctg cggaccgttc catccgtgcc tccggcgagc ccccggagat      799

ccgttatctc ggcgtcgtcg actaccagga ggcctggaat ctgcaggccg agctggcgtc      859

gcaacgcgcg gccggggaga tcggtgacca gctcctcatc ctcgagcacc cgagcgtgta      919

caccgccggc aagcgcacgc agccggagga ccgccccacc aacggcctgc cggtcatcga      979

cgtcgaccgg ggtggccgca                                                 999
```

<210> 38
<211> 132
<212> PRT
<213> Corynebacterium humireducens

<400> 38

```
Met Ala Thr Glu His Ser Leu Pro Gly Asn Tyr Ser Tyr Ser Glu Asp
1               5                  10                  15

His Glu Trp Ile Asp Ala Thr Pro Glu Asp Ala Val Gly Ala Thr Val
            20                  25                  30

Lys Val Gly Ile Thr Ser Val Ala Thr Glu Arg Leu Gly Glu Val Val
        35                  40                  45

Tyr Ala Glu Leu Pro Gln Val Gly Asp Ala Val Thr Ala Gly Glu Pro
    50                  55                  60

Cys Gly Glu Val Glu Ser Thr Lys Ser Val Ser Asp Leu Tyr Ala Pro
65                  70                  75                  80

Val Thr Gly Thr Val Thr Glu Val Asn Asp Ala Val His Asp Asp Tyr
                85                  90                  95

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

```
Glu Val Asp Glu Val Gly Pro Leu Met Thr Ala Ala Glu Tyr Ala Glu
        115                 120                 125

Ala Asn Gly Val
    130
```

<210> 39
<211> 3462
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(3162)
<223> gene gcvP

<400> 39

```
ctgggcaccg cggccatcga gaagcgtccg gtcgtggtga ccgatgacgg cgtcgactcg       60

atcgccatcc gccagatgtg ctacctgccg ttcacctacg accaccaggt catcgacggt      120

gccgacgccg gtcgcttcat caccaccatc aaggaccgcc tggagaccgc ggacttccag      180

tccgacctcg gcctctaagc tctcccgctg agagagaccg ccacctgacc ttcccggtcg      240

ggtggcggtt ttcttcttat aatcggaatc atccggtccc ccatcgagga gcgattccgc      300

atg gcc ctg cac ccg atc acc gat tcc gcc tcc tac ctg gcc cga cac        348
Met Ala Leu His Pro Ile Thr Asp Ser Ala Ser Tyr Leu Ala Arg His
1               5                   10                  15

ctc ggc ccc gac acc gcg gag gag cag gtc atg ctg ggg gcg ctg ggc        396
Leu Gly Pro Asp Thr Ala Glu Glu Gln Val Met Leu Gly Ala Leu Gly
            20                  25                  30

tac ggt tcc ctc gcc gag ctt gtc gac gcc gcc ctg ccc acc gac atc        444
Tyr Gly Ser Leu Ala Glu Leu Val Asp Ala Ala Leu Pro Thr Asp Ile
        35                  40                  45

cgc ctc acc gaa cct ctc ccg cgg cac gcg ccc ctc tcg gag acg gag        492
Arg Leu Thr Glu Pro Leu Pro Arg His Ala Pro Leu Ser Glu Thr Glu
    50                  55                  60

gcg cag gcg cga ctg cgg gag tac gcc tcg cgg aac acg gtg ctc cgt        540
Ala Gln Ala Arg Leu Arg Glu Tyr Ala Ser Arg Asn Thr Val Leu Arg
65                  70                  75                  80

tcc ttt tac ggg cag ggt ttc tcc gac acg gtc act ccc ccg gtg atc        588
Ser Phe Tyr Gly Gln Gly Phe Ser Asp Thr Val Thr Pro Pro Val Ile
                85                  90                  95

cgc cgc ggg gtg ctc gag gcc ccg ggc tgg tac acc gcg tac acg ccg        636
Arg Arg Gly Val Leu Glu Ala Pro Gly Trp Tyr Thr Ala Tyr Thr Pro
            100                 105                 110
```

```
tac cag ccg gag atc tcg cag ggc cgc ctc gag gcg ctg ctc aac ttc        684
Tyr Gln Pro Glu Ile Ser Gln Gly Arg Leu Glu Ala Leu Leu Asn Phe
        115                 120                 125

cag acg atg gtc tcc gag ctc acc ggc ctg ccg gtg gcg aac gcc tcg        732
Gln Thr Met Val Ser Glu Leu Thr Gly Leu Pro Val Ala Asn Ala Ser
    130                 135                 140

ctc ctc gac gag gct tcc gcc acc gcc gaa gcc gtc ggc ctc atg tcg        780
Leu Leu Asp Glu Ala Ser Ala Thr Ala Glu Ala Val Gly Leu Met Ser
145                 150                 155                 160

cgg gcg cag agg aag ggg cgg cgg gtg ctt ctc gac gcc cgc ctc cac        828
Arg Ala Gln Arg Lys Gly Arg Arg Val Leu Leu Asp Ala Arg Leu His
                165                 170                 175

ccc cag gtc ctc gcc gtc gct gcg gag cgg gcc cgg gcg atc gac ctg        876
Pro Gln Val Leu Ala Val Ala Ala Glu Arg Ala Arg Ala Ile Asp Leu
            180                 185                 190

gag gtc gcc gtc gag gac ctg tcc ggc ccg ctg gtg ggt gag gat ctc        924
Glu Val Ala Val Glu Asp Leu Ser Gly Pro Leu Val Gly Glu Asp Leu
        195                 200                 205

tgc ggc gtc gtc atc gcc tac ccc ggc acg gag ggc gac atc gcc gat        972
Cys Gly Val Val Ile Ala Tyr Pro Gly Thr Glu Gly Asp Ile Ala Asp
    210                 215                 220

ccc cgc ccg gtc atc gag gcc gtg cac gca cgc ggg ggt ctg gcc acc       1020
Pro Arg Pro Val Ile Glu Ala Val His Ala Arg Gly Gly Leu Ala Thr
225                 230                 235                 240

gtg gtc acc gat ccc ctg tcg ctg ctc ctg ctc gag tcg ccg ggt gag       1068
Val Val Thr Asp Pro Leu Ser Leu Leu Leu Leu Glu Ser Pro Gly Glu
                245                 250                 255

atg ggg gcg gac atc gcg gtg ggc tcc tcg cag cgt ttc ggc gtg ccc       1116
Met Gly Ala Asp Ile Ala Val Gly Ser Ser Gln Arg Phe Gly Val Pro
            260                 265                 270

ctg ttc tac ggt ggc ccg cac gcc gcg tac atg gcc gtc agt gac gcc       1164
Leu Phe Tyr Gly Gly Pro His Ala Ala Tyr Met Ala Val Ser Asp Ala
        275                 280                 285

ctc aag cgc cag atc ccc ggc cgc ctg gtg ggc gtg tcc gtc gac gcc       1212
Leu Lys Arg Gln Ile Pro Gly Arg Leu Val Gly Val Ser Val Asp Ala
    290                 295                 300

gag ggc gcc ccc gcc tac cgg ctc gcg ctg cag acc cgg gag cag cac       1260
Glu Gly Ala Pro Ala Tyr Arg Leu Ala Leu Gln Thr Arg Glu Gln His
305                 310                 315                 320

atc cgt cgc gag cgg gcg acg tcg aac atc tgc acc gcg cag gcg ctg       1308
Ile Arg Arg Glu Arg Ala Thr Ser Asn Ile Cys Thr Ala Gln Ala Leu
                325                 330                 335

ctg gcg gtc acc gcc ggc atg tac gcc gtc tac cac ggt ccc gag ggg       1356
Leu Ala Val Thr Ala Gly Met Tyr Ala Val Tyr His Gly Pro Glu Gly
```

```
                340                 345                 350

ttg cgt gcc atc gcg gag cgc gtg cac ggt ctg gcc tgt gac ttc gcg      1404
Leu Arg Ala Ile Ala Glu Arg Val His Gly Leu Ala Cys Asp Phe Ala
        355                 360                 365

gcg gcc gtc cgc gcc gcc ggc ggg acg gtg ctg cac gac gcc ttc ttc      1452
Ala Ala Val Arg Ala Ala Gly Gly Thr Val Leu His Asp Ala Phe Phe
    370                 375                 380

gac acc gtc gcg gtg cgg gtg gag gct gca cga ccg atc gtc ggc acg      1500
Asp Thr Val Ala Val Arg Val Glu Ala Ala Arg Pro Ile Val Gly Thr
385                 390                 395                 400

ctc gcg gag gcg ggc tac ctc gtg cgt gcc gtg gac ggc acg acc gtc      1548
Leu Ala Glu Ala Gly Tyr Leu Val Arg Ala Val Asp Gly Thr Thr Val
                405                 410                 415

ggc gtg agc ttc ggt gag tcg gcg gag gag ggg gac gtc gag aag ctc      1596
Gly Val Ser Phe Gly Glu Ser Ala Glu Glu Gly Asp Val Glu Lys Leu
            420                 425                 430

gcc gcc gtc ttc ggc gcc tcc ctg acg gcg ggc acc cgc tgc atc ccc      1644
Ala Ala Val Phe Gly Ala Ser Leu Thr Ala Gly Thr Arg Cys Ile Pro
        435                 440                 445

gcg tcc gtg gcg cgg cag acg ccg acg ctg acg cac ccg gtc ttc tcc      1692
Ala Ser Val Ala Arg Gln Thr Pro Thr Leu Thr His Pro Val Phe Ser
    450                 455                 460

acg ctc cac tcc gag acg cag atg atg cgc tac ctg cgc acg ctc tcg      1740
Thr Leu His Ser Glu Thr Gln Met Met Arg Tyr Leu Arg Thr Leu Ser
465                 470                 475                 480

gac cgg gat ctc gcg ctc gac cgc acg atg atc ccg ctg ggt tcg tgc      1788
Asp Arg Asp Leu Ala Leu Asp Arg Thr Met Ile Pro Leu Gly Ser Cys
                485                 490                 495

acg atg aag ctc aac ccg acc gcc ggg ctg gag acg atc acg tgg ccg      1836
Thr Met Lys Leu Asn Pro Thr Ala Gly Leu Glu Thr Ile Thr Trp Pro
            500                 505                 510

gag ttc gcc gac atg cac ccc ttc gcc ccc gac gac cag gcc gcg ggc      1884
Glu Phe Ala Asp Met His Pro Phe Ala Pro Asp Asp Gln Ala Ala Gly
        515                 520                 525

tgg ctg gcg ctc atc gcg gag ctg gag ggc tgg ctc gcg gag ctc acc      1932
Trp Leu Ala Leu Ile Ala Glu Leu Glu Gly Trp Leu Ala Glu Leu Thr
    530                 535                 540

gga tac gcg aag gtg tcc gtg cag ccc aac gcg ggt tcc cag ggg gag      1980
Gly Tyr Ala Lys Val Ser Val Gln Pro Asn Ala Gly Ser Gln Gly Glu
545                 550                 555                 560

ctg gcc gga ctg ctg gcc atc cgc cgc tac cac gtg gcc aac ggg gac      2028
Leu Ala Gly Leu Leu Ala Ile Arg Arg Tyr His Val Ala Asn Gly Asp
                565                 570                 575

atg gac cgt gat atc tgc ctg gtc ccg gcc tcg gcg cac ggc acg aac      2076
```

```
Met Asp Arg Asp Ile Cys Leu Val Pro Ala Ser Ala His Gly Thr Asn
            580                 585                 590

gcg gcg tcg gcg acg ctg gcg cac ctg cgg gtc gtg gtg gtc ggc acc      2124
Ala Ala Ser Ala Thr Leu Ala His Leu Arg Val Val Val Val Gly Thr
        595                 600                 605

gcc ggg gac ggc tcc atc gac atg gac gac ctc gac gcg aaa ctc gcc      2172
Ala Gly Asp Gly Ser Ile Asp Met Asp Asp Leu Asp Ala Lys Leu Ala
    610                 615                 620

gag cac ggc ccg cag gtg gcc gcg atc atg atc acc tac ccc tcc acg      2220
Glu His Gly Pro Gln Val Ala Ala Ile Met Ile Thr Tyr Pro Ser Thr
625                 630                 635                 640

cac ggc gtc ttc gag gac acc gtg cgc gag gtg tgc gac agg gtg cac      2268
His Gly Val Phe Glu Asp Thr Val Arg Glu Val Cys Asp Arg Val His
                645                 650                 655

gcg gtc ggc ggg cag gtc tac atc gac ggc gcg aac ctc aac gcc ctg      2316
Ala Val Gly Gly Gln Val Tyr Ile Asp Gly Ala Asn Leu Asn Ala Leu
            660                 665                 670

acc ggc ctg gcg ctg ctg ggc cgc atc ggc ggc gac gtc tcc cac ctc      2364
Thr Gly Leu Ala Leu Leu Gly Arg Ile Gly Gly Asp Val Ser His Leu
        675                 680                 685

aac ctg cac aag acg ttc acc atc ccg cac ggc ggc ggt ggc ccg ggc      2412
Asn Leu His Lys Thr Phe Thr Ile Pro His Gly Gly Gly Gly Pro Gly
    690                 695                 700

gtg ggc ccg gtg tgc gtc gcg gag cac ctc gtc ccc ttc ctg ccg gcg      2460
Val Gly Pro Val Cys Val Ala Glu His Leu Val Pro Phe Leu Pro Ala
705                 710                 715                 720

gac ccg acc tcc ctc gac ggc gcc acc ccg gcg gcg gtc ggc acc ggc      2508
Asp Pro Thr Ser Leu Asp Gly Ala Thr Pro Ala Ala Val Gly Thr Gly
                725                 730                 735

gtg ccc gtc tct gcg acg cgc cac ggc tcg gcg ggc gtc ctg cag atc      2556
Val Pro Val Ser Ala Thr Arg His Gly Ser Ala Gly Val Leu Gln Ile
            740                 745                 750

tcc tgg gcg tac atc gcc atg atg ggc acc gac ggc ctc acc cgc gcc      2604
Ser Trp Ala Tyr Ile Ala Met Met Gly Thr Asp Gly Leu Thr Arg Ala
        755                 760                 765

agc gcc gcg gcg atc ctc agc gcg aac tac gtc gcc cac cgc ctg ggc      2652
Ser Ala Ala Ala Ile Leu Ser Ala Asn Tyr Val Ala His Arg Leu Gly
    770                 775                 780

gag gcc ttc ccg gtg ctc tac acc ggc cgc aac ggc ctg gtg gcg cac      2700
Glu Ala Phe Pro Val Leu Tyr Thr Gly Arg Asn Gly Leu Val Ala His
785                 790                 795                 800

gag tgc atc ctc gac ctg cgc gac ctg acg agg cag acc ggc gtc acc      2748
Glu Cys Ile Leu Asp Leu Arg Asp Leu Thr Arg Gln Thr Gly Val Thr
                805                 810                 815
```

```
gcc acg gac gtg gcc aaa cgc ctc atc gac ttc ggc ttc cac gcc ccc      2796
Ala Thr Asp Val Ala Lys Arg Leu Ile Asp Phe Gly Phe His Ala Pro
            820                 825                 830

acg ctc tcc ttc ccc gtc gcc ggt acc ctc atg gtc gag ccg acc gag      2844
Thr Leu Ser Phe Pro Val Ala Gly Thr Leu Met Val Glu Pro Thr Glu
        835                 840                 845

tcc gag gac ctc gcc gag ctc gac cgc ttc atc gag gcg atg ctc acc      2892
Ser Glu Asp Leu Ala Glu Leu Asp Arg Phe Ile Glu Ala Met Leu Thr
    850                 855                 860

atc cgc gcg gag atc gac gag atc agc ggc ggc gac atc gcc tac gag      2940
Ile Arg Ala Glu Ile Asp Glu Ile Ser Gly Gly Asp Ile Ala Tyr Glu
865                 870                 875                 880

gac tcc gtc ctc cac cac gcg ccg ttc acc gcg tgg agc gtg tcc cgc      2988
Asp Ser Val Leu His His Ala Pro Phe Thr Ala Trp Ser Val Ser Arg
                885                 890                 895

gac gac tgg gac cac gcc ttc acc cgt gag cag gcg gcc tgg ccg gtc      3036
Asp Asp Trp Asp His Ala Phe Thr Arg Glu Gln Ala Ala Trp Pro Val
            900                 905                 910

ccc ggt ctg cgc cgc acc aag tac ttc ccg ccg gtc cgc cgc ctc aac      3084
Pro Gly Leu Arg Arg Thr Lys Tyr Phe Pro Pro Val Arg Arg Leu Asn
        915                 920                 925

gag gcc tac ggt gac cgc cac ctc gtg tgc gcc tgc ccg ccg ccc gag      3132
Glu Ala Tyr Gly Asp Arg His Leu Val Cys Ala Cys Pro Pro Pro Glu
    930                 935                 940

gcc ttc gac ctt tcc gag gag aac cag tga ccgacctgcg taccagcccc        3182
Ala Phe Asp Leu Ser Glu Glu Asn Gln
945                 950

ctccacgagc gtcatgtgga gctcggggcc tccttcaccc ccttcggccc gtggaacatg    3242

cccctgcgct acggcaacga gctcgacgag caccgcgccg tccgttccac cgccgggctc    3302

ttcgacctct cgcacatggg tgagatccgc gtgtggggcg cacaggccgc ggagttcctc    3362

gaccatgcgc tgctctccgc cttctccacg ctccccgtgg gtaaggcgcg gtactccatg    3422

cttgtcgacg ccaccggtgc catcctcgac gacctcctca                          3462
```

<210> 40
<211> 953
<212> PRT
<213> Corynebacterium humireducens

<400> 40

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

Leu Gly Pro Asp Thr Ala Glu Glu Gln Val Met Leu Gly Ala Leu Gly
```

```
                20                  25                  30

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

Arg Leu Thr Glu Pro Leu Pro Arg His Ala Pro Leu Ser Glu Thr Glu
    50                  55                  60

Ala Gln Ala Arg Leu Arg Glu Tyr Ala Ser Arg Asn Thr Val Leu Arg
65                  70                  75                  80

Ser Phe Tyr Gly Gln Gly Phe Ser Asp Thr Val Thr Pro Pro Val Ile
                85                  90                  95

Arg Arg Gly Val Leu Glu Ala Pro Gly Trp Tyr Thr Ala Tyr Thr Pro
            100                 105                 110

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

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

Leu Leu Asp Glu Ala Ser Ala Thr Ala Glu Ala Val Gly Leu Met Ser
145                 150                 155                 160

Arg Ala Gln Arg Lys Gly Arg Arg Val Leu Leu Asp Ala Arg Leu His
                165                 170                 175

Pro Gln Val Leu Ala Val Ala Ala Glu Arg Ala Arg Ala Ile Asp Leu
            180                 185                 190

Glu Val Ala Val Glu Asp Leu Ser Gly Pro Leu Val Gly Glu Asp Leu
        195                 200                 205

Cys Gly Val Val Ile Ala Tyr Pro Gly Thr Glu Gly Asp Ile Ala Asp
    210                 215                 220

Pro Arg Pro Val Ile Glu Ala Val His Ala Arg Gly Gly Leu Ala Thr
225                 230                 235                 240

Val Val Thr Asp Pro Leu Ser Leu Leu Leu Leu Glu Ser Pro Gly Glu
                245                 250                 255
```

```
Met Gly Ala Asp Ile Ala Val Gly Ser Ser Gln Arg Phe Gly Val Pro
            260                 265                 270

Leu Phe Tyr Gly Gly Pro His Ala Ala Tyr Met Ala Val Ser Asp Ala
        275                 280                 285

Leu Lys Arg Gln Ile Pro Gly Arg Leu Val Gly Val Ser Val Asp Ala
    290                 295                 300

Glu Gly Ala Pro Ala Tyr Arg Leu Ala Leu Gln Thr Arg Glu Gln His
305                 310                 315                 320

Ile Arg Arg Glu Arg Ala Thr Ser Asn Ile Cys Thr Ala Gln Ala Leu
                325                 330                 335

Leu Ala Val Thr Ala Gly Met Tyr Ala Val Tyr His Gly Pro Glu Gly
            340                 345                 350

Leu Arg Ala Ile Ala Glu Arg Val His Gly Leu Ala Cys Asp Phe Ala
        355                 360                 365

Ala Ala Val Arg Ala Ala Gly Gly Thr Val Leu His Asp Ala Phe Phe
    370                 375                 380

Asp Thr Val Ala Val Arg Val Glu Ala Ala Arg Pro Ile Val Gly Thr
385                 390                 395                 400

Leu Ala Glu Ala Gly Tyr Leu Val Arg Ala Val Asp Gly Thr Thr Val
                405                 410                 415

Gly Val Ser Phe Gly Glu Ser Ala Glu Glu Gly Asp Val Glu Lys Leu
            420                 425                 430

Ala Ala Val Phe Gly Ala Ser Leu Thr Ala Gly Thr Arg Cys Ile Pro
        435                 440                 445

Ala Ser Val Ala Arg Gln Thr Pro Thr Leu Thr His Pro Val Phe Ser
    450                 455                 460

Thr Leu His Ser Glu Thr Gln Met Met Arg Tyr Leu Arg Thr Leu Ser
465                 470                 475                 480

Asp Arg Asp Leu Ala Leu Asp Arg Thr Met Ile Pro Leu Gly Ser Cys
                485                 490                 495
```

```
Thr Met Lys Leu Asn Pro Thr Ala Gly Leu Glu Thr Ile Thr Trp Pro
            500                 505                 510

Glu Phe Ala Asp Met His Pro Phe Ala Pro Asp Asp Gln Ala Ala Gly
        515                 520                 525

Trp Leu Ala Leu Ile Ala Glu Leu Glu Gly Trp Leu Ala Glu Leu Thr
    530                 535                 540

Gly Tyr Ala Lys Val Ser Val Gln Pro Asn Ala Gly Ser Gln Gly Glu
545                 550                 555                 560

Leu Ala Gly Leu Leu Ala Ile Arg Arg Tyr His Val Ala Asn Gly Asp
                565                 570                 575

Met Asp Arg Asp Ile Cys Leu Val Pro Ala Ser Ala His Gly Thr Asn
            580                 585                 590

Ala Ala Ser Ala Thr Leu Ala His Leu Arg Val Val Val Val Gly Thr
        595                 600                 605

Ala Gly Asp Gly Ser Ile Asp Met Asp Asp Leu Asp Ala Lys Leu Ala
    610                 615                 620

Glu His Gly Pro Gln Val Ala Ala Ile Met Ile Thr Tyr Pro Ser Thr
625                 630                 635                 640

His Gly Val Phe Glu Asp Thr Val Arg Glu Val Cys Asp Arg Val His
                645                 650                 655

Ala Val Gly Gly Gln Val Tyr Ile Asp Gly Ala Asn Leu Asn Ala Leu
            660                 665                 670

Thr Gly Leu Ala Leu Leu Gly Arg Ile Gly Gly Asp Val Ser His Leu
        675                 680                 685

Asn Leu His Lys Thr Phe Thr Ile Pro His Gly Gly Gly Gly Pro Gly
    690                 695                 700

Val Gly Pro Val Cys Val Ala Glu His Leu Val Pro Phe Leu Pro Ala
705                 710                 715                 720

Asp Pro Thr Ser Leu Asp Gly Ala Thr Pro Ala Ala Val Gly Thr Gly
                725                 730                 735
```

```
Val Pro Val Ser Ala Thr Arg His Gly Ser Ala Gly Val Leu Gln Ile
            740                 745                 750

Ser Trp Ala Tyr Ile Ala Met Met Gly Thr Asp Gly Leu Thr Arg Ala
        755                 760                 765

Ser Ala Ala Ala Ile Leu Ser Ala Asn Tyr Val Ala His Arg Leu Gly
    770                 775                 780

Glu Ala Phe Pro Val Leu Tyr Thr Gly Arg Asn Gly Leu Val Ala His
785                 790                 795                 800

Glu Cys Ile Leu Asp Leu Arg Asp Leu Thr Arg Gln Thr Gly Val Thr
                805                 810                 815

Ala Thr Asp Val Ala Lys Arg Leu Ile Asp Phe Gly Phe His Ala Pro
            820                 825                 830

Thr Leu Ser Phe Pro Val Ala Gly Thr Leu Met Val Glu Pro Thr Glu
        835                 840                 845

Ser Glu Asp Leu Ala Glu Leu Asp Arg Phe Ile Glu Ala Met Leu Thr
    850                 855                 860

Ile Arg Ala Glu Ile Asp Glu Ile Ser Gly Gly Asp Ile Ala Tyr Glu
865                 870                 875                 880

Asp Ser Val Leu His His Ala Pro Phe Thr Ala Trp Ser Val Ser Arg
                885                 890                 895

Asp Asp Trp Asp His Ala Phe Thr Arg Glu Gln Ala Ala Trp Pro Val
            900                 905                 910

Pro Gly Leu Arg Arg Thr Lys Tyr Phe Pro Pro Val Arg Arg Leu Asn
        915                 920                 925

Glu Ala Tyr Gly Asp Arg His Leu Val Cys Ala Cys Pro Pro Pro Glu
    930                 935                 940

Ala Phe Asp Leu Ser Glu Glu Asn Gln
945                 950
```

<210> 41

<211> 1704
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1404)
<223> gene gcvT

<400> 41
cgagctcgac cgcttcatcg aggcgatgct caccatccgc gcggagatcg acgagatcag 60

cggcggcgac atcgcctacg aggactccgt cctccaccac gcgccgttca ccgcgtggag 120

cgtgtcccgc gacgactggg accacgcctt cacccgtgag caggcggcct ggccggtccc 180

cggtctgcgc cgcaccaagt acttcccgcc ggtccgccgc ctcaacgagg cctacggtga 240

ccgccacctc gtgtgcgcct gcccgccgcc cgaggccttc gacctttccg aggagaacca 300

gtg acc gac ctg cgt acc agc ccc ctc cac gag cgt cat gtg gag ctc 348
Val Thr Asp Leu Arg Thr Ser Pro Leu His Glu Arg His Val Glu Leu
1 5 10 15

ggg gcc tcc ttc acc ccc ttc ggc ccg tgg aac atg ccc ctg cgc tac 396
Gly Ala Ser Phe Thr Pro Phe Gly Pro Trp Asn Met Pro Leu Arg Tyr
20 25 30

ggc aac gag ctc gac gag cac cgc gcc gtc cgt tcc acc gcc ggg ctc 444
Gly Asn Glu Leu Asp Glu His Arg Ala Val Arg Ser Thr Ala Gly Leu
35 40 45

ttc gac ctc tcg cac atg ggt gag atc cgc gtg tgg ggc gca cag gcc 492
Phe Asp Leu Ser His Met Gly Glu Ile Arg Val Trp Gly Ala Gln Ala
50 55 60

gcg gag ttc ctc gac cat gcg ctg ctc tcc gcc ttc tcc acg ctc ccc 540
Ala Glu Phe Leu Asp His Ala Leu Leu Ser Ala Phe Ser Thr Leu Pro
65 70 75 80

gtg ggt aag gcg cgg tac tcc atg ctt gtc gac gcc acc ggt gcc atc 588
Val Gly Lys Ala Arg Tyr Ser Met Leu Val Asp Ala Thr Gly Ala Ile
85 90 95

ctc gac gac ctc ctc acc tac cgc ctc gcc ggg gac gag ttc ctg gtg 636
Leu Asp Asp Leu Leu Thr Tyr Arg Leu Ala Gly Asp Glu Phe Leu Val
100 105 110

gtc ccc aac gcg gcg aac acg gag acc gtg tgg gag gag ttc cgg gcc 684
Val Pro Asn Ala Ala Asn Thr Glu Thr Val Trp Glu Glu Phe Arg Ala
115 120 125

cgc gcc gcc ggc ttc gac gtg gag ctg gcc gac gag tcc gcc gac act 732
Arg Ala Ala Gly Phe Asp Val Glu Leu Ala Asp Glu Ser Ala Asp Thr
130 135 140

gcg ctg ctg gct gtg cag ggc ccc cgc gcc gag cag atc atc gcc gac 780
Ala Leu Leu Ala Val Gln Gly Pro Arg Ala Glu Gln Ile Ile Ala Asp

```
145                 150                 155                 160

ctc gtc gcc ggg gac gac gag tcg gtc gtg cgc acg atg aag ttc tac  828
Leu Val Ala Gly Asp Asp Glu Ser Val Val Arg Thr Met Lys Phe Tyr
                165                 170                 175

tcg gcg gcc ccg ttg acg gtg gcg ggc gtc gat acg ctg ctc gcc cgc  876
Ser Ala Ala Pro Leu Thr Val Ala Gly Val Asp Thr Leu Leu Ala Arg
            180                 185                 190

acc ggc tac acc ggg gag gac ggc ttc gag ctc tac gtc tcc ggc gcg  924
Thr Gly Tyr Thr Gly Glu Asp Gly Phe Glu Leu Tyr Val Ser Gly Ala
        195                 200                 205

gac gcc gct gaa ctg tgg gac gcg ctg ctc aac gcc ggc gcc gcc tac  972
Asp Ala Ala Glu Leu Trp Asp Ala Leu Leu Asn Ala Gly Ala Ala Tyr
    210                 215                 220

gac atg ctg ccc gcc gga ctg gcg gcg cgg gac tcc ctg cgc ctg gag 1020
Asp Met Leu Pro Ala Gly Leu Ala Ala Arg Asp Ser Leu Arg Leu Glu
225                 230                 235                 240

gcc ggg ctc ccc ctc tac ggg cag gag ctc acc cgc gac atc acg ccg 1068
Ala Gly Leu Pro Leu Tyr Gly Gln Glu Leu Thr Arg Asp Ile Thr Pro
                245                 250                 255

gtg gag gcc ggg atg gcc cgc gcc ttc gcc tcg aag gag ggg gac ttc 1116
Val Glu Ala Gly Met Ala Arg Ala Phe Ala Ser Lys Glu Gly Asp Phe
            260                 265                 270

gtc ggc cgc gac gcc ctc gtc ggc agg gag ccg acc agc gcc atc gtc 1164
Val Gly Arg Asp Ala Leu Val Gly Arg Glu Pro Thr Ser Ala Ile Val
        275                 280                 285

ggg ctc cgg ggt ctg ggg cgc cgc gcg gcc cgc gag ggc gcc gag gtc 1212
Gly Leu Arg Gly Leu Gly Arg Arg Ala Ala Arg Glu Gly Ala Glu Val
    290                 295                 300

tac ctc gac ggc gaa cag gtc ggc gtg gtc acc tcc ggg cag ccg gcg 1260
Tyr Leu Asp Gly Glu Gln Val Gly Val Val Thr Ser Gly Gln Pro Ala
305                 310                 315                 320

ccg gtg ctc ggc tac ccg atc gca ctc gcc cgc ctg cgc ccc gac gtc 1308
Pro Val Leu Gly Tyr Pro Ile Ala Leu Ala Arg Leu Arg Pro Asp Val
                325                 330                 335

acc gcg gcc ggc acg gca ctg gag gtg gac atc cgt ggg agg cgg cac 1356
Thr Ala Ala Gly Thr Ala Leu Glu Val Asp Ile Arg Gly Arg Arg His
            340                 345                 350

ccc ttc gag atc gtc gac ctg ccc ttc tac cgc cgc gcc gca cga taa 1404
Pro Phe Glu Ile Val Asp Leu Pro Phe Tyr Arg Arg Ala Ala Arg
        355                 360                 365

cctgaaccca ccaccaacgg aaaggctccc ccaccatggc caccgagcac tccctgcccg 1464

ggaactactc ctactccgag gaccacgagt ggatcgacgc gacgcccgag gacgccgtcg 1524

gcgcgaccgt gaaggtcggc atcacctccg tggccaccga acgcctcggc gaggtcgtct 1584
```

acgcggagct cccgcaggtc ggtgacgccg tcaccgccgg tgaaccgtgc ggcgaggtcg 1644

agtccacgaa gtcggtctcc gacctctacg cgccggtcac gggcaccgtc accgaggtca 1704

<210> 42
<211> 367
<212> PRT
<213> Corynebacterium humireducens

<400> 42

Val Thr Asp Leu Arg Thr Ser Pro Leu His Glu Arg His Val Glu Leu
1 5 10 15

Gly Ala Ser Phe Thr Pro Phe Gly Pro Trp Asn Met Pro Leu Arg Tyr
20 25 30

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

Phe Asp Leu Ser His Met Gly Glu Ile Arg Val Trp Gly Ala Gln Ala
50 55 60

Ala Glu Phe Leu Asp His Ala Leu Leu Ser Ala Phe Ser Thr Leu Pro
65 70 75 80

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

Leu Asp Asp Leu Leu Thr Tyr Arg Leu Ala Gly Asp Glu Phe Leu Val
100 105 110

Val Pro Asn Ala Ala Asn Thr Glu Thr Val Trp Glu Glu Phe Arg Ala
115 120 125

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

Ala Leu Leu Ala Val Gln Gly Pro Arg Ala Glu Gln Ile Ile Ala Asp
145 150 155 160

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

Ser Ala Ala Pro Leu Thr Val Ala Gly Val Asp Thr Leu Leu Ala Arg
180 185 190

```
Thr Gly Tyr Thr Gly Glu Asp Gly Phe Glu Leu Tyr Val Ser Gly Ala
        195                 200                 205

Asp Ala Ala Glu Leu Trp Asp Ala Leu Leu Asn Ala Gly Ala Ala Tyr
    210                 215                 220

Asp Met Leu Pro Ala Gly Leu Ala Ala Arg Asp Ser Leu Arg Leu Glu
225                 230                 235                 240

Ala Gly Leu Pro Leu Tyr Gly Gln Glu Leu Thr Arg Asp Ile Thr Pro
                245                 250                 255

Val Glu Ala Gly Met Ala Arg Ala Phe Ala Ser Lys Glu Gly Asp Phe
            260                 265                 270

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

Gly Leu Arg Gly Leu Gly Arg Arg Ala Ala Arg Glu Gly Ala Glu Val
    290                 295                 300

Tyr Leu Asp Gly Glu Gln Val Gly Val Val Thr Ser Gly Gln Pro Ala
305                 310                 315                 320

Pro Val Leu Gly Tyr Pro Ile Ala Leu Ala Arg Leu Arg Pro Asp Val
                325                 330                 335

Thr Ala Ala Gly Thr Ala Leu Glu Val Asp Ile Arg Gly Arg Arg His
            340                 345                 350

Pro Phe Glu Ile Val Asp Leu Pro Phe Tyr Arg Arg Ala Ala Arg
        355                 360                 365
```

<210> 43
<211> 1899
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1599)
<223> gene glyA

<400> 43
gacaggggga gatagacctc ggcgacctcc acgaggtcga tcgattcgcc gatgccgcgg 60

```
agctgctcga cctcctcctc cgtgagcacc tgcggcatcg attgacgcag ggcacgccag      120

gaggagcggt cgaaatccac gtaggggggtg gcgtccttgg gccgagacat gcgtcccatt      180

gtgtcatctg ccccgtcaac tgtgtcccac tcacccgggg tgcgggggta tgaggtgccc      240

tgtgggcggt atgctgtcca cgaatgccgt gtacccctag aaaggctggc tgtaacgccc      300

atg acc gct gag tct tct gat ctc cgt tac cag gaa ctg tcc gtc ctc         348
Met Thr Ala Glu Ser Ser Asp Leu Arg Tyr Gln Glu Leu Ser Val Leu
1               5                   10                  15

gac ccg gag gtc cac gcc gcc atc ggc ggt gag atc gcc cgt cag cgt         396
Asp Pro Glu Val His Ala Ala Ile Gly Gly Glu Ile Ala Arg Gln Arg
            20                  25                  30

gac ttc ctc gag atg atc gcg tcc gag aac ttc gtc ccc cgt gcc gtc         444
Asp Phe Leu Glu Met Ile Ala Ser Glu Asn Phe Val Pro Arg Ala Val
        35                  40                  45

ctg cag gca cag ggt tcg gtg ttc acc aac aag tac gcc gag ggc tac         492
Leu Gln Ala Gln Gly Ser Val Phe Thr Asn Lys Tyr Ala Glu Gly Tyr
    50                  55                  60

ccg ggg cgt cgt tac tac ggt ggc tgc gag aac gcc gac atc gtc gag         540
Pro Gly Arg Arg Tyr Tyr Gly Gly Cys Glu Asn Ala Asp Ile Val Glu
65                  70                  75                  80

gac ctg gcc cgc gac cgc gcc aag gcc ctg ttc ggc gcc gag ttc gcc         588
Asp Leu Ala Arg Asp Arg Ala Lys Ala Leu Phe Gly Ala Glu Phe Ala
                85                  90                  95

aac gtc cag ccg cac tcc ggc gcc cag gcc aac gcc gcc gtc ctg cac         636
Asn Val Gln Pro His Ser Gly Ala Gln Ala Asn Ala Ala Val Leu His
            100                 105                 110

gcg ctg gcc gac gcc ggc gac aag atc atg ggt ctg tcc ctg gcc cac         684
Ala Leu Ala Asp Ala Gly Asp Lys Ile Met Gly Leu Ser Leu Ala His
        115                 120                 125

ggt ggt cac ctg acc cac ggc atg aag ctc aac ttc tcc ggc aag ctc         732
Gly Gly His Leu Thr His Gly Met Lys Leu Asn Phe Ser Gly Lys Leu
    130                 135                 140

tac gac gtc gtc gcc tac gag gtc gac ccg gag acc cac cgc atc gac         780
Tyr Asp Val Val Ala Tyr Glu Val Asp Pro Glu Thr His Arg Ile Asp
145                 150                 155                 160

atg gac cgc gtc cgc gag cag gcc ctg gcc gag cgc ccg aag gtc ctc         828
Met Asp Arg Val Arg Glu Gln Ala Leu Ala Glu Arg Pro Lys Val Leu
                165                 170                 175

atc gcc ggc tgg tcc gcg tac ccg cgc acc ctc gac ttc gag gcg ttc         876
Ile Ala Gly Trp Ser Ala Tyr Pro Arg Thr Leu Asp Phe Glu Ala Phe
            180                 185                 190

cgc tcc atc gcc gac gag gtc ggc gcg tac ctg tgg acc gac atg gcg         924
Arg Ser Ile Ala Asp Glu Val Gly Ala Tyr Leu Trp Thr Asp Met Ala
```

```
          195                 200                 205

cac ttc gcc ggc ctc gtc gcc gcc gac ctg cac ccg tcc ccg gtc ccg        972
His Phe Ala Gly Leu Val Ala Ala Asp Leu His Pro Ser Pro Val Pro
    210                 215                 220

cac tcc gac gtc gtc tcc acc acc gtc cac aag acg ctg ggt ggc ccg       1020
His Ser Asp Val Val Ser Thr Thr Val His Lys Thr Leu Gly Gly Pro
225                 230                 235                 240

cgt tcc ggc ctg atc gtc gcg aag cag gag tgg gcc aag aag ctc aac       1068
Arg Ser Gly Leu Ile Val Ala Lys Gln Glu Trp Ala Lys Lys Leu Asn
                245                 250                 255

tcc gcc gtc ttc ccg ggc cag cag ggt ggt ccg ctc atg cac gcc atc       1116
Ser Ala Val Phe Pro Gly Gln Gln Gly Gly Pro Leu Met His Ala Ile
            260                 265                 270

gcc gcc aag gcc gtg gca ctg aag gtc gcc ggc acc gac gag ttc aag       1164
Ala Ala Lys Ala Val Ala Leu Lys Val Ala Gly Thr Asp Glu Phe Lys
        275                 280                 285

gac cgt cag gcc cgc acc atc gag ggt gcc aag atc ctg gcc gag cgt       1212
Asp Arg Gln Ala Arg Thr Ile Glu Gly Ala Lys Ile Leu Ala Glu Arg
    290                 295                 300

ctc acc gcc gct gac gcg aag gcc gcc ggc atc gac gtc ctc acc ggt       1260
Leu Thr Ala Ala Asp Ala Lys Ala Ala Gly Ile Asp Val Leu Thr Gly
305                 310                 315                 320

ggc acc gac gtg cac ctg gtc ctc gct gac ctg cgc aac tcc gag atg       1308
Gly Thr Asp Val His Leu Val Leu Ala Asp Leu Arg Asn Ser Glu Met
                325                 330                 335

gac ggc cag cag gcc gaa gac ctc ctc cac gag gtc ggc atc acc gtc       1356
Asp Gly Gln Gln Ala Glu Asp Leu Leu His Glu Val Gly Ile Thr Val
            340                 345                 350

aac cgc aac gcc gtc ccg aac gac ccg cgc ccg ccg atg gtc acc tcc       1404
Asn Arg Asn Ala Val Pro Asn Asp Pro Arg Pro Pro Met Val Thr Ser
        355                 360                 365

ggc ctg cgc atc ggc acc ccg gcc ctg gcc acc cgt ggt ttc gac gcc       1452
Gly Leu Arg Ile Gly Thr Pro Ala Leu Ala Thr Arg Gly Phe Asp Ala
    370                 375                 380

gcc gcc ttc acc gag gtc gcc gac atc atc ggc acc gcc ctg gtc aac       1500
Ala Ala Phe Thr Glu Val Ala Asp Ile Ile Gly Thr Ala Leu Val Asn
385                 390                 395                 400

ggc aag aac gcc gac atc gag gca ctg cgt gcc cgc gtc gcg aag ctg       1548
Gly Lys Asn Ala Asp Ile Glu Ala Leu Arg Ala Arg Val Ala Lys Leu
                405                 410                 415

acc gac cag tac ccg ctg tac gag ggt ctg gag gag tgg aag atc aac       1596
Thr Asp Gln Tyr Pro Leu Tyr Glu Gly Leu Glu Glu Trp Lys Ile Asn
            420                 425                 430

tag gtcttcccgc cctccccgtg cgcgtcctcg tcatagacaa cctcgattcc            1649
```

ttcacctgga atctcgtcgc ctacgtcgag gacgtcaccg gtgtcgcccc cgaggtgatc 1709

accaacaacg aacccggatg ggatgtcgac cgcgtcgcca cctacgacgc cgtcatcatc 1769

tccccgggcc ccggccgccc ggagcgtgag aaggacatcg gcatgtgcct cgatgtcctg 1829

cgcgacgggc gtgtcccgat tctgggggtc tgcctcgggc accaggccct cgcccacgcg 1889

tggggcggca 1899

<210> 44
<211> 432
<212> PRT
<213> Corynebacterium humireducens

<400> 44

Met Thr Ala Glu Ser Ser Asp Leu Arg Tyr Gln Glu Leu Ser Val Leu
1 5 10 15

Asp Pro Glu Val His Ala Ala Ile Gly Gly Glu Ile Ala Arg Gln Arg
20 25 30

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

Leu Gln Ala Gln Gly Ser Val Phe Thr Asn Lys Tyr Ala Glu Gly Tyr
50 55 60

Pro Gly Arg Arg Tyr Tyr Gly Gly Cys Glu Asn Ala Asp Ile Val Glu
65 70 75 80

Asp Leu Ala Arg Asp Arg Ala Lys Ala Leu Phe Gly Ala Glu Phe Ala
85 90 95

Asn Val Gln Pro His Ser Gly Ala Gln Ala Asn Ala Ala Val Leu His
100 105 110

Ala Leu Ala Asp Ala Gly Asp Lys Ile Met Gly Leu Ser Leu Ala His
115 120 125

Gly Gly His Leu Thr His Gly Met Lys Leu Asn Phe Ser Gly Lys Leu
130 135 140

Tyr Asp Val Val Ala Tyr Glu Val Asp Pro Glu Thr His Arg Ile Asp
145 150 155 160

```
Met Asp Arg Val Arg Glu Gln Ala Leu Ala Glu Arg Pro Lys Val Leu
                165                 170                 175

Ile Ala Gly Trp Ser Ala Tyr Pro Arg Thr Leu Asp Phe Glu Ala Phe
            180                 185                 190

Arg Ser Ile Ala Asp Glu Val Gly Ala Tyr Leu Trp Thr Asp Met Ala
        195                 200                 205

His Phe Ala Gly Leu Val Ala Ala Asp Leu His Pro Ser Pro Val Pro
    210                 215                 220

His Ser Asp Val Val Ser Thr Thr Val His Lys Thr Leu Gly Gly Pro
225                 230                 235                 240

Arg Ser Gly Leu Ile Val Ala Lys Gln Glu Trp Ala Lys Lys Leu Asn
                245                 250                 255

Ser Ala Val Phe Pro Gly Gln Gln Gly Gly Pro Leu Met His Ala Ile
            260                 265                 270

Ala Ala Lys Ala Val Ala Leu Lys Val Ala Gly Thr Asp Glu Phe Lys
        275                 280                 285

Asp Arg Gln Ala Arg Thr Ile Glu Gly Ala Lys Ile Leu Ala Glu Arg
    290                 295                 300

Leu Thr Ala Ala Asp Ala Lys Ala Ala Gly Ile Asp Val Leu Thr Gly
305                 310                 315                 320

Gly Thr Asp Val His Leu Val Leu Ala Asp Leu Arg Asn Ser Glu Met
                325                 330                 335

Asp Gly Gln Gln Ala Glu Asp Leu Leu His Glu Val Gly Ile Thr Val
            340                 345                 350

Asn Arg Asn Ala Val Pro Asn Asp Pro Arg Pro Pro Met Val Thr Ser
        355                 360                 365

Gly Leu Arg Ile Gly Thr Pro Ala Leu Ala Thr Arg Gly Phe Asp Ala
    370                 375                 380

Ala Ala Phe Thr Glu Val Ala Asp Ile Ile Gly Thr Ala Leu Val Asn
385                 390                 395                 400
```

```
Gly Lys Asn Ala Asp Ile Glu Ala Leu Arg Ala Arg Val Ala Lys Leu
                405                 410                 415

Thr Asp Gln Tyr Pro Leu Tyr Glu Gly Leu Glu Glu Trp Lys Ile Asn
            420                 425                 430
```

<210> 45
<211> 1932
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1632)
<223> gene hom

<400> 45

```
gcggcgtgcg cggacgagat ccccgccagt gggatcacca ggcacgccac gcaggccgtg       60

agtgcacggg tgatccgacg gcgggacatg ctgactcctg tcactggcag aggcatgggg      120

gtggtgagga cagattaatc gtctgaacgc aatatgtcca gagatgtgac ttatcttatg      180

gagtgtcgtg accccggagt ctgaggaagt ggccgaatcc cggtagggtg gtcacggaaa      240

tctgtcctca gtctgcccgt ccccgacggg cacggaccca cgaccatgtg caggagaacc      300

atg acc gtc act cag cag ccc agc ttc aac ccc ggc aag gga gcc ggc        348
Met Thr Val Thr Gln Gln Pro Ser Phe Asn Pro Gly Lys Gly Ala Gly
1               5                   10                  15

gag ccg gtg ggc gtc gcc att ctc ggc cac ggc acc gtc gga tct gag        396
Glu Pro Val Gly Val Ala Ile Leu Gly His Gly Thr Val Gly Ser Glu
            20                  25                  30

gtg ctg cgc ctg atg ggc gag tac tcc gac gcg ctc gcg cac cgc atc        444
Val Leu Arg Leu Met Gly Glu Tyr Ser Asp Ala Leu Ala His Arg Ile
        35                  40                  45

ggc ggt ccg ctc gag ctc aag ggt gtg gcc gtg tcc gac ctc tcc aag        492
Gly Gly Pro Leu Glu Leu Lys Gly Val Ala Val Ser Asp Leu Ser Lys
    50                  55                  60

ccg cgc gag ggc gtg gac cgt gag ctg ctc acc gat gac gcg ctg agc        540
Pro Arg Glu Gly Val Asp Arg Glu Leu Leu Thr Asp Asp Ala Leu Ser
65                  70                  75                  80

ctc atc aac cgc gac gac gtc gac atc gtc gtc gag gtc atc ggc ggc        588
Leu Ile Asn Arg Asp Asp Val Asp Ile Val Val Glu Val Ile Gly Gly
                85                  90                  95

atc gag tac ccg cgt gag ctg gtc ctg gcc gcc ctg cgc gcc ggc aag        636
Ile Glu Tyr Pro Arg Glu Leu Val Leu Ala Ala Leu Arg Ala Gly Lys
            100                 105                 110
```

```
tcc gtc gtc acc gcc aac aag gcc ctc gtc gcc gcg cac gcc gac gag        684
Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ala Asp Glu
        115                 120                 125

ctt gcc gac gcc gcc gac gcc gcc aac gtc gac ctc tac ttc gag gcc        732
Leu Ala Asp Ala Ala Asp Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala
    130                 135                 140

gcc gtc gcc gcc gcc atc ccg gtc gtc ggc atg ctg cgt cgt tcc ctc        780
Ala Val Ala Ala Ala Ile Pro Val Val Gly Met Leu Arg Arg Ser Leu
145                 150                 155                 160

gcc ggc gac aac atc ctg cgt atc tcc ggc atc gtc aac ggc acc acc        828
Ala Gly Asp Asn Ile Leu Arg Ile Ser Gly Ile Val Asn Gly Thr Thr
                165                 170                 175

aac ttc atc ctc gac gcg atg gag tcc acc ggc gcc agc tac gac gac        876
Asn Phe Ile Leu Asp Ala Met Glu Ser Thr Gly Ala Ser Tyr Asp Asp
            180                 185                 190

gcg ctc gcc gag gcc acc cgt ctg ggc tac gcc gag gcc gac ccg acc        924
Ala Leu Ala Glu Ala Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr
        195                 200                 205

gcc gac gtc gag ggc cac gac gcc gcc tcc aag gcc gcc atc ctc gcc        972
Ala Asp Val Glu Gly His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala
    210                 215                 220

tcc ctg ggc ttc cac acc cgc gtc aag ttc gac gac gtc agc tgc gag       1020
Ser Leu Gly Phe His Thr Arg Val Lys Phe Asp Asp Val Ser Cys Glu
225                 230                 235                 240

ggc atc tcc aag gtc acc gcc gag gac atc gag gcc gcc cgc gac gcc       1068
Gly Ile Ser Lys Val Thr Ala Glu Asp Ile Glu Ala Ala Arg Asp Ala
                245                 250                 255

ggc tac gtg atc aag ctg ctc gcc atc tgt gag cgc gtc acc gac aag       1116
Gly Tyr Val Ile Lys Leu Leu Ala Ile Cys Glu Arg Val Thr Asp Lys
            260                 265                 270

gac ggc gtg gag tcc gtc gcc agc cgc gtc cac ccg acc ctc gtt ccg       1164
Asp Gly Val Glu Ser Val Ala Ser Arg Val His Pro Thr Leu Val Pro
        275                 280                 285

gtc gac cac ccg ctg gcc tcg gtc aac cag tcc tac aac gcc atc ttc       1212
Val Asp His Pro Leu Ala Ser Val Asn Gln Ser Tyr Asn Ala Ile Phe
    290                 295                 300

gtc gag gcc gag gca gcc ggt cgc ctg atg ttc tac ggc aac ggt gcc       1260
Val Glu Ala Glu Ala Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala
305                 310                 315                 320

ggt ggc gcc ccg acc gcc tcc gcc gtc ctc ggt gac ctc gtc ggc gcc       1308
Gly Gly Ala Pro Thr Ala Ser Ala Val Leu Gly Asp Leu Val Gly Ala
                325                 330                 335

gcc cgc aac aag gtc cac ggt ggc cgc gcc ccg ggc gag aac acc tac       1356
Ala Arg Asn Lys Val His Gly Gly Arg Ala Pro Gly Glu Asn Thr Tyr
            340                 345                 350
```

```
gcg aac ctg ccg atc gcc gac ctc ggc gac gtg cgc acc cgc tac cac      1404
Ala Asn Leu Pro Ile Ala Asp Leu Gly Asp Val Arg Thr Arg Tyr His
        355                 360                 365

atc gac atg gag gtc gag gac cgc acc ggt gtc ctc gcc gag ctg tcc      1452
Ile Asp Met Glu Val Glu Asp Arg Thr Gly Val Leu Ala Glu Leu Ser
    370                 375                 380

gcg atc ttc gcc acc cac gac atc tcc ctc aag acc gtc cgc cag gag      1500
Ala Ile Phe Ala Thr His Asp Ile Ser Leu Lys Thr Val Arg Gln Glu
385                 390                 395                 400

gag gcc ggc gac cac gcc cgc ctc atc gtc gtc acg cat tcc gca cgt      1548
Glu Ala Gly Asp His Ala Arg Leu Ile Val Val Thr His Ser Ala Arg
                405                 410                 415

gag gcc gac ctg gcc gcc acc gtc gag gac ctg aag aag gcc ccg gcg      1596
Glu Ala Asp Leu Ala Ala Thr Val Glu Asp Leu Lys Lys Ala Pro Ala
            420                 425                 430

gtc aag tcc gtc gac agc gtc ctg cga ctc atc tag ggagcgttga          1642
Val Lys Ser Val Asp Ser Val Leu Arg Leu Ile
        435                 440

gctgtgagca tccagcttga ggtgggcacc cgggccaccg tcaccgtccc cggctcctcc    1702

gcgaacctgg gccccggatt cgacaccctc ggcctggccg tgggcatcta cgacaccgtc    1762

gaggtcgagg tcatcgagtc gggcctcgag gtcgaggtct tcggcgaggg cgaggacgac    1822

ctgccccgcg acggttccca cctggtggtc aaggccatcc ggtcgggcct caacgccgcc    1882

cacgccgagg ccccgggcct gcgcgtggtg tgcaccaacg ccatcccgca              1932
```

<210> 46
<211> 443
<212> PRT
<213> Corynebacterium humireducens

<400> 46

```
Met Thr Val Thr Gln Gln Pro Ser Phe Asn Pro Gly Lys Gly Ala Gly
1               5                   10                  15

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

Val Leu Arg Leu Met Gly Glu Tyr Ser Asp Ala Leu Ala His Arg Ile
        35                  40                  45

Gly Gly Pro Leu Glu Leu Lys Gly Val Ala Val Ser Asp Leu Ser Lys
    50                  55                  60
```

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

Leu Ile Asn Arg Asp Asp Val Asp Ile Val Val Glu Val Ile Gly Gly
                85                  90                  95

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

Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ala Asp Glu
        115                 120                 125

Leu Ala Asp Ala Ala Asp Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala
    130                 135                 140

Ala Val Ala Ala Ala Ile Pro Val Val Gly Met Leu Arg Arg Ser Leu
145                 150                 155                 160

Ala Gly Asp Asn Ile Leu Arg Ile Ser Gly Ile Val Asn Gly Thr Thr
                165                 170                 175

Asn Phe Ile Leu Asp Ala Met Glu Ser Thr Gly Ala Ser Tyr Asp Asp
            180                 185                 190

Ala Leu Ala Glu Ala Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr
        195                 200                 205

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

Ser Leu Gly Phe His Thr Arg Val Lys Phe Asp Asp Val Ser Cys Glu
225                 230                 235                 240

Gly Ile Ser Lys Val Thr Ala Glu Asp Ile Glu Ala Ala Arg Asp Ala
                245                 250                 255

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

Asp Gly Val Glu Ser Val Ala Ser Arg Val His Pro Thr Leu Val Pro
        275                 280                 285

Val Asp His Pro Leu Ala Ser Val Asn Gln Ser Tyr Asn Ala Ile Phe
    290                 295                 300
```

Val Glu Ala Glu Ala Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala
305 310 315 320

Gly Gly Ala Pro Thr Ala Ser Ala Val Leu Gly Asp Leu Val Gly Ala
325 330 335

Ala Arg Asn Lys Val His Gly Gly Arg Ala Pro Gly Glu Asn Thr Tyr
340 345 350

Ala Asn Leu Pro Ile Ala Asp Leu Gly Asp Val Arg Thr Arg Tyr His
355 360 365

Ile Asp Met Glu Val Glu Asp Arg Thr Gly Val Leu Ala Glu Leu Ser
370 375 380

Ala Ile Phe Ala Thr His Asp Ile Ser Leu Lys Thr Val Arg Gln Glu
385 390 395 400

Glu Ala Gly Asp His Ala Arg Leu Ile Val Val Thr His Ser Ala Arg
405 410 415

Glu Ala Asp Leu Ala Ala Thr Val Glu Asp Leu Lys Lys Ala Pro Ala
420 425 430

Val Lys Ser Val Asp Ser Val Leu Arg Leu Ile
435 440

<210> 47
<211> 1644
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1344)
<223> gene lipA

<400> 47
gcggggtgac catgcacggg ctgagcctga actgctcgaa cacgctcgag cactacgggc 60

acatcgtggc gtgcggcatc gacgacgccg acgtcaccac cctcagcatg gaactggggc 120

gcgacgtcag cgtcggggag gtcacggcac cgcttgtcga cgccctcctg gccgccctcg 180

ccggtgaact cgccgtcgcg gaccacacct tcggatcggc gcccgatccg acgaagattc 240

ccgcgaaaac gcgctgacct ctaagtttat ccctatcagt agaaagagta tggtggcgtt 300

```
gtg act atc gca cct gaa gga cgc aag ctg ctc cgg gtg gag aag cgc        348
Val Thr Ile Ala Pro Glu Gly Arg Lys Leu Leu Arg Val Glu Lys Arg
1               5                  10                  15

aat gcg cag acc ccc atc gag acg aag ccc cgt tgg atc cgc aac gcg        396
Asn Ala Gln Thr Pro Ile Glu Thr Lys Pro Arg Trp Ile Arg Asn Ala
            20                  25                  30

gtg aag acc ggc ccc gag tac gag gac atg aag aag aag gtg gcg ggc        444
Val Lys Thr Gly Pro Glu Tyr Glu Asp Met Lys Lys Lys Val Ala Gly
        35                  40                  45

gcc tcc ctg cac acc gtc tgt cag gag gcg ggc tgc ccc aac atc cac        492
Ala Ser Leu His Thr Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His
    50                  55                  60

gag tgc tgg gag tcc cgc gag gcg acg ttt ctc atc ggc ggc gcc aac        540
Glu Cys Trp Glu Ser Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn
65                  70                  75                  80

tgc tcc cgc cgc tgc gac ttc tgc cag atc aac tcc gcg aag ccg gag        588
Cys Ser Arg Arg Cys Asp Phe Cys Gln Ile Asn Ser Ala Lys Pro Glu
                85                  90                  95

ccg ctg gac cgc gac gag ccg cgc cgc gtg gcc gag tcc gtc cgc gag        636
Pro Leu Asp Arg Asp Glu Pro Arg Arg Val Ala Glu Ser Val Arg Glu
            100                 105                 110

atg ggc ctg aac tac tcc acc atc acc ggc gtg acc cgc gac gac ctc        684
Met Gly Leu Asn Tyr Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu
        115                 120                 125

gag gac gag ggt gcc tgg ctc tac gcg gag gtc gtc cgc cag atc cac        732
Glu Asp Glu Gly Ala Trp Leu Tyr Ala Glu Val Val Arg Gln Ile His
    130                 135                 140

gag ctc aac ccg aac acc ggc gtc gag aac ctc gtg ccc gac ttc tcc        780
Glu Leu Asn Pro Asn Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser
145                 150                 155                 160

ggc cgt tcc gag ctg ctg gag cag gtc ttc gag tcc cgc ccc gag gtg        828
Gly Arg Ser Glu Leu Leu Glu Gln Val Phe Glu Ser Arg Pro Glu Val
                165                 170                 175

ttc gcc cac aac ctg gag acc gtg ccg cgc atc ttc aag cgc atc cgc        876
Phe Ala His Asn Leu Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg
            180                 185                 190

ccg gcc ttc cgc tac gag cgt tcc ctc gac gtg atc cgc cag gcc cac        924
Pro Ala Phe Arg Tyr Glu Arg Ser Leu Asp Val Ile Arg Gln Ala His
        195                 200                 205

gac tac ggg ctg atc acc aag tcg aac ctc atc ctc ggc atg ggc gag        972
Asp Tyr Gly Leu Ile Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu
    210                 215                 220

acc ctc gac gag atc cgt gag gcc ctc acc gac ctg cac agc gcc ggc       1020
Thr Leu Asp Glu Ile Arg Glu Ala Leu Thr Asp Leu His Ser Ala Gly
225                 230                 235                 240
```

```
tgc gac atc atc acc atc acg cag tac ctg cgc ccc ggc ccg atg tac      1068
Cys Asp Ile Ile Thr Ile Thr Gln Tyr Leu Arg Pro Gly Pro Met Tyr
                245                 250                 255

cac ccg atc gac cgc tgg gtg aag ccg gag gag ttc gtc gag cac aag      1116
His Pro Ile Asp Arg Trp Val Lys Pro Glu Glu Phe Val Glu His Lys
            260                 265                 270

gac ttc gcc gag gag ctc ggc ttc ggt gcc gtc atg tcc ggc ccg ctg      1164
Asp Phe Ala Glu Glu Leu Gly Phe Gly Ala Val Met Ser Gly Pro Leu
        275                 280                 285

gtc cgt tcc tcc tac cgt gcg gga cgt ctc tac tcg cag gcg atg gcc      1212
Val Arg Ser Ser Tyr Arg Ala Gly Arg Leu Tyr Ser Gln Ala Met Ala
    290                 295                 300

gcc cgc ggc cgg gag atc ccc gac cac ctc aag cac ctg gcc gag acc      1260
Ala Arg Gly Arg Glu Ile Pro Asp His Leu Lys His Leu Ala Glu Thr
305                 310                 315                 320

tcg cag ggc agc acc gac cag gag gcc acc acc ctc ctg gcc aag tac      1308
Ser Gln Gly Ser Thr Asp Gln Glu Ala Thr Thr Leu Leu Ala Lys Tyr
                325                 330                 335

ggc ccc tcc cag gac aca ccg gtc acc tca cgt tag gcacccaccg           1354
Gly Pro Ser Gln Asp Thr Pro Val Thr Ser Arg
            340                 345

gaccctgacc taaagtagag gccatggcag acgacaagca gaaggcggca gcaaaggccg     1414

cgaaggcaga ggcacgggcc gccaagcggg cgaagagcaa ggagacgcgc gcccagctct     1474

ggcaggcgtt caacatccag cgcaagcagg acaagatgct cgtcccgctg atggtgctct     1534

ccgtcgtggg tgtggccgcg ctcctcttcc tcatcggcct ggcctggggc ggccagtggt     1594

tcacgctcat cctgggtatc ttcctgggtg ccgtcctggc gatgtacatc               1644
```

<210> 48
<211> 347
<212> PRT
<213> Corynebacterium humireducens

<400> 48

```
Val Thr Ile Ala Pro Glu Gly Arg Lys Leu Leu Arg Val Glu Lys Arg
1               5                   10                  15

Asn Ala Gln Thr Pro Ile Glu Thr Lys Pro Arg Trp Ile Arg Asn Ala
            20                  25                  30

Val Lys Thr Gly Pro Glu Tyr Glu Asp Met Lys Lys Lys Val Ala Gly
        35                  40                  45
```

```
Ala Ser Leu His Thr Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His
    50                  55                  60

Glu Cys Trp Glu Ser Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn
65                  70                  75                  80

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

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

Met Gly Leu Asn Tyr Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu
        115                 120                 125

Glu Asp Glu Gly Ala Trp Leu Tyr Ala Glu Val Val Arg Gln Ile His
    130                 135                 140

Glu Leu Asn Pro Asn Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser
145                 150                 155                 160

Gly Arg Ser Glu Leu Leu Glu Gln Val Phe Glu Ser Arg Pro Glu Val
                165                 170                 175

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

Pro Ala Phe Arg Tyr Glu Arg Ser Leu Asp Val Ile Arg Gln Ala His
        195                 200                 205

Asp Tyr Gly Leu Ile Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu
    210                 215                 220

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

Cys Asp Ile Ile Thr Ile Thr Gln Tyr Leu Arg Pro Gly Pro Met Tyr
                245                 250                 255

His Pro Ile Asp Arg Trp Val Lys Pro Glu Glu Phe Val Glu His Lys
            260                 265                 270

Asp Phe Ala Glu Glu Leu Gly Phe Gly Ala Val Met Ser Gly Pro Leu
        275                 280                 285
```

```
Val Arg Ser Ser Tyr Arg Ala Gly Arg Leu Tyr Ser Gln Ala Met Ala
    290                 295                 300

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

Ser Gln Gly Ser Thr Asp Gln Glu Ala Thr Thr Leu Leu Ala Lys Tyr
                325                 330                 335

Gly Pro Ser Gln Asp Thr Pro Val Thr Ser Arg
            340                 345
```

<210> 49
<211> 1389
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1089)
<223> gene lipB

<400> 49

```
gaaggtcggc atcacctccg tggccaccga acgcctcggc gaggtcgtct acgcggagct       60

cccgcaggtc ggtgacgccg tcaccgccgg tgaaccgtgc ggcgaggtcg agtccacgaa      120

gtcggtctcc gacctctacg cgccggtcac gggcaccgtc accgaggtca acgacgcggt      180

ccacgacgac tacgccgtga tcaacgacga ccccttcggc gcgggctggc tcttcgccgt      240

cgaggtcgac gaggtcggac cgctcatgac cgccgccgag tacgcggagg ccaacggcgt      300

gtg acc gcc cgg gac cgg tac cct ggt ccc atc atg act gca ccc cgt        348
Val Thr Ala Arg Asp Arg Tyr Pro Gly Pro Ile Met Thr Ala Pro Arg
1               5                   10                  15

gag ccc ttc ttc cct gcg gac cgt tcc atc cgt gcc tcc ggc gag ccc       396
Glu Pro Phe Phe Pro Ala Asp Arg Ser Ile Arg Ala Ser Gly Glu Pro
            20                  25                  30

ccg gag atc cgt tat ctc ggc gtc gtc gac tac cag gag gcc tgg aat       444
Pro Glu Ile Arg Tyr Leu Gly Val Val Asp Tyr Gln Glu Ala Trp Asn
        35                  40                  45

ctg cag gcc gag ctg gcg tcg caa cgc gcg gcc ggg gag atc ggt gac       492
Leu Gln Ala Glu Leu Ala Ser Gln Arg Ala Ala Gly Glu Ile Gly Asp
    50                  55                  60

cag ctc ctc atc ctc gag cac ccg agc gtg tac acc gcc ggc aag cgc       540
Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr Thr Ala Gly Lys Arg
65                  70                  75                  80
```

```
acg cag ccg gag gac cgc ccc acc aac ggc ctg ccg gtc atc gac gtc        588
Thr Gln Pro Glu Asp Arg Pro Thr Asn Gly Leu Pro Val Ile Asp Val
                85                  90                  95

gac cgg ggt ggc cgc atc acc tgg cac ggc gag gga cag ctg gtg gtc        636
Asp Arg Gly Gly Arg Ile Thr Trp His Gly Glu Gly Gln Leu Val Val
            100                 105                 110

tac ccg atc atc aaa ctg gcc gac ccg gtg gac gtc gtg gac tat gtc        684
Tyr Pro Ile Ile Lys Leu Ala Asp Pro Val Asp Val Val Asp Tyr Val
        115                 120                 125

cgc cgc ctc gag gag gcg gtg atc gcg acg gtg cgg gag gtg ggc gtc        732
Arg Arg Leu Glu Glu Ala Val Ile Ala Thr Val Arg Glu Val Gly Val
    130                 135                 140

ggc aat gcg ggt cgc atc gac ggc cgc tcc gga gtc tgg gtc ccc gcc        780
Gly Asn Ala Gly Arg Ile Asp Gly Arg Ser Gly Val Trp Val Pro Ala
145                 150                 155                 160

gac ggg acc cga cgc gac cgg aag gtg gcg gcg ctc ggc atc cgt gtc        828
Asp Gly Thr Arg Arg Asp Arg Lys Val Ala Ala Leu Gly Ile Arg Val
                165                 170                 175

acc cgc ggg gtg acc atg cac ggg ctg agc ctg aac tgc tcg aac acg        876
Thr Arg Gly Val Thr Met His Gly Leu Ser Leu Asn Cys Ser Asn Thr
            180                 185                 190

ctc gag cac tac ggg cac atc gtg gcg tgc ggc atc gac gac gcc gac        924
Leu Glu His Tyr Gly His Ile Val Ala Cys Gly Ile Asp Asp Ala Asp
        195                 200                 205

gtc acc acc ctc agc atg gaa ctg ggg cgc gac gtc agc gtc ggg gag        972
Val Thr Thr Leu Ser Met Glu Leu Gly Arg Asp Val Ser Val Gly Glu
    210                 215                 220

gtc acg gca ccg ctt gtc gac gcc ctc ctg gcc gcc ctc gcc ggt gaa       1020
Val Thr Ala Pro Leu Val Asp Ala Leu Leu Ala Ala Leu Ala Gly Glu
225                 230                 235                 240

ctc gcc gtc gcg gac cac acc ttc gga tcg gcg ccc gat ccg acg aag       1068
Leu Ala Val Ala Asp His Thr Phe Gly Ser Ala Pro Asp Pro Thr Lys
                245                 250                 255

att ccc gcg aaa acg cgc tga cctctaagtt tatccctatc agtagaaaga          1119
Ile Pro Ala Lys Thr Arg
            260

gtatggtggc gttgtgacta tcgcacctga aggacgcaag ctgctccggg tggagaagcg     1179

caatgcgcag acccccatcg agacgaagcc ccgttggatc cgcaacgcgg tgaagaccgg     1239

ccccgagtac gaggacatga agaagaaggt ggcgggcgcc tccctgcaca ccgtctgtca     1299

ggaggcgggc tgccccaaca tccacgagtg ctgggagtcc cgcgaggcga cgtttctcat     1359

cggcggcgcc aactgctccc gccgctgcga                                      1389
```

<210> 50
<211> 262
<212> PRT
<213> Corynebacterium humireducens

<400> 50

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

Glu Pro Phe Phe Pro Ala Asp Arg Ser Ile Arg Ala Ser Gly Glu Pro
20 25 30

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

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

Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr Thr Ala Gly Lys Arg
65 70 75 80

Thr Gln Pro Glu Asp Arg Pro Thr Asn Gly Leu Pro Val Ile Asp Val
85 90 95

Asp Arg Gly Gly Arg Ile Thr Trp His Gly Glu Gly Gln Leu Val Val
100 105 110

Tyr Pro Ile Ile Lys Leu Ala Asp Pro Val Asp Val Val Asp Tyr Val
115 120 125

Arg Arg Leu Glu Glu Ala Val Ile Ala Thr Val Arg Glu Val Gly Val
130 135 140

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

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

Thr Arg Gly Val Thr Met His Gly Leu Ser Leu Asn Cys Ser Asn Thr
180 185 190

Leu Glu His Tyr Gly His Ile Val Ala Cys Gly Ile Asp Asp Ala Asp
195 200 205

Val Thr Thr Leu Ser Met Glu Leu Gly Arg Asp Val Ser Val Gly Glu
210 215 220

Val Thr Ala Pro Leu Val Asp Ala Leu Leu Ala Ala Leu Ala Gly Glu
225 230 235 240

Leu Ala Val Ala Asp His Thr Phe Gly Ser Ala Pro Asp Pro Thr Lys
245 250 255

Ile Pro Ala Lys Thr Arg
260

<210> 51
<211> 2010
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1710)
<223> gene lpd

<400> 51
caactgacat cacagagaga aggcacacat gtccatcttc gagcagatca tcgtcgccat 60

caacaacttc gtcggcccgg gcatccacgc cctgtcctcc gcttcctcca acgccgcact 120

ggccatcggc ctcttctagg tcgaccccgg aagcatctgc ttatcgacgc cccggccccc 180

ggtcggggcg ttcgtcgttg cggcaccaca gtcccgccac cgtcccaccg cccccacggg 240

ggcgggatcc ttttgtgggg ggcggtgaca cgggggaaac ggtcacctat ccttggtggc 300

gtg act gaa cat tat gac gtt gtt gta ctc ggt gcg ggc ccc ggt ggc 348
Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly
1 5 10 15

tac gtc gcc gcc atc cgc gca gcc cag ctc ggc aag aag gtt gct gtc 396
Tyr Val Ala Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val
20 25 30

gtc gag aag cag tac tgg ggc gga gtc tgc ctc aac gtg ggc tgc atc 444
Val Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile
35 40 45

ccc tcg aag gcg ctg atc aag aac gcc gag atc gcc cac atc ttc acg 492
Pro Ser Lys Ala Leu Ile Lys Asn Ala Glu Ile Ala His Ile Phe Thr
50 55 60

cac gag aag aag acg ttc ggc atc aac ggc gac gtc tcc ttc aac tac 540
His Glu Lys Lys Thr Phe Gly Ile Asn Gly Asp Val Ser Phe Asn Tyr
65 70 75 80

gag gac gcc cac aag cgc tcc cgt cag gtg tcg gag aag atc gtc ggc 588

```
Glu Asp Ala His Lys Arg Ser Arg Gln Val Ser Glu Lys Ile Val Gly
                85                  90                  95

ggc gtc cac tac ctg atg aag aag aac aag atc acc gag atc gac ggc      636
Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Thr Glu Ile Asp Gly
            100                 105                 110

ttc gga acc ttc agg gac gcc aag acc atc gag gtc agc gag ggc aag      684
Phe Gly Thr Phe Arg Asp Ala Lys Thr Ile Glu Val Ser Glu Gly Lys
        115                 120                 125

gac gcc ggc aag gtc gtc acc ttc gac gac tgc atc atc gcc acc ggc      732
Asp Ala Gly Lys Val Val Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly
    130                 135                 140

tcc gtg gtc aac agc ctc cgt ggc gtc gag ttc tcc gag aac gtc gtc      780
Ser Val Val Asn Ser Leu Arg Gly Val Glu Phe Ser Glu Asn Val Val
145                 150                 155                 160

tcc tac gag gag cag atc ctc aac ccg gtc gcc ccg gag aag atg gtc      828
Ser Tyr Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Glu Lys Met Val
                165                 170                 175

atc gtc ggt gcc ggc gcc atc ggc atg gag ttc gcc tac gtg ctc tcc      876
Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Ser
            180                 185                 190

aac tac ggc gtc gac gtc acc gtc atc gag tac atg gac cgt gtc ctg      924
Asn Tyr Gly Val Asp Val Thr Val Ile Glu Tyr Met Asp Arg Val Leu
        195                 200                 205

ccg aac gag gac gag gac gtc tcc aag gtc atc gcc aag gcc tac aag      972
Pro Asn Glu Asp Glu Asp Val Ser Lys Val Ile Ala Lys Ala Tyr Lys
    210                 215                 220

aag atg ggc gtc acg ctc ctc ccg ggc cac gcc acc acc gcc gtg cgc     1020
Lys Met Gly Val Thr Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg
225                 230                 235                 240

gac aac ggc gac tcc gtc gag gtc gac tac cag aag aag ggc tcg gac     1068
Asp Asn Gly Asp Ser Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp
                245                 250                 255

aag acc gag acc atc gtc gcc gac cgc gtc ctc gtc tcc gtc ggc ttc     1116
Lys Thr Glu Thr Ile Val Ala Asp Arg Val Leu Val Ser Val Gly Phe
            260                 265                 270

cgc ccg cgt gtc gag ggc ttc ggc ctg gag aac acc ggc gtc gag ctc     1164
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Glu Leu
        275                 280                 285

acc gag cgc ggt gcc atc gcc atc gac gac ttc atg cgc acc aac gtc     1212
Thr Glu Arg Gly Ala Ile Ala Ile Asp Asp Phe Met Arg Thr Asn Val
    290                 295                 300

gag cac atc tac gcc atc ggt gac gtc acc gcc aag ctg cag ctg gcc     1260
Glu His Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala
305                 310                 315                 320
```

```
cac gtc gcc gag gcg cag ggc atc gtc gcc gcc gag acc atc gcc ggc       1308
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly
                325                 330                 335

gcc gag acc cac gag ctg ggc gac tac atg atg atg ccg cgc gcc acc       1356
Ala Glu Thr His Glu Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr
            340                 345                 350

ttc tgt aac ccg cag gtc gcg tcc ttc ggc tac acc gag gcg cag gcc       1404
Phe Cys Asn Pro Gln Val Ala Ser Phe Gly Tyr Thr Glu Ala Gln Ala
        355                 360                 365

aag gag aag tgg ccg gac cgc gag atc aag gtc gcg tcc ttc ccg ttc       1452
Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe
    370                 375                 380

tcc gcg aac ggc aag gcc gtc ggc ctg gcc gag acc gag ggc ttc gcc       1500
Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Glu Gly Phe Ala
385                 390                 395                 400

aag atc gtc gcc gac gcc gag tac ggc gag ctg ctg ggc ggc cac ctg       1548
Lys Ile Val Ala Asp Ala Glu Tyr Gly Glu Leu Leu Gly Gly His Leu
                405                 410                 415

gtc ggc gcc aac gcg tcc gag ctg ctc aac gag ctg gtc ctc gcg cag       1596
Val Gly Ala Asn Ala Ser Glu Leu Leu Asn Glu Leu Val Leu Ala Gln
            420                 425                 430

aac tac gat ctc acc acc gag gag atc agc cgc gcg gtc cac atc cac       1644
Asn Tyr Asp Leu Thr Thr Glu Glu Ile Ser Arg Ala Val His Ile His
        435                 440                 445

ccg acc ctg tcg gag gcc gtc aag gag gcc gca cac ggc atc gac ggc       1692
Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Asp Gly
    450                 455                 460

cac atg atc aac ttc tag tcccccggaa aaaggggcct cccggctggg              1740
His Met Ile Asn Phe
465

aggccccttt tctcatgctt tccgacgccc ccggggcgtc gccaagcgcc tagttgtagg     1800

gcgcgaccga cgaccggtgg gcgtcgatgg tgatctcctc gtggatcggc gggaacgcgc     1860

gctgcgcgca gttctcccgc gggcacacgc ggcagccggc gccgatcggg gtggcgctgg     1920

acaggtcggc gaggttgagt ccctgcgcgt agaccgtgcg gtcggcgtgg cgggcctcgc     1980

agcccaggcc gatggcgaag agcttgccgg                                      2010
```

<210> 52
<211> 469
<212> PRT
<213> Corynebacterium humireducens

<400> 52

```
Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly
```

```
1               5                   10                  15

Tyr Val Ala Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val
            20                  25                  30

Val Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile
        35                  40                  45

Pro Ser Lys Ala Leu Ile Lys Asn Ala Glu Ile Ala His Ile Phe Thr
    50                  55                  60

His Glu Lys Lys Thr Phe Gly Ile Asn Gly Asp Val Ser Phe Asn Tyr
65                  70                  75                  80

Glu Asp Ala His Lys Arg Ser Arg Gln Val Ser Glu Lys Ile Val Gly
                85                  90                  95

Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Thr Glu Ile Asp Gly
            100                 105                 110

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

Asp Ala Gly Lys Val Val Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly
    130                 135                 140

Ser Val Val Asn Ser Leu Arg Gly Val Glu Phe Ser Glu Asn Val Val
145                 150                 155                 160

Ser Tyr Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Glu Lys Met Val
                165                 170                 175

Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Ser
            180                 185                 190

Asn Tyr Gly Val Asp Val Thr Val Ile Glu Tyr Met Asp Arg Val Leu
        195                 200                 205

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

Lys Met Gly Val Thr Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg
225                 230                 235                 240
```

```
Asp Asn Gly Asp Ser Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp
                245                 250                 255

Lys Thr Glu Thr Ile Val Ala Asp Arg Val Leu Val Ser Val Gly Phe
            260                 265                 270

Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Glu Leu
        275                 280                 285

Thr Glu Arg Gly Ala Ile Ala Ile Asp Asp Phe Met Arg Thr Asn Val
    290                 295                 300

Glu His Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala
305                 310                 315                 320

His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly
                325                 330                 335

Ala Glu Thr His Glu Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr
            340                 345                 350

Phe Cys Asn Pro Gln Val Ala Ser Phe Gly Tyr Thr Glu Ala Gln Ala
        355                 360                 365

Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe
    370                 375                 380

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

Lys Ile Val Ala Asp Ala Glu Tyr Gly Glu Leu Leu Gly Gly His Leu
                405                 410                 415

Val Gly Ala Asn Ala Ser Glu Leu Leu Asn Glu Leu Val Leu Ala Gln
            420                 425                 430

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

Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Asp Gly
    450                 455                 460

His Met Ile Asn Phe
465
```

<210> 53
<211> 1866
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1566)
<223> gene lysC

<400> 53
gccggtgccc gcccaccaca ggggacggct gatcgcgttc cagaaggggg aacccttgag 60

ggagccgtcg gcgggggcct cctccgcgat gcggtggcgc accacggttc cccacgcgat 120

ggtgagggcg gaggccagtg cgaacagcac ggccagcaga ttgctgtgca cctcatccac 180

cttagtgaac gggggccttt ccgcagggcc gggacccgcc cactcgacta ctcggacgac 240

cccggctccg ggtacgatga agcagaactt tggcacccca gacgaaaggc ggcctacacg 300

gtg gct ctg atc gtt cag aaa tat gga ggc tcc tcc ctg gag acc gcg 348
Val Ala Leu Ile Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Thr Ala
1 5 10 15

gag cgg atc cgc gct gtc gcc gaa cgg atc gtc gcc acg aaa aag gcc 396
Glu Arg Ile Arg Ala Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
20 25 30

ggc aac gac gtc gtc gtg gtc tgc tcc gcg atg ggc gac acc acg gac 444
Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
35 40 45

gaa ctc ctg gac ctc gcc gcc cag gtg aac ccg gtt ccg ccg gcc cgt 492
Glu Leu Leu Asp Leu Ala Ala Gln Val Asn Pro Val Pro Pro Ala Arg
50 55 60

gag atg gac atg ctg ctc acc gcg ggt gag cgc atc tcc aac gcg ctg 540
Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65 70 75 80

gtc gcg atg gcg atc tcc tcg ctc ggc gcg aag gcg cag tcc ttc acc 588
Val Ala Met Ala Ile Ser Ser Leu Gly Ala Lys Ala Gln Ser Phe Thr
85 90 95

ggc tcg cag gcc ggt gtg ctc acc acc gag cgt cac ggc aac gcc cgc 636
Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
100 105 110

atc gtc gac gtc acc ccg gac cgc gtc cgc gag gcg ctg gac gag ggc 684
Ile Val Asp Val Thr Pro Asp Arg Val Arg Glu Ala Leu Asp Glu Gly
115 120 125

aac atc tgc atc gtc gcc ggt ttc cag ggc atc aac aag gac acc cgc 732
Asn Ile Cys Ile Val Ala Gly Phe Gln Gly Ile Asn Lys Asp Thr Arg
130 135 140

```
gac gtc acc acc ctg ggt cgt ggc ggt tcc gac acc aca gcg gtg gcc        780
Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
145                 150                 155                 160

ctg gcg gcg gcg ctc aac gcc gac gtg tgc gag atc tac tcc gac gtc        828
Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
                165                 170                 175

gac ggc gtc tac acc gcc gat ccg cgc atc gtc ccg aac gcg cag aag        876
Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
            180                 185                 190

ctc gag aag ctc tcc ttc gag gag atg ctc gag ctg gcg gcc gtc ggt        924
Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
        195                 200                 205

tcg aag atc ctg gtg ctg cgt gcc gtc gag tac gca cgt gcc ttc aat        972
Ser Lys Ile Leu Val Leu Arg Ala Val Glu Tyr Ala Arg Ala Phe Asn
    210                 215                 220

gtt ccc ctg cga gtt cgc tcg tct tac agc aat gac acc ggc acc ctg       1020
Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Thr Gly Thr Leu
225                 230                 235                 240

atc gcc ggt tcg atg gag gat atc ccc gtg gaa gaa gca gtt ctc act       1068
Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
                245                 250                 255

ggc gtt gcc acc gac aag tcc gag gcc aag gtc acc atc ctg ggt att       1116
Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Ile Leu Gly Ile
            260                 265                 270

ccc gac aag ccg ggc gag gcg gcc acc gtc ttc cgc gcc gtc gcg gac       1164
Pro Asp Lys Pro Gly Glu Ala Ala Thr Val Phe Arg Ala Val Ala Asp
        275                 280                 285

gcg gag atc aac atc gac atg gtc ctg cag aac gtc tcc tcc ctg gag       1212
Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Leu Glu
    290                 295                 300

gac ggc acg acc gac atc acc ttc acc tgc ccg cgt gcc gac ggc ccc       1260
Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Pro
305                 310                 315                 320

cgc gcc atc gag ctg ctc aag aag atg cag gcg aag agc ggc tgg tcc       1308
Arg Ala Ile Glu Leu Leu Lys Lys Met Gln Ala Lys Ser Gly Trp Ser
                325                 330                 335

aac gtg ctc tac gac gac cag gtg ggc aag gtc tcc ctc gtg ggt gcc       1356
Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
            340                 345                 350

ggc atg aag tcc cac ccg ggc gtc acc gcc gac ttc gcc gag gcg ctc       1404
Gly Met Lys Ser His Pro Gly Val Thr Ala Asp Phe Ala Glu Ala Leu
        355                 360                 365

cgc gac gcc ggc gtg aac atc gag cta atc tcc acc tcg gag atc cgc       1452
Arg Asp Ala Gly Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
    370                 375                 380
```

```
atc tcg gtg ctc acc cgc gag gcc gac ctg gac gcc gcc gcc cgt gcc       1500
Ile Ser Val Leu Thr Arg Glu Ala Asp Leu Asp Ala Ala Ala Arg Ala
385                 390                 395                 400

ctg cac gag aag ttc gag ctc ggc ggc gac gcc gag gcc acc gtc tac       1548
Leu His Glu Lys Phe Glu Leu Gly Gly Asp Ala Glu Ala Thr Val Tyr
                405                 410                 415

gcc ggc acc ggc cgc tag acaatccctt ccacagagga gctttcactc              1596
Ala Gly Thr Gly Arg
            420

tcatgaccac cattgctgtc gtcggtgcca ccggccaggt cggccgcgtg atgcgctcga     1656

tcctggagga gcgcaacttc ccggccgaca aggtccgttt cttcgcgtcc ccgcgctccg     1716

cgggcaccgt catcgagttc cgcggtgagg acatcaccgt cgaggacctc acccagatca     1776

ccccggagtc cgtcaaggac gtcgacatcg ccctcttctc cgccggtggt tccacctccc     1836

gtgagtgggc cccggtcttc gccgaggccg                                      1866
```

<210> 54
<211> 421
<212> PRT
<213> Corynebacterium humireducens

<400> 54

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

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

Asn Ile Cys Ile Val Ala Gly Phe Gln Gly Ile Asn Lys Asp 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

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 Ala Val Glu Tyr Ala Arg Ala Phe Asn
    210                 215                 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Thr 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 Ile Leu Gly Ile
            260                 265                 270

Pro Asp Lys Pro Gly Glu Ala Ala Thr Val Phe Arg Ala Val Ala Asp
        275                 280                 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Leu Glu
    290                 295                 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Pro
305                 310                 315                 320

Arg Ala Ile Glu Leu Leu Lys Lys Met Gln Ala Lys Ser Gly Trp Ser
                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 Asp Phe Ala Glu Ala Leu
        355                 360                 365

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

Ile Ser Val Leu Thr Arg Glu Ala Asp Leu Asp Ala Ala Ala Arg Ala
385                 390                 395                 400

Leu His Glu Lys Phe Glu Leu Gly Gly Asp Ala Glu Ala Thr Val Tyr
                405                 410                 415

Ala Gly Thr Gly Arg
            420
```

<210> 55
<211> 1794
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1494)
<223> gene metB

<400> 55

```
acctccccgg acgggagaga ctgctcggtg tgatcgaccg gctccgcgcg gcgcagcccg       60

gcctgacgac ggtgctggtg acgcatcacg tggaggagat cgcggcgtcg acaagcgatg      120

tcctgctgct caaggagggc cgcgtcctgg cctccggacc cgtcgacgag acgctgacct      180

cggggaacct gtcggcactc tacgacctgc cggtgtcgtt ggagaaggtc cacggacgct      240

ggttcgcgct ctgcatataa ttcccggatg ctgccgggaa agtgaaccgc ttggtctata      300

gtg gcc gac atg acc cac gga ctt tct ggt ttc tcg tct cgt tcc atc          348
Val Ala Asp Met Thr His Gly Leu Ser Gly Phe Ser Ser Arg Ser Ile
1               5                   10                  15

cat gcc gga tac gag cct gac agc ctc tac ggc ccg atc aac acg ccg         396
His Ala Gly Tyr Glu Pro Asp Ser Leu Tyr Gly Pro Ile Asn Thr Pro
            20                  25                  30

atc tac gcg tcg acc acc ttc gcg cag gac ggc ctc aac gag ctg cgc         444
Ile Tyr Ala Ser Thr Thr Phe Ala Gln Asp Gly Leu Asn Glu Leu Arg
        35                  40                  45

ggt ggc ttc gag tac acc cgc tgc ggc aac ccc acg atc gac gcc ctc         492
Gly Gly Phe Glu Tyr Thr Arg Cys Gly Asn Pro Thr Ile Asp Ala Leu
    50                  55                  60
```

```
gaa aag acc gtc gca gcc ctg gaa ggc gca cag tac ggc cgc gcg ttc        540
Glu Lys Thr Val Ala Ala Leu Glu Gly Ala Gln Tyr Gly Arg Ala Phe
65                  70                  75                  80

tcc tcc ggc atg gcc gcc acc gac gtc atc ctg cgt atc ctc ctg cgc        588
Ser Ser Gly Met Ala Ala Thr Asp Val Ile Leu Arg Ile Leu Leu Arg
                85                  90                  95

ccc ggt gac cac ctc atc ctc ggc cac gac gcc tac ggc ggc acc tgg        636
Pro Gly Asp His Leu Ile Leu Gly His Asp Ala Tyr Gly Gly Thr Trp
            100                 105                 110

cgc ctc atc gac cag gcc ttc ggc cag tgg ggc gtc gag tac acc gtc        684
Arg Leu Ile Asp Gln Ala Phe Gly Gln Trp Gly Val Glu Tyr Thr Val
        115                 120                 125

gtc gac acc acc gac gtt gcc gcc gtc gag gcc gcc ctc cgc ccg aac        732
Val Asp Thr Thr Asp Val Ala Ala Val Glu Ala Ala Leu Arg Pro Asn
    130                 135                 140

acc aag ctc atc tgg ctg gag acc ccg acc aac ccg gcc ctg tcc atc        780
Thr Lys Leu Ile Trp Leu Glu Thr Pro Thr Asn Pro Ala Leu Ser Ile
145                 150                 155                 160

acc gac atc gcc gcc atc gcc gcg atc aag cag cag gcc gcc ctc gtc        828
Thr Asp Ile Ala Ala Ile Ala Ala Ile Lys Gln Gln Ala Ala Leu Val
                165                 170                 175

gtg gac aac acc ttc gcg tcc ccg tac ctg cag cag ccg ctc gcc ctc        876
Val Asp Asn Thr Phe Ala Ser Pro Tyr Leu Gln Gln Pro Leu Ala Leu
            180                 185                 190

ggc gcg gac cac gtc ctg cac tcc gcc acc aag tac ctc ggc ggt cac        924
Gly Ala Asp His Val Leu His Ser Ala Thr Lys Tyr Leu Gly Gly His
        195                 200                 205

tcc gac gtc gtc ggc ggc ctc gtg gtg acc aac tgc gcc gag ttc gac        972
Ser Asp Val Val Gly Gly Leu Val Val Thr Asn Cys Ala Glu Phe Asp
    210                 215                 220

gag cag ctc ctc tgg ttc cag ggc ggc gtc ggc ccc atc ccg tcc ccc       1020
Glu Gln Leu Leu Trp Phe Gln Gly Gly Val Gly Pro Ile Pro Ser Pro
225                 230                 235                 240

ttc gac gcc tac ctc acc gcc cgc ggc atc aag acc ctg gcc gtg cgc       1068
Phe Asp Ala Tyr Leu Thr Ala Arg Gly Ile Lys Thr Leu Ala Val Arg
                245                 250                 255

atg gag cgc cac tgc gac aac gcc gag gcc atc gcc gcg cac ctc gag       1116
Met Glu Arg His Cys Asp Asn Ala Glu Ala Ile Ala Ala His Leu Glu
            260                 265                 270

gcc tcc gac cag gtc gcg acc gtg ctc tac ccc ggc ctc gag tcc cac       1164
Ala Ser Asp Gln Val Ala Thr Val Leu Tyr Pro Gly Leu Glu Ser His
        275                 280                 285

ccg ggc cac gag gtg gcc aag cgc cag atg aag cgc ttc ggc ggc atg       1212
Pro Gly His Glu Val Ala Lys Arg Gln Met Lys Arg Phe Gly Gly Met
    290                 295                 300
```

```
atc tcc gtg cgc ttc cgc tcc gag gag gcc gcc cgc gtc ttc tgc ctg       1260
Ile Ser Val Arg Phe Arg Ser Glu Glu Ala Ala Arg Val Phe Cys Leu
305                 310                 315                 320

aac acc cga ctg atc tgt ctg gcc gag tct ctc ggc ggc gtc gag tcg       1308
Asn Thr Arg Leu Ile Cys Leu Ala Glu Ser Leu Gly Gly Val Glu Ser
                325                 330                 335

ctc gtc gag cac ccg gcc acc atg acc cac cag tcc gcc acc ggc tcc       1356
Leu Val Glu His Pro Ala Thr Met Thr His Gln Ser Ala Thr Gly Ser
            340                 345                 350

cag ctg gag gtc ccg cgt gac ctg gtg cgc atc tcc atc ggc atc gag       1404
Gln Leu Glu Val Pro Arg Asp Leu Val Arg Ile Ser Ile Gly Ile Glu
        355                 360                 365

gac gtc gag gac ctc atc gcg gac atc gac gtc gcc ctc cag gcc gtc       1452
Asp Val Glu Asp Leu Ile Ala Asp Ile Asp Val Ala Leu Gln Ala Val
    370                 375                 380

gcg gcc gcg gag gcg gcc gct gag gcc tcc gtc gac gcc tga               1494
Ala Ala Ala Glu Ala Ala Ala Glu Ala Ser Val Asp Ala
385                 390                 395

gtgatgaccg ccccgcacac ggtcgagagg acatgtgcgg gacggctcct cccgggcggc     1554

gcagtgtcga gacgggtact cctcccgaac atgtgagccc gcccctggct ccggcccccc     1614

cagggcagcc ggatcgccgc cacaccgacc accatgagcg ccaggcccac cgcctggacc     1674

agggtggtcg gtttcctctt cgcccccagc agcccgaagt ggtcgatgag gaggctgccg     1734

accatcatgc cgagcaggat cgtcatgacg gtcagacccg tgccgatgac gggggagagg     1794
```

<210> 56
<211> 397
<212> PRT
<213> Corynebacterium humireducens

<400> 56

```
Val Ala Asp Met Thr His Gly Leu Ser Gly Phe Ser Ser Arg Ser Ile
1               5                   10                  15

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

Ile Tyr Ala Ser Thr Thr Phe Ala Gln Asp Gly Leu Asn Glu Leu Arg
        35                  40                  45

Gly Gly Phe Glu Tyr Thr Arg Cys Gly Asn Pro Thr Ile Asp Ala Leu
    50                  55                  60
```

```
Glu Lys Thr Val Ala Ala Leu Glu Gly Ala Gln Tyr Gly Arg Ala Phe
65                  70                  75                  80

Ser Ser Gly Met Ala Ala Thr Asp Val Ile Leu Arg Ile Leu Leu Arg
                85                  90                  95

Pro Gly Asp His Leu Ile Leu Gly His Asp Ala Tyr Gly Gly Thr Trp
            100                 105                 110

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

Val Asp Thr Thr Asp Val Ala Ala Val Glu Ala Ala Leu Arg Pro Asn
    130                 135                 140

Thr Lys Leu Ile Trp Leu Glu Thr Pro Thr Asn Pro Ala Leu Ser Ile
145                 150                 155                 160

Thr Asp Ile Ala Ala Ile Ala Ala Ile Lys Gln Gln Ala Ala Leu Val
                165                 170                 175

Val Asp Asn Thr Phe Ala Ser Pro Tyr Leu Gln Gln Pro Leu Ala Leu
            180                 185                 190

Gly Ala Asp His Val Leu His Ser Ala Thr Lys Tyr Leu Gly Gly His
        195                 200                 205

Ser Asp Val Val Gly Gly Leu Val Val Thr Asn Cys Ala Glu Phe Asp
    210                 215                 220

Glu Gln Leu Leu Trp Phe Gln Gly Gly Val Gly Pro Ile Pro Ser Pro
225                 230                 235                 240

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

Met Glu Arg His Cys Asp Asn Ala Glu Ala Ile Ala Ala His Leu Glu
            260                 265                 270

Ala Ser Asp Gln Val Ala Thr Val Leu Tyr Pro Gly Leu Glu Ser His
        275                 280                 285

Pro Gly His Glu Val Ala Lys Arg Gln Met Lys Arg Phe Gly Gly Met
    290                 295                 300
```

```
Ile Ser Val Arg Phe Arg Ser Glu Glu Ala Ala Arg Val Phe Cys Leu
305                 310                 315                 320

Asn Thr Arg Leu Ile Cys Leu Ala Glu Ser Leu Gly Gly Val Glu Ser
                325                 330                 335

Leu Val Glu His Pro Ala Thr Met Thr His Gln Ser Ala Thr Gly Ser
            340                 345                 350

Gln Leu Glu Val Pro Arg Asp Leu Val Arg Ile Ser Ile Gly Ile Glu
        355                 360                 365

Asp Val Glu Asp Leu Ile Ala Asp Ile Asp Val Ala Leu Gln Ala Val
    370                 375                 380

Ala Ala Ala Glu Ala Ala Ala Glu Ala Ser Val Asp Ala
385                 390                 395
```

<210> 57
<211> 1581
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1281)
<223> gene metF

<400> 57

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ggttcacggt gtgctccttg ttcagtgggt cattctccct cccagactag cggcgaagcc       60

tcgatcaggg cgggtttccg gatgtgtgga acctggggaa atgaaactga accgcttggt      120

ccatttttgt ccgaaaatcg gccctcgggg gtgaattata ttcatgctag ggtggggtta      180

tcgccgcagg tcacgcggca aaccggaaat agcaccttta ggaaaattac ccgccgcaaa      240

ccgttggctt gctacattca cagccacttg cccaacggga tgtctgaagg aggaaaacac      300

atg aac gca aac gcg ccg cag tac agc gcc aag cgt cga ttc tcc gcc         348
Met Asn Ala Asn Ala Pro Gln Tyr Ser Ala Lys Arg Arg Phe Ser Ala
1               5                   10                  15

tcc gcc ccg ttg gac acc ttc gat ccc gag gaa tgg cgc cag gcc ccc         396
Ser Ala Pro Leu Asp Thr Phe Asp Pro Glu Glu Trp Arg Gln Ala Pro
            20                  25                  30

gtg ccg gag cgc acc tcc ctc tcc ttc gag gtc atg ccc ccg cgc cac         444
Val Pro Glu Arg Thr Ser Leu Ser Phe Glu Val Met Pro Pro Arg His
        35                  40                  45
```

```
gac gcg gac gag gcc aag atc gac gaa ctg ctg gac acg ctg cag tcc        492
Asp Ala Asp Glu Ala Lys Ile Asp Glu Leu Leu Asp Thr Leu Gln Ser
    50                  55                  60

tac aac ccg gac tac atc tcc gtc acc agc tcc cgg aac tcc ggc tgg        540
Tyr Asn Pro Asp Tyr Ile Ser Val Thr Ser Ser Arg Asn Ser Gly Trp
65                  70                  75                  80

ctc gag ggc acc gcg aag ttc atc gcg aag atc agc gcc cag acc cgc        588
Leu Glu Gly Thr Ala Lys Phe Ile Ala Lys Ile Ser Ala Gln Thr Arg
                85                  90                  95

atc ccg acg gtc gcc cac ctg gcc tgc acc gcc ggc acc cgc gag gag        636
Ile Pro Thr Val Ala His Leu Ala Cys Thr Ala Gly Thr Arg Glu Glu
            100                 105                 110

ctc atc ggc tgg atc aac cgg ctc atg gac tcc ggc gtc cgc ggc ctg        684
Leu Ile Gly Trp Ile Asn Arg Leu Met Asp Ser Gly Val Arg Gly Leu
        115                 120                 125

ctc gcc ctc cgc ggc gac ctc gca gaa gga cag acc ggt atg cct gag        732
Leu Ala Leu Arg Gly Asp Leu Ala Glu Gly Gln Thr Gly Met Pro Glu
    130                 135                 140

ggt tac ctc aag cac gcg acc gac ctc atc aac ctc atc cag gag atc        780
Gly Tyr Leu Lys His Ala Thr Asp Leu Ile Asn Leu Ile Gln Glu Ile
145                 150                 155                 160

gag gag gag cag gtc gcc cgc ttc ggc gcc ggc cgc ctc gcc atc ggc        828
Glu Glu Glu Gln Val Ala Arg Phe Gly Ala Gly Arg Leu Ala Ile Gly
                165                 170                 175

gtc gcc gcc tac ccc agc ggc cac gag gag tcg acc agc cgc gac gag        876
Val Ala Ala Tyr Pro Ser Gly His Glu Glu Ser Thr Ser Arg Asp Glu
            180                 185                 190

gac atc gac gtc ctc ctg gcc aag cag cgc ctg ggc gcc gac ttc gcc        924
Asp Ile Asp Val Leu Leu Ala Lys Gln Arg Leu Gly Ala Asp Phe Ala
        195                 200                 205

atc acc cag ctc ttc ttc gac gcc gag gac tac ctc cgc ttc ctg gag        972
Ile Thr Gln Leu Phe Phe Asp Ala Glu Asp Tyr Leu Arg Phe Leu Glu
    210                 215                 220

cgc gcc cgc ctg gca ggc gtc cgc atc ccg ctc atc ccc ggc atc atg       1020
Arg Ala Arg Leu Ala Gly Val Arg Ile Pro Leu Ile Pro Gly Ile Met
225                 230                 235                 240

ccg atg acg agc gtc gcg aga cta cgt cga atg gga cag ctc tcc ggc       1068
Pro Met Thr Ser Val Ala Arg Leu Arg Arg Met Gly Gln Leu Ser Gly
                245                 250                 255

ctt acc gtc ccc gac cgg ctg atc agc cga ctg gag gcg gca ggc ccg       1116
Leu Thr Val Pro Asp Arg Leu Ile Ser Arg Leu Glu Ala Ala Gly Pro
            260                 265                 270

gag agc gag tac cag acg ggc ctc gac ctc acg gcc gag ctc gcg cag       1164
Glu Ser Glu Tyr Gln Thr Gly Leu Asp Leu Thr Ala Glu Leu Ala Gln
        275                 280                 285
```

```
acc atc ctg gac gcc ggt gcc ggg ggg atg cac gtg tac acg ttc aac      1212
Thr Ile Leu Asp Ala Gly Ala Gly Gly Met His Val Tyr Thr Phe Asn
    290                 295                 300

cgg ccg gac acc acc acc gaa ctg ctg gac cgc atc ggc atc acc ccc      1260
Arg Pro Asp Thr Thr Thr Glu Leu Leu Asp Arg Ile Gly Ile Thr Pro
305                 310                 315                 320

gac cct cgg gtt agg gag tga ggcgggagac cgccgccgct gcatctcatg          1311
Asp Pro Arg Val Arg Glu
                325

ttgatagcga cctgctgcac gcaccgggag cccccgaagc agaccaggtt gtacacccaa     1371

gattttccga aaggcctccc ttttcatgtc ttccaccgct ttccccacct tcaccatcga     1431

gggctacccg cgcgtcggcg ccaaccgcga gctcaagaag gccctcgagt ccttctgggc     1491

cggccgcatc gacgaggaga ccttcatctc ctccgcgcac tccatccgcc tggagaacta     1551

cgcccgtctg cgtgacctcg gcctggacca                                      1581
```

<210> 58
<211> 326
<212> PRT
<213> Corynebacterium humireducens

<400> 58

```
Met Asn Ala Asn Ala Pro Gln Tyr Ser Ala Lys Arg Arg Phe Ser Ala
1               5                   10                  15

Ser Ala Pro Leu Asp Thr Phe Asp Pro Glu Glu Trp Arg Gln Ala Pro
            20                  25                  30

Val Pro Glu Arg Thr Ser Leu Ser Phe Glu Val Met Pro Pro Arg His
        35                  40                  45

Asp Ala Asp Glu Ala Lys Ile Asp Glu Leu Leu Asp Thr Leu Gln Ser
    50                  55                  60

Tyr Asn Pro Asp Tyr Ile Ser Val Thr Ser Ser Arg Asn Ser Gly Trp
65                  70                  75                  80

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

Ile Pro Thr Val Ala His Leu Ala Cys Thr Ala Gly Thr Arg Glu Glu
            100                 105                 110
```

```
Leu Ile Gly Trp Ile Asn Arg Leu Met Asp Ser Gly Val Arg Gly Leu
        115                 120                 125

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

Gly Tyr Leu Lys His Ala Thr Asp Leu Ile Asn Leu Ile Gln Glu Ile
145                 150                 155                 160

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

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

Asp Ile Asp Val Leu Leu Ala Lys Gln Arg Leu Gly Ala Asp Phe Ala
        195                 200                 205

Ile Thr Gln Leu Phe Phe Asp Ala Glu Asp Tyr Leu Arg Phe Leu Glu
    210                 215                 220

Arg Ala Arg Leu Ala Gly Val Arg Ile Pro Leu Ile Pro Gly Ile Met
225                 230                 235                 240

Pro Met Thr Ser Val Ala Arg Leu Arg Arg Met Gly Gln Leu Ser Gly
                245                 250                 255

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

Glu Ser Glu Tyr Gln Thr Gly Leu Asp Leu Thr Ala Glu Leu Ala Gln
        275                 280                 285

Thr Ile Leu Asp Ala Gly Ala Gly Gly Met His Val Tyr Thr Phe Asn
    290                 295                 300

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

Asp Pro Arg Val Arg Glu
                325
```

<210> 59
<211> 1695
<212> DNA

<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1395)
<223> gene metX

<400> 59

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tccgcctgtc ggtgggcatc gagaagatca ccgacatcat cgccgacctg gagaacgccc       60

tgaacgccgt ctaagagaca gcttggtcca catacattca cgtcccccac ctggggagac      120

gtggatgtcg gcgacccttc tgtttgcgtg gtcacgcgcg gaaacctacc ctttcaggag      180

accgtgccga atgtaggcac cgaggacgac aaactgtccc ccgggacccc caccagacca      240

ctaggacggt gagtttccat ctctaccctc aacctggccc cccagggcga actcgcgcag      300

gtg cgc atc ggt gat ctc cac acg gag gcc ggt ggc gtc atc aac gac         348
Val Arg Ile Gly Asp Leu His Thr Glu Ala Gly Gly Val Ile Asn Asp
1               5                   10                  15

gtc acc atc gcc tac cgc cgc tgg ggc gag ttc cgg gga gac ccg gac         396
Val Thr Ile Ala Tyr Arg Arg Trp Gly Glu Phe Arg Gly Asp Pro Asp
            20                  25                  30

ggg atg aac aac ctc gtg ctc atc gaa cac gcc ctc acc ggc gac acc         444
Gly Met Asn Asn Leu Val Leu Ile Glu His Ala Leu Thr Gly Asp Thr
        35                  40                  45

aac gtc gcc gac tgg tgg tgt gac ctg ctc ggc ccc ggc cgg gcg ctc         492
Asn Val Ala Asp Trp Trp Cys Asp Leu Leu Gly Pro Gly Arg Ala Leu
    50                  55                  60

gac acc gac gcg tgg tgc atc gtg tgc acc aac gtc atc ggc ggc tgc         540
Asp Thr Asp Ala Trp Cys Ile Val Cys Thr Asn Val Ile Gly Gly Cys
65                  70                  75                  80

cag ggc tcg acc ggc ccc gcc tcc gaa cac ccc gac ggc ggc cgc tgg         588
Gln Gly Ser Thr Gly Pro Ala Ser Glu His Pro Asp Gly Gly Arg Trp
                85                  90                  95

gga tcc cgc ttc ccg gcg atc tcc atc cgc gac cag gtc acc gcg gag         636
Gly Ser Arg Phe Pro Ala Ile Ser Ile Arg Asp Gln Val Thr Ala Glu
            100                 105                 110

aag cag ttc ctc gac gcc ctc ggc gtc tcc cgc atc cac gcc gtc ctc         684
Lys Gln Phe Leu Asp Ala Leu Gly Val Ser Arg Ile His Ala Val Leu
        115                 120                 125

ggc ggt tcc atg ggc ggt gcc cgc acc ctc gag tgg gcg atg atg tac         732
Gly Gly Ser Met Gly Gly Ala Arg Thr Leu Glu Trp Ala Met Met Tyr
    130                 135                 140

ccg gac aag gtc aac gcc gtg tgc gtc atc gcc gtc tcc gcc cgg gcc         780
Pro Asp Lys Val Asn Ala Val Cys Val Ile Ala Val Ser Ala Arg Ala
145                 150                 155                 160
```

```
agc gcc tgg cag atc ggc atc cag tcc gcg cag atc tcc gcc atc gag        828
Ser Ala Trp Gln Ile Gly Ile Gln Ser Ala Gln Ile Ser Ala Ile Glu
                165                 170                 175

cgt gac ccc gcc tgg cag ggc ggc gac ttc tac gac acc ggt gcc tcc        876
Arg Asp Pro Ala Trp Gln Gly Gly Asp Phe Tyr Asp Thr Gly Ala Ser
            180                 185                 190

ccc gac gcc ggc ctc gcc gcc gcc cgc cgc atc gcc cac ctc acc tac        924
Pro Asp Ala Gly Leu Ala Ala Ala Arg Arg Ile Ala His Leu Thr Tyr
        195                 200                 205

cgc ggt gag cag gag ctc gac gag cgt ttc ggc gcc gcc cgc cag gac        972
Arg Gly Glu Gln Glu Leu Asp Glu Arg Phe Gly Ala Ala Arg Gln Asp
    210                 215                 220

ggg gag aac ccg ctg ggc acc ttc cgg gac ccc gcc cag cgt ttc gcc       1020
Gly Glu Asn Pro Leu Gly Thr Phe Arg Asp Pro Ala Gln Arg Phe Ala
225                 230                 235                 240

gtc gag agc tac ctg cag tac cac ggc cgc aag ctg gtc gag cgt ttc       1068
Val Glu Ser Tyr Leu Gln Tyr His Gly Arg Lys Leu Val Glu Arg Phe
                245                 250                 255

gac gcc ggc agc tac gtc acc ctc acc gag gcc ctc aac cgg cac aac       1116
Asp Ala Gly Ser Tyr Val Thr Leu Thr Glu Ala Leu Asn Arg His Asn
            260                 265                 270

atc ggc cgg ggc cgc ggg ggc ctg aac aag gcg ctg gcg gcc tgc acg       1164
Ile Gly Arg Gly Arg Gly Gly Leu Asn Lys Ala Leu Ala Ala Cys Thr
        275                 280                 285

gtg ccg acg atg atc gtc ggc gtc gac acg gac atc ctg tac ccg tac       1212
Val Pro Thr Met Ile Val Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr
    290                 295                 300

cac cag cag gag cac ctc tcc cgc aac gtc ggt gag ctg atg ggc atc       1260
His Gln Gln Glu His Leu Ser Arg Asn Val Gly Glu Leu Met Gly Ile
305                 310                 315                 320

gcc cgg atc tcc tcc cct gtc ggc cac gac gcc ttc ctg gcg gag ttc       1308
Ala Arg Ile Ser Ser Pro Val Gly His Asp Ala Phe Leu Ala Glu Phe
                325                 330                 335

cgg cag atg gac cgc atc ctc cgg cgc ttc ttc gtc ctc agc gtg ctg       1356
Arg Gln Met Asp Arg Ile Leu Arg Arg Phe Phe Val Leu Ser Val Leu
            340                 345                 350

gac gag gac gcc cag gag gac gac ggc tac ctc atc tag caacccgaac       1405
Asp Glu Asp Ala Gln Glu Asp Asp Gly Tyr Leu Ile
        355                 360

gtgccgcgag ggggctccca gccatcggtt gggagccccc tcgcggcacg tttcgcgggg     1465

tcacgagccc agcgcgtcca ccgaggccgc caggaacgcc atcgtccccc cgaggacggt     1525

gcagaaggcg gcgtcgaaac gccgggagcg cacggcgaac accccgacga tgcgggagtc     1585

gcacgcgtag cgcaccacgg ccagccacat gagtgagacg ccgagcacga acgtcgcgcg     1645
```

gcgccagtgc tcggtgagcg cgaagacgct cgccacgacc acgccgagca 1695

<210> 60
<211> 364
<212> PRT
<213> Corynebacterium humireducens

<400> 60

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

Val Thr Ile Ala Tyr Arg Arg Trp Gly Glu Phe Arg Gly Asp Pro Asp
20 25 30

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

Asn Val Ala Asp Trp Trp Cys Asp Leu Leu Gly Pro Gly Arg Ala Leu
50 55 60

Asp Thr Asp Ala Trp Cys Ile Val Cys Thr Asn Val Ile Gly Gly Cys
65 70 75 80

Gln Gly Ser Thr Gly Pro Ala Ser Glu His Pro Asp Gly Gly Arg Trp
85 90 95

Gly Ser Arg Phe Pro Ala Ile Ser Ile Arg Asp Gln Val Thr Ala Glu
100 105 110

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

Gly Gly Ser Met Gly Gly Ala Arg Thr Leu Glu Trp Ala Met Met Tyr
130 135 140

Pro Asp Lys Val Asn Ala Val Cys Val Ile Ala Val Ser Ala Arg Ala
145 150 155 160

Ser Ala Trp Gln Ile Gly Ile Gln Ser Ala Gln Ile Ser Ala Ile Glu
165 170 175

Arg Asp Pro Ala Trp Gln Gly Gly Asp Phe Tyr Asp Thr Gly Ala Ser
180 185 190

```
Pro Asp Ala Gly Leu Ala Ala Ala Arg Arg Ile Ala His Leu Thr Tyr
        195                 200                 205

Arg Gly Glu Gln Glu Leu Asp Glu Arg Phe Gly Ala Ala Arg Gln Asp
    210                 215                 220

Gly Glu Asn Pro Leu Gly Thr Phe Arg Asp Pro Ala Gln Arg Phe Ala
225                 230                 235                 240

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

Asp Ala Gly Ser Tyr Val Thr Leu Thr Glu Ala Leu Asn Arg His Asn
            260                 265                 270

Ile Gly Arg Gly Arg Gly Gly Leu Asn Lys Ala Leu Ala Ala Cys Thr
        275                 280                 285

Val Pro Thr Met Ile Val Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr
    290                 295                 300

His Gln Gln Glu His Leu Ser Arg Asn Val Gly Glu Leu Met Gly Ile
305                 310                 315                 320

Ala Arg Ile Ser Ser Pro Val Gly His Asp Ala Phe Leu Ala Glu Phe
                325                 330                 335

Arg Gln Met Asp Arg Ile Leu Arg Arg Phe Phe Val Leu Ser Val Leu
            340                 345                 350

Asp Glu Asp Ala Gln Glu Asp Asp Gly Tyr Leu Ile
        355                 360
```

<210> 61
<211> 1872
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1572)
<223> gene metY

<400> 61
ccaagttgga gcggcgcggc atcaagttcg cgatggcgcg cgtgaagcag gacctctacc 60

gacgcctcga gcccaccggc ttcatcgacc acgtcggccg ggactacatt ttcgagacgc 120

```
tgcccaccgg ggtgcgggcc tacgccaacc gctaccaggc ccggcacgga cgctggccgg      180

acggggtgcc gcgcgaggtg gtcgagccct gacgcggacg gggtggaccc cgagctcatg      240

cccgcggcgg gtacatttgc attcaggtat tccgtcgccc cgaaaggtgt ctgcatcacc      300

atg cac aac cag acc aag ctc atc cac tcc ggc tat gtc ccg ggc aac         348
Met His Asn Gln Thr Lys Leu Ile His Ser Gly Tyr Val Pro Gly Asn
1               5                   10                  15

aag gac ccc cga cag gtg ccg atc gtg cag tcc acg acc tac acc ttc         396
Lys Asp Pro Arg Gln Val Pro Ile Val Gln Ser Thr Thr Tyr Thr Phe
            20                  25                  30

gac tcc tcc gag gac atc gcg gcg gtg ttc gat gag ccg acc cac gcg         444
Asp Ser Ser Glu Asp Ile Ala Ala Val Phe Asp Glu Pro Thr His Ala
        35                  40                  45

ctg atc tac tcc cgc ttc gcc aac ccg acc gtc atg gcg gtg gag acg         492
Leu Ile Tyr Ser Arg Phe Ala Asn Pro Thr Val Met Ala Val Glu Thr
    50                  55                  60

aag atc gcc gag ctg gag ggc ggt gcc gcg gcg atg gcg acc tcc tcc         540
Lys Ile Ala Glu Leu Glu Gly Gly Ala Ala Ala Met Ala Thr Ser Ser
65                  70                  75                  80

ggc cag gcc gcg acc gcg ctg tcg atc atg aac gtc tgc tcg gcg ggt         588
Gly Gln Ala Ala Thr Ala Leu Ser Ile Met Asn Val Cys Ser Ala Gly
                85                  90                  95

gac tcc ttc gtg gcc tcc tcc gag atc tac ggc ggc acc ctc aac ctc         636
Asp Ser Phe Val Ala Ser Ser Glu Ile Tyr Gly Gly Thr Leu Asn Leu
            100                 105                 110

ttc cac acg acg ctc aag cgt ttc ggc atc gag gtc atc tac gtc gac         684
Phe His Thr Thr Leu Lys Arg Phe Gly Ile Glu Val Ile Tyr Val Asp
        115                 120                 125

cag gac gcc tcc gag gag gag atc gcc gcc gcc ttc aag ccg aac acg         732
Gln Asp Ala Ser Glu Glu Glu Ile Ala Ala Ala Phe Lys Pro Asn Thr
    130                 135                 140

aag gca ctg ttc ggt gag acc atc ggc aac ccg gcg atg agc gtg ctg         780
Lys Ala Leu Phe Gly Glu Thr Ile Gly Asn Pro Ala Met Ser Val Leu
145                 150                 155                 160

gac atc gag aag ttc gcc cgc atc gcc cac ggt cag ggc gtg ccg ctc         828
Asp Ile Glu Lys Phe Ala Arg Ile Ala His Gly Gln Gly Val Pro Leu
                165                 170                 175

atc gtc gac tcc acc ttc gcc acc ccg atg ctg tgc cgc ccc atc gag         876
Ile Val Asp Ser Thr Phe Ala Thr Pro Met Leu Cys Arg Pro Ile Glu
            180                 185                 190

cac ggc gcc gac gtg gtc atc cac tcc acc tcc aag tac atg gac ggc         924
His Gly Ala Asp Val Val Ile His Ser Thr Ser Lys Tyr Met Asp Gly
        195                 200                 205
```

```
cac gcg ctg cag gtc ggc ggc atg atc gtc gac gcc ggc acc ttc gac        972
His Ala Leu Gln Val Gly Gly Met Ile Val Asp Ala Gly Thr Phe Asp
    210                 215                 220

tac acc aac ggc aag ttc ccg ggc ttc acc gag ccg gac gag tcc tac       1020
Tyr Thr Asn Gly Lys Phe Pro Gly Phe Thr Glu Pro Asp Glu Ser Tyr
225                 230                 235                 240

cac ggc gtc gtg tac acc aag gac tac gcc gtt gcc ccc ttc atc atc       1068
His Gly Val Val Tyr Thr Lys Asp Tyr Ala Val Ala Pro Phe Ile Ile
                245                 250                 255

aag gcc cgc atg cag ctg cag cgt gat ttc ggc gcc tac ccg tcc gcg       1116
Lys Ala Arg Met Gln Leu Gln Arg Asp Phe Gly Ala Tyr Pro Ser Ala
            260                 265                 270

cac tcc gcc ttc atg ctc aac cac tcc ctc gag agc ctc gac gtg cgc       1164
His Ser Ala Phe Met Leu Asn His Ser Leu Glu Ser Leu Asp Val Arg
        275                 280                 285

atg cag cgc cac tgc gag aac gca cag agg gtc gcc gag tac ctc gag       1212
Met Gln Arg His Cys Glu Asn Ala Gln Arg Val Ala Glu Tyr Leu Glu
    290                 295                 300

ggc cgc aag gac gtg ctt gtc gac gtc cgc tac ccc gga ctc gac tcc       1260
Gly Arg Lys Asp Val Leu Val Asp Val Arg Tyr Pro Gly Leu Asp Ser
305                 310                 315                 320

tcc ccg tac cgc gag ctg gcg aag aag tac ctc agc ggc aac tcc ggc       1308
Ser Pro Tyr Arg Glu Leu Ala Lys Lys Tyr Leu Ser Gly Asn Ser Gly
                325                 330                 335

gtg ctg tgc atc gac atc aag ggg ggc cgc gag gcc ggc gtg aag ttc       1356
Val Leu Cys Ile Asp Ile Lys Gly Gly Arg Glu Ala Gly Val Lys Phe
            340                 345                 350

atg gac gcc ctc gag ctg gtc acc cgc cag gtg cac gtc gcc gac gcc       1404
Met Asp Ala Leu Glu Leu Val Thr Arg Gln Val His Val Ala Asp Ala
        355                 360                 365

cgt tcc tgc gtg ctg cac ccg gcg tcg acc acg cac cgc cag gtg ccg       1452
Arg Ser Cys Val Leu His Pro Ala Ser Thr Thr His Arg Gln Val Pro
    370                 375                 380

gac gag cag ctg ccg tcc gtc ggc atc acc ccg ggt ctg gtg cgc atc       1500
Asp Glu Gln Leu Pro Ser Val Gly Ile Thr Pro Gly Leu Val Arg Ile
385                 390                 395                 400

tcc gtc ggc ctg gag aac gtc gac gac atc atc gcc gac atc gag cag       1548
Ser Val Gly Leu Glu Asn Val Asp Asp Ile Ile Ala Asp Ile Glu Gln
                405                 410                 415

gcc ctg gag aag tcc cag gcc taa gttcgcttat cgacgccgcc ccggtccctc      1602
Ala Leu Glu Lys Ser Gln Ala
            420

atgtgggacc ggggcggtgg ctttcggggg atggctgcac tttcaccccg actgggtgcg     1662

tgtcgacaac ggggtttggg ggacagcgat gagggtataa gtgcagacac ggagaaggcc     1722
```

cggacactgt gggaggtgtc cgggccttgg gggcgtcgat aagcggtgtc tctagaactc 1782

cggcagcggc agaacagtga gggagaacat cgcgacgatg gccatgacca gcgggatggc 1842

gatcatgatc ggggcggcga tagccgggtt 1872

<210> 62
<211> 423
<212> PRT
<213> Corynebacterium humireducens

<400> 62

Met His Asn Gln Thr Lys Leu Ile His Ser Gly Tyr Val Pro Gly Asn
1 5 10 15

Lys Asp Pro Arg Gln Val Pro Ile Val Gln Ser Thr Thr Tyr Thr Phe
20 25 30

Asp Ser Ser Glu Asp Ile Ala Ala Val Phe Asp Glu Pro Thr His Ala
35 40 45

Leu Ile Tyr Ser Arg Phe Ala Asn Pro Thr Val Met Ala Val Glu Thr
50 55 60

Lys Ile Ala Glu Leu Glu Gly Gly Ala Ala Ala Met Ala Thr Ser Ser
65 70 75 80

Gly Gln Ala Ala Thr Ala Leu Ser Ile Met Asn Val Cys Ser Ala Gly
85 90 95

Asp Ser Phe Val Ala Ser Ser Glu Ile Tyr Gly Gly Thr Leu Asn Leu
100 105 110

Phe His Thr Thr Leu Lys Arg Phe Gly Ile Glu Val Ile Tyr Val Asp
115 120 125

Gln Asp Ala Ser Glu Glu Glu Ile Ala Ala Ala Phe Lys Pro Asn Thr
130 135 140

Lys Ala Leu Phe Gly Glu Thr Ile Gly Asn Pro Ala Met Ser Val Leu
145 150 155 160

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

Ile Val Asp Ser Thr Phe Ala Thr Pro Met Leu Cys Arg Pro Ile Glu
180 185 190

His Gly Ala Asp Val Val Ile His Ser Thr Ser Lys Tyr Met Asp Gly
195 200 205

His Ala Leu Gln Val Gly Gly Met Ile Val Asp Ala Gly Thr Phe Asp
210 215 220

Tyr Thr Asn Gly Lys Phe Pro Gly Phe Thr Glu Pro Asp Glu Ser Tyr
225 230 235 240

His Gly Val Val Tyr Thr Lys Asp Tyr Ala Val Ala Pro Phe Ile Ile
245 250 255

Lys Ala Arg Met Gln Leu Gln Arg Asp Phe Gly Ala Tyr Pro Ser Ala
260 265 270

His Ser Ala Phe Met Leu Asn His Ser Leu Glu Ser Leu Asp Val Arg
275 280 285

Met Gln Arg His Cys Glu Asn Ala Gln Arg Val Ala Glu Tyr Leu Glu
290 295 300

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

Ser Pro Tyr Arg Glu Leu Ala Lys Lys Tyr Leu Ser Gly Asn Ser Gly
325 330 335

Val Leu Cys Ile Asp Ile Lys Gly Gly Arg Glu Ala Gly Val Lys Phe
340 345 350

Met Asp Ala Leu Glu Leu Val Thr Arg Gln Val His Val Ala Asp Ala
355 360 365

Arg Ser Cys Val Leu His Pro Ala Ser Thr Thr His Arg Gln Val Pro
370 375 380

Asp Glu Gln Leu Pro Ser Val Gly Ile Thr Pro Gly Leu Val Arg Ile
385 390 395 400

Ser Val Gly Leu Glu Asn Val Asp Asp Ile Ile Ala Asp Ile Glu Gln
405 410 415

```
Ala Leu Glu Lys Ser Gln Ala
            420

<210>  63
<211>  4014
<212>  DNA
<213>  Corynebacterium humireducens

<220>
<221>  CDS
<222>  (301)..(3714)
<223>  gene pyc

<400>  63
cggcaccgga ccaccgcgac gcccacggca ctgcccacac attggggtgg tgcgcgtggg       60

tttcgctgtt cggaacacct gtcggcccat tccgcagggc gggacagaaa cggcctttcg      120

ggcgcccgtc ccgcggagtg cggaaatgga ccgcaccggg tccaccacct gcagataccc      180

cctgtgacta ggggatactc ccccgaagac aacccctctt cttgcgatac tgtggtgtgc      240

cagagagctc acccgctctc agacacaccc ccgacatgac gttcggaaag gaaccccacc      300

gtg gcc aca acc act ctg cca gcc ttc aca aag gtg ctg gtc gcc aac         348
Val Ala Thr Thr Thr Leu Pro Ala Phe Thr Lys Val Leu Val Ala Asn
1               5                   10                  15

cgc ggc gag atc gcc gtc cgc gcc ttc cgt gcc gcc ttc gag acc ggt        396
Arg Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala Phe Glu Thr Gly
            20                  25                  30

gcc tcc acc gtc gcg gtc tac ccg aag gag gac cgc aac tcg cac cac        444
Ala Ser Thr Val Ala Val Tyr Pro Lys Glu Asp Arg Asn Ser His His
        35                  40                  45

cgc tcc ttc gcc tcc gag gcc gtg cgc atc ggc acc gag gga tcg ccg        492
Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro
    50                  55                  60

gtc aag gcg tac ctc gac atc gac gag atc atc cgc gcc gcc aag aag        540
Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Arg Ala Ala Lys Lys
65                  70                  75                  80

acc cac gcc gac gcc gtc tac ccc ggc tac ggt ttc ctc tcc gag aac        588
Thr His Ala Asp Ala Val Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn
                85                  90                  95

gcc cag ctc gcc cgc gag tgc gcc gag aac ggc ctc acc ttc atc ggc        636
Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Leu Thr Phe Ile Gly
            100                 105                 110

ccg ccg ccg gag gtc ctc gac ctg acc ggc gac aag tcc gcc gcc gtc        684
Pro Pro Pro Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Ala Ala Val
        115                 120                 125
```

```
gag gcc gcc cgg aag gcc gga ctc ccg gtc ctg cag gac tcc gag ccg        732
Glu Ala Ala Arg Lys Ala Gly Leu Pro Val Leu Gln Asp Ser Glu Pro
    130                 135                 140

tcc acc gac atc gac gag ctc gtc gag atg tcg aag gac ttc acc ttc        780
Ser Thr Asp Ile Asp Glu Leu Val Glu Met Ser Lys Asp Phe Thr Phe
145                 150                 155                 160

ccg atc ttc gtc aag gcc gtc gcc ggt ggc ggt gga cgt ggc atg cgc        828
Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly Arg Gly Met Arg
                165                 170                 175

ttc atc gag aag ccc gag gac gtc gcc cag ctg gcc acc gag gcc tcc        876
Phe Ile Glu Lys Pro Glu Asp Val Ala Gln Leu Ala Thr Glu Ala Ser
            180                 185                 190

cgc gag gcg gag gcc gcc ttc ggt gac ggt cat gtc tac ctc gag cgt        924
Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly His Val Tyr Leu Glu Arg
        195                 200                 205

gcg gtg ctc aac ccg cag cac atc gag gtc cag atc ctc gcc gac cac        972
Ala Val Leu Asn Pro Gln His Ile Glu Val Gln Ile Leu Ala Asp His
    210                 215                 220

acc ggc gac gtc atc cac ctc tac gag cgt gac tgc tcc ctg cag cgc       1020
Thr Gly Asp Val Ile His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg
225                 230                 235                 240

cgc cac cag aag gtc gtg gag atc gcc ccg gcc cag cac ctc gac cca       1068
Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro
                245                 250                 255

gcc ctg cgc gac cag atc tgc gcc gac gcc gtg aag ttc tgc cgc tcc       1116
Ala Leu Arg Asp Gln Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser
            260                 265                 270

atc ggc tac gtg tgc gcc ggc acc gtc gag ttc ctc gtc gac gag aac       1164
Ile Gly Tyr Val Cys Ala Gly Thr Val Glu Phe Leu Val Asp Glu Asn
        275                 280                 285

ggc aac cac gtc ttc atc gag atg aac ccg cgc atc cag gtc gag cac       1212
Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His
    290                 295                 300

acc atc acc gag gag gtc acc tcc gtc gac ctg gtc aag gcg cag atg       1260
Thr Ile Thr Glu Glu Val Thr Ser Val Asp Leu Val Lys Ala Gln Met
305                 310                 315                 320

aac atc gcc gcc ggc gcg acc ctc aag gac ctc ggc ctc acg cag gag       1308
Asn Ile Ala Ala Gly Ala Thr Leu Lys Asp Leu Gly Leu Thr Gln Glu
                325                 330                 335

tcc atc aag ctc cac ggc gcg gcc ctg cag tgc cgc atc acc acc gag       1356
Ser Ile Lys Leu His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu
            340                 345                 350

gac ccg gcc aac aac ttc cgc ccg gac acc ggc acc atc acc gcg tac       1404
Asp Pro Ala Asn Asn Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr
        355                 360                 365
```

```
cgc tcc ccg ggt ggc gcg ggc gtg cgt ctc gac ggc gcc gcg tcc ctc        1452
Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Ser Leu
    370                 375                 380

ggc ggc gag atc tcc ccg aac ttc gac tcc ctg ctg gtc aag atg acc        1500
Gly Gly Glu Ile Ser Pro Asn Phe Asp Ser Leu Leu Val Lys Met Thr
385                 390                 395                 400

tgc cgc ggc gcc gac ttc gcc acc gcc gtc gcc cgt gcc cag cgc gcg        1548
Cys Arg Gly Ala Asp Phe Ala Thr Ala Val Ala Arg Ala Gln Arg Ala
                405                 410                 415

ctc aac gag ttc acc atc tcg ggc gtg gcc acc aac atc ggc ttc ctc        1596
Leu Asn Glu Phe Thr Ile Ser Gly Val Ala Thr Asn Ile Gly Phe Leu
            420                 425                 430

cgc gcc ctg ctg cgc gag gag gac ttc cag acc cgc cgc atc tcc acc        1644
Arg Ala Leu Leu Arg Glu Glu Asp Phe Gln Thr Arg Arg Ile Ser Thr
        435                 440                 445

aac ttc atc ggc gag cac ctc cac ctg ctg tcc gcc ccg ccg gcc gac        1692
Asn Phe Ile Gly Glu His Leu His Leu Leu Ser Ala Pro Pro Ala Asp
    450                 455                 460

gac gag gcc ggc cgc atc ctc aac tac ctc gcg gac gtc acc gtc aac        1740
Asp Glu Ala Gly Arg Ile Leu Asn Tyr Leu Ala Asp Val Thr Val Asn
465                 470                 475                 480

cgt ccg cac ggc aag cgc ccc acc gag atc cgt ccg gtg acc aag ctg        1788
Arg Pro His Gly Lys Arg Pro Thr Glu Ile Arg Pro Val Thr Lys Leu
                485                 490                 495

ccg gcc cgc gac gac agc ccg ctg ccg cgc ggt tcc cgc gac gtc ctg        1836
Pro Ala Arg Asp Asp Ser Pro Leu Pro Arg Gly Ser Arg Asp Val Leu
            500                 505                 510

cgt gac ctg ggc ccg cag aag ttc gcc gag cag ctg cgc aac cag gac        1884
Arg Asp Leu Gly Pro Gln Lys Phe Ala Glu Gln Leu Arg Asn Gln Asp
        515                 520                 525

gcc ctg gcc gtc acc gac acc acg ttc cgt gac gcg cac cag tcg ctg        1932
Ala Leu Ala Val Thr Asp Thr Thr Phe Arg Asp Ala His Gln Ser Leu
    530                 535                 540

ctg gcc acc cgc atc cgt tcc tcc gcg ctc gtc gcc gcc gcc gag cac        1980
Leu Ala Thr Arg Ile Arg Ser Ser Ala Leu Val Ala Ala Ala Glu His
545                 550                 555                 560

gtc ggc cgc ctg acc ccg gag ctg ctc tcc gtc gag gcg tgg ggc ggt        2028
Val Gly Arg Leu Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly
                565                 570                 575

gcg acc tac gac gtc gcg atg cgt ttc ctc cac gag gac ccg tgg gag        2076
Ala Thr Tyr Asp Val Ala Met Arg Phe Leu His Glu Asp Pro Trp Glu
            580                 585                 590

cgt ctc gac gac ctg cgc cgc gcc atg ccg aac gtc aac atc cag atg        2124
Arg Leu Asp Asp Leu Arg Arg Ala Met Pro Asn Val Asn Ile Gln Met
```

```
          595                 600                 605

ctg ctg cgc ggc cgc aac acc gtc ggc tac acc tcc tac ccg gac agc      2172
Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Ser Tyr Pro Asp Ser
    610                 615                 620

gtc ggc cag gcc ttc gtc aag gag gcc gcc gac tcc ggc gtc gac atc      2220
Val Gly Gln Ala Phe Val Lys Glu Ala Ala Asp Ser Gly Val Asp Ile
625                 630                 635                 640

ttc cgc atc ttc gac gcc ctc aac gac gtg gac cag atg cgc ccg gcc      2268
Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Asp Gln Met Arg Pro Ala
                645                 650                 655

atc gat gcc gtc ctg gag acc ggc acc acc gtc gcc gag gtc gcc atg      2316
Ile Asp Ala Val Leu Glu Thr Gly Thr Thr Val Ala Glu Val Ala Met
            660                 665                 670

gcc tac tcc ggc aac ctg ctg gac ccg aac gag aag ctc tac acg ctc      2364
Ala Tyr Ser Gly Asn Leu Leu Asp Pro Asn Glu Lys Leu Tyr Thr Leu
        675                 680                 685

gac tac tac ctc cgt ctg gcc gag gag atc gtc gag tcc ggt gcc cac      2412
Asp Tyr Tyr Leu Arg Leu Ala Glu Glu Ile Val Glu Ser Gly Ala His
    690                 695                 700

atc ctg gcc atc aag gac atg gcc ggt ctg ctc cgc ccg acc gcg gcc      2460
Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Thr Ala Ala
705                 710                 715                 720

tcc cgc ctg gtg aag gcg ctg cgc agc aac ttc gac ctg ccg gtg cac      2508
Ser Arg Leu Val Lys Ala Leu Arg Ser Asn Phe Asp Leu Pro Val His
                725                 730                 735

gtg cac acc cac gac acc gcc ggc ggt cag ctg gcg acc tac ctg gcc      2556
Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Leu Ala
            740                 745                 750

gcc gcg cag gcg ggt gcc gac gcc gtc gac ggc gcc tcc gcc ccg ctg      2604
Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Ala Pro Leu
        755                 760                 765

gcc ggc acg acc tcg cag ccc tcg ctg tcc gcg atc gtc gcg gcc ttc      2652
Ala Gly Thr Thr Ser Gln Pro Ser Leu Ser Ala Ile Val Ala Ala Phe
    770                 775                 780

gcc gac acc cac cgc gac acc ggc ctg tcc ctg cag gcc gtg tcc gac      2700
Ala Asp Thr His Arg Asp Thr Gly Leu Ser Leu Gln Ala Val Ser Asp
785                 790                 795                 800

ctc gag ccc tac tgg gag gcc gtg cgc cag ctc tac gcc ccc ttc gag      2748
Leu Glu Pro Tyr Trp Glu Ala Val Arg Gln Leu Tyr Ala Pro Phe Glu
                805                 810                 815

gcg ggc gtg ccc ggc ccg acg ggc cgc gtg tac aag cac gag atc ccg      2796
Ala Gly Val Pro Gly Pro Thr Gly Arg Val Tyr Lys His Glu Ile Pro
            820                 825                 830

ggt ggt cag ctg tcg aac ctg cgc acg cag gcc aag gcc ctg ggt ctg      2844
```

```
Gly Gly Gln Leu Ser Asn Leu Arg Thr Gln Ala Lys Ala Leu Gly Leu
        835                 840                 845

gag gac cgc ttc gag ctc atc gag gac tac tac gcc gcc gtc aac gag      2892
Glu Asp Arg Phe Glu Leu Ile Glu Asp Tyr Tyr Ala Ala Val Asn Glu
    850                 855                 860

atg ctg ggc cgc ccc acc aag gtc acc ccg tcc tcc aag gtc gtc ggc      2940
Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly
865                 870                 875                 880

gac ctg gcg ctc cac ctc gtc ggc gcg ggc gtc gac ccg cac gac ttc      2988
Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp Pro His Asp Phe
                885                 890                 895

gcc aat gac ccg cag aag tac gac atc ccg gac tcc gtg atc gac ttc      3036
Ala Asn Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Asp Phe
            900                 905                 910

ctc cgc ggt gac ctc ggc aac ccg ccc ggt ggc tgg ccg atg ctg cgg      3084
Leu Arg Gly Asp Leu Gly Asn Pro Pro Gly Gly Trp Pro Met Leu Arg
        915                 920                 925

gag aag gcc ctg gca ggt cgt tcc tcc acg cag tcc aag ctt gtc gac      3132
Glu Lys Ala Leu Ala Gly Arg Ser Ser Thr Gln Ser Lys Leu Val Asp
    930                 935                 940

gtc gcc ccg gag gac gag gag gcc ctg cag agc gcg gac cgc cag acc      3180
Val Ala Pro Glu Asp Glu Glu Ala Leu Gln Ser Ala Asp Arg Gln Thr
945                 950                 955                 960

cgc cgc tcg acc ctg gac agg ctg ctg ttc ccg aag cag gcc gcc gag      3228
Arg Arg Ser Thr Leu Asp Arg Leu Leu Phe Pro Lys Gln Ala Ala Glu
                965                 970                 975

ttc gcg gag cac cgc cgc cag tac ggc aac acc gcc gcc ctc gag gac      3276
Phe Ala Glu His Arg Arg Gln Tyr Gly Asn Thr Ala Ala Leu Glu Asp
            980                 985                 990

cgc gtg ttc ttc tac ggc ctc aag  gag ggc gag gag aac  gtc atc cgc    3324
Arg Val Phe Phe Tyr Gly Leu Lys  Glu Gly Glu Glu Asn  Val Ile Arg
        995                 1000                1005

ctc atc  ggg gag cac ggt cag  ccg ccg atg gtc gtg  cgt ctc gac       3369
Leu Ile  Gly Glu His Gly Gln  Pro Pro Met Val Val  Arg Leu Asp
    1010                1015                1020

gcc gtc  ggt gag ccc gac gag  aag ggc atg cgc cag  gtg gtg acc       3414
Ala Val  Gly Glu Pro Asp Glu  Lys Gly Met Arg Gln  Val Val Thr
    1025                1030                1035

aac gtc  aac ggc cag atc cgt  ccg atg aag gtc cgt  gac cgc tcc       3459
Asn Val  Asn Gly Gln Ile Arg  Pro Met Lys Val Arg  Asp Arg Ser
    1040                1045                1050

gtc gag  tcg gtc acc gcc tcc  gcg gag aag gcc gac  acc acc aac       3504
Val Glu  Ser Val Thr Ala Ser  Ala Glu Lys Ala Asp  Thr Thr Asn
    1055                1060                1065
```

```
ccg ggc  cac gtc gcc gcg ccg  ttc gcg ggt gtc gtc  atg gtc acc        3549
Pro Gly  His Val Ala Ala Pro  Phe Ala Gly Val Val  Met Val Thr
    1070                 1075                 1080

gcg aag  gtg ggc gac gag gtc  aag gcc ggc gac ccg  gta gcc gtg        3594
Ala Lys  Val Gly Asp Glu Val  Lys Ala Gly Asp Pro  Val Ala Val
    1085                 1090                 1095

atc gag  gcc atg aag atg gag  gcc acc atc acc gcc  tcc aag gac        3639
Ile Glu  Ala Met Lys Met Glu  Ala Thr Ile Thr Ala  Ser Lys Asp
    1100                 1105                 1110

ggc gtg  gtc gac cgc gtc gcc  ctg gcc cag gcc acg  aag gtg gag        3684
Gly Val  Val Asp Arg Val Ala  Leu Ala Gln Ala Thr  Lys Val Glu
    1115                 1120                 1125

ggc ggc  gac ctc atc gtc gtc  atc gcc tag ccgcacaacg cgaaagcccc      3734
Gly Gly  Asp Leu Ile Val Val  Ile Ala
    1130                 1135

gccactcctt ccgggagtgg cggggcttct ctgtgcgggt gggccgctac ttgatctcga    3794

gcaggacctg gcccttggtc acgccggcac cggcctcgac ggacaggccc tcgaccttgc    3854

ccgacttgtg ggccttgacc gggttctcca tcttcatggc ctcgaggacc acgacgacgt    3914

cgccctcggc gacctcctgg ccgtcctcga cgttgacctt gatgacggtg ccctgcatcg    3974

gggccgccac agcgtcaccg gaggcacctg cggcaccgcc                          4014
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<210> 64
<211> 1137
<212> PRT
<213> Corynebacterium humireducens

<400> 64

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Val Ala Thr Thr Thr Leu Pro Ala Phe Thr Lys Val Leu Val Ala Asn
1               5                  10                  15

Arg Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala Phe Glu Thr Gly
            20                  25                  30

Ala Ser Thr Val Ala Val Tyr Pro Lys Glu Asp Arg Asn Ser His His
        35                  40                  45

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

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

Thr His Ala Asp Ala Val Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn
```

85 90 95

Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Leu Thr Phe Ile Gly
100 105 110

Pro Pro Pro Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Ala Ala Val
115 120 125

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

Ser Thr Asp Ile Asp Glu Leu Val Glu Met Ser Lys Asp Phe Thr Phe
145 150 155 160

Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly Arg Gly Met Arg
165 170 175

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

Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly His Val Tyr Leu Glu Arg
195 200 205

Ala Val Leu Asn Pro Gln His Ile Glu Val Gln Ile Leu Ala Asp His
210 215 220

Thr Gly Asp Val Ile His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg
225 230 235 240

Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro
245 250 255

Ala Leu Arg Asp Gln Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser
260 265 270

Ile Gly Tyr Val Cys Ala Gly Thr Val Glu Phe Leu Val Asp Glu Asn
275 280 285

Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His
290 295 300

Thr Ile Thr Glu Glu Val Thr Ser Val Asp Leu Val Lys Ala Gln Met
305 310 315 320

```
Asn Ile Ala Ala Gly Ala Thr Leu Lys Asp Leu Gly Leu Thr Gln Glu
                325                 330                 335

Ser Ile Lys Leu His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu
            340                 345                 350

Asp Pro Ala Asn Asn Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr
        355                 360                 365

Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Ser Leu
    370                 375                 380

Gly Gly Glu Ile Ser Pro Asn Phe Asp Ser Leu Leu Val Lys Met Thr
385                 390                 395                 400

Cys Arg Gly Ala Asp Phe Ala Thr Ala Val Ala Arg Ala Gln Arg Ala
                405                 410                 415

Leu Asn Glu Phe Thr Ile Ser Gly Val Ala Thr Asn Ile Gly Phe Leu
            420                 425                 430

Arg Ala Leu Leu Arg Glu Glu Asp Phe Gln Thr Arg Arg Ile Ser Thr
        435                 440                 445

Asn Phe Ile Gly Glu His Leu His Leu Leu Ser Ala Pro Pro Ala Asp
    450                 455                 460

Asp Glu Ala Gly Arg Ile Leu Asn Tyr Leu Ala Asp Val Thr Val Asn
465                 470                 475                 480

Arg Pro His Gly Lys Arg Pro Thr Glu Ile Arg Pro Val Thr Lys Leu
                485                 490                 495

Pro Ala Arg Asp Asp Ser Pro Leu Pro Arg Gly Ser Arg Asp Val Leu
            500                 505                 510

Arg Asp Leu Gly Pro Gln Lys Phe Ala Glu Gln Leu Arg Asn Gln Asp
        515                 520                 525

Ala Leu Ala Val Thr Asp Thr Thr Phe Arg Asp Ala His Gln Ser Leu
    530                 535                 540

Leu Ala Thr Arg Ile Arg Ser Ser Ala Leu Val Ala Ala Ala Glu His
545                 550                 555                 560
```

```
Val Gly Arg Leu Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly
                565                 570                 575

Ala Thr Tyr Asp Val Ala Met Arg Phe Leu His Glu Asp Pro Trp Glu
            580                 585                 590

Arg Leu Asp Asp Leu Arg Arg Ala Met Pro Asn Val Asn Ile Gln Met
        595                 600                 605

Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Ser Tyr Pro Asp Ser
    610                 615                 620

Val Gly Gln Ala Phe Val Lys Glu Ala Ala Asp Ser Gly Val Asp Ile
625                 630                 635                 640

Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Asp Gln Met Arg Pro Ala
                645                 650                 655

Ile Asp Ala Val Leu Glu Thr Gly Thr Thr Val Ala Glu Val Ala Met
            660                 665                 670

Ala Tyr Ser Gly Asn Leu Leu Asp Pro Asn Glu Lys Leu Tyr Thr Leu
        675                 680                 685

Asp Tyr Tyr Leu Arg Leu Ala Glu Glu Ile Val Glu Ser Gly Ala His
    690                 695                 700

Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Thr Ala Ala
705                 710                 715                 720

Ser Arg Leu Val Lys Ala Leu Arg Ser Asn Phe Asp Leu Pro Val His
                725                 730                 735

Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Leu Ala
            740                 745                 750

Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Ala Pro Leu
        755                 760                 765

Ala Gly Thr Thr Ser Gln Pro Ser Leu Ser Ala Ile Val Ala Ala Phe
    770                 775                 780

Ala Asp Thr His Arg Asp Thr Gly Leu Ser Leu Gln Ala Val Ser Asp
785                 790                 795                 800
```

```
Leu Glu Pro Tyr Trp Glu Ala Val Arg Gln Leu Tyr Ala Pro Phe Glu
                805                 810                 815

Ala Gly Val Pro Gly Pro Thr Gly Arg Val Tyr Lys His Glu Ile Pro
            820                 825                 830

Gly Gly Gln Leu Ser Asn Leu Arg Thr Gln Ala Lys Ala Leu Gly Leu
        835                 840                 845

Glu Asp Arg Phe Glu Leu Ile Glu Asp Tyr Tyr Ala Ala Val Asn Glu
    850                 855                 860

Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly
865                 870                 875                 880

Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp Pro His Asp Phe
                885                 890                 895

Ala Asn Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Asp Phe
            900                 905                 910

Leu Arg Gly Asp Leu Gly Asn Pro Pro Gly Gly Trp Pro Met Leu Arg
        915                 920                 925

Glu Lys Ala Leu Ala Gly Arg Ser Ser Thr Gln Ser Lys Leu Val Asp
    930                 935                 940

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

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

Phe Ala Glu His Arg Arg Gln Tyr Gly Asn Thr Ala Ala Leu Glu Asp
            980                 985                 990

Arg Val Phe Phe Tyr Gly Leu Lys  Glu Gly Glu Glu Asn  Val Ile Arg
        995                 1000                1005

Leu Ile  Gly Glu His Gly Gln  Pro Pro Met Val Val  Arg Leu Asp
    1010                1015                1020

Ala Val  Gly Glu Pro Asp Glu  Lys Gly Met Arg Gln  Val Val Thr
```

1025 1030 1035

Asn Val Asn Gly Gln Ile Arg Pro Met Lys Val Arg Asp Arg Ser
1040 1045 1050

Val Glu Ser Val Thr Ala Ser Ala Glu Lys Ala Asp Thr Thr Asn
1055 1060 1065

Pro Gly His Val Ala Ala Pro Phe Ala Gly Val Val Met Val Thr
1070 1075 1080

Ala Lys Val Gly Asp Glu Val Lys Ala Gly Asp Pro Val Ala Val
1085 1090 1095

Ile Glu Ala Met Lys Met Glu Ala Thr Ile Thr Ala Ser Lys Asp
1100 1105 1110

Gly Val Val Asp Arg Val Ala Leu Ala Gln Ala Thr Lys Val Glu
1115 1120 1125

Gly Gly Asp Leu Ile Val Val Ile Ala
1130 1135

<210> 65
<211> 2190
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1890)
<223> gene serA

<400> 65
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gatggacaag cccgtggtcc gcgacgtcga cgacagtgac tacacggggg gcgaggaggg 120

cccgaacgcg ttcactgact gaacgggggt gaccggtgga gtggtgtgcc tcatatcggg 180

gcagggtatg ggacaaggcg caaccccaca gactaaagtg ttatccgttc ctcgttcctg 240

gttcggtcgg gtgcgctgac cggccccggg gcctcatttt caaatcagga gatatcacac 300

gtg agc aag ccc gtc gtc ctc atc gcc gac aaa ctg gca cct tcc acc 348
Val Ser Lys Pro Val Val Leu Ile Ala Asp Lys Leu Ala Pro Ser Thr
1 5 10 15

gta gat gcg ctc gga gac gcc gtg gag gtg cgc tgg gtc gac ggc ccg 396
Val Asp Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val Asp Gly Pro

```
                20                  25                  30

aac acc ccg gag ctg ctc gcc gcc gtc ccg gag gca gac gca ctg ctg        444
Asn Thr Pro Glu Leu Leu Ala Ala Val Pro Glu Ala Asp Ala Leu Leu
        35                  40                  45

gtc cgt tcc gcg acc acc gtc acc cgt gag gtc ctc gag gcc gca ccg        492
Val Arg Ser Ala Thr Thr Val Thr Arg Glu Val Leu Glu Ala Ala Pro
    50                  55                  60

aac ctg aag atc gtc ggc cgc gcc ggc gtc ggc ctg gac aac gtc gac        540
Asn Leu Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp Asn Val Asp
65                  70                  75                  80

atc gac gcc gcc acc gag cgt ggc gtc atg gtc gtc aac gcc ccg acc        588
Ile Asp Ala Ala Thr Glu Arg Gly Val Met Val Val Asn Ala Pro Thr
                85                  90                  95

tcc aac atc cac tcc gcc tgc gag cac gcc atc gcc ctg ctc atg gcc        636
Ser Asn Ile His Ser Ala Cys Glu His Ala Ile Ala Leu Leu Met Ala
            100                 105                 110

acc gtg cgc cag atc ccg gcc gcc gac gcc acc ctg cgt gag ggc gag        684
Thr Val Arg Gln Ile Pro Ala Ala Asp Ala Thr Leu Arg Glu Gly Glu
        115                 120                 125

tgg aag cgt tcc gcc ttc aag ggc gtg gag atc ttc ggc aag acc atc        732
Trp Lys Arg Ser Ala Phe Lys Gly Val Glu Ile Phe Gly Lys Thr Ile
    130                 135                 140

ggc atc gtc ggc ttc ggc cac atc ggc cag ctc ttc gcc cag cgt ctg        780
Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala Gln Arg Leu
145                 150                 155                 160

tcc gcc ttc gag acc gag atc atc gcc tac gac ccg tac gcg aac ccg        828
Ser Ala Phe Glu Thr Glu Ile Ile Ala Tyr Asp Pro Tyr Ala Asn Pro
                165                 170                 175

acc cgc gcc gcc cag ctc ggc gtc gag ctg gtc gag ctg gag gag ctg        876
Thr Arg Ala Ala Gln Leu Gly Val Glu Leu Val Glu Leu Glu Glu Leu
            180                 185                 190

gtc tcc cgc gcc gac atc gtc acc atc cac ctt ccg aag acc aag gag        924
Val Ser Arg Ala Asp Ile Val Thr Ile His Leu Pro Lys Thr Lys Glu
        195                 200                 205

acg gcc ggc atg ttc aac gcc gag ctg ctc gcc aag tcc aag aag ggc        972
Thr Ala Gly Met Phe Asn Ala Glu Leu Leu Ala Lys Ser Lys Lys Gly
    210                 215                 220

cag atc atc atc aac gcc gcc cgc ggt ggc ctc gtc gat gag cag gca       1020
Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp Glu Gln Ala
225                 230                 235                 240

ctg gct gac gcc atc aag tcc ggc cac atc tgg ggc gcc ggc ttc gac       1068
Leu Ala Asp Ala Ile Lys Ser Gly His Ile Trp Gly Ala Gly Phe Asp
                245                 250                 255

gtc ttc tcc acc gag ccg tgc acc gac tcc ccg ctg ttc ggc ctg ccg       1116
```

```
Val Phe Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe Gly Leu Pro
            260                 265                 270

gag gtc gtc gtg acc ccg cac ctg ggt gcc tcc acc gaa gag gcc cag      1164
Glu Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu Glu Ala Gln
        275                 280                 285

gac cgt gcc ggc acc gac gtc gcc gcc tcc gtc ctc aag gcc ctg gcc      1212
Asp Arg Ala Gly Thr Asp Val Ala Ala Ser Val Leu Lys Ala Leu Ala
    290                 295                 300

ggc gag ttc gtc ccg gac gcc gtg aac gtc tcc ggc ggc cgc gtc ggc      1260
Gly Glu Phe Val Pro Asp Ala Val Asn Val Ser Gly Gly Arg Val Gly
305                 310                 315                 320

gag gag gtc gcc ctg tgg ttg gac ctg acc cgc aag ctg ggt ctg ctg      1308
Glu Glu Val Ala Leu Trp Leu Asp Leu Thr Arg Lys Leu Gly Leu Leu
                325                 330                 335

gcc ggt cag ctg ctg gac tcc gcc ccg gtc gac ctc gag gtc gag gcc      1356
Ala Gly Gln Leu Leu Asp Ser Ala Pro Val Asp Leu Glu Val Glu Ala
            340                 345                 350

cgc ggc gag ctc tcc acc gag gac gac ctg tcc gtg ctc ggc ctg tcc      1404
Arg Gly Glu Leu Ser Thr Glu Asp Asp Leu Ser Val Leu Gly Leu Ser
        355                 360                 365

gcc gtc cgt ggc ctg ttc tcc gcc acc acc gac gag ccg gtc acc ttc      1452
Ala Val Arg Gly Leu Phe Ser Ala Thr Thr Asp Glu Pro Val Thr Phe
    370                 375                 380

gtc aac gcc ccg cag atc gcg gag agc cgt ggc ctg gac tac aag gtc      1500
Val Asn Ala Pro Gln Ile Ala Glu Ser Arg Gly Leu Asp Tyr Lys Val
385                 390                 395                 400

gac acc gcg acc gag tcc acc acc cac cgt tcc tcc gtc gag gtc aag      1548
Asp Thr Ala Thr Glu Ser Thr Thr His Arg Ser Ser Val Glu Val Lys
                405                 410                 415

gtc atc ggt gcg gac ggc tcc tcc cgc tcc gtc gtc ggt gcc ctg acc      1596
Val Ile Gly Ala Asp Gly Ser Ser Arg Ser Val Val Gly Ala Leu Thr
            420                 425                 430

ggc ctg gag cgc gtc gag aag atc gtg cgc atc gac gag cgc ggc ctg      1644
Gly Leu Glu Arg Val Glu Lys Ile Val Arg Ile Asp Glu Arg Gly Leu
        435                 440                 445

gac atg cgc gcc gag ggt cgc aac ctc ttc ctc gag tac acc gac gcc      1692
Asp Met Arg Ala Glu Gly Arg Asn Leu Phe Leu Glu Tyr Thr Asp Ala
    450                 455                 460

ccg ggc gcc ctg ggc aag gtg ggc tcc cag ctg ggc gac gcc ggc atc      1740
Pro Gly Ala Leu Gly Lys Val Gly Ser Gln Leu Gly Asp Ala Gly Ile
465                 470                 475                 480

aac atc gag gcc gcc gcc ctc acc cag gcc acc aag ggt gac ggc gcc      1788
Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Thr Lys Gly Asp Gly Ala
                485                 490                 495
```

atc ctg atc ctg cgt gtc gac gca gag atc ccg gag gca ctg cag aag 1836
Ile Leu Ile Leu Arg Val Asp Ala Glu Ile Pro Glu Ala Leu Gln Lys
500 505 510

cag atc gcc gag tcc ctg ggt gcc acc aac gat atc cag ctc aac ctg 1884
Gln Ile Ala Glu Ser Leu Gly Ala Thr Asn Asp Ile Gln Leu Asn Leu
515 520 525

gac tag tctccggtcg ccccgtcgac ggcgtgtcgc gtcggtccct cgcggatcgc 1940
Asp

gcggcacgcc gttcgcgttt ctgcgggagg cagtttcatt catgccgcct gaccgggaaa 2000

tgtgcaggta gacagtatgg ttcattccag gcgcgccgtt aatagaccga acggtatgga 2060

ctaactagac ggggaagtgt tgaatgggtc aggcaacgaa ccgactgatc caggagtacc 2120

ccgtgtccga cctcaccccg aaccacaccg ccggcgaacc gctcgagccc atcgacgcgc 2180

agaagctcgc 2190

<210> 66
<211> 529
<212> PRT
<213> Corynebacterium humireducens

<400> 66

Val Ser Lys Pro Val Val Leu Ile Ala Asp Lys Leu Ala Pro Ser Thr
1 5 10 15

Val Asp Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val Asp Gly Pro
20 25 30

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

Val Arg Ser Ala Thr Thr Val Thr Arg Glu Val Leu Glu Ala Ala Pro
50 55 60

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

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

Ser Asn Ile His Ser Ala Cys Glu His Ala Ile Ala Leu Leu Met Ala
100 105 110

Thr Val Arg Gln Ile Pro Ala Ala Asp Ala Thr Leu Arg Glu Gly Glu

```
          115                 120                 125

Trp Lys Arg Ser Ala Phe Lys Gly Val Glu Ile Phe Gly Lys Thr Ile
    130                 135                 140

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

Ser Ala Phe Glu Thr Glu Ile Ile Ala Tyr Asp Pro Tyr Ala Asn Pro
                165                 170                 175

Thr Arg Ala Ala Gln Leu Gly Val Glu Leu Val Glu Leu Glu Glu Leu
            180                 185                 190

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

Thr Ala Gly Met Phe Asn Ala Glu Leu Leu Ala Lys Ser Lys Lys Gly
    210                 215                 220

Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp Glu Gln Ala
225                 230                 235                 240

Leu Ala Asp Ala Ile Lys Ser Gly His Ile Trp Gly Ala Gly Phe Asp
                245                 250                 255

Val Phe Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe Gly Leu Pro
            260                 265                 270

Glu Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu Glu Ala Gln
        275                 280                 285

Asp Arg Ala Gly Thr Asp Val Ala Ala Ser Val Leu Lys Ala Leu Ala
    290                 295                 300

Gly Glu Phe Val Pro Asp Ala Val Asn Val Ser Gly Gly Arg Val Gly
305                 310                 315                 320

Glu Glu Val Ala Leu Trp Leu Asp Leu Thr Arg Lys Leu Gly Leu Leu
                325                 330                 335

Ala Gly Gln Leu Leu Asp Ser Ala Pro Val Asp Leu Glu Val Glu Ala
            340                 345                 350
```

```
Arg Gly Glu Leu Ser Thr Glu Asp Asp Leu Ser Val Leu Gly Leu Ser
        355                 360                 365

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

Val Asn Ala Pro Gln Ile Ala Glu Ser Arg Gly Leu Asp Tyr Lys Val
385                 390                 395                 400

Asp Thr Ala Thr Glu Ser Thr Thr His Arg Ser Ser Val Glu Val Lys
                405                 410                 415

Val Ile Gly Ala Asp Gly Ser Ser Arg Ser Val Val Gly Ala Leu Thr
            420                 425                 430

Gly Leu Glu Arg Val Glu Lys Ile Val Arg Ile Asp Glu Arg Gly Leu
        435                 440                 445

Asp Met Arg Ala Glu Gly Arg Asn Leu Phe Leu Glu Tyr Thr Asp Ala
    450                 455                 460

Pro Gly Ala Leu Gly Lys Val Gly Ser Gln Leu Gly Asp Ala Gly Ile
465                 470                 475                 480

Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Thr Lys Gly Asp Gly Ala
                485                 490                 495

Ile Leu Ile Leu Arg Val Asp Ala Glu Ile Pro Glu Ala Leu Gln Lys
            500                 505                 510

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

Asp
```

<210> 67
<211> 1848
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1548)
<223> gene serB

<400> 67

cgtatccgct ccgagcgccc ggcgttcgag ctgcactacc cgcacatggt tgagcgcatg 60

cgtcgcgagg cacacaccgg tgcccacgac gagcgcgcgg agatcaccca gactccggct 120

ccggccgagg tccgctaaaa gggtttgaca tagacccctc cgactgacac gacccccggt 180

agatccctct accgggggtt gcggcatgtt cgaaaccccc tcccatgaaa gaatgatccc 240

gtggcagatc aagctcagaa ccccgatacc gccgacaccg aagcacagca gcagctgcag 300

gtg	gcg	ctc	cag	ccc	gga	ctg	gag	tcc	gca	gtc	atc	acc	ctc	acc	ggc	348
Val	Ala	Leu	Gln	Pro	Gly	Leu	Glu	Ser	Ala	Val	Ile	Thr	Leu	Thr	Gly	
1				5				10					15			

cgt	gac	cgg	ccg	ggc	gtg	acg	gcc	gcc	ttc	ttc	cgc	gtc	ctg	tcc	gct	396
Arg	Asp	Arg	Pro	Gly	Val	Thr	Ala	Ala	Phe	Phe	Arg	Val	Leu	Ser	Ala	
			20					25					30			

cac	gac	gtc	cag	ctt	ctc	gac	gtc	gag	cag	tcc	cag	ttc	cgt	gga	tac	444
His	Asp	Val	Gln	Leu	Leu	Asp	Val	Glu	Gln	Ser	Gln	Phe	Arg	Gly	Tyr	
		35					40					45				

ctc	tcc	ctc	gcc	gcc	tac	gtg	ggc	gtc	gac	ccg	gag	cgc	gtc	gac	cgt	492
Leu	Ser	Leu	Ala	Ala	Tyr	Val	Gly	Val	Asp	Pro	Glu	Arg	Val	Asp	Arg	
	50					55					60					

ctc	cgc	gag	ggc	ctg	acc	gag	acc	ctc	aag	ggc	cac	ggg	cag	ctc	gcc	540
Leu	Arg	Glu	Gly	Leu	Thr	Glu	Thr	Leu	Lys	Gly	His	Gly	Gln	Leu	Ala	
65					70					75					80	

acc	gtc	gag	atg	gtc	ccg	gag	ggc	cag	cac	tcc	agc	ccg	cgg	tcc	acg	588
Thr	Val	Glu	Met	Val	Pro	Glu	Gly	Gln	His	Ser	Ser	Pro	Arg	Ser	Thr	
				85					90					95		

cac	gtg	gcc	gtc	gtc	ctg	ggc	aac	ccg	gtg	acc	gcc	acc	gac	gtg	tcg	636
His	Val	Ala	Val	Val	Leu	Gly	Asn	Pro	Val	Thr	Ala	Thr	Asp	Val	Ser	
			100					105					110			

gcc	atc	ggt	cag	acg	ctg	gcc	aac	tac	ggc	gcg	aac	atc	gac	cgt	atc	684
Ala	Ile	Gly	Gln	Thr	Leu	Ala	Asn	Tyr	Gly	Ala	Asn	Ile	Asp	Arg	Ile	
		115					120					125				

cgc	ggc	atc	gcg	gac	tac	ccg	atc	acc	ggc	ctg	gag	atc	atg	atc	acg	732
Arg	Gly	Ile	Ala	Asp	Tyr	Pro	Ile	Thr	Gly	Leu	Glu	Ile	Met	Ile	Thr	
	130					135					140					

atc	gcc	aac	ccg	gag	ccg	ggc	ggc	ggc	aag	gcc	atg	cgt	aag	gca	ctg	780
Ile	Ala	Asn	Pro	Glu	Pro	Gly	Gly	Gly	Lys	Ala	Met	Arg	Lys	Ala	Leu	
145					150					155					160	

gcg	gag	ctg	acc	acc	gag	ctg	ggc	gtc	gac	atc	gcc	atc	gag	cgt	gcc	828
Ala	Glu	Leu	Thr	Thr	Glu	Leu	Gly	Val	Asp	Ile	Ala	Ile	Glu	Arg	Ala	
				165					170					175		

ggc	ctg	ctg	cgc	cgc	tcc	aag	cgt	ctg	gtc	atc	ttc	gac	tgc	gac	tcc	876
Gly	Leu	Leu	Arg	Arg	Ser	Lys	Arg	Leu	Val	Ile	Phe	Asp	Cys	Asp	Ser	
			180					185					190			

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acc ctc atc acc ggt gag gtc atc gag atg ctg gcg gcc cac gcc ggc        924
Thr Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala Ala His Ala Gly
        195                 200                 205

aag gag gcc gag gtc gcc gag gtc acc gag cgg gcc atg cgc ggc gag        972
Lys Glu Ala Glu Val Ala Glu Val Thr Glu Arg Ala Met Arg Gly Glu
    210                 215                 220

ctc gac ttc gag gag tcc ctc cgt gag cgc gtc gcc acc ctc gag ggt       1020
Leu Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Ala Thr Leu Glu Gly
225                 230                 235                 240

ctc gac gcc tcc gtc atc gac gag gtc gcc cgc gac atc gtc ctg acc       1068
Leu Asp Ala Ser Val Ile Asp Glu Val Ala Arg Asp Ile Val Leu Thr
                245                 250                 255

ccg ggc gcc cgc acg acc atc cgc acc ctg aag aag atg ggc tac cgc       1116
Pro Gly Ala Arg Thr Thr Ile Arg Thr Leu Lys Lys Met Gly Tyr Arg
            260                 265                 270

acg gcc gtc gtc tcc ggt ggc ttc atc cag gtc ctc gag gac ctg gcc       1164
Thr Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu Glu Asp Leu Ala
        275                 280                 285

gag gac ctc cag ctc gac tac gtc cgc gcg aac acc ctg gag atc gtc       1212
Glu Asp Leu Gln Leu Asp Tyr Val Arg Ala Asn Thr Leu Glu Ile Val
    290                 295                 300

gac ggc aag ctc acc ggc cgc gtg acc ggt gac atc gtc gac cgt gcc       1260
Asp Gly Lys Leu Thr Gly Arg Val Thr Gly Asp Ile Val Asp Arg Ala
305                 310                 315                 320

cgc aag gcg gag ctg ctg cgc gag ttc gcc gag gac tcc ggc ctg cag       1308
Arg Lys Ala Glu Leu Leu Arg Glu Phe Ala Glu Asp Ser Gly Leu Gln
                325                 330                 335

atg tac cag acc gtg gcc gtg ggt gac ggt gcc aac gac atc gac atg       1356
Met Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn Asp Ile Asp Met
            340                 345                 350

ctc tcc gcg gcg ggc ctg ggc atc gcg ttc aac gcc aag ccg gcg ctg       1404
Leu Ser Ala Ala Gly Leu Gly Ile Ala Phe Asn Ala Lys Pro Ala Leu
        355                 360                 365

cgc gag atc gcc gac acc tcc gtc aac cac ccc ttc ctc gac gag gtg       1452
Arg Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe Leu Asp Glu Val
    370                 375                 380

ctc cac atc ctg ggc gtc ccg cgc gag gag atc gac gag tcc gac ctg       1500
Leu His Ile Leu Gly Val Pro Arg Glu Glu Ile Asp Glu Ser Asp Leu
385                 390                 395                 400

gag gac ggc acc ttc cgc cgg gtc ccg ctc gag gtc tcc gca cgg tag       1548
Glu Asp Gly Thr Phe Arg Arg Val Pro Leu Glu Val Ser Ala Arg
                405                 410                 415

tggaggagac cgatccgctc gccctcgcgc acgccctcct gagcgcgcgg gtgagcgaca     1608

accggcacga ccgctccgag aacccggagc agcaggagac cgtgcaggcg atgcagatcg     1668
```

ccctgcacgt gccgaagaca caaccgcccc gccgtaccga cctcctcgag gccgcggcgc 1728

gggcggttgt cgccgtctgc ctctccgaca gggtcgcggg ggacccgtcc tggcgggcgg 1788

ggctggaggg ctggtacgac cacctcatcc gcaaggtgac ccgccgggcc cgcaacaagg 1848

<210> 68
<211> 415
<212> PRT
<213> Corynebacterium humireducens

<400> 68

Val Ala Leu Gln Pro Gly Leu Glu Ser Ala Val Ile Thr Leu Thr Gly
1 5 10 15

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

His Asp Val Gln Leu Leu Asp Val Glu Gln Ser Gln Phe Arg Gly Tyr
35 40 45

Leu Ser Leu Ala Ala Tyr Val Gly Val Asp Pro Glu Arg Val Asp Arg
50 55 60

Leu Arg Glu Gly Leu Thr Glu Thr Leu Lys Gly His Gly Gln Leu Ala
65 70 75 80

Thr Val Glu Met Val Pro Glu Gly Gln His Ser Ser Pro Arg Ser Thr
85 90 95

His Val Ala Val Val Leu Gly Asn Pro Val Thr Ala Thr Asp Val Ser
100 105 110

Ala Ile Gly Gln Thr Leu Ala Asn Tyr Gly Ala Asn Ile Asp Arg Ile
115 120 125

Arg Gly Ile Ala Asp Tyr Pro Ile Thr Gly Leu Glu Ile Met Ile Thr
130 135 140

Ile Ala Asn Pro Glu Pro Gly Gly Gly Lys Ala Met Arg Lys Ala Leu
145 150 155 160

Ala Glu Leu Thr Thr Glu Leu Gly Val Asp Ile Ala Ile Glu Arg Ala
165 170 175

```
Gly Leu Leu Arg Arg Ser Lys Arg Leu Val Ile Phe Asp Cys Asp Ser
            180                 185                 190

Thr Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala Ala His Ala Gly
        195                 200                 205

Lys Glu Ala Glu Val Ala Glu Val Thr Glu Arg Ala Met Arg Gly Glu
    210                 215                 220

Leu Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Ala Thr Leu Glu Gly
225                 230                 235                 240

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

Pro Gly Ala Arg Thr Thr Ile Arg Thr Leu Lys Lys Met Gly Tyr Arg
            260                 265                 270

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

Glu Asp Leu Gln Leu Asp Tyr Val Arg Ala Asn Thr Leu Glu Ile Val
    290                 295                 300

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

Arg Lys Ala Glu Leu Leu Arg Glu Phe Ala Glu Asp Ser Gly Leu Gln
                325                 330                 335

Met Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn Asp Ile Asp Met
            340                 345                 350

Leu Ser Ala Ala Gly Leu Gly Ile Ala Phe Asn Ala Lys Pro Ala Leu
        355                 360                 365

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

Leu His Ile Leu Gly Val Pro Arg Glu Glu Ile Asp Glu Ser Asp Leu
385                 390                 395                 400

Glu Asp Gly Thr Phe Arg Arg Val Pro Leu Glu Val Ser Ala Arg
                405                 410                 415
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<210> 69
<211> 1731
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1431)
<223> gene serC

<400> 69
ctgtgcagtt gtgctgccac cgcacggtgt ttgcgctgct cccttggggg gagggccgcc 60

gtccatgagg tggaacaggg cacagtttag caaatgatgt gatggaggca acagatttca 120

gaaaagcagg tcacccccat tgaatttgcg aggataagcc cctttgccta ccccagcaac 180

taccccgtt gtcggtgtca accctaacac ccgggttccg gtcaacgggt gggaggggag 240

atactaaggt tgttctcgat tggacagcac ttcaccgacc acgaaaggga cgtcatctcc 300

atg acc gag ttc ccc acc ctc ccc gca gat ctc ctc ccg gca gac ggt 348
Met Thr Glu Phe Pro Thr Leu Pro Ala Asp Leu Leu Pro Ala Asp Gly
1 5 10 15

cgt ttc ggc tgc ggc ccc tcc aag gtc cgc ccg gag cag atc cag gcc 396
Arg Phe Gly Cys Gly Pro Ser Lys Val Arg Pro Glu Gln Ile Gln Ala
20 25 30

atc gtc gac ggc ggc cgc gac atc atc ggc acc tcg cac cgc cag ccg 444
Ile Val Asp Gly Gly Arg Asp Ile Ile Gly Thr Ser His Arg Gln Pro
35 40 45

gcc gtg aag aat gtc gtc ggt tcg gtc cgt gag ggc ctc tcc gac ctg 492
Ala Val Lys Asn Val Val Gly Ser Val Arg Glu Gly Leu Ser Asp Leu
50 55 60

ttc tcc ctg ccg gag ggc tac gag atc atc ctg tcc ctc ggt ggc gcc 540
Phe Ser Leu Pro Glu Gly Tyr Glu Ile Ile Leu Ser Leu Gly Gly Ala
65 70 75 80

acc gca ttc tgg gac gcc gcc acc ttc ggc ctc atc gag aag aag tcc 588
Thr Ala Phe Trp Asp Ala Ala Thr Phe Gly Leu Ile Glu Lys Lys Ser
85 90 95

ggt cac ctg tcc tac ggt gag ttc tcc tcc aag ttc gcc aag gcc tcc 636
Gly His Leu Ser Tyr Gly Glu Phe Ser Ser Lys Phe Ala Lys Ala Ser
100 105 110

cag cag gca ccg tgg ctg gat gag ccg acc atc atc gag gcc ccg gcc 684
Gln Gln Ala Pro Trp Leu Asp Glu Pro Thr Ile Ile Glu Ala Pro Ala
115 120 125

ggc gac gcc ccg gag ccg cag gcc atg gag ggc acc gac gtc atc ggc 732
Gly Asp Ala Pro Glu Pro Gln Ala Met Glu Gly Thr Asp Val Ile Gly
130 135 140

```
tgg gcc cac aac gag acc tcc acc ggc gcc atg gtg ccg atc gtc cgc        780
Trp Ala His Asn Glu Thr Ser Thr Gly Ala Met Val Pro Ile Val Arg
145                 150                 155                 160

ccg gag ggc tcc gac ggc tcc ctc atc gtc atc gac gcc acc tcc ggc        828
Pro Glu Gly Ser Asp Gly Ser Leu Ile Val Ile Asp Ala Thr Ser Gly
                165                 170                 175

gcc ggc ggc ctc ccg gtg aac atc gcc gac acc gac gtc tac tac ttc        876
Ala Gly Gly Leu Pro Val Asn Ile Ala Asp Thr Asp Val Tyr Tyr Phe
            180                 185                 190

tcc ccg cag aag tgc ttc gcc tcc gac ggt ggc ctg tgg ctc gcc gcc        924
Ser Pro Gln Lys Cys Phe Ala Ser Asp Gly Gly Leu Trp Leu Ala Ala
        195                 200                 205

atg tcc ccg gcc gcc atg gag cgc atc gcg aag atc aag gag tcc ggc        972
Met Ser Pro Ala Ala Met Glu Arg Ile Ala Lys Ile Lys Glu Ser Gly
    210                 215                 220

cgc cac atc ccg gcg ttc ctg gac ctg cag acc gcc gtc gag aac tcc       1020
Arg His Ile Pro Ala Phe Leu Asp Leu Gln Thr Ala Val Glu Asn Ser
225                 230                 235                 240

ctg aag aac cag acc tac aac acc ccg gcc gtg ggc acc ctg ctc atg       1068
Leu Lys Asn Gln Thr Tyr Asn Thr Pro Ala Val Gly Thr Leu Leu Met
                245                 250                 255

ctg gac aac cag gtc aag tgg atg aac gag aac ggt ggc ctg gac ggc       1116
Leu Asp Asn Gln Val Lys Trp Met Asn Glu Asn Gly Gly Leu Asp Gly
            260                 265                 270

atg gtc gcc cgc acc acc gcc tcc tcc gac gcc ctg tac aac tgg gcc       1164
Met Val Ala Arg Thr Thr Ala Ser Ser Asp Ala Leu Tyr Asn Trp Ala
        275                 280                 285

gag gcc cgc gag gag acc acc ccg tac gtc acc gac aag gcg aag cgc       1212
Glu Ala Arg Glu Glu Thr Thr Pro Tyr Val Thr Asp Lys Ala Lys Arg
    290                 295                 300

tcc ctc gtc gtc ggc acc atc gac ttc gac gac tcc gtc gac gcg gcg       1260
Ser Leu Val Val Gly Thr Ile Asp Phe Asp Asp Ser Val Asp Ala Ala
305                 310                 315                 320

gtc gtc gcc aag gtc ctg cgt gcc aac ggc atc ctc gac gtc gag ccc       1308
Val Val Ala Lys Val Leu Arg Ala Asn Gly Ile Leu Asp Val Glu Pro
                325                 330                 335

tac cgc aag ctg ggc cgc aac cag ctg cgc atc ggc atg ttc ccg gcg       1356
Tyr Arg Lys Leu Gly Arg Asn Gln Leu Arg Ile Gly Met Phe Pro Ala
            340                 345                 350

atc gac tcc cag gac atc gtg acc ctc acc aag gcg atc gac cac gtc       1404
Ile Asp Ser Gln Asp Ile Val Thr Leu Thr Lys Ala Ile Asp His Val
        355                 360                 365

ctc gac tcg ggc gtc gcc gcc aag tag tcgccaggta gtcgcgggca             1451
Leu Asp Ser Gly Val Ala Ala Lys
    370                 375
```

cccgcacacc acccaacatg cgtcggacct cacacggtcc ggcgcatgtc tgcgttaggg 1511

tggtattcat cacgagagaa ggagaacgca tgcgcgagtt gttcctcgtc cctgaagagt 1571

cctcggccac ttccctggtg ttccggaccg aggacggcgg acagttcttc ctcgacgtca 1631

cttcactgga cgtggcctcc acccgtgcgc tcctgcttgc cgacgtcccg gaggacccct 1691

cccccacgga gtccggcacc gccgccgtca ccgccgtcga 1731

<210> 70
<211> 376
<212> PRT
<213> Corynebacterium humireducens

<400> 70

Met Thr Glu Phe Pro Thr Leu Pro Ala Asp Leu Leu Pro Ala Asp Gly
1 5 10 15

Arg Phe Gly Cys Gly Pro Ser Lys Val Arg Pro Glu Gln Ile Gln Ala
20 25 30

Ile Val Asp Gly Gly Arg Asp Ile Ile Gly Thr Ser His Arg Gln Pro
35 40 45

Ala Val Lys Asn Val Val Gly Ser Val Arg Glu Gly Leu Ser Asp Leu
50 55 60

Phe Ser Leu Pro Glu Gly Tyr Glu Ile Ile Leu Ser Leu Gly Gly Ala
65 70 75 80

Thr Ala Phe Trp Asp Ala Ala Thr Phe Gly Leu Ile Glu Lys Lys Ser
85 90 95

Gly His Leu Ser Tyr Gly Glu Phe Ser Ser Lys Phe Ala Lys Ala Ser
100 105 110

Gln Gln Ala Pro Trp Leu Asp Glu Pro Thr Ile Ile Glu Ala Pro Ala
115 120 125

Gly Asp Ala Pro Glu Pro Gln Ala Met Glu Gly Thr Asp Val Ile Gly
130 135 140

Trp Ala His Asn Glu Thr Ser Thr Gly Ala Met Val Pro Ile Val Arg
145 150 155 160

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

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

Ser Pro Gln Lys Cys Phe Ala Ser Asp Gly Gly Leu Trp Leu Ala Ala
        195                 200                 205

Met Ser Pro Ala Ala Met Glu Arg Ile Ala Lys Ile Lys Glu Ser Gly
    210                 215                 220

Arg His Ile Pro Ala Phe Leu Asp Leu Gln Thr Ala Val Glu Asn Ser
225                 230                 235                 240

Leu Lys Asn Gln Thr Tyr Asn Thr Pro Ala Val Gly Thr Leu Leu Met
                245                 250                 255

Leu Asp Asn Gln Val Lys Trp Met Asn Glu Asn Gly Gly Leu Asp Gly
            260                 265                 270

Met Val Ala Arg Thr Thr Ala Ser Ser Asp Ala Leu Tyr Asn Trp Ala
        275                 280                 285

Glu Ala Arg Glu Glu Thr Thr Pro Tyr Val Thr Asp Lys Ala Lys Arg
    290                 295                 300

Ser Leu Val Val Gly Thr Ile Asp Phe Asp Asp Ser Val Asp Ala Ala
305                 310                 315                 320

Val Val Ala Lys Val Leu Arg Ala Asn Gly Ile Leu Asp Val Glu Pro
                325                 330                 335

Tyr Arg Lys Leu Gly Arg Asn Gln Leu Arg Ile Gly Met Phe Pro Ala
            340                 345                 350

Ile Asp Ser Gln Asp Ile Val Thr Leu Thr Lys Ala Ile Asp His Val
        355                 360                 365

Leu Asp Ser Gly Val Ala Ala Lys
    370                 375
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<210> 71
<211> 1665
<212> DNA

<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1365)
<223> gene Alanine-Dehydrogenase

<400> 71
acctctcgct cagccacctg cgccgcgcga cgaactcctc gcggaagtag ccgaggtggg 60

cggtcggccc gccgaaggcg gtgacgccca gcagcccgaa gctgcggatg acctctcctg 120

tggtgccgtt gttcttgtct gcggattcct tcacgctcgt catggtaggg cggggcgtcg 180

agaagtgcgc gtcgagcgac agtaaccggg attacatcat taaccagccg gttccgacga 240

gcgtccggaa ggcgcctagt agagtcagtg gtcatgcgta tcggaatccc gaaggaaatc 300

atg aac atg gag ggc cgc gtg gcc ctc agc ccg ctc ggg gca ggc acc 348
Met Asn Met Glu Gly Arg Val Ala Leu Ser Pro Leu Gly Ala Gly Thr
1 5 10 15

ctc gta gcc gac ggc cat gag gtg att gtt cag gcc ggg gcg ggc gag 396
Leu Val Ala Asp Gly His Glu Val Ile Val Gln Ala Gly Ala Gly Glu
20 25 30

aac tcc tcg ttc acc gat gcc gag tac gag gcg acg ggc gcg cgc gtc 444
Asn Ser Ser Phe Thr Asp Ala Glu Tyr Glu Ala Thr Gly Ala Arg Val
35 40 45

gtc gcc tcc gcg gag gag gcc tgg ggc gcc gag atg gtg ctc aag gtc 492
Val Ala Ser Ala Glu Glu Ala Trp Gly Ala Glu Met Val Leu Lys Val
50 55 60

aag gag ccg ctg ccg gag gag tac ggc ttc ctc cgc ccg gac ctc atc 540
Lys Glu Pro Leu Pro Glu Glu Tyr Gly Phe Leu Arg Pro Asp Leu Ile
65 70 75 80

ctg ttc acc tac ctg cac ctg gcg tcc tcg cgt gag tgc acg aag gcg 588
Leu Phe Thr Tyr Leu His Leu Ala Ser Ser Arg Glu Cys Thr Lys Ala
85 90 95

ctg ctc gac gcc ggc acc ctg tcc ctg gcg tac gag acg gtc ctc gac 636
Leu Leu Asp Ala Gly Thr Leu Ser Leu Ala Tyr Glu Thr Val Leu Asp
100 105 110

gcc cgc ggc ggc ctc ccg ctg ctc acc ccg atg tcc cag gtc gcg ggc 684
Ala Arg Gly Gly Leu Pro Leu Leu Thr Pro Met Ser Gln Val Ala Gly
115 120 125

cgc ctc gcc gtg cag gag ggc gcg cac cac ctc atg agc tcc aag ggg 732
Arg Leu Ala Val Gln Glu Gly Ala His His Leu Met Ser Ser Lys Gly
130 135 140

ggc cgc ggc gtg ctg ctc ggt ggc gtg ccc ggc acc gcc ccg gcg aag 780
Gly Arg Gly Val Leu Leu Gly Gly Val Pro Gly Thr Ala Pro Ala Lys
145 150 155 160

```
gtc gtc gtc ctc ggc ggc ggt cag gtc ggc gcc tcg gcc gtc gcg atc        828
Val Val Val Leu Gly Gly Gly Gln Val Gly Ala Ser Ala Val Ala Ile
                165                 170                 175

gcg cag ggt ctg cgc gcc agc gtc acg gtc ctc gac ctc gac ccg cag        876
Ala Gln Gly Leu Arg Ala Ser Val Thr Val Leu Asp Leu Asp Pro Gln
            180                 185                 190

gtg ctc gcg cgt ttc gac gac ctc tac cag ggc aac gtc cgc acc ctg        924
Val Leu Ala Arg Phe Asp Asp Leu Tyr Gln Gly Asn Val Arg Thr Leu
        195                 200                 205

ctg tcc gac ccg atg acc atc gag acc gag ctt ctc gac gcc gac ctc        972
Leu Ser Asp Pro Met Thr Ile Glu Thr Glu Leu Leu Asp Ala Asp Leu
    210                 215                 220

gtc atc ggc gcc gtc ctc gtc gcc ggc gcg aag gcc ccg acg ctg gtc       1020
Val Ile Gly Ala Val Leu Val Ala Gly Ala Lys Ala Pro Thr Leu Val
225                 230                 235                 240

agc gac gac ctg gtc gcc cgc atg aag cag ggc gcc gtg ctc gtc gac       1068
Ser Asp Asp Leu Val Ala Arg Met Lys Gln Gly Ala Val Leu Val Asp
                245                 250                 255

gtc gcc atc gac cag ggc ggc tgc ttc gag ccc tcc cgc aag acc tcc       1116
Val Ala Ile Asp Gln Gly Gly Cys Phe Glu Pro Ser Arg Lys Thr Ser
            260                 265                 270

cac gag gac ccg acc tac gag gtc cac ggc acc cgc ttc tac tgc gtg       1164
His Glu Asp Pro Thr Tyr Glu Val His Gly Thr Arg Phe Tyr Cys Val
        275                 280                 285

ccc aac atg ccc ggc gcg gtg gcc aac acc tcg acc cgg gcg ctc acc       1212
Pro Asn Met Pro Gly Ala Val Ala Asn Thr Ser Thr Arg Ala Leu Thr
    290                 295                 300

tcg gcg acc ctg ccc tac gtc cgc gcg atc gcg gcg ggc ggc gtg gac       1260
Ser Ala Thr Leu Pro Tyr Val Arg Ala Ile Ala Ala Gly Gly Val Asp
305                 310                 315                 320

cgg gcg gtg gac aac cac ccg ggt ctg gag ccg ggc atc atg acc tgc       1308
Arg Ala Val Asp Asn His Pro Gly Leu Glu Pro Gly Ile Met Thr Cys
                325                 330                 335

gac ggc cgc ctg atc agt gag cca gtg aag gag gcg ttc ccg gat ctt       1356
Asp Gly Arg Leu Ile Ser Glu Pro Val Lys Glu Ala Phe Pro Asp Leu
            340                 345                 350

ctc ggt tga tgagcatcgc cgccacccgc tccatgtgat cccagatctg               1405
Leu Gly

gtggcggtac ccggcgggga tggtctcctc gtcgatgctg tcgagtgaca ccttcatcag    1465

ctccagccag cggatcgcag ccgcgcggtc cacggggaac tcgtggtggc ggcggcgcag    1525

catcggggcg ccgcgcttct cgttgaaggt ggccggtccg ccccagtact gggcgaggaa    1585

ccacttgagg cggttctcgg cgccctccca gtcgtcctcg gggtacatgg gccccaggat    1645
```

gtcgtccgtc ttcacctgcg 1665

<210> 72
<211> 354
<212> PRT
<213> Corynebacterium humireducens

<400> 72

Met Asn Met Glu Gly Arg Val Ala Leu Ser Pro Leu Gly Ala Gly Thr
1 5 10 15

Leu Val Ala Asp Gly His Glu Val Ile Val Gln Ala Gly Ala Gly Glu
20 25 30

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

Val Ala Ser Ala Glu Glu Ala Trp Gly Ala Glu Met Val Leu Lys Val
50 55 60

Lys Glu Pro Leu Pro Glu Glu Tyr Gly Phe Leu Arg Pro Asp Leu Ile
65 70 75 80

Leu Phe Thr Tyr Leu His Leu Ala Ser Ser Arg Glu Cys Thr Lys Ala
85 90 95

Leu Leu Asp Ala Gly Thr Leu Ser Leu Ala Tyr Glu Thr Val Leu Asp
100 105 110

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

Arg Leu Ala Val Gln Glu Gly Ala His His Leu Met Ser Ser Lys Gly
130 135 140

Gly Arg Gly Val Leu Leu Gly Gly Val Pro Gly Thr Ala Pro Ala Lys
145 150 155 160

Val Val Val Leu Gly Gly Gly Gln Val Gly Ala Ser Ala Val Ala Ile
165 170 175

Ala Gln Gly Leu Arg Ala Ser Val Thr Val Leu Asp Leu Asp Pro Gln
180 185 190

Val Leu Ala Arg Phe Asp Asp Leu Tyr Gln Gly Asn Val Arg Thr Leu
195 200 205

Leu Ser Asp Pro Met Thr Ile Glu Thr Glu Leu Leu Asp Ala Asp Leu
210 215 220

Val Ile Gly Ala Val Leu Val Ala Gly Ala Lys Ala Pro Thr Leu Val
225 230 235 240

Ser Asp Asp Leu Val Ala Arg Met Lys Gln Gly Ala Val Leu Val Asp
245 250 255

Val Ala Ile Asp Gln Gly Gly Cys Phe Glu Pro Ser Arg Lys Thr Ser
260 265 270

His Glu Asp Pro Thr Tyr Glu Val His Gly Thr Arg Phe Tyr Cys Val
275 280 285

Pro Asn Met Pro Gly Ala Val Ala Asn Thr Ser Thr Arg Ala Leu Thr
290 295 300

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

Arg Ala Val Asp Asn His Pro Gly Leu Glu Pro Gly Ile Met Thr Cys
325 330 335

Asp Gly Arg Leu Ile Ser Glu Pro Val Lys Glu Ala Phe Pro Asp Leu
340 345 350

Leu Gly

<210> 73
<211> 1515
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1215)
<223> gene cysD

<400> 73
cctgaccccg tacgcggggt gggtcaccgg cctgcgccgc gctgacggac cgacccgggc 60

gcacgccccg gcgctcagcc ttgacgcgac ggggcggctg aagatctcgc cgctggtcac 120

```
gtggtccctc gtggacacgg aggcgttcat cgcggaccac gacctcatcc gacacccccc t      180

gaccacgcag ggctacccgt ccatcgggtg cgccacctgc accctccccg tcgccgacgg      240

ggaggatccc cgggccggcc gctgggccgg acagaacaag acagaatgcg ggctccactc      300

atg acc acc acc acc ctc acc aga ctc tcc ccc cat ctg cag gac ctc        348
Met Thr Thr Thr Thr Leu Thr Arg Leu Ser Pro His Leu Gln Asp Leu
1               5                  10                  15

gag aac gag tcc atc cac atc ctc cgg gag gtg gcc ggg cag ttc gac        396
Glu Asn Glu Ser Ile His Ile Leu Arg Glu Val Ala Gly Gln Phe Asp
            20                  25                  30

cgg gtc ggg ctg ctg ttc tcc ggc ggc aag gac tcc gtc gtc gtg ctc        444
Arg Val Gly Leu Leu Phe Ser Gly Gly Lys Asp Ser Val Val Val Leu
        35                  40                  45

gag ctg gcg cgc cgg gcc ttc gct ccg gcg gcc gtg ccc ttc gag ctg        492
Glu Leu Ala Arg Arg Ala Phe Ala Pro Ala Ala Val Pro Phe Glu Leu
    50                  55                  60

ctc cac gtg gac acc ggc cac aac ttc ccc gag gtc atc gag ttc cgt        540
Leu His Val Asp Thr Gly His Asn Phe Pro Glu Val Ile Glu Phe Arg
65                  70                  75                  80

gac cga gtc gtc gcc gag acc ggc gtg cgg ctg cgc gtc gcg cac gtg        588
Asp Arg Val Val Ala Glu Thr Gly Val Arg Leu Arg Val Ala His Val
                85                  90                  95

cag gac tgg atc gac cgc ggt gac ctc gtc gaa cgt ccc gac ggc acc        636
Gln Asp Trp Ile Asp Arg Gly Asp Leu Val Glu Arg Pro Asp Gly Thr
            100                 105                 110

cgc aat ccc ctg cag acc gtc ccc ctc gtg gag acc atc gcc gag cag        684
Arg Asn Pro Leu Gln Thr Val Pro Leu Val Glu Thr Ile Ala Glu Gln
        115                 120                 125

ggc tac gac gcc gtc ctc ggt ggc gcc cgc cgc gac gag gag cgg gcg        732
Gly Tyr Asp Ala Val Leu Gly Gly Ala Arg Arg Asp Glu Glu Arg Ala
    130                 135                 140

cgc gcc aag gag cgt gtc ttc tcc gtg cgc gac tcc ttc ggc ggc tgg        780
Arg Ala Lys Glu Arg Val Phe Ser Val Arg Asp Ser Phe Gly Gly Trp
145                 150                 155                 160

gat ccg cgc cgc cag cgc ccg gag ctg tgg cac ctc tac aac ggc ggc        828
Asp Pro Arg Arg Gln Arg Pro Glu Leu Trp His Leu Tyr Asn Gly Gly
                165                 170                 175

cac ctg ccg ggc gag aac gtc cgc gtc ttc ccc atc tcc aac tgg acc        876
His Leu Pro Gly Glu Asn Val Arg Val Phe Pro Ile Ser Asn Trp Thr
            180                 185                 190

gag gcc gac atc tgg gag tac atc ggc gcc cgc ggc atc gcg ctg ccg        924
Glu Ala Asp Ile Trp Glu Tyr Ile Gly Ala Arg Gly Ile Ala Leu Pro
        195                 200                 205
```

```
gag atc tac ttc gcg cat gag cgg gcc gtc ttc gag cgg gac ggc atg        972
Glu Ile Tyr Phe Ala His Glu Arg Ala Val Phe Glu Arg Asp Gly Met
    210                 215                 220

tgg ctg acc gcc ggc gag tgg ggt ggg ccc cgc gag ggc gag acc ctc       1020
Trp Leu Thr Ala Gly Glu Trp Gly Gly Pro Arg Glu Gly Glu Thr Leu
225                 230                 235                 240

gag gtc cgc cgc gtg cgc tac cgc acc gtc ggc gac atg tcc tgc acc       1068
Glu Val Arg Arg Val Arg Tyr Arg Thr Val Gly Asp Met Ser Cys Thr
                245                 250                 255

ggt gcg gtg ctc tcc gac gcc acc acg gtc gac gac gtc atc gcc gag       1116
Gly Ala Val Leu Ser Asp Ala Thr Thr Val Asp Asp Val Ile Ala Glu
            260                 265                 270

atc gcc acc tcc acc ctc acc gag cgc ggg gcc acc cgc gcc gac gac       1164
Ile Ala Thr Ser Thr Leu Thr Glu Arg Gly Ala Thr Arg Ala Asp Asp
        275                 280                 285

cgc ctc agt gaa tcc gcc atg gaa gac cgc aag aag gaa ggc tac ttc       1212
Arg Leu Ser Glu Ser Ala Met Glu Asp Arg Lys Lys Glu Gly Tyr Phe
    290                 295                 300

tga tgaccaccac gctcctgcgc acccgcgaga cgctgcgcct gtgcaccgcc            1265

ggctccgtcg acgacggcaa gtccaccctc gtgggccgcc tgctccacga cacccgctcc     1325

gtcctcgccg accagctcgc cgccgtcgag cgcacctccg ccgaccgcgg tttccacggc     1385

ggcctggacc tctcactgct cgtcgacggc ctccgcgccg aacgcgagca gggcatcacc     1445

atcgacgtgg cctaccgcta cttcgccacc gaccgccgca ccttcatcct cgccgacacc     1505

cccggccacg                                                           1515
```

<210> 74
<211> 304
<212> PRT
<213> Corynebacterium humireducens

<400> 74

```
Met Thr Thr Thr Thr Leu Thr Arg Leu Ser Pro His Leu Gln Asp Leu
1               5                   10                  15

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

Arg Val Gly Leu Leu Phe Ser Gly Gly Lys Asp Ser Val Val Val Leu
        35                  40                  45

Glu Leu Ala Arg Arg Ala Phe Ala Pro Ala Ala Val Pro Phe Glu Leu
    50                  55                  60
```

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

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

Gln Asp Trp Ile Asp Arg Gly Asp Leu Val Glu Arg Pro Asp Gly Thr
100 105 110

Arg Asn Pro Leu Gln Thr Val Pro Leu Val Glu Thr Ile Ala Glu Gln
115 120 125

Gly Tyr Asp Ala Val Leu Gly Gly Ala Arg Arg Asp Glu Glu Arg Ala
130 135 140

Arg Ala Lys Glu Arg Val Phe Ser Val Arg Asp Ser Phe Gly Gly Trp
145 150 155 160

Asp Pro Arg Arg Gln Arg Pro Glu Leu Trp His Leu Tyr Asn Gly Gly
165 170 175

His Leu Pro Gly Glu Asn Val Arg Val Phe Pro Ile Ser Asn Trp Thr
180 185 190

Glu Ala Asp Ile Trp Glu Tyr Ile Gly Ala Arg Gly Ile Ala Leu Pro
195 200 205

Glu Ile Tyr Phe Ala His Glu Arg Ala Val Phe Glu Arg Asp Gly Met
210 215 220

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

Glu Val Arg Arg Val Arg Tyr Arg Thr Val Gly Asp Met Ser Cys Thr
245 250 255

Gly Ala Val Leu Ser Asp Ala Thr Thr Val Asp Asp Val Ile Ala Glu
260 265 270

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

Arg Leu Ser Glu Ser Ala Met Glu Asp Arg Lys Lys Glu Gly Tyr Phe
290 295 300

<210> 75
<211> 1575
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1275)
<223> gene cysH

<400> 75
cgtgcgcatc gccgtcaacg gctgccccaa ctcgtgtgcc cgcacgcagg tcgcggacat 60

cggcttcaag ggccagaccg tcaccgacgc cgacggcaac cgggtcgagg gcttccaggt 120

gcacctcggc gggtcgatga gcctcaacgc caacttcggc cgcaagctcc gcggccacaa 180

ggtgctcgcc gacgacatcg gggactacgt cacccgcgtg gtcacccact tccgggacca 240

gcgccgaccg gaggagacct tccaggagtg ggtccagcgc gccgccgagg aggacctcca 300

gtg agt ttc cgt cgc gcc ccc aac ccg aac cgc aac cat ccg ctg cac 348
Val Ser Phe Arg Arg Ala Pro Asn Pro Asn Arg Asn His Pro Leu His
1 5 10 15

tgc ccg tgg tgc gcc ggc gag gat ctg ctg ccc aac acg gag gac gac 396
Cys Pro Trp Cys Ala Gly Glu Asp Leu Leu Pro Asn Thr Glu Asp Asp
20 25 30

ttc gcc tgg ctg tgc cgc gac tgc acc cgg gtg ttc tcc gtc cgc tac 444
Phe Ala Trp Leu Cys Arg Asp Cys Thr Arg Val Phe Ser Val Arg Tyr
35 40 45

cac ggg cag gac gcc ccg gcg cgc cga ccg gcc ccg gca ctc tcc acg 492
His Gly Gln Asp Ala Pro Ala Arg Arg Pro Ala Pro Ala Leu Ser Thr
50 55 60

agt gcg gcg atc cag ctc tcc ctg tcc cgt cgc ggc cac ctc aac gac 540
Ser Ala Ala Ile Gln Leu Ser Leu Ser Arg Arg Gly His Leu Asn Asp
65 70 75 80

ccc gcc gtc agc ccg gca ggc ccc acc gcc acc ggg gac ctg ccg ggg 588
Pro Ala Val Ser Pro Ala Gly Pro Thr Ala Thr Gly Asp Leu Pro Gly
85 90 95

gcg gtg cgg gag gag aac gcg cgg ctc gtc gag aag cac gcg gat gag 636
Ala Val Arg Glu Glu Asn Ala Arg Leu Val Glu Lys His Ala Asp Glu
100 105 110

ctg tac gac gcc ccc gcc gac gtc atc ctg gcg tgg gcc cgg gag cac 684
Leu Tyr Asp Ala Pro Ala Asp Val Ile Leu Ala Trp Ala Arg Glu His
115 120 125

gtg ccg ggt cgc ctc gcg gtg acg ctc tcg atg gag aac acc gtc ctc 732
Val Pro Gly Arg Leu Ala Val Thr Leu Ser Met Glu Asn Thr Val Leu
130 135 140

```
gcg gag ctg gcc gcc cgg cac acg ccc gac gcc gac ctg ctc ttc ctc        780
Ala Glu Leu Ala Ala Arg His Thr Pro Asp Ala Asp Leu Leu Phe Leu
145                 150                 155                 160

gac acc ggc tac cac ttc gag gag acg ctg gcg gtg gcg cgg gac gtc        828
Asp Thr Gly Tyr His Phe Glu Glu Thr Leu Ala Val Ala Arg Asp Val
                165                 170                 175

gac agg cgg tac ccg cag acg ctg gtg acc gcg acg ccg acg ctc acc        876
Asp Arg Arg Tyr Pro Gln Thr Leu Val Thr Ala Thr Pro Thr Leu Thr
            180                 185                 190

cgg gcg gag cag gac gcc gcc tac ggg ccc ggc ctg tac cgg cgc gac        924
Arg Ala Glu Gln Asp Ala Ala Tyr Gly Pro Gly Leu Tyr Arg Arg Asp
        195                 200                 205

ccg gcc gcg tgc tgc cgc atg cgc aag gtc gag ccg ctg gcc gtg cac        972
Pro Ala Ala Cys Cys Arg Met Arg Lys Val Glu Pro Leu Ala Val His
    210                 215                 220

ctg acc ccg tac gcg ggg tgg gtc acc ggc ctg cgc cgc gct gac gga       1020
Leu Thr Pro Tyr Ala Gly Trp Val Thr Gly Leu Arg Arg Ala Asp Gly
225                 230                 235                 240

ccg acc cgg gcg cac gcc ccg gcg ctc agc ctt gac gcg acg ggg cgg       1068
Pro Thr Arg Ala His Ala Pro Ala Leu Ser Leu Asp Ala Thr Gly Arg
                245                 250                 255

ctg aag atc tcg ccg ctg gtc acg tgg tcc ctc gtg gac acg gag gcg       1116
Leu Lys Ile Ser Pro Leu Val Thr Trp Ser Leu Val Asp Thr Glu Ala
            260                 265                 270

ttc atc gcg gac cac gac ctc atc cga cac ccc ctg acc acg cag ggc       1164
Phe Ile Ala Asp His Asp Leu Ile Arg His Pro Leu Thr Thr Gln Gly
        275                 280                 285

tac ccg tcc atc ggg tgc gcc acc tgc acc ctc ccc gtc gcc gac ggg       1212
Tyr Pro Ser Ile Gly Cys Ala Thr Cys Thr Leu Pro Val Ala Asp Gly
    290                 295                 300

gag gat ccc cgg gcc ggc cgc tgg gcc gga cag aac aag aca gaa tgc       1260
Glu Asp Pro Arg Ala Gly Arg Trp Ala Gly Gln Asn Lys Thr Glu Cys
305                 310                 315                 320

ggg ctc cac tca tga ccaccaccac cctcaccaga ctctcccccc atctgcagga       1315
Gly Leu His Ser

cctcgagaac gagtccatcc acatcctccg ggaggtggcc gggcagttcg accgggtcgg      1375

gctgctgttc tccggcggca aggactccgt cgtcgtgctc gagctggcgc gccgggcctt      1435

cgctccggcg gccgtgccct tcgagctgct ccacgtggac accggccaca acttccccga      1495

ggtcatcgag ttccgtgacc gagtcgtcgc cgagaccggc gtgcggctgc gcgtcgcgca      1555

cgtgcaggac tggatcgacc                                                 1575
```

<210> 76
<211> 324
<212> PRT
<213> Corynebacterium humireducens

<400> 76

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

Cys Pro Trp Cys Ala Gly Glu Asp Leu Leu Pro Asn Thr Glu Asp Asp
20 25 30

Phe Ala Trp Leu Cys Arg Asp Cys Thr Arg Val Phe Ser Val Arg Tyr
35 40 45

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

Ser Ala Ala Ile Gln Leu Ser Leu Ser Arg Arg Gly His Leu Asn Asp
65 70 75 80

Pro Ala Val Ser Pro Ala Gly Pro Thr Ala Thr Gly Asp Leu Pro Gly
85 90 95

Ala Val Arg Glu Glu Asn Ala Arg Leu Val Glu Lys His Ala Asp Glu
100 105 110

Leu Tyr Asp Ala Pro Ala Asp Val Ile Leu Ala Trp Ala Arg Glu His
115 120 125

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

Ala Glu Leu Ala Ala Arg His Thr Pro Asp Ala Asp Leu Leu Phe Leu
145 150 155 160

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

Asp Arg Arg Tyr Pro Gln Thr Leu Val Thr Ala Thr Pro Thr Leu Thr
180 185 190

Arg Ala Glu Gln Asp Ala Ala Tyr Gly Pro Gly Leu Tyr Arg Arg Asp
195 200 205

```
Pro Ala Ala Cys Cys Arg Met Arg Lys Val Glu Pro Leu Ala Val His
    210                 215                 220

Leu Thr Pro Tyr Ala Gly Trp Val Thr Gly Leu Arg Arg Ala Asp Gly
225                 230                 235                 240

Pro Thr Arg Ala His Ala Pro Ala Leu Ser Leu Asp Ala Thr Gly Arg
                245                 250                 255

Leu Lys Ile Ser Pro Leu Val Thr Trp Ser Leu Val Asp Thr Glu Ala
            260                 265                 270

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

Tyr Pro Ser Ile Gly Cys Ala Thr Cys Thr Leu Pro Val Ala Asp Gly
    290                 295                 300

Glu Asp Pro Arg Ala Gly Arg Trp Ala Gly Gln Asn Lys Thr Glu Cys
305                 310                 315                 320

Gly Leu His Ser
```

<210> 77
<211> 2295
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1995)
<223> gene cysI

<400> 77

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gaaagtagca cccctgggcg gtaatgcaag cgaaaaggcg acttcaattc agggtccggg       60

catcgctctt cgacgccccc aattcaattc agtgaatgta tgtcggatat aaacactacg      120

tacagccatg atcgggaaag ttgcccaaaa tcatgacgta tctacatctc tccaccattg      180

ccatgaactg atctgtctgc tctaatccac tgcagacgcc ccggcagggg ctccgtggcg      240

gcgcccggcg ccgaatccac gtgaatgaaa tagacagaac agttcagtag ggagatggtc      300

atg gac acg acc acc acg atc gag aag gca ccc cgc cgc gag cgc ccc         348
Met Asp Thr Thr Thr Thr Ile Glu Lys Ala Pro Arg Arg Glu Arg Pro
1               5                   10                  15
```

```
aga cgc gcc cgc aag ccg gag ggc cag tgg cgg atc gac ggc acc acg        396
Arg Arg Ala Arg Lys Pro Glu Gly Gln Trp Arg Ile Asp Gly Thr Thr
            20                  25                  30

ccg ctc aac cac gtg gag gag gtg aag cag gac ggc gac atc ctc gcc        444
Pro Leu Asn His Val Glu Glu Val Lys Gln Asp Gly Asp Ile Leu Ala
        35                  40                  45

gtc tac gac cgg gtg gtc aac atc tac tcg aag cag ggt ttc gac tcc        492
Val Tyr Asp Arg Val Val Asn Ile Tyr Ser Lys Gln Gly Phe Asp Ser
    50                  55                  60

atc ccc gcc gac gac ctc gcc ccg cgc ttc aag tgg ctg ggc ctg tac        540
Ile Pro Ala Asp Asp Leu Ala Pro Arg Phe Lys Trp Leu Gly Leu Tyr
65                  70                  75                  80

acg cag cgc cgc cag gat ctc ggc ggt gag ctc acc ggc cag ctg ccc        588
Thr Gln Arg Arg Gln Asp Leu Gly Gly Glu Leu Thr Gly Gln Leu Pro
                85                  90                  95

gac gcc gag ctg cag gac cgc tac ttc atg atg cgc gtg cgt ttc gag        636
Asp Ala Glu Leu Gln Asp Arg Tyr Phe Met Met Arg Val Arg Phe Glu
            100                 105                 110

ggc ggc cag gta acc ccg gcc cgc ctc cgc gcg gtg ggg gag atc tcc        684
Gly Gly Gln Val Thr Pro Ala Arg Leu Arg Ala Val Gly Glu Ile Ser
        115                 120                 125

cgc gac tac gcc cgc agc acc gcg gac ttc acc gat cgg cag aac atc        732
Arg Asp Tyr Ala Arg Ser Thr Ala Asp Phe Thr Asp Arg Gln Asn Ile
    130                 135                 140

cag ctg cac tgg ctg cgc atc gag gac atc ccg gcg atc tgg gag aag        780
Gln Leu His Trp Leu Arg Ile Glu Asp Ile Pro Ala Ile Trp Glu Lys
145                 150                 155                 160

ctc gac tcc gtg ggg ctc agc ccc ctg ctg ggc tgc ggt gac gtg ccg        828
Leu Asp Ser Val Gly Leu Ser Pro Leu Leu Gly Cys Gly Asp Val Pro
                165                 170                 175

cgc atc atc ctc ggc tcc ccg gtc gcg ggg gtc gcc gcc gag gag atc        876
Arg Ile Ile Leu Gly Ser Pro Val Ala Gly Val Ala Ala Glu Glu Ile
            180                 185                 190

atc gac gcc acc ccg gcg atc gag cgg atc cag cgc gag cac ctg ccg        924
Ile Asp Ala Thr Pro Ala Ile Glu Arg Ile Gln Arg Glu His Leu Pro
        195                 200                 205

aac ccg gag ttc cac aac ctg ccg cgc aag ttc aag tcc gcg atc tcc        972
Asn Pro Glu Phe His Asn Leu Pro Arg Lys Phe Lys Ser Ala Ile Ser
    210                 215                 220

ggc cac tcg cgc cag gac gtc acc cac gag atc cag gac gtc gcc ttc       1020
Gly His Ser Arg Gln Asp Val Thr His Glu Ile Gln Asp Val Ala Phe
225                 230                 235                 240

atc ggt tcc gtc cac ccc gag cac ggc ccg ggt ttc gag tgc ttc gtc       1068
Ile Gly Ser Val His Pro Glu His Gly Pro Gly Phe Glu Cys Phe Val
                245                 250                 255
```

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ggc ggt ggc ctg tcc acc aac ccg atg ctc gcg cag tcg ctc ggc gcg      1116
Gly Gly Gly Leu Ser Thr Asn Pro Met Leu Ala Gln Ser Leu Gly Ala
            260                 265                 270

tgg atc ccg ctg gag gac gtg ccg gac gtg tgg gcc ggc gtc gcc cgg      1164
Trp Ile Pro Leu Glu Asp Val Pro Asp Val Trp Ala Gly Val Ala Arg
        275                 280                 285

atc ttc cgc gac tac ggt tac cgc cgc ctg cgg aat cgt gcc cgt ctc      1212
Ile Phe Arg Asp Tyr Gly Tyr Arg Arg Leu Arg Asn Arg Ala Arg Leu
    290                 295                 300

aag ttc ctc gtg gcg gaa tgg ggg atc gag aag ttc cgg gac gtc ctc      1260
Lys Phe Leu Val Ala Glu Trp Gly Ile Glu Lys Phe Arg Asp Val Leu
305                 310                 315                 320

gag acg gag tac ctc gga cgc ccg ctc atc gac gga ccc cgc cag ccc      1308
Glu Thr Glu Tyr Leu Gly Arg Pro Leu Ile Asp Gly Pro Arg Gln Pro
                325                 330                 335

acc aac ccc ggc tac cgc gac cac atc ggc atc cac ccg cag aag gac      1356
Thr Asn Pro Gly Tyr Arg Asp His Ile Gly Ile His Pro Gln Lys Asp
            340                 345                 350

ggc cgc ttc tac ctg ggc gtg aag ccg acc gtc ggg cac acc acc ggt      1404
Gly Arg Phe Tyr Leu Gly Val Lys Pro Thr Val Gly His Thr Thr Gly
        355                 360                 365

gag cag ctc atc gcc atc gcc gag gtg gcg gag cgt ttc ggc atc gag      1452
Glu Gln Leu Ile Ala Ile Ala Glu Val Ala Glu Arg Phe Gly Ile Glu
    370                 375                 380

cgc atc cgc acc acc tcg gag aag gag ctg ctc ttc ctc gac gtc gag      1500
Arg Ile Arg Thr Thr Ser Glu Lys Glu Leu Leu Phe Leu Asp Val Glu
385                 390                 395                 400

cgc acc gac ctc acc gcc ctg gcc gcc gcc ctc gac gag acc ggc ctg      1548
Arg Thr Asp Leu Thr Ala Leu Ala Ala Ala Leu Asp Glu Thr Gly Leu
                405                 410                 415

tac tcg aag ccg agc gag tgg cgc cgc aac atc atc tcg tgc acc ggc      1596
Tyr Ser Lys Pro Ser Glu Trp Arg Arg Asn Ile Ile Ser Cys Thr Gly
            420                 425                 430

ctg gag ttc tgc aaa ctg gcg cac gcg acg acc aag tcg cgt gcc gtg      1644
Leu Glu Phe Cys Lys Leu Ala His Ala Thr Thr Lys Ser Arg Ala Val
        435                 440                 445

gcc ctg gtc gac gag ctg gag gaa cgc gtc ggc gac atc gac gtg ccc      1692
Ala Leu Val Asp Glu Leu Glu Glu Arg Val Gly Asp Ile Asp Val Pro
    450                 455                 460

gtg cgc atc gcc gtc aac ggc tgc ccc aac tcg tgt gcc cgc acg cag      1740
Val Arg Ile Ala Val Asn Gly Cys Pro Asn Ser Cys Ala Arg Thr Gln
465                 470                 475                 480

gtc gcg gac atc ggc ttc aag ggc cag acc gtc acc gac gcc gac ggc      1788
Val Ala Asp Ile Gly Phe Lys Gly Gln Thr Val Thr Asp Ala Asp Gly
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                485                 490                 495

aac cgg gtc gag ggc ttc cag gtg cac ctc ggc ggg tcg atg agc ctc      1836
Asn Arg Val Glu Gly Phe Gln Val His Leu Gly Gly Ser Met Ser Leu
            500                 505                 510

aac gcc aac ttc ggc cgc aag ctc cgc ggc cac aag gtg ctc gcc gac      1884
Asn Ala Asn Phe Gly Arg Lys Leu Arg Gly His Lys Val Leu Ala Asp
        515                 520                 525

gac atc ggg gac tac gtc acc cgc gtg gtc acc cac ttc cgg gac cag      1932
Asp Ile Gly Asp Tyr Val Thr Arg Val Val Thr His Phe Arg Asp Gln
    530                 535                 540

cgc cga ccg gag gag acc ttc cag gag tgg gtc cag cgc gcc gcc gag      1980
Arg Arg Pro Glu Glu Thr Phe Gln Glu Trp Val Gln Arg Ala Ala Glu
545                 550                 555                 560

gag gac ctc cag tga gtttccgtcg cgcccccaac ccgaaccgca accatccgct      2035
Glu Asp Leu Gln

gcactgcccg tggtgcgccg gcgaggatct gctgcccaac acggaggacg acttcgcctg      2095

gctgtgccgc gactgcaccc gggtgttctc cgtccgctac cacgggcagg acgccccggc      2155

gcgccgaccg gccccggcac tctccacgag tgcggcgatc cagctctccc tgtcccgtcg      2215

cggccacctc aacgaccccg ccgtcagccc ggcaggcccc accgccaccg gggacctgcc      2275

gggggcggtg cgggaggaga                                                 2295
```

<210> 78
<211> 564
<212> PRT
<213> Corynebacterium humireducens

<400> 78

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Met Asp Thr Thr Thr Thr Ile Glu Lys Ala Pro Arg Arg Glu Arg Pro
1               5                   10                  15

Arg Arg Ala Arg Lys Pro Glu Gly Gln Trp Arg Ile Asp Gly Thr Thr
            20                  25                  30

Pro Leu Asn His Val Glu Glu Val Lys Gln Asp Gly Asp Ile Leu Ala
        35                  40                  45

Val Tyr Asp Arg Val Val Asn Ile Tyr Ser Lys Gln Gly Phe Asp Ser
    50                  55                  60

Ile Pro Ala Asp Asp Leu Ala Pro Arg Phe Lys Trp Leu Gly Leu Tyr
65                  70                  75                  80
```

Thr Gln Arg Arg Gln Asp Leu Gly Gly Glu Leu Thr Gly Gln Leu Pro
85 90 95

Asp Ala Glu Leu Gln Asp Arg Tyr Phe Met Met Arg Val Arg Phe Glu
100 105 110

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

Arg Asp Tyr Ala Arg Ser Thr Ala Asp Phe Thr Asp Arg Gln Asn Ile
130 135 140

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

Leu Asp Ser Val Gly Leu Ser Pro Leu Leu Gly Cys Gly Asp Val Pro
165 170 175

Arg Ile Ile Leu Gly Ser Pro Val Ala Gly Val Ala Ala Glu Glu Ile
180 185 190

Ile Asp Ala Thr Pro Ala Ile Glu Arg Ile Gln Arg Glu His Leu Pro
195 200 205

Asn Pro Glu Phe His Asn Leu Pro Arg Lys Phe Lys Ser Ala Ile Ser
210 215 220

Gly His Ser Arg Gln Asp Val Thr His Glu Ile Gln Asp Val Ala Phe
225 230 235 240

Ile Gly Ser Val His Pro Glu His Gly Pro Gly Phe Glu Cys Phe Val
245 250 255

Gly Gly Gly Leu Ser Thr Asn Pro Met Leu Ala Gln Ser Leu Gly Ala
260 265 270

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

Ile Phe Arg Asp Tyr Gly Tyr Arg Arg Leu Arg Asn Arg Ala Arg Leu
290 295 300

Lys Phe Leu Val Ala Glu Trp Gly Ile Glu Lys Phe Arg Asp Val Leu
305 310 315 320

Glu Thr Glu Tyr Leu Gly Arg Pro Leu Ile Asp Gly Pro Arg Gln Pro
325 330 335

Thr Asn Pro Gly Tyr Arg Asp His Ile Gly Ile His Pro Gln Lys Asp
340 345 350

Gly Arg Phe Tyr Leu Gly Val Lys Pro Thr Val Gly His Thr Thr Gly
355 360 365

Glu Gln Leu Ile Ala Ile Ala Glu Val Ala Glu Arg Phe Gly Ile Glu
370 375 380

Arg Ile Arg Thr Thr Ser Glu Lys Glu Leu Leu Phe Leu Asp Val Glu
385 390 395 400

Arg Thr Asp Leu Thr Ala Leu Ala Ala Ala Leu Asp Glu Thr Gly Leu
405 410 415

Tyr Ser Lys Pro Ser Glu Trp Arg Arg Asn Ile Ile Ser Cys Thr Gly
420 425 430

Leu Glu Phe Cys Lys Leu Ala His Ala Thr Thr Lys Ser Arg Ala Val
435 440 445

Ala Leu Val Asp Glu Leu Glu Glu Arg Val Gly Asp Ile Asp Val Pro
450 455 460

Val Arg Ile Ala Val Asn Gly Cys Pro Asn Ser Cys Ala Arg Thr Gln
465 470 475 480

Val Ala Asp Ile Gly Phe Lys Gly Gln Thr Val Thr Asp Ala Asp Gly
485 490 495

Asn Arg Val Glu Gly Phe Gln Val His Leu Gly Gly Ser Met Ser Leu
500 505 510

Asn Ala Asn Phe Gly Arg Lys Leu Arg Gly His Lys Val Leu Ala Asp
515 520 525

Asp Ile Gly Asp Tyr Val Thr Arg Val Val Thr His Phe Arg Asp Gln
530 535 540

Arg Arg Pro Glu Glu Thr Phe Gln Glu Trp Val Gln Arg Ala Ala Glu

545 550 555 560

Glu Asp Leu Gln

<210> 79
<211> 1989
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1689)
<223> gene cysJ

<400> 79
acgtggattc ggcgccgggc gccgccacgg agcccctgcc ggggcgtctg cagtggatta 60

gagcagacag atcagttcat ggcaatggtg gagagatgta gatacgtcat gattttgggc 120

aactttcccg atcatggctg tacgtagtgt ttatatccga catacattca ctgaattgaa 180

ttgggggcgt cgaagagcga tgcccggacc ctgaattgaa gtcgcctttt cgcttgcatt 240

accgcccagg ggtgctactt tcacagacca gtcagtctag tgatttcccg aaaggaaccc 300

atg agc cag ccc acc ctc cgc atc gcc gtc atc ggc gcc ggc ccc gcc 348
Met Ser Gln Pro Thr Leu Arg Ile Ala Val Ile Gly Ala Gly Pro Ala
1 5 10 15

ggc atc tac gcc tcc gac ctc ctg gtg aag aac gcc gcc tcc atc ggc 396
Gly Ile Tyr Ala Ser Asp Leu Leu Val Lys Asn Ala Ala Ser Ile Gly
20 25 30

cgt gag gtc cac gtc gac ctc atc gag aag ctg ccc gcc ccc ttc ggg 444
Arg Glu Val His Val Asp Leu Ile Glu Lys Leu Pro Ala Pro Phe Gly
35 40 45

ctc atc cgc tac ggc gtc gcc ccc gac cac ccg cgc atc aag ggc atc 492
Leu Ile Arg Tyr Gly Val Ala Pro Asp His Pro Arg Ile Lys Gly Ile
50 55 60

atc acc tcc ctg cac cgc gtc ctc gac cgc ccc gag atc cgc ctg ctc 540
Ile Thr Ser Leu His Arg Val Leu Asp Arg Pro Glu Ile Arg Leu Leu
65 70 75 80

ggc aac atc gag atc ggc cgc gac gtc acc gtc gag gag ctg cgc gaa 588
Gly Asn Ile Glu Ile Gly Arg Asp Val Thr Val Glu Glu Leu Arg Glu
85 90 95

cac tac gac gcc gtc atc ttc gcc acc ggc gcc atc gcc gac cgc gac 636
His Tyr Asp Ala Val Ile Phe Ala Thr Gly Ala Ile Ala Asp Arg Asp
100 105 110

ctg gac atc ccg ggc gtc gac gcg cag ggc tcc ttc ggc gcc gcc gac 684
Leu Asp Ile Pro Gly Val Asp Ala Gln Gly Ser Phe Gly Ala Ala Asp

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          115                 120                 125

ttc gtc ggc ttc tac gac ggc aac ccc gag ttc ccc cgc acc tgg gac        732
Phe Val Gly Phe Tyr Asp Gly Asn Pro Glu Phe Pro Arg Thr Trp Asp
    130                 135                 140

ctg tcc gcg cag tcc gtc gcc gtc atc ggc gtg ggc aac gtg ggc ctc        780
Leu Ser Ala Gln Ser Val Ala Val Ile Gly Val Gly Asn Val Gly Leu
145                 150                 155                 160

gac gtc gcg cgc gtc ctg tcc aag acc gcc gac gaa ctc aac gtc acc        828
Asp Val Ala Arg Val Leu Ser Lys Thr Ala Asp Glu Leu Asn Val Thr
                165                 170                 175

gag atc ccc gac aac gtc tac gag acc ctc cgc acc aac cag gcc acc        876
Glu Ile Pro Asp Asn Val Tyr Glu Thr Leu Arg Thr Asn Gln Ala Thr
            180                 185                 190

gag gtc cac gtc ttc ggc cgc cgc ggc ccc gcg cag gcc aag ttc acc        924
Glu Val His Val Phe Gly Arg Arg Gly Pro Ala Gln Ala Lys Phe Thr
        195                 200                 205

ccg cag gaa ctc aag gaa ctc gac cac tcc ccc acc gtc aac gtc gtc        972
Pro Gln Glu Leu Lys Glu Leu Asp His Ser Pro Thr Val Asn Val Val
    210                 215                 220

gtc gac ccc gag gac atc gac tac gac gac gcc agc atc gag gcc cgc       1020
Val Asp Pro Glu Asp Ile Asp Tyr Asp Asp Ala Ser Ile Glu Ala Arg
225                 230                 235                 240

agc agc tcc aag tcg cag gac ctc gtg tgc cag acc ctc gag ggc tac       1068
Ser Ser Ser Lys Ser Gln Asp Leu Val Cys Gln Thr Leu Glu Gly Tyr
                245                 250                 255

gcc atc cgc gaa ccc aag gac gcc ccg cac acc ctg cag atc cac ctc       1116
Ala Ile Arg Glu Pro Lys Asp Ala Pro His Thr Leu Gln Ile His Leu
            260                 265                 270

ttc gag tct ccc acc gag atc ctc acc cgc gac ggc cgt gtc gtc ggc       1164
Phe Glu Ser Pro Thr Glu Ile Leu Thr Arg Asp Gly Arg Val Val Gly
        275                 280                 285

ctg cgc acc gaa cgc acc gaa ctc gac ggc acc ggc cac gtc cgc ggc       1212
Leu Arg Thr Glu Arg Thr Glu Leu Asp Gly Thr Gly His Val Arg Gly
    290                 295                 300

acc ggc acc ttc acc gac tgg ccc gtc cag gcc gtc tac cgc gcc gtc       1260
Thr Gly Thr Phe Thr Asp Trp Pro Val Gln Ala Val Tyr Arg Ala Val
305                 310                 315                 320

ggc tac cgc tcc gag ccg gtg ccg ggc gtg ccc ttc aac cat gtc gag       1308
Gly Tyr Arg Ser Glu Pro Val Pro Gly Val Pro Phe Asn His Val Glu
                325                 330                 335

cat gtg atc ccg aac gac ggc ggc cac gtc ctc gac ccc gcc ggc acc       1356
His Val Ile Pro Asn Asp Gly Gly His Val Leu Asp Pro Ala Gly Thr
            340                 345                 350

ccc gtc ccc ggc ctc tac gcc acc ggc tgg atc aag cgc ggc ccc gtc       1404
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Pro Val Pro Gly Leu Tyr Ala Thr Gly Trp Ile Lys Arg Gly Pro Val
        355                 360                 365

gga ctc atc ggc aac acc aag tcc gac gcc aag gag acc acc gac ctc      1452
Gly Leu Ile Gly Asn Thr Lys Ser Asp Ala Lys Glu Thr Thr Asp Leu
    370                 375                 380

ctg ctc gcc gac gcc gcc gcc gga ctt ctc gac gcc ccc ctc cac ccc      1500
Leu Leu Ala Asp Ala Ala Ala Gly Leu Leu Asp Ala Pro Leu His Pro
385                 390                 395                 400

gcc gac gcc ttc ctc cag ctt ctc gac gcc cgc ggc atc ccc gtc acc      1548
Ala Asp Ala Phe Leu Gln Leu Leu Asp Ala Arg Gly Ile Pro Val Thr
                405                 410                 415

acc tgg gag ggc tgg tac cgg ctc gac gcc gcc gag cgc gcc ctc ggc      1596
Thr Trp Glu Gly Trp Tyr Arg Leu Asp Ala Ala Glu Arg Ala Leu Gly
            420                 425                 430

gag gcc tcc ggc gtg gag ggc aag gag cgc cgg aag atc gtc gaa tgg      1644
Glu Ala Ser Gly Val Glu Gly Lys Glu Arg Arg Lys Ile Val Glu Trp
        435                 440                 445

gag gag atg gtc agc cac gca cac atc acc ccg gcc tat gtg tga          1689
Glu Glu Met Val Ser His Ala His Ile Thr Pro Ala Tyr Val
    450                 455                 460

tttctcaggc tcagggccgg cagctgagac tgggcagcgc tatgccacgg gccatgacac     1749

gccgggccgg ataaaaattc ctgaccctga gtcgatctaa ctgcggtaac ggtccggtag     1809

gcgaattgtt accgatcagc aaccgtccaa attcataccc actaatgtga tcactgttac     1869

tctcaagagt ggaaagtaca actgacaatt cttaaggaga aacatcatgc gcggtagcgg     1929

actcatctgg accatcgtcg gcatcctggc catcatcgcc ctagtcatct ggatcatgtc     1989


<210>  80
<211>  462
<212>  PRT
<213>  Corynebacterium humireducens

<400>  80

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

Gly Ile Tyr Ala Ser Asp Leu Leu Val Lys Asn Ala Ala Ser Ile Gly
            20                  25                  30

Arg Glu Val His Val Asp Leu Ile Glu Lys Leu Pro Ala Pro Phe Gly
        35                  40                  45

Leu Ile Arg Tyr Gly Val Ala Pro Asp His Pro Arg Ile Lys Gly Ile
    50                  55                  60
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Ile Thr Ser Leu His Arg Val Leu Asp Arg Pro Glu Ile Arg Leu Leu
65 70 75 80

Gly Asn Ile Glu Ile Gly Arg Asp Val Thr Val Glu Glu Leu Arg Glu
85 90 95

His Tyr Asp Ala Val Ile Phe Ala Thr Gly Ala Ile Ala Asp Arg Asp
100 105 110

Leu Asp Ile Pro Gly Val Asp Ala Gln Gly Ser Phe Gly Ala Ala Asp
115 120 125

Phe Val Gly Phe Tyr Asp Gly Asn Pro Glu Phe Pro Arg Thr Trp Asp
130 135 140

Leu Ser Ala Gln Ser Val Ala Val Ile Gly Val Gly Asn Val Gly Leu
145 150 155 160

Asp Val Ala Arg Val Leu Ser Lys Thr Ala Asp Glu Leu Asn Val Thr
165 170 175

Glu Ile Pro Asp Asn Val Tyr Glu Thr Leu Arg Thr Asn Gln Ala Thr
180 185 190

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

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

Val Asp Pro Glu Asp Ile Asp Tyr Asp Asp Ala Ser Ile Glu Ala Arg
225 230 235 240

Ser Ser Ser Lys Ser Gln Asp Leu Val Cys Gln Thr Leu Glu Gly Tyr
245 250 255

Ala Ile Arg Glu Pro Lys Asp Ala Pro His Thr Leu Gln Ile His Leu
260 265 270

Phe Glu Ser Pro Thr Glu Ile Leu Thr Arg Asp Gly Arg Val Val Gly
275 280 285

Leu Arg Thr Glu Arg Thr Glu Leu Asp Gly Thr Gly His Val Arg Gly

290 295 300

Thr Gly Thr Phe Thr Asp Trp Pro Val Gln Ala Val Tyr Arg Ala Val
305 310 315 320

Gly Tyr Arg Ser Glu Pro Val Pro Gly Val Pro Phe Asn His Val Glu
325 330 335

His Val Ile Pro Asn Asp Gly Gly His Val Leu Asp Pro Ala Gly Thr
340 345 350

Pro Val Pro Gly Leu Tyr Ala Thr Gly Trp Ile Lys Arg Gly Pro Val
355 360 365

Gly Leu Ile Gly Asn Thr Lys Ser Asp Ala Lys Glu Thr Thr Asp Leu
370 375 380

Leu Leu Ala Asp Ala Ala Ala Gly Leu Leu Asp Ala Pro Leu His Pro
385 390 395 400

Ala Asp Ala Phe Leu Gln Leu Leu Asp Ala Arg Gly Ile Pro Val Thr
405 410 415

Thr Trp Glu Gly Trp Tyr Arg Leu Asp Ala Ala Glu Arg Ala Leu Gly
420 425 430

Glu Ala Ser Gly Val Glu Gly Lys Glu Arg Arg Lys Ile Val Glu Trp
435 440 445

Glu Glu Met Val Ser His Ala His Ile Thr Pro Ala Tyr Val
450 455 460

<210> 81
<211> 1869
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1569)
<223> gene cysN

<400> 81
cgcgctgccg gagatctact tcgcgcatga gcgggccgtc ttcgagcggg acggcatgtg 60

gctgaccgcc ggcgagtggg gtgggccccg cgagggcgag accctcgagg tccgccgcgt 120

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gcgctaccgc accgtcggcg acatgtcctg caccggtgcg gtgctctccg acgccaccac      180

ggtcgacgac gtcatcgccg agatcgccac ctccaccctc accgagcgcg gggccacccg      240

cgccgacgac cgcctcagtg aatccgccat ggaagaccgc aagaaggaag gctacttctg      300

atg acc acc acg ctc ctg cgc acc cgc gag acg ctg cgc ctg tgc acc         348
Met Thr Thr Thr Leu Leu Arg Thr Arg Glu Thr Leu Arg Leu Cys Thr
1               5                  10                  15

gcc ggc tcc gtc gac gac ggc aag tcc acc ctc gtg ggc cgc ctg ctc        396
Ala Gly Ser Val Asp Asp Gly Lys Ser Thr Leu Val Gly Arg Leu Leu
            20                  25                  30

cac gac acc cgc tcc gtc ctc gcc gac cag ctc gcc gcc gtc gag cgc        444
His Asp Thr Arg Ser Val Leu Ala Asp Gln Leu Ala Ala Val Glu Arg
        35                  40                  45

acc tcc gcc gac cgc ggt ttc cac ggc ggc ctg gac ctc tca ctg ctc        492
Thr Ser Ala Asp Arg Gly Phe His Gly Gly Leu Asp Leu Ser Leu Leu
    50                  55                  60

gtc gac ggc ctc cgc gcc gaa cgc gag cag ggc atc acc atc gac gtg        540
Val Asp Gly Leu Arg Ala Glu Arg Glu Gln Gly Ile Thr Ile Asp Val
65                  70                  75                  80

gcc tac cgc tac ttc gcc acc gac cgc cgc acc ttc atc ctc gcc gac        588
Ala Tyr Arg Tyr Phe Ala Thr Asp Arg Arg Thr Phe Ile Leu Ala Asp
                85                  90                  95

acc ccc ggc cac gtg cag tac acg cgc aac acc gtc acc ggc gtg tcc        636
Thr Pro Gly His Val Gln Tyr Thr Arg Asn Thr Val Thr Gly Val Ser
            100                 105                 110

acg tcg cag gtg gtc gtc ctg ctt gtc gac gcc cgc cac ggc gtc gtc        684
Thr Ser Gln Val Val Val Leu Leu Val Asp Ala Arg His Gly Val Val
        115                 120                 125

gag cag acc cgc cgc cac ctc acc gtc gcg gcg ctc ctc ggg gtg cgc        732
Glu Gln Thr Arg Arg His Leu Thr Val Ala Ala Leu Leu Gly Val Arg
    130                 135                 140

aca gtg ctc ctc gcg gtg aat aag atc gac ctc gtt gac tgg tcc gag        780
Thr Val Leu Leu Ala Val Asn Lys Ile Asp Leu Val Asp Trp Ser Glu
145                 150                 155                 160

gcc gtc ttc cgg gac atc gag gcg gag ttc acg tcg ctg gcc acc gac        828
Ala Val Phe Arg Asp Ile Glu Ala Glu Phe Thr Ser Leu Ala Thr Asp
                165                 170                 175

gtc ggc gtc gac gac gcg cac gtc atc ccc gtc tcc gcg ctg ctg ggc        876
Val Gly Val Asp Asp Ala His Val Ile Pro Val Ser Ala Leu Leu Gly
            180                 185                 190

gac aac gtc gtc gaa ccc tcg gcg aac ctc ccc tgg tac gag ggg ccg        924
Asp Asn Val Val Glu Pro Ser Ala Asn Leu Pro Trp Tyr Glu Gly Pro
        195                 200                 205

acg gtg ctg gaa ctg ctc gag agc gtc gag gtc cac cgc ggc cgc gcc        972
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Thr Val Leu Glu Leu Leu Glu Ser Val Glu Val His Arg Gly Arg Ala
    210                 215                 220

cac gcc ctc ggc ttc cgc ctg ccg atc cag tac gtc atc cgc gag cac      1020
His Ala Leu Gly Phe Arg Leu Pro Ile Gln Tyr Val Ile Arg Glu His
225                 230                 235                 240

tcc tcc gac tac cgc ggc tac gcc ggg cgt gtc gac gcc ggc gtg ctc      1068
Ser Ser Asp Tyr Arg Gly Tyr Ala Gly Arg Val Asp Ala Gly Val Leu
                245                 250                 255

acc gtc ggc gac acc gtc cac ctc ccc gag ggg cgc acc agc acc gtc      1116
Thr Val Gly Asp Thr Val His Leu Pro Glu Gly Arg Thr Ser Thr Val
            260                 265                 270

acc cac atc gac acc gcc gac ggc gag gtc cgc tcc gcc cac gcc ggt      1164
Thr His Ile Asp Thr Ala Asp Gly Glu Val Arg Ser Ala His Ala Gly
        275                 280                 285

gac tcc gtg gtc ctg cgc ctg gcc gac gac atc gac ctc atc cgc ggc      1212
Asp Ser Val Val Leu Arg Leu Ala Asp Asp Ile Asp Leu Ile Arg Gly
    290                 295                 300

gac ctc atc gcc ggt gag gac cgc ccg gag ccg acc cgc tcc ttc gcc      1260
Asp Leu Ile Ala Gly Glu Asp Arg Pro Glu Pro Thr Arg Ser Phe Ala
305                 310                 315                 320

gcc aca ctc gtc gga ctc ggc gac cgc acc ctg cgc ccc ggc tcc ccc      1308
Ala Thr Leu Val Gly Leu Gly Asp Arg Thr Leu Arg Pro Gly Ser Pro
                325                 330                 335

gtg aag gtc cgc tac ggc acc tca ctc gtg cgg gga cgc gtc gcg gcg      1356
Val Lys Val Arg Tyr Gly Thr Ser Leu Val Arg Gly Arg Val Ala Ala
            340                 345                 350

atc gag cgg ctg ctc gac atc gac ggc cgc acc gac cac ctc tcc ccg      1404
Ile Glu Arg Leu Leu Asp Ile Asp Gly Arg Thr Asp His Leu Ser Pro
        355                 360                 365

gac gac ctc ggc ctc aac gac atc gcc cac gtg cgt atc gac gtc gcc      1452
Asp Asp Leu Gly Leu Asn Asp Ile Ala His Val Arg Ile Asp Val Ala
    370                 375                 380

acc gag ctc ccc gtc gag ccc tac gcc gcc cgc ggc gcc gtc ggc tcc      1500
Thr Glu Leu Pro Val Glu Pro Tyr Ala Ala Arg Gly Ala Val Gly Ser
385                 390                 395                 400

ttc ctg ctc atc gac cag gcc agc ggc gac acc ctc gcc gcc ggg ctc      1548
Phe Leu Leu Ile Asp Gln Ala Ser Gly Asp Thr Leu Ala Ala Gly Leu
                405                 410                 415

gtc ggc cac cgg ctc cgc tga cccgtgaccg ccctgctcac cctctcccac          1599
Val Gly His Arg Leu Arg
            420

gggtcccgcc acccgcgcgc cgccgccggc gtcgaccgcc tcacccgggc ggccggggag     1659

gtgctgggcg tcaccgcccg cgccgcccac ctcgagttcg acacccccctc cctcatcgac    1719
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gccgcccgcg acctcgtcgc ccgcggccac gaccacgccg tggtcgtccc cctgctgttc 1779

accgacgcct tccacgcgcg tcacgacgtc cccgccgccc tcgacgcggc ccgccgcgcc 1839

accggcctgc ggctcacgcc cgcccggggc 1869

<210> 82
<211> 422
<212> PRT
<213> Corynebacterium humireducens

<400> 82

Met Thr Thr Thr Leu Leu Arg Thr Arg Glu Thr Leu Arg Leu Cys Thr
1 5 10 15

Ala Gly Ser Val Asp Asp Gly Lys Ser Thr Leu Val Gly Arg Leu Leu
20 25 30

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

Thr Ser Ala Asp Arg Gly Phe His Gly Gly Leu Asp Leu Ser Leu Leu
50 55 60

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

Ala Tyr Arg Tyr Phe Ala Thr Asp Arg Arg Thr Phe Ile Leu Ala Asp
85 90 95

Thr Pro Gly His Val Gln Tyr Thr Arg Asn Thr Val Thr Gly Val Ser
100 105 110

Thr Ser Gln Val Val Val Leu Leu Val Asp Ala Arg His Gly Val Val
115 120 125

Glu Gln Thr Arg Arg His Leu Thr Val Ala Ala Leu Leu Gly Val Arg
130 135 140

Thr Val Leu Leu Ala Val Asn Lys Ile Asp Leu Val Asp Trp Ser Glu
145 150 155 160

Ala Val Phe Arg Asp Ile Glu Ala Glu Phe Thr Ser Leu Ala Thr Asp
165 170 175

Val Gly Val Asp Asp Ala His Val Ile Pro Val Ser Ala Leu Leu Gly

180 185 190

Asp Asn Val Val Glu Pro Ser Ala Asn Leu Pro Trp Tyr Glu Gly Pro
195 200 205

Thr Val Leu Glu Leu Leu Glu Ser Val Glu Val His Arg Gly Arg Ala
210 215 220

His Ala Leu Gly Phe Arg Leu Pro Ile Gln Tyr Val Ile Arg Glu His
225 230 235 240

Ser Ser Asp Tyr Arg Gly Tyr Ala Gly Arg Val Asp Ala Gly Val Leu
245 250 255

Thr Val Gly Asp Thr Val His Leu Pro Glu Gly Arg Thr Ser Thr Val
260 265 270

Thr His Ile Asp Thr Ala Asp Gly Glu Val Arg Ser Ala His Ala Gly
275 280 285

Asp Ser Val Val Leu Arg Leu Ala Asp Asp Ile Asp Leu Ile Arg Gly
290 295 300

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

Ala Thr Leu Val Gly Leu Gly Asp Arg Thr Leu Arg Pro Gly Ser Pro
325 330 335

Val Lys Val Arg Tyr Gly Thr Ser Leu Val Arg Gly Arg Val Ala Ala
340 345 350

Ile Glu Arg Leu Leu Asp Ile Asp Gly Arg Thr Asp His Leu Ser Pro
355 360 365

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

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

Phe Leu Leu Ile Asp Gln Ala Ser Gly Asp Thr Leu Ala Ala Gly Leu
405 410 415

Val Gly His Arg Leu Arg
420

<210> 83
<211> 1248
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(948)
<223> gene cysY

<400> 83
ggactcggcg accgcaccct gcgccccggc tcccccgtga aggtccgcta cggcacctca 60

ctcgtgcggg gacgcgtcgc ggcgatcgag cggctgctcg acatcgacgg ccgcaccgac 120

cacctctccc cggacgacct cggcctcaac gacatcgccc acgtgcgtat cgacgtcgcc 180

accgagctcc ccgtcgagcc ctacgccgcc cgcggcgccg tcggctcctt cctgctcatc 240

gaccaggcca gcggcgacac cctcgccgcc gggctcgtcg gccaccggct ccgctgaccc 300

gtg acc gcc ctg ctc acc ctc tcc cac ggg tcc cgc cac ccg cgc gcc 348
Val Thr Ala Leu Leu Thr Leu Ser His Gly Ser Arg His Pro Arg Ala
1 5 10 15

gcc gcc ggc gtc gac cgc ctc acc cgg gcg gcc ggg gag gtg ctg ggc 396
Ala Ala Gly Val Asp Arg Leu Thr Arg Ala Ala Gly Glu Val Leu Gly
20 25 30

gtc acc gcc cgc gcc gcc cac ctc gag ttc gac acc ccc tcc ctc atc 444
Val Thr Ala Arg Ala Ala His Leu Glu Phe Asp Thr Pro Ser Leu Ile
35 40 45

gac gcc gcc cgc gac ctc gtc gcc cgc ggc cac gac cac gcc gtg gtc 492
Asp Ala Ala Arg Asp Leu Val Ala Arg Gly His Asp His Ala Val Val
50 55 60

gtc ccc ctg ctg ttc acc gac gcc ttc cac gcg cgt cac gac gtc ccc 540
Val Pro Leu Leu Phe Thr Asp Ala Phe His Ala Arg His Asp Val Pro
65 70 75 80

gcc gcc ctc gac gcg gcc cgc cgc gcc acc ggc ctg cgg ctc acg ccc 588
Ala Ala Leu Asp Ala Ala Arg Arg Ala Thr Gly Leu Arg Leu Thr Pro
85 90 95

gcc cgg ggc ctc ggc acc ggc ccc gac atc gcc gac gtc ctt gcc cgc 636
Ala Arg Gly Leu Gly Thr Gly Pro Asp Ile Ala Asp Val Leu Ala Arg
100 105 110

cac acc cgc ccc cgc aac ccg gac ctc gtc ctc ggg cac gtc gga tcc 684
His Thr Arg Pro Arg Asn Pro Asp Leu Val Leu Gly His Val Gly Ser
115 120 125

tcc tcc gtc gca gcc gag gcc gcc gtc cgg tcg ctg gcc gac ctc ctc 732

```
Ser Ser Val Ala Ala Glu Ala Ala Val Arg Ser Leu Ala Asp Leu Leu
    130                 135                 140

gcc gcc cgc ctc ggg cgg gac gtc gcg gtg gtg cgg gcg acg ggg gag      780
Ala Ala Arg Leu Gly Arg Asp Val Ala Val Val Arg Ala Thr Gly Glu
145                 150                 155                 160

aag gcg gcg tcg ata agc agc ggt gcc cac ctc gtc ccc ctc ttc gtc      828
Lys Ala Ala Ser Ile Ser Ser Gly Ala His Leu Val Pro Leu Phe Val
                165                 170                 175

acc gac gcc ctg ctg ctc gac cgc ctg cgc gcc gcc caa ccc cac gcg      876
Thr Asp Ala Leu Leu Leu Asp Arg Leu Arg Ala Ala Gln Pro His Ala
            180                 185                 190

acc tcc gac cgc ccg ctc acc gac gcc ctc cgc gac gtc gtg gcg gcg      924
Thr Ser Asp Arg Pro Leu Thr Asp Ala Leu Arg Asp Val Val Ala Ala
        195                 200                 205

cgg tac cgg gcc gcc ctc acc tag gaacccacca tgaacacact cctgctcatc      978
Arg Tyr Arg Ala Ala Leu Thr
    210                 215

gccctcgcgg ggctcgccgc ccagctcgtc gacggcggcc tcggcatggg cttcggcgcc     1038

acctccacca cgatcctcat cgtgctcgcc ggactcggcc ccgccacagc cagcgccgtc     1098

gtccacaccg cggaactggg caccaccctc gtctccggcg tctcgcactg gcgtttcgga     1158

aacgtcgact ggcaggtcgt ccgccgcctc gccatccccg gtgccgtggg cgccttcgcc     1218

ggggcaaccg tgctctccca cttatcgacg                                      1248
```

<210> 84
<211> 215
<212> PRT
<213> Corynebacterium humireducens

<400> 84

```
Val Thr Ala Leu Leu Thr Leu Ser His Gly Ser Arg His Pro Arg Ala
1               5                   10                  15

Ala Ala Gly Val Asp Arg Leu Thr Arg Ala Ala Gly Glu Val Leu Gly
            20                  25                  30

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

Asp Ala Ala Arg Asp Leu Val Ala Arg Gly His Asp His Ala Val Val
    50                  55                  60

Val Pro Leu Leu Phe Thr Asp Ala Phe His Ala Arg His Asp Val Pro
65                  70                  75                  80
```

Ala Ala Leu Asp Ala Ala Arg Arg Ala Thr Gly Leu Arg Leu Thr Pro
85 90 95

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

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

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

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

Lys Ala Ala Ser Ile Ser Ser Gly Ala His Leu Val Pro Leu Phe Val
165 170 175

Thr Asp Ala Leu Leu Leu Asp Arg Leu Arg Ala Ala Gln Pro His Ala
180 185 190

Thr Ser Asp Arg Pro Leu Thr Asp Ala Leu Arg Asp Val Val Ala Ala
195 200 205

Arg Tyr Arg Ala Ala Leu Thr
210 215

<210> 85
<211> 1515
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1215)
<223> gene cysZ

<400> 85
gacctcgtcc tcgggcacgt cggatcctcc tccgtcgcag ccgaggccgc cgtccggtcg 60

ctggccgacc tcctcgccgc ccgcctcggg cgggacgtcg cggtggtgcg ggcgacgggg 120

gagaaggcgg cgtcgataag cagcggtgcc cacctcgtcc ccctcttcgt caccgacgcc 180

ctgctgctcg accgcctgcg cgccgcccaa ccccacgcga cctccgaccg cccgctcacc 240

gacgccctcc gcgacgtcgt ggcggcgcgg taccgggccg ccctcaccta ggaacccacc 300

```
atg aac aca ctc ctg ctc atc gcc ctc gcg ggg ctc gcc gcc cag ctc        348
Met Asn Thr Leu Leu Leu Ile Ala Leu Ala Gly Leu Ala Ala Gln Leu
1               5                   10                  15

gtc gac ggc ggc ctc ggc atg ggc ttc ggc gcc acc tcc acc acg atc        396
Val Asp Gly Gly Leu Gly Met Gly Phe Gly Ala Thr Ser Thr Thr Ile
            20                  25                  30

ctc atc gtg ctc gcc gga ctc ggc ccc gcc aca gcc agc gcc gtc gtc        444
Leu Ile Val Leu Ala Gly Leu Gly Pro Ala Thr Ala Ser Ala Val Val
        35                  40                  45

cac acc gcg gaa ctg ggc acc acc ctc gtc tcc ggc gtc tcg cac tgg        492
His Thr Ala Glu Leu Gly Thr Thr Leu Val Ser Gly Val Ser His Trp
    50                  55                  60

cgt ttc gga aac gtc gac tgg cag gtc gtc cgc cgc ctc gcc atc ccc        540
Arg Phe Gly Asn Val Asp Trp Gln Val Val Arg Arg Leu Ala Ile Pro
65                  70                  75                  80

ggt gcc gtg ggc gcc ttc gcc ggg gca acc gtg ctc tcc cac tta tcg        588
Gly Ala Val Gly Ala Phe Ala Gly Ala Thr Val Leu Ser His Leu Ser
                85                  90                  95

acg cag gcc gcc gcc ccc gtc acc gcc acg atc ctc acc ctc atc ggc        636
Thr Gln Ala Ala Ala Pro Val Thr Ala Thr Ile Leu Thr Leu Ile Gly
            100                 105                 110

gcc aac ctc gtg tgg cgc ttc tcc cgc gga cgc atc cac ccg cgc cgc        684
Ala Asn Leu Val Trp Arg Phe Ser Arg Gly Arg Ile His Pro Arg Arg
        115                 120                 125

gcc ggg aag ggg cac tcg cgc ggc ttc ctc ggc ggg ctc ggc ctg ttc        732
Ala Gly Lys Gly His Ser Arg Gly Phe Leu Gly Gly Leu Gly Leu Phe
    130                 135                 140

ggc ggc ttc atc gac gcc tcc gga ggc ggc ggc tgg ggc ccg gtg acc        780
Gly Gly Phe Ile Asp Ala Ser Gly Gly Gly Gly Trp Gly Pro Val Thr
145                 150                 155                 160

acc tcg acc ctg atg acg ctg ggg cgg gcg gaa ccg cgc cgc atc gtc        828
Thr Ser Thr Leu Met Thr Leu Gly Arg Ala Glu Pro Arg Arg Ile Val
                165                 170                 175

ggc acg gtc aac acc gcc gag ttc ctg gtc acc gcc gcg gcg acc gcc        876
Gly Thr Val Asn Thr Ala Glu Phe Leu Val Thr Ala Ala Ala Thr Ala
            180                 185                 190

ggc ttc gtc atc ggc ctg tgg gac gac ctg gtg gcc aac ctc gcg gcc        924
Gly Phe Val Ile Gly Leu Trp Asp Asp Leu Val Ala Asn Leu Ala Ala
        195                 200                 205

gtg ctc gcg ctg ctc atc ggc ggt gtc atc gcc gcg ccg gtc gcc gcg        972
Val Leu Ala Leu Leu Ile Gly Gly Val Ile Ala Ala Pro Val Ala Ala
    210                 215                 220

tgg ctg gtc acc cgc ctc aac ccg gcc gcc ctc ggc ggc gtc gtg ggc       1020
Trp Leu Val Thr Arg Leu Asn Pro Ala Ala Leu Gly Gly Val Val Gly
```

225 230 235 240

acc ctg ctg gtc gcg ctg aac ctc ccc aag gtg ctg ccc ttc gcc gga 1068
Thr Leu Leu Val Ala Leu Asn Leu Pro Lys Val Leu Pro Phe Ala Gly
245 250 255

gga ccg gtg ctg ctg gcc gtc atc gtc gtc ggc ctg ggc ttc tcg tgg 1116
Gly Pro Val Leu Leu Ala Val Ile Val Val Gly Leu Gly Phe Ser Trp
260 265 270

gtc ggc tgg cga cgc tcc ctc cgt gcc cgc gcc gcc gcc ggg cag ccc 1164
Val Gly Trp Arg Arg Ser Leu Arg Ala Arg Ala Ala Ala Gly Gln Pro
275 280 285

gtc acc gga acg acg agc acc ccc acc gga cag tcg gtg ggg gtg cgg 1212
Val Thr Gly Thr Thr Ser Thr Pro Thr Gly Gln Ser Val Gly Val Arg
290 295 300

tag ggcgggggct acagggcggc gacgtcgccg atgacgtaca cggccgggga 1265

cccgatgcgg ttcccggcca tcgtcgtggc cagggttccc aacgtgcacc ggaaggaacg 1325

ctgcccagtg gtggtgccct cctggatgac ggcggccggg gtgtgggggt cgaggccggc 1385

gtcgacaagc gtggcggtga tggcggcgac gttgcgcaca cccatgatca ccgagatcgt 1445

gccgcccgcc cgcgccagcg cggcccagtc gacgagcgag tccgggtgcc ccggcggcag 1505

atgcccggag 1515

<210> 86
<211> 304
<212> PRT
<213> Corynebacterium humireducens

<400> 86

Met Asn Thr Leu Leu Leu Ile Ala Leu Ala Gly Leu Ala Ala Gln Leu
1 5 10 15

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

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

His Thr Ala Glu Leu Gly Thr Thr Leu Val Ser Gly Val Ser His Trp
50 55 60

Arg Phe Gly Asn Val Asp Trp Gln Val Val Arg Arg Leu Ala Ile Pro
65 70 75 80

Gly Ala Val Gly Ala Phe Ala Gly Ala Thr Val Leu Ser His Leu Ser

85 90 95

Thr Gln Ala Ala Ala Pro Val Thr Ala Thr Ile Leu Thr Leu Ile Gly
100 105 110

Ala Asn Leu Val Trp Arg Phe Ser Arg Gly Arg Ile His Pro Arg Arg
115 120 125

Ala Gly Lys Gly His Ser Arg Gly Phe Leu Gly Gly Leu Gly Leu Phe
130 135 140

Gly Gly Phe Ile Asp Ala Ser Gly Gly Gly Gly Trp Gly Pro Val Thr
145 150 155 160

Thr Ser Thr Leu Met Thr Leu Gly Arg Ala Glu Pro Arg Arg Ile Val
165 170 175

Gly Thr Val Asn Thr Ala Glu Phe Leu Val Thr Ala Ala Ala Thr Ala
180 185 190

Gly Phe Val Ile Gly Leu Trp Asp Asp Leu Val Ala Asn Leu Ala Ala
195 200 205

Val Leu Ala Leu Leu Ile Gly Gly Val Ile Ala Ala Pro Val Ala Ala
210 215 220

Trp Leu Val Thr Arg Leu Asn Pro Ala Ala Leu Gly Gly Val Val Gly
225 230 235 240

Thr Leu Leu Val Ala Leu Asn Leu Pro Lys Val Leu Pro Phe Ala Gly
245 250 255

Gly Pro Val Leu Leu Ala Val Ile Val Val Gly Leu Gly Phe Ser Trp
260 265 270

Val Gly Trp Arg Arg Ser Leu Arg Ala Arg Ala Ala Ala Gly Gln Pro
275 280 285

Val Thr Gly Thr Thr Ser Thr Pro Thr Gly Gln Ser Val Gly Val Arg
290 295 300

<210> 87
<211> 2916
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(2616)
<223> gene metE

<400> 87
gactggaggc ggcaggcccg gagagcgagt accagacggg cctcgacctc acggccgagc 60

tcgcgcagac catcctggac gccggtgccg gggggatgca cgtgtacacg ttcaaccggc 120

cggacaccac caccgaactg ctggaccgca tcggcatcac ccccgaccct cgggttaggg 180

agtgaggcgg gagaccgccg ccgctgcatc tcatgttgat agcgacctgc tgcacgcacc 240

gggagccccc gaagcagacc aggttgtaca cccaagattt tccgaaaggc ctccctttc 300

atg tct tcc acc gct ttc ccc acc ttc acc atc gag ggc tac ccg cgc 348
Met Ser Ser Thr Ala Phe Pro Thr Phe Thr Ile Glu Gly Tyr Pro Arg
1 5 10 15

gtc ggc gcc aac cgc gag ctc aag aag gcc ctc gag tcc ttc tgg gcc 396
Val Gly Ala Asn Arg Glu Leu Lys Lys Ala Leu Glu Ser Phe Trp Ala
20 25 30

ggc cgc atc gac gag gag acc ttc atc tcc tcc gcg cac tcc atc cgc 444
Gly Arg Ile Asp Glu Glu Thr Phe Ile Ser Ser Ala His Ser Ile Arg
35 40 45

ctg gag aac tac gcc cgt ctg cgt gac ctc ggc ctg gac cag gac tac 492
Leu Glu Asn Tyr Ala Arg Leu Arg Asp Leu Gly Leu Asp Gln Asp Tyr
50 55 60

gcc atc ccg gcc gac gtc gcc ctc tac gac cag gtg ctc gag acc ggc 540
Ala Ile Pro Ala Asp Val Ala Leu Tyr Asp Gln Val Leu Glu Thr Gly
65 70 75 80

gtc acc gtc ggc ctg atc ggt ggc gac gcc gcc gag gtc gac ctc acc 588
Val Thr Val Gly Leu Ile Gly Gly Asp Ala Ala Glu Val Asp Leu Thr
85 90 95

gag tac ttc gcc ctg gcc cgc ggc acc gcc gag cgt tcc ccg ctc gag 636
Glu Tyr Phe Ala Leu Ala Arg Gly Thr Ala Glu Arg Ser Pro Leu Glu
100 105 110

atg acc aag tgg ttc gac acc aac tac cac tac ctc gtc ccg gag gtc 684
Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Val
115 120 125

gcc gag gac acc gtc atc acc ccg cgc ccg cag cgc atc ctc gac atc 732
Ala Glu Asp Thr Val Ile Thr Pro Arg Pro Gln Arg Ile Leu Asp Ile
130 135 140

gtc gcc gag gcc aag gag gcc ggc cac acc gtc cgt ccg ttc ctg gtc 780
Val Ala Glu Ala Lys Glu Ala Gly His Thr Val Arg Pro Phe Leu Val
145 150 155 160

ggc ccg gtc acc ctg ctg gcc aag tcc aag gcc gcc gag aac gcc ggc 828

```
Gly Pro Val Thr Leu Leu Ala Lys Ser Lys Ala Ala Glu Asn Ala Gly
                165                 170                 175

gag ggc ttc aac ccg ctg tcc cgc ctc gag gac ctc acc gcc gcc tac  876
Glu Gly Phe Asn Pro Leu Ser Arg Leu Glu Asp Leu Thr Ala Ala Tyr
            180                 185                 190

gcc cag gtc ctc gcc gcc ctc aag gag gcc ggc gtg gag tgg gtc cag  924
Ala Gln Val Leu Ala Ala Leu Lys Glu Ala Gly Val Glu Trp Val Gln
        195                 200                 205

ctc gcc gag ccg gcc ctg gtc gcc gac ctg acc atc cgt tcc gac gcc  972
Leu Ala Glu Pro Ala Leu Val Ala Asp Leu Thr Ile Arg Ser Asp Ala
    210                 215                 220

gac ctg gcc gcc gac gcg aag gcc acc tac gag gcg ctc ctc ggc tcc 1020
Asp Leu Ala Ala Asp Ala Lys Ala Thr Tyr Glu Ala Leu Leu Gly Ser
225                 230                 235                 240

gag gac cgc ccg cag gtc ctc atc acc acc ccc tac ggt gcc ctg cgc 1068
Glu Asp Arg Pro Gln Val Leu Ile Thr Thr Pro Tyr Gly Ala Leu Arg
                245                 250                 255

aac ggc ctc gac gcc ctc gtc gcc gcc aag ccg gag gcc ctg cag gtc 1116
Asn Gly Leu Asp Ala Leu Val Ala Ala Lys Pro Glu Ala Leu Gln Val
            260                 265                 270

gac ctc gca ccg gtc acc ctc gcc aac gag gag ggc tac gtc gag cgc 1164
Asp Leu Ala Pro Val Thr Leu Ala Asn Glu Glu Gly Tyr Val Glu Arg
        275                 280                 285

gtc gcc aag gca gtc gcc ggc acc ggc atc acc ctg gcc gcc ggc gtc 1212
Val Ala Lys Ala Val Ala Gly Thr Gly Ile Thr Leu Ala Ala Gly Val
    290                 295                 300

atc gac ggc cgc aac atc tgg gcc gcc gac ctg cgc gag cgc ctc tcc 1260
Ile Asp Gly Arg Asn Ile Trp Ala Ala Asp Leu Arg Glu Arg Leu Ser
305                 310                 315                 320

gtc ctg gag gag ctg aag aag ggc ggc gtc gag aag atc gcc gtc acc 1308
Val Leu Glu Glu Leu Lys Lys Gly Gly Val Glu Lys Ile Ala Val Thr
                325                 330                 335

tcc tcc gtc tcc ctg cag cac gtc ccg cac acc gtc tcc gtg gag aag 1356
Ser Ser Val Ser Leu Gln His Val Pro His Thr Val Ser Val Glu Lys
            340                 345                 350

aac ctc ccg gtc gac gtc gcc ggc tgg ctc tcc ttc gcc gac gag aag 1404
Asn Leu Pro Val Asp Val Ala Gly Trp Leu Ser Phe Ala Asp Glu Lys
        355                 360                 365

atc ggc gag gca cag gcc ctg gcc acc gca ctc gag ggc ggc tcc gtc 1452
Ile Gly Glu Ala Gln Ala Leu Ala Thr Ala Leu Glu Gly Gly Ser Val
    370                 375                 380

gcc gcc gca gac gcc ttc gcc cgc tcc gac cgc gcc gtg cgc acc cgt 1500
Ala Ala Ala Asp Ala Phe Ala Arg Ser Asp Arg Ala Val Arg Thr Arg
385                 390                 395                 400
```

```
cgt gag tcc gcc cgc acc cac aac cag gcc gtc cag gac cgc gtc gcc       1548
Arg Glu Ser Ala Arg Thr His Asn Gln Ala Val Gln Asp Arg Val Ala
                405                 410                 415

gct ctg ccg gac ggc cag gtc gca cgc gag ccg gag ttc gag ggc cgc       1596
Ala Leu Pro Asp Gly Gln Val Ala Arg Glu Pro Glu Phe Glu Gly Arg
            420                 425                 430

gtc gag gca cag aag gtg ctc aac ctg ccg aag ctg ccg acc acc acg       1644
Val Glu Ala Gln Lys Val Leu Asn Leu Pro Lys Leu Pro Thr Thr Thr
        435                 440                 445

atc ggc tcc ttc ccg cag acc acc gag atc cgc aag gca cgc gcc gac       1692
Ile Gly Ser Phe Pro Gln Thr Thr Glu Ile Arg Lys Ala Arg Ala Asp
    450                 455                 460

cac cgc tcc ggc gcc ctc acc gac gag cag tac acc gac gcc ctc aag       1740
His Arg Ser Gly Ala Leu Thr Asp Glu Gln Tyr Thr Asp Ala Leu Lys
465                 470                 475                 480

gac gag gtc aag tcc gtc atc gag ctg cag gag cgc ctc ggc atc gac       1788
Asp Glu Val Lys Ser Val Ile Glu Leu Gln Glu Arg Leu Gly Ile Asp
                485                 490                 495

gtc ctc gtc cac ggc gag ccc gag cgc aac gac atg gtc cag tac ttc       1836
Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe
            500                 505                 510

gcc gag ctt ctc gac ggc ttc gtg acc acc gag cac ggc tgg gtc cag       1884
Ala Glu Leu Leu Asp Gly Phe Val Thr Thr Glu His Gly Trp Val Gln
        515                 520                 525

tcc tac ggc tcc cgc tgc acc cgc ccg tcc atc gtc gtc ggc gac gtc       1932
Ser Tyr Gly Ser Arg Cys Thr Arg Pro Ser Ile Val Val Gly Asp Val
    530                 535                 540

tcc cgc ccg aag gcc atg acc gtc gag tgg gcc aag tac gcc cag tcc       1980
Ser Arg Pro Lys Ala Met Thr Val Glu Trp Ala Lys Tyr Ala Gln Ser
545                 550                 555                 560

ctc tcc gac aag cac gtc aag ggc atg ctg acc ggc ccg gtc acc atc       2028
Leu Ser Asp Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile
                565                 570                 575

ctc gcg tgg tcc ttc acc cgt gac gac gtt ccg aag tcc gtc tcc gcc       2076
Leu Ala Trp Ser Phe Thr Arg Asp Asp Val Pro Lys Ser Val Ser Ala
            580                 585                 590

gac cag atc ggc gtc gcc ctc gcc gac gag gtc gcc gac ctc gag gcc       2124
Asp Gln Ile Gly Val Ala Leu Ala Asp Glu Val Ala Asp Leu Glu Ala
        595                 600                 605

gcc ggc atc aac gtc atc cag atc gac gag ccg gcc ctg cgc gag ctg       2172
Ala Gly Ile Asn Val Ile Gln Ile Asp Glu Pro Ala Leu Arg Glu Leu
    610                 615                 620

ctg ccg ctg cgt gag gag gac cgc ccg gca tac ctg gac tgg gcc gtc       2220
Leu Pro Leu Arg Glu Glu Asp Arg Pro Ala Tyr Leu Asp Trp Ala Val
625                 630                 635                 640
```

```
cgc tcc ttc cgc ctc gtc tcc ctg gac gcg aag ccg acc acc cag atc      2268
Arg Ser Phe Arg Leu Val Ser Leu Asp Ala Lys Pro Thr Thr Gln Ile
                645                 650                 655

cac acc cac ctc tgc tac tcg gag ttc ggg cag atc atc gac gcc gtc      2316
His Thr His Leu Cys Tyr Ser Glu Phe Gly Gln Ile Ile Asp Ala Val
            660                 665                 670

gcc gcc ctc gac gcc gac gtc acc tcc atc gag gcc gcc cgc tcc cgc      2364
Ala Ala Leu Asp Ala Asp Val Thr Ser Ile Glu Ala Ala Arg Ser Arg
        675                 680                 685

atg gag ctg ctg ggt gac ctg gac gag tcc ttc cac tcc gag atc ggc      2412
Met Glu Leu Leu Gly Asp Leu Asp Glu Ser Phe His Ser Glu Ile Gly
    690                 695                 700

ccg ggc atc tgg gac atc cac tcc ccg cgc gtc ccg gac gtc gcc gag      2460
Pro Gly Ile Trp Asp Ile His Ser Pro Arg Val Pro Asp Val Ala Glu
705                 710                 715                 720

ctc acc gag ctg atc aag gcc gcc ctg gtc aac gtc ccg acc gag cgc      2508
Leu Thr Glu Leu Ile Lys Ala Ala Leu Val Asn Val Pro Thr Glu Arg
                725                 730                 735

ctc tgg gtc aac ccg gac tgc ggt ctg aag acc cgc ggc tac gcc gag      2556
Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Tyr Ala Glu
            740                 745                 750

acc gag gcg tcc ctg cgc aac atg gtc ctc gcc cgc gac ctc gtg gtc      2604
Thr Glu Ala Ser Leu Arg Asn Met Val Leu Ala Arg Asp Leu Val Val
        755                 760                 765

gag tcc ctg taa cacctgcgta gcaactacgt tgcgggcccg gttccacttc          2656
Glu Ser Leu
    770

ggtggggccg ggcccctcgt gattccgggg gcggctagcg ctcgtcgatg acctccgcga    2716

aggcggccac cttccggcgg agatcctcga tgagggcgtc cccgtccctc cgggacttct    2776

cctccgacgc cgggtcatcc cagcctgtct cccagtggtg gtgggaccgc cagtggtcgc    2836

accatgcgta gagccgctgc gtcagcgact cggacaggcc gtagtcccgt ggcgccatca    2896

gataggtgtc cgtgccgttc                                               2916
```

<210> 88
<211> 771
<212> PRT
<213> Corynebacterium humireducens

<400> 88

```
Met Ser Ser Thr Ala Phe Pro Thr Phe Thr Ile Glu Gly Tyr Pro Arg
1               5                  10                  15
```

```
Val Gly Ala Asn Arg Glu Leu Lys Lys Ala Leu Glu Ser Phe Trp Ala
            20                  25                  30

Gly Arg Ile Asp Glu Glu Thr Phe Ile Ser Ser Ala His Ser Ile Arg
        35                  40                  45

Leu Glu Asn Tyr Ala Arg Leu Arg Asp Leu Gly Leu Asp Gln Asp Tyr
    50                  55                  60

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

Val Thr Val Gly Leu Ile Gly Gly Asp Ala Ala Glu Val Asp Leu Thr
                85                  90                  95

Glu Tyr Phe Ala Leu Ala Arg Gly Thr Ala Glu Arg Ser Pro Leu Glu
            100                 105                 110

Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Val
        115                 120                 125

Ala Glu Asp Thr Val Ile Thr Pro Arg Pro Gln Arg Ile Leu Asp Ile
    130                 135                 140

Val Ala Glu Ala Lys Glu Ala Gly His Thr Val Arg Pro Phe Leu Val
145                 150                 155                 160

Gly Pro Val Thr Leu Leu Ala Lys Ser Lys Ala Ala Glu Asn Ala Gly
                165                 170                 175

Glu Gly Phe Asn Pro Leu Ser Arg Leu Glu Asp Leu Thr Ala Ala Tyr
            180                 185                 190

Ala Gln Val Leu Ala Ala Leu Lys Glu Ala Gly Val Glu Trp Val Gln
        195                 200                 205

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

Asp Leu Ala Ala Asp Ala Lys Ala Thr Tyr Glu Ala Leu Leu Gly Ser
225                 230                 235                 240

Glu Asp Arg Pro Gln Val Leu Ile Thr Thr Pro Tyr Gly Ala Leu Arg
                245                 250                 255
```

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

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

Val Ala Lys Ala Val Ala Gly Thr Gly Ile Thr Leu Ala Ala Gly Val
290 295 300

Ile Asp Gly Arg Asn Ile Trp Ala Ala Asp Leu Arg Glu Arg Leu Ser
305 310 315 320

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

Ser Ser Val Ser Leu Gln His Val Pro His Thr Val Ser Val Glu Lys
340 345 350

Asn Leu Pro Val Asp Val Ala Gly Trp Leu Ser Phe Ala Asp Glu Lys
355 360 365

Ile Gly Glu Ala Gln Ala Leu Ala Thr Ala Leu Glu Gly Gly Ser Val
370 375 380

Ala Ala Ala Asp Ala Phe Ala Arg Ser Asp Arg Ala Val Arg Thr Arg
385 390 395 400

Arg Glu Ser Ala Arg Thr His Asn Gln Ala Val Gln Asp Arg Val Ala
405 410 415

Ala Leu Pro Asp Gly Gln Val Ala Arg Glu Pro Glu Phe Glu Gly Arg
420 425 430

Val Glu Ala Gln Lys Val Leu Asn Leu Pro Lys Leu Pro Thr Thr Thr
435 440 445

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

His Arg Ser Gly Ala Leu Thr Asp Glu Gln Tyr Thr Asp Ala Leu Lys
465 470 475 480

Asp Glu Val Lys Ser Val Ile Glu Leu Gln Glu Arg Leu Gly Ile Asp
485 490 495

Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe
500 505 510

Ala Glu Leu Leu Asp Gly Phe Val Thr Thr Glu His Gly Trp Val Gln
515 520 525

Ser Tyr Gly Ser Arg Cys Thr Arg Pro Ser Ile Val Val Gly Asp Val
530 535 540

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

Leu Ser Asp Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile
565 570 575

Leu Ala Trp Ser Phe Thr Arg Asp Asp Val Pro Lys Ser Val Ser Ala
580 585 590

Asp Gln Ile Gly Val Ala Leu Ala Asp Glu Val Ala Asp Leu Glu Ala
595 600 605

Ala Gly Ile Asn Val Ile Gln Ile Asp Glu Pro Ala Leu Arg Glu Leu
610 615 620

Leu Pro Leu Arg Glu Glu Asp Arg Pro Ala Tyr Leu Asp Trp Ala Val
625 630 635 640

Arg Ser Phe Arg Leu Val Ser Leu Asp Ala Lys Pro Thr Thr Gln Ile
645 650 655

His Thr His Leu Cys Tyr Ser Glu Phe Gly Gln Ile Ile Asp Ala Val
660 665 670

Ala Ala Leu Asp Ala Asp Val Thr Ser Ile Glu Ala Ala Arg Ser Arg
675 680 685

Met Glu Leu Leu Gly Asp Leu Asp Glu Ser Phe His Ser Glu Ile Gly
690 695 700

Pro Gly Ile Trp Asp Ile His Ser Pro Arg Val Pro Asp Val Ala Glu
705 710 715 720

Leu Thr Glu Leu Ile Lys Ala Ala Leu Val Asn Val Pro Thr Glu Arg

725 730 735

Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Tyr Ala Glu
740 745 750

Thr Glu Ala Ser Leu Arg Asn Met Val Leu Ala Arg Asp Leu Val Val
755 760 765

Glu Ser Leu
770

<210> 89
<211> 1200
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(900)
<223> gene ptH1

<400> 89
gcgaacttgg cgtcgaagtc gttcgacagg tcgacctccg gcaggggcg gtcgccggcg 60

acacggcgga cgtcggcaag cgactcgaag ggcgcctgcc gcgtgaacag attgacggcg 120

tagggccccg tgacctgcgc cagctgctcc tccaggagcg cggcgggcgc gccgcccggc 180

gcgaggaaac cgagggaacc ggcggctgcg gcggcgtcga caagcgcggg cgacgagggg 240

ccgccggcca tgggcgcgac gatgatctgc gggatgtcca tgtgtgagag actatcgggc 300

gtg ttc aag atc ttc gac ctc ttc cgc cgc aag cag acg acc ccg gcg 348
Val Phe Lys Ile Phe Asp Leu Phe Arg Arg Lys Gln Thr Thr Pro Ala
1 5 10 15

ctc agc gcc gac tgg atc atc ctc ggc ctg ggc aac ccg ggg ccg aaa 396
Leu Ser Ala Asp Trp Ile Ile Leu Gly Leu Gly Asn Pro Gly Pro Lys
20 25 30

tac gcc gcc acg cgc cac aac gtg ggc tac atg gcc gtc gac gag ctt 444
Tyr Ala Ala Thr Arg His Asn Val Gly Tyr Met Ala Val Asp Glu Leu
35 40 45

ctc gac gcc acc ccg ctc cag ccc ctc ccc ggt acg aag gca ctg cac 492
Leu Asp Ala Thr Pro Leu Gln Pro Leu Pro Gly Thr Lys Ala Leu His
50 55 60

gcg aag acg atg atc gcg ggg cag gac gtg ctc gtg ctg cgt tcg acg 540
Ala Lys Thr Met Ile Ala Gly Gln Asp Val Leu Val Leu Arg Ser Thr
65 70 75 80

acc tac atg aac ctc tcc ggc gag gct gtc gcc cca ctc gcg gag cag 588
Thr Tyr Met Asn Leu Ser Gly Glu Ala Val Ala Pro Leu Ala Glu Gln

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                85                  90                  95

ctc ggg gtg ccg gcg gag cgg atc atc gcc atc cac gac gag ctc gac      636
Leu Gly Val Pro Ala Glu Arg Ile Ile Ala Ile His Asp Glu Leu Asp
            100                 105                 110

ctg ccg gtg ggc acc gtg cgg gtg aag aag ggc ggc aac gag aac ggc      684
Leu Pro Val Gly Thr Val Arg Val Lys Lys Gly Gly Asn Glu Asn Gly
        115                 120                 125

cac aac ggc ctg aag tcc atg acc gag cac ctg ggc acc cgc gac tac      732
His Asn Gly Leu Lys Ser Met Thr Glu His Leu Gly Thr Arg Asp Tyr
    130                 135                 140

ctg cgg gtg cgc atc ggc atc gcc cgc ccg ccg cag ggc gtg tcg gtg      780
Leu Arg Val Arg Ile Gly Ile Ala Arg Pro Pro Gln Gly Val Ser Val
145                 150                 155                 160

acc gac cat gtc ctc ggc ccc atc gac ggc ggc gag aac atc cgc ctg      828
Thr Asp His Val Leu Gly Pro Ile Asp Gly Gly Glu Asn Ile Arg Leu
                165                 170                 175

gcc gcc gag gcg gcg cgg ctc atc gtc gag cag ggg ctg ggc agg gcg      876
Ala Ala Glu Ala Ala Arg Leu Ile Val Glu Gln Gly Leu Gly Arg Ala
            180                 185                 190

cag aac gtc atc cac gcg cgg tga tcgcccccgg gcgctgctgc accaaagggg      930
Gln Asn Val Ile His Ala Arg
        195

gtattcgagt cggggcattg atcgggtgac gcccacgcgc tacccgatca atgcctcagt      990

tcgaataccc cctcggcccc ggcggccccg caggatctac ttcgccatct gcgcgacgag     1050

cttctccagg tcgccgagca tcgtctccag ctcgccgagg cgacgctcct gcggggagaa     1110

cacgccctcc tccgcgtcgt tgaaggtcga caggtacacc tggttgcgca cgtcgtactg     1170

ctggaagttg ccgacgatct gccgccagct                                     1200
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<210> 90
<211> 199
<212> PRT
<213> Corynebacterium humireducens

<400> 90

```
Val Phe Lys Ile Phe Asp Leu Phe Arg Arg Lys Gln Thr Thr Pro Ala
1               5                   10                  15

Leu Ser Ala Asp Trp Ile Ile Leu Gly Leu Gly Asn Pro Gly Pro Lys
            20                  25                  30

Tyr Ala Ala Thr Arg His Asn Val Gly Tyr Met Ala Val Asp Glu Leu
        35                  40                  45
```

Leu Asp Ala Thr Pro Leu Gln Pro Leu Pro Gly Thr Lys Ala Leu His
50 55 60

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

Thr Tyr Met Asn Leu Ser Gly Glu Ala Val Ala Pro Leu Ala Glu Gln
85 90 95

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

Leu Pro Val Gly Thr Val Arg Val Lys Lys Gly Gly Asn Glu Asn Gly
115 120 125

His Asn Gly Leu Lys Ser Met Thr Glu His Leu Gly Thr Arg Asp Tyr
130 135 140

Leu Arg Val Arg Ile Gly Ile Ala Arg Pro Pro Gln Gly Val Ser Val
145 150 155 160

Thr Asp His Val Leu Gly Pro Ile Asp Gly Gly Glu Asn Ile Arg Leu
165 170 175

Ala Ala Glu Ala Ala Arg Leu Ile Val Glu Gln Gly Leu Gly Arg Ala
180 185 190

Gln Asn Val Ile His Ala Arg
195

<210> 91
<211> 1146
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(846)
<223> gene ptH2

<400> 91
aggagatcgt cgtgtccgtc gagggcatcg aggccggcaa cgtcatcaac gccggtgaca 60

tcaccctgcc ggaggacgtc accctggtcg acgacgccga gctgctcgtc ttcaacatca 120

ccttcgagga ggtcgccgac gttccggagg agggcgagga ggccaccgaa gacgctgtcg 180

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gcgaggccgg caaggacgag gctgccgagg gcgaggagta gtcactcccc ttccgccacg      240

tgtgacgccc ctgaccggcc ggtcaggggc gtctcccctt ttctgtgcca gactgatcgg      300

gtg act gat tct cca ctt ctc atc gtc ggc ctg ggt aac ccg ggc gcg        348
Val Thr Asp Ser Pro Leu Leu Ile Val Gly Leu Gly Asn Pro Gly Ala
1               5                  10                  15

aag tac gcc gac acc cgc cac aac atc ggc gtc atg ctt ctc gac gag        396
Lys Tyr Ala Asp Thr Arg His Asn Ile Gly Val Met Leu Leu Asp Glu
            20                  25                  30

ctc gcc tcc cgc atc acc ccc gtc ccc gcc agc ttc gcc gtg cac aag        444
Leu Ala Ser Arg Ile Thr Pro Val Pro Ala Ser Phe Ala Val His Lys
        35                  40                  45

cgc acg aac acc gag gtc gcc gag gtc cgt cat cgc ggc cgt cgc ctc        492
Arg Thr Asn Thr Glu Val Ala Glu Val Arg His Arg Gly Arg Arg Leu
    50                  55                  60

gtg ctg gcc cgg acc cgc ggc tac atg aac gtc tcc ggt gga ccg gtg        540
Val Leu Ala Arg Thr Arg Gly Tyr Met Asn Val Ser Gly Gly Pro Val
65                  70                  75                  80

aag gca ctg gcg acc ttc ttc agg atc gcc ccc ggc gac atc atc gtc        588
Lys Ala Leu Ala Thr Phe Phe Arg Ile Ala Pro Gly Asp Ile Ile Val
                85                  90                  95

gcc cac gac gaa ctc gag ctg gac ttc ggc gag cac cgc ctc cgc acc        636
Ala His Asp Glu Leu Glu Leu Asp Phe Gly Glu His Arg Leu Arg Thr
            100                 105                 110

ggc ggc ggc gac cac ggc cac aac ggc ctg aag tcc gtg acc aag tcg        684
Gly Gly Gly Asp His Gly His Asn Gly Leu Lys Ser Val Thr Lys Ser
        115                 120                 125

ctg gga acg aag gag tac cag cgc ctg gcg ctc ggc atc ggc cgt ccg        732
Leu Gly Thr Lys Glu Tyr Gln Arg Leu Ala Leu Gly Ile Gly Arg Pro
    130                 135                 140

ccc ggg cgt atg gac ccc gcc gcc ttc gtg ctc aag ccc ttc acc cgc        780
Pro Gly Arg Met Asp Pro Ala Ala Phe Val Leu Lys Pro Phe Thr Arg
145                 150                 155                 160

cag gag gcc ggg gag ctg ccc ttc ctg ctc tcc gac gcc gcc gac gaa        828
Gln Glu Ala Gly Glu Leu Pro Phe Leu Leu Ser Asp Ala Ala Asp Glu
                165                 170                 175

ctc gaa cgc gcc ctc tga cctcccaggg tggaacctgg tcccggaagg                876
Leu Glu Arg Ala Leu
            180

ttccggacgc tgcccgggtg tctagatggt gagctcctcc ggggccgcct ccccctcgcg      936

ccgggcgatg atcttgtgga tctggtactc ccactcctgc agctcctccg gcagctcccc      996

cttcgagggg tcacggagat actcgcgacg cccggcgtcg tagccccaca gccagtcgac     1056

gtagcggtac caggacgtgc ggccggcctg gcggaaggtc tcgttgcgga tcaggcggga     1116
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gacgccgtcg acgtgccaca gctcccccca 1146

<210> 92
<211> 181
<212> PRT
<213> Corynebacterium humireducens

<400> 92

Val Thr Asp Ser Pro Leu Leu Ile Val Gly Leu Gly Asn Pro Gly Ala
1 5 10 15

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

Leu Ala Ser Arg Ile Thr Pro Val Pro Ala Ser Phe Ala Val His Lys
35 40 45

Arg Thr Asn Thr Glu Val Ala Glu Val Arg His Arg Gly Arg Arg Leu
50 55 60

Val Leu Ala Arg Thr Arg Gly Tyr Met Asn Val Ser Gly Gly Pro Val
65 70 75 80

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

Ala His Asp Glu Leu Glu Leu Asp Phe Gly Glu His Arg Leu Arg Thr
100 105 110

Gly Gly Gly Asp His Gly His Asn Gly Leu Lys Ser Val Thr Lys Ser
115 120 125

Leu Gly Thr Lys Glu Tyr Gln Arg Leu Ala Leu Gly Ile Gly Arg Pro
130 135 140

Pro Gly Arg Met Asp Pro Ala Ala Phe Val Leu Lys Pro Phe Thr Arg
145 150 155 160

Gln Glu Ala Gly Glu Leu Pro Phe Leu Leu Ser Asp Ala Ala Asp Glu
165 170 175

Leu Glu Arg Ala Leu
180

<210> 93
<211> 1389
<212> DNA
<213> Corynbacterium humireducens

<220>
<221> CDS
<222> (301)..(1089)
<223> gene lplA

<400> 93
gaaggtcggc atcacctccg tggccaccga acgcctcggc gaggtcgtct acgcggagct 60

cccgcaggtc ggtgacgccg tcaccgccgg tgaaccgtgc ggcgaggtcg agtccacgaa 120

gtcggtctcc gacctctacg cgccggtcac gggcaccgtc accgaggtca acgacgcggt 180

ccacgacgac tacgccgtga tcaacgacga ccccttcggc gcgggctggc tcttcgccgt 240

cgaggtcgac gaggtcggac cgctcatgac cgccgccgag tacgcggagg ccaacggcgt 300

gtg acc gcc cgg gac cgg tac cct ggt ccc atc atg act gca ccc cgt 348
Val Thr Ala Arg Asp Arg Tyr Pro Gly Pro Ile Met Thr Ala Pro Arg
1 5 10 15

gag ccc ttc ttc cct gcg gac cgt tcc atc cgt gcc tcc ggc gag ccc 396
Glu Pro Phe Phe Pro Ala Asp Arg Ser Ile Arg Ala Ser Gly Glu Pro
20 25 30

ccg gag atc cgt tat ctc ggc gtc gtc gac tac cag gag gcc tgg aat 444
Pro Glu Ile Arg Tyr Leu Gly Val Val Asp Tyr Gln Glu Ala Trp Asn
35 40 45

ctg cag gcc gag ctg gcg tcg caa cgc gcg gcc ggg gag atc ggt gac 492
Leu Gln Ala Glu Leu Ala Ser Gln Arg Ala Ala Gly Glu Ile Gly Asp
50 55 60

cag ctc ctc atc ctc gag cac ccg agc gtg tac acc gcc ggc aag cgc 540
Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr Thr Ala Gly Lys Arg
65 70 75 80

acg cag ccg gag gac cgc ccc acc aac ggc ctg ccg gtc atc gac gtc 588
Thr Gln Pro Glu Asp Arg Pro Thr Asn Gly Leu Pro Val Ile Asp Val
85 90 95

gac cgg ggt ggc cgc atc acc tgg cac ggc gag gga cag ctg gtg gtc 636
Asp Arg Gly Gly Arg Ile Thr Trp His Gly Glu Gly Gln Leu Val Val
100 105 110

tac ccg atc atc aaa ctg gcc gac ccg gtg gac gtc gtg gac tat gtc 684
Tyr Pro Ile Ile Lys Leu Ala Asp Pro Val Asp Val Val Asp Tyr Val
115 120 125

cgc cgc ctc gag gag gcg gtg atc gcg acg gtg cgg gag gtg ggc gtc 732
Arg Arg Leu Glu Glu Ala Val Ile Ala Thr Val Arg Glu Val Gly Val
130 135 140

```
ggc aat gcg ggt cgc atc gac ggc cgc tcc gga gtc tgg gtc ccc gcc        780
Gly Asn Ala Gly Arg Ile Asp Gly Arg Ser Gly Val Trp Val Pro Ala
145                 150                 155                 160

gac ggg acc cga cgc gac cgg aag gtg gcg gcg ctc ggc atc cgt gtc        828
Asp Gly Thr Arg Arg Asp Arg Lys Val Ala Ala Leu Gly Ile Arg Val
                165                 170                 175

acc cgc ggg gtg acc atg cac ggg ctg agc ctg aac tgc tcg aac acg        876
Thr Arg Gly Val Thr Met His Gly Leu Ser Leu Asn Cys Ser Asn Thr
            180                 185                 190

ctc gag cac tac ggg cac atc gtg gcg tgc ggc atc gac gac gcc gac        924
Leu Glu His Tyr Gly His Ile Val Ala Cys Gly Ile Asp Asp Ala Asp
        195                 200                 205

gtc acc acc ctc agc atg gaa ctg ggg cgc gac gtc agc gtc ggg gag        972
Val Thr Thr Leu Ser Met Glu Leu Gly Arg Asp Val Ser Val Gly Glu
    210                 215                 220

gtc acg gca ccg ctt gtc gac gcc ctc ctg gcc gcc ctc gcc ggt gaa       1020
Val Thr Ala Pro Leu Val Asp Ala Leu Leu Ala Ala Leu Ala Gly Glu
225                 230                 235                 240

ctc gcc gtc gcg gac cac acc ttc gga tcg gcg ccc gat ccg acg aag       1068
Leu Ala Val Ala Asp His Thr Phe Gly Ser Ala Pro Asp Pro Thr Lys
                245                 250                 255

att ccc gcg aaa acg cgc tga cctctaagtt tatccctatc agtagaaaga          1119
Ile Pro Ala Lys Thr Arg
            260

gtatggtggc gttgtgacta tcgcacctga aggacgcaag ctgctccggg tggagaagcg     1179

caatgcgcag acccccatcg agacgaagcc ccgttggatc cgcaacgcgg tgaagaccgg     1239

ccccgagtac gaggacatga agaagaaggt ggcgggcgcc tccctgcaca ccgtctgtca     1299

ggaggcgggc tgccccaaca tccacgagtg ctgggagtcc cgcgaggcga cgtttctcat     1359

cggcggcgcc aactgctccc gccgctgcga                                      1389
```

<210> 94
<211> 262
<212> PRT
<213> Corynbacterium humireducens

<400> 94

```
Val Thr Ala Arg Asp Arg Tyr Pro Gly Pro Ile Met Thr Ala Pro Arg
1               5                   10                  15

Glu Pro Phe Phe Pro Ala Asp Arg Ser Ile Arg Ala Ser Gly Glu Pro
            20                  25                  30
```

```
Pro Glu Ile Arg Tyr Leu Gly Val Val Asp Tyr Gln Glu Ala Trp Asn
        35                  40                  45

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

Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr Thr Ala Gly Lys Arg
65                  70                  75                  80

Thr Gln Pro Glu Asp Arg Pro Thr Asn Gly Leu Pro Val Ile Asp Val
                85                  90                  95

Asp Arg Gly Gly Arg Ile Thr Trp His Gly Glu Gly Gln Leu Val Val
            100                 105                 110

Tyr Pro Ile Ile Lys Leu Ala Asp Pro Val Asp Val Val Asp Tyr Val
        115                 120                 125

Arg Arg Leu Glu Glu Ala Val Ile Ala Thr Val Arg Glu Val Gly Val
    130                 135                 140

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

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

Thr Arg Gly Val Thr Met His Gly Leu Ser Leu Asn Cys Ser Asn Thr
            180                 185                 190

Leu Glu His Tyr Gly His Ile Val Ala Cys Gly Ile Asp Asp Ala Asp
        195                 200                 205

Val Thr Thr Leu Ser Met Glu Leu Gly Arg Asp Val Ser Val Gly Glu
    210                 215                 220

Val Thr Ala Pro Leu Val Asp Ala Leu Leu Ala Ala Leu Ala Gly Glu
225                 230                 235                 240

Leu Ala Val Ala Asp His Thr Phe Gly Ser Ala Pro Asp Pro Thr Lys
                245                 250                 255

Ile Pro Ala Lys Thr Arg
            260
```

<210> 95
<211> 2010
<212> DNA
<213> Corynbacterium humireducens

<220>
<221> CDS
<222> (301)..(1710)
<223> gene gcvL

<400> 95
caactgacat cacagagaga aggcacacat gtccatcttc gagcagatca tcgtcgccat 60

caacaacttc gtcggcccgg gcatccacgc cctgtcctcc gcttcctcca acgccgcact 120

ggccatcggc ctcttctagg tcgaccccgg aagcatctgc ttatcgacgc cccggccccc 180

ggtcggggcg ttcgtcgttg cggcaccaca gtcccgccac cgtcccaccg cccccacggg 240

ggcgggatcc ttttgtgggg ggcggtgaca cgggggaaac ggtcacctat ccttggtggc 300

gtg act gaa cat tat gac gtt gtt gta ctc ggt gcg ggc ccc ggt ggc 348
Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly
1 5 10 15

tac gtc gcc gcc atc cgc gca gcc cag ctc ggc aag aag gtt gct gtc 396
Tyr Val Ala Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val
20 25 30

gtc gag aag cag tac tgg ggc gga gtc tgc ctc aac gtg ggc tgc atc 444
Val Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile
35 40 45

ccc tcg aag gcg ctg atc aag aac gcc gag atc gcc cac atc ttc acg 492
Pro Ser Lys Ala Leu Ile Lys Asn Ala Glu Ile Ala His Ile Phe Thr
50 55 60

cac gag aag aag acg ttc ggc atc aac ggc gac gtc tcc ttc aac tac 540
His Glu Lys Lys Thr Phe Gly Ile Asn Gly Asp Val Ser Phe Asn Tyr
65 70 75 80

gag gac gcc cac aag cgc tcc cgt cag gtg tcg gag aag atc gtc ggc 588
Glu Asp Ala His Lys Arg Ser Arg Gln Val Ser Glu Lys Ile Val Gly
85 90 95

ggc gtc cac tac ctg atg aag aag aac aag atc acc gag atc gac ggc 636
Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Thr Glu Ile Asp Gly
100 105 110

ttc gga acc ttc agg gac gcc aag acc atc gag gtc agc gag ggc aag 684
Phe Gly Thr Phe Arg Asp Ala Lys Thr Ile Glu Val Ser Glu Gly Lys
115 120 125

gac gcc ggc aag gtc gtc acc ttc gac gac tgc atc atc gcc acc ggc 732
Asp Ala Gly Lys Val Val Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly
130 135 140

```
tcc gtg gtc aac agc ctc cgt ggc gtc gag ttc tcc gag aac gtc gtc        780
Ser Val Val Asn Ser Leu Arg Gly Val Glu Phe Ser Glu Asn Val Val
145                 150                 155                 160

tcc tac gag gag cag atc ctc aac ccg gtc gcc ccg gag aag atg gtc        828
Ser Tyr Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Glu Lys Met Val
                165                 170                 175

atc gtc ggt gcc ggc gcc atc ggc atg gag ttc gcc tac gtg ctc tcc        876
Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Ser
            180                 185                 190

aac tac ggc gtc gac gtc acc gtc atc gag tac atg gac cgt gtc ctg        924
Asn Tyr Gly Val Asp Val Thr Val Ile Glu Tyr Met Asp Arg Val Leu
        195                 200                 205

ccg aac gag gac gag gac gtc tcc aag gtc atc gcc aag gcc tac aag        972
Pro Asn Glu Asp Glu Asp Val Ser Lys Val Ile Ala Lys Ala Tyr Lys
    210                 215                 220

aag atg ggc gtc acg ctc ctc ccg ggc cac gcc acc acc gcc gtg cgc       1020
Lys Met Gly Val Thr Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg
225                 230                 235                 240

gac aac ggc gac tcc gtc gag gtc gac tac cag aag aag ggc tcg gac       1068
Asp Asn Gly Asp Ser Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp
                245                 250                 255

aag acc gag acc atc gtc gcc gac cgc gtc ctc gtc tcc gtc ggc ttc       1116
Lys Thr Glu Thr Ile Val Ala Asp Arg Val Leu Val Ser Val Gly Phe
            260                 265                 270

cgc ccg cgt gtc gag ggc ttc ggc ctg gag aac acc ggc gtc gag ctc       1164
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Glu Leu
        275                 280                 285

acc gag cgc ggt gcc atc gcc atc gac gac ttc atg cgc acc aac gtc       1212
Thr Glu Arg Gly Ala Ile Ala Ile Asp Asp Phe Met Arg Thr Asn Val
    290                 295                 300

gag cac atc tac gcc atc ggt gac gtc acc gcc aag ctg cag ctg gcc       1260
Glu His Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala
305                 310                 315                 320

cac gtc gcc gag gcg cag ggc atc gtc gcc gcc gag acc atc gcc ggc       1308
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly
                325                 330                 335

gcc gag acc cac gag ctg ggc gac tac atg atg atg ccg cgc gcc acc       1356
Ala Glu Thr His Glu Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr
            340                 345                 350

ttc tgt aac ccg cag gtc gcg tcc ttc ggc tac acc gag gcg cag gcc       1404
Phe Cys Asn Pro Gln Val Ala Ser Phe Gly Tyr Thr Glu Ala Gln Ala
        355                 360                 365

aag gag aag tgg ccg gac cgc gag atc aag gtc gcg tcc ttc ccg ttc       1452
Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe
    370                 375                 380
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tcc gcg aac ggc aag gcc gtc ggc ctg gcc gag acc gag ggc ttc gcc        1500
Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Glu Gly Phe Ala
385                 390                 395                 400

aag atc gtc gcc gac gcc gag tac ggc gag ctg ctg ggc ggc cac ctg        1548
Lys Ile Val Ala Asp Ala Glu Tyr Gly Glu Leu Leu Gly Gly His Leu
                405                 410                 415

gtc ggc gcc aac gcg tcc gag ctg ctc aac gag ctg gtc ctc gcg cag        1596
Val Gly Ala Asn Ala Ser Glu Leu Leu Asn Glu Leu Val Leu Ala Gln
            420                 425                 430

aac tac gat ctc acc acc gag gag atc agc cgc gcg gtc cac atc cac        1644
Asn Tyr Asp Leu Thr Thr Glu Glu Ile Ser Arg Ala Val His Ile His
        435                 440                 445

ccg acc ctg tcg gag gcc gtc aag gag gcc gca cac ggc atc gac ggc        1692
Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Asp Gly
    450                 455                 460

cac atg atc aac ttc tag tccccggaa aaaggggcct cccggctggg                1740
His Met Ile Asn Phe
465

aggccccttt tctcatgctt tccgacgccc ccggggcgtc gccaagcgcc tagttgtagg      1800

gcgcgaccga cgaccggtgg gcgtcgatgg tgatctcctc gtggatcggc gggaacgcgc      1860

gctgcgcgca gttctcccgc gggcacacgc ggcagccggc gccgatcggg gtggcgctgg      1920

acaggtcggc gaggttgagt ccctgcgcgt agaccgtgcg gtcggcgtgg cgggcctcgc      1980

agcccaggcc gatggcgaag agcttgccgg                                       2010
```

<210> 96
<211> 469
<212> PRT
<213> Corynbacterium humireducens

<400> 96

```
Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly
1               5                   10                  15

Tyr Val Ala Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val
            20                  25                  30

Val Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile
        35                  40                  45

Pro Ser Lys Ala Leu Ile Lys Asn Ala Glu Ile Ala His Ile Phe Thr
    50                  55                  60
```

```
His Glu Lys Lys Thr Phe Gly Ile Asn Gly Asp Val Ser Phe Asn Tyr
65                  70                  75                  80

Glu Asp Ala His Lys Arg Ser Arg Gln Val Ser Glu Lys Ile Val Gly
                85                  90                  95

Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Thr Glu Ile Asp Gly
            100                 105                 110

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

Asp Ala Gly Lys Val Val Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly
    130                 135                 140

Ser Val Val Asn Ser Leu Arg Gly Val Glu Phe Ser Glu Asn Val Val
145                 150                 155                 160

Ser Tyr Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Glu Lys Met Val
                165                 170                 175

Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Ser
            180                 185                 190

Asn Tyr Gly Val Asp Val Thr Val Ile Glu Tyr Met Asp Arg Val Leu
        195                 200                 205

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

Lys Met Gly Val Thr Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg
225                 230                 235                 240

Asp Asn Gly Asp Ser Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp
                245                 250                 255

Lys Thr Glu Thr Ile Val Ala Asp Arg Val Leu Val Ser Val Gly Phe
            260                 265                 270

Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Glu Leu
        275                 280                 285

Thr Glu Arg Gly Ala Ile Ala Ile Asp Asp Phe Met Arg Thr Asn Val
    290                 295                 300
```

```
Glu His Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala
305                 310                 315                 320

His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly
                325                 330                 335

Ala Glu Thr His Glu Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr
            340                 345                 350

Phe Cys Asn Pro Gln Val Ala Ser Phe Gly Tyr Thr Glu Ala Gln Ala
        355                 360                 365

Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe
    370                 375                 380

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

Lys Ile Val Ala Asp Ala Glu Tyr Gly Glu Leu Leu Gly Gly His Leu
                405                 410                 415

Val Gly Ala Asn Ala Ser Glu Leu Leu Asn Glu Leu Val Leu Ala Gln
            420                 425                 430

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

Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Asp Gly
    450                 455                 460

His Met Ile Asn Phe
465
```

<210> 97
<211> 2442
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS

<222> (301)..(2142)
<223> gene ilvB

<400> 97

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cttgtggtag cagcgcggcg cctgccgtaa cgaccctacc cagtcgtctc gacaagcgcc       60

ctcgacagca cccaccatca gtgctgtacg ggggctttgt ctttagatgg tcgcaggtca      120

cttgtgccga cgacagccac caggccgacc ccttccgcac caagggaaga gtcaccaggt      180

agcgtttcaa ttgcattgtc cttgtgaaat taggagcttg ataacgtggc agcttcgcaa      240

acgcccaccc cggccacggt cgccaagaag tccccgggag ccgagaacgc acccgagcgg      300

atg acc ggc gcc cag gcg atc gtc cgg tcc ctc gag gag ctc ggc acc        348
Met Thr Gly Ala Gln Ala Ile Val Arg Ser Leu Glu Glu Leu Gly Thr
1               5                   10                  15

gac atc gtc ttc ggc ctg ccc ggc ggt gcc atc ctc ccc ctg tac gac       396
Asp Ile Val Phe Gly Leu Pro Gly Gly Ala Ile Leu Pro Leu Tyr Asp
            20                  25                  30

ccc ctc ttc tcc tcg aag aag ctg cgt cac gtg ctg gtg cgc cac gag       444
Pro Leu Phe Ser Ser Lys Lys Leu Arg His Val Leu Val Arg His Glu
        35                  40                  45

cag ggc tcg ggc cac gct gcc acc ggt tac gca cag gtc acc ggc aag       492
Gln Gly Ser Gly His Ala Ala Thr Gly Tyr Ala Gln Val Thr Gly Lys
    50                  55                  60

gtc ggc gtc tgc atc gcc acc tcc ggc ccg ggt gcc acc aac ctg gtc       540
Val Gly Val Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
65                  70                  75                  80

acc ccg ctg gcc gac gcc aac ctg gac tcc gtc ccg atg gtc gcc att       588
Thr Pro Leu Ala Asp Ala Asn Leu Asp Ser Val Pro Met Val Ala Ile
                85                  90                  95

acc ggc cag gtc ggc cgt tcc ctg ctg ggc acc gac gcc ttc cag gag       636
Thr Gly Gln Val Gly Arg Ser Leu Leu Gly Thr Asp Ala Phe Gln Glu
            100                 105                 110

gcc gac atc cgg ggt gtg acc atg ccg atc acg aag cac aac ttc atg       684
Ala Asp Ile Arg Gly Val Thr Met Pro Ile Thr Lys His Asn Phe Met
        115                 120                 125

gtc acc gac ccc aac gac atc gcc cgc acc ctg atg gag gcc ttc cac       732
Val Thr Asp Pro Asn Asp Ile Ala Arg Thr Leu Met Glu Ala Phe His
    130                 135                 140

ctc gct ctg acc ggt cgc ccg ggc ccc gtc ctg gtc gac atc ccg aag       780
Leu Ala Leu Thr Gly Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys
145                 150                 155                 160

gac atc cag aac gcg gag ttc gac ttc gtc tgg ccg ccg aag atg gat       828
Asp Ile Gln Asn Ala Glu Phe Asp Phe Val Trp Pro Pro Lys Met Asp
                165                 170                 175

ctg ccg ggc tac aag ccg gtc acc acg ccg cac tcc cgc cag atc acc       876
```

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

cag gcc gtc cag atg atc gcc gag gcc gag cgt ccc tgc ctc tac gtc      924
Gln Ala Val Gln Met Ile Ala Glu Ala Glu Arg Pro Cys Leu Tyr Val
        195                 200                 205

ggc ggc ggc gtc atc aag gcc gac gcc aac aag gag ctg ctg gag ttc      972
Gly Gly Gly Val Ile Lys Ala Asp Ala Asn Lys Glu Leu Leu Glu Phe
    210                 215                 220

gcc gag tac acc ggc gtc ccg gtc gtc acc acc ctc atg gcc ctg ggc     1020
Ala Glu Tyr Thr Gly Val Pro Val Val Thr Thr Leu Met Ala Leu Gly
225                 230                 235                 240

gcg ttc ccg gag tcc cac ccg ctg cac atg ggc atg ccg ggc atg cac     1068
Ala Phe Pro Glu Ser His Pro Leu His Met Gly Met Pro Gly Met His
                245                 250                 255

ggc gcc gtc ccg gcc gtc ggt gcc atg cag ggc gct gac ctg ctc atc     1116
Gly Ala Val Pro Ala Val Gly Ala Met Gln Gly Ala Asp Leu Leu Ile
            260                 265                 270

acc atc ggc gcg cgt ttc gac gac cgc gtc acc ggc aac ctc gac gag     1164
Thr Ile Gly Ala Arg Phe Asp Asp Arg Val Thr Gly Asn Leu Asp Glu
        275                 280                 285

ttc gcc ccg gac gcc cag gtc atc cac gcc gac atc gac ccg gcc gag     1212
Phe Ala Pro Asp Ala Gln Val Ile His Ala Asp Ile Asp Pro Ala Glu
    290                 295                 300

atc ggc aag atc cgc gag gcc gcc gtc ccg atc gtc ggc gac gcc cgc     1260
Ile Gly Lys Ile Arg Glu Ala Ala Val Pro Ile Val Gly Asp Ala Arg
305                 310                 315                 320

gag gtc ctc tcc gca ctc ctg cgc acc tac aag tcc tcc aag aac ctc     1308
Glu Val Leu Ser Ala Leu Leu Arg Thr Tyr Lys Ser Ser Lys Asn Leu
                325                 330                 335

acc ccg ccg aag atc acc gag tgg gtc gag tac ctg acg gac ctc aag     1356
Thr Pro Pro Lys Ile Thr Glu Trp Val Glu Tyr Leu Thr Asp Leu Lys
            340                 345                 350

gag cgc ttc ccg cgc ggc tac gac gag cag tcg gac ggc atg atg agc     1404
Glu Arg Phe Pro Arg Gly Tyr Asp Glu Gln Ser Asp Gly Met Met Ser
        355                 360                 365

ccg cag ttc gtc atc gag acc ctg tcc aag gag gtc ggc ccg gac gcg     1452
Pro Gln Phe Val Ile Glu Thr Leu Ser Lys Glu Val Gly Pro Asp Ala
    370                 375                 380

atc tac gtc gcc ggc gtc ggc cag cac cag atg tgg gcc gcg cag ttc     1500
Ile Tyr Val Ala Gly Val Gly Gln His Gln Met Trp Ala Ala Gln Phe
385                 390                 395                 400

atc gac ttc gag aag ccg cgc acc tgg ctc aac tcc ggt ggt ctg ggc     1548
Ile Asp Phe Glu Lys Pro Arg Thr Trp Leu Asn Ser Gly Gly Leu Gly
                405                 410                 415
```

```
acg atg ggc tac tcc atc ccc gcc gcc atg ggc gcc aag gcc ggt ctg      1596
Thr Met Gly Tyr Ser Ile Pro Ala Ala Met Gly Ala Lys Ala Gly Leu
            420                 425                 430

ccg gac gcc gag gtc tgg gcc atc gac ggt gac ggc tgc ttc cag atg      1644
Pro Asp Ala Glu Val Trp Ala Ile Asp Gly Asp Gly Cys Phe Gln Met
        435                 440                 445

acc aac cag gag ctc acc acc gcc gcg gtc gag ggc ttc ccg atc aag      1692
Thr Asn Gln Glu Leu Thr Thr Ala Ala Val Glu Gly Phe Pro Ile Lys
    450                 455                 460

gtc gcc ctg atc aac aac ggc aac ctg ggc atg gtc cgc cag tgg cag      1740
Val Ala Leu Ile Asn Asn Gly Asn Leu Gly Met Val Arg Gln Trp Gln
465                 470                 475                 480

acc ctg ttc tac ggt ggc cgc tac tcg aac acg aag ctg cgt gag cag      1788
Thr Leu Phe Tyr Gly Gly Arg Tyr Ser Asn Thr Lys Leu Arg Glu Gln
                485                 490                 495

gac gag tac gtg ccg gac ttc gtc acg ctg tcc gag gcg ctc ggc tgc      1836
Asp Glu Tyr Val Pro Asp Phe Val Thr Leu Ser Glu Ala Leu Gly Cys
            500                 505                 510

gtc gcc ttc cgc gtc acc cgc gag gag gac gtc ctg ccg acg atc cag      1884
Val Ala Phe Arg Val Thr Arg Glu Glu Asp Val Leu Pro Thr Ile Gln
        515                 520                 525

aag gca cgc gag atc aac gac cgc ccg gtc gtc atc gac ttc atc gtc      1932
Lys Ala Arg Glu Ile Asn Asp Arg Pro Val Val Ile Asp Phe Ile Val
    530                 535                 540

ggt gag gac gcc cag gtc tgg ccg atg gtc gcc gcc ggc gcc tcc aac      1980
Gly Glu Asp Ala Gln Val Trp Pro Met Val Ala Ala Gly Ala Ser Asn
545                 550                 555                 560

tcg gac atc gag tac gca cgt ggt ctg cgc ccc ttc ttc gag ggt gac      2028
Ser Asp Ile Glu Tyr Ala Arg Gly Leu Arg Pro Phe Phe Glu Gly Asp
                565                 570                 575

gag tcc gcg ggt gag tcc ccg gcc gac atc cac ggt gtc atg gag aac      2076
Glu Ser Ala Gly Glu Ser Pro Ala Asp Ile His Gly Val Met Glu Asn
            580                 585                 590

gcc cag gag gag acc gtc gag gaa gtc ctc gag gag cgc gcg aac gac      2124
Ala Gln Glu Glu Thr Val Glu Glu Val Leu Glu Glu Arg Ala Asn Asp
        595                 600                 605

agc gag aag gag aac tag gacaatggcg aacaccgaca tcatccgcaa             2172
Ser Glu Lys Glu Asn
    610

caccctcagc gtcctggtcc aggacgtcga cggcatcatc tcccgcgtcg caggcatgtt    2232

cacccgccgt ggctacaacc tggtgtccat cgtctcggcg cacaccgaca ccccgggcat    2292

cagccgcatc accatcgtgg tcgacgccaa cgagctggtc atcgagcagg tcaccaagca    2352

gctcaacaag atcatcccgg tgctcaaggt cgtccgcctc gaggaggaca ccaccatcgc    2412
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ccgcgccatc atgctggtga aggtcaacgc 2442

<210> 98
<211> 613
<212> PRT
<213> Corynebacterium humireducens

<400> 98

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

Asp Ile Val Phe Gly Leu Pro Gly Gly Ala Ile Leu Pro Leu Tyr Asp
20 25 30

Pro Leu Phe Ser Ser Lys Lys Leu Arg His Val Leu Val Arg His Glu
35 40 45

Gln Gly Ser Gly His Ala Ala Thr Gly Tyr Ala Gln Val Thr Gly Lys
50 55 60

Val Gly Val Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
65 70 75 80

Thr Pro Leu Ala Asp Ala Asn Leu Asp Ser Val Pro Met Val Ala Ile
85 90 95

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

Ala Asp Ile Arg Gly Val Thr Met Pro Ile Thr Lys His Asn Phe Met
115 120 125

Val Thr Asp Pro Asn Asp Ile Ala Arg Thr Leu Met Glu Ala Phe His
130 135 140

Leu Ala Leu Thr Gly Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys
145 150 155 160

Asp Ile Gln Asn Ala Glu Phe Asp Phe Val Trp Pro Pro Lys Met Asp
165 170 175

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

Gln Ala Val Gln Met Ile Ala Glu Ala Glu Arg Pro Cys Leu Tyr Val
195 200 205

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

Ala Glu Tyr Thr Gly Val Pro Val Val Thr Thr Leu Met Ala Leu Gly
225 230 235 240

Ala Phe Pro Glu Ser His Pro Leu His Met Gly Met Pro Gly Met His
245 250 255

Gly Ala Val Pro Ala Val Gly Ala Met Gln Gly Ala Asp Leu Leu Ile
260 265 270

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

Phe Ala Pro Asp Ala Gln Val Ile His Ala Asp Ile Asp Pro Ala Glu
290 295 300

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

Glu Val Leu Ser Ala Leu Leu Arg Thr Tyr Lys Ser Ser Lys Asn Leu
325 330 335

Thr Pro Pro Lys Ile Thr Glu Trp Val Glu Tyr Leu Thr Asp Leu Lys
340 345 350

Glu Arg Phe Pro Arg Gly Tyr Asp Glu Gln Ser Asp Gly Met Met Ser
355 360 365

Pro Gln Phe Val Ile Glu Thr Leu Ser Lys Glu Val Gly Pro Asp Ala
370 375 380

Ile Tyr Val Ala Gly Val Gly Gln His Gln Met Trp Ala Ala Gln Phe
385 390 395 400

Ile Asp Phe Glu Lys Pro Arg Thr Trp Leu Asn Ser Gly Gly Leu Gly
405 410 415

Thr Met Gly Tyr Ser Ile Pro Ala Ala Met Gly Ala Lys Ala Gly Leu
420 425 430

```
Pro Asp Ala Glu Val Trp Ala Ile Asp Gly Asp Gly Cys Phe Gln Met
        435                 440                 445

Thr Asn Gln Glu Leu Thr Thr Ala Ala Val Glu Gly Phe Pro Ile Lys
    450                 455                 460

Val Ala Leu Ile Asn Asn Gly Asn Leu Gly Met Val Arg Gln Trp Gln
465                 470                 475                 480

Thr Leu Phe Tyr Gly Gly Arg Tyr Ser Asn Thr Lys Leu Arg Glu Gln
                485                 490                 495

Asp Glu Tyr Val Pro Asp Phe Val Thr Leu Ser Glu Ala Leu Gly Cys
            500                 505                 510

Val Ala Phe Arg Val Thr Arg Glu Glu Asp Val Leu Pro Thr Ile Gln
        515                 520                 525

Lys Ala Arg Glu Ile Asn Asp Arg Pro Val Val Ile Asp Phe Ile Val
    530                 535                 540

Gly Glu Asp Ala Gln Val Trp Pro Met Val Ala Ala Gly Ala Ser Asn
545                 550                 555                 560

Ser Asp Ile Glu Tyr Ala Arg Gly Leu Arg Pro Phe Phe Glu Gly Asp
                565                 570                 575

Glu Ser Ala Gly Glu Ser Pro Ala Asp Ile His Gly Val Met Glu Asn
            580                 585                 590

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

Ser Glu Lys Glu Asn
    610
```

<210> 99
<211> 1614
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1314)
<223> gene ilvC

<400> 99

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ccgcgcccgc atcgtcgacg tggcccagga gtccgtggtc atcgaggcca ccggtacccc       60

gggcaagctg cgcgccctgc tggaggtcct cgagcccttc ggtatccgtg agctcatcca       120

gtccggtcag atcgccctca accgcggtcc gaagacgatg gcaccgtcca agtaacaccc       180

cctcatccca cctggtgaga caacacgcat gaaagtccca ccaggtgggg taccctgtc        240

tcatgttgtg gtacaaacaa caacagcact tgtataagac gaaaggcgag tttttctccc       300

atg gct att gaa ctg ctt tac gac gcc gac gct gac ctc tcc ctc atc          348
Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile
1               5                   10                  15

cag ggc cgc aag gtc gcc atc atc ggc tac ggc tcc cag ggc cac gcc         396
Gln Gly Arg Lys Val Ala Ile Ile Gly Tyr Gly Ser Gln Gly His Ala
            20                  25                  30

cac gcc cag aac ctg cgt gac tcc ggc gtc gag gtc tgc atc ggc ctg         444
His Ala Gln Asn Leu Arg Asp Ser Gly Val Glu Val Cys Ile Gly Leu
        35                  40                  45

cgc gac ggc tcc aag tcc gcg gag aag gcc aag gag gcc ggc ttc gag         492
Arg Asp Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
    50                  55                  60

gtc aag tcc aac gcc gac gcc gcc gcc tgg gca gac gtc atc atg ctg         540
Val Lys Ser Asn Ala Asp Ala Ala Ala Trp Ala Asp Val Ile Met Leu
65                  70                  75                  80

ctc gcc ccg gac acc tcc cag aag tcc atc tac gag aac gac atc gag         588
Leu Ala Pro Asp Thr Ser Gln Lys Ser Ile Tyr Glu Asn Asp Ile Glu
                85                  90                  95

ccg aac ctc aac gac ggt gac gcc ctg ctg ttc ggc cac ggc ctg aac         636
Pro Asn Leu Asn Asp Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
            100                 105                 110

gtc cac ttc ggc ctg atc aag ccg gcc gag aac atc gtc gtc ggc atg         684
Val His Phe Gly Leu Ile Lys Pro Ala Glu Asn Ile Val Val Gly Met
        115                 120                 125

gtc gcc ccg aag ggc ccg ggc cac ctc gtc cgt cgt cag ttc gtc gac         732
Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
    130                 135                 140

ggc aag ggc gtc ccc tgc ctc atc gcc gtc gac cag gac ccg aag ggc         780
Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Lys Gly
145                 150                 155                 160

aac ggc aag gac ctg ctg ctg tcc tac gcc gcc gcc atc ggt ggt gcc         828
Asn Gly Lys Asp Leu Leu Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala
                165                 170                 175

cgt gca ggc gtc atc ccg acc acc ttc gag gct gag acc gtc acc gac         876
Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp
            180                 185                 190
```

```
ctg ttc ggt gag cag gcc gtc ctc tgc ggt ggc acc gag gag ctc gtc        924
Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val
        195                 200                 205

aag acc ggc ttc gag gtt ctg gtc gag gct ggc tac gag ccg gag atg        972
Lys Thr Gly Phe Glu Val Leu Val Glu Ala Gly Tyr Glu Pro Glu Met
    210                 215                 220

gcc tac ttc gag tgc ctc cac gag ctc aag ctg atc gtt gac ctc atg       1020
Ala Tyr Phe Glu Cys Leu His Glu Leu Lys Leu Ile Val Asp Leu Met
225                 230                 235                 240

ttc gag ggc ggc atc gcc aac atg aac tac tcc gtc tcc gac acc gcc       1068
Phe Glu Gly Gly Ile Ala Asn Met Asn Tyr Ser Val Ser Asp Thr Ala
                245                 250                 255

gag ttc ggt ggc tac ctc tcc ggc ccg cgc gtc atc gac gcc ggc acc       1116
Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Gly Thr
            260                 265                 270

aag gag cgc atg aag gac atc ctg acc gac atc cag gac ggc acc ttc       1164
Lys Glu Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe
        275                 280                 285

acc aag cgc ctc atc gcc aac gtc gag aac ggc aac aag gag ctc gag       1212
Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Lys Glu Leu Glu
    290                 295                 300

ggt ctg cgc gag gag tac gcc aag cac cag atc gag gag acc ggc gcc       1260
Gly Leu Arg Glu Glu Tyr Ala Lys His Gln Ile Glu Glu Thr Gly Ala
305                 310                 315                 320

aag ctg cgt gac ctc atg agc tgg gtc aag gtc gag atc acc gag acc       1308
Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Glu Ile Thr Glu Thr
                325                 330                 335

gcc taa gcccccacgc ttgtcgacgc cccaccggtt cgccggtggg gcgttcgtct        1364
Ala

ttgccgggcc agctgagggg cctgcctcag gggtggagca ggtcgagcag gtgccgccgg    1424

agggcggggt cggggtcggc gtcgcgacgc gggcgggggа ggtccacggt gatgtcggcg    1484

atgaccgtgg cgtcgggggа gggggacatg acgaggatgc ggtcggagag caggatcgcc    1544

tcgtcgacgt cgtgggtgac catgacgacg gtgcggcggt cggactccca cagggagagc    1604

agctccagct                                                          1614

<210>  100
<211>  337
<212>  PRT
<213>  Corynebacterium humireducens

<400>  100
```

```
Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile
1               5                  10                  15

Gln Gly Arg Lys Val Ala Ile Ile Gly Tyr Gly Ser Gln Gly His Ala
            20                  25                  30

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

Arg Asp Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
    50                  55                  60

Val Lys Ser Asn Ala Asp Ala Ala Ala Trp Ala Asp Val Ile Met Leu
65                  70                  75                  80

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

Pro Asn Leu Asn Asp Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
            100                 105                 110

Val His Phe Gly Leu Ile Lys Pro Ala Glu Asn Ile Val Val Gly Met
        115                 120                 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
    130                 135                 140

Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Lys Gly
145                 150                 155                 160

Asn Gly Lys Asp Leu Leu Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala
                165                 170                 175

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

Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val
        195                 200                 205

Lys Thr Gly Phe Glu Val Leu Val Glu Ala Gly Tyr Glu Pro Glu Met
    210                 215                 220

Ala Tyr Phe Glu Cys Leu His Glu Leu Lys Leu Ile Val Asp Leu Met
225                 230                 235                 240
```

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

Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Gly Thr
            260                 265                 270

Lys Glu Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe
        275                 280                 285

Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Lys Glu Leu Glu
    290                 295                 300

Gly Leu Arg Glu Glu Tyr Ala Lys His Gln Ile Glu Glu Thr Gly Ala
305                 310                 315                 320

Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Glu Ile Thr Glu Thr
                325                 330                 335

Ala
```

<210> 101
<211> 2439
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(2139)
<223> gene ilvD

<400> 101

```
gaggacgtct ccggcatcgg cttcaagggc tcccgcgccc tgctgaccac ccgcgacggc       60

accgagcacg ccatgcccgg cgtgaccttc aactccctgc cgcagctggc ggaggcctcc      120

cagggccgga tccccgatgt cctcacctcc gcccaggagg cggccgacga caaggtcacc      180

atcatccacc gcgacgggca gcagatcctc atctccaagg aggagtacgc tgctcgacag      240

gccgcgcagc aggccaaccg ctcgtcctct gacaaccctg aaaaacctgaa ggagcagtaa      300

gtg ttc ccg ctt cga tcc aaa gtc acc acc gtc gga cgc aac gcc gcc          348
Val Phe Pro Leu Arg Ser Lys Val Thr Thr Val Gly Arg Asn Ala Ala
1               5                   10                  15

gga gcc cgc gcc ctg tgg cgc gcc acg ggc acc aag gag cac gag ttc        396
Gly Ala Arg Ala Leu Trp Arg Ala Thr Gly Thr Lys Glu His Glu Phe
            20                  25                  30
```

```
ggt aag ccg atc gtc gcg atc gtg aac tcc tac acc cag ttc gtc ccg        444
Gly Lys Pro Ile Val Ala Ile Val Asn Ser Tyr Thr Gln Phe Val Pro
        35                  40                  45

ggc cac gtc cac ctg aag aac gtg ggc gac atc gtc gcg gac gcc gtc        492
Gly His Val His Leu Lys Asn Val Gly Asp Ile Val Ala Asp Ala Val
    50                  55                  60

cgt gcc gcc ggt ggc gtg ccg aag gag ttc cac acc atc gcc gtc gac        540
Arg Ala Ala Gly Gly Val Pro Lys Glu Phe His Thr Ile Ala Val Asp
65                  70                  75                  80

gac ggc atc gcc atg gga cac ggc ggc atg ctc tac tcg ctg ccc agc        588
Asp Gly Ile Ala Met Gly His Gly Gly Met Leu Tyr Ser Leu Pro Ser
                85                  90                  95

cgt gag atc atc gcc gac tct gtc gag tac atg gtc aac gcc cac acc        636
Arg Glu Ile Ile Ala Asp Ser Val Glu Tyr Met Val Asn Ala His Thr
            100                 105                 110

gcc gac gcg atg gtc tgc atc tcc aac tgc gac aag atc acc ccg ggc        684
Ala Asp Ala Met Val Cys Ile Ser Asn Cys Asp Lys Ile Thr Pro Gly
        115                 120                 125

atg ctc aac gcc gcg ctg cgt ctc aac atc ccg gcc gtg ttc gtc tcc        732
Met Leu Asn Ala Ala Leu Arg Leu Asn Ile Pro Ala Val Phe Val Ser
    130                 135                 140

ggc ggt ccg atg gag gcc ggc aag gcc gtc gtc gtc gac ggc gtc gcc        780
Gly Gly Pro Met Glu Ala Gly Lys Ala Val Val Val Asp Gly Val Ala
145                 150                 155                 160

cag acc ccg acc gac ctc atc acc gcc atc gcc gcc tcc gcc gac gac        828
Gln Thr Pro Thr Asp Leu Ile Thr Ala Ile Ala Ala Ser Ala Asp Asp
                165                 170                 175

aac gtc tcc gat gag ggc ctg gcc acc atc gag gag tcg gcc tgc ccg        876
Asn Val Ser Asp Glu Gly Leu Ala Thr Ile Glu Glu Ser Ala Cys Pro
            180                 185                 190

acc tgt ggc tcc tgc tcc ggc atg ttc acc gcc aac tcg atg aac tgc        924
Thr Cys Gly Ser Cys Ser Gly Met Phe Thr Ala Asn Ser Met Asn Cys
        195                 200                 205

ctc acc gag gcc ctg ggc ctg tcc ctg ccg ggc aac ggc acg acg ctg        972
Leu Thr Glu Ala Leu Gly Leu Ser Leu Pro Gly Asn Gly Thr Thr Leu
    210                 215                 220

gcc acc cac tcc gcc cgc cgt cgt ctc ttc gag cag gcc ggc gag acc       1020
Ala Thr His Ser Ala Arg Arg Arg Leu Phe Glu Gln Ala Gly Glu Thr
225                 230                 235                 240

atc gtc gag ctg tgc agg cgc tac tac ggc gag gag gac gag tcc gtc       1068
Ile Val Glu Leu Cys Arg Arg Tyr Tyr Gly Glu Glu Asp Glu Ser Val
                245                 250                 255

ctg ccg cgc aac atc gcc acc aag gac gcc ttc cgc aac gcg atg gcc       1116
Leu Pro Arg Asn Ile Ala Thr Lys Asp Ala Phe Arg Asn Ala Met Ala
            260                 265                 270
```

```
ctc gac atg gcc atg ggc ggc tcc acc aac acg atc ctc cac acg ctg      1164
Leu Asp Met Ala Met Gly Gly Ser Thr Asn Thr Ile Leu His Thr Leu
        275                 280                 285

gcc gcc gcc cag gag ggt gag gtc gac ttc acc ctg gcg gac atc gag      1212
Ala Ala Ala Gln Glu Gly Glu Val Asp Phe Thr Leu Ala Asp Ile Glu
    290                 295                 300

gag atc tcc cac cag gtg ccg tgc atc tcc aag gtc gcc ccg aac ggc      1260
Glu Ile Ser His Gln Val Pro Cys Ile Ser Lys Val Ala Pro Asn Gly
305                 310                 315                 320

atc tac cac atc gag gac gtc cac cgc gcc ggc ggc atc ccg gcc atc      1308
Ile Tyr His Ile Glu Asp Val His Arg Ala Gly Gly Ile Pro Ala Ile
                325                 330                 335

ctc ggc gag ctg cgt cgc gcg aac ctg ctc aac gag gac gtc cac tcc      1356
Leu Gly Glu Leu Arg Arg Ala Asn Leu Leu Asn Glu Asp Val His Ser
            340                 345                 350

atc acc tac gac tcc ctc gac gag tgg ctg ggt gac tgg gac atc cgt      1404
Ile Thr Tyr Asp Ser Leu Asp Glu Trp Leu Gly Asp Trp Asp Ile Arg
        355                 360                 365

ggc ggc cgg gcc atc gac gcc gcg acc gag ctc ttc cac gcc gcc ccg      1452
Gly Gly Arg Ala Ile Asp Ala Ala Thr Glu Leu Phe His Ala Ala Pro
    370                 375                 380

ggt ggc gtg cgc acc acg gag ccc ttc tcc acc gac aac cgc tgg gac      1500
Gly Gly Val Arg Thr Thr Glu Pro Phe Ser Thr Asp Asn Arg Trp Asp
385                 390                 395                 400

agc ctg gac acc gac ccg gtc aac ggc tgc atc cac gac gtc gag cac      1548
Ser Leu Asp Thr Asp Pro Val Asn Gly Cys Ile His Asp Val Glu His
                405                 410                 415

gcc cac tcc gcg gac ggc ggc ctg gtg gtc ctg cgc ggc aac ctg gcg      1596
Ala His Ser Ala Asp Gly Gly Leu Val Val Leu Arg Gly Asn Leu Ala
            420                 425                 430

ccg gac ggc tcc gtc ctc aag acc gcc ggc gtc gag gag gag ctg tgg      1644
Pro Asp Gly Ser Val Leu Lys Thr Ala Gly Val Glu Glu Glu Leu Trp
        435                 440                 445

acc ttc acc ggc ccg gcc cgc gtc gtc gac agc cag gag gag gcc gtc      1692
Thr Phe Thr Gly Pro Ala Arg Val Val Asp Ser Gln Glu Glu Ala Val
    450                 455                 460

tcc atc atc ctc aag cgc gag gtc cag ccg ggt gag gtc gtc gtc atc      1740
Ser Ile Ile Leu Lys Arg Glu Val Gln Pro Gly Glu Val Val Val Ile
465                 470                 475                 480

cgt tac gag ggt cct tcc ggt ggc ccg ggc atg cag gag atg ctg cac      1788
Arg Tyr Glu Gly Pro Ser Gly Gly Pro Gly Met Gln Glu Met Leu His
                485                 490                 495

ccg acg tcc ttc ctc aag ggt gcc ggc ctg ggc aag aag tgc gcc ctc      1836
Pro Thr Ser Phe Leu Lys Gly Ala Gly Leu Gly Lys Lys Cys Ala Leu
```

```
                500                 505                 510

atc acc gac ggc cgt ttc tcc ggc ggc acc tcc ggc ttg tcg atc ggc      1884
Ile Thr Asp Gly Arg Phe Ser Gly Gly Thr Ser Gly Leu Ser Ile Gly
        515                 520                 525

cac atc tcc ccg gag gcc gcc cac ggt ggt ctc atc ggc ctg atc cgc      1932
His Ile Ser Pro Glu Ala Ala His Gly Gly Leu Ile Gly Leu Ile Arg
    530                 535                 540

aac ggt gac ccg atc acc atc gac gtc cac acc cgt cgt ctc tcc ctc      1980
Asn Gly Asp Pro Ile Thr Ile Asp Val His Thr Arg Arg Leu Ser Leu
545                 550                 555                 560

gac ctg ccg gac gag gag atc gag gcc cgc cgc gcc gag atg gag gcc      2028
Asp Leu Pro Asp Glu Glu Ile Glu Ala Arg Arg Ala Glu Met Glu Ala
                565                 570                 575

tcc gag aag ccg tgg acc gcg aac cgc gag cgc aag gtc tcc aag gca      2076
Ser Glu Lys Pro Trp Thr Ala Asn Arg Glu Arg Lys Val Ser Lys Ala
            580                 585                 590

ctg cgt gcg tac gcc gcc atg gcc acc tcc gcc gat aag ggc gcc gtc      2124
Leu Arg Ala Tyr Ala Ala Met Ala Thr Ser Ala Asp Lys Gly Ala Val
        595                 600                 605

cgc cag gtg gac taa cattgtccgc gtgaccacga caaacaagcc cgcgatcctg      2179
Arg Gln Val Asp
    610

ccccacaccg ccatcctgag gatggtggtg gccctggggc tgatcgcggg cttcggcgtc    2239

accggacgcc agatgatgat caccgacttc cccatcgaca tgatcatcta catggagggc    2299

gtgcgggcct tcctcgacgg cgccgagatg tacgccgtgc cgatgtacgc cggctccctg    2359

gccctgccgt tcatctatcc cccgttcggc gccctcgtca tggtgccgct cacccgttac    2419

gagcatgacc tggccggcga                                               2439
```

<210> 102
<211> 612
<212> PRT
<213> Corynebacterium humireducens

<400> 102

```
Val Phe Pro Leu Arg Ser Lys Val Thr Thr Val Gly Arg Asn Ala Ala
1               5                   10                  15

Gly Ala Arg Ala Leu Trp Arg Ala Thr Gly Thr Lys Glu His Glu Phe
            20                  25                  30

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

```
Gly His Val His Leu Lys Asn Val Gly Asp Ile Val Ala Asp Ala Val
    50                  55                  60

Arg Ala Ala Gly Gly Val Pro Lys Glu Phe His Thr Ile Ala Val Asp
65                  70                  75                  80

Asp Gly Ile Ala Met Gly His Gly Gly Met Leu Tyr Ser Leu Pro Ser
                85                  90                  95

Arg Glu Ile Ile Ala Asp Ser Val Glu Tyr Met Val Asn Ala His Thr
            100                 105                 110

Ala Asp Ala Met Val Cys Ile Ser Asn Cys Asp Lys Ile Thr Pro Gly
        115                 120                 125

Met Leu Asn Ala Ala Leu Arg Leu Asn Ile Pro Ala Val Phe Val Ser
    130                 135                 140

Gly Gly Pro Met Glu Ala Gly Lys Ala Val Val Val Asp Gly Val Ala
145                 150                 155                 160

Gln Thr Pro Thr Asp Leu Ile Thr Ala Ile Ala Ala Ser Ala Asp Asp
                165                 170                 175

Asn Val Ser Asp Glu Gly Leu Ala Thr Ile Glu Glu Ser Ala Cys Pro
            180                 185                 190

Thr Cys Gly Ser Cys Ser Gly Met Phe Thr Ala Asn Ser Met Asn Cys
        195                 200                 205

Leu Thr Glu Ala Leu Gly Leu Ser Leu Pro Gly Asn Gly Thr Thr Leu
    210                 215                 220

Ala Thr His Ser Ala Arg Arg Arg Leu Phe Glu Gln Ala Gly Glu Thr
225                 230                 235                 240

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

Leu Pro Arg Asn Ile Ala Thr Lys Asp Ala Phe Arg Asn Ala Met Ala
            260                 265                 270

Leu Asp Met Ala Met Gly Gly Ser Thr Asn Thr Ile Leu His Thr Leu
        275                 280                 285
```

Ala Ala Ala Gln Glu Gly Glu Val Asp Phe Thr Leu Ala Asp Ile Glu
290 295 300

Glu Ile Ser His Gln Val Pro Cys Ile Ser Lys Val Ala Pro Asn Gly
305 310 315 320

Ile Tyr His Ile Glu Asp Val His Arg Ala Gly Gly Ile Pro Ala Ile
325 330 335

Leu Gly Glu Leu Arg Arg Ala Asn Leu Leu Asn Glu Asp Val His Ser
340 345 350

Ile Thr Tyr Asp Ser Leu Asp Glu Trp Leu Gly Asp Trp Asp Ile Arg
355 360 365

Gly Gly Arg Ala Ile Asp Ala Ala Thr Glu Leu Phe His Ala Ala Pro
370 375 380

Gly Gly Val Arg Thr Thr Glu Pro Phe Ser Thr Asp Asn Arg Trp Asp
385 390 395 400

Ser Leu Asp Thr Asp Pro Val Asn Gly Cys Ile His Asp Val Glu His
405 410 415

Ala His Ser Ala Asp Gly Gly Leu Val Val Leu Arg Gly Asn Leu Ala
420 425 430

Pro Asp Gly Ser Val Leu Lys Thr Ala Gly Val Glu Glu Glu Leu Trp
435 440 445

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

Ser Ile Ile Leu Lys Arg Glu Val Gln Pro Gly Glu Val Val Val Ile
465 470 475 480

Arg Tyr Glu Gly Pro Ser Gly Gly Pro Gly Met Gln Glu Met Leu His
485 490 495

Pro Thr Ser Phe Leu Lys Gly Ala Gly Leu Gly Lys Lys Cys Ala Leu
500 505 510

Ile Thr Asp Gly Arg Phe Ser Gly Gly Thr Ser Gly Leu Ser Ile Gly

515 520 525

His Ile Ser Pro Glu Ala Ala His Gly Gly Leu Ile Gly Leu Ile Arg
530 535 540

Asn Gly Asp Pro Ile Thr Ile Asp Val His Thr Arg Arg Leu Ser Leu
545 550 555 560

Asp Leu Pro Asp Glu Glu Ile Glu Ala Arg Arg Ala Glu Met Glu Ala
565 570 575

Ser Glu Lys Pro Trp Thr Ala Asn Arg Glu Arg Lys Val Ser Lys Ala
580 585 590

Leu Arg Ala Tyr Ala Ala Met Ala Thr Ser Ala Asp Lys Gly Ala Val
595 600 605

Arg Gln Val Asp
610

<210> 103
<211> 1725
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1425)
<223> gene ilvE

<400> 103
gatctcgttg gccttgcccg tggcaccgac ggcggtgagg gcgtcgagga cctcgcggga 60

ggcggcgtcg tcgagaagga cggaggccgg cagctccggg ccgtcctcac cgcagaggac 120

ggggacgagc agtgcgtcgg gggtcttcgg ggccttcttg gccagctcga cggcgggggt 180

ggtgccgcgg gcgggaaggg tgaaagtggg gttcgccatg gaaagtacct cctgagattg 240

acaagcgatg aacccagctt atagagatca cctctgggtc gtcggtgtag cgtgttcccc 300

atg acg tct ctc aat ttc acc gtg aac cgt acg agc acc ccg acg tcc 348
Met Thr Ser Leu Asn Phe Thr Val Asn Arg Thr Ser Thr Pro Thr Ser
1 5 10 15

gat gag gcg cgc gag gag att ctg cag aat ccg cgg ttc ggc aag aac 396
Asp Glu Ala Arg Glu Glu Ile Leu Gln Asn Pro Arg Phe Gly Lys Asn
20 25 30

ttc acc gat cac atg gtc acc atc gag tgg tcc gag gac aag ggc tgg 444
Phe Thr Asp His Met Val Thr Ile Glu Trp Ser Glu Asp Lys Gly Trp

```
          35                  40                  45

cac gac gcc cgc gtg cgt ccc tac gag gcc atc ccg atg gat ccc gcg        492
His Asp Ala Arg Val Arg Pro Tyr Glu Ala Ile Pro Met Asp Pro Ala
    50                  55                  60

acc acg gtg ttc cac tac ggc cag gcg atc ttc gag ggc atc aag gcc        540
Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala
65                  70                  75                  80

tac cgt cag ccg gac ggc tcc atc gcc acc ttc cgc ccg gag cgc aac        588
Tyr Arg Gln Pro Asp Gly Ser Ile Ala Thr Phe Arg Pro Glu Arg Asn
                85                  90                  95

gcc gag cgc atg cag cgt tcc gcc gag cgc atg gcc atg ccg ccg ctg        636
Ala Glu Arg Met Gln Arg Ser Ala Glu Arg Met Ala Met Pro Pro Leu
            100                 105                 110

ccg acc gag gac ttc ctc gag acg ctc cgc ctg ctt gtc gac gtc gac        684
Pro Thr Glu Asp Phe Leu Glu Thr Leu Arg Leu Leu Val Asp Val Asp
        115                 120                 125

cgt gac tgg gtc ccc gcc gcc ggc ggc gag gcc agc ctc tac ctg cgt        732
Arg Asp Trp Val Pro Ala Ala Gly Gly Glu Ala Ser Leu Tyr Leu Arg
    130                 135                 140

ccc ttc atg atc tcc acc gag gtc tcc ctg ggc gtc agc ccg gcc aac        780
Pro Phe Met Ile Ser Thr Glu Val Ser Leu Gly Val Ser Pro Ala Asn
145                 150                 155                 160

cgg tac acc ttc ttc gtc atc gcc tcc ccg gtc ggg gcg tac ttc acc        828
Arg Tyr Thr Phe Phe Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
                165                 170                 175

ggt ggc gtc aag ccg gtc tcc gtg tgg ctg agc gag gac tac gtc cgt        876
Gly Gly Val Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
            180                 185                 190

gcc gcc ccg ggt ggc acc ggt gcc gcg aag ttc gcc ggc aac tac gcc        924
Ala Ala Pro Gly Gly Thr Gly Ala Ala Lys Phe Ala Gly Asn Tyr Ala
        195                 200                 205

gcc tcc ctg ctc gcg cag gcg cag gcg gag gag aag ggc tgc gac cag        972
Ala Ser Leu Leu Ala Gln Ala Gln Ala Glu Glu Lys Gly Cys Asp Gln
    210                 215                 220

gtc gtg tgg ctc gac gcc atc gag cac acc tac atc gag gag atg ggt       1020
Val Val Trp Leu Asp Ala Ile Glu His Thr Tyr Ile Glu Glu Met Gly
225                 230                 235                 240

ggc atg aac ctg ttc ttc gtg tac ggc tcg ggt gac gac gtc acc gtg       1068
Gly Met Asn Leu Phe Phe Val Tyr Gly Ser Gly Asp Asp Val Thr Val
                245                 250                 255

gcc acc ccc gag ctc tcc ggc tcc ctc ctg ccg ggc gtc acc cgc gac       1116
Ala Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Val Thr Arg Asp
            260                 265                 270

tcc ctc ctg cag gtc gcc cgc gat ctc ggc cac cgc acc gag gag cgg       1164
```

```
Ser Leu Leu Gln Val Ala Arg Asp Leu Gly His Arg Thr Glu Glu Arg
        275                 280                 285

agg atc tcc aag ttc gac tgg cgc gac gac gtc gcc tcc ggt gcg atg      1212
Arg Ile Ser Lys Phe Asp Trp Arg Asp Asp Val Ala Ser Gly Ala Met
    290                 295                 300

acc gag gcc atg gcc tgc ggc aca gcc gcc gtg atc acc ccg gtc ggc      1260
Thr Glu Ala Met Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly
305                 310                 315                 320

cgg gtc ctg tcc aac gac ggc gag ttc cag atc aat gac aac cag ccg      1308
Arg Val Leu Ser Asn Asp Gly Glu Phe Gln Ile Asn Asp Asn Gln Pro
                325                 330                 335

ggt gag gtc acc atg gcc atg cgc gag cgt ctc acc gac atc cag cgc      1356
Gly Glu Val Thr Met Ala Met Arg Glu Arg Leu Thr Asp Ile Gln Arg
            340                 345                 350

ggc ctg tac gag gac acc cac ggc tgg gtg cac acc ctc gtc ccg gct      1404
Gly Leu Tyr Glu Asp Thr His Gly Trp Val His Thr Leu Val Pro Ala
        355                 360                 365

gag gac cag ccg gcg gac tag tcggccagca gctcggcggc ggcccgcacc          1455
Glu Asp Gln Pro Ala Asp
    370

agcgggagcg ccgctagcgc gccggtgccc tggccggcgt tcatgtccag ggcgacgaga     1515

ggcgtgagtt cgagggcctg cagcgcgatg aggtgcgcgg gctccggggt cagctgccct     1575

gcctggcacc agggggcggt gccgggggag agacgttccg cgaggtaggc ggcgacggtg     1635

acgggggcgc cgtcgagaag cacgggggtg cggcgtgccg cggcctgcgc gatgaaggcc     1695

accagtgcca ccaggtccgg ggaggcgatc                                      1725
```

<210> 104
<211> 374
<212> PRT
<213> Corynebacterium humireducens

<400> 104

```
Met Thr Ser Leu Asn Phe Thr Val Asn Arg Thr Ser Thr Pro Thr Ser
1               5                  10                  15

Asp Glu Ala Arg Glu Glu Ile Leu Gln Asn Pro Arg Phe Gly Lys Asn
            20                  25                  30

Phe Thr Asp His Met Val Thr Ile Glu Trp Ser Glu Asp Lys Gly Trp
        35                  40                  45

His Asp Ala Arg Val Arg Pro Tyr Glu Ala Ile Pro Met Asp Pro Ala
    50                  55                  60
```

Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala
65 70 75 80

Tyr Arg Gln Pro Asp Gly Ser Ile Ala Thr Phe Arg Pro Glu Arg Asn
85 90 95

Ala Glu Arg Met Gln Arg Ser Ala Glu Arg Met Ala Met Pro Pro Leu
100 105 110

Pro Thr Glu Asp Phe Leu Glu Thr Leu Arg Leu Leu Val Asp Val Asp
115 120 125

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

Pro Phe Met Ile Ser Thr Glu Val Ser Leu Gly Val Ser Pro Ala Asn
145 150 155 160

Arg Tyr Thr Phe Phe Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
165 170 175

Gly Gly Val Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
180 185 190

Ala Ala Pro Gly Gly Thr Gly Ala Ala Lys Phe Ala Gly Asn Tyr Ala
195 200 205

Ala Ser Leu Leu Ala Gln Ala Gln Ala Glu Glu Lys Gly Cys Asp Gln
210 215 220

Val Val Trp Leu Asp Ala Ile Glu His Thr Tyr Ile Glu Glu Met Gly
225 230 235 240

Gly Met Asn Leu Phe Phe Val Tyr Gly Ser Gly Asp Asp Val Thr Val
245 250 255

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

Ser Leu Leu Gln Val Ala Arg Asp Leu Gly His Arg Thr Glu Glu Arg
275 280 285

Arg Ile Ser Lys Phe Asp Trp Arg Asp Asp Val Ala Ser Gly Ala Met

290 295 300

Thr Glu Ala Met Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly
305 310 315 320

Arg Val Leu Ser Asn Asp Gly Glu Phe Gln Ile Asn Asp Asn Gln Pro
325 330 335

Gly Glu Val Thr Met Ala Met Arg Glu Arg Leu Thr Asp Ile Gln Arg
340 345 350

Gly Leu Tyr Glu Asp Thr His Gly Trp Val His Thr Leu Val Pro Ala
355 360 365

Glu Asp Gln Pro Ala Asp
370

<210> 105
<211> 1896
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1596)
<223> gene ilvA

<400> 105
gccgatcggg gccagcgaga gggccgcacc cggggccgag tggacgacgg ggttgtccac 60

gacagcggcg tgggccgggg cgatgaggga gacactggtg gcgagcgccg cgcacagcgc 120

gacagcggaa cggcgaaggg acacggggag aactcctgtg gtcggtgggg tgcagatcgt 180

gtgacatggt ggaccagtga catgacacca atctcaattc cggaccacct gcaggtgaac 240

agtcggtgaa gtgggctgca acgccgtggc cggtggacag ggggactaca ctgagtcccc 300

atg agt gac acc cgg tct gcc gta acc acc ttc gag cct gtc cgc gcc 348
Met Ser Asp Thr Arg Ser Ala Val Thr Thr Phe Glu Pro Val Arg Ala
1 5 10 15

tcg gac att cag ctg gcg cag gca cgg atc tcc tcc gtc atc gag ccc 396
Ser Asp Ile Gln Leu Ala Gln Ala Arg Ile Ser Ser Val Ile Glu Pro
20 25 30

acc ccg ctc cag tac tgc ccc cgc ctc tcc gag gag acc ggc tgc gag 444
Thr Pro Leu Gln Tyr Cys Pro Arg Leu Ser Glu Glu Thr Gly Cys Glu
35 40 45

gtg tac ctc aaa cgc gag gac ctg cag gac gtg cgc tcc tac aag atc 492
Val Tyr Leu Lys Arg Glu Asp Leu Gln Asp Val Arg Ser Tyr Lys Ile

```
     50                  55                  60

cgc ggc gcc tac tac gcc atg gcc aac ctc gac gag cag cag cgg gac      540
Arg Gly Ala Tyr Tyr Ala Met Ala Asn Leu Asp Glu Gln Gln Arg Asp
65                  70                  75                  80

gcc ggc atc gtc gcc gcc tcc gcc ggc aac cac gca cag ggt gtc gcc      588
Ala Gly Ile Val Ala Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala
                85                  90                  95

tac gcc tgc cgc acg atg ggc atc cgg ggt cgc atc ttc gtc ccc aac      636
Tyr Ala Cys Arg Thr Met Gly Ile Arg Gly Arg Ile Phe Val Pro Asn
            100                 105                 110

cag acg ccg aag cag aag cgt gac cgc atc atg gtc cac ggc ggt gac      684
Gln Thr Pro Lys Gln Lys Arg Asp Arg Ile Met Val His Gly Gly Asp
        115                 120                 125

atg gtg gag ctg gtc gtc acc ggc aac aac ttc gac gag gcc gcc gag      732
Met Val Glu Leu Val Val Thr Gly Asn Asn Phe Asp Glu Ala Ala Glu
    130                 135                 140

gcc gcg cgt gcc gac gcc gcc gag cgc ggc gcc acc atg atc gag ccc      780
Ala Ala Arg Ala Asp Ala Ala Glu Arg Gly Ala Thr Met Ile Glu Pro
145                 150                 155                 160

ttc gac gcc cgc gac acc gtc atc ggt cag ggg acc atc gcg gcg gag      828
Phe Asp Ala Arg Asp Thr Val Ile Gly Gln Gly Thr Ile Ala Ala Glu
                165                 170                 175

atc ctc acg cag ctc acg tcc atc ggc aag tcc ctc gac acg gtg ctc      876
Ile Leu Thr Gln Leu Thr Ser Ile Gly Lys Ser Leu Asp Thr Val Leu
            180                 185                 190

gtg ccg gtc ggc ggc ggt ggc ctc ctg gcc ggt gtc gcc agc tac ctc      924
Val Pro Val Gly Gly Gly Gly Leu Leu Ala Gly Val Ala Ser Tyr Leu
        195                 200                 205

gcc gac atg gcg ccg cgc acc gcg atc gtc ggc gtc gag ccg ggc ggt      972
Ala Asp Met Ala Pro Arg Thr Ala Ile Val Gly Val Glu Pro Gly Gly
    210                 215                 220

gcc gcc tcc ctc cag gcc gcc ctg cgt gcc gac gcc ccc gtc acc ctc     1020
Ala Ala Ser Leu Gln Ala Ala Leu Arg Ala Asp Ala Pro Val Thr Leu
225                 230                 235                 240

tcc gcg gtc gac ccc ttc gtc gac ggc gcc gcc gtc aag cgc atc ggt     1068
Ser Ala Val Asp Pro Phe Val Asp Gly Ala Ala Val Lys Arg Ile Gly
                245                 250                 255

gac ctg ccc ttc gac atc atc gaa cgc aac aag ggc cgc atc cac gtc     1116
Asp Leu Pro Phe Asp Ile Ile Glu Arg Asn Lys Gly Arg Ile His Val
            260                 265                 270

atg gac gtc tcc gag ggc gcc gtg tgc acc gag atg ctc gac ctg tac     1164
Met Asp Val Ser Glu Gly Ala Val Cys Thr Glu Met Leu Asp Leu Tyr
        275                 280                 285

cag aac gag ggc atc atc acc gag ccc gcc ggt gca ctg tcg gtc acg     1212
```

```
Gln Asn Glu Gly Ile Ile Thr Glu Pro Ala Gly Ala Leu Ser Val Thr
    290                 295                 300

ggc ctg aag gag atg aag ctc cag cag gac tcc atc gtg gtg tgc atc      1260
Gly Leu Lys Glu Met Lys Leu Gln Gln Asp Ser Ile Val Val Cys Ile
305                 310                 315                 320

atc tcc ggc ggc aac aac gac gtg ctg cgc tac gcc gag atc atg gag      1308
Ile Ser Gly Gly Asn Asn Asp Val Leu Arg Tyr Ala Glu Ile Met Glu
                325                 330                 335

cgc tcc ctg gtg cac cgc ggc ctc aag cac tac ttc ctg gtg aac ttc      1356
Arg Ser Leu Val His Arg Gly Leu Lys His Tyr Phe Leu Val Asn Phe
            340                 345                 350

ccg cag gag ccg ggc cag ctg cgc cac ttc ctc aac gac atc ctc ggc      1404
Pro Gln Glu Pro Gly Gln Leu Arg His Phe Leu Asn Asp Ile Leu Gly
        355                 360                 365

ccc gac gac gac atc acc ctc ttc gag tac ctc aag cgc aac aac cgg      1452
Pro Asp Asp Asp Ile Thr Leu Phe Glu Tyr Leu Lys Arg Asn Asn Arg
    370                 375                 380

gag acc ggt gcc gcg ctc gtc ggc ctc gag ctc ggc cgg gcc agc gac      1500
Glu Thr Gly Ala Ala Leu Val Gly Leu Glu Leu Gly Arg Ala Ser Asp
385                 390                 395                 400

ctc gac ccg ctg ctc gag cgg atg aac gcc tcc cgc atc gag tgc cag      1548
Leu Asp Pro Leu Leu Glu Arg Met Asn Ala Ser Arg Ile Glu Cys Gln
                405                 410                 415

cac ctc aag ccg aac acc ccc gag tac gag tac ctg gtc aac acc tag      1596
His Leu Lys Pro Asn Thr Pro Glu Tyr Glu Tyr Leu Val Asn Thr
            420                 425                 430

gggtctctac ctgcgcagga gcgcgaactc ccacgggccc aggcgcgtgt cgtcgaggcc    1656

gacctccggt tccgtgaagg agtagatgag ctcgccgccg taggggcgc ggacctccgc     1716

gtcggagagg ttggccacga ggatcacgtc ctcccagccc atcgccagcc agccgtcccc    1776

ggtctcgacg gtgaggcggg agagatcggc gcgggagagg ccgagctcgc ggcgcagacg    1836

cagcagctcc cggtaggcgg cgtggatctc ctgctgctcc tccgtgaagt cccagtccag    1896
```

<210> 106
<211> 431
<212> PRT
<213> Corynebacterium humireducens

<400> 106

```
Met Ser Asp Thr Arg Ser Ala Val Thr Thr Phe Glu Pro Val Arg Ala
1               5                   10                  15

Ser Asp Ile Gln Leu Ala Gln Ala Arg Ile Ser Ser Val Ile Glu Pro
            20                  25                  30
```

Thr Pro Leu Gln Tyr Cys Pro Arg Leu Ser Glu Glu Thr Gly Cys Glu
35 40 45

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

Arg Gly Ala Tyr Tyr Ala Met Ala Asn Leu Asp Glu Gln Gln Arg Asp
65 70 75 80

Ala Gly Ile Val Ala Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala
85 90 95

Tyr Ala Cys Arg Thr Met Gly Ile Arg Gly Arg Ile Phe Val Pro Asn
100 105 110

Gln Thr Pro Lys Gln Lys Arg Asp Arg Ile Met Val His Gly Gly Asp
115 120 125

Met Val Glu Leu Val Val Thr Gly Asn Asn Phe Asp Glu Ala Ala Glu
130 135 140

Ala Ala Arg Ala Asp Ala Ala Glu Arg Gly Ala Thr Met Ile Glu Pro
145 150 155 160

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

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

Val Pro Val Gly Gly Gly Gly Leu Leu Ala Gly Val Ala Ser Tyr Leu
195 200 205

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

Ala Ala Ser Leu Gln Ala Ala Leu Arg Ala Asp Ala Pro Val Thr Leu
225 230 235 240

Ser Ala Val Asp Pro Phe Val Asp Gly Ala Ala Val Lys Arg Ile Gly
245 250 255

Asp Leu Pro Phe Asp Ile Ile Glu Arg Asn Lys Gly Arg Ile His Val

260 265 270

Met Asp Val Ser Glu Gly Ala Val Cys Thr Glu Met Leu Asp Leu Tyr
275 280 285

Gln Asn Glu Gly Ile Ile Thr Glu Pro Ala Gly Ala Leu Ser Val Thr
290 295 300

Gly Leu Lys Glu Met Lys Leu Gln Gln Asp Ser Ile Val Val Cys Ile
305 310 315 320

Ile Ser Gly Gly Asn Asn Asp Val Leu Arg Tyr Ala Glu Ile Met Glu
325 330 335

Arg Ser Leu Val His Arg Gly Leu Lys His Tyr Phe Leu Val Asn Phe
340 345 350

Pro Gln Glu Pro Gly Gln Leu Arg His Phe Leu Asn Asp Ile Leu Gly
355 360 365

Pro Asp Asp Asp Ile Thr Leu Phe Glu Tyr Leu Lys Arg Asn Asn Arg
370 375 380

Glu Thr Gly Ala Ala Leu Val Gly Leu Glu Leu Gly Arg Ala Ser Asp
385 390 395 400

Leu Asp Pro Leu Leu Glu Arg Met Asn Ala Ser Arg Ile Glu Cys Gln
405 410 415

His Leu Lys Pro Asn Thr Pro Glu Tyr Glu Tyr Leu Val Asn Thr
420 425 430

<210> 107
<211> 2043
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1743)
<223> gene thrC

<400> 107
cggggcagca ccgcgatggc cacgacgagg acgagcagga ccgcggtgac ggtggctacg 60

```
gtacgtgtgt tacctcggga ggccacgggg cgctcactcc tctgtgcgac tctctgcgac      120

tctgtacgac tctgtgcgac gcggcgtgga caacgccgcc cggcaggggc gtgcggccgc      180

agtaccccgt agcgtactca actgcttttc ccgggaaagg ggaattcacc gggatccccg      240

ccccggcgtg cgggtgggat gttgcgcatg cttccagccc cgccacgtat ggttgtccac      300

gtg gat tac att tcg acg cgc gac tcc tcc cgt act ccc gcc acc ttc         348
Val Asp Tyr Ile Ser Thr Arg Asp Ser Ser Arg Thr Pro Ala Thr Phe
1               5                   10                  15

acc gac atc ctg ctc ggt gga ctg gcc ccc gac ggc ggc ctc tac ctg         396
Thr Asp Ile Leu Leu Gly Gly Leu Ala Pro Asp Gly Gly Leu Tyr Leu
            20                  25                  30

ccc gcc gag tac ccg cag atc agc gat gag cag ctg acg cag tgg cgg         444
Pro Ala Glu Tyr Pro Gln Ile Ser Asp Glu Gln Leu Thr Gln Trp Arg
        35                  40                  45

tct ctc ctg cag gag aag ggg tac gcc gcc ctg gcg gcg gag atc ctc         492
Ser Leu Leu Gln Glu Lys Gly Tyr Ala Ala Leu Ala Ala Glu Ile Leu
    50                  55                  60

aag ctc ttc gtc gac gac atc ccg gcg gag gat ctc gag ggc atc gcc         540
Lys Leu Phe Val Asp Asp Ile Pro Ala Glu Asp Leu Glu Gly Ile Ala
65                  70                  75                  80

gcc cgc gcc tac acc tcc ccg aag ttc gcg cac gag gag atc gtc ccc         588
Ala Arg Ala Tyr Thr Ser Pro Lys Phe Ala His Glu Glu Ile Val Pro
                85                  90                  95

gtg acc gag ctc gag gac ggc ctg tgg atc ggc cac ctc tcc gag ggc         636
Val Thr Glu Leu Glu Asp Gly Leu Trp Ile Gly His Leu Ser Glu Gly
            100                 105                 110

ccg acc gcc gcg ttc aag gac atg gcg atg cag ctg ctc ggc gag ctc         684
Pro Thr Ala Ala Phe Lys Asp Met Ala Met Gln Leu Leu Gly Glu Leu
        115                 120                 125

ttc gag tac gag ctg gcc cgt cgc ggg gag acc ctc aac atc ctg ggt         732
Phe Glu Tyr Glu Leu Ala Arg Arg Gly Glu Thr Leu Asn Ile Leu Gly
    130                 135                 140

gcg acc tcg ggt gac acg ggt tcc tcc gcc gag tac gcg atg cgc ggc         780
Ala Thr Ser Gly Asp Thr Gly Ser Ser Ala Glu Tyr Ala Met Arg Gly
145                 150                 155                 160

cgt aag ggc atc cgt gtc ttc atg ctg acc ccg gcc ggt cgc atg acc         828
Arg Lys Gly Ile Arg Val Phe Met Leu Thr Pro Ala Gly Arg Met Thr
                165                 170                 175

ccg ttc cag cag gcg cag atg ttc ggc ctg cag gac ccc aac atc ttc         876
Pro Phe Gln Gln Ala Gln Met Phe Gly Leu Gln Asp Pro Asn Ile Phe
            180                 185                 190

aac atc gcc ctg gac ggc gtc ttc gac gac tgc cag gac gtg gtc aag         924
Asn Ile Ala Leu Asp Gly Val Phe Asp Asp Cys Gln Asp Val Val Lys
```

```
                195                 200                 205

gcg gtg tcc gcc gac gcc ggg ttc aag gcc gag aac cgt atc ggt gcg        972
Ala Val Ser Ala Asp Ala Gly Phe Lys Ala Glu Asn Arg Ile Gly Ala
    210                 215                 220

gtc aac tcg atc aac tgg gcc cgc ctc atg gcg cag atc gtc tac tac       1020
Val Asn Ser Ile Asn Trp Ala Arg Leu Met Ala Gln Ile Val Tyr Tyr
225                 230                 235                 240

gtc tcc tcc tgg ctg agg atc acc gag agc aac gac cag aag gtc tcc       1068
Val Ser Ser Trp Leu Arg Ile Thr Glu Ser Asn Asp Gln Lys Val Ser
                245                 250                 255

ttc tcc gtg ccg acc ggc aac ttc ggt gac atc tgc gcc ggc cac atc       1116
Phe Ser Val Pro Thr Gly Asn Phe Gly Asp Ile Cys Ala Gly His Ile
            260                 265                 270

gcc cgt cag atg ggt ctg ccg atc gac cgt ctc atc gtc gcc acc aac       1164
Ala Arg Gln Met Gly Leu Pro Ile Asp Arg Leu Ile Val Ala Thr Asn
        275                 280                 285

gag aac gac gtc ctc gac gag ttc ttc cgc acc ggc aac tac cgt ccg       1212
Glu Asn Asp Val Leu Asp Glu Phe Phe Arg Thr Gly Asn Tyr Arg Pro
    290                 295                 300

cgc ccg gcg gag gag acc ctg gag acg tcc tcg ccg tcg atg gac atc       1260
Arg Pro Ala Glu Glu Thr Leu Glu Thr Ser Ser Pro Ser Met Asp Ile
305                 310                 315                 320

tcc cgt gcc tcc aac ttc gag cgt ttc gtc ttc gac ctg ctg ggc cgt       1308
Ser Arg Ala Ser Asn Phe Glu Arg Phe Val Phe Asp Leu Leu Gly Arg
                325                 330                 335

gac gcc gcg cgc gtc gcg cag cac ttc ggc gtc gac gtc cgc gcc gac       1356
Asp Ala Ala Arg Val Ala Gln His Phe Gly Val Asp Val Arg Ala Asp
            340                 345                 350

ggt ttc tcg ctt gcc gac gac ccc gcg ttc ccg gcc gcc gca gag aag       1404
Gly Phe Ser Leu Ala Asp Asp Pro Ala Phe Pro Ala Ala Ala Glu Lys
        355                 360                 365

tac ggc ttc gcc tcc ggt cgt tcc acc cac cag gac cgc ctc gac acg       1452
Tyr Gly Phe Ala Ser Gly Arg Ser Thr His Gln Asp Arg Leu Asp Thr
    370                 375                 380

atc agg gac gtg tgg gag cgc ctg ggc atc atg ctc gac ccg cac acc       1500
Ile Arg Asp Val Trp Glu Arg Leu Gly Ile Met Leu Asp Pro His Thr
385                 390                 395                 400

gcc gac ggc gtg aag gtc gcc cgc gag tgg cgt tcc gag atc gac ggc       1548
Ala Asp Gly Val Lys Val Ala Arg Glu Trp Arg Ser Glu Ile Asp Gly
                405                 410                 415

ccg atc gtg tgc ctg gag acc gcc ctg ccg gtg aag ttc tcc gag acc       1596
Pro Ile Val Cys Leu Glu Thr Ala Leu Pro Val Lys Phe Ser Glu Thr
            420                 425                 430

atc gag gag gcc acc ggc gtg cag ccg gag acc ccg gag cgt ttc gcc       1644
```

```
Ile Glu Glu Ala Thr Gly Val Gln Pro Glu Thr Pro Glu Arg Phe Ala
        435                 440                 445

ggc atc ctc gac gcc gag cgc cac gtg acg gac ctg ccg aac gac gcg      1692
Gly Ile Leu Asp Ala Glu Arg His Val Thr Asp Leu Pro Asn Asp Ala
    450                 455                 460

gag acc gtc aag aag ttc atc acc gac tcc atc cgc acc acc gag gtg      1740
Glu Thr Val Lys Lys Phe Ile Thr Asp Ser Ile Arg Thr Thr Glu Val
465                 470                 475                 480

taa ccgtcgtggc catggagttc aagatgggtc aggagtactt ccaggacttc           1793

gacccggaga agttcgccgc gatgatcaag gcgcaggccg aggctgaggc tgacgctgcg    1853

gccggggaag acggcgtcga caagcagtga acatccgcgt ctgggcgggt ctggtcgcac    1913

tgaccaccgc cggcgtgggg tcgctcatcg cctggtccgt cgaggaccag cggcagcacc    1973

ccacgcccat cgccgaggtg atcgcggcgg cgccgacgca ggtcccgacg gagttccgtg    2033

cccctgcggt                                                          2043
```

<210> 108
<211> 480
<212> PRT
<213> Corynebacterium humireducens

<400> 108

```
Val Asp Tyr Ile Ser Thr Arg Asp Ser Ser Arg Thr Pro Ala Thr Phe
1               5                   10                  15

Thr Asp Ile Leu Leu Gly Gly Leu Ala Pro Asp Gly Gly Leu Tyr Leu
            20                  25                  30

Pro Ala Glu Tyr Pro Gln Ile Ser Asp Glu Gln Leu Thr Gln Trp Arg
        35                  40                  45

Ser Leu Leu Gln Glu Lys Gly Tyr Ala Ala Leu Ala Ala Glu Ile Leu
    50                  55                  60

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

Ala Arg Ala Tyr Thr Ser Pro Lys Phe Ala His Glu Glu Ile Val Pro
                85                  90                  95

Val Thr Glu Leu Glu Asp Gly Leu Trp Ile Gly His Leu Ser Glu Gly
            100                 105                 110
```

Pro Thr Ala Ala Phe Lys Asp Met Ala Met Gln Leu Leu Gly Glu Leu
115 120 125

Phe Glu Tyr Glu Leu Ala Arg Arg Gly Glu Thr Leu Asn Ile Leu Gly
130 135 140

Ala Thr Ser Gly Asp Thr Gly Ser Ser Ala Glu Tyr Ala Met Arg Gly
145 150 155 160

Arg Lys Gly Ile Arg Val Phe Met Leu Thr Pro Ala Gly Arg Met Thr
165 170 175

Pro Phe Gln Gln Ala Gln Met Phe Gly Leu Gln Asp Pro Asn Ile Phe
180 185 190

Asn Ile Ala Leu Asp Gly Val Phe Asp Asp Cys Gln Asp Val Val Lys
195 200 205

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

Val Asn Ser Ile Asn Trp Ala Arg Leu Met Ala Gln Ile Val Tyr Tyr
225 230 235 240

Val Ser Ser Trp Leu Arg Ile Thr Glu Ser Asn Asp Gln Lys Val Ser
245 250 255

Phe Ser Val Pro Thr Gly Asn Phe Gly Asp Ile Cys Ala Gly His Ile
260 265 270

Ala Arg Gln Met Gly Leu Pro Ile Asp Arg Leu Ile Val Ala Thr Asn
275 280 285

Glu Asn Asp Val Leu Asp Glu Phe Phe Arg Thr Gly Asn Tyr Arg Pro
290 295 300

Arg Pro Ala Glu Glu Thr Leu Glu Thr Ser Ser Pro Ser Met Asp Ile
305 310 315 320

Ser Arg Ala Ser Asn Phe Glu Arg Phe Val Phe Asp Leu Leu Gly Arg
325 330 335

Asp Ala Ala Arg Val Ala Gln His Phe Gly Val Asp Val Arg Ala Asp
340 345 350

Gly Phe Ser Leu Ala Asp Asp Pro Ala Phe Pro Ala Ala Ala Glu Lys
355 360 365

Tyr Gly Phe Ala Ser Gly Arg Ser Thr His Gln Asp Arg Leu Asp Thr
370 375 380

Ile Arg Asp Val Trp Glu Arg Leu Gly Ile Met Leu Asp Pro His Thr
385 390 395 400

Ala Asp Gly Val Lys Val Ala Arg Glu Trp Arg Ser Glu Ile Asp Gly
405 410 415

Pro Ile Val Cys Leu Glu Thr Ala Leu Pro Val Lys Phe Ser Glu Thr
420 425 430

Ile Glu Glu Ala Thr Gly Val Gln Pro Glu Thr Pro Glu Arg Phe Ala
435 440 445

Gly Ile Leu Asp Ala Glu Arg His Val Thr Asp Leu Pro Asn Asp Ala
450 455 460

Glu Thr Val Lys Lys Phe Ile Thr Asp Ser Ile Arg Thr Thr Glu Val
465 470 475 480

<210> 109
<211> 2448
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(2148)
<223> gene leuA

<400> 109
gggtcgatgc cgtggagcag ggcttttcac gtttcttcac aaaactgcgt tgcgccgggg 60

gagggagtgt gtagacttca cagcatgttc tcccgcgcga acctccttct tcttcgccgc 120

ggcgggtccc aggtccagta acgaagcgac cggcaccccg tcgcggagtt tggtgttgcc 180

ggtcgctgct cccgctgaat agcccattca tcagcggtga gacctcgcag gctactacag 240

tgaaggccgt tgtcggcccc tggtagtccg cagccacaga cagacccgaa aaggaaactc 300

atg tcc ccg aac gac tcc ttc atc tcc gcc ccc tcc gag atc cgc acc 348

```
Met Ser Pro Asn Asp Ser Phe Ile Ser Ala Pro Ser Glu Ile Arg Thr
1               5                  10                  15

ccg gac gga ccg cgc cgc gag ggc cag ccc ttc tgg aac aag cag cgc  396
Pro Asp Gly Pro Arg Arg Glu Gly Gln Pro Phe Trp Asn Lys Gln Arg
            20                  25                  30

aac tcc tcc atg ccg gta cac cgc tac cgc ccc ttc gcc gag gcc gtc  444
Asn Ser Ser Met Pro Val His Arg Tyr Arg Pro Phe Ala Glu Ala Val
        35                  40                  45

gag gac atc gtt ctg ccg gac cgc acc tgg ccg gac aag aag atc acc  492
Glu Asp Ile Val Leu Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr
    50                  55                  60

gcc gcc ccg cag tgg tgt gcg gtc gac ctg cgt gac ggc aac cag gcg  540
Ala Ala Pro Gln Trp Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala
65                  70                  75                  80

ctc atc gac ccg atg agc ccg gaa cgc aag cgc cgc atg ttc aac ctg  588
Leu Ile Asp Pro Met Ser Pro Glu Arg Lys Arg Arg Met Phe Asn Leu
                85                  90                  95

ctg gtg cag atg ggc tac aag gag atc gag gtt ggt ttc ccg tcc gcc  636
Leu Val Gln Met Gly Tyr Lys Glu Ile Glu Val Gly Phe Pro Ser Ala
            100                 105                 110

tcc cag acc gac ttc gac ttc gtc cgc gag atc atc gag cag gac atg  684
Ser Gln Thr Asp Phe Asp Phe Val Arg Glu Ile Ile Glu Gln Asp Met
        115                 120                 125

atc ccg gag gac gtc acc atc cag gtc ctg gtc cag gcc cgt gag cac  732
Ile Pro Glu Asp Val Thr Ile Gln Val Leu Val Gln Ala Arg Glu His
    130                 135                 140

ctg atc cgc cgc acc ttc gag gcg tgc gag ggc gcg aag aac gtc atc  780
Leu Ile Arg Arg Thr Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile
145                 150                 155                 160

gtc cac ttc tac aac tcc acc tcc gag ctg cag cgc cgc gtc gtg ttc  828
Val His Phe Tyr Asn Ser Thr Ser Glu Leu Gln Arg Arg Val Val Phe
                165                 170                 175

cgc aag gat aag ccg gcc atc aag cag ctg gcc gtc gac gcc gcc gag  876
Arg Lys Asp Lys Pro Ala Ile Lys Gln Leu Ala Val Asp Ala Ala Glu
            180                 185                 190

ctg atc cag acc atc gcc cag gac tac ccg ggc acc aac tgg cgt tgg  924
Leu Ile Gln Thr Ile Ala Gln Asp Tyr Pro Gly Thr Asn Trp Arg Trp
        195                 200                 205

cag tac tcc ccg gag tcc ttc acc ggc acc gag ctg gag ttc gcc ctc  972
Gln Tyr Ser Pro Glu Ser Phe Thr Gly Thr Glu Leu Glu Phe Ala Leu
    210                 215                 220

gag gtc tgc aac gcc gtc atc gag gtc atg gcg ccc acc ccg gac aac 1020
Glu Val Cys Asn Ala Val Ile Glu Val Met Ala Pro Thr Pro Asp Asn
225                 230                 235                 240
```

```
ccg atc aac atc aac ctg ccg tcc acc gtc gag atg atc acc ccg aac      1068
Pro Ile Asn Ile Asn Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn
                245                 250                 255

gtc tac gcc gac tcc atc gag tgg atg cac cgc aac ctg gac cgc cgt      1116
Val Tyr Ala Asp Ser Ile Glu Trp Met His Arg Asn Leu Asp Arg Arg
            260                 265                 270

gac tcc gtc atc ctg tcg ctg cac ccc cac aac gac cgt ggt gag ggc      1164
Asp Ser Val Ile Leu Ser Leu His Pro His Asn Asp Arg Gly Glu Gly
        275                 280                 285

gtc gcc gcc gcc gag ctg ggc tac ctg gcc ggc gcc gac cgc atc gag      1212
Val Ala Ala Ala Glu Leu Gly Tyr Leu Ala Gly Ala Asp Arg Ile Glu
    290                 295                 300

ggc tgc ctg ttc ggc aac ggt gag cgc acc ggt aac gtc tgc ctg gtc      1260
Gly Cys Leu Phe Gly Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val
305                 310                 315                 320

acc ctg ggc ctg aac atg ctc acc cag ggc gtc gac ccg cag atc gac      1308
Thr Leu Gly Leu Asn Met Leu Thr Gln Gly Val Asp Pro Gln Ile Asp
                325                 330                 335

ttc tcc gac atc cgc cag atc cgc agc acc gtc gag tac tgc aac cag      1356
Phe Ser Asp Ile Arg Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln
            340                 345                 350

ctg cga gtc ccg gag cgt cac ccc tac ggc ggc gac ctg gtc ttc acc      1404
Leu Arg Val Pro Glu Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr
        355                 360                 365

gcc ttc tcc ggc tcc cac cag gac gcc gtc aac aag ggc ctc gac gcc      1452
Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala
    370                 375                 380

atg gcc gcc aag gtc aag ccg ggc gcc aac aac acc gag gtc acc tgg      1500
Met Ala Ala Lys Val Lys Pro Gly Ala Asn Asn Thr Glu Val Thr Trp
385                 390                 395                 400

gag gag ctg ggc aag gcc gtc tgg gag gtt ccc tac ctg ccc atc gac      1548
Glu Glu Leu Gly Lys Ala Val Trp Glu Val Pro Tyr Leu Pro Ile Asp
                405                 410                 415

ccg aag gac gtc ggc cgc gac tac gag gcc gtc atc cgc gtc aac tcc      1596
Pro Lys Asp Val Gly Arg Asp Tyr Glu Ala Val Ile Arg Val Asn Ser
            420                 425                 430

cag tcc ggt aag ggc ggc gtc gcc tac atc atg aag acg gat cac ggc      1644
Gln Ser Gly Lys Gly Gly Val Ala Tyr Ile Met Lys Thr Asp His Gly
        435                 440                 445

atc aac ctg ccg cgt cag atg cag gcc gag ttc tcc tcc gtc gtc cag      1692
Ile Asn Leu Pro Arg Gln Met Gln Ala Glu Phe Ser Ser Val Val Gln
    450                 455                 460

gcg atc acc gac tcc gag ggc gga gag gtc aac tcc aag gag atg tgg      1740
Ala Ile Thr Asp Ser Glu Gly Gly Glu Val Asn Ser Lys Glu Met Trp
465                 470                 475                 480
```

```
gac gtc ttc gcc acc gag tac ctg gat gtc acc gag ccg gtg gag gag      1788
Asp Val Phe Ala Thr Glu Tyr Leu Asp Val Thr Glu Pro Val Glu Glu
                485                 490                 495

gtc tcc atc cgc atc gtc aac gcc gag acc gac acc gac gag gcc acc      1836
Val Ser Ile Arg Ile Val Asn Ala Glu Thr Asp Thr Asp Glu Ala Thr
            500                 505                 510

gtc acc gcc acc gtc atc cac aag ggc tcc gag aag gag atc acc ggc      1884
Val Thr Ala Thr Val Ile His Lys Gly Ser Glu Lys Glu Ile Thr Gly
        515                 520                 525

acc ggc aac ggc ccc gtc gcc gcc tac gcc aac gcc ctg gag cag ctg      1932
Thr Gly Asn Gly Pro Val Ala Ala Tyr Ala Asn Ala Leu Glu Gln Leu
    530                 535                 540

ggc atc gac gcg gag gtc cag ttc tac tcc cag cag gcc cgc tcc tcg      1980
Gly Ile Asp Ala Glu Val Gln Phe Tyr Ser Gln Gln Ala Arg Ser Ser
545                 550                 555                 560

ggc gat gac gcc gag gcc gcc tgc tac atc tac gcc acg gtc aac ggc      2028
Gly Asp Asp Ala Glu Ala Ala Cys Tyr Ile Tyr Ala Thr Val Asn Gly
                565                 570                 575

tcc gcc gcc tgg ggc gtc ggt atc gcg ggc tcc atc acc cgc gcc tcc      2076
Ser Ala Ala Trp Gly Val Gly Ile Ala Gly Ser Ile Thr Arg Ala Ser
            580                 585                 590

atc aag gca ctg acc tcc gcg gtc aac cgt gcc atc aag gtc gag gcc      2124
Ile Lys Ala Leu Thr Ser Ala Val Asn Arg Ala Ile Lys Val Glu Ala
        595                 600                 605

tcc gtg ctg gcc ggc ggc gtc tag accgcctgag tcacgggagg ggagtgcgcg      2178
Ser Val Leu Ala Gly Gly Val
    610                 615

gccgcgcact cccctccttc cgtatctcac cgcccctacc ggcccctacc agcacagtcc      2238

ccgcaggaga ggcactagac tctgaacaat gaccacgacc ccagaccacg gcgattccgc      2298

agctgagacc ccgcctgccg tcgagccggc gttccccttc gtcgctctga cggtccaggc      2358

cacggggatc catccgtcga ccgcccgcct ggtggccgtc gacgtcctga ccttcgacga      2418

ggacggggag atcggcgagg agttccacac                                      2448
```

<210> 110
<211> 615
<212> PRT
<213> Corynebacterium humireducens

<400> 110

```
Met Ser Pro Asn Asp Ser Phe Ile Ser Ala Pro Ser Glu Ile Arg Thr
1               5                   10                  15
```

```
Pro Asp Gly Pro Arg Arg Glu Gly Gln Pro Phe Trp Asn Lys Gln Arg
            20                  25                  30

Asn Ser Ser Met Pro Val His Arg Tyr Arg Pro Phe Ala Glu Ala Val
        35                  40                  45

Glu Asp Ile Val Leu Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr
    50                  55                  60

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

Leu Ile Asp Pro Met Ser Pro Glu Arg Lys Arg Arg Met Phe Asn Leu
                85                  90                  95

Leu Val Gln Met Gly Tyr Lys Glu Ile Glu Val Gly Phe Pro Ser Ala
            100                 105                 110

Ser Gln Thr Asp Phe Asp Phe Val Arg Glu Ile Ile Glu Gln Asp Met
        115                 120                 125

Ile Pro Glu Asp Val Thr Ile Gln Val Leu Val Gln Ala Arg Glu His
    130                 135                 140

Leu Ile Arg Arg Thr Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile
145                 150                 155                 160

Val His Phe Tyr Asn Ser Thr Ser Glu Leu Gln Arg Arg Val Val Phe
                165                 170                 175

Arg Lys Asp Lys Pro Ala Ile Lys Gln Leu Ala Val Asp Ala Ala Glu
            180                 185                 190

Leu Ile Gln Thr Ile Ala Gln Asp Tyr Pro Gly Thr Asn Trp Arg Trp
        195                 200                 205

Gln Tyr Ser Pro Glu Ser Phe Thr Gly Thr Glu Leu Glu Phe Ala Leu
    210                 215                 220

Glu Val Cys Asn Ala Val Ile Glu Val Met Ala Pro Thr Pro Asp Asn
225                 230                 235                 240

Pro Ile Asn Ile Asn Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn
                245                 250                 255
```

Val Tyr Ala Asp Ser Ile Glu Trp Met His Arg Asn Leu Asp Arg Arg
260 265 270

Asp Ser Val Ile Leu Ser Leu His Pro His Asn Asp Arg Gly Glu Gly
275 280 285

Val Ala Ala Ala Glu Leu Gly Tyr Leu Ala Gly Ala Asp Arg Ile Glu
290 295 300

Gly Cys Leu Phe Gly Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val
305 310 315 320

Thr Leu Gly Leu Asn Met Leu Thr Gln Gly Val Asp Pro Gln Ile Asp
325 330 335

Phe Ser Asp Ile Arg Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln
340 345 350

Leu Arg Val Pro Glu Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr
355 360 365

Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala
370 375 380

Met Ala Ala Lys Val Lys Pro Gly Ala Asn Asn Thr Glu Val Thr Trp
385 390 395 400

Glu Glu Leu Gly Lys Ala Val Trp Glu Val Pro Tyr Leu Pro Ile Asp
405 410 415

Pro Lys Asp Val Gly Arg Asp Tyr Glu Ala Val Ile Arg Val Asn Ser
420 425 430

Gln Ser Gly Lys Gly Gly Val Ala Tyr Ile Met Lys Thr Asp His Gly
435 440 445

Ile Asn Leu Pro Arg Gln Met Gln Ala Glu Phe Ser Ser Val Val Gln
450 455 460

Ala Ile Thr Asp Ser Glu Gly Gly Glu Val Asn Ser Lys Glu Met Trp
465 470 475 480

Asp Val Phe Ala Thr Glu Tyr Leu Asp Val Thr Glu Pro Val Glu Glu
485 490 495

```
Val Ser Ile Arg Ile Val Asn Ala Glu Thr Asp Thr Asp Glu Ala Thr
            500                 505                 510

Val Thr Ala Thr Val Ile His Lys Gly Ser Glu Lys Glu Ile Thr Gly
        515                 520                 525

Thr Gly Asn Gly Pro Val Ala Ala Tyr Ala Asn Ala Leu Glu Gln Leu
    530                 535                 540

Gly Ile Asp Ala Glu Val Gln Phe Tyr Ser Gln Gln Ala Arg Ser Ser
545                 550                 555                 560

Gly Asp Asp Ala Glu Ala Ala Cys Tyr Ile Tyr Ala Thr Val Asn Gly
                565                 570                 575

Ser Ala Ala Trp Gly Val Gly Ile Ala Gly Ser Ile Thr Arg Ala Ser
            580                 585                 590

Ile Lys Ala Leu Thr Ser Ala Val Asn Arg Ala Ile Lys Val Glu Ala
        595                 600                 605

Ser Val Leu Ala Gly Gly Val
    610                 615
```

<210> 111
<211> 1614
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1314)
<223> gene leuB

<400> 111

```
ctggtcgtag tactcgtagt catagacgcg gacgtcgtcg ccgagcgcgg ccgccttctc        60

cggggaaccg gtgacggcgg cgacgagctc gacgtcgtcg agactgcgga gcgccgggag       120

gaaggcctgc tgggtgatct ggccgacacc gacgacagcg aaacggacag gggagtcata       180

tgcgtgtgtg ctcatggccc caggctacgg actcgaaacg tgcggcgttg agcgcacgag       240

gggaggggtg ggctgataga atcgccgcca gttcagcagg tgagaaagga atcccacaga       300

atg aaa ctt gca gtc att ggc gga gac ggc atc ggc ccg gag gtc acc          348
Met Lys Leu Ala Val Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr
1               5                   10                  15
```

```
gaa gag gcg ctc aag gtc ctc cgc acc gtc cgc gac gac atc gag acc        396
Glu Glu Ala Leu Lys Val Leu Arg Thr Val Arg Asp Asp Ile Glu Thr
            20                  25                  30

acc gac tac gat ctc ggc gca cgt cgc tac ctg cgc aac ggt gag ctg        444
Thr Asp Tyr Asp Leu Gly Ala Arg Arg Tyr Leu Arg Asn Gly Glu Leu
        35                  40                  45

ctc acc gac gcc gac ctc gac tcc ctc cgc gag cac gac gcc atc ctc        492
Leu Thr Asp Ala Asp Leu Asp Ser Leu Arg Glu His Asp Ala Ile Leu
    50                  55                  60

ctc ggc gcc atc ggc gcc ccg gac acc gtc gcg ccg ggc gtc ctc gag        540
Leu Gly Ala Ile Gly Ala Pro Asp Thr Val Ala Pro Gly Val Leu Glu
65                  70                  75                  80

cgt ggc ctg ctg ctc aag atg cgt ttc gcc ctc gac cac cac gtc aac        588
Arg Gly Leu Leu Leu Lys Met Arg Phe Ala Leu Asp His His Val Asn
                85                  90                  95

ctg cgt ccc tcc aag ctc tac gag ggc gtc gag tcc ccg ctg aag aac        636
Leu Arg Pro Ser Lys Leu Tyr Glu Gly Val Glu Ser Pro Leu Lys Asn
            100                 105                 110

ccg ggc gag atc gac ttc gtc gtc gtc cgc gag ggc acc gag ggc gcc        684
Pro Gly Glu Ile Asp Phe Val Val Val Arg Glu Gly Thr Glu Gly Ala
        115                 120                 125

tac acc ggc aac ggc ggc gcc atc cgc gtg ggc acc ccg cac gag gtc        732
Tyr Thr Gly Asn Gly Gly Ala Ile Arg Val Gly Thr Pro His Glu Val
    130                 135                 140

gcc aac gag acc tcc gtc aac acc cgc tac ggc gcc gag cgc gtc gtc        780
Ala Asn Glu Thr Ser Val Asn Thr Arg Tyr Gly Ala Glu Arg Val Val
145                 150                 155                 160

cgc tac gcc ttc gag ctg gcc atg acc cgc cgc aag cac gtc acc ctg        828
Arg Tyr Ala Phe Glu Leu Ala Met Thr Arg Arg Lys His Val Thr Leu
                165                 170                 175

gtc cac aag acc aac gtg ctc gtc cac ggc ggc ggc atg tgg cag cgc        876
Val His Lys Thr Asn Val Leu Val His Gly Gly Gly Met Trp Gln Arg
            180                 185                 190

acc gtc gac gag gtc gcc acg gag tac cct gag gtc acc gtc gac tac        924
Thr Val Asp Glu Val Ala Thr Glu Tyr Pro Glu Val Thr Val Asp Tyr
        195                 200                 205

gcg cac atc gac gcc gcg acg atc tac atg atc acc gac ccc tcc cgc        972
Ala His Ile Asp Ala Ala Thr Ile Tyr Met Ile Thr Asp Pro Ser Arg
    210                 215                 220

ttc gac gtc atc gtc acc gac aac ctc ttc ggc gac atc atc acc gat       1020
Phe Asp Val Ile Val Thr Asp Asn Leu Phe Gly Asp Ile Ile Thr Asp
225                 230                 235                 240

gag gcc ggt gcc gtc tcc ggt ggc atc ggc ctc gcc gcc tcc ggc aac       1068
Glu Ala Gly Ala Val Ser Gly Gly Ile Gly Leu Ala Ala Ser Gly Asn
```

```
                    245                 250                 255

atc gac gcc acc cgc acc aac ccg tcc atg ttc gag ccg gtc cac ggc      1116
Ile Asp Ala Thr Arg Thr Asn Pro Ser Met Phe Glu Pro Val His Gly
            260                 265                 270

tcc gca ccg gac atc gcc ggc cag ggc atc gcc gac ccg acc gcc gcc      1164
Ser Ala Pro Asp Ile Ala Gly Gln Gly Ile Ala Asp Pro Thr Ala Ala
        275                 280                 285

atc ctc tcc gcc gcg atg ctg ctg cgt cac ctc ggt gac gag gac aac      1212
Ile Leu Ser Ala Ala Met Leu Leu Arg His Leu Gly Asp Glu Asp Asn
    290                 295                 300

gcc gca cgg atc gag gcc gcg gtg gcc gag gac gtc gcc aag cgt gag      1260
Ala Ala Arg Ile Glu Ala Ala Val Ala Glu Asp Val Ala Lys Arg Glu
305                 310                 315                 320

ggg cag atc cgc acc acc gag gtc ggc gac cgc atc gcc gcc gcc ctc      1308
Gly Gln Ile Arg Thr Thr Glu Val Gly Asp Arg Ile Ala Ala Ala Leu
                325                 330                 335

aag tag tctgtcggca gcagacagac gccatatata taaggagcat tcgtgaggcg      1364
Lys

acgtacagca ctactggccc tggccaccac cctggccatg gtcaccggat gctccacctc   1424

ggcggacacc ggtgacgggg acgaccggaa gcccggcacc cccgccctgg agatgacctc   1484

ctccgaggtc atcgccgacg ccgccggcaa cggcgtcgac acctccgccc gcctcttcga   1544

ggaggcggag accgtcgtgg tcgccgccga cacccctgag gaccaggccc ggggcgccca   1604

cctggcgatc                                                          1614
```

<210> 112
<211> 337
<212> PRT
<213> Corynebacterium humireducens

<400> 112

```
Met Lys Leu Ala Val Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr
1               5                   10                  15

Glu Glu Ala Leu Lys Val Leu Arg Thr Val Arg Asp Asp Ile Glu Thr
            20                  25                  30

Thr Asp Tyr Asp Leu Gly Ala Arg Arg Tyr Leu Arg Asn Gly Glu Leu
        35                  40                  45

Leu Thr Asp Ala Asp Leu Asp Ser Leu Arg Glu His Asp Ala Ile Leu
    50                  55                  60
```

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

Arg Gly Leu Leu Leu Lys Met Arg Phe Ala Leu Asp His His Val Asn
                85                  90                  95

Leu Arg Pro Ser Lys Leu Tyr Glu Gly Val Glu Ser Pro Leu Lys Asn
            100                 105                 110

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

Tyr Thr Gly Asn Gly Gly Ala Ile Arg Val Gly Thr Pro His Glu Val
    130                 135                 140

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

Arg Tyr Ala Phe Glu Leu Ala Met Thr Arg Arg Lys His Val Thr Leu
                165                 170                 175

Val His Lys Thr Asn Val Leu Val His Gly Gly Gly Met Trp Gln Arg
            180                 185                 190

Thr Val Asp Glu Val Ala Thr Glu Tyr Pro Glu Val Thr Val Asp Tyr
        195                 200                 205

Ala His Ile Asp Ala Ala Thr Ile Tyr Met Ile Thr Asp Pro Ser Arg
    210                 215                 220

Phe Asp Val Ile Val Thr Asp Asn Leu Phe Gly Asp Ile Ile Thr Asp
225                 230                 235                 240

Glu Ala Gly Ala Val Ser Gly Gly Ile Gly Leu Ala Ala Ser Gly Asn
                245                 250                 255

Ile Asp Ala Thr Arg Thr Asn Pro Ser Met Phe Glu Pro Val His Gly
            260                 265                 270

Ser Ala Pro Asp Ile Ala Gly Gln Gly Ile Ala Asp Pro Thr Ala Ala
        275                 280                 285

Ile Leu Ser Ala Ala Met Leu Leu Arg His Leu Gly Asp Glu Asp Asn
    290                 295                 300
```

```
Ala Ala Arg Ile Glu Ala Ala Val Ala Glu Asp Val Ala Lys Arg Glu
305                 310                 315                 320

Gly Gln Ile Arg Thr Thr Glu Val Gly Asp Arg Ile Ala Ala Ala Leu
                325                 330                 335

Lys
```

<210> 113
<211> 2019
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1719)
<223> gene leuC

<400> 113

```
gctggtcccg gccgccggtg ccgagggcgg tgagtgcggt gccggtggtc cagcggccgt       60

cgtcgccgcg ggcgaggatg cggtgtgtct cgagggcggt ggcgaggcgg tgggcggtgg      120

cgcggggcag gccggtggtc tcgcacagtt cggtgaggga gaggggatgg ggggcgacgg      180

ccatcatgat ggcgacggcc cgatcgagca ccttgatccc tgacactgcg ctatactgtc      240

ccataccacg atactaacat ctcaccttgt gagatttcac agatggaaag gtggacatcc      300

atg gcc gag aag ctc acg ctg gcc gag aag gtg tgg aac gac cat att         348
Met Ala Glu Lys Leu Thr Leu Ala Glu Lys Val Trp Asn Asp His Ile
1               5                   10                  15

gtc gcg aag ggc gag aac ggc gag ccc gat ctc ctc tac att gac ctg         396
Val Ala Lys Gly Glu Asn Gly Glu Pro Asp Leu Leu Tyr Ile Asp Leu
            20                  25                  30

cag ctc ctg cac gag gtg acc tcc ccg cag gcc ttc gac gga ctg cgc         444
Gln Leu Leu His Glu Val Thr Ser Pro Gln Ala Phe Asp Gly Leu Arg
        35                  40                  45

ctc gcc ggc cgc aag ctc cgc cgc ccg gac ctg cac ctg gcc acc gag         492
Leu Ala Gly Arg Lys Leu Arg Arg Pro Asp Leu His Leu Ala Thr Glu
    50                  55                  60

gac cac aac gtg ccc acc gag ggc atc gtc tcc ggc tcc ctc ctg gag         540
Asp His Asn Val Pro Thr Glu Gly Ile Val Ser Gly Ser Leu Leu Glu
65                  70                  75                  80

atc aag gag gcc acc tcc cgc acg cag gtc gag acc ctg cgc aag aac         588
Ile Lys Glu Ala Thr Ser Arg Thr Gln Val Glu Thr Leu Arg Lys Asn
                85                  90                  95
```

```
tgc gag gag ttc ggc atc cgc ctg cac ccg atg ggc gac gtc aag cag        636
Cys Glu Glu Phe Gly Ile Arg Leu His Pro Met Gly Asp Val Lys Gln
            100                 105                 110

ggc atc gtc cac acc gtc ggc ccg cag ctg ggc gcc acc cag ccg ggc        684
Gly Ile Val His Thr Val Gly Pro Gln Leu Gly Ala Thr Gln Pro Gly
        115                 120                 125

atg acc atc gtc tgc ggc gac tcc cac acc tcc acc cac ggt gcc ttc        732
Met Thr Ile Val Cys Gly Asp Ser His Thr Ser Thr His Gly Ala Phe
    130                 135                 140

ggc tcc atc gcc atg ggc atc ggc acc tcc gag gtc gag cac gtc atg        780
Gly Ser Ile Ala Met Gly Ile Gly Thr Ser Glu Val Glu His Val Met
145                 150                 155                 160

gcg acc cag acc ctg ccg ctc aag ccg ttc aag acc atg gcc atc gag        828
Ala Thr Gln Thr Leu Pro Leu Lys Pro Phe Lys Thr Met Ala Ile Glu
                165                 170                 175

gtc tcc ggc gag ctg cag gag ggc gtc acc gcc aag gac ctc atc ttg        876
Val Ser Gly Glu Leu Gln Glu Gly Val Thr Ala Lys Asp Leu Ile Leu
            180                 185                 190

gcg atc atc gcc aag atc ggc acc ggc ggc ggc cag ggc cac atc atc        924
Ala Ile Ile Ala Lys Ile Gly Thr Gly Gly Gly Gln Gly His Ile Ile
        195                 200                 205

gag tac cgc ggc gag gcc atc gag aag ctc tcg atg gag gcc cgg atg        972
Glu Tyr Arg Gly Glu Ala Ile Glu Lys Leu Ser Met Glu Ala Arg Met
    210                 215                 220

acc atc tgc aac atg tcc atc gag gcc ggt gcc cgt gcc ggc atg gtc       1020
Thr Ile Cys Asn Met Ser Ile Glu Ala Gly Ala Arg Ala Gly Met Val
225                 230                 235                 240

gcc ccc gac cag aag acc ttc gac tac gtc cag ggc cgc gag ttc gcc       1068
Ala Pro Asp Gln Lys Thr Phe Asp Tyr Val Gln Gly Arg Glu Phe Ala
                245                 250                 255

ccc acc ggc gag gac tgg gac gcc gcc gtc gcc tac tgg aag acc ctg       1116
Pro Thr Gly Glu Asp Trp Asp Ala Ala Val Ala Tyr Trp Lys Thr Leu
            260                 265                 270

ccg acc gac gag ggc gcc gag ttc gac acc gtc gtc gag atc gac ggc       1164
Pro Thr Asp Glu Gly Ala Glu Phe Asp Thr Val Val Glu Ile Asp Gly
        275                 280                 285

tcc gcg ctg acc ccg ttc gtc acc tgg ggc acc aac ccg ggc cag ggc       1212
Ser Ala Leu Thr Pro Phe Val Thr Trp Gly Thr Asn Pro Gly Gln Gly
    290                 295                 300

ctg ccc ctg tcc gcg aac gtc ccg gac ccg gag gac ttc acc aac gag       1260
Leu Pro Leu Ser Ala Asn Val Pro Asp Pro Glu Asp Phe Thr Asn Glu
305                 310                 315                 320

gcc gac aag gcc gcc gcg gag aag gcc ctg gcc tac atg gac ctc acc       1308
Ala Asp Lys Ala Ala Ala Glu Lys Ala Leu Ala Tyr Met Asp Leu Thr
```

```
                    325                 330                 335

ccg ggc acc ccg ctg cgg gac atc aag atc gac acc gtc ttc ctc ggc      1356
Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile Asp Thr Val Phe Leu Gly
            340                 345                 350

tcc tgc acc aac gcc cgc atc gag gac ctg cgc gct gcc gcc gag gtc      1404
Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu Arg Ala Ala Ala Glu Val
        355                 360                 365

gtc gag ggc cgc acg atc gcc ccg aac acc cgc atg ctc gtc gtc ccg      1452
Val Glu Gly Arg Thr Ile Ala Pro Asn Thr Arg Met Leu Val Val Pro
    370                 375                 380

tcc tcg acg ctg gtc aag cag cag gcc gag gag gag ggg ctg gac aag      1500
Ser Ser Thr Leu Val Lys Gln Gln Ala Glu Glu Glu Gly Leu Asp Lys
385                 390                 395                 400

atc ttc acc gac ttc ggc gcc gag tgg cgc acc gcc ggc tgc tcc atg      1548
Ile Phe Thr Asp Phe Gly Ala Glu Trp Arg Thr Ala Gly Cys Ser Met
                405                 410                 415

tgc ctg ggc atg aac ccg gac cag ctg gcc ccg ggc gag cgc tcc gcc      1596
Cys Leu Gly Met Asn Pro Asp Gln Leu Ala Pro Gly Glu Arg Ser Ala
            420                 425                 430

tcc acc tcg aac cgt aac ttc gag ggc cgg cag ggc ccg ggc ggc cgc      1644
Ser Thr Ser Asn Arg Asn Phe Glu Gly Arg Gln Gly Pro Gly Gly Arg
        435                 440                 445

acc cac ctg gtg tcc ccg ccg gtc gcc gcc gcc acc gcc gtc ctc ggc      1692
Thr His Leu Val Ser Pro Pro Val Ala Ala Ala Thr Ala Val Leu Gly
    450                 455                 460

cac ctg gct tcc ccc gca gac ctc tga ccacgccgac caccaaggag            1739
His Leu Ala Ser Pro Ala Asp Leu
465                 470

ataaaaacag tggagaagtt caccacccac accggcgtcg gcgtcccgct gacccgctcg     1799

aacgtcgaca ccgaccagat catccccgcc gtctacctca agcgcgtcac ccgcacgggc     1859

ttcgatgacg gcctgttcgc cgagtggcgc aaggacgatt ccttcgtcct caaccaggag     1919

ccctaccgca acggctccgt cctggtcgcc ggccccgact tcggcaccgg ctcctcccgt     1979

gagcacgccg tctgggccct catggactac ggcttccgcg                           2019
```

<210> 114
<211> 472
<212> PRT
<213> Corynebacterium humireducens

<400> 114

```
Met Ala Glu Lys Leu Thr Leu Ala Glu Lys Val Trp Asn Asp His Ile
1               5                   10                  15
```

Val Ala Lys Gly Glu Asn Gly Glu Pro Asp Leu Leu Tyr Ile Asp Leu
20 25 30

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

Leu Ala Gly Arg Lys Leu Arg Arg Pro Asp Leu His Leu Ala Thr Glu
50 55 60

Asp His Asn Val Pro Thr Glu Gly Ile Val Ser Gly Ser Leu Leu Glu
65 70 75 80

Ile Lys Glu Ala Thr Ser Arg Thr Gln Val Glu Thr Leu Arg Lys Asn
85 90 95

Cys Glu Glu Phe Gly Ile Arg Leu His Pro Met Gly Asp Val Lys Gln
100 105 110

Gly Ile Val His Thr Val Gly Pro Gln Leu Gly Ala Thr Gln Pro Gly
115 120 125

Met Thr Ile Val Cys Gly Asp Ser His Thr Ser Thr His Gly Ala Phe
130 135 140

Gly Ser Ile Ala Met Gly Ile Gly Thr Ser Glu Val Glu His Val Met
145 150 155 160

Ala Thr Gln Thr Leu Pro Leu Lys Pro Phe Lys Thr Met Ala Ile Glu
165 170 175

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

Ala Ile Ile Ala Lys Ile Gly Thr Gly Gly Gly Gln Gly His Ile Ile
195 200 205

Glu Tyr Arg Gly Glu Ala Ile Glu Lys Leu Ser Met Glu Ala Arg Met
210 215 220

Thr Ile Cys Asn Met Ser Ile Glu Ala Gly Ala Arg Ala Gly Met Val
225 230 235 240

Ala Pro Asp Gln Lys Thr Phe Asp Tyr Val Gln Gly Arg Glu Phe Ala
245 250 255

Pro Thr Gly Glu Asp Trp Asp Ala Ala Val Ala Tyr Trp Lys Thr Leu
260 265 270

Pro Thr Asp Glu Gly Ala Glu Phe Asp Thr Val Val Glu Ile Asp Gly
275 280 285

Ser Ala Leu Thr Pro Phe Val Thr Trp Gly Thr Asn Pro Gly Gln Gly
290 295 300

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

Ala Asp Lys Ala Ala Ala Glu Lys Ala Leu Ala Tyr Met Asp Leu Thr
325 330 335

Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile Asp Thr Val Phe Leu Gly
340 345 350

Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu Arg Ala Ala Ala Glu Val
355 360 365

Val Glu Gly Arg Thr Ile Ala Pro Asn Thr Arg Met Leu Val Val Pro
370 375 380

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

Ile Phe Thr Asp Phe Gly Ala Glu Trp Arg Thr Ala Gly Cys Ser Met
405 410 415

Cys Leu Gly Met Asn Pro Asp Gln Leu Ala Pro Gly Glu Arg Ser Ala
420 425 430

Ser Thr Ser Asn Arg Asn Phe Glu Gly Arg Gln Gly Pro Gly Gly Arg
435 440 445

Thr His Leu Val Ser Pro Pro Val Ala Ala Ala Thr Ala Val Leu Gly
450 455 460

His Leu Ala Ser Pro Ala Asp Leu
465 470

<210> 115

<211> 1197
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(897)
<223> gene leuD

<400> 115
cccgtcctcg acgctggtca agcagcaggc cgaggaggag gggctggaca agatcttcac 60

cgacttcggc gccgagtggc gcaccgccgg ctgctccatg tgcctgggca tgaacccgga 120

ccagctggcc ccgggcgagc gctccgcctc cacctcgaac cgtaacttcg agggccggca 180

gggcccgggc ggccgcaccc acctggtgtc cccgccggtc gccgccgcca ccgccgtcct 240

cggccacctg gcttcccccg cagacctctg accacgccga ccaccaagga gataaaaaca 300

gtg gag aag ttc acc acc cac acc ggc gtc ggc gtc ccg ctg acc cgc 348
Val Glu Lys Phe Thr Thr His Thr Gly Val Gly Val Pro Leu Thr Arg
1 5 10 15

tcg aac gtc gac acc gac cag atc atc ccc gcc gtc tac ctc aag cgc 396
Ser Asn Val Asp Thr Asp Gln Ile Ile Pro Ala Val Tyr Leu Lys Arg
20 25 30

gtc acc cgc acg ggc ttc gat gac ggc ctg ttc gcc gag tgg cgc aag 444
Val Thr Arg Thr Gly Phe Asp Asp Gly Leu Phe Ala Glu Trp Arg Lys
35 40 45

gac gat tcc ttc gtc ctc aac cag gag ccc tac cgc aac ggc tcc gtc 492
Asp Asp Ser Phe Val Leu Asn Gln Glu Pro Tyr Arg Asn Gly Ser Val
50 55 60

ctg gtc gcc ggc ccc gac ttc ggc acc ggc tcc tcc cgt gag cac gcc 540
Leu Val Ala Gly Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His Ala
65 70 75 80

gtc tgg gcc ctc atg gac tac ggc ttc cgc gtc gtg ctg tcc tcc cgc 588
Val Trp Ala Leu Met Asp Tyr Gly Phe Arg Val Val Leu Ser Ser Arg
85 90 95

ttc gcc gac atc ttc cgc ggc aac tcc ggc aag gcc ggc ctg ctg gcc 636
Phe Ala Asp Ile Phe Arg Gly Asn Ser Gly Lys Ala Gly Leu Leu Ala
100 105 110

gcc cag atg gag gag gcc gat atc gag ctg ctg tgg aag cag ctc gag 684
Ala Gln Met Glu Glu Ala Asp Ile Glu Leu Leu Trp Lys Gln Leu Glu
115 120 125

gct gag ccg ggc ctg gag atc acc gtc gac ctc gag tcc cgc acc gtc 732
Ala Glu Pro Gly Leu Glu Ile Thr Val Asp Leu Glu Ser Arg Thr Val
130 135 140

acc gcc ggc gag aac acc tac cag ttc tcc gtc gac gac tac acc cgc 780
Thr Ala Gly Glu Asn Thr Tyr Gln Phe Ser Val Asp Asp Tyr Thr Arg

```
145                 150                 155                 160

tgg cgc ctc atg gag ggc ctc gac gac atc ggc ctg acc ctg cgc gac      828
Trp Arg Leu Met Glu Gly Leu Asp Asp Ile Gly Leu Thr Leu Arg Asp
                165                 170                 175

gag cag gcc atc acc gac tac gag gcg aag cgc ccc gtg tac aag ccg      876
Glu Gln Ala Ile Thr Asp Tyr Glu Ala Lys Arg Pro Val Tyr Lys Pro
            180                 185                 190

acc atc acc gcg gag gtg tga gtcatgtccg acaaccgttt cgacgaggga         927
Thr Ile Thr Ala Glu Val
        195

atccgcatcc gccgcgaggt catgggcgac gatttcgtcg acgccgccct gacccgcaac     987

gccggcaccg acggcgagga cctgcagcac cacatcaccg ccaccgtctg gggttcggtg    1047

tggacccgcg agggcctgtc caagcgtgac cgcagcctgc tcaacatcgg catgctcgtc    1107

gccctgcgcg cgaccgagga actgcgcgga catgtccgcg gcggcctgcg taacggcctg    1167

acccgcgagg agatcaccga ggcgatcatc                                     1197
```

<210> 116
<211> 198
<212> PRT
<213> Corynebacterium humireducens

<400> 116

```
Val Glu Lys Phe Thr Thr His Thr Gly Val Gly Val Pro Leu Thr Arg
1               5                   10                  15

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

Val Thr Arg Thr Gly Phe Asp Asp Gly Leu Phe Ala Glu Trp Arg Lys
        35                  40                  45

Asp Asp Ser Phe Val Leu Asn Gln Glu Pro Tyr Arg Asn Gly Ser Val
    50                  55                  60

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

Val Trp Ala Leu Met Asp Tyr Gly Phe Arg Val Val Leu Ser Ser Arg
                85                  90                  95

Phe Ala Asp Ile Phe Arg Gly Asn Ser Gly Lys Ala Gly Leu Leu Ala
            100                 105                 110
```

```
Ala Gln Met Glu Glu Ala Asp Ile Glu Leu Leu Trp Lys Gln Leu Glu
        115                 120                 125

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

Thr Ala Gly Glu Asn Thr Tyr Gln Phe Ser Val Asp Asp Tyr Thr Arg
145                 150                 155                 160

Trp Arg Leu Met Glu Gly Leu Asp Asp Ile Gly Leu Thr Leu Arg Asp
                165                 170                 175

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

Thr Ile Thr Ala Glu Val
        195
```

<210> 117
<211> 1398
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1098)
<223> gene panB

<400> 117

```
ccgggcgcaa ggcggacgta ctcgtcattc cgccaacccc ggatgattct ctgacgctct       60

gccccggtgg cacgcgtggt gctgatcacc ggcccccccga cctggttcat gtccgcagtc      120

tcccatcagc gcctgcggca cgcacctcca cacgtcggtg gcgttgtgag gcacccgctt      180

gttcgcgagc tccgggagtt ttcccaggtc aggttttcct ggggtgaaca agagggtact      240

tccgcacaca tgccttccgt gggaacaggg gggcatatac tcttgcccat ggtttcccgg      300

atg cgt acc cgc cat ttc gcc cag gcc aag gcc gag ggc cgc aag atc         348
Met Arg Thr Arg His Phe Ala Gln Ala Lys Ala Glu Gly Arg Lys Ile
1               5                   10                  15

tcc tgc ctg acc gcc tac gac gcg ccc acc gcc gcg atc ttc gat gag        396
Ser Cys Leu Thr Ala Tyr Asp Ala Pro Thr Ala Ala Ile Phe Asp Glu
            20                  25                  30

gcg ggc atc gac ctg ctc ctc gtc ggc gat tcc gcc gcc aac gtc gtc        444
Ala Gly Ile Asp Leu Leu Leu Val Gly Asp Ser Ala Ala Asn Val Val
        35                  40                  45
```

```
ctg ggc cag gac tcg acc ctg tcg atc acg gtc gag gag atg atg acc        492
Leu Gly Gln Asp Ser Thr Leu Ser Ile Thr Val Glu Glu Met Met Thr
    50                  55                  60

atg gcg acc gcc gtc gcc cgc ggc acc gaa cgc gcc ttc gtg gtc acc        540
Met Ala Thr Ala Val Ala Arg Gly Thr Glu Arg Ala Phe Val Val Thr
65                  70                  75                  80

gac ctg ccc ttc ggc tcc tac gag gtc tcc ccc gcc cag gcg ctg gag        588
Asp Leu Pro Phe Gly Ser Tyr Glu Val Ser Pro Ala Gln Ala Leu Glu
                85                  90                  95

acg gcc gcc cgg ttc atg aag cag acc ggt gtc gcc gcg gtg aag atc        636
Thr Ala Ala Arg Phe Met Lys Gln Thr Gly Val Ala Ala Val Lys Ile
            100                 105                 110

gag ggc ggc gtc gag atc gcc ccg acg atc cgc acg ctc gtc gac gcc        684
Glu Gly Gly Val Glu Ile Ala Pro Thr Ile Arg Thr Leu Val Asp Ala
        115                 120                 125

ggc atc ccc gtc atg gcc cac atc ggc tac acc ccg cag tcc gag cac        732
Gly Ile Pro Val Met Ala His Ile Gly Tyr Thr Pro Gln Ser Glu His
    130                 135                 140

gcc ctc ggc ggc tac gtc gtc cag ggt cgc ggg gag gcc gcg gag aag        780
Ala Leu Gly Gly Tyr Val Val Gln Gly Arg Gly Glu Ala Ala Glu Lys
145                 150                 155                 160

ctg cgc gcc gac gcc ctc gcc gtc cag gag gcc ggc gcc ttc gcc gtc        828
Leu Arg Ala Asp Ala Leu Ala Val Gln Glu Ala Gly Ala Phe Ala Val
                165                 170                 175

gtc ctc gag atg gtc ccc gcc ggc atc gcc ggg gag atc acc cgc gag        876
Val Leu Glu Met Val Pro Ala Gly Ile Ala Gly Glu Ile Thr Arg Glu
            180                 185                 190

ctc acc atc ccg acg atc ggc atc ggc gcc ggc gcc gac acc gac ggc        924
Leu Thr Ile Pro Thr Ile Gly Ile Gly Ala Gly Ala Asp Thr Asp Gly
        195                 200                 205

cag gtc ctc gtg tgg acc gac gcc ttc ggt ctc acg cgc ggc cgt acg        972
Gln Val Leu Val Trp Thr Asp Ala Phe Gly Leu Thr Arg Gly Arg Thr
    210                 215                 220

ccg cgt ttc gcg cgt cgt tac gcg gag atc ggg gac atg ctc ctc gac       1020
Pro Arg Phe Ala Arg Arg Tyr Ala Glu Ile Gly Asp Met Leu Leu Asp
225                 230                 235                 240

gcc gcc cgt gcc tac cgc acc gac gtc gag tcc ggc tcc ttc ccg gac       1068
Ala Ala Arg Ala Tyr Arg Thr Asp Val Glu Ser Gly Ser Phe Pro Asp
                245                 250                 255

gag tcc gag tcc ttc cgg gac gag cag tga ccgtcgtcgc gcgcactgtc         1118
Glu Ser Glu Ser Phe Arg Asp Glu Gln
            260                 265

gcgcagctgc gttccgccgt cgccgatctg cagggttccg tcggcctcgt gccgaccatg     1178

ggtgcgctcc acgagggtca cggccgtctg gtgtccctgg ccgccgagga gaactcctcg     1238
```

gtggtggtga gcatcttcgt caacccgttg cagttcaccg acctcggcga ctgcgacgac 1298

ttccgccact acccgcgtga cctggacaag gacgtcgcct tcctggagaa gctcggcgtc 1358

gacgtcgtgt tcgcgccgac cgacgaggcg atgtacccgg 1398

<210> 118
<211> 265
<212> PRT
<213> Corynebacterium humireducens

<400> 118

Met Arg Thr Arg His Phe Ala Gln Ala Lys Ala Glu Gly Arg Lys Ile
1 5 10 15

Ser Cys Leu Thr Ala Tyr Asp Ala Pro Thr Ala Ala Ile Phe Asp Glu
20 25 30

Ala Gly Ile Asp Leu Leu Leu Val Gly Asp Ser Ala Ala Asn Val Val
35 40 45

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

Met Ala Thr Ala Val Ala Arg Gly Thr Glu Arg Ala Phe Val Val Thr
65 70 75 80

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

Thr Ala Ala Arg Phe Met Lys Gln Thr Gly Val Ala Ala Val Lys Ile
100 105 110

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

Gly Ile Pro Val Met Ala His Ile Gly Tyr Thr Pro Gln Ser Glu His
130 135 140

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

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

```
Val Leu Glu Met Val Pro Ala Gly Ile Ala Gly Glu Ile Thr Arg Glu
            180                 185                 190

Leu Thr Ile Pro Thr Ile Gly Ile Gly Ala Gly Ala Asp Thr Asp Gly
        195                 200                 205

Gln Val Leu Val Trp Thr Asp Ala Phe Gly Leu Thr Arg Gly Arg Thr
    210                 215                 220

Pro Arg Phe Ala Arg Arg Tyr Ala Glu Ile Gly Asp Met Leu Leu Asp
225                 230                 235                 240

Ala Ala Arg Ala Tyr Arg Thr Asp Val Glu Ser Gly Ser Phe Pro Asp
                245                 250                 255

Glu Ser Glu Ser Phe Arg Asp Glu Gln
            260                 265
```

<210> 119
<211> 1452
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1152)
<223> gene panC

<400> 119

```
cctcgccgtc caggaggccg gcgccttcgc cgtcgtcctc gagatggtcc ccgccggcat       60

cgccggggag atcacccgcg agctcaccat cccgacgatc ggcatcggcg ccggcgccga      120

caccgacggc caggtcctcg tgtggaccga cgccttcggt ctcacgcgcg gccgtacgcc      180

gcgtttcgcg cgtcgttacg cggagatcgg ggacatgctc ctcgacgccg cccgtgccta      240

ccgcaccgac gtcgagtccg gctccttccc ggacgagtcc gagtccttcc gggacgagca      300

gtg acc gtc gtc gcg cgc act gtc gcg cag ctg cgt tcc gcc gtc gcc         348
Val Thr Val Val Ala Arg Thr Val Ala Gln Leu Arg Ser Ala Val Ala
1               5                   10                  15

gat ctg cag ggt tcc gtc ggc ctc gtg ccg acc atg ggt gcg ctc cac       396
Asp Leu Gln Gly Ser Val Gly Leu Val Pro Thr Met Gly Ala Leu His
            20                  25                  30

gag ggt cac ggc cgt ctg gtg tcc ctg gcc gcc gag gag aac tcc tcg       444
Glu Gly His Gly Arg Leu Val Ser Leu Ala Ala Glu Glu Asn Ser Ser
        35                  40                  45

gtg gtg gtg agc atc ttc gtc aac ccg ttg cag ttc acc gac ctc ggc       492
```

```
Val Val Val Ser Ile Phe Val Asn Pro Leu Gln Phe Thr Asp Leu Gly
    50                  55                  60

gac tgc gac gac ttc cgc cac tac ccg cgt gac ctg gac aag gac gtc      540
Asp Cys Asp Asp Phe Arg His Tyr Pro Arg Asp Leu Asp Lys Asp Val
65                  70                  75                  80

gcc ttc ctg gag aag ctc ggc gtc gac gtc gtg ttc gcg ccg acc gac      588
Ala Phe Leu Glu Lys Leu Gly Val Asp Val Val Phe Ala Pro Thr Asp
                85                  90                  95

gag gcg atg tac ccg gac ggc ctg ccc cag gtg tgg gtg cgg gcc ggc      636
Glu Ala Met Tyr Pro Asp Gly Leu Pro Gln Val Trp Val Arg Ala Gly
            100                 105                 110

gag atg ggt gag cgc ctc gag ggc gcc tcc cgt ccc ggc cac ttc gac      684
Glu Met Gly Glu Arg Leu Glu Gly Ala Ser Arg Pro Gly His Phe Asp
        115                 120                 125

ggc gtg acc acc gtg gtg gcc aag ctg ttc cag ctc atc cag ccg gac      732
Gly Val Thr Thr Val Val Ala Lys Leu Phe Gln Leu Ile Gln Pro Asp
    130                 135                 140

cgc gcc tac ttc ggt gag aag gac gcg cag cag ctg gcg atc atc cag      780
Arg Ala Tyr Phe Gly Glu Lys Asp Ala Gln Gln Leu Ala Ile Ile Gln
145                 150                 155                 160

cgc atg gtc atg gac ctg gac ttc ccg ctg cag atc cgc ccg gtg ccg      828
Arg Met Val Met Asp Leu Asp Phe Pro Leu Gln Ile Arg Pro Val Pro
                165                 170                 175

atc atc cgc ggt gcc gac ggc ctg gcc gag tcc tcc cgc aac cag cac      876
Ile Ile Arg Gly Ala Asp Gly Leu Ala Glu Ser Ser Arg Asn Gln His
            180                 185                 190

ctc acc ccc gag gcg cgg gag cag gcg ctc gtc ctg ccg cgc acc ctg      924
Leu Thr Pro Glu Ala Arg Glu Gln Ala Leu Val Leu Pro Arg Thr Leu
        195                 200                 205

gcc gcg ctg cgt gac cgc gcc gcc gcc ggt gac ccc ctc gac gtc gag      972
Ala Ala Leu Arg Asp Arg Ala Ala Ala Gly Asp Pro Leu Asp Val Glu
    210                 215                 220

ggt gcc cgc gag gcg ctg cgc tcc gcc gag ggc gtg gaa ctc gac cac     1020
Gly Ala Arg Glu Ala Leu Arg Ser Ala Glu Gly Val Glu Leu Asp His
225                 230                 235                 240

ctc gag gtc gtc gac gcc gcg acg ctg ctg ccg gtc tcc gag gtc ggc     1068
Leu Glu Val Val Asp Ala Ala Thr Leu Leu Pro Val Ser Glu Val Gly
                245                 250                 255

gcc ggc gcg ctg gcc gtc gcc gcg atc cac gtg ggt ggc acg cgg ctc     1116
Ala Gly Ala Leu Ala Val Ala Ala Ile His Val Gly Gly Thr Arg Leu
            260                 265                 270

atc gac aac gtg cga ctg ctt ccg ccg cgc gct tag cgtaggggcc          1162
Ile Asp Asn Val Arg Leu Leu Pro Pro Arg Ala
        275                 280
```

gacgccgacg atcgtcgccg aaccggggcc gagccagtcc ccgtagccca ccaggtgcag 1222

cggcagcccc cggtcgagga cccgccggaa gggacgcagc gccgggcgga agccggtgca 1282

ccagatgagg tgctccgcgt ccacctcgtc gaggctgcgg aacagcggcg tcgcccgcag 1342

gcggccggag tcccgcgcgg ccttcaccgc gggcaggacc acgatgtccc cgagctcgga 1402

gtccgccccc gggtcctcct ccccgcgcag gatcgccagg gcccgcaggc 1452

<210> 120
<211> 283
<212> PRT
<213> Corynebacterium humireducens

<400> 120

Val Thr Val Val Ala Arg Thr Val Ala Gln Leu Arg Ser Ala Val Ala
1 5 10 15

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

Glu Gly His Gly Arg Leu Val Ser Leu Ala Ala Glu Glu Asn Ser Ser
35 40 45

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

Asp Cys Asp Asp Phe Arg His Tyr Pro Arg Asp Leu Asp Lys Asp Val
65 70 75 80

Ala Phe Leu Glu Lys Leu Gly Val Asp Val Val Phe Ala Pro Thr Asp
85 90 95

Glu Ala Met Tyr Pro Asp Gly Leu Pro Gln Val Trp Val Arg Ala Gly
100 105 110

Glu Met Gly Glu Arg Leu Glu Gly Ala Ser Arg Pro Gly His Phe Asp
115 120 125

Gly Val Thr Thr Val Val Ala Lys Leu Phe Gln Leu Ile Gln Pro Asp
130 135 140

Arg Ala Tyr Phe Gly Glu Lys Asp Ala Gln Gln Leu Ala Ile Ile Gln
145 150 155 160

Arg Met Val Met Asp Leu Asp Phe Pro Leu Gln Ile Arg Pro Val Pro

165 170 175

Ile Ile Arg Gly Ala Asp Gly Leu Ala Glu Ser Ser Arg Asn Gln His
180 185 190

Leu Thr Pro Glu Ala Arg Glu Gln Ala Leu Val Leu Pro Arg Thr Leu
195 200 205

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

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

Leu Glu Val Val Asp Ala Ala Thr Leu Leu Pro Val Ser Glu Val Gly
245 250 255

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

Ile Asp Asn Val Arg Leu Leu Pro Pro Arg Ala
275 280

<210> 121
<211> 1116
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(816)
<223> gene ilvH

<400> 121
gcgtcacccg cgaggaggac gtcctgccga cgatccagaa ggcacgcgag atcaacgacc 60

gcccggtcgt catcgacttc atcgtcggtg aggacgccca ggtctggccg atggtcgccg 120

ccggcgcctc caactcggac atcgagtacg cacgtggtct gcgccccttc ttcgagggtg 180

acgagtccgc gggtgagtcc ccggccgaca tccacggtgt catggagaac gcccaggagg 240

agaccgtcga ggaagtcctc gaggagcgcg cgaacgacag cgagaaggag aactaggaca 300

atg gcg aac acc gac atc atc cgc aac acc ctc agc gtc ctg gtc cag 348
Met Ala Asn Thr Asp Ile Ile Arg Asn Thr Leu Ser Val Leu Val Gln
1 5 10 15

gac gtc gac ggc atc atc tcc cgc gtc gca ggc atg ttc acc cgc cgt 396
Asp Val Asp Gly Ile Ile Ser Arg Val Ala Gly Met Phe Thr Arg Arg

```
                20                  25                  30

ggc tac aac ctg gtg tcc atc gtc tcg gcg cac acc gac acc ccg ggc        444
Gly Tyr Asn Leu Val Ser Ile Val Ser Ala His Thr Asp Thr Pro Gly
        35                  40                  45

atc agc cgc atc acc atc gtg gtc gac gcc aac gag ctg gtc atc gag        492
Ile Ser Arg Ile Thr Ile Val Val Asp Ala Asn Glu Leu Val Ile Glu
    50                  55                  60

cag gtc acc aag cag ctc aac aag atc atc ccg gtg ctc aag gtc gtc        540
Gln Val Thr Lys Gln Leu Asn Lys Ile Ile Pro Val Leu Lys Val Val
65                  70                  75                  80

cgc ctc gag gag gac acc acc atc gcc cgc gcc atc atg ctg gtg aag        588
Arg Leu Glu Glu Asp Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys
                85                  90                  95

gtc aac gcc gac aac acc aac cgc ccg cag gtc gtc gac gcc gcg aac        636
Val Asn Ala Asp Asn Thr Asn Arg Pro Gln Val Val Asp Ala Ala Asn
            100                 105                 110

atc ttc cgc gcc cgc atc gtc gac gtg gcc cag gag tcc gtg gtc atc        684
Ile Phe Arg Ala Arg Ile Val Asp Val Ala Gln Glu Ser Val Val Ile
        115                 120                 125

gag gcc acc ggt acc ccg ggc aag ctg cgc gcc ctg ctg gag gtc ctc        732
Glu Ala Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Glu Val Leu
    130                 135                 140

gag ccc ttc ggt atc cgt gag ctc atc cag tcc ggt cag atc gcc ctc        780
Glu Pro Phe Gly Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu
145                 150                 155                 160

aac cgc ggt ccg aag acg atg gca ccg tcc aag taa cacccccтca              826
Asn Arg Gly Pro Lys Thr Met Ala Pro Ser Lys
                165                 170

tcccacctgg tgagacaaca cgcatgaaag tcccaccagg tggggtaccc ctgtctcatg       886

ttgtggtaca aacaacaaca gcacttgtat aagacgaaag gcgagttttt ctcccatggc       946

tattgaactg ctttacgacg ccgacgctga cctctccctc atccagggcc gcaaggtcgc      1006

catcatcggc tacggctccc agggccacgc ccacgcccag aacctgcgtg actccggcgt      1066

cgaggtctgc atcggcctgc gcgacggctc caagtccgcg gagaaggcca                 1116
```

<210> 122
<211> 171
<212> PRT
<213> Corynebacterium humireducens

<400> 122

```
Met Ala Asn Thr Asp Ile Ile Arg Asn Thr Leu Ser Val Leu Val Gln
1               5                   10                  15
```

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

Gly Tyr Asn Leu Val Ser Ile Val Ser Ala His Thr Asp Thr Pro Gly
35 40 45

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

Gln Val Thr Lys Gln Leu Asn Lys Ile Ile Pro Val Leu Lys Val Val
65 70 75 80

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

Val Asn Ala Asp Asn Thr Asn Arg Pro Gln Val Val Asp Ala Ala Asn
100 105 110

Ile Phe Arg Ala Arg Ile Val Asp Val Ala Gln Glu Ser Val Val Ile
115 120 125

Glu Ala Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Glu Val Leu
130 135 140

Glu Pro Phe Gly Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu
145 150 155 160

Asn Arg Gly Pro Lys Thr Met Ala Pro Ser Lys
165 170

<210> 123
<211> 1944
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1644)
<223> gene gdh

<400> 123
gaaggtggcg gcggtgccct cacccccgtc ggccatggga gcgagggtga tctcggcgtc 60

ccggatgatc gagcggacac cctcgccgat cagccgtgcg gcctgatcgg cggtggcagt 120

```
gcccttgaag gagtcggggg cgatgatgat gtggaccatg ggaagcagtc taggggtagt      180

gggagtgaca tattcaactc cggagtgact tgcatgaacc gcgccgcccg tgaaaactat      240

aggccgttag aaaaccccat cccccgggct gcccgcgact gcgggccgga aaggactcgt      300

atg tct att gac gag cag gtc tcc tcc tac tac aac atg ctg ctc aag         348
Met Ser Ile Asp Glu Gln Val Ser Ser Tyr Tyr Asn Met Leu Leu Lys
1               5                  10                  15

cgg aac gca gga gag ccg gag ttc cac cag gca gtc gca gaa gtt ctc         396
Arg Asn Ala Gly Glu Pro Glu Phe His Gln Ala Val Ala Glu Val Leu
            20                  25                  30

gcc tcc ctc aag atc gtc ctg gag aag gat ccg cac tac gcg gac tac         444
Ala Ser Leu Lys Ile Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr
        35                  40                  45

ggc ctc atc cag cgc ctg tgc gag ccg gag cgc cag ctc atc ttc cgt         492
Gly Leu Ile Gln Arg Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg
    50                  55                  60

gtg ccg tgg atc gac gac aac ggc gtg gta cag gtc aac cgt ggt ttc         540
Val Pro Trp Ile Asp Asp Asn Gly Val Val Gln Val Asn Arg Gly Phe
65                  70                  75                  80

cga gta cag ttc aac tcc gcc ctc ggc ccg tac aag ggc ggc cta cgc         588
Arg Val Gln Phe Asn Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg
                85                  90                  95

ttc cac ccg tcc gtc aac ctg ggc atc atc aag ttc ctc ggc ttc gag         636
Phe His Pro Ser Val Asn Leu Gly Ile Ile Lys Phe Leu Gly Phe Glu
            100                 105                 110

cag atc ttc aag aac tcc ctc acc ggc ctg ccc atc ggc ggc ggc aag         684
Gln Ile Phe Lys Asn Ser Leu Thr Gly Leu Pro Ile Gly Gly Gly Lys
        115                 120                 125

ggc ggc tcc gac ttc gac ccg aag ggc aag tcc gag ctc gag atc atg         732
Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Glu Leu Glu Ile Met
    130                 135                 140

cgt ttc tgc cag tcc ttc atg acc gag ctg cac aag cac atc ggc gag         780
Arg Phe Cys Gln Ser Phe Met Thr Glu Leu His Lys His Ile Gly Glu
145                 150                 155                 160

tac aag gac gtc ccc gcc ggt gac atc ggc gtc ggc ggc cgg gag atc         828
Tyr Lys Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Ile
                165                 170                 175

ggt ttc ctc ttc ggc cag tac cgt cgt ctg gcc ggc cag cac gag tcc         876
Gly Phe Leu Phe Gly Gln Tyr Arg Arg Leu Ala Gly Gln His Glu Ser
            180                 185                 190

ggc gtc ctc acc ggc aag ggc ctc gcc tgg ggt ggc tcc ctc gtg cgc         924
Gly Val Leu Thr Gly Lys Gly Leu Ala Trp Gly Gly Ser Leu Val Arg
        195                 200                 205
```

```
acc gag gcc acc ggc tac ggc gcc gtc tac ctc acg cag gag atg atg        972
Thr Glu Ala Thr Gly Tyr Gly Ala Val Tyr Leu Thr Gln Glu Met Met
    210                 215                 220

aag gcc cac ggc gac tcc ctc tcc ggt tcg aag gtc atc gtc tcc ggc       1020
Lys Ala His Gly Asp Ser Leu Ser Gly Ser Lys Val Ile Val Ser Gly
225                 230                 235                 240

tcc ggc aac gtc gcc atc tac gcc atc gag aag gcc cag gag ctc ggc       1068
Ser Gly Asn Val Ala Ile Tyr Ala Ile Glu Lys Ala Gln Glu Leu Gly
                245                 250                 255

gcc acc gtc gtc ggc ttc tcc gac tcc tcc ggc tgg gtc tcc acc ccg       1116
Ala Thr Val Val Gly Phe Ser Asp Ser Ser Gly Trp Val Ser Thr Pro
            260                 265                 270

aac ggc gtc gac gtc gag ctg ctc cac gac gtc aag gag aag cgc cgc       1164
Asn Gly Val Asp Val Glu Leu Leu His Asp Val Lys Glu Lys Arg Arg
        275                 280                 285

gag cgc gtc tcc tgc tac gcc gag gag gcc acc ggc gcg acc ttc cac       1212
Glu Arg Val Ser Cys Tyr Ala Glu Glu Ala Thr Gly Ala Thr Phe His
    290                 295                 300

gcc gag ggc tcc atc tgg gac ctc gcc gcc gac gtc gcc ctc ccg tgc       1260
Ala Glu Gly Ser Ile Trp Asp Leu Ala Ala Asp Val Ala Leu Pro Cys
305                 310                 315                 320

gcc acc cag aac gag ctc aac ggc gac cac gcc cgc acc ctg gcc gac       1308
Ala Thr Gln Asn Glu Leu Asn Gly Asp His Ala Arg Thr Leu Ala Asp
                325                 330                 335

aac ggc atc cgc tac gtc gcc gag ggc gcc aac atg ccc tcc acc ccg       1356
Asn Gly Ile Arg Tyr Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro
            340                 345                 350

gag gcc atc gag gtc ttc cgt gag cgc ggt atc ttc ttc gcc ccg ggc       1404
Glu Ala Ile Glu Val Phe Arg Glu Arg Gly Ile Phe Phe Ala Pro Gly
        355                 360                 365

aag gcc gcc aac gcc ggt ggc gtg gcc acc tcc gcc ctg gag atg cag       1452
Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln
    370                 375                 380

cag aac gcc tcc cgt gac tcc tgg tcc ttc gag tac acg gac cag cgc       1500
Gln Asn Ala Ser Arg Asp Ser Trp Ser Phe Glu Tyr Thr Asp Gln Arg
385                 390                 395                 400

ctg cac aag atc atg tcc aag atc ttc cgc acc atg tcc cgc act gcc       1548
Leu His Lys Ile Met Ser Lys Ile Phe Arg Thr Met Ser Arg Thr Ala
                405                 410                 415

gca gag tac ggc cac gag ggc aac tac gtc gtc ggc tcc aac atc gcc       1596
Ala Glu Tyr Gly His Glu Gly Asn Tyr Val Val Gly Ser Asn Ile Ala
            420                 425                 430

ggc ttc aag aag gtc gcc gac gcg atg ctc gcg cag ggc gtc atc taa       1644
Gly Phe Lys Lys Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile
        435                 440                 445
```

ggctctccac aggattccct gacccccctgg ccctgccgca ccacacattg tgcggcaggg 1704

ccagtaatct ttgagtcatg tatagagtct tcgaagccct ggacgagctc aaccagaccg 1764

tggagcaggc ctacggcgtg cccatgacct ccaactgcat ggtgccgcgc aacgacaccc 1824

tcgcgcttct cgacgatctg cgtaacgccc tgcccgtcga gatcgacgac gcccaggatg 1884

tcctggacca gcgcgacgag atcctccgcg gggccgagga ccgggcccgc gacatgatcg 1944

<210> 124
<211> 447
<212> PRT
<213> Corynebacterium humireducens

<400> 124

Met Ser Ile Asp Glu Gln Val Ser Ser Tyr Tyr Asn 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

Ala 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 Ile Asp Asp Asn Gly Val Val Gln 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 Ile 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 Glu Leu Glu Ile Met
130 135 140

Arg Phe Cys Gln Ser Phe Met Thr Glu Leu His Lys His Ile Gly Glu
145 150 155 160

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

Gly Phe Leu Phe Gly Gln Tyr Arg Arg Leu Ala Gly Gln His Glu Ser
180 185 190

Gly Val Leu Thr Gly Lys Gly Leu Ala Trp Gly Gly Ser Leu Val Arg
195 200 205

Thr Glu Ala Thr Gly Tyr Gly Ala Val Tyr Leu Thr Gln Glu Met Met
210 215 220

Lys Ala His Gly Asp Ser Leu Ser Gly Ser Lys Val Ile Val Ser Gly
225 230 235 240

Ser Gly Asn Val Ala Ile Tyr Ala Ile Glu Lys Ala Gln Glu Leu Gly
245 250 255

Ala Thr Val Val Gly Phe Ser Asp Ser Ser Gly Trp Val Ser Thr Pro
260 265 270

Asn Gly Val Asp Val Glu Leu Leu His Asp Val Lys Glu Lys Arg Arg
275 280 285

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

Ala Glu Gly Ser Ile Trp Asp Leu Ala Ala Asp Val Ala Leu Pro Cys
305 310 315 320

Ala Thr Gln Asn Glu Leu Asn Gly Asp His Ala Arg Thr Leu Ala Asp
325 330 335

Asn Gly Ile Arg Tyr Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro
340 345 350

Glu Ala Ile Glu Val Phe Arg Glu Arg Gly Ile Phe Phe Ala 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 Gln Arg
385 390 395 400

```
Leu His Lys Ile Met Ser Lys Ile Phe Arg Thr Met Ser Arg Thr Ala
                405                 410                 415

Ala Glu Tyr Gly His Glu Gly Asn Tyr Val Val Gly Ser 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> 125
<211> 2037
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1737)
<223> gene glutaminsynthetase_1

<400> 125

```
agcgagccgg ggccggtctc ggggaggccg agtttctctc cggggtaccg gccgggtgcg      60

aaggggtcct cgtgttcgcc ggggatctgg gggccgtcga gccagctacg cttggggttc     120

gccataccgt agacattagc cgggggcgtg cgggcagggg aaactcgagt ttcctgcgac     180

tattgatcgg tcaacagata gcagtttaga atgagcgaca ggtaataggg agcggtgccc     240

gcacctgtag actggctgag ataccgcacg acctagagcg tcaacaacca aggagtcatc     300

gtg gcc ttc aac acg atc gaa gaa gtc gtc aag tac atc aag gat gaa        348
Val Ala Phe Asn Thr Ile Glu Glu Val Val Lys Tyr Ile Lys Asp Glu
1               5                   10                  15

aac gtc gag ttc gtc gac gtc cgc ttc acg gac gtc ccg ggc acc gag       396
Asn Val Glu Phe Val Asp Val Arg Phe Thr Asp Val Pro Gly Thr Glu
            20                  25                  30

cac cac ttc acc atc ccc gcc tcg atg ttc gac gag gag gcg gcg gag       444
His His Phe Thr Ile Pro Ala Ser Met Phe Asp Glu Glu Ala Ala Glu
        35                  40                  45

gaa ggc ctc gcc ttc gac ggc tcc tcc atc cgc ggc ttc acc acg atc       492
Glu Gly Leu Ala Phe Asp Gly Ser Ser Ile Arg Gly Phe Thr Thr Ile
    50                  55                  60

gac gag tcc gac atg aac ctc ctg ccg gac ctc aag acc gcc aag ctc       540
Asp Glu Ser Asp Met Asn Leu Leu Pro Asp Leu Lys Thr Ala Lys Leu
65                  70                  75                  80

gac ccc ttc cgc gag gcc aag acg ctg aac atc aag ttc ttc gtc cac       588
Asp Pro Phe Arg Glu Ala Lys Thr Leu Asn Ile Lys Phe Phe Val His
                85                  90                  95
```

```
gac ccc ttc acc cgc gag ccc ttc tcc cgc gac ccc cgc aac gtc gcc        636
Asp Pro Phe Thr Arg Glu Pro Phe Ser Arg Asp Pro Arg Asn Val Ala
            100                 105                 110

cgc aag gcc gag gag tac ctc gcc tcc acc ggc atc gcc gac acc tgc        684
Arg Lys Ala Glu Glu Tyr Leu Ala Ser Thr Gly Ile Ala Asp Thr Cys
        115                 120                 125

ttc ttc ggc gcc gag gcc gag ttc tac ctc ttc gac acc gtc cgg ttc        732
Phe Phe Gly Ala Glu Ala Glu Phe Tyr Leu Phe Asp Thr Val Arg Phe
    130                 135                 140

gag acc tcc acc aac ggc ggc ttc tac gag gtc gac tcc gac gag ggc        780
Glu Thr Ser Thr Asn Gly Gly Phe Tyr Glu Val Asp Ser Asp Glu Gly
145                 150                 155                 160

tgg tgg aac cgc ggc aag gag gag cgt ctc gac ggc cgc cgc aac ctc        828
Trp Trp Asn Arg Gly Lys Glu Glu Arg Leu Asp Gly Arg Arg Asn Leu
                165                 170                 175

ggc tac acc aac cgc gtc aag ggc gga tac ttc ccg gtc gcc ccc tac        876
Gly Tyr Thr Asn Arg Val Lys Gly Gly Tyr Phe Pro Val Ala Pro Tyr
            180                 185                 190

gac cag acc gtg gac atc cgt gac tcc atg gtg cgc cac ctg cag aac        924
Asp Gln Thr Val Asp Ile Arg Asp Ser Met Val Arg His Leu Gln Asn
        195                 200                 205

gcc gac ttc cac atc gag cgc ttc cac aag gag gtg ggc acg ggc ggc        972
Ala Asp Phe His Ile Glu Arg Phe His Lys Glu Val Gly Thr Gly Gly
    210                 215                 220

cag cag gag atc aac tac cgc ttc aac acc ctg ctc cac gcc gcc gat       1020
Gln Gln Glu Ile Asn Tyr Arg Phe Asn Thr Leu Leu His Ala Ala Asp
225                 230                 235                 240

gat ctg cag acc ttc aag tac atc atc aag aac acc gcc ttc aac gcc       1068
Asp Leu Gln Thr Phe Lys Tyr Ile Ile Lys Asn Thr Ala Phe Asn Ala
                245                 250                 255

ggc aag acg gcc acg ttc atg ccc aag ccc atc gcc ggc gac aac ggt       1116
Gly Lys Thr Ala Thr Phe Met Pro Lys Pro Ile Ala Gly Asp Asn Gly
            260                 265                 270

tcc ggc atg cac gcc cac cag tcg ctg tgg aag gac ggc gag ccg ctc       1164
Ser Gly Met His Ala His Gln Ser Leu Trp Lys Asp Gly Glu Pro Leu
        275                 280                 285

ttc cac gac gag tcc ggc tac gcc ggc ctg tcc gac atg gcc cgc tac       1212
Phe His Asp Glu Ser Gly Tyr Ala Gly Leu Ser Asp Met Ala Arg Tyr
    290                 295                 300

tac atc ggc ggc atc ctc cac cac gcc ggc gcc gtc ctg gcc ttc acc       1260
Tyr Ile Gly Gly Ile Leu His His Ala Gly Ala Val Leu Ala Phe Thr
305                 310                 315                 320

aac ccg acg ctg aac tcc tac cac cgc ctg gtc aag ggc ttc gag gca       1308
Asn Pro Thr Leu Asn Ser Tyr His Arg Leu Val Lys Gly Phe Glu Ala
                325                 330                 335
```

```
ccg atc aac ctg gtg tac tcc cag cgc aac cgc tcc gcc gcg atc cgc      1356
Pro Ile Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Ala Ile Arg
            340                 345                 350

atc ccg atc acc ggc tcc aac ccg aag gcc aag cgc atc gag ttc cgc      1404
Ile Pro Ile Thr Gly Ser Asn Pro Lys Ala Lys Arg Ile Glu Phe Arg
        355                 360                 365

gcc ccg gac ccg tcc ggc aac ccg tac ctc ggc ttc gcc gcg atg atg      1452
Ala Pro Asp Pro Ser Gly Asn Pro Tyr Leu Gly Phe Ala Ala Met Met
    370                 375                 380

ctc gcc ggc ctc gac ggc atc aag aac cgc atc gag ccg atg gcc ccg      1500
Leu Ala Gly Leu Asp Gly Ile Lys Asn Arg Ile Glu Pro Met Ala Pro
385                 390                 395                 400

gtg gac aag gac ctc tac gag ctc ccg ccg gag gag gcc gcc gcc atc      1548
Val Asp Lys Asp Leu Tyr Glu Leu Pro Pro Glu Glu Ala Ala Ala Ile
                405                 410                 415

ccg cag gcc ccg acc tcc ctc gag gcc tcc ctg gcc gcc ctg cag gag      1596
Pro Gln Ala Pro Thr Ser Leu Glu Ala Ser Leu Ala Ala Leu Gln Glu
            420                 425                 430

gac aac gac ttc ctc acc gag ggt gac gtg ttc acc gag gac ctc atc      1644
Asp Asn Asp Phe Leu Thr Glu Gly Asp Val Phe Thr Glu Asp Leu Ile
        435                 440                 445

gag gcc tac atc cag ctc aag tac gac aac gag atc acc ccg gcc cgt      1692
Glu Ala Tyr Ile Gln Leu Lys Tyr Asp Asn Glu Ile Thr Pro Ala Arg
    450                 455                 460

ctg cgc ccg acg ccg ctg gag ttc gag ctg tac tac gac tgc tga          1737
Leu Arg Pro Thr Pro Leu Glu Phe Glu Leu Tyr Tyr Asp Cys
465                 470                 475

ccatgccccc accgcaaccc ccgcgccgga gctttccgac gcgggggttg cgcgcctctc     1797

ccctgtcagc taactgacag taactatact ttccaccgtg aacatatccc tggcaggccc     1857

ccgtcgcctc gcatccctca tcctgtcact gttcctggcg ttgtccctgg ccccgcggc      1917

acacgccgcc accggcagcc cccaggaatt cgtcccctac accgacagcc acggcacaag     1977

ttcgaactac cacttctacc cctccggccg cgagaacgcc ggactcctcg tccacctcga     2037
```

<210> 126
<211> 478
<212> PRT
<213> Corynebacterium humireducens

<400> 126

```
Val Ala Phe Asn Thr Ile Glu Glu Val Val Lys Tyr Ile Lys Asp Glu
1               5                   10                  15
```

```
Asn Val Glu Phe Val Asp Val Arg Phe Thr Asp Val Pro Gly Thr Glu
            20                  25                  30

His His Phe Thr Ile Pro Ala Ser Met Phe Asp Glu Glu Ala Ala Glu
        35                  40                  45

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

Asp Glu Ser Asp Met Asn Leu Leu Pro Asp Leu Lys Thr Ala Lys Leu
65                  70                  75                  80

Asp Pro Phe Arg Glu Ala Lys Thr Leu Asn Ile Lys Phe Phe Val His
                85                  90                  95

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

Arg Lys Ala Glu Glu Tyr Leu Ala Ser Thr Gly Ile Ala Asp Thr Cys
        115                 120                 125

Phe Phe Gly Ala Glu Ala Glu Phe Tyr Leu Phe Asp Thr Val Arg Phe
    130                 135                 140

Glu Thr Ser Thr Asn Gly Gly Phe Tyr Glu Val Asp Ser Asp Glu Gly
145                 150                 155                 160

Trp Trp Asn Arg Gly Lys Glu Glu Arg Leu Asp Gly Arg Arg Asn Leu
                165                 170                 175

Gly Tyr Thr Asn Arg Val Lys Gly Gly Tyr Phe Pro Val Ala Pro Tyr
            180                 185                 190

Asp Gln Thr Val Asp Ile Arg Asp Ser Met Val Arg His Leu Gln Asn
        195                 200                 205

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

Gln Gln Glu Ile Asn Tyr Arg Phe Asn Thr Leu Leu His Ala Ala Asp
225                 230                 235                 240

Asp Leu Gln Thr Phe Lys Tyr Ile Ile Lys Asn Thr Ala Phe Asn Ala
                245                 250                 255
```

```
Gly Lys Thr Ala Thr Phe Met Pro Lys Pro Ile Ala Gly Asp Asn Gly
            260                 265                 270

Ser Gly Met His Ala His Gln Ser Leu Trp Lys Asp Gly Glu Pro Leu
        275                 280                 285

Phe His Asp Glu Ser Gly Tyr Ala Gly Leu Ser Asp Met Ala Arg Tyr
    290                 295                 300

Tyr Ile Gly Gly Ile Leu His His Ala Gly Ala Val Leu Ala Phe Thr
305                 310                 315                 320

Asn Pro Thr Leu Asn Ser Tyr His Arg Leu Val Lys Gly Phe Glu Ala
                325                 330                 335

Pro Ile Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Ala Ile Arg
            340                 345                 350

Ile Pro Ile Thr Gly Ser Asn Pro Lys Ala Lys Arg Ile Glu Phe Arg
        355                 360                 365

Ala Pro Asp Pro Ser Gly Asn Pro Tyr Leu Gly Phe Ala Ala Met Met
    370                 375                 380

Leu Ala Gly Leu Asp Gly Ile Lys Asn Arg Ile Glu Pro Met Ala Pro
385                 390                 395                 400

Val Asp Lys Asp Leu Tyr Glu Leu Pro Pro Glu Glu Ala Ala Ala Ile
                405                 410                 415

Pro Gln Ala Pro Thr Ser Leu Glu Ala Ser Leu Ala Ala Leu Gln Glu
            420                 425                 430

Asp Asn Asp Phe Leu Thr Glu Gly Asp Val Phe Thr Glu Asp Leu Ile
        435                 440                 445

Glu Ala Tyr Ile Gln Leu Lys Tyr Asp Asn Glu Ile Thr Pro Ala Arg
    450                 455                 460

Leu Arg Pro Thr Pro Leu Glu Phe Glu Leu Tyr Tyr Asp Cys
465                 470                 475
```

<210> 127
<211> 2037

<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1737)
<223> gene glutaminsynthetase_2

<400> 127
catccccggc aaccgctggt gggacatgac cgaggagggc atcctgccga aggagcgcct 60

ggtgaacatc ggcgacatcg ccgccggccg tgccctgggc cgcgagaacg acgagcagat 120

cttctgctac tccatcggcg gcatgcccgt ggaggacgtc gcctgggcct gggacgtcta 180

ccacaacgcc ctggagaagg gcatcggcac caggctcaac ctgtgggaca cccccaccct 240

caagtaagcc cctcaagcaa gacacctgaa cacaacaatc taggagccct gacacctgtc 300

gtg tcc ttc cag tcc acc acc gac ctg atc gac ttc atg cgc gat gag 348
Val Ser Phe Gln Ser Thr Thr Asp Leu Ile Asp Phe Met Arg Asp Glu
1 5 10 15

ggg gtg gag tac ctg gac atc cgt ttc acc gat gtc ccc ggc aca gaa 396
Gly Val Glu Tyr Leu Asp Ile Arg Phe Thr Asp Val Pro Gly Thr Glu
20 25 30

cac gcg ctg acg gtt ccc gcc gcg gcg ctg acc gag gag acc gcg gcg 444
His Ala Leu Thr Val Pro Ala Ala Ala Leu Thr Glu Glu Thr Ala Ala
35 40 45

gag ggc ttc gcc ttc gac ggc tcg tcg atc gca ggt ttc acc tcg gtc 492
Glu Gly Phe Ala Phe Asp Gly Ser Ser Ile Ala Gly Phe Thr Ser Val
50 55 60

gac gag tcc gac atg acc ctc atg ccg gac gtc tcg acg gcc tac gtg 540
Asp Glu Ser Asp Met Thr Leu Met Pro Asp Val Ser Thr Ala Tyr Val
65 70 75 80

gac ccc ttc cgt cac cgg aag acg gtg aac atg cag ttc ttc gtc cac 588
Asp Pro Phe Arg His Arg Lys Thr Val Asn Met Gln Phe Phe Val His
85 90 95

gac ccc ttc acc cgc gag gcg ttc tcc cgc gat ccg cgc aac atc gcc 636
Asp Pro Phe Thr Arg Glu Ala Phe Ser Arg Asp Pro Arg Asn Ile Ala
100 105 110

cgc aag gcg gag gag tac atg cgt gcc tcc ggc atc gcc gac gag tgc 684
Arg Lys Ala Glu Glu Tyr Met Arg Ala Ser Gly Ile Ala Asp Glu Cys
115 120 125

tac atc ggc gcc gag gcc gag ttc ttc gtc ttc gac tcg gtc cgc tac 732
Tyr Ile Gly Ala Glu Ala Glu Phe Phe Val Phe Asp Ser Val Arg Tyr
130 135 140

tcc acc gac gtc cac cgt tcc ttc cac cag gtc gac tcc gac gag ggc 780
Ser Thr Asp Val His Arg Ser Phe His Gln Val Asp Ser Asp Glu Gly
145 150 155 160

```
tgg tgg aac tcc gac gcg gag acc atg atc gac ggt tcc ccg aac ctg        828
Trp Trp Asn Ser Asp Ala Glu Thr Met Ile Asp Gly Ser Pro Asn Leu
                165                 170                 175

ggc aac aag atc cgc gtc aac gac ggc tac ttc ccc gtc gcc ccc tac        876
Gly Asn Lys Ile Arg Val Asn Asp Gly Tyr Phe Pro Val Ala Pro Tyr
            180                 185                 190

gac aag acg atc ccg gtg cgc gac gag atc gcg cac aac ctc tcg cag        924
Asp Lys Thr Ile Pro Val Arg Asp Glu Ile Ala His Asn Leu Ser Gln
        195                 200                 205

gtc ggt ttc gag atc gag cgt ttc cac cac gag gtc tcc acg ggt ggc        972
Val Gly Phe Glu Ile Glu Arg Phe His His Glu Val Ser Thr Gly Gly
    210                 215                 220

atc cag gag gtg aac tac cgc ttc aac acc ctc ctg cac gcg gcg gat       1020
Ile Gln Glu Val Asn Tyr Arg Phe Asn Thr Leu Leu His Ala Ala Asp
225                 230                 235                 240

gac ctg cag aag ttc aag tac atc gtg aag aac acc gcc gac gcc cac       1068
Asp Leu Gln Lys Phe Lys Tyr Ile Val Lys Asn Thr Ala Asp Ala His
                245                 250                 255

ggc aag gtc gcc acc ttc atg ccg aag ccg ctt ctc gac gac ggc ggc       1116
Gly Lys Val Ala Thr Phe Met Pro Lys Pro Leu Leu Asp Asp Gly Gly
            260                 265                 270

tgc ggc atg cac gcc cac cag tcc ctg tgg aag gac ggc cga ccg ctg       1164
Cys Gly Met His Ala His Gln Ser Leu Trp Lys Asp Gly Arg Pro Leu
        275                 280                 285

ttc cac gac gag gaa ggt tac gcc ggc ctc tcc gag acc gcc cgc cac       1212
Phe His Asp Glu Glu Gly Tyr Ala Gly Leu Ser Glu Thr Ala Arg His
    290                 295                 300

tac atc ggt ggc ctg ctg gcc cac gcc ccg gcg gtc ctg gcg ttc acc       1260
Tyr Ile Gly Gly Leu Leu Ala His Ala Pro Ala Val Leu Ala Phe Thr
305                 310                 315                 320

aac ccg acg gtc aac tcc tac cgt cgc ctc tac tcc ggt ttc gag gcc       1308
Asn Pro Thr Val Asn Ser Tyr Arg Arg Leu Tyr Ser Gly Phe Glu Ala
                325                 330                 335

ccg gtg aac ctg gtg tac tcc cag cgc aac cgt tcc gcc gcg atc cgt       1356
Pro Val Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Ala Ile Arg
            340                 345                 350

atc ccg gtg acc ggc ccc tcc gcc gcc gcc aag cgc atc gag ttc cgc       1404
Ile Pro Val Thr Gly Pro Ser Ala Ala Ala Lys Arg Ile Glu Phe Arg
        355                 360                 365

gcc ccg gac ccc tcc ggc aac ccc tac ctc ggt ttc gcg gcc cag ctg       1452
Ala Pro Asp Pro Ser Gly Asn Pro Tyr Leu Gly Phe Ala Ala Gln Leu
    370                 375                 380

ctg gcc ggt ctg gac ggc atc aag aac cgc atc gag ccg ggc gac ccg       1500
Leu Ala Gly Leu Asp Gly Ile Lys Asn Arg Ile Glu Pro Gly Asp Pro
```

385 390 395 400

gtg gac aag gac ctc tac gag ctg gag ccg gag gag gcc gac aag gtg 1548
Val Asp Lys Asp Leu Tyr Glu Leu Glu Pro Glu Glu Ala Asp Lys Val
405 410 415

ccg cgc gtc ccg cac tcc ctg gag tcc tcg ctg tac gcc ctg gag aac 1596
Pro Arg Val Pro His Ser Leu Glu Ser Ser Leu Tyr Ala Leu Glu Asn
420 425 430

gac cac gag ttc ctc acc gag ggc gac gtg ttc acc gag gac ctc atc 1644
Asp His Glu Phe Leu Thr Glu Gly Asp Val Phe Thr Glu Asp Leu Ile
435 440 445

gag gcc tac atc cag ctg aag tac gac aac gag atc aac ccg atg cgc 1692
Glu Ala Tyr Ile Gln Leu Lys Tyr Asp Asn Glu Ile Asn Pro Met Arg
450 455 460

caa ggc ccg acg ccg aag gag ttc gag ctc tac ttc aac tgc tag 1737
Gln Gly Pro Thr Pro Lys Glu Phe Glu Leu Tyr Phe Asn Cys
465 470 475

gttcagcagg catgcggcgc agttacgtcc tcggggcgac agagcacacg gacctccggg 1797

gcatccggcg ggtgctcgca cgctaccgct acgacgcgcc gtgggtgctt ctcgacgccc 1857

gccccgtcct cgaggtctcc tggttcgggg agggcgcggt gtcgttctac gccaccactc 1917

ccccgctgcc tcccgacccc gccctggccc gcctcctctt cgacctcggg tcctgcggac 1977

tgctgctcgg ggtgtcgccg gggccgccgg acatcgtcat ctgcggtggt cacagtacgg 2037

<210> 128
<211> 478
<212> PRT
<213> Corynebacterium humireducens

<400> 128

Val Ser Phe Gln Ser Thr Thr Asp Leu Ile Asp Phe Met Arg Asp Glu
1 5 10 15

Gly Val Glu Tyr Leu Asp Ile Arg Phe Thr Asp Val Pro Gly Thr Glu
20 25 30

His Ala Leu Thr Val Pro Ala Ala Ala Leu Thr Glu Glu Thr Ala Ala
35 40 45

Glu Gly Phe Ala Phe Asp Gly Ser Ser Ile Ala Gly Phe Thr Ser Val
50 55 60

Asp Glu Ser Asp Met Thr Leu Met Pro Asp Val Ser Thr Ala Tyr Val
65 70 75 80

Asp Pro Phe Arg His Arg Lys Thr Val Asn Met Gln Phe Phe Val His
85 90 95

Asp Pro Phe Thr Arg Glu Ala Phe Ser Arg Asp Pro Arg Asn Ile Ala
100 105 110

Arg Lys Ala Glu Glu Tyr Met Arg Ala Ser Gly Ile Ala Asp Glu Cys
115 120 125

Tyr Ile Gly Ala Glu Ala Glu Phe Phe Val Phe Asp Ser Val Arg Tyr
130 135 140

Ser Thr Asp Val His Arg Ser Phe His Gln Val Asp Ser Asp Glu Gly
145 150 155 160

Trp Trp Asn Ser Asp Ala Glu Thr Met Ile Asp Gly Ser Pro Asn Leu
165 170 175

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

Asp Lys Thr Ile Pro Val Arg Asp Glu Ile Ala His Asn Leu Ser Gln
195 200 205

Val Gly Phe Glu Ile Glu Arg Phe His His Glu Val Ser Thr Gly Gly
210 215 220

Ile Gln Glu Val Asn Tyr Arg Phe Asn Thr Leu Leu His Ala Ala Asp
225 230 235 240

Asp Leu Gln Lys Phe Lys Tyr Ile Val Lys Asn Thr Ala Asp Ala His
245 250 255

Gly Lys Val Ala Thr Phe Met Pro Lys Pro Leu Leu Asp Asp Gly Gly
260 265 270

Cys Gly Met His Ala His Gln Ser Leu Trp Lys Asp Gly Arg Pro Leu
275 280 285

Phe His Asp Glu Glu Gly Tyr Ala Gly Leu Ser Glu Thr Ala Arg His
290 295 300

Tyr Ile Gly Gly Leu Leu Ala His Ala Pro Ala Val Leu Ala Phe Thr
305 310 315 320

Asn Pro Thr Val Asn Ser Tyr Arg Arg Leu Tyr Ser Gly Phe Glu Ala
325 330 335

Pro Val Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Ala Ile Arg
340 345 350

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

Ala Pro Asp Pro Ser Gly Asn Pro Tyr Leu Gly Phe Ala Ala Gln Leu
370 375 380

Leu Ala Gly Leu Asp Gly Ile Lys Asn Arg Ile Glu Pro Gly Asp Pro
385 390 395 400

Val Asp Lys Asp Leu Tyr Glu Leu Glu Pro Glu Glu Ala Asp Lys Val
405 410 415

Pro Arg Val Pro His Ser Leu Glu Ser Ser Leu Tyr Ala Leu Glu Asn
420 425 430

Asp His Glu Phe Leu Thr Glu Gly Asp Val Phe Thr Glu Asp Leu Ile
435 440 445

Glu Ala Tyr Ile Gln Leu Lys Tyr Asp Asn Glu Ile Asn Pro Met Arg
450 455 460

Gln Gly Pro Thr Pro Lys Glu Phe Glu Leu Tyr Phe Asn Cys
465 470 475

<210> 129
<211> 2241
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1941)
<223> gene glutamate synthase

<400> 129
ctggggttcc gcgtcgaagg acaccatcaa actggcccgc ctggccaccc agaccggcct 60

gttccccgtg tacgaggcgg agtacggcga gatcacctcg gtgaagaaga tccgccgccc 120

cgccccggtc gaggactacc tccgcctcca gcgccgctac gcgcacctgt tccggaagga 180

```
cgcggacccg tccgtcatcg agcggctcca ggcgctggcg gaccgcaaca tccgccgcta      240

caacctcatc gacgaagaga ccctcgacga gttcgtcagg ttcgaaggag acgacgcaca      300

gtg agt acc ggt aac cac gtc aac atc ggc atg ccc ttc gcc atc acc          348
Val Ser Thr Gly Asn His Val Asn Ile Gly Met Pro Phe Ala Ile Thr
1               5                  10                  15

ctg cag acc ggc tcc tcc ctg gcg aac aag acc ggc tcc tgg cgc agc         396
Leu Gln Thr Gly Ser Ser Leu Ala Asn Lys Thr Gly Ser Trp Arg Ser
            20                  25                  30

gag cgg ccc gtg tac gtc gac ctg ctg ccg ccc tgc aac aag gcg tgt         444
Glu Arg Pro Val Tyr Val Asp Leu Leu Pro Pro Cys Asn Lys Ala Cys
        35                  40                  45

ccc gcc ggc ggg aac atc cag ggc tgg ctg tac cac gcc gag gag ggc         492
Pro Ala Gly Gly Asn Ile Gln Gly Trp Leu Tyr His Ala Glu Glu Gly
    50                  55                  60

gac tac gag tcc gcc tgg cgc gag atc atg gtg gac aac ccg ctg ccc         540
Asp Tyr Glu Ser Ala Trp Arg Glu Ile Met Val Asp Asn Pro Leu Pro
65                  70                  75                  80

gcc gtc atg ggg cgt gtc tgc tac cac acc tgc cag acc gcc tgt aac         588
Ala Val Met Gly Arg Val Cys Tyr His Thr Cys Gln Thr Ala Cys Asn
                85                  90                  95

cgc gcg gag gtc gac gag gcc gtc ggc atc aac gcg gtc gag cgc ttc         636
Arg Ala Glu Val Asp Glu Ala Val Gly Ile Asn Ala Val Glu Arg Phe
            100                 105                 110

ctc ggg gac cgt gcc atc gag gag ggg tgg cag gtc gaa ccc gtc aag         684
Leu Gly Asp Arg Ala Ile Glu Glu Gly Trp Gln Val Glu Pro Val Lys
        115                 120                 125

gac ccc tcc ggc cgg agg gtc ctc gtc gtg ggt tcc ggc ccc tcc ggc         732
Asp Pro Ser Gly Arg Arg Val Leu Val Val Gly Ser Gly Pro Ser Gly
    130                 135                 140

ctg tcc gcg gcc tac cac ctc gcc cga ctc ggc cac gag gtg acg gtc         780
Leu Ser Ala Ala Tyr His Leu Ala Arg Leu Gly His Glu Val Thr Val
145                 150                 155                 160

cgc gac cgg ggt gag cgg ccg ggc ggc atg atg cgc tac ggc atc ccc         828
Arg Asp Arg Gly Glu Arg Pro Gly Gly Met Met Arg Tyr Gly Ile Pro
                165                 170                 175

tcc tac cgc ctg ccc cgc cac atc ctc gac gcc gag atc gcg cgc atc         876
Ser Tyr Arg Leu Pro Arg His Ile Leu Asp Ala Glu Ile Ala Arg Ile
            180                 185                 190

gcg gcc ctg ggc gtc acc ttc gag cag ggg gtc acc gtc acc gac gtc         924
Ala Ala Leu Gly Val Thr Phe Glu Gln Gly Val Thr Val Thr Asp Val
        195                 200                 205

gag tcc gaa ctc gag ctt ttc gac gcc gtc ttc acc gcc gtc ggt gcc         972
Glu Ser Glu Leu Glu Leu Phe Asp Ala Val Phe Thr Ala Val Gly Ala
```

```
        210                 215                 220

    cag ctg ggc cgc aac gtg gag gtg ccc gcc ggg tcg gcg gcg acc atc      1020
    Gln Leu Gly Arg Asn Val Glu Val Pro Ala Gly Ser Ala Ala Thr Ile
5   225                 230                 235                 240

    atg aac gcc gtt gac ctg ctg cgt gac acc gag gcc ggg gag gcg ccg      1068
    Met Asn Ala Val Asp Leu Leu Arg Asp Thr Glu Ala Gly Glu Ala Pro
                    245                 250                 255
10
    ctg ctc ggt cgt cgg gtc gtg gtc tac ggc ggc ggc aac aca gcc gtc      1116
    Leu Leu Gly Arg Arg Val Val Val Tyr Gly Gly Gly Asn Thr Ala Val
                260                 265                 270

15  gac gcc gcc cgc acc gcg cgt cgt ctc ggg gcg acc gag tcg gtc atc      1164
    Asp Ala Ala Arg Thr Ala Arg Arg Leu Gly Ala Thr Glu Ser Val Ile
            275                 280                 285

    ctc tac cgc cgc acc cgc gac cac atg agc gcc cac gac tcc gag gtc      1212
20  Leu Tyr Arg Arg Thr Arg Asp His Met Ser Ala His Asp Ser Glu Val
        290                 295                 300

    atg gag gcc gag gag gag ggc atc acc atg cgc tgg ctg tcc acc gtc      1260
    Met Glu Ala Glu Glu Glu Gly Ile Thr Met Arg Trp Leu Ser Thr Val
25  305                 310                 315                 320

    gac cac gtc gag gag ggc tcc atc agg atc gag aag atg gac atc gac      1308
    Asp His Val Glu Glu Gly Ser Ile Arg Ile Glu Lys Met Asp Ile Asp
                    325                 330                 335
30
    gcc gac ggc cac ctc acc ccg acc ggt gag tac gag gag ctc gcc gcc      1356
    Ala Asp Gly His Leu Thr Pro Thr Gly Glu Tyr Glu Glu Leu Ala Ala
                340                 345                 350

35  gac tcc ctc gtc atg gcg ctg ggc cag gag tcg gac ctc tcc ctg ctc      1404
    Asp Ser Leu Val Met Ala Leu Gly Gln Glu Ser Asp Leu Ser Leu Leu
            355                 360                 365

    gag ggc gtg gag ggg gtg gag atc tcc cgc ggc gtc gtc gcc gtc gac      1452
40  Glu Gly Val Glu Gly Val Glu Ile Ser Arg Gly Val Val Ala Val Asp
        370                 375                 380

    gag cag atg atg acc gga cgt gcg ggc gtc ttc gcc ggc ggc gac atg      1500
    Glu Gln Met Met Thr Gly Arg Ala Gly Val Phe Ala Gly Gly Asp Met
45  385                 390                 395                 400

    gtg ccg agc gag aag aac gtc acc gtc gcc atc ggc cac ggc aag aag      1548
    Val Pro Ser Glu Lys Asn Val Thr Val Ala Ile Gly His Gly Lys Lys
                    405                 410                 415
50
    gcg gcc cgg tac atc gac ggt tgg ctc cgt ggc gaa ccc tac gtg ccc      1596
    Ala Ala Arg Tyr Ile Asp Gly Trp Leu Arg Gly Glu Pro Tyr Val Pro
                420                 425                 430

55  gcc gtc aag cct gca gac gcg act ctc gac cgt atg gag acc tgg tac      1644
    Ala Val Lys Pro Ala Asp Ala Thr Leu Asp Arg Met Glu Thr Trp Tyr
            435                 440                 445

    tac tca gag gcc ccg cac cag gtg cgc gaa cgc ctc gag ggc gcc cgc      1692
```

```
Tyr Ser Glu Ala Pro His Gln Val Arg Glu Arg Leu Glu Gly Ala Arg
    450                 455                 460

cgc gcc tcc acc ttt gac gag gtc gtc cgg gga ctc gac gcc gac tcc      1740
Arg Ala Ser Thr Phe Asp Glu Val Val Arg Gly Leu Asp Ala Asp Ser
465                 470                 475                 480

gcc ctg ctc gag gca cgc cgc tgc atg tcg tgc ggc aac tgc ttc ggc      1788
Ala Leu Leu Glu Ala Arg Arg Cys Met Ser Cys Gly Asn Cys Phe Gly
                485                 490                 495

tgc gac aac tgc ttc ggc gtc tgc ccg gac aac gcg gtc acc aaa ttg      1836
Cys Asp Asn Cys Phe Gly Val Cys Pro Asp Asn Ala Val Thr Lys Leu
            500                 505                 510

gcg ccg ggt gag tac gag ttc aag tac gac tac tgc aag ggc tgc ggc      1884
Ala Pro Gly Glu Tyr Glu Phe Lys Tyr Asp Tyr Cys Lys Gly Cys Gly
        515                 520                 525

atc tgc gcg gag gag tgc ccg tgc ggc gcg atc tcc atg att ccc gag      1932
Ile Cys Ala Glu Glu Cys Pro Cys Gly Ala Ile Ser Met Ile Pro Glu
    530                 535                 540

gag aac tga ggagaactga ccgcccgcaa caagttagag tatgggcacc              1981
Glu Asn
545

aacgtcgtcc cctgaccaga aggatcccca tgcgccgcac cctcatcgcc ctcggcaccg     2041

ccaccgccct caccctgggg gcggtcccgg ccgcccacgc ccagcccgcg aacgccgtca     2101

ccgcccagat cgaggagctg ccggccgaca tgcgggcagg ctcctccggc gcggagaagc     2161

tctcctccgc ctccaccgag gccgagaagc aggagggtgc cctgctgctg ggacgcgact     2221

ggctgctcgg tttcgccgcg                                                2241


<210>  130
<211>  546
<212>  PRT
<213>  Corynebacterium humireducens

<400>  130

Val Ser Thr Gly Asn His Val Asn Ile Gly Met Pro Phe Ala Ile Thr
1               5                   10                  15

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

Glu Arg Pro Val Tyr Val Asp Leu Leu Pro Pro Cys Asn Lys Ala Cys
        35                  40                  45

Pro Ala Gly Gly Asn Ile Gln Gly Trp Leu Tyr His Ala Glu Glu Gly
    50                  55                  60
```

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

Ala Val Met Gly Arg Val Cys Tyr His Thr Cys Gln Thr Ala Cys Asn
85 90 95

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

Leu Gly Asp Arg Ala Ile Glu Glu Gly Trp Gln Val Glu Pro Val Lys
115 120 125

Asp Pro Ser Gly Arg Arg Val Leu Val Val Gly Ser Gly Pro Ser Gly
130 135 140

Leu Ser Ala Ala Tyr His Leu Ala Arg Leu Gly His Glu Val Thr Val
145 150 155 160

Arg Asp Arg Gly Glu Arg Pro Gly Gly Met Met Arg Tyr Gly Ile Pro
165 170 175

Ser Tyr Arg Leu Pro Arg His Ile Leu Asp Ala Glu Ile Ala Arg Ile
180 185 190

Ala Ala Leu Gly Val Thr Phe Glu Gln Gly Val Thr Val Thr Asp Val
195 200 205

Glu Ser Glu Leu Glu Leu Phe Asp Ala Val Phe Thr Ala Val Gly Ala
210 215 220

Gln Leu Gly Arg Asn Val Glu Val Pro Ala Gly Ser Ala Ala Thr Ile
225 230 235 240

Met Asn Ala Val Asp Leu Leu Arg Asp Thr Glu Ala Gly Glu Ala Pro
245 250 255

Leu Leu Gly Arg Arg Val Val Val Tyr Gly Gly Gly Asn Thr Ala Val
260 265 270

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

Leu Tyr Arg Arg Thr Arg Asp His Met Ser Ala His Asp Ser Glu Val

290 295 300

Met Glu Ala Glu Glu Glu Gly Ile Thr Met Arg Trp Leu Ser Thr Val
305 310 315 320

Asp His Val Glu Glu Gly Ser Ile Arg Ile Glu Lys Met Asp Ile Asp
325 330 335

Ala Asp Gly His Leu Thr Pro Thr Gly Glu Tyr Glu Glu Leu Ala Ala
340 345 350

Asp Ser Leu Val Met Ala Leu Gly Gln Glu Ser Asp Leu Ser Leu Leu
355 360 365

Glu Gly Val Glu Gly Val Glu Ile Ser Arg Gly Val Val Ala Val Asp
370 375 380

Glu Gln Met Met Thr Gly Arg Ala Gly Val Phe Ala Gly Gly Asp Met
385 390 395 400

Val Pro Ser Glu Lys Asn Val Thr Val Ala Ile Gly His Gly Lys Lys
405 410 415

Ala Ala Arg Tyr Ile Asp Gly Trp Leu Arg Gly Glu Pro Tyr Val Pro
420 425 430

Ala Val Lys Pro Ala Asp Ala Thr Leu Asp Arg Met Glu Thr Trp Tyr
435 440 445

Tyr Ser Glu Ala Pro His Gln Val Arg Glu Arg Leu Glu Gly Ala Arg
450 455 460

Arg Ala Ser Thr Phe Asp Glu Val Val Arg Gly Leu Asp Ala Asp Ser
465 470 475 480

Ala Leu Leu Glu Ala Arg Arg Cys Met Ser Cys Gly Asn Cys Phe Gly
485 490 495

Cys Asp Asn Cys Phe Gly Val Cys Pro Asp Asn Ala Val Thr Lys Leu
500 505 510

Ala Pro Gly Glu Tyr Glu Phe Lys Tyr Asp Tyr Cys Lys Gly Cys Gly
515 520 525

Ile Cys Ala Glu Glu Cys Pro Cys Gly Ala Ile Ser Met Ile Pro Glu
530 535 540

Glu Asn
545

<210> 131
<211> 2817
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(2517)
<223> gene isocitrate dehydrogenase

<400> 131
cgccgacgta gtgccagccc gcgtcgaggg cgggctgcaa cgccttgacg gactcctcga 60

cggtcgcgcg cacctcctgc aggagcacca cgtcagccgg ggactgctcc agccaggcca 120

gcatgcccgg attgtcctcg ttgcgctgct tgacggcggc gcggattcca ttgacgttga 180

cggaggtgat ggtcagactc ataggaacca ccatatcgcc gttggtggca gggcccctgc 240

cccgccgggt atccttagcc gttgacactg ccgagattga agaaagcgtt agggagttac 300

atg gca aag atc atc tgg acc cgc acc gac gag gcc ccg ctg ctc gcg 348
Met Ala Lys Ile Ile Trp Thr Arg Thr Asp Glu Ala Pro Leu Leu Ala
1 5 10 15

acc tat tcg ttc aag cct gtt gtt gag gcc ttc gcc gcc acc gcg ggt 396
Thr Tyr Ser Phe Lys Pro Val Val Glu Ala Phe Ala Ala Thr Ala Gly
20 25 30

atc gat gtc gag acc cgc gac atc tcc ctg gcc ggc cgc atc ctg gcc 444
Ile Asp Val Glu Thr Arg Asp Ile Ser Leu Ala Gly Arg Ile Leu Ala
35 40 45

cag ttc ccg gac cgc ctc acc gag gag cag cga gtc gct gac gcc ctc 492
Gln Phe Pro Asp Arg Leu Thr Glu Glu Gln Arg Val Ala Asp Ala Leu
50 55 60

acc gag ctc ggc gac ctg gcc aag acc ccg gaa gcc aac atc atc aag 540
Thr Glu Leu Gly Asp Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys
65 70 75 80

ctc ccg aac atc tcg gcg tcc gtc ccg cag ctc aag gca gcc atc aag 588
Leu Pro Asn Ile Ser Ala Ser Val Pro Gln Leu Lys Ala Ala Ile Lys
85 90 95

gag ctg cag gac cag gga tac gac ctc ccc gac tac gtc gac tcc ccg 636
Glu Leu Gln Asp Gln Gly Tyr Asp Leu Pro Asp Tyr Val Asp Ser Pro
100 105 110

gag acc gac gag gag aag gac gcc cgc aag cgc tac gac gta gta aag 684

```
Glu Thr Asp Glu Glu Lys Asp Ala Arg Lys Arg Tyr Asp Val Val Lys
        115                 120                 125

ggt tcc gct gtg aac ccg gta ctc cgt gag ggc aac tcc gac cgt cgt      732
Gly Ser Ala Val Asn Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg
    130                 135                 140

gcc ccg gag gcc gtg aag aac ttc gtc cgc aag aac ccg cac cgc atg      780
Ala Pro Glu Ala Val Lys Asn Phe Val Arg Lys Asn Pro His Arg Met
145                 150                 155                 160

ggt gag tgg tcc gcc gac tcc aag acc aac gtc gcc acc atg gac tcc      828
Gly Glu Trp Ser Ala Asp Ser Lys Thr Asn Val Ala Thr Met Asp Ser
                165                 170                 175

gac gac ttc cgt cac aac gag cag tcc gtc atc ctc ccg gcc gag gac      876
Asp Asp Phe Arg His Asn Glu Gln Ser Val Ile Leu Pro Ala Glu Asp
            180                 185                 190

acc ctc tcc ttc gtc cac gtc gcc acc gac ggc acc gag acc aag ctc      924
Thr Leu Ser Phe Val His Val Ala Thr Asp Gly Thr Glu Thr Lys Leu
        195                 200                 205

cgc gac gac ctc aag gtc ctc gag ggc gag gtc gtc gac ggc acc gtc      972
Arg Asp Asp Leu Lys Val Leu Glu Gly Glu Val Val Asp Gly Thr Val
    210                 215                 220

atg cgc gcc gcc gcc ctg cag gag ttc ctg gcc gag cag gtc aag cgc     1020
Met Arg Ala Ala Ala Leu Gln Glu Phe Leu Ala Glu Gln Val Lys Arg
225                 230                 235                 240

gcc cag gac gag ggc atc ctg ttc tcc gtc cac ctc aag gcc acc atg     1068
Ala Gln Asp Glu Gly Ile Leu Phe Ser Val His Leu Lys Ala Thr Met
                245                 250                 255

atg aag gtc tcc gac ccg atc atc ttc ggc tac gtc gtc cgc gcc ttc     1116
Met Lys Val Ser Asp Pro Ile Ile Phe Gly Tyr Val Val Arg Ala Phe
            260                 265                 270

ttc gcc gac gtc tac gag aag tac ggc gag gag ctg ctg gcc gcc ggt     1164
Phe Ala Asp Val Tyr Glu Lys Tyr Gly Glu Glu Leu Leu Ala Ala Gly
        275                 280                 285

ctc gac ggc gag aac ggc ctc ggc gcc atc ttc tcc gga ctc gag gaa     1212
Leu Asp Gly Glu Asn Gly Leu Gly Ala Ile Phe Ser Gly Leu Glu Glu
    290                 295                 300

ctg gag aac ggc gag gag atc cgc cgt gcc ttc gac gag gcc ctc gag     1260
Leu Glu Asn Gly Glu Glu Ile Arg Arg Ala Phe Asp Glu Ala Leu Glu
305                 310                 315                 320

aac ggc cct gac ctg gcg atg gtg aac tcc gac aag ggc atc acc aac     1308
Asn Gly Pro Asp Leu Ala Met Val Asn Ser Asp Lys Gly Ile Thr Asn
                325                 330                 335

ctg cac gtc ccg tcc gac gtc atc gtc gac gcc tcc atg ccc gcc atg     1356
Leu His Val Pro Ser Asp Val Ile Val Asp Ala Ser Met Pro Ala Met
            340                 345                 350
```

```
atc cgc acc tcc ggc cag atg tgg aac aag gac gac aag acc cag gac      1404
Ile Arg Thr Ser Gly Gln Met Trp Asn Lys Asp Asp Lys Thr Gln Asp
        355                 360                 365

acc ctg gcc gtc atc ccg gac tcc tcc tac gcc ggc gtc ttc cag acc      1452
Thr Leu Ala Val Ile Pro Asp Ser Ser Tyr Ala Gly Val Phe Gln Thr
    370                 375                 380

gtc atc gac gac tgc aag gcc aac ggc gcc ttc gac ccg acc acc atg      1500
Val Ile Asp Asp Cys Lys Ala Asn Gly Ala Phe Asp Pro Thr Thr Met
385                 390                 395                 400

ggc acc gtc ccg aac gtc ggc ctc atg gcc cag aag gcc gag gag tac      1548
Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln Lys Ala Glu Glu Tyr
                405                 410                 415

ggc tcc cac gac aag acc ttc cgc atc gcc gcg gac ggc aag gtc gag      1596
Gly Ser His Asp Lys Thr Phe Arg Ile Ala Ala Asp Gly Lys Val Glu
            420                 425                 430

gtc cgc aac tcc gcc ggt gac gtc ctg ctc gag cac gag gtc tcc gag      1644
Val Arg Asn Ser Ala Gly Asp Val Leu Leu Glu His Glu Val Ser Glu
        435                 440                 445

ggc gac atc tgg cgc gcc tgc cag acc aag gac gcc ccg atc cag gac      1692
Gly Asp Ile Trp Arg Ala Cys Gln Thr Lys Asp Ala Pro Ile Gln Asp
    450                 455                 460

tgg gtc aag ctg gcc gtc gac cgc gcc cgc atc tcc ggc atg ccg gcc      1740
Trp Val Lys Leu Ala Val Asp Arg Ala Arg Ile Ser Gly Met Pro Ala
465                 470                 475                 480

gtc ttc tgg ctg gac ccg gag cgc gcc cac gac cgc aac ctc acc acc      1788
Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp Arg Asn Leu Thr Thr
                485                 490                 495

ctg gtg gag aag tac ctg gcc gac cac gac acc gag ggc ctg gac atc      1836
Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile
            500                 505                 510

cgc atc ctc tcc ccg gtc gag gcg acc cag ctg tcc gtc gac cgc atc      1884
Arg Ile Leu Ser Pro Val Glu Ala Thr Gln Leu Ser Val Asp Arg Ile
        515                 520                 525

cgc cgc ggc gag gac acc atc tcc gtg acc ggt aac gtc ctg cgt gac      1932
Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp
    530                 535                 540

tac aac acc gac ctc ttc ccg atc ctc gag ctg ggc acc tcc gcc aag      1980
Tyr Asn Thr Asp Leu Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys
545                 550                 555                 560

atg ctc tcc gtc gtg ccg ctg atg gcc ggt ggc ggc ctc ttc gag acc      2028
Met Leu Ser Val Val Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr
                565                 570                 575

ggt gcc ggt ggc tcc gcc ccg aag cac gtc cag cag gtc gtc gag gag      2076
Gly Ala Gly Gly Ser Ala Pro Lys His Val Gln Gln Val Val Glu Glu
            580                 585                 590
```

```
aac cac ctg cgc tgg gac tcc ctc ggt gag ttc ctc gcc ctg gcc gag      2124
Asn His Leu Arg Trp Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu
        595                 600                 605

tcc ctg cgc cac gtc gcc cgc acc cag gac aac gcg aag gcc gcc gtc      2172
Ser Leu Arg His Val Ala Arg Thr Gln Asp Asn Ala Lys Ala Ala Val
    610                 615                 620

ctg gcc gac gcc ctg gac aag gcc acc gag aag gtc ctg tcc gag ggc      2220
Leu Ala Asp Ala Leu Asp Lys Ala Thr Glu Lys Val Leu Ser Glu Gly
625                 630                 635                 640

aag tcc ccg tcc cgc aag gtc ggc gag atc gac aac cgt ggc tcc cac      2268
Lys Ser Pro Ser Arg Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His
                645                 650                 655

ttc tac ctc gcg tcc tac tgg gcc gag gcc ctg gcc gca cag tcc gac      2316
Phe Tyr Leu Ala Ser Tyr Trp Ala Glu Ala Leu Ala Ala Gln Ser Asp
            660                 665                 670

gac gcc gag ctg gcc gcg acc ttc cag ccg gtc gcc gag gcc ctg gcc      2364
Asp Ala Glu Leu Ala Ala Thr Phe Gln Pro Val Ala Glu Ala Leu Ala
        675                 680                 685

gcc gac gcc gcg acc atc gac cag gag ctc atc gac aac cag ggt tcc      2412
Ala Asp Ala Ala Thr Ile Asp Gln Glu Leu Ile Asp Asn Gln Gly Ser
    690                 695                 700

gcc gtg gac ctc ggc ggc tac tac gcc ccg tcc gat gag aag acc tcc      2460
Ala Val Asp Leu Gly Gly Tyr Tyr Ala Pro Ser Asp Glu Lys Thr Ser
705                 710                 715                 720

gac gtg atg cgt ccg tcc gcg aag ttc aac gag atc atc gac ggt ctg      2508
Asp Val Met Arg Pro Ser Ala Lys Phe Asn Glu Ile Ile Asp Gly Leu
                725                 730                 735

aag aag taa cccccgcttt ccgacgccgc cctgccccgc caccggggca              2557
Lys Lys

gggcggcgtc gcctttgggc agggccccgg acgaaccact tggtctaccg tcccctttatt   2617

tttattcatg cgccctgaac tgcggagaca gggtttggac agacagctcg gtttacgtcg    2677

aaaagcggtg cgccgtactc ttctcccatg acccgatacg acaactccgc agcagaccag    2737

tgggacttcg agacccgctc catccacgcc ggccagaacc cggaccccgc gaccggttcc    2797

cgtaaccagc cgatccacct                                               2817
```

<210> 132
<211> 738
<212> PRT
<213> Corynebacterium humireducens

<400> 132

```
Met Ala Lys Ile Ile Trp Thr Arg Thr Asp Glu Ala Pro Leu Leu Ala
1               5                  10                  15

Thr Tyr Ser Phe Lys Pro Val Val Glu Ala Phe Ala Ala Thr Ala Gly
            20                  25                  30

Ile Asp Val Glu Thr Arg Asp Ile Ser Leu Ala Gly Arg Ile Leu Ala
        35                  40                  45

Gln Phe Pro Asp Arg Leu Thr Glu Glu Gln Arg Val Ala Asp Ala Leu
    50                  55                  60

Thr Glu Leu Gly Asp Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys
65                  70                  75                  80

Leu Pro Asn Ile Ser Ala Ser Val Pro Gln Leu Lys Ala Ala Ile Lys
                85                  90                  95

Glu Leu Gln Asp Gln Gly Tyr Asp Leu Pro Asp Tyr Val Asp Ser Pro
            100                 105                 110

Glu Thr Asp Glu Glu Lys Asp Ala Arg Lys Arg Tyr Asp Val Val Lys
        115                 120                 125

Gly Ser Ala Val Asn Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg
    130                 135                 140

Ala Pro Glu Ala Val Lys Asn Phe Val Arg Lys Asn Pro His Arg Met
145                 150                 155                 160

Gly Glu Trp Ser Ala Asp Ser Lys Thr Asn Val Ala Thr Met Asp Ser
                165                 170                 175

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

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

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

Met Arg Ala Ala Ala Leu Gln Glu Phe Leu Ala Glu Gln Val Lys Arg
225                 230                 235                 240
```

```
Ala Gln Asp Glu Gly Ile Leu Phe Ser Val His Leu Lys Ala Thr Met
                245                 250                 255

Met Lys Val Ser Asp Pro Ile Ile Phe Gly Tyr Val Val Arg Ala Phe
            260                 265                 270

Phe Ala Asp Val Tyr Glu Lys Tyr Gly Glu Glu Leu Leu Ala Ala Gly
        275                 280                 285

Leu Asp Gly Glu Asn Gly Leu Gly Ala Ile Phe Ser Gly Leu Glu Glu
    290                 295                 300

Leu Glu Asn Gly Glu Glu Ile Arg Arg Ala Phe Asp Glu Ala Leu Glu
305                 310                 315                 320

Asn Gly Pro Asp Leu Ala Met Val Asn Ser Asp Lys Gly Ile Thr Asn
                325                 330                 335

Leu His Val Pro Ser Asp Val Ile Val Asp Ala Ser Met Pro Ala Met
            340                 345                 350

Ile Arg Thr Ser Gly Gln Met Trp Asn Lys Asp Asp Lys Thr Gln Asp
        355                 360                 365

Thr Leu Ala Val Ile Pro Asp Ser Ser Tyr Ala Gly Val Phe Gln Thr
    370                 375                 380

Val Ile Asp Asp Cys Lys Ala Asn Gly Ala Phe Asp Pro Thr Thr Met
385                 390                 395                 400

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

Gly Ser His Asp Lys Thr Phe Arg Ile Ala Ala Asp Gly Lys Val Glu
            420                 425                 430

Val Arg Asn Ser Ala Gly Asp Val Leu Leu Glu His Glu Val Ser Glu
        435                 440                 445

Gly Asp Ile Trp Arg Ala Cys Gln Thr Lys Asp Ala Pro Ile Gln Asp
    450                 455                 460

Trp Val Lys Leu Ala Val Asp Arg Ala Arg Ile Ser Gly Met Pro Ala
465                 470                 475                 480
```

Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp Arg Asn Leu Thr Thr
485 490 495

Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile
500 505 510

Arg Ile Leu Ser Pro Val Glu Ala Thr Gln Leu Ser Val Asp Arg Ile
515 520 525

Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp
530 535 540

Tyr Asn Thr Asp Leu Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys
545 550 555 560

Met Leu Ser Val Val Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr
565 570 575

Gly Ala Gly Gly Ser Ala Pro Lys His Val Gln Gln Val Val Glu Glu
580 585 590

Asn His Leu Arg Trp Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu
595 600 605

Ser Leu Arg His Val Ala Arg Thr Gln Asp Asn Ala Lys Ala Ala Val
610 615 620

Leu Ala Asp Ala Leu Asp Lys Ala Thr Glu Lys Val Leu Ser Glu Gly
625 630 635 640

Lys Ser Pro Ser Arg Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His
645 650 655

Phe Tyr Leu Ala Ser Tyr Trp Ala Glu Ala Leu Ala Ala Gln Ser Asp
660 665 670

Asp Ala Glu Leu Ala Ala Thr Phe Gln Pro Val Ala Glu Ala Leu Ala
675 680 685

Ala Asp Ala Ala Thr Ile Asp Gln Glu Leu Ile Asp Asn Gln Gly Ser
690 695 700

Ala Val Asp Leu Gly Gly Tyr Tyr Ala Pro Ser Asp Glu Lys Thr Ser

705 710 715 720

Asp Val Met Arg Pro Ser Ala Lys Phe Asn Glu Ile Ile Asp Gly Leu
725 730 735

Lys Lys

<210> 133
<211> 3378
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(3078)
<223> gene aconitathydrase

<400> 133
aggtcatcgg tgtcgatgcc ggcgggaatc atcgtggtgc ggcttctttc gcatggggcg 60

gcgtgcggac accgctattt ctatcctccg cgggtgtggc gggggtggcg acgcgccgga 120

cacacagcga aaagccacaa acaagacgct cgtactgtta gaattgcagc ggtcgttggt 180

ccgaatccct acacttgggg acgtaccacc gcgttctgcc ggtgcacgcc taccttgacc 240

ggggtagacg ggtgcgggta acgaacattc cagttcaatg aagaggaaat ggagctccct 300

gtg acc gaa agc aag aac tcc ttc aac gcc aag cgc acc ctc gag gtc 348
Val Thr Glu Ser Lys Asn Ser Phe Asn Ala Lys Arg Thr Leu Glu Val
1 5 10 15

ggc gag aag tcc tac gac tac ttc gcc ctc gac gcc gtg ccg ggc atg 396
Gly Glu Lys Ser Tyr Asp Tyr Phe Ala Leu Asp Ala Val Pro Gly Met
20 25 30

gag aag ctg ccg tac tcc ctg aag gtt ctc ggc gag aac ctt ctg cgt 444
Glu Lys Leu Pro Tyr Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg
35 40 45

acc gag gac ggc gca aac atc acc acc gag cac atc gag gca atc gcc 492
Thr Glu Asp Gly Ala Asn Ile Thr Thr Glu His Ile Glu Ala Ile Ala
50 55 60

aac tgg gat ccg aag gct gag ccc tcc atc gag atc cag ttc acc ccg 540
Asn Trp Asp Pro Lys Ala Glu Pro Ser Ile Glu Ile Gln Phe Thr Pro
65 70 75 80

gca cgt gtc ctc atg cag gac ttc acc ggt gtc gcc tgt gca gtc gac 588
Ala Arg Val Leu Met Gln Asp Phe Thr Gly Val Ala Cys Ala Val Asp
85 90 95

ctg gcc acc atg cgc gag gcc gtg aag acc ctg ggc ggc gac ccg gac 636
Leu Ala Thr Met Arg Glu Ala Val Lys Thr Leu Gly Gly Asp Pro Asp

```
                100                 105                 110

gac gtc aac ccg ctg aac ccg gcc gag atg gtc atc gac cac tcc gtc        684
Asp Val Asn Pro Leu Asn Pro Ala Glu Met Val Ile Asp His Ser Val
        115                 120                 125

atc gtc gag gca ttc ggt acc tcc gcc gct ctg gag aag aac gtc gag        732
Ile Val Glu Ala Phe Gly Thr Ser Ala Ala Leu Glu Lys Asn Val Glu
    130                 135                 140

atc gag tac cag cgc aac gag gag cgc tac cag ttc ctc cgc tgg ggt        780
Ile Glu Tyr Gln Arg Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly
145                 150                 155                 160

gcc gag aac ttc tcc aac ttc cgc gtc gtt ccc ccg gga acc ggc atc        828
Ala Glu Asn Phe Ser Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile
                165                 170                 175

gtc cac cag gtc aac atc gag tac ctg tcc cgc gtt gtc ttc gac aac        876
Val His Gln Val Asn Ile Glu Tyr Leu Ser Arg Val Val Phe Asp Asn
            180                 185                 190

aac ggc ctc gcc tac ccg gac acc tgc atc ggc acc gac tcc cac acc        924
Asn Gly Leu Ala Tyr Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr
        195                 200                 205

acc atg gag aac ggc ctg gga atc ctg ggc tgg ggc gtc ggc ggc atc        972
Thr Met Glu Asn Gly Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile
    210                 215                 220

gag gcc gag gct gcc atg ctg ggc cag ccg gtc tcc atg ctc atc ccg       1020
Glu Ala Glu Ala Ala Met Leu Gly Gln Pro Val Ser Met Leu Ile Pro
225                 230                 235                 240

cgc gtc gtc ggc ttc aag ctg acc ggt gag atc ccg gcc ggc gtc acc       1068
Arg Val Val Gly Phe Lys Leu Thr Gly Glu Ile Pro Ala Gly Val Thr
                245                 250                 255

gcc acc gac gtg gtc ctc acc atc acc gag atg ctg cgt aac cac ggc       1116
Ala Thr Asp Val Val Leu Thr Ile Thr Glu Met Leu Arg Asn His Gly
            260                 265                 270

gtc gtc cag aag ttc gtc gag ttc tac ggc aac ggc gtc aag tcc gtc       1164
Val Val Gln Lys Phe Val Glu Phe Tyr Gly Asn Gly Val Lys Ser Val
        275                 280                 285

ccg ctg gcg aac cgc gcc acc atc ggc aac atg tcc ccg gag ttc ggc       1212
Pro Leu Ala Asn Arg Ala Thr Ile Gly Asn Met Ser Pro Glu Phe Gly
    290                 295                 300

tcc acc tgt gcc atg ttc ccg atc gac gag gag acc atc aag tac ctc       1260
Ser Thr Cys Ala Met Phe Pro Ile Asp Glu Glu Thr Ile Lys Tyr Leu
305                 310                 315                 320

gag ctc acc ggc cgc tcc gag gag gac atc gcc cgc gtc gag gca tac       1308
Glu Leu Thr Gly Arg Ser Glu Glu Asp Ile Ala Arg Val Glu Ala Tyr
                325                 330                 335

gcc aag gct cag ggc atg tgg ctc tac gag gac gcc ccg gag gcc gag       1356
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Ala Lys Ala Gln Gly Met Trp Leu Tyr Glu Asp Ala Pro Glu Ala Glu
            340                 345                 350

tac tcc gag tac ctc gag ctg gac ctc tcc acc gtc gtc ccg tcc atc      1404
Tyr Ser Glu Tyr Leu Glu Leu Asp Leu Ser Thr Val Val Pro Ser Ile
        355                 360                 365

gcc ggc ccg aag cgc ccg cag gac cgc atc ctc ctc tcc gag gcc aag      1452
Ala Gly Pro Lys Arg Pro Gln Asp Arg Ile Leu Leu Ser Glu Ala Lys
    370                 375                 380

gca cag ttc cgc aag gac ctg ccg acc tac gcc tcc gac gag gtc gct      1500
Ala Gln Phe Arg Lys Asp Leu Pro Thr Tyr Ala Ser Asp Glu Val Ala
385                 390                 395                 400

gag ccg gtc cgc gcc acc aag gcc gtc ggc gac gac tac aac cag tcc      1548
Glu Pro Val Arg Ala Thr Lys Ala Val Gly Asp Asp Tyr Asn Gln Ser
                405                 410                 415

ttc ccg ggc aac ggc gag tcc gct gcc gac tcc gcc gag ggc cgc gcc      1596
Phe Pro Gly Asn Gly Glu Ser Ala Ala Asp Ser Ala Glu Gly Arg Ala
            420                 425                 430

tcc aag ccg gtc atc gtc gag tcc ccg cag ggc ggc gag tac acc ctc      1644
Ser Lys Pro Val Ile Val Glu Ser Pro Gln Gly Gly Glu Tyr Thr Leu
        435                 440                 445

gac cac ggc atg gtg gcc atc gcc tcc atc acc tcc tgc acc aac acc      1692
Asp His Gly Met Val Ala Ile Ala Ser Ile Thr Ser Cys Thr Asn Thr
    450                 455                 460

tcc aac ccg tcc gtg ctg gtc gca gcc ggc ctg ctg gcc cgc aag gcc      1740
Ser Asn Pro Ser Val Leu Val Ala Ala Gly Leu Leu Ala Arg Lys Ala
465                 470                 475                 480

aac gag ctg ggc ctg aag tcc aag ccg tgg gtc aag acc atc tgc gcc      1788
Asn Glu Leu Gly Leu Lys Ser Lys Pro Trp Val Lys Thr Ile Cys Ala
                485                 490                 495

ccg ggc tcc cag gtc gtc gac ggt tac ttc aag cgc gcc gac ctc tgg      1836
Pro Gly Ser Gln Val Val Asp Gly Tyr Phe Lys Arg Ala Asp Leu Trp
            500                 505                 510

aag gat ctg gag gcc ctg ggc ttc tac ctc tcc ggc ttc ggc tgc acc      1884
Lys Asp Leu Glu Ala Leu Gly Phe Tyr Leu Ser Gly Phe Gly Cys Thr
        515                 520                 525

tcc tgc atc ggc aac tcc ggt ccg ctc ccg gct gag gtc tcc tcc gcc      1932
Ser Cys Ile Gly Asn Ser Gly Pro Leu Pro Ala Glu Val Ser Ser Ala
    530                 535                 540

atc aac gag cac gac ctg gcc gcc acc gca gtc ctg tcc ggc aac cgt      1980
Ile Asn Glu His Asp Leu Ala Ala Thr Ala Val Leu Ser Gly Asn Arg
545                 550                 555                 560

aac ttc gag ggt cgt atc tcc ccc gac gtc aag atg aac tac ctg gcc      2028
Asn Phe Glu Gly Arg Ile Ser Pro Asp Val Lys Met Asn Tyr Leu Ala
                565                 570                 575
```

```
tcc ccg ccg ctg gtc atc gcc tac gcc atc gcc ggc acc atg gac ttc      2076
Ser Pro Pro Leu Val Ile Ala Tyr Ala Ile Ala Gly Thr Met Asp Phe
            580                 585                 590

gac ttc gag acc gat gcc ctg ggt cag gac aag gac ggc aac gac gtc      2124
Asp Phe Glu Thr Asp Ala Leu Gly Gln Asp Lys Asp Gly Asn Asp Val
        595                 600                 605

ttc ctg aag gac atc tgg ccc tcc acc gag gag atc gag gag acc atc      2172
Phe Leu Lys Asp Ile Trp Pro Ser Thr Glu Glu Ile Glu Glu Thr Ile
    610                 615                 620

gcg gcc tcc atc tcc cgc gag ctg tac gag gcc gac tac gct gac gtc      2220
Ala Ala Ser Ile Ser Arg Glu Leu Tyr Glu Ala Asp Tyr Ala Asp Val
625                 630                 635                 640

ttc aag ggc gac aag cag tgg cag gag ctc gac atc ccg acc ggc aag      2268
Phe Lys Gly Asp Lys Gln Trp Gln Glu Leu Asp Ile Pro Thr Gly Lys
                645                 650                 655

acc ttc gag tgg gac gag aac tcc tcc tac atc cgt aag gca ccg tac      2316
Thr Phe Glu Trp Asp Glu Asn Ser Ser Tyr Ile Arg Lys Ala Pro Tyr
            660                 665                 670

ttc gac ggc atg ccg ctc gag ccg cag ccg gtc gag gac atc aag ggc      2364
Phe Asp Gly Met Pro Leu Glu Pro Gln Pro Val Glu Asp Ile Lys Gly
        675                 680                 685

gcc cgc gtc ctc gcc aag ctc ggc gac tcc gtg acc acc gac cac atc      2412
Ala Arg Val Leu Ala Lys Leu Gly Asp Ser Val Thr Thr Asp His Ile
    690                 695                 700

tcc ccg gcc tcc tcc atc aag ccg ggc acc ccg gca gcc cag tac ctg      2460
Ser Pro Ala Ser Ser Ile Lys Pro Gly Thr Pro Ala Ala Gln Tyr Leu
705                 710                 715                 720

gac tcc atg ggt gtc gag cgc aag gac tac aac tcc ctg ggc tcc cgt      2508
Asp Ser Met Gly Val Glu Arg Lys Asp Tyr Asn Ser Leu Gly Ser Arg
                725                 730                 735

cgt ggt aac cac gag gtc atg gtc cgc ggt acc ttc gcg aac atc cgc      2556
Arg Gly Asn His Glu Val Met Val Arg Gly Thr Phe Ala Asn Ile Arg
            740                 745                 750

ctg gcc aac cag ctg gtc gac gtc acc ggt ggc tac acc cgt gac ttc      2604
Leu Ala Asn Gln Leu Val Asp Val Thr Gly Gly Tyr Thr Arg Asp Phe
        755                 760                 765

acc cag gag ggt ggc ccg cag gcc tac atc tac gac gcc gcc atg aac      2652
Thr Gln Glu Gly Gly Pro Gln Ala Tyr Ile Tyr Asp Ala Ala Met Asn
    770                 775                 780

tac aag gag gcc ggc acc ccg ctg gtc gtc ctg ggt ggc aag gag tac      2700
Tyr Lys Glu Ala Gly Thr Pro Leu Val Val Leu Gly Gly Lys Glu Tyr
785                 790                 795                 800

ggc acc ggt tcc tcc cgt gac tgg gcc gcg aag ggc acc atc ctg ctc      2748
Gly Thr Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr Ile Leu Leu
                805                 810                 815
```

```
ggc gtg aag gcc gtc atc acc gag tcc ttc gag cgt atc cac cgc tcg      2796
Gly Val Lys Ala Val Ile Thr Glu Ser Phe Glu Arg Ile His Arg Ser
            820                 825                 830

aac ctg atc ggt atg ggt gtc atc ccg ctg cag ttc ccg gag ggc gag      2844
Asn Leu Ile Gly Met Gly Val Ile Pro Leu Gln Phe Pro Glu Gly Glu
        835                 840                 845

tcc cac gag tcc ctg ggc ctg gac ggc acc gag gtc ttc gac atc gag      2892
Ser His Glu Ser Leu Gly Leu Asp Gly Thr Glu Val Phe Asp Ile Glu
    850                 855                 860

ggc atc acc gcc ctg aac gag ggc gag acc ccg aag acc gtc aag gtc      2940
Gly Ile Thr Ala Leu Asn Glu Gly Glu Thr Pro Lys Thr Val Lys Val
865                 870                 875                 880

acc gcc acc aag gag gac ggc tcc acc gtg gag ttc gac gcg att gtc      2988
Thr Ala Thr Lys Glu Asp Gly Ser Thr Val Glu Phe Asp Ala Ile Val
                885                 890                 895

cgc atc gac acc ccg ggt gag gcc gac tac tac cgc aac ggc ggc atc      3036
Arg Ile Asp Thr Pro Gly Glu Ala Asp Tyr Tyr Arg Asn Gly Gly Ile
            900                 905                 910

ctg cag tac gtc ctg cgt cag atg atc gct gct gcc aag taa              3078
Leu Gln Tyr Val Leu Arg Gln Met Ile Ala Ala Ala Lys
        915                 920                 925

gcgagcatcc tcccgcagtg tgaactgcct ctgagagggg gctgcatccc cggctaaggc     3138

gtcacgccac cggggagagc agccccctct ccccttttcc cctattcccc cgacaggagt     3198

cccctcatgc ccgtggtcag cgacaccgag ttgacgcgtc gtcagaccga gatcctcgaa     3258

ggcgcgcggc gttgcttcgc cgagtacggc tacgagggcg ccacggtgcg ccgcctcgag     3318

gaggccacgg gcaagtcgcg gggtgcgatc ttccaccact tcggtgacaa ggagaacctc     3378
```

<210> 134
<211> 925
<212> PRT
<213> Corynebacterium humireducens

<400> 134

```
Val Thr Glu Ser Lys Asn Ser Phe Asn Ala Lys Arg Thr Leu Glu Val
1               5                  10                  15

Gly Glu Lys Ser Tyr Asp Tyr Phe Ala Leu Asp Ala Val Pro Gly Met
            20                  25                  30

Glu Lys Leu Pro Tyr Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg
        35                  40                  45
```

```
Thr Glu Asp Gly Ala Asn Ile Thr Thr Glu His Ile Glu Ala Ile Ala
     50                  55                  60

Asn Trp Asp Pro Lys Ala Glu Pro Ser Ile Glu Ile Gln Phe Thr Pro
65                  70                  75                  80

Ala Arg Val Leu Met Gln Asp Phe Thr Gly Val Ala Cys Ala Val Asp
                85                  90                  95

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

Asp Val Asn Pro Leu Asn Pro Ala Glu Met Val Ile Asp His Ser Val
        115                 120                 125

Ile Val Glu Ala Phe Gly Thr Ser Ala Ala Leu Glu Lys Asn Val Glu
    130                 135                 140

Ile Glu Tyr Gln Arg Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly
145                 150                 155                 160

Ala Glu Asn Phe Ser Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile
                165                 170                 175

Val His Gln Val Asn Ile Glu Tyr Leu Ser Arg Val Val Phe Asp Asn
            180                 185                 190

Asn Gly Leu Ala Tyr Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr
        195                 200                 205

Thr Met Glu Asn Gly Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile
    210                 215                 220

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

Arg Val Val Gly Phe Lys Leu Thr Gly Glu Ile Pro Ala Gly Val Thr
                245                 250                 255

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

Val Val Gln Lys Phe Val Glu Phe Tyr Gly Asn Gly Val Lys Ser Val
        275                 280                 285
```

```
Pro Leu Ala Asn Arg Ala Thr Ile Gly Asn Met Ser Pro Glu Phe Gly
    290                 295                 300

Ser Thr Cys Ala Met Phe Pro Ile Asp Glu Glu Thr Ile Lys Tyr Leu
305                 310                 315                 320

Glu Leu Thr Gly Arg Ser Glu Glu Asp Ile Ala Arg Val Glu Ala Tyr
                325                 330                 335

Ala Lys Ala Gln Gly Met Trp Leu Tyr Glu Asp Ala Pro Glu Ala Glu
            340                 345                 350

Tyr Ser Glu Tyr Leu Glu Leu Asp Leu Ser Thr Val Val Pro Ser Ile
        355                 360                 365

Ala Gly Pro Lys Arg Pro Gln Asp Arg Ile Leu Leu Ser Glu Ala Lys
    370                 375                 380

Ala Gln Phe Arg Lys Asp Leu Pro Thr Tyr Ala Ser Asp Glu Val Ala
385                 390                 395                 400

Glu Pro Val Arg Ala Thr Lys Ala Val Gly Asp Asp Tyr Asn Gln Ser
                405                 410                 415

Phe Pro Gly Asn Gly Glu Ser Ala Ala Asp Ser Ala Glu Gly Arg Ala
            420                 425                 430

Ser Lys Pro Val Ile Val Glu Ser Pro Gln Gly Gly Glu Tyr Thr Leu
        435                 440                 445

Asp His Gly Met Val Ala Ile Ala Ser Ile Thr Ser Cys Thr Asn Thr
    450                 455                 460

Ser Asn Pro Ser Val Leu Val Ala Ala Gly Leu Leu Ala Arg Lys Ala
465                 470                 475                 480

Asn Glu Leu Gly Leu Lys Ser Lys Pro Trp Val Lys Thr Ile Cys Ala
                485                 490                 495

Pro Gly Ser Gln Val Val Asp Gly Tyr Phe Lys Arg Ala Asp Leu Trp
            500                 505                 510

Lys Asp Leu Glu Ala Leu Gly Phe Tyr Leu Ser Gly Phe Gly Cys Thr
        515                 520                 525
```

Ser Cys Ile Gly Asn Ser Gly Pro Leu Pro Ala Glu Val Ser Ser Ala
530 535 540

Ile Asn Glu His Asp Leu Ala Ala Thr Ala Val Leu Ser Gly Asn Arg
545 550 555 560

Asn Phe Glu Gly Arg Ile Ser Pro Asp Val Lys Met Asn Tyr Leu Ala
565 570 575

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

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

Phe Leu Lys Asp Ile Trp Pro Ser Thr Glu Glu Ile Glu Glu Thr Ile
610 615 620

Ala Ala Ser Ile Ser Arg Glu Leu Tyr Glu Ala Asp Tyr Ala Asp Val
625 630 635 640

Phe Lys Gly Asp Lys Gln Trp Gln Glu Leu Asp Ile Pro Thr Gly Lys
645 650 655

Thr Phe Glu Trp Asp Glu Asn Ser Ser Tyr Ile Arg Lys Ala Pro Tyr
660 665 670

Phe Asp Gly Met Pro Leu Glu Pro Gln Pro Val Glu Asp Ile Lys Gly
675 680 685

Ala Arg Val Leu Ala Lys Leu Gly Asp Ser Val Thr Thr Asp His Ile
690 695 700

Ser Pro Ala Ser Ser Ile Lys Pro Gly Thr Pro Ala Ala Gln Tyr Leu
705 710 715 720

Asp Ser Met Gly Val Glu Arg Lys Asp Tyr Asn Ser Leu Gly Ser Arg
725 730 735

Arg Gly Asn His Glu Val Met Val Arg Gly Thr Phe Ala Asn Ile Arg
740 745 750

Leu Ala Asn Gln Leu Val Asp Val Thr Gly Gly Tyr Thr Arg Asp Phe

```
          755                 760                 765

Thr Gln Glu Gly Gly Pro Gln Ala Tyr Ile Tyr Asp Ala Ala Met Asn
    770                 775                 780

Tyr Lys Glu Ala Gly Thr Pro Leu Val Val Leu Gly Gly Lys Glu Tyr
785                 790                 795                 800

Gly Thr Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr Ile Leu Leu
                805                 810                 815

Gly Val Lys Ala Val Ile Thr Glu Ser Phe Glu Arg Ile His Arg Ser
            820                 825                 830

Asn Leu Ile Gly Met Gly Val Ile Pro Leu Gln Phe Pro Glu Gly Glu
        835                 840                 845

Ser His Glu Ser Leu Gly Leu Asp Gly Thr Glu Val Phe Asp Ile Glu
    850                 855                 860

Gly Ile Thr Ala Leu Asn Glu Gly Glu Thr Pro Lys Thr Val Lys Val
865                 870                 875                 880

Thr Ala Thr Lys Glu Asp Gly Ser Thr Val Glu Phe Asp Ala Ile Val
                885                 890                 895

Arg Ile Asp Thr Pro Gly Glu Ala Asp Tyr Tyr Arg Asn Gly Gly Ile
            900                 905                 910

Leu Gln Tyr Val Leu Arg Gln Met Ile Ala Ala Ala Lys
        915                 920                 925
```

<210> 135
<211> 1752
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1452)
<223> gene citrate synthase

<400> 135
agctgctctc cgcccagcag ctcgaggagc tcggcttcaa cgccgtcatc tacccggtga 60

ccaccctgcg catcgccatg ggacaggtcg aggaggctct cgcggagatc gccgccaccg 120

```
gcacccagac cgggtgggtc gaccgcatgc agcaccgctc ccgcctctac gaactgctcc      180

gctacaacga gtacaacgcc ttcgaccagg aggttttcac gtactccgcc gacacctacc      240

agcccacctt ccagtagccc accagcaact cctgacattc cttgaaaggg gatgagtacc      300

atg tcc gac aac acc aac atc gag gtc cgc aag ggt ctc tac ggc gtg         348
Met Ser Asp Asn Thr Asn Ile Glu Val Arg Lys Gly Leu Tyr Gly Val
1               5                  10                  15

atc gcc gac tac acc gca gtc tcc aag gtc atg ccg gag acc aac tcc         396
Ile Ala Asp Tyr Thr Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser
            20                  25                  30

ctg acc tac cgc gga tac gcc gtc cag gac ctc gtc gca gag tgc tcc         444
Leu Thr Tyr Arg Gly Tyr Ala Val Gln Asp Leu Val Ala Glu Cys Ser
        35                  40                  45

ttc gag gag gtc ttc tac ctc ctg tgg aac ggt gag ctg ccg aac gag         492
Phe Glu Glu Val Phe Tyr Leu Leu Trp Asn Gly Glu Leu Pro Asn Glu
    50                  55                  60

gag cag ctg gcg gag ttc aac agg cgc ggc cgt tcc tac cgc aag ctc         540
Glu Gln Leu Ala Glu Phe Asn Arg Arg Gly Arg Ser Tyr Arg Lys Leu
65                  70                  75                  80

gac gcc ggc ctg atc gca ctc atc cac tcc ctg ccg ctc gac tgt cac         588
Asp Ala Gly Leu Ile Ala Leu Ile His Ser Leu Pro Leu Asp Cys His
                85                  90                  95

ccg atg gac gtc atg cgc acc gcc gtg tcc tac atg ggc acc aag gac         636
Pro Met Asp Val Met Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp
            100                 105                 110

tcc gag cac ttc acc ccg gac gcc gac cac atc acc cac gtc ggc cac         684
Ser Glu His Phe Thr Pro Asp Ala Asp His Ile Thr His Val Gly His
        115                 120                 125

aac ctc ctc gcc cag ctg ccg atg gtg ctg gcc atg gac atc cgc cgc         732
Asn Leu Leu Ala Gln Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg
    130                 135                 140

cgt cag ggc ctc gac atc gtc gcc ccg gac ccg gac aag tcc gtc gcc         780
Arg Gln Gly Leu Asp Ile Val Ala Pro Asp Pro Asp Lys Ser Val Ala
145                 150                 155                 160

cac aac ctg ctg tcg atg gtc ttc ggc aac ggc ccg gag tcc ccg gcg         828
His Asn Leu Leu Ser Met Val Phe Gly Asn Gly Pro Glu Ser Pro Ala
                165                 170                 175

tcc aac ccg gac gac gtg cgt gac ttc gag aag tcg ctc atc ctc tac         876
Ser Asn Pro Asp Asp Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr
            180                 185                 190

gcc gag cac tcc ttc aac gcc tcg acc ttc acc tcg cgt gtg atc acc         924
Ala Glu His Ser Phe Asn Ala Ser Thr Phe Thr Ser Arg Val Ile Thr
        195                 200                 205

tcg acc cgc tcg gac gtc tac tcc gcg atc acc ggt gcc atc ggc gcc         972
```

```
Ser Thr Arg Ser Asp Val Tyr Ser Ala Ile Thr Gly Ala Ile Gly Ala
    210                 215                 220

ctc aag ggc ccg ctg cac ggc ggc gcc aac gag ttc gtc atg cac acc      1020
Leu Lys Gly Pro Leu His Gly Gly Ala Asn Glu Phe Val Met His Thr
225                 230                 235                 240

atg ctg gag atc gac gac ccg gag aag gcc gcc gac tgg gtc aac aac      1068
Met Leu Glu Ile Asp Asp Pro Glu Lys Ala Ala Asp Trp Val Asn Asn
                245                 250                 255

gcc ctg gac aac aag gac ctc atc atg ggc ttc ggt cac cgc gtg tac      1116
Ala Leu Asp Asn Lys Asp Leu Ile Met Gly Phe Gly His Arg Val Tyr
            260                 265                 270

aag aag ggt gac tcg cgt gtc ccg tcc atg gag gcg tcc ttc cgt gac      1164
Lys Lys Gly Asp Ser Arg Val Pro Ser Met Glu Ala Ser Phe Arg Asp
        275                 280                 285

ctc gcc gag cgt cac gac ggc gcc aag tgg gtc gcc atg tac gag aac      1212
Leu Ala Glu Arg His Asp Gly Ala Lys Trp Val Ala Met Tyr Glu Asn
    290                 295                 300

atg cgc gac gcc atg gac gcc cgc acc ggc atc aag ccg aac ctg gac      1260
Met Arg Asp Ala Met Asp Ala Arg Thr Gly Ile Lys Pro Asn Leu Asp
305                 310                 315                 320

ttc ccg gcc ggc ccg gcg tac cac ctg ctc ggc ttc ccg gtc gac ttc      1308
Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe Pro Val Asp Phe
                325                 330                 335

ttc acc ccg ctg ttc gtc gtc gcc cgc atc gcc ggc tgg acc gcc cac      1356
Phe Thr Pro Leu Phe Val Val Ala Arg Ile Ala Gly Trp Thr Ala His
            340                 345                 350

atc gtg gag cag tac aac gac aac tcc ctg att cgt ccg ctc tcc gcc      1404
Ile Val Glu Gln Tyr Asn Asp Asn Ser Leu Ile Arg Pro Leu Ser Ala
        355                 360                 365

tac aac ggc ccc gag cag cgc cag gtc acc ccg ctg gcc gcc cgt tag      1452
Tyr Asn Gly Pro Glu Gln Arg Gln Val Thr Pro Leu Ala Ala Arg
    370                 375                 380

ccccacggcc ggcaccggac caccgcgacg cccacggcac tgcccacaca ctggggtggt    1512

gcgcgtgggt ttcgctgttc ggaacacctg tcggcccatt ccgcagggcg ggacagaaac    1572

ggcctttcgg gcgcccgtcc cgcggagtgc ggaaatggac cgcaccgggt cccaccacctg    1632

cagatacccc ctgtgactag gggatactcc cccgaagaca accctctttc ctgcgatact    1692

gtggtgtgcc agagagctca cccgctctca gacacacccc cgacatgacg ctcggaaagg    1752
```

<210> 136
<211> 383
<212> PRT
<213> Corynebacterium humireducens

<400> 136

Met Ser Asp Asn Thr Asn Ile Glu Val Arg Lys Gly Leu Tyr Gly Val
1 5 10 15

Ile Ala Asp Tyr Thr Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser
20 25 30

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

Phe Glu Glu Val Phe Tyr Leu Leu Trp Asn Gly Glu Leu Pro Asn Glu
50 55 60

Glu Gln Leu Ala Glu Phe Asn Arg Arg Gly Arg Ser Tyr Arg Lys Leu
65 70 75 80

Asp Ala Gly Leu Ile Ala Leu Ile His Ser Leu Pro Leu Asp Cys His
85 90 95

Pro Met Asp Val Met Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp
100 105 110

Ser Glu His Phe Thr Pro Asp Ala Asp His Ile Thr His Val Gly His
115 120 125

Asn Leu Leu Ala Gln Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg
130 135 140

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

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

Ser Asn Pro Asp Asp Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr
180 185 190

Ala Glu His Ser Phe Asn Ala Ser Thr Phe Thr Ser Arg Val Ile Thr
195 200 205

Ser Thr Arg Ser Asp Val Tyr Ser Ala Ile Thr Gly Ala Ile Gly Ala
210 215 220

Leu Lys Gly Pro Leu His Gly Gly Ala Asn Glu Phe Val Met His Thr

225 230 235 240

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

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

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

Leu Ala Glu Arg His Asp Gly Ala Lys Trp Val Ala Met Tyr Glu Asn
290 295 300

Met Arg Asp Ala Met Asp Ala Arg Thr Gly Ile Lys Pro Asn Leu Asp
305 310 315 320

Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe Pro Val Asp Phe
325 330 335

Phe Thr Pro Leu Phe Val Val Ala Arg Ile Ala Gly Trp Thr Ala His
340 345 350

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

Tyr Asn Gly Pro Glu Gln Arg Gln Val Thr Pro Leu Ala Ala Arg
370 375 380

<210> 137
<211> 3372
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(3072)
<223> gene pepc

<400> 137
cggttccgtc aagaccgact cggtcgccga gatcgtcggt cagcccgacg tcgacggtgg 60

tctcgtcggt ggcgcctcgc tcgacggcga ggagttcgcc aagctggcgg ccgccgcggc 120

gtccgtcgtc tagcatcacc tcatccaccg gccccgggca ctgaacattc agtgcccggg 180

gccggtgtcc tttctccggg gaatatggtg cgcaatcccc acgcacggcc gtcatatgcg 240

```
tcatgatggg gaggcgaacc gcatccccgc cttcttcgag tacgaacagg gagacactca      300

atg acc gtc cgc gat cat ctg cag gaa gac atc cgc tac ctc ggc cgt        348
Met Thr Val Arg Asp His Leu Gln Glu Asp Ile Arg Tyr Leu Gly Arg
1               5                   10                  15

atc ctc ggc cag gtc atc gcg gaa cag gag ggc gag gac gtg ttc aac        396
Ile Leu Gly Gln Val Ile Ala Glu Gln Glu Gly Glu Asp Val Phe Asn
            20                  25                  30

ctc gtc gag cac gcc cgc cag cag gcc ttc gag gtg gcc aag ggc aac        444
Leu Val Glu His Ala Arg Gln Gln Ala Phe Glu Val Ala Lys Gly Asn
        35                  40                  45

gcc tcc ctg gag gtg ctc gtc gac ctg ttc cgg aac atc gag ccg gag        492
Ala Ser Leu Glu Val Leu Val Asp Leu Phe Arg Asn Ile Glu Pro Glu
    50                  55                  60

cgc gcg acc ccg gtg atc cgg gcg ttc agc cac ttc gcc ctg atg gcg        540
Arg Ala Thr Pro Val Ile Arg Ala Phe Ser His Phe Ala Leu Met Ala
65                  70                  75                  80

aac ctc gcg gag gac atc cac gac gac ttc cac cgg gag cgc atc ctc        588
Asn Leu Ala Glu Asp Ile His Asp Asp Phe His Arg Glu Arg Ile Leu
                85                  90                  95

gat gag ggc ggg gcc ccc gac tcc acc ctc aac gcc acg tgg gag aag        636
Asp Glu Gly Gly Ala Pro Asp Ser Thr Leu Asn Ala Thr Trp Glu Lys
            100                 105                 110

ttc cgg gag gcc ggc gtc agt gcc gcg gac atc gag agg tcg ctg tct        684
Phe Arg Glu Ala Gly Val Ser Ala Ala Asp Ile Glu Arg Ser Leu Ser
        115                 120                 125

gcc ggg ctc gtc gcc ccg gtg ctc acc gcc cac ccg acg gag acc cgc        732
Ala Gly Leu Val Ala Pro Val Leu Thr Ala His Pro Thr Glu Thr Arg
    130                 135                 140

cgc cgc acc gtc ttc gac gcc cag aag cac atc acc gag ctc atg ctg        780
Arg Arg Thr Val Phe Asp Ala Gln Lys His Ile Thr Glu Leu Met Leu
145                 150                 155                 160

cag cgg cac gcc gtc cag gac gcg gag ccg aac gcc cgc acc gag gac        828
Gln Arg His Ala Val Gln Asp Ala Glu Pro Asn Ala Arg Thr Glu Asp
                165                 170                 175

cgt ctc gcg gag atc gag cgc aac atc cgc cgc cgc atg acc atc ctg        876
Arg Leu Ala Glu Ile Glu Arg Asn Ile Arg Arg Arg Met Thr Ile Leu
            180                 185                 190

tgg cag acc gcg ctc atc cgg cag gcc cgc ccc cgc atc gag gac gag        924
Trp Gln Thr Ala Leu Ile Arg Gln Ala Arg Pro Arg Ile Glu Asp Glu
        195                 200                 205

atc gag gtc ggc ctg cgc tac tac acg ctc tcc ctg ctc cgg gag atc        972
Ile Glu Val Gly Leu Arg Tyr Tyr Thr Leu Ser Leu Leu Arg Glu Ile
    210                 215                 220

ccg gcg ctc aac cgg cac gtc gtc gac acg ctc acg gag cgt ttc ggc       1020
```

```
Pro Ala Leu Asn Arg His Val Val Asp Thr Leu Thr Glu Arg Phe Gly
225                 230                 235                 240

gcc gac ctg cgc aac agc gcc ggt cag gcc atc gtc cgc ccg ggc tcc      1068
Ala Asp Leu Arg Asn Ser Ala Gly Gln Ala Ile Val Arg Pro Gly Ser
                245                 250                 255

tgg atc ggc ggc gac cac gac ggc aac ccc ttc gtc acc gcc gac aca      1116
Trp Ile Gly Gly Asp His Asp Gly Asn Pro Phe Val Thr Ala Asp Thr
            260                 265                 270

ctg gac tac gct tcc cga cgc gcc gcc cag acc gtc ctc aag tac tac      1164
Leu Asp Tyr Ala Ser Arg Arg Ala Ala Gln Thr Val Leu Lys Tyr Tyr
        275                 280                 285

gtc acg cag ctc cac gcc ctc gag cac gag ctg agc ctc tcc gac cgc      1212
Val Thr Gln Leu His Ala Leu Glu His Glu Leu Ser Leu Ser Asp Arg
    290                 295                 300

atg acc tcc gtc acc gtg gag ctc gtc gcc ctc gcc ggg cgg gga aag      1260
Met Thr Ser Val Thr Val Glu Leu Val Ala Leu Ala Gly Arg Gly Lys
305                 310                 315                 320

aac gac gtc ccc tcg cgt gtc gac gag ccc tac cgc cgc gcc gtc cac      1308
Asn Asp Val Pro Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Val His
                325                 330                 335

ggc gtc cgg ggc cgc atc ctc gcc acg acc gcg gcg ctc atc ggg gag      1356
Gly Val Arg Gly Arg Ile Leu Ala Thr Thr Ala Ala Leu Ile Gly Glu
            340                 345                 350

gac gcc gtc gag ggc gtc tgg cac cgc gag cat gag ccc tac ggc tcc      1404
Asp Ala Val Glu Gly Val Trp His Arg Glu His Glu Pro Tyr Gly Ser
        355                 360                 365

ccg cag gag ttc gag gcg gac ctc agg gtc atc gac acc tcg ctg cgt      1452
Pro Gln Glu Phe Glu Ala Asp Leu Arg Val Ile Asp Thr Ser Leu Arg
    370                 375                 380

gcc tcc cac gac gag atc atc gcc gac gac cgt ctc agc tcc atc cgg      1500
Ala Ser His Asp Glu Ile Ile Ala Asp Asp Arg Leu Ser Ser Ile Arg
385                 390                 395                 400

gcg gcc gtc gcc tcc ttc ggg ttc cac ctg tac tcg atc gac ctg cga      1548
Ala Ala Val Ala Ser Phe Gly Phe His Leu Tyr Ser Ile Asp Leu Arg
                405                 410                 415

cag aac tcc gag tcc ttc gag aac gtc ctc acc gag gtc ttc gcc acc      1596
Gln Asn Ser Glu Ser Phe Glu Asn Val Leu Thr Glu Val Phe Ala Thr
            420                 425                 430

gcg cac gtc cac ccc aac tac gac acg ctg cgg gag gag gtg aag atc      1644
Ala His Val His Pro Asn Tyr Asp Thr Leu Arg Glu Glu Val Lys Ile
        435                 440                 445

gag ctg ctc acc cgc gaa ctg cag acc ccg cgc ccc ctc gtc ccg cgc      1692
Glu Leu Leu Thr Arg Glu Leu Gln Thr Pro Arg Pro Leu Val Pro Arg
    450                 455                 460
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ggc tac cgg ggc ttc tcc gag ccg acc cag cgg gag ctc gac ctc atc      1740
Gly Tyr Arg Gly Phe Ser Glu Pro Thr Gln Arg Glu Leu Asp Leu Ile
465                 470                 475                 480

tcc cag gcc gcg gac tcc gtc gcc cgc ttc ggc gag cag atg atc ccg      1788
Ser Gln Ala Ala Asp Ser Val Ala Arg Phe Gly Glu Gln Met Ile Pro
                485                 490                 495

cac cag atc atc tcc atg gcg cag tcg gtc agc gac atc ctc gag ccg      1836
His Gln Ile Ile Ser Met Ala Gln Ser Val Ser Asp Ile Leu Glu Pro
            500                 505                 510

atg gtg ctg ctc aag gag gtc ggc ctc atc cag gcc aac ggc cag ggc      1884
Met Val Leu Leu Lys Glu Val Gly Leu Ile Gln Ala Asn Gly Gln Gly
        515                 520                 525

ccg acc ggc agc gtc gac atc atc ccg ctg ttc gag acg atc gac gac      1932
Pro Thr Gly Ser Val Asp Ile Ile Pro Leu Phe Glu Thr Ile Asp Asp
    530                 535                 540

ctc cag gcc ggc gcc ggc atc ctc cgt gag ctg tgg gac ctg ccg atc      1980
Leu Gln Ala Gly Ala Gly Ile Leu Arg Glu Leu Trp Asp Leu Pro Ile
545                 550                 555                 560

tac cgg gcg tac ctc gcc cag cgc ggc gac atc cag gag gtc atg ctc      2028
Tyr Arg Ala Tyr Leu Ala Gln Arg Gly Asp Ile Gln Glu Val Met Leu
                565                 570                 575

ggc tac tcg gac tcc aac aag gac ggc ggc tac ttc gcc gcc aac tgg      2076
Gly Tyr Ser Asp Ser Asn Lys Asp Gly Gly Tyr Phe Ala Ala Asn Trp
            580                 585                 590

gcg ctc tac gac gcc gag acc gac ctg gtg aag gtc ggc cgc gag tac      2124
Ala Leu Tyr Asp Ala Glu Thr Asp Leu Val Lys Val Gly Arg Glu Tyr
        595                 600                 605

ggt gtg cgc ctg cga ctc ttc cac ggc cgc ggc ggc acc gtc ggc cgt      2172
Gly Val Arg Leu Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly Arg
    610                 615                 620

ggt ggc ggc ccc tcc tac gac gcg ctc ctc gcc cag ccg cag ggg gcg      2220
Gly Gly Gly Pro Ser Tyr Asp Ala Leu Leu Ala Gln Pro Gln Gly Ala
625                 630                 635                 640

gtc gac ggt tcc gtg cgc atc acc gag cag ggc gag atc atc tcg gcc      2268
Val Asp Gly Ser Val Arg Ile Thr Glu Gln Gly Glu Ile Ile Ser Ala
                645                 650                 655

aag tac ggc tcc ccg cgt acg gcc cgc cgc aac ctg gag gca ctg gtc      2316
Lys Tyr Gly Ser Pro Arg Thr Ala Arg Arg Asn Leu Glu Ala Leu Val
            660                 665                 670

tcc gcg acg ctc gag gcc agc ctg ctc acc gtc gac gac ctc gcc gac      2364
Ser Ala Thr Leu Glu Ala Ser Leu Leu Thr Val Asp Asp Leu Ala Asp
        675                 680                 685

cgg gcc cgc gcg acg cag ata atg agc gaa ctc gcg cag atc tcc cgc      2412
Arg Ala Arg Ala Thr Gln Ile Met Ser Glu Leu Ala Gln Ile Ser Arg
    690                 695                 700
```

```
cgc aag tac tcc gag ctc gtc cac gag gac ccg ggg ttc atc ccg tac      2460
Arg Lys Tyr Ser Glu Leu Val His Glu Asp Pro Gly Phe Ile Pro Tyr
705                 710                 715                 720

ttc acc cag tcg acc ccg ctc gac gag atc ggc tcc ctc aac atc ggc      2508
Phe Thr Gln Ser Thr Pro Leu Asp Glu Ile Gly Ser Leu Asn Ile Gly
                725                 730                 735

tcc cgc ccg acc gcc cgc aag cag acc aag ggc gtc gac gat ctc cgc      2556
Ser Arg Pro Thr Ala Arg Lys Gln Thr Lys Gly Val Asp Asp Leu Arg
            740                 745                 750

gcc atc ccg tgg gtg ctc gcc tgg tcc cag tcg cgt gtg ctg ctg ccg      2604
Ala Ile Pro Trp Val Leu Ala Trp Ser Gln Ser Arg Val Leu Leu Pro
        755                 760                 765

ggc tgg ttc ggc gtc ggc acg gcc ctg gcc gag tgg atc ggg gag ggg      2652
Gly Trp Phe Gly Val Gly Thr Ala Leu Ala Glu Trp Ile Gly Glu Gly
    770                 775                 780

gag gac agg gac gag cgc atc gcc gag ctg cgg gag ctc tac gag tcc      2700
Glu Asp Arg Asp Glu Arg Ile Ala Glu Leu Arg Glu Leu Tyr Glu Ser
785                 790                 795                 800

tgg ccc ttc ttc acc tcg atc atg tcc aac atg gcg cag gtc atg tcg      2748
Trp Pro Phe Phe Thr Ser Ile Met Ser Asn Met Ala Gln Val Met Ser
                805                 810                 815

aag gcg ggc atg gat ctc gcg gag ctc tac gcc cgg ctc atc gac gac      2796
Lys Ala Gly Met Asp Leu Ala Glu Leu Tyr Ala Arg Leu Ile Asp Asp
            820                 825                 830

cgg gag gtc gcc gag cgc gtc cac ggt gtc atc acg gag gag ttc gag      2844
Arg Glu Val Ala Glu Arg Val His Gly Val Ile Thr Glu Glu Phe Glu
        835                 840                 845

ctc acc cgc gag atg ttc agc acc gtc acc ggc agc gcc gag ctg ctc      2892
Leu Thr Arg Glu Met Phe Ser Thr Val Thr Gly Ser Ala Glu Leu Leu
    850                 855                 860

gcc gac aac ccg gcg ctg gcc cgt tcg gtg cgc agg cgc ttc ccg tac      2940
Ala Asp Asn Pro Ala Leu Ala Arg Ser Val Arg Arg Arg Phe Pro Tyr
865                 870                 875                 880

ctg ctg ccg ctc aac atc atc cag ctg gag ctg ctg cgc cgc cac cgt      2988
Leu Leu Pro Leu Asn Ile Ile Gln Leu Glu Leu Leu Arg Arg His Arg
                885                 890                 895

gcc ggc gac tcc cga cgc gcc gtg tcc cgc ggc atc cag ctg acg atg      3036
Ala Gly Asp Ser Arg Arg Ala Val Ser Arg Gly Ile Gln Leu Thr Met
            900                 905                 910

aac gga ctc gcc acc gca ctg cgc aac tcc ggg tag acctggtgta          3082
Asn Gly Leu Ala Thr Ala Leu Arg Asn Ser Gly
        915                 920

gactgagccg gagtttgtgc cgcccgattc ccgcaaagga ccttcatgac cctcgcactc    3142
```

cagatcatcc tcgtgctcac cgccgtgctc atgacggtgt tcgttctgct gcacaagggt 3202

aagggcggcg gcctgtccag cctcttcggt ggcggcatgc agtcgaacct ctcgggttcg 3262

acggtcgtcg agaagaacct cgaccgctac acgatcctca tggccgtcat ctggatcgcc 3322

tgcatcgtgg cgctgaacct catccaggct ttcgccggct aggttcaatg 3372

<210> 138
<211> 923
<212> PRT
<213> Corynebacterium humireducens

<400> 138

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

Ile Leu Gly Gln Val Ile Ala Glu Gln Glu Gly Glu Asp Val Phe Asn
20 25 30

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

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

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

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

Asp Glu Gly Gly Ala Pro Asp Ser Thr Leu Asn Ala Thr Trp Glu Lys
100 105 110

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

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

Arg Arg Thr Val Phe Asp Ala Gln Lys His Ile Thr Glu Leu Met Leu
145 150 155 160

Gln Arg His Ala Val Gln Asp Ala Glu Pro Asn Ala Arg Thr Glu Asp
165 170 175

```
Arg Leu Ala Glu Ile Glu Arg Asn Ile Arg Arg Arg Met Thr Ile Leu
            180                 185                 190

Trp Gln Thr Ala Leu Ile Arg Gln Ala Arg Pro Arg Ile Glu Asp Glu
        195                 200                 205

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

Pro Ala Leu Asn Arg His Val Val Asp Thr Leu Thr Glu Arg Phe Gly
225                 230                 235                 240

Ala Asp Leu Arg Asn Ser Ala Gly Gln Ala Ile Val Arg Pro Gly Ser
                245                 250                 255

Trp Ile Gly Gly Asp His Asp Gly Asn Pro Phe Val Thr Ala Asp Thr
            260                 265                 270

Leu Asp Tyr Ala Ser Arg Arg Ala Ala Gln Thr Val Leu Lys Tyr Tyr
        275                 280                 285

Val Thr Gln Leu His Ala Leu Glu His Glu Leu Ser Leu Ser Asp Arg
    290                 295                 300

Met Thr Ser Val Thr Val Glu Leu Val Ala Leu Ala Gly Arg Gly Lys
305                 310                 315                 320

Asn Asp Val Pro Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Val His
                325                 330                 335

Gly Val Arg Gly Arg Ile Leu Ala Thr Thr Ala Ala Leu Ile Gly Glu
            340                 345                 350

Asp Ala Val Glu Gly Val Trp His Arg Glu His Glu Pro Tyr Gly Ser
        355                 360                 365

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

Ala Ser His Asp Glu Ile Ile Ala Asp Asp Arg Leu Ser Ser Ile Arg
385                 390                 395                 400

Ala Ala Val Ala Ser Phe Gly Phe His Leu Tyr Ser Ile Asp Leu Arg
                405                 410                 415
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Gln Asn Ser Glu Ser Phe Glu Asn Val Leu Thr Glu Val Phe Ala Thr
420 425 430

Ala His Val His Pro Asn Tyr Asp Thr Leu Arg Glu Glu Val Lys Ile
435 440 445

Glu Leu Leu Thr Arg Glu Leu Gln Thr Pro Arg Pro Leu Val Pro Arg
450 455 460

Gly Tyr Arg Gly Phe Ser Glu Pro Thr Gln Arg Glu Leu Asp Leu Ile
465 470 475 480

Ser Gln Ala Ala Asp Ser Val Ala Arg Phe Gly Glu Gln Met Ile Pro
485 490 495

His Gln Ile Ile Ser Met Ala Gln Ser Val Ser Asp Ile Leu Glu Pro
500 505 510

Met Val Leu Leu Lys Glu Val Gly Leu Ile Gln Ala Asn Gly Gln Gly
515 520 525

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

Leu Gln Ala Gly Ala Gly Ile Leu Arg Glu Leu Trp Asp Leu Pro Ile
545 550 555 560

Tyr Arg Ala Tyr Leu Ala Gln Arg Gly Asp Ile Gln Glu Val Met Leu
565 570 575

Gly Tyr Ser Asp Ser Asn Lys Asp Gly Gly Tyr Phe Ala Ala Asn Trp
580 585 590

Ala Leu Tyr Asp Ala Glu Thr Asp Leu Val Lys Val Gly Arg Glu Tyr
595 600 605

Gly Val Arg Leu Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly Arg
610 615 620

Gly Gly Gly Pro Ser Tyr Asp Ala Leu Leu Ala Gln Pro Gln Gly Ala
625 630 635 640

Val Asp Gly Ser Val Arg Ile Thr Glu Gln Gly Glu Ile Ile Ser Ala

645 650 655

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

Ser Ala Thr Leu Glu Ala Ser Leu Leu Thr Val Asp Asp Leu Ala Asp
675 680 685

Arg Ala Arg Ala Thr Gln Ile Met Ser Glu Leu Ala Gln Ile Ser Arg
690 695 700

Arg Lys Tyr Ser Glu Leu Val His Glu Asp Pro Gly Phe Ile Pro Tyr
705 710 715 720

Phe Thr Gln Ser Thr Pro Leu Asp Glu Ile Gly Ser Leu Asn Ile Gly
725 730 735

Ser Arg Pro Thr Ala Arg Lys Gln Thr Lys Gly Val Asp Asp Leu Arg
740 745 750

Ala Ile Pro Trp Val Leu Ala Trp Ser Gln Ser Arg Val Leu Leu Pro
755 760 765

Gly Trp Phe Gly Val Gly Thr Ala Leu Ala Glu Trp Ile Gly Glu Gly
770 775 780

Glu Asp Arg Asp Glu Arg Ile Ala Glu Leu Arg Glu Leu Tyr Glu Ser
785 790 795 800

Trp Pro Phe Phe Thr Ser Ile Met Ser Asn Met Ala Gln Val Met Ser
805 810 815

Lys Ala Gly Met Asp Leu Ala Glu Leu Tyr Ala Arg Leu Ile Asp Asp
820 825 830

Arg Glu Val Ala Glu Arg Val His Gly Val Ile Thr Glu Glu Phe Glu
835 840 845

Leu Thr Arg Glu Met Phe Ser Thr Val Thr Gly Ser Ala Glu Leu Leu
850 855 860

Ala Asp Asn Pro Ala Leu Ala Arg Ser Val Arg Arg Arg Phe Pro Tyr
865 870 875 880

Leu Leu Pro Leu Asn Ile Ile Gln Leu Glu Leu Leu Arg Arg His Arg
885 890 895

Ala Gly Asp Ser Arg Arg Ala Val Ser Arg Gly Ile Gln Leu Thr Met
900 905 910

Asn Gly Leu Ala Thr Ala Leu Arg Asn Ser Gly
915 920

<210> 139
<211> 2346
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(2046)
<223> gene pyruvate dehydrogenase

<400> 139
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atgatccaca gcgcctgcac ctcggaggtg tggagctgtc tgcgcagctc ggggagcgcg 120

gtgaagagga tcgagttgtc caccccgacc atcagcagcc ccagggagat gatggcgagg 180

aaggcccacc gctgggccgg ggtggagtcg acgttgtcga ggtgcgtcac gcagcggaac 240

tgtaccgacc gttcgttaca gtttcaacgc ggggcatgaa tcctccgtac gctcgggacc 300

atg gca cgc acc tac gca cag cag ctc gtc gac gcc ctc gag agg cag 348
Met Ala Arg Thr Tyr Ala Gln Gln Leu Val Asp Ala Leu Glu Arg Gln
1 5 10 15

ggc gtg gaa cgg atc tac gga gtc gtc ggg gac agc ctc aac ccc atc 396
Gly Val Glu Arg Ile Tyr Gly Val Val Gly Asp Ser Leu Asn Pro Ile
20 25 30

gtc gac gcc gtc cgc acc tcc ccg atc gag tgg atc cac gtc cgc aac 444
Val Asp Ala Val Arg Thr Ser Pro Ile Glu Trp Ile His Val Arg Asn
35 40 45

gag gag gcc gcc gcc ttc gcc gcc ggc gcc gag tcc ctc ctc acc ggc 492
Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Leu Thr Gly
50 55 60

cgc ctc gcc gtg tgc gcg ggc tcc tgc ggc ccc ggc aac ctc cac ctc 540
Arg Leu Ala Val Cys Ala Gly Ser Cys Gly Pro Gly Asn Leu His Leu
65 70 75 80

atc cag ggt ctc tac gac gcc cac cgc aac ggc gcc cac gtc ctc gcc 588
Ile Gln Gly Leu Tyr Asp Ala His Arg Asn Gly Ala His Val Leu Ala
85 90 95

ctg gcc tcc cac atc ccc agc aac cag atc ggt acc tca tac ttc cag 636

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Leu Ala Ser His Ile Pro Ser Asn Gln Ile Gly Thr Ser Tyr Phe Gln
            100                 105                 110

gag acc cac ccc gaa cag ctc ttc gcg gaa tgt tcc ggt tac tgc gag      684
Glu Thr His Pro Glu Gln Leu Phe Ala Glu Cys Ser Gly Tyr Cys Glu
        115                 120                 125

atg gtc aac tcc gcc gac cag ggc gcc cgc gtc ctg cac cac gcg atc      732
Met Val Asn Ser Ala Asp Gln Gly Ala Arg Val Leu His His Ala Ile
    130                 135                 140

cag tcg acg atg gcc ggg cag ggc gtg tcc gtg ctg gtc atc ccg ggg      780
Gln Ser Thr Met Ala Gly Gln Gly Val Ser Val Leu Val Ile Pro Gly
145                 150                 155                 160

gac atc gcc acg cag gac gcc ggc gac gac cgg ttc ctg cag tcc acc      828
Asp Ile Ala Thr Gln Asp Ala Gly Asp Asp Arg Phe Leu Gln Ser Thr
                165                 170                 175

gtc gcc acc ggc cgc ccc gtg ctc cac ccc gac gcc cgc gag gcc gcc      876
Val Ala Thr Gly Arg Pro Val Leu His Pro Asp Ala Arg Glu Ala Ala
            180                 185                 190

gcc ctg gtc gcg gcc atc aac gcc gcc gac acg gtg acc ctg ttc tgc      924
Ala Leu Val Ala Ala Ile Asn Ala Ala Asp Thr Val Thr Leu Phe Cys
        195                 200                 205

ggc gca ggc gta cgc gac gcc cgc gag cag gtc ctc gcc ctg gcg gag      972
Gly Ala Gly Val Arg Asp Ala Arg Glu Gln Val Leu Ala Leu Ala Glu
    210                 215                 220

aag atc aag gcc ccc atc ggc cac gcc ctc ggc ggc aag atg cac atc     1020
Lys Ile Lys Ala Pro Ile Gly His Ala Leu Gly Gly Lys Met His Ile
225                 230                 235                 240

cag cac gac aac ccc ttc gac gtc ggc atg tcc ggg ctc ctc ggc tac     1068
Gln His Asp Asn Pro Phe Asp Val Gly Met Ser Gly Leu Leu Gly Tyr
                245                 250                 255

ggc gcc tgc cac gac gca ctg cac gac gcc gac ctg ctc atc ctc ctg     1116
Gly Ala Cys His Asp Ala Leu His Asp Ala Asp Leu Leu Ile Leu Leu
            260                 265                 270

ggc acc gac ttc ccc tac acc gag ttc ctg ccc acc ggg aac gtc gcg     1164
Gly Thr Asp Phe Pro Tyr Thr Glu Phe Leu Pro Thr Gly Asn Val Ala
        275                 280                 285

cag gtc gac agc gac gcc gcg cac atc ggc cgc cgc acc acg gtg cac     1212
Gln Val Asp Ser Asp Ala Ala His Ile Gly Arg Arg Thr Thr Val His
    290                 295                 300

cac ccg gtg gtc ggc gac gtc ggc gcc acc ctc gac acc atc ctc ccg     1260
His Pro Val Val Gly Asp Val Gly Ala Thr Leu Asp Thr Ile Leu Pro
305                 310                 315                 320

cac ctg gag gag aag acc gac cgc agc ttc ctc gac ggg atg ctc cgc     1308
His Leu Glu Glu Lys Thr Asp Arg Ser Phe Leu Asp Gly Met Leu Arg
                325                 330                 335
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aag cac gcc cgg acg ctg gag aag gtc gtg gag gtg tac acg cgg gac      1356
Lys His Ala Arg Thr Leu Glu Lys Val Val Glu Val Tyr Thr Arg Asp
            340                 345                 350

gtc ggg aag cac acc ccc atc cac ccg gag tac ctc gcc gcc gtc ctc      1404
Val Gly Lys His Thr Pro Ile His Pro Glu Tyr Leu Ala Ala Val Leu
        355                 360                 365

gac gag ctc gcc gcc gac gac gcc gtg ttc acc gtc gac acc ggc atg      1452
Asp Glu Leu Ala Ala Asp Asp Ala Val Phe Thr Val Asp Thr Gly Met
    370                 375                 380

tgc aac gtg tgg gcc gcg cgc tac ctc acc ccc aac gga cga cgc gcg      1500
Cys Asn Val Trp Ala Ala Arg Tyr Leu Thr Pro Asn Gly Arg Arg Ala
385                 390                 395                 400

cag atc ggc tcc ctc cgc cac ggc acg atg gcc aac gcg ctg ccg cac      1548
Gln Ile Gly Ser Leu Arg His Gly Thr Met Ala Asn Ala Leu Pro His
                405                 410                 415

gcc atc ggc gcg cag ttc gcc gac cgg aac cgt cag gtc atc agc ctc      1596
Ala Ile Gly Ala Gln Phe Ala Asp Arg Asn Arg Gln Val Ile Ser Leu
            420                 425                 430

aac ggc gac ggc ggc ctc gcc atg ctc ctc ggc gaa ctg ctc acc gtg      1644
Asn Gly Asp Gly Gly Leu Ala Met Leu Leu Gly Glu Leu Leu Thr Val
        435                 440                 445

gaa ctc cac gac ctg ccc gtg aag atg gtc gtg ttc aac aac tcc tcg      1692
Glu Leu His Asp Leu Pro Val Lys Met Val Val Phe Asn Asn Ser Ser
    450                 455                 460

ctc ggc atg gtc aaa ctc gag atg ctc gtc gag ggc atg ccc cag cac      1740
Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Met Pro Gln His
465                 470                 475                 480

ggc acc gac cac ggg cag gtc gac ttc gcg gcg atc gcg gcc gcc gcg      1788
Gly Thr Asp His Gly Gln Val Asp Phe Ala Ala Ile Ala Ala Ala Ala
                485                 490                 495

ggc atc cac tcc gtg ctc atc gac gac ccc gcc acc ctc cgc gag cag      1836
Gly Ile His Ser Val Leu Ile Asp Asp Pro Ala Thr Leu Arg Glu Gln
            500                 505                 510

ctc gcc gcg gcg ctc gcc cac ccc ggg ccc gtg ctc atc gac gtc cgc      1884
Leu Ala Ala Ala Leu Ala His Pro Gly Pro Val Leu Ile Asp Val Arg
        515                 520                 525

acc gac ccc gac gcc ctc tcc ctc ccg ccg gag atc acc tgg gag atg      1932
Thr Asp Pro Asp Ala Leu Ser Leu Pro Pro Glu Ile Thr Trp Glu Met
    530                 535                 540

ctc atc ggc ttc tcc cgg gcc gcg acc cgt acc gtc ctc ggc ggc ggc      1980
Leu Ile Gly Phe Ser Arg Ala Ala Thr Arg Thr Val Leu Gly Gly Gly
545                 550                 555                 560

gtc ggc gag atg gtg cac ctc gcg cgc acg aac ctg cgc aac atc ggc      2028
Val Gly Glu Met Val His Leu Ala Arg Thr Asn Leu Arg Asn Ile Gly
                565                 570                 575
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gcg gcc ggg gcg gtc tag tctgggcgtc atgaccccga ccgtccggat 2076
Ala Ala Gly Ala Val
580

cgacctcgcc cgcctcgacg cgaacatcgc cgcgcaaccc gggcggctgc gaccgcacgt 2136

gaagacccac aagatcctgg agatcgcccg ccggcagctc gcggcgggtg cccacggcct 2196

cacggtcgcg acggtggggg aggcggaggt cttcgccgag gtctgcgacg acatcttcat 2256

cgcctacccc gtctgggccg acaagaggct gcgcgacctg gccgggaggg tgcggctgag 2316

cgtcggctgc gactcgctgg ccgccgccga 2346

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<211> 581
<212> PRT
<213> Corynebacterium humireducens

<400> 140

Met Ala Arg Thr Tyr Ala Gln Gln Leu Val Asp Ala Leu Glu Arg Gln
1 5 10 15

Gly Val Glu Arg Ile Tyr Gly Val Val Gly Asp Ser Leu Asn Pro Ile
20 25 30

Val Asp Ala Val Arg Thr Ser Pro Ile Glu Trp Ile His Val Arg Asn
35 40 45

Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Leu Thr Gly
50 55 60

Arg Leu Ala Val Cys Ala Gly Ser Cys Gly Pro Gly Asn Leu His Leu
65 70 75 80

Ile Gln Gly Leu Tyr Asp Ala His Arg Asn Gly Ala His Val Leu Ala
85 90 95

Leu Ala Ser His Ile Pro Ser Asn Gln Ile Gly Thr Ser Tyr Phe Gln
100 105 110

Glu Thr His Pro Glu Gln Leu Phe Ala Glu Cys Ser Gly Tyr Cys Glu
115 120 125

Met Val Asn Ser Ala Asp Gln Gly Ala Arg Val Leu His His Ala Ile
130 135 140

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

Asp Ile Ala Thr Gln Asp Ala Gly Asp Asp Arg Phe Leu Gln Ser Thr
                165                 170                 175

Val Ala Thr Gly Arg Pro Val Leu His Pro Asp Ala Arg Glu Ala Ala
            180                 185                 190

Ala Leu Val Ala Ala Ile Asn Ala Ala Asp Thr Val Thr Leu Phe Cys
        195                 200                 205

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

Lys Ile Lys Ala Pro Ile Gly His Ala Leu Gly Gly Lys Met His Ile
225                 230                 235                 240

Gln His Asp Asn Pro Phe Asp Val Gly Met Ser Gly Leu Leu Gly Tyr
                245                 250                 255

Gly Ala Cys His Asp Ala Leu His Asp Ala Asp Leu Leu Ile Leu Leu
            260                 265                 270

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

Gln Val Asp Ser Asp Ala Ala His Ile Gly Arg Arg Thr Thr Val His
    290                 295                 300

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

His Leu Glu Glu Lys Thr Asp Arg Ser Phe Leu Asp Gly Met Leu Arg
                325                 330                 335

Lys His Ala Arg Thr Leu Glu Lys Val Val Glu Val Tyr Thr Arg Asp
            340                 345                 350

Val Gly Lys His Thr Pro Ile His Pro Glu Tyr Leu Ala Ala Val Leu
        355                 360                 365

Asp Glu Leu Ala Ala Asp Asp Ala Val Phe Thr Val Asp Thr Gly Met
    370                 375                 380
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```
Cys Asn Val Trp Ala Ala Arg Tyr Leu Thr Pro Asn Gly Arg Arg Ala
385                 390                 395                 400

Gln Ile Gly Ser Leu Arg His Gly Thr Met Ala Asn Ala Leu Pro His
                405                 410                 415

Ala Ile Gly Ala Gln Phe Ala Asp Arg Asn Arg Gln Val Ile Ser Leu
            420                 425                 430

Asn Gly Asp Gly Gly Leu Ala Met Leu Leu Gly Glu Leu Leu Thr Val
        435                 440                 445

Glu Leu His Asp Leu Pro Val Lys Met Val Val Phe Asn Asn Ser Ser
    450                 455                 460

Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Met Pro Gln His
465                 470                 475                 480

Gly Thr Asp His Gly Gln Val Asp Phe Ala Ala Ile Ala Ala Ala Ala
                485                 490                 495

Gly Ile His Ser Val Leu Ile Asp Asp Pro Ala Thr Leu Arg Glu Gln
            500                 505                 510

Leu Ala Ala Ala Leu Ala His Pro Gly Pro Val Leu Ile Asp Val Arg
        515                 520                 525

Thr Asp Pro Asp Ala Leu Ser Leu Pro Pro Glu Ile Thr Trp Glu Met
    530                 535                 540

Leu Ile Gly Phe Ser Arg Ala Ala Thr Arg Thr Val Leu Gly Gly Gly
545                 550                 555                 560

Val Gly Glu Met Val His Leu Ala Arg Thr Asn Leu Arg Asn Ile Gly
                565                 570                 575

Ala Ala Gly Ala Val
            580
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<210> 141
<211> 2010
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1710)
<223> gene pyruvate kinase_1

<400> 141
acgagctgct gtggaacctc ctcatcttcg ggctgctcat cctcatcgac cgccgcttcc 60

gcatcgcacc gggtggactg ttcgccctct acgtcgccgg ttacacgctg ggccgtttct 120

ggatcgagct catgcgcgac gattccgcca cgatgatcct cggccagcgg gtcaacacct 180

gggtctccgc cgtggtgttc ctcgtctcga tcgcggtatt cgtgtggttg cagcgacgtc 240

agcgggctgt tgtccgagaa acagagtagg ttggtagccg tgtctagacg aaccaagatt 300

gtg tgc acc ctc ggt cct gcc gtc gcc tcc aag gac gcg atc acg cgt 348
Val Cys Thr Leu Gly Pro Ala Val Ala Ser Lys Asp Ala Ile Thr Arg
1 5 10 15

ctg gtg gag gac ggc atg gac gtc gcc cgc ctg aac ttc tcc cac ggt 396
Leu Val Glu Asp Gly Met Asp Val Ala Arg Leu Asn Phe Ser His Gly
20 25 30

gat cac ccc gat cac gag cag aac tac aag tgg gtc cgg gaa gcc acc 444
Asp His Pro Asp His Glu Gln Asn Tyr Lys Trp Val Arg Glu Ala Thr
35 40 45

gat gag acc ggc cgt gcc gtc ggc atc ctc gct gac ctc cag ggc ccg 492
Asp Glu Thr Gly Arg Ala Val Gly Ile Leu Ala Asp Leu Gln Gly Pro
50 55 60

aag atc cgc ctc ggt cgc ttc atc gac ggt gcc acc gtc tgg gag acc 540
Lys Ile Arg Leu Gly Arg Phe Ile Asp Gly Ala Thr Val Trp Glu Thr
65 70 75 80

ggt gag gtc atc cgc atc acc gtg gac gat gtc gag ggc acg cac gac 588
Gly Glu Val Ile Arg Ile Thr Val Asp Asp Val Glu Gly Thr His Asp
85 90 95

cgc gtg tcc acc acc tac aag aac ctc gcg cag gac gcc aag ccc ggc 636
Arg Val Ser Thr Thr Tyr Lys Asn Leu Ala Gln Asp Ala Lys Pro Gly
100 105 110

gac cgt ctg ctc gtc gac gac ggc aag gtc ggc ctg acc tgc ctc gag 684
Asp Arg Leu Leu Val Asp Asp Gly Lys Val Gly Leu Thr Cys Leu Glu
115 120 125

gtc gac ggc aac gac gtc gtc tgc gag gtc acc gag ggc ggc ccc gtc 732
Val Asp Gly Asn Asp Val Val Cys Glu Val Thr Glu Gly Gly Pro Val
130 135 140

tcc aac aac aag ggc gtc tcc ctc ccg ggc atg gac atc tct gtg ccg 780
Ser Asn Asn Lys Gly Val Ser Leu Pro Gly Met Asp Ile Ser Val Pro
145 150 155 160

gcg ctg tcg gag aag gac atc gcc gac ctc gag ttc gcc ctc aag ctg 828
Ala Leu Ser Glu Lys Asp Ile Ala Asp Leu Glu Phe Ala Leu Lys Leu
165 170 175

```
ggc gtc gac ttc atc gcc ctg tcc ttc gtc cgc tcc ccg gcg gac gtc        876
Gly Val Asp Phe Ile Ala Leu Ser Phe Val Arg Ser Pro Ala Asp Val
            180                 185                 190

gac ctc gtc cac gag gtc atg gac cgc gtc ggc cgc cac gtg ccg gtc        924
Asp Leu Val His Glu Val Met Asp Arg Val Gly Arg His Val Pro Val
        195                 200                 205

atc gcg aag ctg gag aag ccg gag gcc gtc cac gcc ctc gag tcc atc        972
Ile Ala Lys Leu Glu Lys Pro Glu Ala Val His Ala Leu Glu Ser Ile
    210                 215                 220

gtc ctc gcc ttc gac gcc atc atg gtc gcc cgc ggt gac ctc ggc gtc       1020
Val Leu Ala Phe Asp Ala Ile Met Val Ala Arg Gly Asp Leu Gly Val
225                 230                 235                 240

gag gtg ccg ctg gag cag gtc ccg ctg gtg cag aag cgg gcc atc cag       1068
Glu Val Pro Leu Glu Gln Val Pro Leu Val Gln Lys Arg Ala Ile Gln
                245                 250                 255

atc gcc cgc gag aac gcg aag ccg gtc att gtc gcc acg cag atg ctc       1116
Ile Ala Arg Glu Asn Ala Lys Pro Val Ile Val Ala Thr Gln Met Leu
            260                 265                 270

gac tcc atg atc gag aac tcc acc ccg acc cgc gcc gag gcc tcc gac       1164
Asp Ser Met Ile Glu Asn Ser Thr Pro Thr Arg Ala Glu Ala Ser Asp
        275                 280                 285

gtc gcc aac gcc gtc ctc gac ggc gcc gac gcg gtc atg ctc tcc ggt       1212
Val Ala Asn Ala Val Leu Asp Gly Ala Asp Ala Val Met Leu Ser Gly
    290                 295                 300

gag acc tcc atc ggt gtg gac ccg cac aac gtc gtg cgc acc atg gcc       1260
Glu Thr Ser Ile Gly Val Asp Pro His Asn Val Val Arg Thr Met Ala
305                 310                 315                 320

cgc atc gtc acc cag gcc gag acc gac ggc cac gtg ccg ccg ctg agc       1308
Arg Ile Val Thr Gln Ala Glu Thr Asp Gly His Val Pro Pro Leu Ser
                325                 330                 335

cat gtc ccg cgc acc aag cgg ggc gtc atc tcc tac tcg gcc cgt gac       1356
His Val Pro Arg Thr Lys Arg Gly Val Ile Ser Tyr Ser Ala Arg Asp
            340                 345                 350

atc gcc gag cgt ctc aac gcc cgc gcc ctg gtc tgc ttc acc acc tcc       1404
Ile Ala Glu Arg Leu Asn Ala Arg Ala Leu Val Cys Phe Thr Thr Ser
        355                 360                 365

ggt gac acc gcc cgc cgt gtc gcc cgc ctg cac tcg cac ctg ccg ctg       1452
Gly Asp Thr Ala Arg Arg Val Ala Arg Leu His Ser His Leu Pro Leu
    370                 375                 380

ctg gtg ttc acc ccg cac ccg gcg gtc cgt tcg cag ctg gcc ctc acc       1500
Leu Val Phe Thr Pro His Pro Ala Val Arg Ser Gln Leu Ala Leu Thr
385                 390                 395                 400

tgg ggc gcc gag acc ttc ctc tgc gcc cag gcc ctg tcc acc gac gac       1548
Trp Gly Ala Glu Thr Phe Leu Cys Ala Gln Ala Leu Ser Thr Asp Asp
```

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                405                 410                 415

atg atg gcc gag ctg gac cgt tcc ctg ctc gcc atg gac gac tac cac      1596
Met Met Ala Glu Leu Asp Arg Ser Leu Leu Ala Met Asp Asp Tyr His
            420                 425                 430

cgc gac gac atg atg gtc gtc gtc gcc ggc acc ccg ccc ggg gtc tcc      1644
Arg Asp Asp Met Met Val Val Val Ala Gly Thr Pro Pro Gly Val Ser
        435                 440                 445

ggc aac acg aac atg atc cac gtc cac ctg ctg ggc gag gac acg agt      1692
Gly Asn Thr Asn Met Ile His Val His Leu Leu Gly Glu Asp Thr Ser
    450                 455                 460

tcc ccg acc ggc agg tag ccggagaaca gaaaaaggag cggcggagag             1740
Ser Pro Thr Gly Arg
465

gatcatcctc tccgccgctc ctgtcgtgtg cggctacttc accggggtcg gctccagctt     1800

ccacacctca cgcgcgtagt cgttgatggt gcggtcggag gagaaacggc ccgaggcgca     1860

gatgttcgcc cagcacatac gcgcccagtg caggcggtcg gcgtagtcgg cggccatgcg     1920

gtcgcgggtc tcgcggtagt cggcgaagtc accgaggacg tagtagacgt ccggggtctc     1980

ccagccgccg ccgtcgagaa gcgaggaacg                                      2010
```

<210> 142
<211> 469
<212> PRT
<213> Corynebacterium humireducens

<400> 142

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Val Cys Thr Leu Gly Pro Ala Val Ala Ser Lys Asp Ala Ile Thr Arg
1               5                   10                  15

Leu Val Glu Asp Gly Met Asp Val Ala Arg Leu Asn Phe Ser His Gly
            20                  25                  30

Asp His Pro Asp His Glu Gln Asn Tyr Lys Trp Val Arg Glu Ala Thr
        35                  40                  45

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

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

Gly Glu Val Ile Arg Ile Thr Val Asp Asp Val Glu Gly Thr His Asp
                85                  90                  95
```

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Arg Val Ser Thr Thr Tyr Lys Asn Leu Ala Gln Asp Ala Lys Pro Gly
            100                 105                 110

Asp Arg Leu Leu Val Asp Asp Gly Lys Val Gly Leu Thr Cys Leu Glu
        115                 120                 125

Val Asp Gly Asn Asp Val Val Cys Glu Val Thr Glu Gly Gly Pro Val
    130                 135                 140

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

Ala Leu Ser Glu Lys Asp Ile Ala Asp Leu Glu Phe Ala Leu Lys Leu
                165                 170                 175

Gly Val Asp Phe Ile Ala Leu Ser Phe Val Arg Ser Pro Ala Asp Val
            180                 185                 190

Asp Leu Val His Glu Val Met Asp Arg Val Gly Arg His Val Pro Val
        195                 200                 205

Ile Ala Lys Leu Glu Lys Pro Glu Ala Val His Ala Leu Glu Ser Ile
    210                 215                 220

Val Leu Ala Phe Asp Ala Ile Met Val Ala Arg Gly Asp Leu Gly Val
225                 230                 235                 240

Glu Val Pro Leu Glu Gln Val Pro Leu Val Gln Lys Arg Ala Ile Gln
                245                 250                 255

Ile Ala Arg Glu Asn Ala Lys Pro Val Ile Val Ala Thr Gln Met Leu
            260                 265                 270

Asp Ser Met Ile Glu Asn Ser Thr Pro Thr Arg Ala Glu Ala Ser Asp
        275                 280                 285

Val Ala Asn Ala Val Leu Asp Gly Ala Asp Ala Val Met Leu Ser Gly
    290                 295                 300

Glu Thr Ser Ile Gly Val Asp Pro His Asn Val Val Arg Thr Met Ala
305                 310                 315                 320

Arg Ile Val Thr Gln Ala Glu Thr Asp Gly His Val Pro Pro Leu Ser
                325                 330                 335
```

His Val Pro Arg Thr Lys Arg Gly Val Ile Ser Tyr Ser Ala Arg Asp
340 345 350

Ile Ala Glu Arg Leu Asn Ala Arg Ala Leu Val Cys Phe Thr Thr Ser
355 360 365

Gly Asp Thr Ala Arg Arg Val Ala Arg Leu His Ser His Leu Pro Leu
370 375 380

Leu Val Phe Thr Pro His Pro Ala Val Arg Ser Gln Leu Ala Leu Thr
385 390 395 400

Trp Gly Ala Glu Thr Phe Leu Cys Ala Gln Ala Leu Ser Thr Asp Asp
405 410 415

Met Met Ala Glu Leu Asp Arg Ser Leu Leu Ala Met Asp Asp Tyr His
420 425 430

Arg Asp Asp Met Met Val Val Val Ala Gly Thr Pro Pro Gly Val Ser
435 440 445

Gly Asn Thr Asn Met Ile His Val His Leu Leu Gly Glu Asp Thr Ser
450 455 460

Ser Pro Thr Gly Arg
465

<210> 143
<211> 2472
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(2172)
<223> gene pyruvate kinase 2

<400> 143
atccagaacc aggacgtcgc tctgccggtg tccgcgtacc tcgacggcga gtacgggcag 60

aaggacctct acatcggcac cccggcgatc atcaaccgcg ccggaatcgc ccgcacggtc 120

gagctgaagc tcaacgagca cgaggcggag cgcttcgccc actcggctga cacgctgcgc 180

gcgatcaagg aggagttctt ccccgccgac tgacggcttc cccgagatgc cgaacctccc 240

gaacacaggc acaatatggg ggtatcaccc attttgtcgt gcgcgtacgg gaggacagcc 300

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gtg gat gcc agg ctg cag gaa ctg atc acc gag gtc gac ggt ctc atc        348
Val Asp Ala Arg Leu Gln Glu Leu Ile Thr Glu Val Asp Gly Leu Ile
1               5                   10                  15

gac tgc ctc aag gag gtc gag gag cag gtg gcc ccc gcg atc ggg cgg        396
Asp Cys Leu Lys Glu Val Glu Glu Gln Val Ala Pro Ala Ile Gly Arg
            20                  25                  30

gtc gcc gag aac cac cgc cac ggc gcg gtg aac ctc gtc cac tac gcc        444
Val Ala Glu Asn His Arg His Gly Ala Val Asn Leu Val His Tyr Ala
        35                  40                  45

gag ctg cgg cag cac gac gtc cgc gcg gtc cag ggc ggc ctg gcc tcc        492
Glu Leu Arg Gln His Asp Val Arg Ala Val Gln Gly Gly Leu Ala Ser
    50                  55                  60

atc ggc gcc acc cgc ctg tcg acg gcg gag ccg gcc gtc ctc gcc cgt        540
Ile Gly Ala Thr Arg Leu Ser Thr Ala Glu Pro Ala Val Leu Ala Arg
65                  70                  75                  80

ctc cac gcg gcg cgg aac gtg ctc tcc gcc tac aac ggt gag cag ctc        588
Leu His Ala Ala Arg Asn Val Leu Ser Ala Tyr Asn Gly Glu Gln Leu
                85                  90                  95

aag tac acc ggc agc gag gtc cgt gac gcc ttc gcc acc gcc gac gac        636
Lys Tyr Thr Gly Ser Glu Val Arg Asp Ala Phe Ala Thr Ala Asp Asp
            100                 105                 110

atc ctc gag gac cac gcc ctg cag ctc ctc ggc tac tcc tcc gag gag        684
Ile Leu Glu Asp His Ala Leu Gln Leu Leu Gly Tyr Ser Ser Glu Glu
        115                 120                 125

acg cac tcc cgc atc atg gtg acc ctg ccg acg gag gca ggc gag gac        732
Thr His Ser Arg Ile Met Val Thr Leu Pro Thr Glu Ala Gly Glu Asp
    130                 135                 140

ctc gac ctg gtc cgc ggt ttc gtc gag gcc ggc atg gag ctg gcc cgc        780
Leu Asp Leu Val Arg Gly Phe Val Glu Ala Gly Met Glu Leu Ala Arg
145                 150                 155                 160

atc aac tgc gcc cac gac ggc ccc gag gtg tgg agg cgc atg atc gac        828
Ile Asn Cys Ala His Asp Gly Pro Glu Val Trp Arg Arg Met Ile Asp
                165                 170                 175

aac gtc cac acc gcc gcc cgc gag gcc ggc cgg gag atc agg atc gcc        876
Asn Val His Thr Ala Ala Arg Glu Ala Gly Arg Glu Ile Arg Ile Ala
            180                 185                 190

atg gac ctg gcg ggc ccg aag gtc cgc acc ggg gag atc gag ccg ggc        924
Met Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu Ile Glu Pro Gly
        195                 200                 205

ccg gag gtc ggc cgc gcc cgc gtc acc cgc gag gac acc ggc gtg gtg        972
Pro Glu Val Gly Arg Ala Arg Val Thr Arg Glu Asp Thr Gly Val Val
    210                 215                 220

gtc acc ccg tcg aag atc tgg ctc acc ccc gcc gac ctg gcc gac gac       1020
Val Thr Pro Ser Lys Ile Trp Leu Thr Pro Ala Asp Leu Ala Asp Asp
```

```
225                 230                 235                 240

gag gtc ccg ccg gtc ccc gcc gga ctg ccg ggc cgc ccg acg ctg ccg  1068
Glu Val Pro Pro Val Pro Ala Gly Leu Pro Gly Arg Pro Thr Leu Pro
                245                 250                 255

ctg cgc gtc gag cgt gac tgg ctg gag gcc ctg gag atc ggc tcc gag  1116
Leu Arg Val Glu Arg Asp Trp Leu Glu Ala Leu Glu Ile Gly Ser Glu
            260                 265                 270

atc acc ttc cac gac aac cgc gac gcg aag cgc cgg ttc acc gtc acc  1164
Ile Thr Phe His Asp Asn Arg Asp Ala Lys Arg Arg Phe Thr Val Thr
        275                 280                 285

cgc atc gag ggg cag ggg gtg ctg ctg gag ggg cgt cgc aac gcc tac  1212
Arg Ile Glu Gly Gln Gly Val Leu Leu Glu Gly Arg Arg Asn Ala Tyr
    290                 295                 300

gtc tcc aac tcc acc ctc ctc gag acc gac tgg acc aag acc cgc gtc  1260
Val Ser Asn Ser Thr Leu Leu Glu Thr Asp Trp Thr Lys Thr Arg Val
305                 310                 315                 320

tcc ggc gtc ccg ccg acc gag cag cgc ctg cgt ctg agc atc gga gac  1308
Ser Gly Val Pro Pro Thr Glu Gln Arg Leu Arg Leu Ser Ile Gly Asp
                325                 330                 335

acg ctc atc ctc acc gac gac cag acc ccc gcc gtc gtc gcc ccg gac  1356
Thr Leu Ile Leu Thr Asp Asp Gln Thr Pro Ala Val Val Ala Pro Asp
            340                 345                 350

gtc acc ccg cgc atc ggc tgc acg ctg ccg gag gcc gtc gcc gcc atc  1404
Val Thr Pro Arg Ile Gly Cys Thr Leu Pro Glu Ala Val Ala Ala Ile
        355                 360                 365

gag gtc ggg cag aag gtg ctt ttc gac gac ggc tcg atc gcc gcc cgc  1452
Glu Val Gly Gln Lys Val Leu Phe Asp Asp Gly Ser Ile Ala Ala Arg
    370                 375                 380

gcc gtc gac aag cag gtc acg gag cag ggc cac cac gag gtg cgc ctc  1500
Ala Val Asp Lys Gln Val Thr Glu Gln Gly His His Glu Val Arg Leu
385                 390                 395                 400

gag gtg acc tac gcc ggg ccg gag ggc acc aag ctc gcc gcg tac aag  1548
Glu Val Thr Tyr Ala Gly Pro Glu Gly Thr Lys Leu Ala Ala Tyr Lys
                405                 410                 415

ggc atc aac ctg ccg gac acc gtc ctg ccg ctg ccg agc ctc acc gag  1596
Gly Ile Asn Leu Pro Asp Thr Val Leu Pro Leu Pro Ser Leu Thr Glu
            420                 425                 430

gag gac atc gag gcg ttc cgc ttc gtg gcc gag cac ggt gac atc gcg  1644
Glu Asp Ile Glu Ala Phe Arg Phe Val Ala Glu His Gly Asp Ile Ala
        435                 440                 445

aac gtc tcc ttc att cgc gac gcc gac gac gtc aac ttc gtg ctc gac  1692
Asn Val Ser Phe Ile Arg Asp Ala Asp Asp Val Asn Phe Val Leu Asp
    450                 455                 460

acc ctc gag cag atc gcg cag gag tcc gac gac ccg gag cgc gtc cgc  1740
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```
Thr Leu Glu Gln Ile Ala Gln Glu Ser Asp Asp Pro Glu Arg Val Arg
465                 470                 475                 480

aac ctc ggc atc gtg ctc aag atc gag acg atc ccc gcc tac gag ggc      1788
Asn Leu Gly Ile Val Leu Lys Ile Glu Thr Ile Pro Ala Tyr Glu Gly
                485                 490                 495

ctg tgc agc gtc ctg ctc gcc ggc atg cgc cac ccc aac ctc gga gtc      1836
Leu Cys Ser Val Leu Leu Ala Gly Met Arg His Pro Asn Leu Gly Val
            500                 505                 510

atg atc gcc cgc ggc gac ctg gcc gtc gag ctc ggc ttc gag cgc atg      1884
Met Ile Ala Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Glu Arg Met
        515                 520                 525

gcc gag gtc ccg cgc ctc atc gcc cag atg gcg gag gcc gcc cac gtg      1932
Ala Glu Val Pro Arg Leu Ile Ala Gln Met Ala Glu Ala Ala His Val
    530                 535                 540

ccc gtc atc atg gcc acc cag gtg ctc gag aac ctg gcc aag tcc ggc      1980
Pro Val Ile Met Ala Thr Gln Val Leu Glu Asn Leu Ala Lys Ser Gly
545                 550                 555                 560

ctg ccg acc cgc gcc gag atc acc gac gcc gcg tac gcc ctg cgc tcc      2028
Leu Pro Thr Arg Ala Glu Ile Thr Asp Ala Ala Tyr Ala Leu Arg Ser
                565                 570                 575

gag gcc gtg atg ctc aac aag ggc ccg cac atc acc gac gcg atc cgc      2076
Glu Ala Val Met Leu Asn Lys Gly Pro His Ile Thr Asp Ala Ile Arg
            580                 585                 590

atc ctc cac acc ctg tcg acc aag ctc ggc cgt tcc cag cgc aag aac      2124
Ile Leu His Thr Leu Ser Thr Lys Leu Gly Arg Ser Gln Arg Lys Asn
        595                 600                 605

cgc cag atg ctc cgc cag atc tcg agc tgg atg ccc ggg aat gag tag      2172
Arg Gln Met Leu Arg Gln Ile Ser Ser Trp Met Pro Gly Asn Glu
    610                 615                 620

atgaccgccg cacccaggat catcgcccac cgcggttact ccgcgaagta ccccgagttg     2232

acgcccgtcg ccttcgagcg ggcgctggaa ctgcccgtcc acggcatcga gtgcgatgta     2292

cgcctcagcc tcgacgggga ggtggtggtg ttgcatgacc cgctcatcga ccgcgtcgcg     2352

gacggctccg ggcgggtctc ccgcatgacg gtggacgccc tgcgtgacca caactacggc     2412

accgccgagc tgccgcagga catgctcacc ctcccggagc tgctggagat ggtggagccg     2472
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<210> 144
<211> 623
<212> PRT
<213> Corynebacterium humireducens

<400> 144

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Val Asp Ala Arg Leu Gln Glu Leu Ile Thr Glu Val Asp Gly Leu Ile
1               5                   10                  15
```

Asp Cys Leu Lys Glu Val Glu Glu Gln Val Ala Pro Ala Ile Gly Arg
20 25 30

Val Ala Glu Asn His Arg His Gly Ala Val Asn Leu Val His Tyr Ala
35 40 45

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

Ile Gly Ala Thr Arg Leu Ser Thr Ala Glu Pro Ala Val Leu Ala Arg
65 70 75 80

Leu His Ala Ala Arg Asn Val Leu Ser Ala Tyr Asn Gly Glu Gln Leu
85 90 95

Lys Tyr Thr Gly Ser Glu Val Arg Asp Ala Phe Ala Thr Ala Asp Asp
100 105 110

Ile Leu Glu Asp His Ala Leu Gln Leu Leu Gly Tyr Ser Ser Glu Glu
115 120 125

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

Leu Asp Leu Val Arg Gly Phe Val Glu Ala Gly Met Glu Leu Ala Arg
145 150 155 160

Ile Asn Cys Ala His Asp Gly Pro Glu Val Trp Arg Arg Met Ile Asp
165 170 175

Asn Val His Thr Ala Ala Arg Glu Ala Gly Arg Glu Ile Arg Ile Ala
180 185 190

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

Pro Glu Val Gly Arg Ala Arg Val Thr Arg Glu Asp Thr Gly Val Val
210 215 220

Val Thr Pro Ser Lys Ile Trp Leu Thr Pro Ala Asp Leu Ala Asp Asp
225 230 235 240

Glu Val Pro Pro Val Pro Ala Gly Leu Pro Gly Arg Pro Thr Leu Pro

245 250 255

Leu Arg Val Glu Arg Asp Trp Leu Glu Ala Leu Glu Ile Gly Ser Glu
260 265 270

Ile Thr Phe His Asp Asn Arg Asp Ala Lys Arg Arg Phe Thr Val Thr
275 280 285

Arg Ile Glu Gly Gln Gly Val Leu Leu Glu Gly Arg Arg Asn Ala Tyr
290 295 300

Val Ser Asn Ser Thr Leu Leu Glu Thr Asp Trp Thr Lys Thr Arg Val
305 310 315 320

Ser Gly Val Pro Pro Thr Glu Gln Arg Leu Arg Leu Ser Ile Gly Asp
325 330 335

Thr Leu Ile Leu Thr Asp Asp Gln Thr Pro Ala Val Val Ala Pro Asp
340 345 350

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

Glu Val Gly Gln Lys Val Leu Phe Asp Asp Gly Ser Ile Ala Ala Arg
370 375 380

Ala Val Asp Lys Gln Val Thr Glu Gln Gly His His Glu Val Arg Leu
385 390 395 400

Glu Val Thr Tyr Ala Gly Pro Glu Gly Thr Lys Leu Ala Ala Tyr Lys
405 410 415

Gly Ile Asn Leu Pro Asp Thr Val Leu Pro Leu Pro Ser Leu Thr Glu
420 425 430

Glu Asp Ile Glu Ala Phe Arg Phe Val Ala Glu His Gly Asp Ile Ala
435 440 445

Asn Val Ser Phe Ile Arg Asp Ala Asp Asp Val Asn Phe Val Leu Asp
450 455 460

Thr Leu Glu Gln Ile Ala Gln Glu Ser Asp Asp Pro Glu Arg Val Arg
465 470 475 480

Asn Leu Gly Ile Val Leu Lys Ile Glu Thr Ile Pro Ala Tyr Glu Gly
485 490 495

Leu Cys Ser Val Leu Leu Ala Gly Met Arg His Pro Asn Leu Gly Val
500 505 510

Met Ile Ala Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Glu Arg Met
515 520 525

Ala Glu Val Pro Arg Leu Ile Ala Gln Met Ala Glu Ala Ala His Val
530 535 540

Pro Val Ile Met Ala Thr Gln Val Leu Glu Asn Leu Ala Lys Ser Gly
545 550 555 560

Leu Pro Thr Arg Ala Glu Ile Thr Asp Ala Ala Tyr Ala Leu Arg Ser
565 570 575

Glu Ala Val Met Leu Asn Lys Gly Pro His Ile Thr Asp Ala Ile Arg
580 585 590

Ile Leu His Thr Leu Ser Thr Lys Leu Gly Arg Ser Gln Arg Lys Asn
595 600 605

Arg Gln Met Leu Arg Gln Ile Ser Ser Trp Met Pro Gly Asn Glu
610 615 620

<210> 145
<211> 1878
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1578)
<223> gene enolase

<400> 145
ccctgggggc ggcgcacctg ctgtgtacca acggtgggga cctcagcacc ccggagggct 60

ggtcccgggc gatctacgcc tacaaccgtt ccgaggccta cctcatcgac gtgcgtgacg 120

cggccgcgtc ctatgccctg aaccagccgg cccggtgacg gccacccctg gttgccccct 180

gcaatcgtcg ggttgtagcc cctggtggcg gtttttctgg aagaattgtc cccggacgcg 240

tgtcgagagc gcgcgacgat gacgaactcc catctcatat ggctatagga ggccccaaaa 300

gtg gct gac atc att cac gtt ttc gca cga gag atc atg gat tcc cgt 348

```
Val Ala Asp Ile Ile His Val Phe Ala Arg Glu Ile Met Asp Ser Arg
1               5                  10                  15

ggc aac ccg acc gtc gag gcc ggc gtt gtg ctg gat gac gga acc ctc        396
Gly Asn Pro Thr Val Glu Ala Gly Val Val Leu Asp Asp Gly Thr Leu
            20                  25                  30

gcc acc gcc ggt gtc ccc tcc ggc gcc tcc acc ggt gtc cac gag gca        444
Ala Thr Ala Gly Val Pro Ser Gly Ala Ser Thr Gly Val His Glu Ala
        35                  40                  45

cac gag ctg cgt gac ggc ggc gac cgc tac ctg ggc aag ggt gtc ctg        492
His Glu Leu Arg Asp Gly Gly Asp Arg Tyr Leu Gly Lys Gly Val Leu
    50                  55                  60

aag gcc gtc gag aac gtc aac gag gag atc gcc gac gag ctg gcc ggc        540
Lys Ala Val Glu Asn Val Asn Glu Glu Ile Ala Asp Glu Leu Ala Gly
65                  70                  75                  80

ttc gag gcc gat gac cag cgc gcc atc gac cag gcc atg atc cag ctg        588
Phe Glu Ala Asp Asp Gln Arg Ala Ile Asp Gln Ala Met Ile Gln Leu
                85                  90                  95

gac ggc acc gac aac aag gcc cgc ctg ggt gcc aac gcc atc ctg ggt        636
Asp Gly Thr Asp Asn Lys Ala Arg Leu Gly Ala Asn Ala Ile Leu Gly
            100                 105                 110

gtc tcc atg gct gtg gcc cgc gcc gcc gcc gag tcc gcc ggc ctg ccg        684
Val Ser Met Ala Val Ala Arg Ala Ala Ala Glu Ser Ala Gly Leu Pro
        115                 120                 125

ctc tac cgt tac gtc ggt ggc ccg aac gca cac gtg ctg ccg gtc ccg        732
Leu Tyr Arg Tyr Val Gly Gly Pro Asn Ala His Val Leu Pro Val Pro
    130                 135                 140

atg atg aac atc ctc aac ggt ggc gcc cac gcc gac tcc ggc gtc gac        780
Met Met Asn Ile Leu Asn Gly Gly Ala His Ala Asp Ser Gly Val Asp
145                 150                 155                 160

gtc cag gag ttc atg atc gcc ccg atc ggt gcc gag acc ttc tcc gag        828
Val Gln Glu Phe Met Ile Ala Pro Ile Gly Ala Glu Thr Phe Ser Glu
                165                 170                 175

gct ctg cag gtc ggc gcc gag gtg tac cac acc ctg aag tcc gtc atc        876
Ala Leu Gln Val Gly Ala Glu Val Tyr His Thr Leu Lys Ser Val Ile
            180                 185                 190

cag gag aag ggc ctg tcc acc ggc ctg ggc gac gag ggc ggt ttc gcc        924
Gln Glu Lys Gly Leu Ser Thr Gly Leu Gly Asp Glu Gly Gly Phe Ala
        195                 200                 205

ccg tcc gtc gag tcc acc cgt gcg gcc ctg gac ctc atc gtc gag gcc        972
Pro Ser Val Glu Ser Thr Arg Ala Ala Leu Asp Leu Ile Val Glu Ala
    210                 215                 220

gtc gag aag gcc ggc tac aag ctg ggc gac gat gtc gcc ctg gcc ctg       1020
Val Glu Lys Ala Gly Tyr Lys Leu Gly Asp Asp Val Ala Leu Ala Leu
225                 230                 235                 240
```

```
gac gtc gcc tcc tcc gag ttc ttc aag gac ggc aag tac cac ttc gag      1068
Asp Val Ala Ser Ser Glu Phe Phe Lys Asp Gly Lys Tyr His Phe Glu
                245                 250                 255

ggc aag gag ctc tcc gcc gag gag atg tcc aag gtc tac gag gag ctc      1116
Gly Lys Glu Leu Ser Ala Glu Glu Met Ser Lys Val Tyr Glu Glu Leu
            260                 265                 270

atc aac gag tac ccg atc gtc tcc atc gag gat ccg ctg cag gag gac      1164
Ile Asn Glu Tyr Pro Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp
        275                 280                 285

gac tgg gac ggc tac gtc gcc ctg acc gcc gcc atc ggt gac aag gtc      1212
Asp Trp Asp Gly Tyr Val Ala Leu Thr Ala Ala Ile Gly Asp Lys Val
    290                 295                 300

cag ctg gtc ggc gac gac ttc ttc gtc acc aac ccg gcc cgc ctg aag      1260
Gln Leu Val Gly Asp Asp Phe Phe Val Thr Asn Pro Ala Arg Leu Lys
305                 310                 315                 320

gag ggc atc gcc aag aag gcc gcc aac tcc atc ctg gtg aag gtc aac      1308
Glu Gly Ile Ala Lys Lys Ala Ala Asn Ser Ile Leu Val Lys Val Asn
                325                 330                 335

cag atc ggt acc ctc acc gag acc ttc gac gcc gtc gag atg gcc cac      1356
Gln Ile Gly Thr Leu Thr Glu Thr Phe Asp Ala Val Glu Met Ala His
            340                 345                 350

cgt gcg ggc tac acc tcg atg atg tcc cac cgt tcc ggt gag acc gag      1404
Arg Ala Gly Tyr Thr Ser Met Met Ser His Arg Ser Gly Glu Thr Glu
        355                 360                 365

gac acc acc atc gcc gac ctg gct gtc gca ctg aac tgc ggc cag atc      1452
Asp Thr Thr Ile Ala Asp Leu Ala Val Ala Leu Asn Cys Gly Gln Ile
    370                 375                 380

aag acc ggt gcc ccg gcc cgc tcc gag cgc gtc gcc aag tac aac cag      1500
Lys Thr Gly Ala Pro Ala Arg Ser Glu Arg Val Ala Lys Tyr Asn Gln
385                 390                 395                 400

ctg ctg cgc atc gag cag gag ctc ggc gac gcc gcc gtc tac gcc ggc      1548
Leu Leu Arg Ile Glu Gln Glu Leu Gly Asp Ala Ala Val Tyr Ala Gly
                405                 410                 415

cgc tcc gcc ttc ccg cgc ttc cag aag taa ctgacagcgc tttccgacgc        1598
Arg Ser Ala Phe Pro Arg Phe Gln Lys
            420                 425

ccccgtgcac cccggtgcac gggggcgtcc ccgtatccgt gggggaggac accatggcat    1658

tcttcggcag acgtagggca cggccccggc tggagcccga cttcgtgcac acctggaccg    1718

gtgagcagct ggtccggatc gcggagggcg tcgacctggg caccctccgg gccggtgtacg   1778

ggcgtctcga cgccacctca cggatccact tcctcttcga cttcggtgcc ctcttctccg    1838

acgggtacct cttcgagctc tgggagcggc gtctcctgga                          1878
```

<210> 146
<211> 425
<212> PRT
<213> Corynebacterium humireducens

<400> 146

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

Gly Asn Pro Thr Val Glu Ala Gly Val Val Leu Asp Asp Gly Thr Leu
20 25 30

Ala Thr Ala Gly Val Pro Ser Gly Ala Ser Thr Gly Val His Glu Ala
35 40 45

His Glu Leu Arg Asp Gly Gly Asp Arg Tyr Leu Gly Lys Gly Val Leu
50 55 60

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

Phe Glu Ala Asp Asp Gln Arg Ala Ile Asp Gln Ala Met Ile Gln Leu
85 90 95

Asp Gly Thr Asp Asn Lys Ala Arg Leu Gly Ala Asn Ala Ile Leu Gly
100 105 110

Val Ser Met Ala Val Ala Arg Ala Ala Ala Glu Ser Ala Gly Leu Pro
115 120 125

Leu Tyr Arg Tyr Val Gly Gly Pro Asn Ala His Val Leu Pro Val Pro
130 135 140

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

Val Gln Glu Phe Met Ile Ala Pro Ile Gly Ala Glu Thr Phe Ser Glu
165 170 175

Ala Leu Gln Val Gly Ala Glu Val Tyr His Thr Leu Lys Ser Val Ile
180 185 190

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

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

Val Glu Lys Ala Gly Tyr Lys Leu Gly Asp Asp Val Ala Leu Ala Leu
225 230 235 240

Asp Val Ala Ser Ser Glu Phe Phe Lys Asp Gly Lys Tyr His Phe Glu
245 250 255

Gly Lys Glu Leu Ser Ala Glu Glu Met Ser Lys Val Tyr Glu Glu Leu
260 265 270

Ile Asn Glu Tyr Pro Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp
275 280 285

Asp Trp Asp Gly Tyr Val Ala Leu Thr Ala Ala Ile Gly Asp Lys Val
290 295 300

Gln Leu Val Gly Asp Asp Phe Phe Val Thr Asn Pro Ala Arg Leu Lys
305 310 315 320

Glu Gly Ile Ala Lys Lys Ala Ala Asn Ser Ile Leu Val Lys Val Asn
325 330 335

Gln Ile Gly Thr Leu Thr Glu Thr Phe Asp Ala Val Glu Met Ala His
340 345 350

Arg Ala Gly Tyr Thr Ser Met Met Ser His Arg Ser Gly Glu Thr Glu
355 360 365

Asp Thr Thr Ile Ala Asp Leu Ala Val Ala Leu Asn Cys Gly Gln Ile
370 375 380

Lys Thr Gly Ala Pro Ala Arg Ser Glu Arg Val Ala Lys Tyr Asn Gln
385 390 395 400

Leu Leu Arg Ile Glu Gln Glu Leu Gly Asp Ala Ala Val Tyr Ala Gly
405 410 415

Arg Ser Ala Phe Pro Arg Phe Gln Lys
420 425

<210> 147
<211> 1347
<212> DNA

<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1047)
<223> gene gpmA

<400> 147
tcgccgtctc cgaggggggag acgggagtgc ttgtcgacgg ccacgacacc ggcgactggg 60

ccgacgccct ggagaacctc ctcgacgacg acgacacccg cctgcggatg gcgaccgacg 120

ccgtccagca cgccgcgaac ttctcgtggt cgaactccgc cgcccagctg gcggcggtgt 180

acgccgaggc cctgagcctg gaggtcgaca actgcccgca acgccgcgaa cgggccgaag 240

ggctctaaac ggggggtatt aatccgcacg ctaccggcgg aatcgtggca tattggagac 300

atg acc aac gga aag ctc att ctt ctt cgc cac ggg cag agc cag tgg 348
Met Thr Asn Gly Lys Leu Ile Leu Leu Arg His Gly Gln Ser Gln Trp
1 5 10 15

aac aaa tcg aac cag ttc acc ggc tgg gtg gac gtt gac ctg acc gag 396
Asn Lys Ser Asn Gln Phe Thr Gly Trp Val Asp Val Asp Leu Thr Glu
20 25 30

cag ggc gtc gcc gag gct gtc cgc ggc ggc gag atg ctc aag gag gct 444
Gln Gly Val Ala Glu Ala Val Arg Gly Gly Glu Met Leu Lys Glu Ala
35 40 45

ggt ctc ctg ccg gac atc gtc tac acc tcc ctg ctg cgt cgt gcc atc 492
Gly Leu Leu Pro Asp Ile Val Tyr Thr Ser Leu Leu Arg Arg Ala Ile
50 55 60

cgc acc gcg aac atc gcg ctc aac gcc gcc gac cgt cac tgg atc ccg 540
Arg Thr Ala Asn Ile Ala Leu Asn Ala Ala Asp Arg His Trp Ile Pro
65 70 75 80

gtc gtc cgc gac tgg cgt ctc aac gag cgc cac tac ggt gcg ctg cag 588
Val Val Arg Asp Trp Arg Leu Asn Glu Arg His Tyr Gly Ala Leu Gln
85 90 95

ggc ctg gac aag gcc gag acc aag gac aag tac ggc gac gag cag ttc 636
Gly Leu Asp Lys Ala Glu Thr Lys Asp Lys Tyr Gly Asp Glu Gln Phe
100 105 110

atg gcg tgg cgt cgt tcc tac gac acc ccg ccg ccg gag ctg gcc gac 684
Met Ala Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Glu Leu Ala Asp
115 120 125

gac gcc gag tac tcc cag tcc gac gat gtg cgc tac gcc gcc ctg gag 732
Asp Ala Glu Tyr Ser Gln Ser Asp Asp Val Arg Tyr Ala Ala Leu Glu
130 135 140

aac gca ccg cgt acc gag tgc ctc ctg gac gtc gtc aag cgt ttc atc 780
Asn Ala Pro Arg Thr Glu Cys Leu Leu Asp Val Val Lys Arg Phe Ile
145 150 155 160

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ccg tac tac cag gag gag atc gag ccg cgc gtc aag cgt ggc gag acc        828
Pro Tyr Tyr Gln Glu Glu Ile Glu Pro Arg Val Lys Arg Gly Glu Thr
                165                 170                 175

gtc ctc gtc gcc gcg cac ggc aac tcc ctg cgc gcg ctg gtc aag cac        876
Val Leu Val Ala Ala His Gly Asn Ser Leu Arg Ala Leu Val Lys His
            180                 185                 190

ctg gac aac atc tcg gac gag gac atc gcg gcc ctc aac atc ccg acc        924
Leu Asp Asn Ile Ser Asp Glu Asp Ile Ala Ala Leu Asn Ile Pro Thr
        195                 200                 205

ggc atc ccg ctg gtc tac gag ctg gat gct gac ggc aag gtc gtc aac        972
Gly Ile Pro Leu Val Tyr Glu Leu Asp Ala Asp Gly Lys Val Val Asn
    210                 215                 220

ccg ggc ggc acc tac ctc gac ccc gag gcg gcc gcc gcc ggt gct gcc       1020
Pro Gly Gly Thr Tyr Leu Asp Pro Glu Ala Ala Ala Ala Gly Ala Ala
225                 230                 235                 240

gct gtc gcg gca cag ggt ggc aag tag cctgtagggc gtgtccgccg              1067
Ala Val Ala Ala Gln Gly Gly Lys
                245

ttctcgcgtt cctgttgggc gtcgccgtca ccggcgtcgc ctttccggcg ttgaactggg      1127

cacgtaagcg gatagtccgc caccgttcct cggccacgct cgaggacaac caggtcacca      1187

ccgtcggcca ggtcctgcac ctggccatcc agggttcccc cacgggcgtc accgtcgtcg      1247

accgcggcgg tgaggtgatc ctgtcgaacg cccgcgccca cgagatggcc ctcgtccacg      1307

accgcaccct caacgagcag gtgtggcagg tggcggggga                            1347
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<210> 148
<211> 248
<212> PRT
<213> Corynebacterium humireducens

<400> 148

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

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

Gln Gly Val Ala Glu Ala Val Arg Gly Gly Glu Met Leu Lys Glu Ala
        35                  40                  45

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

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

Val Val Arg Asp Trp Arg Leu Asn Glu Arg His Tyr Gly Ala Leu Gln
85 90 95

Gly Leu Asp Lys Ala Glu Thr Lys Asp Lys Tyr Gly Asp Glu Gln Phe
100 105 110

Met Ala Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Glu Leu Ala Asp
115 120 125

Asp Ala Glu Tyr Ser Gln Ser Asp Asp Val Arg Tyr Ala Ala Leu Glu
130 135 140

Asn Ala Pro Arg Thr Glu Cys Leu Leu Asp Val Val Lys Arg Phe Ile
145 150 155 160

Pro Tyr Tyr Gln Glu Glu Ile Glu Pro Arg Val Lys Arg Gly Glu Thr
165 170 175

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

Leu Asp Asn Ile Ser Asp Glu Asp Ile Ala Ala Leu Asn Ile Pro Thr
195 200 205

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

Pro Gly Gly Thr Tyr Leu Asp Pro Glu Ala Ala Ala Ala Gly Ala Ala
225 230 235 240

Ala Val Ala Ala Gln Gly Gly Lys
245

<210> 149
<211> 1818
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1518)
<223> gene pgk

<400> 149

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cgatccgcac ggctccatct tcgacgccgg cctgaccaag gtcatcggcg accaggtcaa      60

ggtcgtctcc tggtacgaca acgagtgggg ctacacctgc cagctcctgc gcctgaccga     120

gctcgtcgcc tccaagctct aggaccgcga ccccgcactt ccccggcctc cggctgagac     180

cgggggagtg cgcccctgtg gcccggggtg tgcctcggca cacgtcgggc ctcagggcta     240

tccacccccc cagatcagcc gccccttttct catctgaaga caaaagtcaa ggagacagcc     300

atg acc gtg aag act ctg cag gac ctg ctc gac gag ggc gtc gac ggc        348
Met Thr Val Lys Thr Leu Gln Asp Leu Leu Asp Glu Gly Val Asp Gly
1               5                  10                  15

cgc cac atc ctc gtc cgc tcc gac ttc aac gtc ccg ctc aac gac gcc        396
Arg His Ile Leu Val Arg Ser Asp Phe Asn Val Pro Leu Asn Asp Ala
            20                  25                  30

ggt gag atc acc gac gcg ggc cgc atc acc gcc tcc ctg ccc acc ctc        444
Gly Glu Ile Thr Asp Ala Gly Arg Ile Thr Ala Ser Leu Pro Thr Leu
        35                  40                  45

aag gcg ctc gtc gag ggt ggc gcg aag gtc atc gtc atg gcc cac ctg        492
Lys Ala Leu Val Glu Gly Gly Ala Lys Val Ile Val Met Ala His Leu
    50                  55                  60

ggc cgc ccg aag ggc gag gtc aac ccg aag tac tcc ctg gcc ccg gtc        540
Gly Arg Pro Lys Gly Glu Val Asn Pro Lys Tyr Ser Leu Ala Pro Val
65                  70                  75                  80

gcc gag gcc ctc tcc gag gca ctc ggc cag tac gtc gcc ctc gcc ggc        588
Ala Glu Ala Leu Ser Glu Ala Leu Gly Gln Tyr Val Ala Leu Ala Gly
                85                  90                  95

gac gtc acc ggt gag gac gcc cac gag cgc gcc aac ggc ctg acc gag        636
Asp Val Thr Gly Glu Asp Ala His Glu Arg Ala Asn Gly Leu Thr Glu
            100                 105                 110

ggc gac gtc ctg ctc ctc gag aac gtg cgt ttc gac gcc cgc gag acc        684
Gly Asp Val Leu Leu Leu Glu Asn Val Arg Phe Asp Ala Arg Glu Thr
        115                 120                 125

tcc aag gac gag gcc gag cgc ggc gcc ttc gcc gac gag ctc gcc gcc        732
Ser Lys Asp Glu Ala Glu Arg Gly Ala Phe Ala Asp Glu Leu Ala Ala
    130                 135                 140

ctg gcc gcc gac aac ggc gcc ttc gtc tcc gac ggt ttc ggt gtc gtc        780
Leu Ala Ala Asp Asn Gly Ala Phe Val Ser Asp Gly Phe Gly Val Val
145                 150                 155                 160

cac cgt gcg cag gcc tcc gtc tac gac gtc gcc aag cgt ctc ccg gcc        828
His Arg Ala Gln Ala Ser Val Tyr Asp Val Ala Lys Arg Leu Pro Ala
                165                 170                 175

tac gcc ggc aac ctg gtg gag aag gag atc tcc gtc ctg gag aag acc        876
Tyr Ala Gly Asn Leu Val Glu Lys Glu Ile Ser Val Leu Glu Lys Thr
            180                 185                 190

gcc acc aac ccg gag tcc ccg tac gtc gtc gtc ctc ggc ggc tcc aag        924
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Ala Thr Asn Pro Glu Ser Pro Tyr Val Val Val Leu Gly Gly Ser Lys
        195                 200                 205

gtc tcc gac aag ctg ggc gtc atc gag gct ctg gcc ggc aag gcc gac  972
Val Ser Asp Lys Leu Gly Val Ile Glu Ala Leu Ala Gly Lys Ala Asp
    210                 215                 220

aag atc atc atc ggt ggc ggc atg tgc tac acc ttc ctc aac gcc cag 1020
Lys Ile Ile Ile Gly Gly Gly Met Cys Tyr Thr Phe Leu Asn Ala Gln
225                 230                 235                 240

ggc tac aac acc cag aag tcc ctg ctg cag gag gag atg atc gac acc 1068
Gly Tyr Asn Thr Gln Lys Ser Leu Leu Gln Glu Glu Met Ile Asp Thr
                245                 250                 255

tgc aag gac ctc ctc gag cgt ttc ggc gac aag atc gtc ctc ccg gtg 1116
Cys Lys Asp Leu Leu Glu Arg Phe Gly Asp Lys Ile Val Leu Pro Val
            260                 265                 270

gac ctc gtg gcc gcc gcc gag ttc tcc gcc gac tcc gag cac aag gtc 1164
Asp Leu Val Ala Ala Ala Glu Phe Ser Ala Asp Ser Glu His Lys Val
        275                 280                 285

gtc gcc ctc gac gag atc ccg gag ggc tgg ctg tcc ccg gac atc ggc 1212
Val Ala Leu Asp Glu Ile Pro Glu Gly Trp Leu Ser Pro Asp Ile Gly
    290                 295                 300

ccg gag tcc gtc aag aag ttc gcc gac gtc ctc gcc acc tcc aag acc 1260
Pro Glu Ser Val Lys Lys Phe Ala Asp Val Leu Ala Thr Ser Lys Thr
305                 310                 315                 320

gtc ttc tgg aac ggc ccg atg ggt gtc ttc gag atg gca ccg ttc tcc 1308
Val Phe Trp Asn Gly Pro Met Gly Val Phe Glu Met Ala Pro Phe Ser
                325                 330                 335

aag ggc acc gag ggc gtc gcc aag gcc atc atc gac gcg acc gcg aac 1356
Lys Gly Thr Glu Gly Val Ala Lys Ala Ile Ile Asp Ala Thr Ala Asn
            340                 345                 350

aac ggt tcc ttc tcc gtc gtc ggt ggc ggc gac tcc gca gcc tcc gtc 1404
Asn Gly Ser Phe Ser Val Val Gly Gly Gly Asp Ser Ala Ala Ser Val
        355                 360                 365

cgc gtg ctc ggc ctg gac gag gac ggc ttc tcc cac atc tcc acc ggc 1452
Arg Val Leu Gly Leu Asp Glu Asp Gly Phe Ser His Ile Ser Thr Gly
    370                 375                 380

ggc ggc gcc tcc ctc gag ttc ctc gag ggc aag gag ctc ccg ggc gtt 1500
Gly Gly Ala Ser Leu Glu Phe Leu Glu Gly Lys Glu Leu Pro Gly Val
385                 390                 395                 400

tcc gtc ctg gac cgc taa gcacttacca cccactctga aaggagtgcc         1548
Ser Val Leu Asp Arg
                405

ccacccatgg cacgcacccc cctcatcgcc ggcaactgga agatgaacct ggaccaccac 1608

caggccatcg ccaccgtgca gaagctcgac ttcgccctgc cgaaggagta ctacgagaag 1668
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gtcgacgtcg ccgtcaccgt cccgttcacc gacctccgtt ccgtgcagac gctcgtcgac 1728

ggggacaagc tcaaggtcac ctacggtgcc caggacgtct cccggcacga gtccggcgcg 1788

tacaccggtg aggtctccgc tcagatgctc 1818

<210> 150
<211> 405
<212> PRT
<213> Corynebacterium humireducens

<400> 150

Met Thr Val Lys Thr Leu Gln Asp Leu Leu Asp Glu Gly Val Asp Gly
1 5 10 15

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

Gly Glu Ile Thr Asp Ala Gly Arg Ile Thr Ala Ser Leu Pro Thr Leu
35 40 45

Lys Ala Leu Val Glu Gly Gly Ala Lys Val Ile Val Met Ala His Leu
50 55 60

Gly Arg Pro Lys Gly Glu Val Asn Pro Lys Tyr Ser Leu Ala Pro Val
65 70 75 80

Ala Glu Ala Leu Ser Glu Ala Leu Gly Gln Tyr Val Ala Leu Ala Gly
85 90 95

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

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

Ser Lys Asp Glu Ala Glu Arg Gly Ala Phe Ala Asp Glu Leu Ala Ala
130 135 140

Leu Ala Ala Asp Asn Gly Ala Phe Val Ser Asp Gly Phe Gly Val Val
145 150 155 160

His Arg Ala Gln Ala Ser Val Tyr Asp Val Ala Lys Arg Leu Pro Ala
165 170 175

Tyr Ala Gly Asn Leu Val Glu Lys Glu Ile Ser Val Leu Glu Lys Thr

180 185 190

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

Val Ser Asp Lys Leu Gly Val Ile Glu Ala Leu Ala Gly Lys Ala Asp
210 215 220

Lys Ile Ile Ile Gly Gly Gly Met Cys Tyr Thr Phe Leu Asn Ala Gln
225 230 235 240

Gly Tyr Asn Thr Gln Lys Ser Leu Leu Gln Glu Glu Met Ile Asp Thr
245 250 255

Cys Lys Asp Leu Leu Glu Arg Phe Gly Asp Lys Ile Val Leu Pro Val
260 265 270

Asp Leu Val Ala Ala Ala Glu Phe Ser Ala Asp Ser Glu His Lys Val
275 280 285

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

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

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

Lys Gly Thr Glu Gly Val Ala Lys Ala Ile Ile Asp Ala Thr Ala Asn
340 345 350

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

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

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

Ser Val Leu Asp Arg
405

<210> 151
<211> 2058
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1758)
<223> gene glyceraldehyde_3_phopshatdehydrogenase 1

<400> 151
gcggcgggcg ggcgcagcgt ggcgagccgg gccttcagcg gccgcgtcgc ccgcggactg 60

gaaacggact tcacccggaa caacccggac atcccgccga tctaccccta cctcgtgtcg 120

ctgcaggccg cggaacggcg ggaacgcccg cgggaactgg cctactgcct cgtcggggtg 180

ggcgtcgaga agctcggggg tggccccgcg gcggggattc tggctcgact cgcgcctgaa 240

caggcaattt cacgctaaag tcgtggggac gtttcccttt actttcggag gtaaaaagca 300

gtg acc gcc cac gcg cag cct gag cac aac aac tgg aac gag aag atc 348
Val Thr Ala His Ala Gln Pro Glu His Asn Asn Trp Asn Glu Lys Ile
1 5 10 15

gcc ctc gct cag gag atg ctg ccg ctg atc ggc cag ctc cac cgc aac 396
Ala Leu Ala Gln Glu Met Leu Pro Leu Ile Gly Gln Leu His Arg Asn
20 25 30

aac gat gtc gtc gtc tcc atc ttc gga cga ctg ctt gtc ggc gcg acg 444
Asn Asp Val Val Val Ser Ile Phe Gly Arg Leu Leu Val Gly Ala Thr
35 40 45

gac atc gac atc atc aag gcg cac cgt tac gcg cgc cgc gtc gcc gac 492
Asp Ile Asp Ile Ile Lys Ala His Arg Tyr Ala Arg Arg Val Ala Asp
50 55 60

cgt gag atg aag ctc gat cag acc ctc ccg gtc ctg cgc gag ctc gtc 540
Arg Glu Met Lys Leu Asp Gln Thr Leu Pro Val Leu Arg Glu Leu Val
65 70 75 80

gac atg gac ctc ggc acc gcc tcc atc gac ctg ggc cgc ctg gcc acc 588
Asp Met Asp Leu Gly Thr Ala Ser Ile Asp Leu Gly Arg Leu Ala Thr
85 90 95

ggc ttc gag aag tcc ggc ggc acc gac ctg cgt gcc tac ctg gac gag 636
Gly Phe Glu Lys Ser Gly Gly Thr Asp Leu Arg Ala Tyr Leu Asp Glu
100 105 110

cag ctc gcc gac atc gtc ggc aag cgc tcc gag acc gag ccg cgc gac 684
Gln Leu Ala Asp Ile Val Gly Lys Arg Ser Glu Thr Glu Pro Arg Asp
115 120 125

gtc gtc ctc tac ggc ttc ggc cgc atc ggc cgc ctc ctg gcc cgc atc 732
Val Val Leu Tyr Gly Phe Gly Arg Ile Gly Arg Leu Leu Ala Arg Ile
130 135 140

ctc atc tcc cgt gag gcc acc tac ggc ggc gtc cgc ctc cgc gcg gtg 780

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Leu Ile Ser Arg Glu Ala Thr Tyr Gly Gly Val Arg Leu Arg Ala Val
145                 150                 155                 160

gtg gta cgc aag aac tcc gag gac gac atc gtc aag cgt gcc tcc ctc  828
Val Val Arg Lys Asn Ser Glu Asp Asp Ile Val Lys Arg Ala Ser Leu
                165                 170                 175

ctg cgc cgt gac tcc gtg cac ggc gcc ttc gac ggc acg atc acc gtc  876
Leu Arg Arg Asp Ser Val His Gly Ala Phe Asp Gly Thr Ile Thr Val
            180                 185                 190

gac aag gag aac aac gtc atc tgg gcc aac ggc acc aag atc cag atc  924
Asp Lys Glu Asn Asn Val Ile Trp Ala Asn Gly Thr Lys Ile Gln Ile
        195                 200                 205

atc tac tcc aac tcc ccg gcc gag gtc gac tac acc gcc tac ggc atc  972
Ile Tyr Ser Asn Ser Pro Ala Glu Val Asp Tyr Thr Ala Tyr Gly Ile
    210                 215                 220

aat gac gcc atc gtg gtg gac aac acc ggc atc tgg cgc gac cgc gag 1020
Asn Asp Ala Ile Val Val Asp Asn Thr Gly Ile Trp Arg Asp Arg Glu
225                 230                 235                 240

gga ctg tcc cag cac ctg cag tcc aag ggc gtc tcc cgc gtc gtc ctc 1068
Gly Leu Ser Gln His Leu Gln Ser Lys Gly Val Ser Arg Val Val Leu
                245                 250                 255

acc gcc ccg ggc aag ggc gac ctg ccg aac atc gtc tac ggc atc aac 1116
Thr Ala Pro Gly Lys Gly Asp Leu Pro Asn Ile Val Tyr Gly Ile Asn
            260                 265                 270

gac gac atg atc acc gac gac gag cag atc atc acc gcc gcc tcc tgc 1164
Asp Asp Met Ile Thr Asp Asp Glu Gln Ile Ile Thr Ala Ala Ser Cys
        275                 280                 285

acc acc aac ggc atc acc ccg gtc ctg aag gtc atc aac gac cgc tac 1212
Thr Thr Asn Gly Ile Thr Pro Val Leu Lys Val Ile Asn Asp Arg Tyr
    290                 295                 300

ggc gtc gag cac ggt cac gtc gag acc gtc cac tcc ttc acc aac gac 1260
Gly Val Glu His Gly His Val Glu Thr Val His Ser Phe Thr Asn Asp
305                 310                 315                 320

cag aac ctc atc gac aac ttc cac aag ggc acc cgc cgt ggc cgt gcc 1308
Gln Asn Leu Ile Asp Asn Phe His Lys Gly Thr Arg Arg Gly Arg Ala
                325                 330                 335

gcc tcc ctc aac atg gtc ctc acc gag acc ggc gcc gcc aag gcc gtc 1356
Ala Ser Leu Asn Met Val Leu Thr Glu Thr Gly Ala Ala Lys Ala Val
            340                 345                 350

tcc aag gcc ctg ccg gag ttc gag ggc aag ctc acc ggc aac gcc atc 1404
Ser Lys Ala Leu Pro Glu Phe Glu Gly Lys Leu Thr Gly Asn Ala Ile
        355                 360                 365

cgc gtc ccc acc ccg aac gtc tcc atg gcg gtg ctc aac ctc acc ctg 1452
Arg Val Pro Thr Pro Asn Val Ser Met Ala Val Leu Asn Leu Thr Leu
    370                 375                 380
```

```
gag aag gag gtc gac cgc gag gag gtc aac aac ttc ctg cgc aag gtc      1500
Glu Lys Glu Val Asp Arg Glu Glu Val Asn Asn Phe Leu Arg Lys Val
385                 390                 395                 400

tcc ctg cac tcc gac ctg cgc cag cag atc tcc tac atc aac tcc ccg      1548
Ser Leu His Ser Asp Leu Arg Gln Gln Ile Ser Tyr Ile Asn Ser Pro
                405                 410                 415

gag gtc gtg tcc acc gac ttc gtc ggc agc acc cac gcc ggc atc gtc      1596
Glu Val Val Ser Thr Asp Phe Val Gly Ser Thr His Ala Gly Ile Val
            420                 425                 430

gac ggc ctg gcc acc atc gcc tcc ggc aag cac ctc gtg ctc tac gtc      1644
Asp Gly Leu Ala Thr Ile Ala Ser Gly Lys His Leu Val Leu Tyr Val
        435                 440                 445

tgg tac gac aac gag ttc ggc tac tcc aac cag gtc atc cgc atc gtc      1692
Trp Tyr Asp Asn Glu Phe Gly Tyr Ser Asn Gln Val Ile Arg Ile Val
    450                 455                 460

gag gag gtc gcc ggc gcc cgc ccg gag atc tac ccg cgt cgc ctg gag      1740
Glu Glu Val Ala Gly Ala Arg Pro Glu Ile Tyr Pro Arg Arg Leu Glu
465                 470                 475                 480

gcc tct gag ctg aag tag cttttccagg atcagcttca agctgccgca             1788
Ala Ser Glu Leu Lys
                485

gcgacaggcc cggttctcca cgtggagaac cgggcctgtc gcattcagga ggggcggcag    1848

cggcacaggc agatgaagaa tcgtcgtcgg tgtgtccgct cactgcgcct ggtgttaggc    1908

ccgtgctcta cacccgcccg ctgccggtta cggcaatcat ggccaggagc aggtgctgac    1968

cggtctgaca ggcgcctacg ctcacccagt caactgctga ctgggacatt gacttgagga    2028

tgcgtgcttc ccggcgtatg tggtcccttg                                     2058
```

<210> 152
<211> 485
<212> PRT
<213> Corynebacterium humireducens

<400> 152

```
Val Thr Ala His Ala Gln Pro Glu His Asn Asn Trp Asn Glu Lys Ile
1               5                   10                  15

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

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

Asp Ile Asp Ile Ile Lys Ala His Arg Tyr Ala Arg Arg Val Ala Asp
```

50 55 60

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

Asp Met Asp Leu Gly Thr Ala Ser Ile Asp Leu Gly Arg Leu Ala Thr
85 90 95

Gly Phe Glu Lys Ser Gly Gly Thr Asp Leu Arg Ala Tyr Leu Asp Glu
100 105 110

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

Val Val Leu Tyr Gly Phe Gly Arg Ile Gly Arg Leu Leu Ala Arg Ile
130 135 140

Leu Ile Ser Arg Glu Ala Thr Tyr Gly Gly Val Arg Leu Arg Ala Val
145 150 155 160

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

Leu Arg Arg Asp Ser Val His Gly Ala Phe Asp Gly Thr Ile Thr Val
180 185 190

Asp Lys Glu Asn Asn Val Ile Trp Ala Asn Gly Thr Lys Ile Gln Ile
195 200 205

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

Asn Asp Ala Ile Val Val Asp Asn Thr Gly Ile Trp Arg Asp Arg Glu
225 230 235 240

Gly Leu Ser Gln His Leu Gln Ser Lys Gly Val Ser Arg Val Val Leu
245 250 255

Thr Ala Pro Gly Lys Gly Asp Leu Pro Asn Ile Val Tyr Gly Ile Asn
260 265 270

Asp Asp Met Ile Thr Asp Asp Glu Gln Ile Ile Thr Ala Ala Ser Cys
275 280 285

Thr Thr Asn Gly Ile Thr Pro Val Leu Lys Val Ile Asn Asp Arg Tyr
290 295 300

Gly Val Glu His Gly His Val Glu Thr Val His Ser Phe Thr Asn Asp
305 310 315 320

Gln Asn Leu Ile Asp Asn Phe His Lys Gly Thr Arg Arg Gly Arg Ala
325 330 335

Ala Ser Leu Asn Met Val Leu Thr Glu Thr Gly Ala Ala Lys Ala Val
340 345 350

Ser Lys Ala Leu Pro Glu Phe Glu Gly Lys Leu Thr Gly Asn Ala Ile
355 360 365

Arg Val Pro Thr Pro Asn Val Ser Met Ala Val Leu Asn Leu Thr Leu
370 375 380

Glu Lys Glu Val Asp Arg Glu Glu Val Asn Asn Phe Leu Arg Lys Val
385 390 395 400

Ser Leu His Ser Asp Leu Arg Gln Gln Ile Ser Tyr Ile Asn Ser Pro
405 410 415

Glu Val Val Ser Thr Asp Phe Val Gly Ser Thr His Ala Gly Ile Val
420 425 430

Asp Gly Leu Ala Thr Ile Ala Ser Gly Lys His Leu Val Leu Tyr Val
435 440 445

Trp Tyr Asp Asn Glu Phe Gly Tyr Ser Asn Gln Val Ile Arg Ile Val
450 455 460

Glu Glu Val Ala Gly Ala Arg Pro Glu Ile Tyr Pro Arg Arg Leu Glu
465 470 475 480

Ala Ser Glu Leu Lys
485

<210> 153
<211> 1605
<212> DNA
<213> Corynebacterium humireducens

<220>

<221> CDS
<222> (301)..(1305)
<223> gene glyceraldehyde_3_phopshatdehydrogenase 2

<400> 153
gctccattcg ggggtgaatc gggcatgtgt gaccgatatt attcgccggt gtccggagga 60

ccgcccggtg cccggccgcc tgcgaccccc cgttgacaac gactttcggg aagtggggcg 120

gaccggaatg tgagggcaaa cataatcgga aatccgcgga tgtctgaaaa tgtctgattc 180

ttcgctgcac agcggggtaa gtgccgctaa actgtcgctt gatgggccgt gaacgccagt 240

cactacgacg gacagtgcgg tcacatccgg acacgtgtac tcaaacccga ggagaaaatt 300

gtg acc atc cgc gtt ggc atc aac ggc ttc ggc cgt atc ggc cgt aac 348
Val Thr Ile Arg Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn
1 5 10 15

ttc tac cgc gca gtc ctg gag cgc agc gag gcc atc gag atc gtc gcc 396
Phe Tyr Arg Ala Val Leu Glu Arg Ser Glu Ala Ile Glu Ile Val Ala
20 25 30

gtc aac gac ctc acc gac aac aag acg ctg tcg acc ctc ctg aag tac 444
Val Asn Asp Leu Thr Asp Asn Lys Thr Leu Ser Thr Leu Leu Lys Tyr
35 40 45

gac tcc atc ctc ggc aag ctg ccg ggc gag gtc tcg ttc gac gac gac 492
Asp Ser Ile Leu Gly Lys Leu Pro Gly Glu Val Ser Phe Asp Asp Asp
50 55 60

tcc atc acc tac gac ggc aag acc atc gcc gtc tcc gct gag cgc gac 540
Ser Ile Thr Tyr Asp Gly Lys Thr Ile Ala Val Ser Ala Glu Arg Asp
65 70 75 80

ccg aag aac ctg gac tgg gcc gcc cac aac gtg gac atc gtc atc gag 588
Pro Lys Asn Leu Asp Trp Ala Ala His Asn Val Asp Ile Val Ile Glu
85 90 95

tcc acc ggc ttc ttc acc gac gcc gag gca gcc aag gcc cac atc gag 636
Ser Thr Gly Phe Phe Thr Asp Ala Glu Ala Ala Lys Ala His Ile Glu
100 105 110

gcc ggc gcc aag aag gtc atc atc tcc gcc ccg gcc tcc aac gag gac 684
Ala Gly Ala Lys Lys Val Ile Ile Ser Ala Pro Ala Ser Asn Glu Asp
115 120 125

gcg acc ttc gtc tac ggc gtc aac cac cag gac tac gac ccg gag aac 732
Ala Thr Phe Val Tyr Gly Val Asn His Gln Asp Tyr Asp Pro Glu Asn
130 135 140

cac aac gtc atc tcc gcc gca tcc tgc acc acc aac tgc ctg gcc ccg 780
His Asn Val Ile Ser Ala Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro
145 150 155 160

atg gcc aag gtc ctc aac gac aag ctc ggc atc gag cgc ggc ctg atg 828
Met Ala Lys Val Leu Asn Asp Lys Leu Gly Ile Glu Arg Gly Leu Met
165 170 175

```
acc acc atc cac gcc tac acc ggt gac cag cgt ctg cac gac gcc ccg        876
Thr Thr Ile His Ala Tyr Thr Gly Asp Gln Arg Leu His Asp Ala Pro
            180                 185                 190

cac aag gac ctg cgc cgc gcc cgc gcc gcc gcc gtc aac atc gtg ccc        924
His Lys Asp Leu Arg Arg Ala Arg Ala Ala Ala Val Asn Ile Val Pro
        195                 200                 205

acc tcc acc ggt gcc gcc aag gcc gtc tcc ctg gtc ctg ccg gag ctg        972
Thr Ser Thr Gly Ala Ala Lys Ala Val Ser Leu Val Leu Pro Glu Leu
    210                 215                 220

aag ggc aag ctg gac ggc tac gca ctg cgc gtc ccg acc atc acc ggt       1020
Lys Gly Lys Leu Asp Gly Tyr Ala Leu Arg Val Pro Thr Ile Thr Gly
225                 230                 235                 240

tcc gcc acc gac ctc acc ttc acc gcc tcc cgc gag acc tct gtc gag       1068
Ser Ala Thr Asp Leu Thr Phe Thr Ala Ser Arg Glu Thr Ser Val Glu
                245                 250                 255

gag gtc aac gcc ttc atc aag gag gcc gcg cag ggc gag ttc ggt gag       1116
Glu Val Asn Ala Phe Ile Lys Glu Ala Ala Gln Gly Glu Phe Gly Glu
            260                 265                 270

acc ctg gcc tac acc gag gat ccg atc gtc tcc acc gac atc gtc acc       1164
Thr Leu Ala Tyr Thr Glu Asp Pro Ile Val Ser Thr Asp Ile Val Thr
        275                 280                 285

gat ccg cac ggc tcc atc ttc gac gcc ggc ctg acc aag gtc atc ggc       1212
Asp Pro His Gly Ser Ile Phe Asp Ala Gly Leu Thr Lys Val Ile Gly
    290                 295                 300

gac cag gtc aag gtc gtc tcc tgg tac gac aac gag tgg ggc tac acc       1260
Asp Gln Val Lys Val Val Ser Trp Tyr Asp Asn Glu Trp Gly Tyr Thr
305                 310                 315                 320

tgc cag ctc ctg cgc ctg acc gag ctc gtc gcc tcc aag ctc tag           1305
Cys Gln Leu Leu Arg Leu Thr Glu Leu Val Ala Ser Lys Leu
                325                 330

gaccgcgacc ccgcacttcc ccggcctccg gctgagaccg ggggagtgcg ccccctgtggc    1365

ccggggtgtg cctcggcaca cgtcgggcct cagggctatc cacccccctca gatcagccgc    1425

ccctttctca tctgaagaca aaagtcaagg agacagccat gaccgtgaag actctgcagg    1485

acctgctcga cgagggcgtc gacggccgcc acatcctcgt ccgctccgac ttcaacgtcc    1545

cgctcaacga cgccggtgag atcaccgacg cgggccgcat caccgcctcc ctgcccaccc    1605
```

<210> 154
<211> 334
<212> PRT
<213> Corynebacterium humireducens

<400> 154

Val Thr Ile Arg Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn

```
1               5                   10                  15

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

Val Asn Asp Leu Thr Asp Asn Lys Thr Leu Ser Thr Leu Leu Lys Tyr
        35                  40                  45

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

Ser Ile Thr Tyr Asp Gly Lys Thr Ile Ala Val Ser Ala Glu Arg Asp
65                  70                  75                  80

Pro Lys Asn Leu Asp Trp Ala Ala His Asn Val Asp Ile Val Ile Glu
                85                  90                  95

Ser Thr Gly Phe Phe Thr Asp Ala Glu Ala Ala Lys Ala His Ile Glu
            100                 105                 110

Ala Gly Ala Lys Lys Val Ile Ile Ser Ala Pro Ala Ser Asn Glu Asp
        115                 120                 125

Ala Thr Phe Val Tyr Gly Val Asn His Gln Asp Tyr Asp Pro Glu Asn
    130                 135                 140

His Asn Val Ile Ser Ala Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro
145                 150                 155                 160

Met Ala Lys Val Leu Asn Asp Lys Leu Gly Ile Glu Arg Gly Leu Met
                165                 170                 175

Thr Thr Ile His Ala Tyr Thr Gly Asp Gln Arg Leu His Asp Ala Pro
            180                 185                 190

His Lys Asp Leu Arg Arg Ala Arg Ala Ala Ala Val Asn Ile Val Pro
        195                 200                 205

Thr Ser Thr Gly Ala Ala Lys Ala Val Ser Leu Val Leu Pro Glu Leu
    210                 215                 220

Lys Gly Lys Leu Asp Gly Tyr Ala Leu Arg Val Pro Thr Ile Thr Gly
225                 230                 235                 240
```

Ser Ala Thr Asp Leu Thr Phe Thr Ala Ser Arg Glu Thr Ser Val Glu
245 250 255

Glu Val Asn Ala Phe Ile Lys Glu Ala Ala Gln Gly Glu Phe Gly Glu
260 265 270

Thr Leu Ala Tyr Thr Glu Asp Pro Ile Val Ser Thr Asp Ile Val Thr
275 280 285

Asp Pro His Gly Ser Ile Phe Asp Ala Gly Leu Thr Lys Val Ile Gly
290 295 300

Asp Gln Val Lys Val Val Ser Trp Tyr Asp Asn Glu Trp Gly Tyr Thr
305 310 315 320

Cys Gln Leu Leu Arg Leu Thr Glu Leu Val Ala Ser Lys Leu
325 330

<210> 155
<211> 1380
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1080)
<223> gene tpiA

<400> 155
aagaccgtct tctggaacgg cccgatgggt gtcttcgaga tggcaccgtt ctccaagggc 60

accgagggcg tcgccaaggc catcatcgac gcgaccgcga acaacggttc cttctccgtc 120

gtcggtggcg gcgactccgc agcctccgtc cgcgtgctcg gcctggacga ggacggcttc 180

tcccacatct ccaccggcgg cggcgcctcc ctcgagttcc tcgagggcaa ggagctcccg 240

ggcgtttccg tcctggaccg ctaagcactt accacccact ctgaaaggag tgccccaccc 300

atg gca cgc acc ccc ctc atc gcc ggc aac tgg aag atg aac ctg gac 348
Met Ala Arg Thr Pro Leu Ile Ala Gly Asn Trp Lys Met Asn Leu Asp
1 5 10 15

cac cac cag gcc atc gcc acc gtg cag aag ctc gac ttc gcc ctg ccg 396
His His Gln Ala Ile Ala Thr Val Gln Lys Leu Asp Phe Ala Leu Pro
20 25 30

aag gag tac tac gag aag gtc gac gtc gcc gtc acc gtc ccg ttc acc 444
Lys Glu Tyr Tyr Glu Lys Val Asp Val Ala Val Thr Val Pro Phe Thr
35 40 45

gac ctc cgt tcc gtg cag acg ctc gtc gac ggg gac aag ctc aag gtc 492

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

acc tac ggt gcc cag gac gtc tcc cgg cac gag tcc ggc gcg tac acc      540
Thr Tyr Gly Ala Gln Asp Val Ser Arg His Glu Ser Gly Ala Tyr Thr
65                  70                  75                  80

ggt gag gtc tcc gct cag atg ctc gcc aag ctc ggc tgc acc tgg gtc      588
Gly Glu Val Ser Ala Gln Met Leu Ala Lys Leu Gly Cys Thr Trp Val
                85                  90                  95

gtc gtc ggc cac tcc gag cgc cgc gag tac cac aac gag tcc gac gag      636
Val Val Gly His Ser Glu Arg Arg Glu Tyr His Asn Glu Ser Asp Glu
            100                 105                 110

ctg gtc gcc gcg aag gcc gct gcc gcc ctc cgc cac ggc atg agc ccg      684
Leu Val Ala Ala Lys Ala Ala Ala Ala Leu Arg His Gly Met Ser Pro
        115                 120                 125

atc gtg tgc gtc ggc gag ccg ctg gag atc cgc gag gcc ggc acc cac      732
Ile Val Cys Val Gly Glu Pro Leu Glu Ile Arg Glu Ala Gly Thr His
    130                 135                 140

gtc gac tac gtc gtc gag cag acc cgt gcc tcc ctg gcc ggc ctg tcc      780
Val Asp Tyr Val Val Glu Gln Thr Arg Ala Ser Leu Ala Gly Leu Ser
145                 150                 155                 160

gcc gag gac ctg tcc aac acc gtc atc gcc tac gag ccc gtg tgg gcc      828
Ala Glu Asp Leu Ser Asn Thr Val Ile Ala Tyr Glu Pro Val Trp Ala
                165                 170                 175

atc ggc acc ggc aag gtc gcc tcc gcg gcc gat gcc cag gag gtc tgt      876
Ile Gly Thr Gly Lys Val Ala Ser Ala Ala Asp Ala Gln Glu Val Cys
            180                 185                 190

gcg gcg atc cgc ggt ctc gtc cgc gag ctg gcc ggt gac gag gtc gcc      924
Ala Ala Ile Arg Gly Leu Val Arg Glu Leu Ala Gly Asp Glu Val Ala
        195                 200                 205

gac ggc atc cgc atc ctc tac ggc ggt tcc gtc aag acc gac tcg gtc      972
Asp Gly Ile Arg Ile Leu Tyr Gly Gly Ser Val Lys Thr Asp Ser Val
    210                 215                 220

gcc gag atc gtc ggt cag ccc gac gtc gac ggt ggt ctc gtc ggt ggc     1020
Ala Glu Ile Val Gly Gln Pro Asp Val Asp Gly Gly Leu Val Gly Gly
225                 230                 235                 240

gcc tcg ctc gac ggc gag gag ttc gcc aag ctg gcg gcc gcc gcg gcg     1068
Ala Ser Leu Asp Gly Glu Glu Phe Ala Lys Leu Ala Ala Ala Ala Ala
                245                 250                 255

tcc gtc gtc tag catcacctca tccaccggcc ccgggcactg aacattcagt         1120
Ser Val Val

gcccggggcc ggtgtccttt ctccggggaa tatggtgcgc aatccccacg cacggccgtc   1180

atatgcgtca tgatggggag gcgaaccgca tccccgcctt cttcgagtac gaacagggag   1240
```

acactcaatg accgtccgcg atcatctgca ggaagacatc cgctacctcg gccgtatcct 1300

cggccaggtc atcgcggaac aggagggcga ggacgtgttc aacctcgtcg agcacgcccg 1360

ccagcaggcc ttcgaggtgg 1380

<210> 156
<211> 259
<212> PRT
<213> Corynebacterium humireducens

<400> 156

Met Ala Arg Thr Pro Leu Ile Ala Gly Asn Trp Lys Met Asn Leu Asp
1 5 10 15

His His Gln Ala Ile Ala Thr Val Gln Lys Leu Asp Phe Ala Leu Pro
20 25 30

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

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

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

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

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

Leu Val Ala Ala Lys Ala Ala Ala Ala Leu Arg His Gly Met Ser Pro
115 120 125

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

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

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

Ile Gly Thr Gly Lys Val Ala Ser Ala Ala Asp Ala Gln Glu Val Cys

180 185 190

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

Asp Gly Ile Arg Ile Leu Tyr Gly Gly Ser Val Lys Thr Asp Ser Val
210 215 220

Ala Glu Ile Val Gly Gln Pro Asp Val Asp Gly Gly Leu Val Gly Gly
225 230 235 240

Ala Ser Leu Asp Gly Glu Glu Phe Ala Lys Leu Ala Ala Ala Ala Ala
245 250 255

Ser Val Val

<210> 157
<211> 1632
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1332)
<223> gene frutcosebisphosphataldolase

<400> 157
ccgactggac cgccgacgcc cgcctgccgc acaacttcgg cctggcgccg tcgtcactgc 60

cggaggccct cggcgtcctg cgtatcgacg aacgcgatct ctccgtccag ctctccggct 120

ggatgctgct ggaggccgcc gcccgggtgt ccacctacgc ggagacccag cggtcctgat 180

ccccgcgcgc ggggcggggg gggaggtgac gcgggttttc cgccctctgt tgcgagcgcg 240

ggaggccaaa gggaggcata ctggtatacg gacctgtttg ctaacccgga ggatcaccct 300

atg cct atc gcg act ccc gaa atc tac aac gag atg ctc gac agg gcc 348
Met Pro Ile Ala Thr Pro Glu Ile Tyr Asn Glu Met Leu Asp Arg Ala
1 5 10 15

aag gag ggc ggc tac gcc ttc ccg gcc atc aac tgc acc tcc tcg gag 396
Lys Glu Gly Gly Tyr Ala Phe Pro Ala Ile Asn Cys Thr Ser Ser Glu
20 25 30

acc atc aac gcc gct ctc cgc ggc ttc gcc gag gcc gag tcc gac ggc 444
Thr Ile Asn Ala Ala Leu Arg Gly Phe Ala Glu Ala Glu Ser Asp Gly
35 40 45

atc atc cag ttc tcc acc ggt ggc gcc gaa ttc ggc tcc ggt ctg tcc 492
Ile Ile Gln Phe Ser Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ser

```
     50                  55                  60

gtg aag aac aag gtc gcc ggc gcc gtc gcc ctg gcc tcc ttc gcg cat        540
Val Lys Asn Lys Val Ala Gly Ala Val Ala Leu Ala Ser Phe Ala His
65                  70                  75                  80

gag gcc gcc aag cac tac ggc gtc aac gtc gcc ctg cac acc gac cac        588
Glu Ala Ala Lys His Tyr Gly Val Asn Val Ala Leu His Thr Asp His
                85                  90                  95

tgc cag aag gag gtg ctc gac gag ttc gtg cgc ccg ctg ctg gcc atc        636
Cys Gln Lys Glu Val Leu Asp Glu Phe Val Arg Pro Leu Leu Ala Ile
            100                 105                 110

tcc cag gag cgc gtc gac gcc ggt gag ctc ccg ctc ttc cag tcc cac        684
Ser Gln Glu Arg Val Asp Ala Gly Glu Leu Pro Leu Phe Gln Ser His
        115                 120                 125

atg tgg gac ggt tcc gct gtc ccg atc gac gag aac ctg gag atc gcg        732
Met Trp Asp Gly Ser Ala Val Pro Ile Asp Glu Asn Leu Glu Ile Ala
    130                 135                 140

aag gag ctg ctg gag aag tcc cgc aag gcg aac att atc ctc gag atc        780
Lys Glu Leu Leu Glu Lys Ser Arg Lys Ala Asn Ile Ile Leu Glu Ile
145                 150                 155                 160

gag atc ggt gtc gtc ggc ggc gag gag gac ggt gtc gag gcc aag gcc        828
Glu Ile Gly Val Val Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala
                165                 170                 175

ggc gcc aac ctc tac acc acc gag gag gac ttc gag aag acc atc gac        876
Gly Ala Asn Leu Tyr Thr Thr Glu Glu Asp Phe Glu Lys Thr Ile Asp
            180                 185                 190

gcc atc ggc acc ggt gag aac ggc cgc tac ctg ctg gcc gcg acc ttc        924
Ala Ile Gly Thr Gly Glu Asn Gly Arg Tyr Leu Leu Ala Ala Thr Phe
        195                 200                 205

ggc aac gtc cac ggc gtg tac aag ccg ggc aac gtg aag ctg cgt ccg        972
Gly Asn Val His Gly Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro
    210                 215                 220

gag gtc ctg ctc gag ggc cag aag gtg gcc cgc cgc aag ctg ggt ctg       1020
Glu Val Leu Leu Glu Gly Gln Lys Val Ala Arg Arg Lys Leu Gly Leu
225                 230                 235                 240

ggc gac gac gcc ctg ccg ttc gac ttc gtc ttc cac ggt ggc tcc ggc       1068
Gly Asp Asp Ala Leu Pro Phe Asp Phe Val Phe His Gly Gly Ser Gly
                245                 250                 255

tcc gag aag gag aag atc gag gag gcg ctg cgt tac ggc acc atc aag       1116
Ser Glu Lys Glu Lys Ile Glu Glu Ala Leu Arg Tyr Gly Thr Ile Lys
            260                 265                 270

atg aac gtc gac acg gac acc cag tac gcg ttc acc cgt ccg atc gtc       1164
Met Asn Val Asp Thr Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val
        275                 280                 285

acg cac atg ttc cag aac tac gac ggc gtc ctc aag atc gac ggc gag       1212
```

```
Thr His Met Phe Gln Asn Tyr Asp Gly Val Leu Lys Ile Asp Gly Glu
    290                 295                 300

gtg ggc aac aag aag gcc tac gac ccg cgt tcc tac ctg aag aag gcc      1260
Val Gly Asn Lys Lys Ala Tyr Asp Pro Arg Ser Tyr Leu Lys Lys Ala
305                 310                 315                 320

gag cag tcg atg gct gag cgc gtc atc gag gcc tgc cag gac ctg cac      1308
Glu Gln Ser Met Ala Glu Arg Val Ile Glu Ala Cys Gln Asp Leu His
                325                 330                 335

tcc gtg ggc aag acc gtc aag tag tcttctccac ccgaggaaag ccccgccctg      1362
Ser Val Gly Lys Thr Val Lys
            340

tgcggggctt tctgcgctta gtatcggtgc atggccaaac tgagaatcgg caccctggaa      1422

cgtctccgcc agctcgaggg ctcgttggag tcccgggcgc tgcgcgtgcg gaagcgcttc      1482

ttccggatcg tgcaggtcgc ggtggccgcg ggggtgtcgt tctgggtggc gcagtccctc      1542

atcgggcatc cggtcccgtt cttcgcgccg atcacggtga tcatcatcct ggggctcacc      1602

ggcggcgacc gcatccggcg ggccctggag                                      1632
```

<210> 158
<211> 343
<212> PRT
<213> Corynebacterium humireducens

<400> 158

```
Met Pro Ile Ala Thr Pro Glu Ile Tyr Asn Glu Met Leu Asp Arg Ala
1               5                   10                  15

Lys Glu Gly Gly Tyr Ala Phe Pro Ala Ile Asn Cys Thr Ser Ser Glu
            20                  25                  30

Thr Ile Asn Ala Ala Leu Arg Gly Phe Ala Glu Ala Glu Ser Asp Gly
        35                  40                  45

Ile Ile Gln Phe Ser Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ser
    50                  55                  60

Val Lys Asn Lys Val Ala Gly Ala Val Ala Leu Ala Ser Phe Ala His
65                  70                  75                  80

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

Cys Gln Lys Glu Val Leu Asp Glu Phe Val Arg Pro Leu Leu Ala Ile
            100                 105                 110
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Ser Gln Glu Arg Val Asp Ala Gly Glu Leu Pro Leu Phe Gln Ser His
115 120 125

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

Lys Glu Leu Leu Glu Lys Ser Arg Lys Ala Asn Ile Ile Leu Glu Ile
145 150 155 160

Glu Ile Gly Val Val Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala
165 170 175

Gly Ala Asn Leu Tyr Thr Thr Glu Glu Asp Phe Glu Lys Thr Ile Asp
180 185 190

Ala Ile Gly Thr Gly Glu Asn Gly Arg Tyr Leu Leu Ala Ala Thr Phe
195 200 205

Gly Asn Val His Gly Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro
210 215 220

Glu Val Leu Leu Glu Gly Gln Lys Val Ala Arg Arg Lys Leu Gly Leu
225 230 235 240

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

Ser Glu Lys Glu Lys Ile Glu Glu Ala Leu Arg Tyr Gly Thr Ile Lys
260 265 270

Met Asn Val Asp Thr Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val
275 280 285

Thr His Met Phe Gln Asn Tyr Asp Gly Val Leu Lys Ile Asp Gly Glu
290 295 300

Val Gly Asn Lys Lys Ala Tyr Asp Pro Arg Ser Tyr Leu Lys Lys Ala
305 310 315 320

Glu Gln Ser Met Ala Glu Arg Val Ile Glu Ala Cys Gln Asp Leu His
325 330 335

Ser Val Gly Lys Thr Val Lys

340

<210> 159
<211> 1566
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1266)
<223> gene 1-phosphofructokinase

<400> 159
agaacaccac aaaatccact agttagcaac gatccagaca ggcaaccctt gacaaacgga 60

cacaatcgga caatgatgat gttgtaacac cacattaaat gtgacttaat tcatcatttt 120

cataacgtcc cgcccgggac agccccggag cgccccgatc cccgggtcgc gccccatagg 180

attgatccag ctcaggacct gttcggtcac ccgaccggac accgctccgg gcacgcgtcc 240

cccgccaccc agcggacacg ccgcaacgac acgtttttcc gaacggacag ggagcccgcc 300

gtg att ctc acc ctc acc ccc aac ccc agc atc gac gcg acc atg caa 348
Val Ile Leu Thr Leu Thr Pro Asn Pro Ser Ile Asp Ala Thr Met Gln
1 5 10 15

ctg ggg acg cgg ctg cgc cgc ggg ctc gtc cac cgt ccc tcc tcc atc 396
Leu Gly Thr Arg Leu Arg Arg Gly Leu Val His Arg Pro Ser Ser Ile
20 25 30

tcc cag gtg gcc ggc gga aaa ggc gtc aac gtc acg cac gcc ctg acc 444
Ser Gln Val Ala Gly Gly Lys Gly Val Asn Val Thr His Ala Leu Thr
35 40 45

ctc gcg gac aaa ctc agc ctc gcc ctc ttc ccg gcg gac ggc aac gac 492
Leu Ala Asp Lys Leu Ser Leu Ala Leu Phe Pro Ala Asp Gly Asn Asp
50 55 60

ccc ttc gtc gcc ctg gcc cgc cag tcc ggg atc ccc ttc cac gcc atc 540
Pro Phe Val Ala Leu Ala Arg Gln Ser Gly Ile Pro Phe His Ala Ile
65 70 75 80

ccg gtg tcc gag ggc gtc cgc atc aac acc acc ctc act gaa ccg gac 588
Pro Val Ser Glu Gly Val Arg Ile Asn Thr Thr Leu Thr Glu Pro Asp
85 90 95

ggg acc acc acc aag atc aac ggc ctc ggc gcg cag atc gag ccg ccc 636
Gly Thr Thr Thr Lys Ile Asn Gly Leu Gly Ala Gln Ile Glu Pro Pro
100 105 110

acc cgc cgc atc atc gag gag acc gtc gtc cgc ctc gcc gcg aac gcc 684
Thr Arg Arg Ile Ile Glu Glu Thr Val Val Arg Leu Ala Ala Asn Ala
115 120 125

tcc tgg ctg gtc atg gcc ggt tcc ctg ccg ccc ggg gtc ccc acc ggc 732
Ser Trp Leu Val Met Ala Gly Ser Leu Pro Pro Gly Val Pro Thr Gly

```
          130                 135                 140

tgg tac acg gaa ctc atc acc acc gtc cgc gcg acg cac ccg gac ctg        780
Trp Tyr Thr Glu Leu Ile Thr Thr Val Arg Ala Thr His Pro Asp Leu
145                 150                 155                 160

ccg gtg gcc gtc gac acg tcc gac gcc gcg atg atc gcc ctc ggc gag        828
Pro Val Ala Val Asp Thr Ser Asp Ala Ala Met Ile Ala Leu Gly Glu
                165                 170                 175

ggc ttc gag gtc gcc gcc ccg acc ctc atc aag ccc aac ggc atg gag        876
Gly Phe Glu Val Ala Ala Pro Thr Leu Ile Lys Pro Asn Gly Met Glu
            180                 185                 190

ctc ggg cag ctc gtc gac cgt gac ggc gag cac ctc gag gcg gcc gcc        924
Leu Gly Gln Leu Val Asp Arg Asp Gly Glu His Leu Glu Ala Ala Ala
        195                 200                 205

gcc cgc ggc gac ttc tcc ccg gtc atc gac gcg gcc cgc gtc gtc gtc        972
Ala Arg Gly Asp Phe Ser Pro Val Ile Asp Ala Ala Arg Val Val Val
    210                 215                 220

gac cgc ggc gtc aac gag gtc ctg gtg acg ctc ggc gtc gcc gga gcc       1020
Asp Arg Gly Val Asn Glu Val Leu Val Thr Leu Gly Val Ala Gly Ala
225                 230                 235                 240

gcc ctc gtc acc gcg cag ggc gtc tgg ctc gcc acc cct ccc ccg gtc       1068
Ala Leu Val Thr Ala Gln Gly Val Trp Leu Ala Thr Pro Pro Pro Val
                245                 250                 255

gac gtc atg tcc acc gtc ggc gcg ggc gac agc tcg ctc gcc ggg tac       1116
Asp Val Met Ser Thr Val Gly Ala Gly Asp Ser Ser Leu Ala Gly Tyr
            260                 265                 270

ctc atg gcc cgc gcg gag ggc ggc agt ccc gcc gac tgc ctg gcc cgc       1164
Leu Met Ala Arg Ala Glu Gly Gly Ser Pro Ala Asp Cys Leu Ala Arg
        275                 280                 285

gcc gtc gcc tac ggc acc gcc gcc acc ggc ctg ccc ggc acc acc att       1212
Ala Val Ala Tyr Gly Thr Ala Ala Thr Gly Leu Pro Gly Thr Thr Ile
    290                 295                 300

cct tcc ccc gca caa ctg aat ctc gag gaa acc cat gtc cgt cat atc       1260
Pro Ser Pro Ala Gln Leu Asn Leu Glu Glu Thr His Val Arg His Ile
305                 310                 315                 320

tcc tga cctggtacac ctggacgccg acctcggcgg cacgaccacc gaggtgatca       1316
Ser

ccgccctggc gggcgtcgtc cacgccgccg gccgcgccag ctccccgcaa ctgctcgccg     1376

acgccgccct cgcccgtgag gcccagaacc ccaccggtgt gcccggccgc gtcgccatcc     1436

cccactgccg ttccgccgcc gtcgaggtcc cgaccctggc cttcgcccga cttgtcgcgcc     1496

ccgtcgactt cggcggtccc gacggcgacg ccgagctcgt cttcctcatc gccgcccccg     1556

agggcggcgg                                                           1566
```

<210> 160
<211> 321
<212> PRT
<213> Corynebacterium humireducens

<400> 160

Val Ile Leu Thr Leu Thr Pro Asn Pro Ser Ile Asp Ala Thr Met Gln
1 5 10 15

Leu Gly Thr Arg Leu Arg Arg Gly Leu Val His Arg Pro Ser Ser Ile
20 25 30

Ser Gln Val Ala Gly Gly Lys Gly Val Asn Val Thr His Ala Leu Thr
35 40 45

Leu Ala Asp Lys Leu Ser Leu Ala Leu Phe Pro Ala Asp Gly Asn Asp
50 55 60

Pro Phe Val Ala Leu Ala Arg Gln Ser Gly Ile Pro Phe His Ala Ile
65 70 75 80

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

Gly Thr Thr Thr Lys Ile Asn Gly Leu Gly Ala Gln Ile Glu Pro Pro
100 105 110

Thr Arg Arg Ile Ile Glu Glu Thr Val Val Arg Leu Ala Ala Asn Ala
115 120 125

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

Trp Tyr Thr Glu Leu Ile Thr Thr Val Arg Ala Thr His Pro Asp Leu
145 150 155 160

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

Gly Phe Glu Val Ala Ala Pro Thr Leu Ile Lys Pro Asn Gly Met Glu
180 185 190

Leu Gly Gln Leu Val Asp Arg Asp Gly Glu His Leu Glu Ala Ala Ala
195 200 205

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

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

Ala Leu Val Thr Ala Gln Gly Val Trp Leu Ala Thr Pro Pro Pro Val
245 250 255

Asp Val Met Ser Thr Val Gly Ala Gly Asp Ser Ser Leu Ala Gly Tyr
260 265 270

Leu Met Ala Arg Ala Glu Gly Gly Ser Pro Ala Asp Cys Leu Ala Arg
275 280 285

Ala Val Ala Tyr Gly Thr Ala Ala Thr Gly Leu Pro Gly Thr Thr Ile
290 295 300

Pro Ser Pro Ala Gln Leu Asn Leu Glu Glu Thr His Val Arg His Ile
305 310 315 320

Ser

<210> 161
<211> 1632
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1332)
<223> gene 6-phosphofructokinase

<400> 161
tggtgtgggc gcccaactcg gcgacggcga tgcggaccgt cgacatcgcc tacatgggtg 60

cggcggccgg cgtgtacaac acggggcgcc agaccggtgc ggtcctcggc gcggccgggg 120

tgggggcggc gatgcaggtc ggtgcggcca cggccgggtt cgtgccgggt ctcgctctgt 180

cgctgctgct ccccgtggcc gtcctcggtc tggggctggt ggcggtcgcc ttcttcgaga 240

ccccgccaca cgccgaacca cagggtgccg aacagcgggc cggggactaa agtggtctcc 300

atg cga ctt gcc acc ctc acc tcc ggc ggc gac tgc ccc ggc ctc aac 348
Met Arg Leu Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro Gly Leu Asn
1 5 10 15

```
gcc gtc atc cgc ggc atc gtc cgt acc gcc agc tcc gag ttc ggt tcc   396
Ala Val Ile Arg Gly Ile Val Arg Thr Ala Ser Ser Glu Phe Gly Ser
            20                  25                  30

acc gtc gtg gga tac cag gac ggc tgg cag ggc ctg ctg gag gac cgc   444
Thr Val Val Gly Tyr Gln Asp Gly Trp Gln Gly Leu Leu Glu Asp Arg
        35                  40                  45

cgc gtc gac ctc tac gac gac gag cac atc gac cgc atc ctc ctg cgc   492
Arg Val Asp Leu Tyr Asp Asp Glu His Ile Asp Arg Ile Leu Leu Arg
    50                  55                  60

ggt ggc acg atc ctg ggc acc ggt cgt ctg cac ccg gac aag ttc aag   540
Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp Lys Phe Lys
65                  70                  75                  80

gcg ggg ctc gac cag atc aag cag aac ctg gat gac gcg ggc atc gac   588
Ala Gly Leu Asp Gln Ile Lys Gln Asn Leu Asp Asp Ala Gly Ile Asp
                85                  90                  95

gcc ctc atc ccg atc ggc ggc gag ggc acc ctc aag ggc gcg aag tgg   636
Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp
            100                 105                 110

ctg tcc gac aac ggc atc ccg gtc gtc ggc gtg ccg aag acc atc gac   684
Leu Ser Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys Thr Ile Asp
        115                 120                 125

aac gac gtc tac ggc acc gac tac acc ttc ggc ttc gac acc gcc gtc   732
Asn Asp Val Tyr Gly Thr Asp Tyr Thr Phe Gly Phe Asp Thr Ala Val
    130                 135                 140

gcc gtg gcc acc gac gcc gtc gac cgt ctg cac acc acc gcc gag tcc   780
Ala Val Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr Ala Glu Ser
145                 150                 155                 160

cac aac cgc atc ctc atc gtc gag gtc atg ggc cgt cac gtc ggc tgg   828
His Asn Arg Ile Leu Ile Val Glu Val Met Gly Arg His Val Gly Trp
                165                 170                 175

atc gcg ctg cac gcg ggc atg gcc ggc ggc gcg cac tac acc gtg atc   876
Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr Thr Val Ile
            180                 185                 190

ccg gag gtg ccc ttc gac atc tcc gag atc tgc aag aag atg gag cgc   924
Pro Glu Val Pro Phe Asp Ile Ser Glu Ile Cys Lys Lys Met Glu Arg
        195                 200                 205

cgc ttc cag atg ggc gag aag tac ggc atc atc gtc gtc gcc gag ggc   972
Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val Ala Glu Gly
    210                 215                 220

gcc gcg ccc aag gag ggc acg atg gag ctc aag tcc ggt ggc gtc gac  1020
Ala Ala Pro Lys Glu Gly Thr Met Glu Leu Lys Ser Gly Gly Val Asp
225                 230                 235                 240

cag ttc ggc cac gag atc ttc acc ggc atc ggc cag cag atc gcc gac  1068
Gln Phe Gly His Glu Ile Phe Thr Gly Ile Gly Gln Gln Ile Ala Asp
```

```
                  245                 250                 255

gag atc cac gcc cgc ctc ggc cat gac gtc cgc acc tcc gtc ctg ggc      1116
Glu Ile His Ala Arg Leu Gly His Asp Val Arg Thr Ser Val Leu Gly
             260                 265                 270

cac atc cag cgc ggt ggc acc ccg acc gcc ttc gac cgc gtc ctg gcc      1164
His Ile Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg Val Leu Ala
        275                 280                 285

acc cgt tac ggc gtc cgc gcg acc cgc tcc gcc cac cgc ggc gag ttc      1212
Thr Arg Tyr Gly Val Arg Ala Thr Arg Ser Ala His Arg Gly Glu Phe
    290                 295                 300

ggc acc tgc gtg gcg ctc aag ggt gag cgg atc gag aac atc acg ctg      1260
Gly Thr Cys Val Ala Leu Lys Gly Glu Arg Ile Glu Asn Ile Thr Leu
305                 310                 315                 320

gag aag gcc gtg ggc acc ctc aag acc gtg ccg atg gac cgc tgg ctc      1308
Glu Lys Ala Val Gly Thr Leu Lys Thr Val Pro Met Asp Arg Trp Leu
                325                 330                 335

acc gcc cag gcc atg ttc ggc tag gtgcgcgacc tccatctgga cacctgccgg      1362
Thr Ala Gln Ala Met Phe Gly
             340

ctgctcgtcg tcggcatcaa cccgggtctg gtgtcggagc gcgtcgacgc gcccttcgcc      1422

cgcccgggca accgtttctg gccggcgctc cacgccgccg gcatcacgga gacgcttgtc      1482

gacgcccgcg acggcctcac cgccgcccac cacgcggagc tgctgcggcg gggcctcggc      1542

ttcacgaacg tcgtgccgcg ggccacggcg gtggcctccg agctgacccg cgaggagtac      1602

ctggcgggtg gggcggtgct ggcggagaag                                       1632


<210>  162
<211>  343
<212>  PRT
<213>  Corynebacterium humireducens

<400>  162

Met Arg Leu Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro Gly Leu Asn
1               5                   10                  15

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

Thr Val Val Gly Tyr Gln Asp Gly Trp Gln Gly Leu Leu Glu Asp Arg
        35                  40                  45

Arg Val Asp Leu Tyr Asp Asp Glu His Ile Asp Arg Ile Leu Leu Arg
    50                  55                  60
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Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp Lys Phe Lys
65 70 75 80

Ala Gly Leu Asp Gln Ile Lys Gln Asn Leu Asp Asp Ala Gly Ile Asp
85 90 95

Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp
100 105 110

Leu Ser Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys Thr Ile Asp
115 120 125

Asn Asp Val Tyr Gly Thr Asp Tyr Thr Phe Gly Phe Asp Thr Ala Val
130 135 140

Ala Val Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr Ala Glu Ser
145 150 155 160

His Asn Arg Ile Leu Ile Val Glu Val Met Gly Arg His Val Gly Trp
165 170 175

Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr Thr Val Ile
180 185 190

Pro Glu Val Pro Phe Asp Ile Ser Glu Ile Cys Lys Lys Met Glu Arg
195 200 205

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

Ala Ala Pro Lys Glu Gly Thr Met Glu Leu Lys Ser Gly Gly Val Asp
225 230 235 240

Gln Phe Gly His Glu Ile Phe Thr Gly Ile Gly Gln Gln Ile Ala Asp
245 250 255

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

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

Thr Arg Tyr Gly Val Arg Ala Thr Arg Ser Ala His Arg Gly Glu Phe
290 295 300

Gly Thr Cys Val Ala Leu Lys Gly Glu Arg Ile Glu Asn Ile Thr Leu
305 310 315 320

Glu Lys Ala Val Gly Thr Leu Lys Thr Val Pro Met Asp Arg Trp Leu
325 330 335

Thr Ala Gln Ala Met Phe Gly
340

<210> 163
<211> 1932
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1632)
<223> gene lysA

<400> 163
cggacctctc cctgctcacc cacgagcggg agggcgacct catccgcacc ctcggcgagt 60

tcccgaacgt ggtcaaggcc gcggcggaac tgcgtgagcc gcaccgtatc gcccgttatg 120

ccgaggaact ggccggcgtg ttccaccgct tctacgacaa ctgccagatc ctgccgaagg 180

cggacgaaga ggccgccccg atccacaccg cccgcctggc gctggctgcg gccacccgcc 240

agaccctggc caacgcgctc ggcctggtcg gtgtcaccgc cccggagagg atgtaagcgc 300

atg acc tcg gat ttc aac gat ctg ccg gcc cac gtc tgg ccg cgc aac 348
Met Thr Ser Asp Phe Asn Asp Leu Pro Ala His Val Trp Pro Arg Asn
1 5 10 15

gcc gcg cgc cag gag gac ggc gtg gtc acc gtc gcg ggt gtc ccg ctg 396
Ala Ala Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu
20 25 30

ccg gag atc gcc gag gag ttc ggt acc ccg gtc ttc gtc gtc gac gag 444
Pro Glu Ile Ala Glu Glu Phe Gly Thr Pro Val Phe Val Val Asp Glu
35 40 45

gac gac ttc cgt tcc cgc tgc cag gac atg gcc cgc gcc ttc ggc ggc 492
Asp Asp Phe Arg Ser Arg Cys Gln Asp Met Ala Arg Ala Phe Gly Gly
50 55 60

ccg gag cac gtc cac tac gcc tcc aag gcg ttc ctc acc cgc acc gtc 540
Pro Glu His Val His Tyr Ala Ser Lys Ala Phe Leu Thr Arg Thr Val
65 70 75 80

gcc cgc tgg gtc gac gag gag ggg ctg tcg ctc gac gtc gcc tcg ctc 588

```
Ala Arg Trp Val Asp Glu Glu Gly Leu Ser Leu Asp Val Ala Ser Leu
                85                  90                  95

aac gag ctg cgg atc gcg ctg gcc gcc gag ttc ccc gcc gcc cgc atc      636
Asn Glu Leu Arg Ile Ala Leu Ala Ala Glu Phe Pro Ala Ala Arg Ile
            100                 105                 110

acc gcg cac ggc aac aac aag ggc ccg tcc ttc ctg cgg gcg tgc gtc      684
Thr Ala His Gly Asn Asn Lys Gly Pro Ser Phe Leu Arg Ala Cys Val
        115                 120                 125

acc gag ggc gtc ggc cac gtc gtc ctc gac tcc gag cag gag ctc gag      732
Thr Glu Gly Val Gly His Val Val Leu Asp Ser Glu Gln Glu Leu Glu
    130                 135                 140

ctt ctc gac gcc atc gcc gcc ggc gcc ggc gtc atc cag aag gtg atg      780
Leu Leu Asp Ala Ile Ala Ala Gly Ala Gly Val Ile Gln Lys Val Met
145                 150                 155                 160

atc cgc gtc aag ccg ggc atc gag gcg cac acc cac gag gcc atc gcc      828
Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Ala Ile Ala
                165                 170                 175

acg tcc cac gag gac cag aag ttc ggc ttc tcc ctg gcc tcc ggc tcg      876
Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser
            180                 185                 190

gcg ttc cgc gcc gcg gag gcc gcc gtc cgc gcc gag aac ctc gag ctc      924
Ala Phe Arg Ala Ala Glu Ala Ala Val Arg Ala Glu Asn Leu Glu Leu
        195                 200                 205

gtg ggc ctg cac tgc cac gtc ggc tcc cag gtc ttc gac gcc cgg ggc      972
Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Arg Gly
    210                 215                 220

ttc acg atg gcc gcc gac cgc gtg ctg ggc ctc tac tcg cag atc cac     1020
Phe Thr Met Ala Ala Asp Arg Val Leu Gly Leu Tyr Ser Gln Ile His
225                 230                 235                 240

cgc gaa ctc ggc gtg cag ctg ccc gag ctc gat ctc ggc ggc ggc tac     1068
Arg Glu Leu Gly Val Gln Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr
                245                 250                 255

ggc atc gcc tac acc gag gac gag cag ccc ctc aac gtc gac gag gtc     1116
Gly Ile Ala Tyr Thr Glu Asp Glu Gln Pro Leu Asn Val Asp Glu Val
            260                 265                 270

gcc cac gac ctg ctc acc gcc gtg gcc aag acc gcc gcg gag ctg ggc     1164
Ala His Asp Leu Leu Thr Ala Val Ala Lys Thr Ala Ala Glu Leu Gly
        275                 280                 285

atc gac gcc ccc gcc gtc ctc gtc gag ccg ggc cgc gcc atc gcc ggc     1212
Ile Asp Ala Pro Ala Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly
    290                 295                 300

ccc ggc acg gtg acg gtc tac gag gtc ggc acc gtc aag gac gtc acc     1260
Pro Gly Thr Val Thr Val Tyr Glu Val Gly Thr Val Lys Asp Val Thr
305                 310                 315                 320
```

```
gtc tcc gag gac gag aag cga cgc tac ctc tcc gtc gac ggc ggc atg      1308
Val Ser Glu Asp Glu Lys Arg Arg Tyr Leu Ser Val Asp Gly Gly Met
                325                 330                 335

tcc gac aac atc cgc ccg gcc ctc tac gac gcg ctt tac gac gcc cgc      1356
Ser Asp Asn Ile Arg Pro Ala Leu Tyr Asp Ala Leu Tyr Asp Ala Arg
            340                 345                 350

gtg gtc aac cgt ttc acc gag ggc gag gag atc tcc tcc cgc ctc gtc      1404
Val Val Asn Arg Phe Thr Glu Gly Glu Glu Ile Ser Ser Arg Leu Val
        355                 360                 365

ggt tcc cac tgc gag tcc ggc gac att ctc gtc cgc gac gcg cgc tac      1452
Gly Ser His Cys Glu Ser Gly Asp Ile Leu Val Arg Asp Ala Arg Tyr
    370                 375                 380

ccc gac gac atc gtg gtc ggg gac ctc atg gcc gtc gcc gcg acc ggc      1500
Pro Asp Asp Ile Val Val Gly Asp Leu Met Ala Val Ala Ala Thr Gly
385                 390                 395                 400

gcc tac gcc tac gcc atg tcc tcg cgc tac aac gcc ttc ggc cgt ccg      1548
Ala Tyr Ala Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Gly Arg Pro
                405                 410                 415

ccg gtc gtc gcg gtg cgt gcc ggc aag acg aag ctc atg ctg cgc cgc      1596
Pro Val Val Ala Val Arg Ala Gly Lys Thr Lys Leu Met Leu Arg Arg
            420                 425                 430

gag acc gtc gag gac att ctc gcg ctg gag acg tag aaccgacgcc           1642
Glu Thr Val Glu Asp Ile Leu Ala Leu Glu Thr
        435                 440

cgggcagggc gtcagtggaa gaggcccttg aggctgccgg cgtcctccag cagcgccacg     1702

acgagcgagg tgtggatgga accgagcggc acgcccctgg cgggcgtcgg cgcggtcgac     1762

gggtccgggg tggaggaacg ggtcggcgtc gtggacgact cttcgcggtc gacggtgccg     1822

gaggctcccg tggcgcacat gcgcagctcc gcccggtagg cgtccgcctc cgcctgggct     1882

cccggggtgc gctcccaggc ccgcagccag gcctcgtcgg cggccacgga                1932
```

<210> 164
<211> 443
<212> PRT
<213> Corynebacterium humireducens

<400> 164

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

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

Pro Glu Ile Ala Glu Glu Phe Gly Thr Pro Val Phe Val Val Asp Glu
```

35 40 45

Asp Asp Phe Arg Ser Arg Cys Gln Asp Met Ala Arg Ala Phe Gly Gly
50 55 60

Pro Glu His Val His Tyr Ala Ser Lys Ala Phe Leu Thr Arg Thr Val
65 70 75 80

Ala Arg Trp Val Asp Glu Glu Gly Leu Ser Leu Asp Val Ala Ser Leu
85 90 95

Asn Glu Leu Arg Ile Ala Leu Ala Ala Glu Phe Pro Ala Ala Arg Ile
100 105 110

Thr Ala His Gly Asn Asn Lys Gly Pro Ser Phe Leu Arg Ala Cys Val
115 120 125

Thr Glu Gly Val Gly His Val Val Leu Asp Ser Glu Gln Glu Leu Glu
130 135 140

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

Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Ala Ile Ala
165 170 175

Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser
180 185 190

Ala Phe Arg Ala Ala Glu Ala Ala Val Arg Ala Glu Asn Leu Glu Leu
195 200 205

Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Arg Gly
210 215 220

Phe Thr Met Ala Ala Asp Arg Val Leu Gly Leu Tyr Ser Gln Ile His
225 230 235 240

Arg Glu Leu Gly Val Gln Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr
245 250 255

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

Ala His Asp Leu Leu Thr Ala Val Ala Lys Thr Ala Ala Glu Leu Gly
275 280 285

Ile Asp Ala Pro Ala Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly
290 295 300

Pro Gly Thr Val Thr Val Tyr Glu Val Gly Thr Val Lys Asp Val Thr
305 310 315 320

Val Ser Glu Asp Glu Lys Arg Arg Tyr Leu Ser Val Asp Gly Gly Met
325 330 335

Ser Asp Asn Ile Arg Pro Ala Leu Tyr Asp Ala Leu Tyr Asp Ala Arg
340 345 350

Val Val Asn Arg Phe Thr Glu Gly Glu Glu Ile Ser Ser Arg Leu Val
355 360 365

Gly Ser His Cys Glu Ser Gly Asp Ile Leu Val Arg Asp Ala Arg Tyr
370 375 380

Pro Asp Asp Ile Val Val Gly Asp Leu Met Ala Val Ala Ala Thr Gly
385 390 395 400

Ala Tyr Ala Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Gly Arg Pro
405 410 415

Pro Val Val Ala Val Arg Ala Gly Lys Thr Lys Leu Met Leu Arg Arg
420 425 430

Glu Thr Val Glu Asp Ile Leu Ala Leu Glu Thr
435 440

<210> 165
<211> 1770
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1470)
<223> gene aat

<400> 165
cgcctacgcg ctcaccgtcg tcctggccgc cgagaactac ccggccgccc cggtcaccgg 60

tggggtcatc accggtgacg tcgtgaatga cccgtccaag gtcctccacg ccggtaccgc 120

```
gcgcaacgag gccggcgagc tggtctccgc cggtggccgc gtgctcaaca tcgtgggcgt      180

cggcaagacc ctcgaggagg cgcgtgacga cgcctacgcc accatcgagc agatccagct      240

cgagggttcc ttctaccgcg gcgacatcgc actgccggcc gtggagggac ggatctccct      300

gtg acc ggt cgg cag ctc gtc agc gac cgc ggc cag gtc cag ccc ttc         348
Val Thr Gly Arg Gln Leu Val Ser Asp Arg Gly Gln Val Gln Pro Phe
1               5                   10                  15

cgc gtc atg cag atg ctc gac atc gtg cac cga cgc gcc cgc gag ggg         396
Arg Val Met Gln Met Leu Asp Ile Val His Arg Arg Ala Arg Glu Gly
            20                  25                  30

aag cac acc atc atg ctg tgc gcc ggg cag ccc tcc acg ggt gcc ccg         444
Lys His Thr Ile Met Leu Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro
        35                  40                  45

gcc ccg gtc ctg acc gcg gcg gag gag tcc ctc cac gcc tcg ccc ctc         492
Ala Pro Val Leu Thr Ala Ala Glu Glu Ser Leu His Ala Ser Pro Leu
    50                  55                  60

ggg tac acc gag gtg gtc ggt gac cgc gac ctc cgg gag atc gtc gcg         540
Gly Tyr Thr Glu Val Val Gly Asp Arg Asp Leu Arg Glu Ile Val Ala
65                  70                  75                  80

gcc tgg cac tcc gac acc tac ggc gtg cac acc agc gcg gac aac gtg         588
Ala Trp His Ser Asp Thr Tyr Gly Val His Thr Ser Ala Asp Asn Val
                85                  90                  95

gtg atc acc acc ggc tcc tcc ggt ggc ttc gtc gcg tcc ttc ctg gcc         636
Val Ile Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Leu Ala
            100                 105                 110

gtg ctc gac cac ggc gac gcc gtc gcc ctg tcc tgc ccc ggt tac ccg         684
Val Leu Asp His Gly Asp Ala Val Ala Leu Ser Cys Pro Gly Tyr Pro
        115                 120                 125

gcg tac cgc aac atc ctg gag tcc ctc ggg gcg cgg gtg gtc aac ctc         732
Ala Tyr Arg Asn Ile Leu Glu Ser Leu Gly Ala Arg Val Val Asn Leu
    130                 135                 140

gtg tgc gac gag tcg acc cgc ttc cag ccg acg gcc gcg atg ctc gag         780
Val Cys Asp Glu Ser Thr Arg Phe Gln Pro Thr Ala Ala Met Leu Glu
145                 150                 155                 160

gca ctg ccg gag gct gac agg ccg cgg gcg gtg atc gtc acc tcc ccg         828
Ala Leu Pro Glu Ala Asp Arg Pro Arg Ala Val Ile Val Thr Ser Pro
                165                 170                 175

ggc aac ccc tcc ggc acg acc atc gac ccc gcg gag ctc gag cgc atc         876
Gly Asn Pro Ser Gly Thr Thr Ile Asp Pro Ala Glu Leu Glu Arg Ile
            180                 185                 190

gcc cgc tgg tgc gag gac aac gac gcc gtg ctc atc tcc gac gag gac         924
Ala Arg Trp Cys Glu Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp
        195                 200                 205
```

```
tac cac ggc atg tcc ttc ggc cgc ccc ctg gcc acc gca cgc cag ttc        972
Tyr His Gly Met Ser Phe Gly Arg Pro Leu Ala Thr Ala Arg Gln Phe
    210                 215                 220

tcc gac cgg gcg atc gtc gtg ggc acg ctg tcg aag tac tac tcc atg       1020
Ser Asp Arg Ala Ile Val Val Gly Thr Leu Ser Lys Tyr Tyr Ser Met
225                 230                 235                 240

acc ggc tgg cgc gtc ggc tgg ctc atc ctc ccc gac gag ctg gtc acc       1068
Thr Gly Trp Arg Val Gly Trp Leu Ile Leu Pro Asp Glu Leu Val Thr
                245                 250                 255

ccc gtg gag aac ctg cag gcc tcg ctg gcg ctc tgc ccg ccg gcg atc       1116
Pro Val Glu Asn Leu Gln Ala Ser Leu Ala Leu Cys Pro Pro Ala Ile
            260                 265                 270

tcg cag gtc gcc ggg cgt gcc gcc ttc acc ccg gag gcg cgc gcc gaa       1164
Ser Gln Val Ala Gly Arg Ala Ala Phe Thr Pro Glu Ala Arg Ala Glu
        275                 280                 285

ctc gac tcc cac gtc gag cgc tac cgc gcc gcc cgc gcg gtg ctg ctc       1212
Leu Asp Ser His Val Glu Arg Tyr Arg Ala Ala Arg Ala Val Leu Leu
    290                 295                 300

gag gag ctg ccg gcg gcc ggt ttc acc acc atg gcg gaa ccc gac ggc       1260
Glu Glu Leu Pro Ala Ala Gly Phe Thr Thr Met Ala Glu Pro Asp Gly
305                 310                 315                 320

ggg ctc tac ctg tgg ctc gac gtc tcc cac gtc acc gac gac tcc gag       1308
Gly Leu Tyr Leu Trp Leu Asp Val Ser His Val Thr Asp Asp Ser Glu
                325                 330                 335

gcc tgg tgc cac gag ctc gtc gag gag atc ggc gtg gcc ttc gcg ccg       1356
Ala Trp Cys His Glu Leu Val Glu Glu Ile Gly Val Ala Phe Ala Pro
            340                 345                 350

ggc gtc gac ttc gac ccg atc aac ggt cac aag tgg gtc cgc ctc acg       1404
Gly Val Asp Phe Asp Pro Ile Asn Gly His Lys Trp Val Arg Leu Thr
        355                 360                 365

ctg tgc gcc ccg gag gag gag acc cgc gag gcg atc cgg cgc ctc ggc       1452
Leu Cys Ala Pro Glu Glu Glu Thr Arg Glu Ala Ile Arg Arg Leu Gly
    370                 375                 380

gag tac gtg cgt cgc tga ccgcgcggcg acctgcggcg cgggggaaac               1500
Glu Tyr Val Arg Arg
385

ggcccggatc cggggactcc cgggccaccc ccgccgctgg tcatgcgata atcgggggcg      1560

tggctgagaa gaagaagatc gcgaacgtcc tgtccaaccg ctacgcctcc gcggagctga      1620

gcaacctgtg gagcccggag tacaagatca tcctggagcg tcagctctgg atcgccgtga      1680

tgaaggcgca gaaggatctg ggtgtcgaca tcccggctga ggccatcgac gcctacgagg      1740

ccgtcatcga ccgggtcgac ctcgagtcga                                       1770
```

<210> 166
<211> 389
<212> PRT
<213> Corynebacterium humireducens

<400> 166

Val Thr Gly Arg Gln Leu Val Ser Asp Arg Gly Gln Val Gln Pro Phe
1 5 10 15

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

Lys His Thr Ile Met Leu Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro
35 40 45

Ala Pro Val Leu Thr Ala Ala Glu Glu Ser Leu His Ala Ser Pro Leu
50 55 60

Gly Tyr Thr Glu Val Val Gly Asp Arg Asp Leu Arg Glu Ile Val Ala
65 70 75 80

Ala Trp His Ser Asp Thr Tyr Gly Val His Thr Ser Ala Asp Asn Val
85 90 95

Val Ile Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Leu Ala
100 105 110

Val Leu Asp His Gly Asp Ala Val Ala Leu Ser Cys Pro Gly Tyr Pro
115 120 125

Ala Tyr Arg Asn Ile Leu Glu Ser Leu Gly Ala Arg Val Val Asn Leu
130 135 140

Val Cys Asp Glu Ser Thr Arg Phe Gln Pro Thr Ala Ala Met Leu Glu
145 150 155 160

Ala Leu Pro Glu Ala Asp Arg Pro Arg Ala Val Ile Val Thr Ser Pro
165 170 175

Gly Asn Pro Ser Gly Thr Thr Ile Asp Pro Ala Glu Leu Glu Arg Ile
180 185 190

Ala Arg Trp Cys Glu Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp
195 200 205

```
Tyr His Gly Met Ser Phe Gly Arg Pro Leu Ala Thr Ala Arg Gln Phe
    210                 215                 220

Ser Asp Arg Ala Ile Val Val Gly Thr Leu Ser Lys Tyr Tyr Ser Met
225                 230                 235                 240

Thr Gly Trp Arg Val Gly Trp Leu Ile Leu Pro Asp Glu Leu Val Thr
                245                 250                 255

Pro Val Glu Asn Leu Gln Ala Ser Leu Ala Leu Cys Pro Pro Ala Ile
            260                 265                 270

Ser Gln Val Ala Gly Arg Ala Ala Phe Thr Pro Glu Ala Arg Ala Glu
        275                 280                 285

Leu Asp Ser His Val Glu Arg Tyr Arg Ala Ala Arg Ala Val Leu Leu
    290                 295                 300

Glu Glu Leu Pro Ala Ala Gly Phe Thr Thr Met Ala Glu Pro Asp Gly
305                 310                 315                 320

Gly Leu Tyr Leu Trp Leu Asp Val Ser His Val Thr Asp Asp Ser Glu
                325                 330                 335

Ala Trp Cys His Glu Leu Val Glu Glu Ile Gly Val Ala Phe Ala Pro
            340                 345                 350

Gly Val Asp Phe Asp Pro Ile Asn Gly His Lys Trp Val Arg Leu Thr
        355                 360                 365

Leu Cys Ala Pro Glu Glu Glu Thr Arg Glu Ala Ile Arg Arg Leu Gly
    370                 375                 380

Glu Tyr Val Arg Arg
385
```

<210> 167
<211> 1281
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(981)
<223> gene lysE

<400> 167
gaaggcgatc acctggatgc cgtagcccac cgccgccggg tcgaggcgcg tgtggaagcc 60

ggtgatcacg cccccgttct ccagcgcccg cagccgccgc aggcaggtgc ttgacgacgc 120

ccccgtatga tgcgccagtt ctgcggcggt gatgcgtgca ttgttctgga tcagtgacag 180

aatcatgcgg tcaatgtcgt ccatacgccg gattctgtca cacgtgcagt cccggcgtcc 240

cccggtgaat gaaaagttca ggagtatcgg ccgcggcgcc gggcgggcac gataccgggc 300

atg gac atc acg gac ctc ctg agc ttc tgg gcg gtc agc ctc ctg ctg 348
Met Asp Ile Thr Asp Leu Leu Ser Phe Trp Ala Val Ser Leu Leu Leu
1 5 10 15

atc gtc acc ccg ggc ccc gac tgg gcg ttc gtg ctc ggg cac gct ttc 396
Ile Val Thr Pro Gly Pro Asp Trp Ala Phe Val Leu Gly His Ala Phe
20 25 30

cga cgc cgc ccc ctc gcc ccg ccc ctt ctc ggc atc ggc ctg ggc tac 444
Arg Arg Arg Pro Leu Ala Pro Pro Leu Leu Gly Ile Gly Leu Gly Tyr
35 40 45

ctc ggc ctg acc acc gtg gtg gcc ggc ggc ctc ggg gcg ctc gtg gcc 492
Leu Gly Leu Thr Thr Val Val Ala Gly Gly Leu Gly Ala Leu Val Ala
50 55 60

cgt cac ccc gcg ctg ctc acg ctc gtc acc gtc gcc ggt gtc ctg gtg 540
Arg His Pro Ala Leu Leu Thr Leu Val Thr Val Ala Gly Val Leu Val
65 70 75 80

ctc ctg cgt ctc ggc tgg cag atg atg cgc gcg gcg ctg gcc ggg ccc 588
Leu Leu Arg Leu Gly Trp Gln Met Met Arg Ala Ala Leu Ala Gly Pro
85 90 95

gtc acg gtg gag gtg gac acc gcg gac ccg gct gtc ccg gag ggg ccg 636
Val Thr Val Glu Val Asp Thr Ala Asp Pro Ala Val Pro Glu Gly Pro
100 105 110

gcc ggc ggg gga gtg gcg acg ctg acg cgc ccg cag gtg ggc gtc gag 684
Ala Gly Gly Gly Val Ala Thr Leu Thr Arg Pro Gln Val Gly Val Glu
115 120 125

aag cac gcg gtg gtc acc ggg gcc gcg gtg agt ggc ctc aac ccc aag 732
Lys His Ala Val Val Thr Gly Ala Ala Val Ser Gly Leu Asn Pro Lys
130 135 140

ggg ctc atg ctg ttc atc gcg ctg ctg ccc cag ttc gtg ggc gcg gag 780
Gly Leu Met Leu Phe Ile Ala Leu Leu Pro Gln Phe Val Gly Ala Glu
145 150 155 160

gcg acg tgg ccg gtg tgg acg cag atg ttc gtc ctc gga ctg gtg ttc 828
Ala Thr Trp Pro Val Trp Thr Gln Met Phe Val Leu Gly Leu Val Phe
165 170 175

atc gcc tcg gcg acc gtg ttc tac gcg ctg ctc ggc gtt ttc gcc ggg 876
Ile Ala Ser Ala Thr Val Phe Tyr Ala Leu Leu Gly Val Phe Ala Gly
180 185 190

cgg gtg ctg gcg ggc tcg gag cgg gcc tcc cgg atc ctc acc ggc gtg 924
Arg Val Leu Ala Gly Ser Glu Arg Ala Ser Arg Ile Leu Thr Gly Val
195 200 205

gcc ggc ggg gcg atg atg tgt gtc gcg gca ggg atg ctc gcg cag cac 972
Ala Gly Gly Ala Met Met Cys Val Ala Ala Gly Met Leu Ala Gln His
210 215 220

ctc ctc tga tgggggtagt tgagtagggg cattcatcgg gtgcgagttc 1021
Leu Leu
225

cgcgcctccc gatgaatgcc cctgctcgga taccctccta ctccacgtgc gccggcgtcg 1081

acggcgacac cagcggcatc ggcgcgtact cggcacgcag ctcgcgcagc ttccgggcgt 1141

gctcggagag gcggacgtcc tcggtggtac gggggacgaa ctggcgggcg ggcagggcgt 1201

tgccgtcggc gtccgtcgcc aggtaggtga cggtggcgtg gatggcggtc tgcaggttct 1261

cgcggccccc gcgcgggttg 1281

<210> 168
<211> 226
<212> PRT
<213> Corynebacterium humireducens

<400> 168

Met Asp Ile Thr Asp Leu Leu Ser Phe Trp Ala Val Ser Leu Leu Leu
1 5 10 15

Ile Val Thr Pro Gly Pro Asp Trp Ala Phe Val Leu Gly His Ala Phe
20 25 30

Arg Arg Arg Pro Leu Ala Pro Pro Leu Leu Gly Ile Gly Leu Gly Tyr
35 40 45

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

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

Leu Leu Arg Leu Gly Trp Gln Met Met Arg Ala Ala Leu Ala Gly Pro
85 90 95

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

Ala Gly Gly Gly Val Ala Thr Leu Thr Arg Pro Gln Val Gly Val Glu

115 120 125

Lys His Ala Val Val Thr Gly Ala Ala Val Ser Gly Leu Asn Pro Lys
130 135 140

Gly Leu Met Leu Phe Ile Ala Leu Leu Pro Gln Phe Val Gly Ala Glu
145 150 155 160

Ala Thr Trp Pro Val Trp Thr Gln Met Phe Val Leu Gly Leu Val Phe
165 170 175

Ile Ala Ser Ala Thr Val Phe Tyr Ala Leu Leu Gly Val Phe Ala Gly
180 185 190

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

Ala Gly Gly Ala Met Met Cys Val Ala Ala Gly Met Leu Ala Gln His
210 215 220

Leu Leu
225

<210> 169
<211> 1347
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1047)
<223> gene dapB

<400> 169
ccggtgccga aggagtcgag ccaggtgcgc agggagttgc ggttgactcc gagatcggag 60

gcgatcgcgt tgatcgttgc tccgggagtc gactcgtaca acgccactgc gtcacgcttg 120

aactgctcgg tgtaggtctt gcgtggcatg gtggaaaggt acctcacttc ccagcgaaa 180

tgctggtttc agcgtgtcca ccatcaaggg gtcaggtccg ctggtgatgt tgatgcgcat 240

gcaacgattc tatgcgccta gactggggca ctgaatcttt caggaactca aggaggaacc 300

atg gcg atc aag gtg gga gtg ctc ggc gcg aag ggc cgt gtc ggc tcg 348
Met Ala Ile Lys Val Gly Val Leu Gly Ala Lys Gly Arg Val Gly Ser
1 5 10 15

gcg gtg tgc gag ggc gtc aac ggg gcg gag ggc ctc gag ctc gtc gcg 396

```
Ala Val Cys Glu Gly Val Asn Gly Ala Glu Gly Leu Glu Leu Val Ala
            20                  25                  30

cag gtc gat cag gac gat gac ctg cag ctg ctt ctc gac gcc ggg gcg        444
Gln Val Asp Gln Asp Asp Asp Leu Gln Leu Leu Leu Asp Ala Gly Ala
        35                  40                  45

gag gtc gtc gtc gac ttc acc act ccg ggt tcc gtg atg ggc aac ctg        492
Glu Val Val Val Asp Phe Thr Thr Pro Gly Ser Val Met Gly Asn Leu
    50                  55                  60

gag ttc tgc atc gcc aac ggc atc cac gcg gtg gtc ggc acc acc ggc        540
Glu Phe Cys Ile Ala Asn Gly Ile His Ala Val Val Gly Thr Thr Gly
65                  70                  75                  80

ttc gac gag gag cgc ctc gcg cag gtc cgt gag tgg tgt gcc gcc gag        588
Phe Asp Glu Glu Arg Leu Ala Gln Val Arg Glu Trp Cys Ala Ala Glu
                85                  90                  95

ggg gcg ggc aac gtc ctc atc gcc ccg aac ttc gcg atc tct gca gtg        636
Gly Ala Gly Asn Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val
            100                 105                 110

ctg gcc atg gag ttc gcg cgg cag gcc gcc cgc ttc ttc gac tcc gcc        684
Leu Ala Met Glu Phe Ala Arg Gln Ala Ala Arg Phe Phe Asp Ser Ala
        115                 120                 125

gag gtc gtc gag tac cac cac ccc tac aag ctg gac gcc ccc tcc ggc        732
Glu Val Val Glu Tyr His His Pro Tyr Lys Leu Asp Ala Pro Ser Gly
    130                 135                 140

acc gcg atc cac acc gcg cag ggc atc gcc gcc gcc cgc cgg gag gcc        780
Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Arg Glu Ala
145                 150                 155                 160

ggc ctc ggc ccc atc ccg gat gcc acc gag cag acc ctc gag ggt gcc        828
Gly Leu Gly Pro Ile Pro Asp Ala Thr Glu Gln Thr Leu Glu Gly Ala
                165                 170                 175

cgc ggc gcc gac gtc gac ggc gtg cgt gtc cac ggc gtg cgc atg acc        876
Arg Gly Ala Asp Val Asp Gly Val Arg Val His Gly Val Arg Met Thr
            180                 185                 190

ggc atg gtc gcc cac gag gac atc atc ttc ggt gcc cag ggc cag tcc        924
Gly Met Val Ala His Glu Asp Ile Ile Phe Gly Ala Gln Gly Gln Ser
        195                 200                 205

ctg acc atc cgc cag gac tcc tac gac cgc acc tcc ttc gtg ccg ggc        972
Leu Thr Ile Arg Gln Asp Ser Tyr Asp Arg Thr Ser Phe Val Pro Gly
    210                 215                 220

gtg ctc ctc ggt gtc cgt gag atc gcg aac cac gac ggc ctg acc gtg       1020
Val Leu Leu Gly Val Arg Glu Ile Ala Asn His Asp Gly Leu Thr Val
225                 230                 235                 240

ggg ctc gac agc tac ctg gga ctc tag atggccaagc ccgtcgacct            1067
Gly Leu Asp Ser Tyr Leu Gly Leu
                245
```

ggacgtccag ctcatcgcgg ccacgcagtt caccccgccc gccggggtcg actgggaggc 1127

cgacgacacc gccaccggcg ccgaggcgct cgtcgagttc gcgggccgcg cctgctacga 1187

gaccttcgac aaacccaacc cgcgcaccgc ggccaacgac gcctacctcc gccacatcat 1247

ggaggtcgga cacaccgcac tgctcgagca cgccaccgcg acgctctaca tccgcggcat 1307

ctcccgctcc gccacccacg agctggtccg ccaccgcaac 1347

<210> 170
<211> 248
<212> PRT
<213> Corynebacterium humireducens

<400> 170

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

Ala Val Cys Glu Gly Val Asn Gly Ala Glu Gly Leu Glu Leu Val Ala
20 25 30

Gln Val Asp Gln Asp Asp Asp Leu Gln Leu Leu Leu Asp Ala Gly Ala
35 40 45

Glu Val Val Val Asp Phe Thr Thr Pro Gly Ser Val Met Gly Asn Leu
50 55 60

Glu Phe Cys Ile Ala Asn Gly Ile His Ala Val Val Gly Thr Thr Gly
65 70 75 80

Phe Asp Glu Glu Arg Leu Ala Gln Val Arg Glu Trp Cys Ala Ala Glu
85 90 95

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

Leu Ala Met Glu Phe Ala Arg Gln Ala Ala Arg Phe Phe Asp Ser Ala
115 120 125

Glu Val Val Glu Tyr His His Pro Tyr Lys Leu Asp Ala Pro Ser Gly
130 135 140

Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Arg Glu Ala
145 150 155 160

Gly Leu Gly Pro Ile Pro Asp Ala Thr Glu Gln Thr Leu Glu Gly Ala

165 170 175

Arg Gly Ala Asp Val Asp Gly Val Arg Val His Gly Val Arg Met Thr
180 185 190

Gly Met Val Ala His Glu Asp Ile Ile Phe Gly Ala Gln Gly Gln Ser
195 200 205

Leu Thr Ile Arg Gln Asp Ser Tyr Asp Arg Thr Ser Phe Val Pro Gly
210 215 220

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

Gly Leu Asp Ser Tyr Leu Gly Leu
245

<210> 171
<211> 2145
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1845)
<223> gene glucose-6-phosphate dehydrogenase

<400> 171
cgaccctcta cgtcaccgag ctggccggcc cggagaccgt caacaccatg ccggagccga 60

ccatcgacgc cgtgctcgag cagggtggcc tccacggcga caccctgagc ggcaccgcgg 120

acgacgcgca ggccgtcttc gagcagctgg tgcaggtcgg catcgacatg gaggacgtct 180

tcgcggtgct ggagcgcgag ggcgtcgaga agttcgtgtc ctcctggtcc gagctgctcg 240

actccatgga gtcccgactg cgctagcagt cccctccccg acaggaaagg acctgagcgc 300

atg ccc ctc ccc gtg acc ggc acc gac gcc tgg atc aac ccg ctg cgg 348
Met Pro Leu Pro Val Thr Gly Thr Asp Ala Trp Ile Asn Pro Leu Arg
1 5 10 15

aac acc gtc gac aag cgg ctg ccc cgc atc gcc ggc ccc tcc ggc atg 396
Asn Thr Val Asp Lys Arg Leu Pro Arg Ile Ala Gly Pro Ser Gly Met
20 25 30

gtg atc ttc ggc gtg acc ggt gac ctg gcc cgc aag aag ctg ctc ccg 444
Val Ile Phe Gly Val Thr Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro
35 40 45

gcc atc tac gac ctg gcc aac cgt ggc ctc ctg ccg gcc ggt ttc acc 492
Ala Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Ala Gly Phe Thr

```
     50                  55                  60

ctc atc ggt ttc ggc cgt cgt ccc tgg agc aaa ccc gag ttc gag gag        540
Leu Ile Gly Phe Gly Arg Arg Pro Trp Ser Lys Pro Glu Phe Glu Glu
65                  70                  75                  80

tac gtg cgg gag gcc gtc gag agc ggc gcc cgc acc gag ttc cgc gaa        588
Tyr Val Arg Glu Ala Val Glu Ser Gly Ala Arg Thr Glu Phe Arg Glu
                85                  90                  95

cac gtg tgg gag cgg ctg gcc gag ggc atg cac ttc gtc gag ggc aac        636
His Val Trp Glu Arg Leu Ala Glu Gly Met His Phe Val Glu Gly Asn
            100                 105                 110

ttc gac gac gag ggc ttc gac cgc ctc gcc gcc acc ctc gcc gag atg        684
Phe Asp Asp Glu Gly Phe Asp Arg Leu Ala Ala Thr Leu Ala Glu Met
        115                 120                 125

gac acc tcc cgc ggc acg gcg ggc aac tgg gcc ttc tac ctg tcg gtc        732
Asp Thr Ser Arg Gly Thr Ala Gly Asn Trp Ala Phe Tyr Leu Ser Val
    130                 135                 140

ccg ccg gac ttc ttc acc gcc gtc tgc cac cag ctg gag cgc tcc ggc        780
Pro Pro Asp Phe Phe Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly
145                 150                 155                 160

ctg gcg gag gcc ggt gag gag tcg tgg cgt cgc gtg atc atc gag aag        828
Leu Ala Glu Ala Gly Glu Glu Ser Trp Arg Arg Val Ile Ile Glu Lys
                165                 170                 175

ccc ttc ggc cac gac cag gac acg gcc cgg gag ctc aac cgg gtg gtc        876
Pro Phe Gly His Asp Gln Asp Thr Ala Arg Glu Leu Asn Arg Val Val
            180                 185                 190

aac gcc gtc ttc ccg gag gag tcg gtg ttc cgc atc gac cac tac ctg        924
Asn Ala Val Phe Pro Glu Glu Ser Val Phe Arg Ile Asp His Tyr Leu
        195                 200                 205

ggc aag gag acg gtg cag aac atc ctg gcg ctg cgc ttc gcc aac cag        972
Gly Lys Glu Thr Val Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln
    210                 215                 220

ctc ttc gac ccg atc tgg aac gcg cac tac gtc gac cac gtg cag atc       1020
Leu Phe Asp Pro Ile Trp Asn Ala His Tyr Val Asp His Val Gln Ile
225                 230                 235                 240

acc atg gcc gag gac atc ggt ctc ggt ggt cgg gcc ggc tac tac gac       1068
Thr Met Ala Glu Asp Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp
                245                 250                 255

ggc atc ggc gcc gcc cgc gac gtc atg cag aac cac ctc ctc cag ctc       1116
Gly Ile Gly Ala Ala Arg Asp Val Met Gln Asn His Leu Leu Gln Leu
            260                 265                 270

ctg gcg ctg gtg gcc atg gag gag ccc atc gcc ttc gac ccg gct gag       1164
Leu Ala Leu Val Ala Met Glu Glu Pro Ile Ala Phe Asp Pro Ala Glu
        275                 280                 285

ctg cag gcg gag aag gtc aag gtc ctg cgc gcg acc aac ccc gtc ttc       1212
```

```
Leu Gln Ala Glu Lys Val Lys Val Leu Arg Ala Thr Asn Pro Val Phe
    290                 295                 300

ccg ctg aac aag acc acc gcc cgt ggc cag tac gcg gcg ggc tgg cag      1260
Pro Leu Asn Lys Thr Thr Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln
305                 310                 315                 320

ggc tcg cac aag gtg cgt ggc ctg cgt gag gag gag ggt ttc gac ccg      1308
Gly Ser His Lys Val Arg Gly Leu Arg Glu Glu Glu Gly Phe Asp Pro
                325                 330                 335

gac tcc acc acg gag acc tac gcc gcc tgc acc ctg gag atc aac tcc      1356
Asp Ser Thr Thr Glu Thr Tyr Ala Ala Cys Thr Leu Glu Ile Asn Ser
            340                 345                 350

cgc cgc tgg gcg ggc gtg ccc ttc tac ctg cgg acc ggc aag cgc ctg      1404
Arg Arg Trp Ala Gly Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu
        355                 360                 365

ggg cgc cgc gtc acg gag atc gcc ctc gtg ttc aag gag gcg ccg cac      1452
Gly Arg Arg Val Thr Glu Ile Ala Leu Val Phe Lys Glu Ala Pro His
    370                 375                 380

cag ccc ttc ctc gag ggg cag acg tcc tcg ctg ggg cag aac gcg atc      1500
Gln Pro Phe Leu Glu Gly Gln Thr Ser Ser Leu Gly Gln Asn Ala Ile
385                 390                 395                 400

gtc atc cgc gtc cag ccc gac gag ggc gtg ctc atg cgc ttc ggc tcc      1548
Val Ile Arg Val Gln Pro Asp Glu Gly Val Leu Met Arg Phe Gly Ser
                405                 410                 415

aag gtg ccc ggc tcc gcg atg gag gtc cgt gac gtc aac atg gac ttc      1596
Lys Val Pro Gly Ser Ala Met Glu Val Arg Asp Val Asn Met Asp Phe
            420                 425                 430

tcc tac gcg gag gcc ttc acc gag gcg tcc ccg gag gcc tat gag cgg      1644
Ser Tyr Ala Glu Ala Phe Thr Glu Ala Ser Pro Glu Ala Tyr Glu Arg
        435                 440                 445

ctc atc ctc gat gcg ctt ctc gac gag tcc tcg ctc ttc ccc acc aac      1692
Leu Ile Leu Asp Ala Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn
    450                 455                 460

gag gag gtc gag ctc tcc tgg gcg atc ctg gac ccg atc ctc gag ttc      1740
Glu Glu Val Glu Leu Ser Trp Ala Ile Leu Asp Pro Ile Leu Glu Phe
465                 470                 475                 480

tgg gct gag aag ggc cag ccc gag gag tac gag tcc ggc acc tgg ggg      1788
Trp Ala Glu Lys Gly Gln Pro Glu Glu Tyr Glu Ser Gly Thr Trp Gly
                485                 490                 495

ccc gcc tcc gcc gac cgc atg ctg gaa cgg acc ggc cgc gcc tgg cgc      1836
Pro Ala Ser Ala Asp Arg Met Leu Glu Arg Thr Gly Arg Ala Trp Arg
            500                 505                 510

cgc ccc tga cctggaaggg acccgacttg aagatcgaac tgccggacac              1885
Arg Pro
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cgacacccgg aacatcgccg ccagcctgct cgaggcccgg gagcacaact cccagaccac 1945

cgggcgggtg ctcaccctca tcgtcgtcgc cgcgctcgac gacgacgtcg accacatcat 2005

ctccgtcacc cgcgacgcct cccacgagca ccccgcccgt gtgctggtgc tgctcaccgg 2065

ccgggaggac gctgactcgc gtctcgacgc cgaggtgcgc gtcggcggtc acgccggcgc 2125

ctcggagatg gtcatcatgc 2145

<210> 172
<211> 514
<212> PRT
<213> Corynebacterium humireducens

<400> 172

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

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

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

Ala Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Ala Gly Phe Thr
50 55 60

Leu Ile Gly Phe Gly Arg Arg Pro Trp Ser Lys Pro Glu Phe Glu Glu
65 70 75 80

Tyr Val Arg Glu Ala Val Glu Ser Gly Ala Arg Thr Glu Phe Arg Glu
85 90 95

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

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

Asp Thr Ser Arg Gly Thr Ala Gly Asn Trp Ala Phe Tyr Leu Ser Val
130 135 140

Pro Pro Asp Phe Phe Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly
145 150 155 160

Leu Ala Glu Ala Gly Glu Glu Ser Trp Arg Arg Val Ile Ile Glu Lys

165 170 175

Pro Phe Gly His Asp Gln Asp Thr Ala Arg Glu Leu Asn Arg Val Val
180 185 190

Asn Ala Val Phe Pro Glu Glu Ser Val Phe Arg Ile Asp His Tyr Leu
195 200 205

Gly Lys Glu Thr Val Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln
210 215 220

Leu Phe Asp Pro Ile Trp Asn Ala His Tyr Val Asp His Val Gln Ile
225 230 235 240

Thr Met Ala Glu Asp Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp
245 250 255

Gly Ile Gly Ala Ala Arg Asp Val Met Gln Asn His Leu Leu Gln Leu
260 265 270

Leu Ala Leu Val Ala Met Glu Glu Pro Ile Ala Phe Asp Pro Ala Glu
275 280 285

Leu Gln Ala Glu Lys Val Lys Val Leu Arg Ala Thr Asn Pro Val Phe
290 295 300

Pro Leu Asn Lys Thr Thr Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln
305 310 315 320

Gly Ser His Lys Val Arg Gly Leu Arg Glu Glu Glu Gly Phe Asp Pro
325 330 335

Asp Ser Thr Thr Glu Thr Tyr Ala Ala Cys Thr Leu Glu Ile Asn Ser
340 345 350

Arg Arg Trp Ala Gly Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu
355 360 365

Gly Arg Arg Val Thr Glu Ile Ala Leu Val Phe Lys Glu Ala Pro His
370 375 380

Gln Pro Phe Leu Glu Gly Gln Thr Ser Ser Leu Gly Gln Asn Ala Ile
385 390 395 400

Val Ile Arg Val Gln Pro Asp Glu Gly Val Leu Met Arg Phe Gly Ser
405 410 415

Lys Val Pro Gly Ser Ala Met Glu Val Arg Asp Val Asn Met Asp Phe
420 425 430

Ser Tyr Ala Glu Ala Phe Thr Glu Ala Ser Pro Glu Ala Tyr Glu Arg
435 440 445

Leu Ile Leu Asp Ala Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn
450 455 460

Glu Glu Val Glu Leu Ser Trp Ala Ile Leu Asp Pro Ile Leu Glu Phe
465 470 475 480

Trp Ala Glu Lys Gly Gln Pro Glu Glu Tyr Glu Ser Gly Thr Trp Gly
485 490 495

Pro Ala Ser Ala Asp Arg Met Leu Glu Arg Thr Gly Arg Ala Trp Arg
500 505 510

Arg Pro

<210> 173
<211> 2055
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1755)
<223> gene gnd

<400> 173
aaggctgccc acggactcgg ccagcgcgca gaacacgccc ccgttgacca ggccgacggg 60

ctgccggtgc tggtccccca cctcgaggcg ggcgcggacg cggccgtcgg cgatctgcgt 120

gtagacgatc ccgaggtggg cgtcgaggcc gacgttgcgg tcgttgagct gcgcgagctg 180

cgcggcgtcg agggccttgc ctgtcccggc gaggcggaag aggtcggtga aactgtaggt 240

ctcggtcatg agtgccgact ctactgaccc ttcgaaaatg gtgtgtctaa actctgtgcc 300

atg acc tcc cct gag aat ctc gcc cag atc ggc gtc gtc gga ctc gcc 348
Met Thr Ser Pro Glu Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala
1 5 10 15

gtc atg ggt tcc aac ctg gcc cgc aac ttc gcc cgc aac ggc cac acc 396

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Val Met Gly Ser Asn Leu Ala Arg Asn Phe Ala Arg Asn Gly His Thr
            20                  25                  30

gtc gcc gtg tac aac cgt tcc ccc gag aag acc cgc gac ctc atc gcc        444
Val Ala Val Tyr Asn Arg Ser Pro Glu Lys Thr Arg Asp Leu Ile Ala
        35                  40                  45

gag cac ggt gac gag ggc acc ttc ctc gcc tcc gag acc gtc gag gac        492
Glu His Gly Asp Glu Gly Thr Phe Leu Ala Ser Glu Thr Val Glu Asp
    50                  55                  60

ttc gtc gcc tcc ctc gag cgc ccg cgt aag gcg atc atc atg gtc cag        540
Phe Val Ala Ser Leu Glu Arg Pro Arg Lys Ala Ile Ile Met Val Gln
65                  70                  75                  80

gcc ggc gcg gcc acc gac gcg gtg atc aac cag ctg gcc gac gcc atg        588
Ala Gly Ala Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met
                85                  90                  95

gag gac ggc gac atc atc atc gac ggc ggc aac gcc ctc tac agc gac        636
Glu Asp Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Ser Asp
            100                 105                 110

acc atc cgc cgg gag cgg gag atg gcc gag cgc aac cgt cac ttc gtc        684
Thr Ile Arg Arg Glu Arg Glu Met Ala Glu Arg Asn Arg His Phe Val
        115                 120                 125

ggc gcc ggc atc tcc ggc ggc gag gag ggg gcc ctc aac ggc ccg tcg        732
Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser
    130                 135                 140

atc atg ccg ggt ggc ccg aag gag tcc tgg gag acc ctc ggc ccg ctg        780
Ile Met Pro Gly Gly Pro Lys Glu Ser Trp Glu Thr Leu Gly Pro Leu
145                 150                 155                 160

ctg gag tcc gtc gct gcc gtc gtc gac ggc acc ccg tgt gtc acg cac        828
Leu Glu Ser Val Ala Ala Val Val Asp Gly Thr Pro Cys Val Thr His
                165                 170                 175

atc ggc ccg gac ggt gcg ggc cac ttc gtc aag atg gtc cac aac ggc        876
Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly
            180                 185                 190

atc gag tac gcc gac atg cag gtc atc ggc gag gcg tac cag ctg ctg        924
Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr Gln Leu Leu
        195                 200                 205

cgc tac ggc gcg ggc atg agc ccg gcc gag atc tcc gag gtc ttc cgc        972
Arg Tyr Gly Ala Gly Met Ser Pro Ala Glu Ile Ser Glu Val Phe Arg
    210                 215                 220

gag tgg aac tcc ggc gac ctc gac tcc tac ctc atc gag atc acc gcc       1020
Glu Trp Asn Ser Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala
225                 230                 235                 240

gag gtc ctc gcg cag gtc gac gcc gag acg ggg aag ccg ctc atc gac       1068
Glu Val Leu Ala Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp
                245                 250                 255
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gtc atc gtc gac gcc gcc ggc cag aag ggc acc ggc cgc tgg acc gtc      1116
Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val
            260                 265                 270

aag gcc gcc ctc gac ctg ggc atc ccg gtc acc ggc atc ggc gag gcc      1164
Lys Ala Ala Leu Asp Leu Gly Ile Pro Val Thr Gly Ile Gly Glu Ala
        275                 280                 285

gtc ttc gcc cgc gcc ctg tcc tcc tcc ctc gag cag cgt gcc gcc gcg      1212
Val Phe Ala Arg Ala Leu Ser Ser Ser Leu Glu Gln Arg Ala Ala Ala
    290                 295                 300

cag ggc gtg ctg ccc gcc ggt gag ctc gcc acc ttc gag tcc ctg ggt      1260
Gln Gly Val Leu Pro Ala Gly Glu Leu Ala Thr Phe Glu Ser Leu Gly
305                 310                 315                 320

ctg gac cgc gac gcc ttc atc gag gac gtc cgc cgc gcc ctc tac gcc      1308
Leu Asp Arg Asp Ala Phe Ile Glu Asp Val Arg Arg Ala Leu Tyr Ala
                325                 330                 335

tcc aag ctg gtc gcc tac gcg cag ggc ttc gac gag atc cgg gcc ggc      1356
Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Arg Ala Gly
            340                 345                 350

tcc gcc gag cac gcc tgg gac gtc gac ccc cgc gac ctg gcc acc atc      1404
Ser Ala Glu His Ala Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile
        355                 360                 365

tgg cgg ggc ggc tgc atc atc cgc gcc aag ttc ctc aac cgc atc gtc      1452
Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val
    370                 375                 380

gag gcc tac gac gcc gac ccg cag ctg ccg tcc ctg ctt ctc gac gcc      1500
Glu Ala Tyr Asp Ala Asp Pro Gln Leu Pro Ser Leu Leu Leu Asp Ala
385                 390                 395                 400

tac ttc ctc gac gag ctg cgc gac ctc atc gac tcc tgg cgt cgc gtc      1548
Tyr Phe Leu Asp Glu Leu Arg Asp Leu Ile Asp Ser Trp Arg Arg Val
                405                 410                 415

atc gtc gcc gcc acc cag ctg ggc ctg ccg gtg ccg gtg ttc gcg tcc      1596
Ile Val Ala Ala Thr Gln Leu Gly Leu Pro Val Pro Val Phe Ala Ser
            420                 425                 430

tcc ctg tcc tac tac gac tcg ctg cgc gcc gag cgt ctg ccg gcc gcc      1644
Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala
        435                 440                 445

gtg atc cag ggc cag cgt gac tac ttc ggt gcg cac acc tac ggg cgc      1692
Val Ile Gln Gly Gln Arg Asp Tyr Phe Gly Ala His Thr Tyr Gly Arg
    450                 455                 460

gtc gac aag ccg ggt gcc ttc cac acc ctg tgg tcc ggg gac cgc agc      1740
Val Asp Lys Pro Gly Ala Phe His Thr Leu Trp Ser Gly Asp Arg Ser
465                 470                 475                 480

gag atc gag gtg taa tgcccgtgtg ggcgaggatc tcccgtttcc tgccggcggc      1795
Glu Ile Glu Val
```

ggccatcgtg gtggtgaccg ccagggcagt gcaggaggtc cttgcccacg ggcagtgggc 1855

ggtgtggcgg ctgtcgcggc gggagacccg cctgttcgtc gaggtattcc ggacggtgct 1915

gggcctgttc ctcgtcgtcg gcctcacccg ggtggtcgcc gcgcctccct cccccacgga 1975

actggccgga tgggcgctca ccttggggtt cctgtggatc ctcaccctca cggagacgga 2035

acccggcccc gaccccgagc 2055

<210> 174
<211> 484
<212> PRT
<213> Corynebacterium humireducens

<400> 174

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

Val Met Gly Ser Asn Leu Ala Arg Asn Phe Ala Arg Asn Gly His Thr
20 25 30

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

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

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

Ala Gly Ala Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met
85 90 95

Glu Asp Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Ser Asp
100 105 110

Thr Ile Arg Arg Glu Arg Glu Met Ala Glu Arg Asn Arg His Phe Val
115 120 125

Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser
130 135 140

Ile Met Pro Gly Gly Pro Lys Glu Ser Trp Glu Thr Leu Gly Pro Leu
145 150 155 160

Leu Glu Ser Val Ala Ala Val Val Asp Gly Thr Pro Cys Val Thr His
165 170 175

Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly
180 185 190

Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr Gln Leu Leu
195 200 205

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

Glu Trp Asn Ser Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala
225 230 235 240

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

Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val
260 265 270

Lys Ala Ala Leu Asp Leu Gly Ile Pro Val Thr Gly Ile Gly Glu Ala
275 280 285

Val Phe Ala Arg Ala Leu Ser Ser Ser Leu Glu Gln Arg Ala Ala Ala
290 295 300

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

Leu Asp Arg Asp Ala Phe Ile Glu Asp Val Arg Arg Ala Leu Tyr Ala
325 330 335

Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Arg Ala Gly
340 345 350

Ser Ala Glu His Ala Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile
355 360 365

Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val
370 375 380

Glu Ala Tyr Asp Ala Asp Pro Gln Leu Pro Ser Leu Leu Leu Asp Ala
385 390 395 400

Tyr Phe Leu Asp Glu Leu Arg Asp Leu Ile Asp Ser Trp Arg Arg Val
405 410 415

Ile Val Ala Ala Thr Gln Leu Gly Leu Pro Val Pro Val Phe Ala Ser
420 425 430

Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala
435 440 445

Val Ile Gln Gly Gln Arg Asp Tyr Phe Gly Ala His Thr Tyr Gly Arg
450 455 460

Val Asp Lys Pro Gly Ala Phe His Thr Leu Trp Ser Gly Asp Arg Ser
465 470 475 480

Glu Ile Glu Val

<210> 175
<211> 2103
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1803)
<223> gene mqo

<400> 175
cgagaatgtc ctcataccag tcggagaagg cgggaacgct catgatgacc acactagtgg 60

gggtacgggg gcaggggcg ggggagtgag gggcgtcgat aagttcgtgt tttccggacc 120

ttcgtcacac ccccgtgaac ctaaggcgta aggttgatgt ttaccggaca aggggagcgg 180

atctgtgccg aggacgtcag agtccgcacc cggaattgtc ctgcccaccg ggagtagtgc 240

cgacacccgg tgtgggccat gactggccag aaccttcgac gacgaatgag gtaatgcaag 300

gtg tcc acc gaa aac aag aac gct ccc aag gtc act gac gag gtc gat 348
Val Ser Thr Glu Asn Lys Asn Ala Pro Lys Val Thr Asp Glu Val Asp
1 5 10 15

gtc gcc ctc gtc ggc gcg ggt gtc atg agc gcc acc ctg ggt gcg atg 396
Val Ala Leu Val Gly Ala Gly Val Met Ser Ala Thr Leu Gly Ala Met
20 25 30

atc cgc gag ctc gag ccg agc tgg tcc cag atg atc ttc gag cgc ctg 444
Ile Arg Glu Leu Glu Pro Ser Trp Ser Gln Met Ile Phe Glu Arg Leu
35 40 45

```
gac ggc ccc gcc cag gag tcc tcc tcc ccg tgg aac aac gcc ggt acc        492
Asp Gly Pro Ala Gln Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr
    50                  55                  60

ggc cac tcc gca ctc tgc gag ctg aac tac acc ccc gag gtc aac ggc        540
Gly His Ser Ala Leu Cys Glu Leu Asn Tyr Thr Pro Glu Val Asn Gly
65                  70                  75                  80

aag atc gag gtg gcc aag gcc atc ggc atc aac gag aag ttc cag gtc        588
Lys Ile Glu Val Ala Lys Ala Ile Gly Ile Asn Glu Lys Phe Gln Val
                85                  90                  95

tcc cgc cag ttc tgg tcc cac cag atc gac cac ggc gtg ctg gac gac        636
Ser Arg Gln Phe Trp Ser His Gln Ile Asp His Gly Val Leu Asp Asp
            100                 105                 110

ccc aag gag tgg atc aac ccc gtc gcc cac ctg gcc ttc gcc cag ggc        684
Pro Lys Glu Trp Ile Asn Pro Val Ala His Leu Ala Phe Ala Gln Gly
        115                 120                 125

gac gac cag gtc gac tac ctc aag cgc cgc cac gag gcg ctg gcc gac        732
Asp Asp Gln Val Asp Tyr Leu Lys Arg Arg His Glu Ala Leu Ala Asp
    130                 135                 140

aac atc ctc ttc ccg ggc atg gag tgg gtc gag gac gac gcc aag ttc        780
Asn Ile Leu Phe Pro Gly Met Glu Trp Val Glu Asp Asp Ala Lys Phe
145                 150                 155                 160

gcc gag cgc ctc ccg gtc atg tcc gag ggc cgt gac ttc gcc gcc gag        828
Ala Glu Arg Leu Pro Val Met Ser Glu Gly Arg Asp Phe Ala Ala Glu
                165                 170                 175

aag gtc gcc tac tcc ggc acc gac atc ggc acc gac gtc aac ttc ggt        876
Lys Val Ala Tyr Ser Gly Thr Asp Ile Gly Thr Asp Val Asn Phe Gly
            180                 185                 190

gcc ctg acc gag cag ttc ctc act gcc gcc gag gcc tcc ggc acg gag        924
Ala Leu Thr Glu Gln Phe Leu Thr Ala Ala Glu Ala Ser Gly Thr Glu
        195                 200                 205

atc cgc tac ggc cac gag gtc aag aac atc aag aag gac ggt ggc aag        972
Ile Arg Tyr Gly His Glu Val Lys Asn Ile Lys Lys Asp Gly Gly Lys
    210                 215                 220

tgg aag atc acc gtc aag aac gtc cac acg ggt gac acc tcc gtg gtc       1020
Trp Lys Ile Thr Val Lys Asn Val His Thr Gly Asp Thr Ser Val Val
225                 230                 235                 240

aag gcc aag ttc gtg ttc gtc ggc gcc ggc ggc tac gcc ctc gac ctg       1068
Lys Ala Lys Phe Val Phe Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu
                245                 250                 255

ctg cgc aag gca ggc gtc ccg gag gtc agc ggt tac gcc ggc ttc ccg       1116
Leu Arg Lys Ala Gly Val Pro Glu Val Ser Gly Tyr Ala Gly Phe Pro
            260                 265                 270

gtg tcc ggc ctg tgg ctg cgc tgc acc aac gag gag ctg atc aac cag       1164
Val Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Asn Gln
        275                 280                 285
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cac gac gcc aag gtc tac ggc aag gcc aag gtc ggt gcc ccg ccg atg      1212
His Asp Ala Lys Val Tyr Gly Lys Ala Lys Val Gly Ala Pro Pro Met
    290                 295                 300

tcc gtc ccg cac ctt gac acc cgc gtc atc gac ggc aag aag ggc ctc      1260
Ser Val Pro His Leu Asp Thr Arg Val Ile Asp Gly Lys Lys Gly Leu
305                 310                 315                 320

ctg ttc ggc ccc tac ggc ggc tgg agc ccg aag ttc ctc aag gag ggt      1308
Leu Phe Gly Pro Tyr Gly Gly Trp Ser Pro Lys Phe Leu Lys Glu Gly
                325                 330                 335

tcg tac ctc gac ctg ttc aag tcg atc cgc ctg gac aac ctc ccg tcc      1356
Ser Tyr Leu Asp Leu Phe Lys Ser Ile Arg Leu Asp Asn Leu Pro Ser
            340                 345                 350

tac ctc ggt gtc gcc gcc cag gag ttc gcc ctg acc aag tac ctc atc      1404
Tyr Leu Gly Val Ala Ala Gln Glu Phe Ala Leu Thr Lys Tyr Leu Ile
        355                 360                 365

acc gag gtg gcg aag gac ttc gag aag cgc ctc gtc gac ctg cgt gac      1452
Thr Glu Val Ala Lys Asp Phe Glu Lys Arg Leu Val Asp Leu Arg Asp
    370                 375                 380

tac gtc ccg tcc gcc aag gcc gag gac tgg gag acc gtg gtc gcc ggt      1500
Tyr Val Pro Ser Ala Lys Ala Glu Asp Trp Glu Thr Val Val Ala Gly
385                 390                 395                 400

cag cgc gtc cag gtg atc aag ccg gcc cgc gcg ccg cgc ttc ggc tcc      1548
Gln Arg Val Gln Val Ile Lys Pro Ala Arg Ala Pro Arg Phe Gly Ser
                405                 410                 415

ctc gag ttc ggc acc gcc ctg atc aac agc acc gac ggc tcc atc gcc      1596
Leu Glu Phe Gly Thr Ala Leu Ile Asn Ser Thr Asp Gly Ser Ile Ala
            420                 425                 430

ggc ctg ctg ggt gcc tcc ccg ggt gcc tcc atc gcc ccg gcc gcc atg      1644
Gly Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ala Ala Met
        435                 440                 445

ctc gag ctc gtc gag cgc tgc ttc ggt gac cgc atg atc cag tgg ggc      1692
Leu Glu Leu Val Glu Arg Cys Phe Gly Asp Arg Met Ile Gln Trp Gly
    450                 455                 460

ccg aag ctc aag gag atg atc ccg tcc tac ggc acc aag ctg ggc gac      1740
Pro Lys Leu Lys Glu Met Ile Pro Ser Tyr Gly Thr Lys Leu Gly Asp
465                 470                 475                 480

gac gag aag atg ttc aac gag ctc tgg gac tac acc cag aag acc ctg      1788
Asp Glu Lys Met Phe Asn Glu Leu Trp Asp Tyr Thr Gln Lys Thr Leu
                485                 490                 495

aag ctc gag aag tag ttccactgtg agggccgcga ccaccgggtc gcggccttcg      1843
Lys Leu Glu Lys
            500

ccgattccgt aggctggtgg ccatgcaacg catcgtgccc accatctggt tcaaccggaa    1903
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cgccgacgag gccgccgagt tctacgccga cgtcttcccc gacacgcttg tcgacgcccg 1963

cgtcccccac cccgaatccg gcgagaccct caccgtcgac gtgctcatcg acggctaccg 2023

cgtcaccctc ctcaacggtg ggccggagtt cggcccgacc cccgcgatca gcttcttcgt 2083

caacttcgac ccctccccgca 2103

<210> 176
<211> 500
<212> PRT
<213> Corynebacterium humireducens

<400> 176

Val Ser Thr Glu Asn Lys Asn Ala Pro Lys Val Thr Asp Glu Val Asp
1 5 10 15

Val Ala Leu Val Gly Ala Gly Val Met Ser Ala Thr Leu Gly Ala Met
20 25 30

Ile Arg Glu Leu Glu Pro Ser Trp Ser Gln Met Ile Phe Glu Arg Leu
35 40 45

Asp Gly Pro Ala Gln Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr
50 55 60

Gly His Ser Ala Leu Cys Glu Leu Asn Tyr Thr Pro Glu Val Asn Gly
65 70 75 80

Lys Ile Glu Val Ala Lys Ala Ile Gly Ile Asn Glu Lys Phe Gln Val
85 90 95

Ser Arg Gln Phe Trp Ser His Gln Ile Asp His Gly Val Leu Asp Asp
100 105 110

Pro Lys Glu Trp Ile Asn Pro Val Ala His Leu Ala Phe Ala Gln Gly
115 120 125

Asp Asp Gln Val Asp Tyr Leu Lys Arg Arg His Glu Ala Leu Ala Asp
130 135 140

Asn Ile Leu Phe Pro Gly Met Glu Trp Val Glu Asp Asp Ala Lys Phe
145 150 155 160

Ala Glu Arg Leu Pro Val Met Ser Glu Gly Arg Asp Phe Ala Ala Glu
165 170 175

```
Lys Val Ala Tyr Ser Gly Thr Asp Ile Gly Thr Asp Val Asn Phe Gly
            180                 185                 190

Ala Leu Thr Glu Gln Phe Leu Thr Ala Ala Glu Ala Ser Gly Thr Glu
        195                 200                 205

Ile Arg Tyr Gly His Glu Val Lys Asn Ile Lys Lys Asp Gly Gly Lys
    210                 215                 220

Trp Lys Ile Thr Val Lys Asn Val His Thr Gly Asp Thr Ser Val Val
225                 230                 235                 240

Lys Ala Lys Phe Val Phe Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu
                245                 250                 255

Leu Arg Lys Ala Gly Val Pro Glu Val Ser Gly Tyr Ala Gly Phe Pro
            260                 265                 270

Val Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Asn Gln
        275                 280                 285

His Asp Ala Lys Val Tyr Gly Lys Ala Lys Val Gly Ala Pro Pro Met
    290                 295                 300

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

Leu Phe Gly Pro Tyr Gly Gly Trp Ser Pro Lys Phe Leu Lys Glu Gly
                325                 330                 335

Ser Tyr Leu Asp Leu Phe Lys Ser Ile Arg Leu Asp Asn Leu Pro Ser
            340                 345                 350

Tyr Leu Gly Val Ala Ala Gln Glu Phe Ala Leu Thr Lys Tyr Leu Ile
        355                 360                 365

Thr Glu Val Ala Lys Asp Phe Glu Lys Arg Leu Val Asp Leu Arg Asp
    370                 375                 380

Tyr Val Pro Ser Ala Lys Ala Glu Asp Trp Glu Thr Val Val Ala Gly
385                 390                 395                 400

Gln Arg Val Gln Val Ile Lys Pro Ala Arg Ala Pro Arg Phe Gly Ser
                405                 410                 415
```

Leu Glu Phe Gly Thr Ala Leu Ile Asn Ser Thr Asp Gly Ser Ile Ala
420 425 430

Gly Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ala Ala Met
435 440 445

Leu Glu Leu Val Glu Arg Cys Phe Gly Asp Arg Met Ile Gln Trp Gly
450 455 460

Pro Lys Leu Lys Glu Met Ile Pro Ser Tyr Gly Thr Lys Leu Gly Asp
465 470 475 480

Asp Glu Lys Met Phe Asn Glu Leu Trp Asp Tyr Thr Gln Lys Thr Leu
485 490 495

Lys Leu Glu Lys
500

<210> 177
<211> 3357
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(3057)
<223> gene aceE

<400> 177
gtgggagatg accctcgttg ccgccccttg tgggctggtt gtgacctcgg gggtgggagc 60

cggggtttgc aatctccgcc acacacctcg cggagaggcg ggacaggcct gcgacaaggg 120

gcgatgggac gtcgataagc ggaacgccgg acccgttcat cttcgcaagc tttacaggaa 180

tgcagaacta cgttggccaa tgaaaacacg tatcctggac tggacactcg ggcctgtccg 240

gaccaccttg ccggcgggcc cgttgctcca ccacgacacc cagaaacctg aggcacatc 300

atg gca gat gac ctg aac gcg aac ggc cgc aag ggc aac tcc cac tac 348
Met Ala Asp Asp Leu Asn Ala Asn Gly Arg Lys Gly Asn Ser His Tyr
1 5 10 15

ccg gcg atc cgc gac ggc gtc gcg tcc tac ctc aaa gac acc gac ccg 396
Pro Ala Ile Arg Asp Gly Val Ala Ser Tyr Leu Lys Asp Thr Asp Pro
20 25 30

gag gag acc cag gag tgg atg gac tcc ctc gac ggt ctc ctc gcg gag 444
Glu Glu Thr Gln Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Ala Glu
35 40 45

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aag gac ccg gcc cgc gcc cgc tac ctc atg ctc cgc atg ctg gag cgc        492
Lys Asp Pro Ala Arg Ala Arg Tyr Leu Met Leu Arg Met Leu Glu Arg
    50                  55                  60

gcg gcc ctc aag cgt gtc ccg ctg ccg aac ctg acc tcc aca gac ttc        540
Ala Ala Leu Lys Arg Val Pro Leu Pro Asn Leu Thr Ser Thr Asp Phe
65                  70                  75                  80

gtc aac acg atc ccc acc acc atg gag ccg gag ttc ccg ggt gac gag        588
Val Asn Thr Ile Pro Thr Thr Met Glu Pro Glu Phe Pro Gly Asp Glu
                85                  90                  95

gag atg gag aag cgc tac cgc cgc tgg atg cgc tgg aac gcc gcc atc        636
Glu Met Glu Lys Arg Tyr Arg Arg Trp Met Arg Trp Asn Ala Ala Ile
            100                 105                 110

atg gtg cac cgc gcc cag cgc ccc ggc atc ggc gtc ggc ggc cac atc        684
Met Val His Arg Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His Ile
        115                 120                 125

tcc acc tac gcc tcc gcc gcc ccg ctc tac gag gtc ggc ttc aat cac        732
Ser Thr Tyr Ala Ser Ala Ala Pro Leu Tyr Glu Val Gly Phe Asn His
    130                 135                 140

ttc tgg cgc ggc aag gac cac ccg ggc ggc ggc gac cag atc ttc ttc        780
Phe Trp Arg Gly Lys Asp His Pro Gly Gly Gly Asp Gln Ile Phe Phe
145                 150                 155                 160

cag ggc cac gcc tcc ccc ggc atc tac gcc cgc gcc ttc ctc gag ggg        828
Gln Gly His Ala Ser Pro Gly Ile Tyr Ala Arg Ala Phe Leu Glu Gly
                165                 170                 175

cgc ctg agc gag gac gac ctc gac ggc ttc cgc cag gag gtc tcc cgc        876
Arg Leu Ser Glu Asp Asp Leu Asp Gly Phe Arg Gln Glu Val Ser Arg
            180                 185                 190

ggt gag ggc aac ggc atc ccg tcc tac ccg cac ccg cac ggc atg cct        924
Gly Glu Gly Asn Gly Ile Pro Ser Tyr Pro His Pro His Gly Met Pro
        195                 200                 205

gat ttc tgg gag ttc ccg acc gtc tcc atg gga ctg ggc ccg atg gac        972
Asp Phe Trp Glu Phe Pro Thr Val Ser Met Gly Leu Gly Pro Met Asp
    210                 215                 220

gcg atc tac cag gca cgt ttc aac cgt tac ctg cac aac cgc ggc atc       1020
Ala Ile Tyr Gln Ala Arg Phe Asn Arg Tyr Leu His Asn Arg Gly Ile
225                 230                 235                 240

aag gac acc tcc gac cag cac gtg tgg gcc ttc ctc ggc gac ggc gag       1068
Lys Asp Thr Ser Asp Gln His Val Trp Ala Phe Leu Gly Asp Gly Glu
                245                 250                 255

atg gac gag ccg gag tcc cgc ggc ctc atc cag cac gcc gcg ctg aac       1116
Met Asp Glu Pro Glu Ser Arg Gly Leu Ile Gln His Ala Ala Leu Asn
            260                 265                 270

aac ctg gac aac ctc acc ttc gtg gtc aac tgc aac ctg cag cgt ctc       1164
Asn Leu Asp Asn Leu Thr Phe Val Val Asn Cys Asn Leu Gln Arg Leu
```

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          275                 280                 285

gac ggc ccg gtc cgc ggc aac acg cag atc atc cag gag ctc gag tcc      1212
Asp Gly Pro Val Arg Gly Asn Thr Gln Ile Ile Gln Glu Leu Glu Ser
    290                 295                 300

ttc ttc cgg ggt gcc ggc tgg tcc gtc atc aag gtc atc tgg ggc cgc      1260
Phe Phe Arg Gly Ala Gly Trp Ser Val Ile Lys Val Ile Trp Gly Arg
305                 310                 315                 320

gag tgg gac gcc ctg ctg gag aag gac gag tcc ggc gcg ctg gtc aac      1308
Glu Trp Asp Ala Leu Leu Glu Lys Asp Glu Ser Gly Ala Leu Val Asn
                325                 330                 335

gtc atg aac acc acc ccg gac ggt gac tac cag acc ttc aag gcc aac      1356
Val Met Asn Thr Thr Pro Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn
            340                 345                 350

gac ggc gcc tac gtc cgc gag cac ttc ttc ggc cgc gac gag cgc acc      1404
Asp Gly Ala Tyr Val Arg Glu His Phe Phe Gly Arg Asp Glu Arg Thr
        355                 360                 365

gcc aaa ctc gtc gag gac atg acc gac gag gag atc tgg gcc ctg ccg      1452
Ala Lys Leu Val Glu Asp Met Thr Asp Glu Glu Ile Trp Ala Leu Pro
    370                 375                 380

cgc ggt ggc cac gac tac cgc aag gtc cac gcc gcc tac aag cgg gcg      1500
Arg Gly Gly His Asp Tyr Arg Lys Val His Ala Ala Tyr Lys Arg Ala
385                 390                 395                 400

ctg gag acc aag gac cgc ccg acc gtc atc ctc gcg ttc acc atc aag      1548
Leu Glu Thr Lys Asp Arg Pro Thr Val Ile Leu Ala Phe Thr Ile Lys
                405                 410                 415

ggc tac ggc ctg ggc cac aac ttc gag ggc cgc aac gcg acg cac cag      1596
Gly Tyr Gly Leu Gly His Asn Phe Glu Gly Arg Asn Ala Thr His Gln
            420                 425                 430

atg aag aag ctc gcc gcc gag gac ctg aag aac ttc cgc gac aag cag      1644
Met Lys Lys Leu Ala Ala Glu Asp Leu Lys Asn Phe Arg Asp Lys Gln
        435                 440                 445

tcc atc ccg atc ccg gac gag gtc ctc gag gcc gac ccg tac ctg ccg      1692
Ser Ile Pro Ile Pro Asp Glu Val Leu Glu Ala Asp Pro Tyr Leu Pro
    450                 455                 460

ccg tac tac cac ccg ggc gag gac gcc ccg gag atc cag tac atg aag      1740
Pro Tyr Tyr His Pro Gly Glu Asp Ala Pro Glu Ile Gln Tyr Met Lys
465                 470                 475                 480

aag cgt cgt cag gag ctg ggc ggt ttc atc ccg gag cgt cgc cag acc      1788
Lys Arg Arg Gln Glu Leu Gly Gly Phe Ile Pro Glu Arg Arg Gln Thr
                485                 490                 495

tac acc ccg ctg cag gtc ccg gac atc gag aag ctg cgc agc gtg cgc      1836
Tyr Thr Pro Leu Gln Val Pro Asp Ile Glu Lys Leu Arg Ser Val Arg
            500                 505                 510

aag ggc tcc ggc aag cag gag gtc gcc tcc acc atg gcg ctc gtg cgt      1884
```

```
Lys Gly Ser Gly Lys Gln Glu Val Ala Ser Thr Met Ala Leu Val Arg
        515                 520                 525

gcc ttc aag gag ctc atg cgt gac aag gag ctg ggc cgc cgc gtc gtg      1932
Ala Phe Lys Glu Leu Met Arg Asp Lys Glu Leu Gly Arg Arg Val Val
    530                 535                 540

ccg atc atc ccg gac gag gcc cgc acc ttc ggc ctc gac tcc tgg ttc      1980
Pro Ile Ile Pro Asp Glu Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe
545                 550                 555                 560

ccg acc ctg aag atc tac aac ccg cac ggc cag aac tac gtg ccg gtc      2028
Pro Thr Leu Lys Ile Tyr Asn Pro His Gly Gln Asn Tyr Val Pro Val
                565                 570                 575

gac cat gac ctc atg ctg tcc tac cgg gag gcc acc gac ggc cag atc      2076
Asp His Asp Leu Met Leu Ser Tyr Arg Glu Ala Thr Asp Gly Gln Ile
            580                 585                 590

ctc cac gag ggc atc aac gag gcc ggt tcc gtc gcg tcc ttc atg gcc      2124
Leu His Glu Gly Ile Asn Glu Ala Gly Ser Val Ala Ser Phe Met Ala
        595                 600                 605

gcc ggc acc tcc tac gcc acc cac ggc gaa gcg atg atc ccg ctg tac      2172
Ala Gly Thr Ser Tyr Ala Thr His Gly Glu Ala Met Ile Pro Leu Tyr
    610                 615                 620

atc ttc tac tcg atg ttc ggt ttc cag cgc acc ggc gac ggc atc tgg      2220
Ile Phe Tyr Ser Met Phe Gly Phe Gln Arg Thr Gly Asp Gly Ile Trp
625                 630                 635                 640

gcc gcc gcc gac cag atg gcc cgt ggc ttc ctc atc ggc gcc acc gcc      2268
Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Leu Ile Gly Ala Thr Ala
                645                 650                 655

ggc cgc acc acc ctg acg ggt gag ggc ctg cag cac atg gac ggc cac      2316
Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln His Met Asp Gly His
            660                 665                 670

tcg cag atc ctc gcc tcc acg aac ccg ggc gtc gtg tcc tac gac ccg      2364
Ser Gln Ile Leu Ala Ser Thr Asn Pro Gly Val Val Ser Tyr Asp Pro
        675                 680                 685

gcg ttc gcc tac gag atc gcg cac ctg ctc cat gag ggc atc gac cgc      2412
Ala Phe Ala Tyr Glu Ile Ala His Leu Leu His Glu Gly Ile Asp Arg
    690                 695                 700

atg tac ggc ccg ggc cgc ggt gag aac gtc atc tac tac ctc acc gtg      2460
Met Tyr Gly Pro Gly Arg Gly Glu Asn Val Ile Tyr Tyr Leu Thr Val
705                 710                 715                 720

tac aac gag ccg gtc ccg cag ccg gcc gag ccg gag aac ctc gac gtc      2508
Tyr Asn Glu Pro Val Pro Gln Pro Ala Glu Pro Glu Asn Leu Asp Val
                725                 730                 735

gag ggc ctg cac aag ggc atg tac ctg ttc tcc cgc gcg gag gag ctc      2556
Glu Gly Leu His Lys Gly Met Tyr Leu Phe Ser Arg Ala Glu Glu Leu
            740                 745                 750
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gag gtc gag gac ggc cac gag gcc tcc atc ctg gcc tcc ggc atc ggc      2604
Glu Val Glu Asp Gly His Glu Ala Ser Ile Leu Ala Ser Gly Ile Gly
        755                 760                 765

atg cag tgg gcg ctc aag gcc cag cag atg ctg gcc gag gag tac aac      2652
Met Gln Trp Ala Leu Lys Ala Gln Gln Met Leu Ala Glu Glu Tyr Asn
    770                 775                 780

gtg cgt gcc aac gtc ttc tcc gtc acc tcc tgg gtc gag ctg gcc cgc      2700
Val Arg Ala Asn Val Phe Ser Val Thr Ser Trp Val Glu Leu Ala Arg
785                 790                 795                 800

gag ggt gcg gcg aag aac aag gag cag ctg cgc aac ccg gcc gca gag      2748
Glu Gly Ala Ala Lys Asn Lys Glu Gln Leu Arg Asn Pro Ala Ala Glu
                805                 810                 815

atc gag gag gcc ttc gcc acc agg cag ctg aag cag gtc gac ggc ggc      2796
Ile Glu Glu Ala Phe Ala Thr Arg Gln Leu Lys Gln Val Asp Gly Gly
            820                 825                 830

acc ttc gtg gcc gtc tcc gac ttc gcg acc gac ctg cag gag cag atc      2844
Thr Phe Val Ala Val Ser Asp Phe Ala Thr Asp Leu Gln Glu Gln Ile
        835                 840                 845

cgc gcc tac gtc ccg ggc gag tac atc gtc ctg ggc gcc gac ggc ttc      2892
Arg Ala Tyr Val Pro Gly Glu Tyr Ile Val Leu Gly Ala Asp Gly Phe
    850                 855                 860

ggc ttc tcc gac acc cgt ccg gcc gcc cgc cgc ttc ttc aac atc gac      2940
Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp
865                 870                 875                 880

gcc gag tcc atc gtc gtc gcg gtc ctc atg ggc ctg gcc cgc gag ggc      2988
Ala Glu Ser Ile Val Val Ala Val Leu Met Gly Leu Ala Arg Glu Gly
                885                 890                 895

aag atc gac atc tct gtg gcc cag cag gcc gcc gag aag tac cag ctg      3036
Lys Ile Asp Ile Ser Val Ala Gln Gln Ala Ala Glu Lys Tyr Gln Leu
            900                 905                 910

gac gat ccg acc gct gtg taa ctgatccccc ggtcaaggcc ctgctccggc         3087
Asp Asp Pro Thr Ala Val
        915

agggccttgc tgctttcccg cttgtcgacg cccctctcac tccctgttga ggtaccgcgg     3147

ccaggaggtg tcgcgggtgg ccagcgagat ctccaccgcg gtgtcgagct ccgctgccag     3207

gggctcgggc agcttgtgcc ggagcgcgtc gccgaggcgc gcgatgacct ccaggcgcag     3267

caggttgcgg gtctccgtga tgtagatgcg cgggtaccgg gtggccagct cgacctcgga     3327

ggggtcggcg ggcccgccgt acatctcgac                                      3357
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<210> 178
<211> 918
<212> PRT
<213> Corynebacterium humireducens

<400> 178

Met Ala Asp Asp Leu Asn Ala Asn Gly Arg Lys Gly Asn Ser His Tyr
1 5 10 15

Pro Ala Ile Arg Asp Gly Val Ala Ser Tyr Leu Lys Asp Thr Asp Pro
20 25 30

Glu Glu Thr Gln Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Ala Glu
35 40 45

Lys Asp Pro Ala Arg Ala Arg Tyr Leu Met Leu Arg Met Leu Glu Arg
50 55 60

Ala Ala Leu Lys Arg Val Pro Leu Pro Asn Leu Thr Ser Thr Asp Phe
65 70 75 80

Val Asn Thr Ile Pro Thr Thr Met Glu Pro Glu Phe Pro Gly Asp Glu
85 90 95

Glu Met Glu Lys Arg Tyr Arg Arg Trp Met Arg Trp Asn Ala Ala Ile
100 105 110

Met Val His Arg Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His Ile
115 120 125

Ser Thr Tyr Ala Ser Ala Ala Pro Leu Tyr Glu Val Gly Phe Asn His
130 135 140

Phe Trp Arg Gly Lys Asp His Pro Gly Gly Gly Asp Gln Ile Phe Phe
145 150 155 160

Gln Gly His Ala Ser Pro Gly Ile Tyr Ala Arg Ala Phe Leu Glu Gly
165 170 175

Arg Leu Ser Glu Asp Asp Leu Asp Gly Phe Arg Gln Glu Val Ser Arg
180 185 190

Gly Glu Gly Asn Gly Ile Pro Ser Tyr Pro His Pro His Gly Met Pro
195 200 205

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

Ala Ile Tyr Gln Ala Arg Phe Asn Arg Tyr Leu His Asn Arg Gly Ile
225 230 235 240

Lys Asp Thr Ser Asp Gln His Val Trp Ala Phe Leu Gly Asp Gly Glu
245 250 255

Met Asp Glu Pro Glu Ser Arg Gly Leu Ile Gln His Ala Ala Leu Asn
260 265 270

Asn Leu Asp Asn Leu Thr Phe Val Val Asn Cys Asn Leu Gln Arg Leu
275 280 285

Asp Gly Pro Val Arg Gly Asn Thr Gln Ile Ile Gln Glu Leu Glu Ser
290 295 300

Phe Phe Arg Gly Ala Gly Trp Ser Val Ile Lys Val Ile Trp Gly Arg
305 310 315 320

Glu Trp Asp Ala Leu Leu Glu Lys Asp Glu Ser Gly Ala Leu Val Asn
325 330 335

Val Met Asn Thr Thr Pro Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn
340 345 350

Asp Gly Ala Tyr Val Arg Glu His Phe Phe Gly Arg Asp Glu Arg Thr
355 360 365

Ala Lys Leu Val Glu Asp Met Thr Asp Glu Glu Ile Trp Ala Leu Pro
370 375 380

Arg Gly Gly His Asp Tyr Arg Lys Val His Ala Ala Tyr Lys Arg Ala
385 390 395 400

Leu Glu Thr Lys Asp Arg Pro Thr Val Ile Leu Ala Phe Thr Ile Lys
405 410 415

Gly Tyr Gly Leu Gly His Asn Phe Glu Gly Arg Asn Ala Thr His Gln
420 425 430

Met Lys Lys Leu Ala Ala Glu Asp Leu Lys Asn Phe Arg Asp Lys Gln
435 440 445

Ser Ile Pro Ile Pro Asp Glu Val Leu Glu Ala Asp Pro Tyr Leu Pro
450 455 460

Pro Tyr Tyr His Pro Gly Glu Asp Ala Pro Glu Ile Gln Tyr Met Lys
465 470 475 480

Lys Arg Arg Gln Glu Leu Gly Gly Phe Ile Pro Glu Arg Arg Gln Thr
485 490 495

Tyr Thr Pro Leu Gln Val Pro Asp Ile Glu Lys Leu Arg Ser Val Arg
500 505 510

Lys Gly Ser Gly Lys Gln Glu Val Ala Ser Thr Met Ala Leu Val Arg
515 520 525

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

Pro Ile Ile Pro Asp Glu Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe
545 550 555 560

Pro Thr Leu Lys Ile Tyr Asn Pro His Gly Gln Asn Tyr Val Pro Val
565 570 575

Asp His Asp Leu Met Leu Ser Tyr Arg Glu Ala Thr Asp Gly Gln Ile
580 585 590

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

Ala Gly Thr Ser Tyr Ala Thr His Gly Glu Ala Met Ile Pro Leu Tyr
610 615 620

Ile Phe Tyr Ser Met Phe Gly Phe Gln Arg Thr Gly Asp Gly Ile Trp
625 630 635 640

Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Leu Ile Gly Ala Thr Ala
645 650 655

Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln His Met Asp Gly His
660 665 670

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

Ala Phe Ala Tyr Glu Ile Ala His Leu Leu His Glu Gly Ile Asp Arg
690 695 700

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Met Tyr Gly Pro Gly Arg Gly Glu Asn Val Ile Tyr Tyr Leu Thr Val
705                 710                 715                 720

Tyr Asn Glu Pro Val Pro Gln Pro Ala Glu Pro Glu Asn Leu Asp Val
                725                 730                 735

Glu Gly Leu His Lys Gly Met Tyr Leu Phe Ser Arg Ala Glu Glu Leu
            740                 745                 750

Glu Val Glu Asp Gly His Glu Ala Ser Ile Leu Ala Ser Gly Ile Gly
        755                 760                 765

Met Gln Trp Ala Leu Lys Ala Gln Gln Met Leu Ala Glu Glu Tyr Asn
    770                 775                 780

Val Arg Ala Asn Val Phe Ser Val Thr Ser Trp Val Glu Leu Ala Arg
785                 790                 795                 800

Glu Gly Ala Ala Lys Asn Lys Glu Gln Leu Arg Asn Pro Ala Ala Glu
                805                 810                 815

Ile Glu Glu Ala Phe Ala Thr Arg Gln Leu Lys Gln Val Asp Gly Gly
            820                 825                 830

Thr Phe Val Ala Val Ser Asp Phe Ala Thr Asp Leu Gln Glu Gln Ile
        835                 840                 845

Arg Ala Tyr Val Pro Gly Glu Tyr Ile Val Leu Gly Ala Asp Gly Phe
    850                 855                 860

Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp
865                 870                 875                 880

Ala Glu Ser Ile Val Val Ala Val Leu Met Gly Leu Ala Arg Glu Gly
                885                 890                 895

Lys Ile Asp Ile Ser Val Ala Gln Gln Ala Ala Glu Lys Tyr Gln Leu
            900                 905                 910

Asp Asp Pro Thr Ala Val
        915
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<210> 179

<211> 1752
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1452)
<223> gene gltA

<400> 179
agctgctctc cgcccagcag ctcgaggagc tcggcttcaa cgccgtcatc tacccggtga 60

ccaccctgcg catcgccatg ggacaggtcg aggaggctct cgcggagatc gccgccaccg 120

gcacccagac cgggtgggtc gaccgcatgc agcaccgctc ccgcctctac gaactgctcc 180

gctacaacga gtacaacgcc ttcgaccagg aggttttcac gtactccgcc gacacctacc 240

agcccacctt ccagtagccc accagcaact cctgacattc cttgaaaggg gatgagtacc 300

atg tcc gac aac acc aac atc gag gtc cgc aag ggt ctc tac ggc gtg 348
Met Ser Asp Asn Thr Asn Ile Glu Val Arg Lys Gly Leu Tyr Gly Val
1 5 10 15

atc gcc gac tac acc gca gtc tcc aag gtc atg ccg gag acc aac tcc 396
Ile Ala Asp Tyr Thr Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser
20 25 30

ctg acc tac cgc gga tac gcc gtc cag gac ctc gtc gca gag tgc tcc 444
Leu Thr Tyr Arg Gly Tyr Ala Val Gln Asp Leu Val Ala Glu Cys Ser
35 40 45

ttc gag gag gtc ttc tac ctc ctg tgg aac ggt gag ctg ccg aac gag 492
Phe Glu Glu Val Phe Tyr Leu Leu Trp Asn Gly Glu Leu Pro Asn Glu
50 55 60

gag cag ctg gcg gag ttc aac agg cgc ggc cgt tcc tac cgc aag ctc 540
Glu Gln Leu Ala Glu Phe Asn Arg Arg Gly Arg Ser Tyr Arg Lys Leu
65 70 75 80

gac gcc ggc ctg atc gca ctc atc cac tcc ctg ccg ctc gac tgt cac 588
Asp Ala Gly Leu Ile Ala Leu Ile His Ser Leu Pro Leu Asp Cys His
85 90 95

ccg atg gac gtc atg cgc acc gcc gtg tcc tac atg ggc acc aag gac 636
Pro Met Asp Val Met Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp
100 105 110

tcc gag cac ttc acc ccg gac gcc gac cac atc acc cac gtc ggc cac 684
Ser Glu His Phe Thr Pro Asp Ala Asp His Ile Thr His Val Gly His
115 120 125

aac ctc ctc gcc cag ctg ccg atg gtg ctg gcc atg gac atc cgc cgc 732
Asn Leu Leu Ala Gln Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg
130 135 140

cgt cag ggc ctc gac atc gtc gcc ccg gac ccg gac aag tcc gtc gcc 780
Arg Gln Gly Leu Asp Ile Val Ala Pro Asp Pro Asp Lys Ser Val Ala

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145                 150                 155                 160

cac aac ctg ctg tcg atg gtc ttc ggc aac ggc ccg gag tcc ccg gcg  828
His Asn Leu Leu Ser Met Val Phe Gly Asn Gly Pro Glu Ser Pro Ala
                165                 170                 175

tcc aac ccg gac gac gtg cgt gac ttc gag aag tcg ctc atc ctc tac  876
Ser Asn Pro Asp Asp Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr
            180                 185                 190

gcc gag cac tcc ttc aac gcc tcg acc ttc acc tcg cgt gtg atc acc  924
Ala Glu His Ser Phe Asn Ala Ser Thr Phe Thr Ser Arg Val Ile Thr
        195                 200                 205

tcg acc cgc tcg gac gtc tac tcc gcg atc acc ggt gcc atc ggc gcc  972
Ser Thr Arg Ser Asp Val Tyr Ser Ala Ile Thr Gly Ala Ile Gly Ala
    210                 215                 220

ctc aag ggc ccg ctg cac ggc ggc gcc aac gag ttc gtc atg cac acc 1020
Leu Lys Gly Pro Leu His Gly Gly Ala Asn Glu Phe Val Met His Thr
225                 230                 235                 240

atg ctg gag atc gac gac ccg gag aag gcc gcc gac tgg gtc aac aac 1068
Met Leu Glu Ile Asp Asp Pro Glu Lys Ala Ala Asp Trp Val Asn Asn
                245                 250                 255

gcc ctg gac aac aag gac ctc atc atg ggc ttc ggt cac cgc gtg tac 1116
Ala Leu Asp Asn Lys Asp Leu Ile Met Gly Phe Gly His Arg Val Tyr
            260                 265                 270

aag aag ggt gac tcg cgt gtc ccg tcc atg gag gcg tcc ttc cgt gac 1164
Lys Lys Gly Asp Ser Arg Val Pro Ser Met Glu Ala Ser Phe Arg Asp
        275                 280                 285

ctc gcc gag cgt cac gac ggc gcc aag tgg gtc gcc atg tac gag aac 1212
Leu Ala Glu Arg His Asp Gly Ala Lys Trp Val Ala Met Tyr Glu Asn
    290                 295                 300

atg cgc gac gcc atg gac gcc cgc acc ggc atc aag ccg aac ctg gac 1260
Met Arg Asp Ala Met Asp Ala Arg Thr Gly Ile Lys Pro Asn Leu Asp
305                 310                 315                 320

ttc ccg gcc ggc ccg gcg tac cac ctg ctc ggc ttc ccg gtc gac ttc 1308
Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe Pro Val Asp Phe
                325                 330                 335

ttc acc ccg ctg ttc gtc gtc gcc cgc atc gcc ggc tgg acc gcc cac 1356
Phe Thr Pro Leu Phe Val Val Ala Arg Ile Ala Gly Trp Thr Ala His
            340                 345                 350

atc gtg gag cag tac aac gac aac tcc ctg att cgt ccg ctc tcc gcc 1404
Ile Val Glu Gln Tyr Asn Asp Asn Ser Leu Ile Arg Pro Leu Ser Ala
        355                 360                 365

tac aac ggc ccc gag cag cgc cag gtc acc ccg ctg gcc gcc cgt tag 1452
Tyr Asn Gly Pro Glu Gln Arg Gln Val Thr Pro Leu Ala Ala Arg
    370                 375                 380

ccccacggcc ggcaccggac caccgcgacg cccacggcac tgcccacaca ttggggtggt 1512
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gcgcgtgggt ttcgctgttc ggaacacctg tcggcccatt ccgcagggcg ggacagaaac 1572

ggcctttcgg gcgcccgtcc cgcggagtgc ggaaatggac cgcaccgggt ccaccacctg 1632

cagatacccc ctgtgactag gggatactcc cccgaagaca accctctttc ttgcgatact 1692

gtggtgtgcc agagagctca cccgctctca gacacacccc cgacatgacg ttcggaaagg 1752

<210> 180
<211> 383
<212> PRT
<213> Corynebacterium humireducens

<400> 180

Met Ser Asp Asn Thr Asn Ile Glu Val Arg Lys Gly Leu Tyr Gly Val
1 5 10 15

Ile Ala Asp Tyr Thr Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser
20 25 30

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

Phe Glu Glu Val Phe Tyr Leu Leu Trp Asn Gly Glu Leu Pro Asn Glu
50 55 60

Glu Gln Leu Ala Glu Phe Asn Arg Arg Gly Arg Ser Tyr Arg Lys Leu
65 70 75 80

Asp Ala Gly Leu Ile Ala Leu Ile His Ser Leu Pro Leu Asp Cys His
85 90 95

Pro Met Asp Val Met Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp
100 105 110

Ser Glu His Phe Thr Pro Asp Ala Asp His Ile Thr His Val Gly His
115 120 125

Asn Leu Leu Ala Gln Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg
130 135 140

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

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

Ser Asn Pro Asp Asp Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr
180 185 190

Ala Glu His Ser Phe Asn Ala Ser Thr Phe Thr Ser Arg Val Ile Thr
195 200 205

Ser Thr Arg Ser Asp Val Tyr Ser Ala Ile Thr Gly Ala Ile Gly Ala
210 215 220

Leu Lys Gly Pro Leu His Gly Gly Ala Asn Glu Phe Val Met His Thr
225 230 235 240

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

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

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

Leu Ala Glu Arg His Asp Gly Ala Lys Trp Val Ala Met Tyr Glu Asn
290 295 300

Met Arg Asp Ala Met Asp Ala Arg Thr Gly Ile Lys Pro Asn Leu Asp
305 310 315 320

Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe Pro Val Asp Phe
325 330 335

Phe Thr Pro Leu Phe Val Val Ala Arg Ile Ala Gly Trp Thr Ala His
340 345 350

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

Tyr Asn Gly Pro Glu Gln Arg Gln Val Thr Pro Leu Ala Ala Arg
370 375 380

<210> 181
<211> 1578
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1278)
<223> gene mdh

<400> 181
gaacatgcgg ggtcgtccct ccgggggcac gggtcggggt ggaagggtct ggaaggggc 60

ggtgccggcg ggtctgtgcg ggccgcaacc ggcgctgtga tccatcgtgc ctgatgtatc 120

ggtcggtggt ggggcggtgc ggctgagaag atgctggacc acccgatgta gcgacgttct 180

tccagcggaa acagccggat ctccggcgag gttacgccca tccgggggtg gcggctcgga 240

acggtctttg aggctagact cgcaggcgtt gatgcattag accgctcgaa aggatcccgc 300

atg acc cag aac ccc gtg aag atc gcc gtc acc ggt gcc gcc ggc aac 348
Met Thr Gln Asn Pro Val Lys Ile Ala Val Thr Gly Ala Ala Gly Asn
1 5 10 15

atc gcc tac tcc ctc ctg tgg cgc atc gcc gca ggt gac gtc tac ggc 396
Ile Ala Tyr Ser Leu Leu Trp Arg Ile Ala Ala Gly Asp Val Tyr Gly
20 25 30

cgc gac acc ccg atc gag ctc acc ctc ctc gag atc ccg gcc gcc gta 444
Arg Asp Thr Pro Ile Glu Leu Thr Leu Leu Glu Ile Pro Ala Ala Val
35 40 45

cgc ggc gcc gag ggc gtg gcc atg gag ctc aac gac tcc gcc ttc ccc 492
Arg Gly Ala Glu Gly Val Ala Met Glu Leu Asn Asp Ser Ala Phe Pro
50 55 60

ctc ctg cgc aac atc acc gtc acc gac agc gcc gac gtc gcc ttc gac 540
Leu Leu Arg Asn Ile Thr Val Thr Asp Ser Ala Asp Val Ala Phe Asp
65 70 75 80

ggc gcc aac gcc gcc ttc ctt gtc ggc gcg aag ccg cgc ggt gca ggc 588
Gly Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro Arg Gly Ala Gly
85 90 95

gag gag cgc gcc gac ctg ctg aag aac aac ggc ggc atc ttc ggc ccg 636
Glu Glu Arg Ala Asp Leu Leu Lys Asn Asn Gly Gly Ile Phe Gly Pro
100 105 110

cag ggc agg gcc atc aac gac cgc gcc gcg gac gac gtc cgc gtg ctc 684
Gln Gly Arg Ala Ile Asn Asp Arg Ala Ala Asp Asp Val Arg Val Leu
115 120 125

gtc gtc ggc aac ccg gcc aac acc aac gcc ctg atc gcc cag cgc aac 732
Val Val Gly Asn Pro Ala Asn Thr Asn Ala Leu Ile Ala Gln Arg Asn
130 135 140

gcc ccg gac gtc ccg gcc gag cgt ttc acc gcg ctg atg cgc ctg gac 780
Ala Pro Asp Val Pro Ala Glu Arg Phe Thr Ala Leu Met Arg Leu Asp
145 150 155 160

cac agc cgt gcg ctg tcc cag ctg gcc gag aag ctc ggc gtg ctc acc 828
His Ser Arg Ala Leu Ser Gln Leu Ala Glu Lys Leu Gly Val Leu Thr

```
                    165                 170                 175

acc gac ttc gag aac gtc gtc gtg tgg ggc aac cac tcc gcg acc cag        876
Thr Asp Phe Glu Asn Val Val Val Trp Gly Asn His Ser Ala Thr Gln
            180                 185                 190

ttc ccg gac gtg acc ttc gcc acc gtc aag ggt gag ccg gtc atc gag        924
Phe Pro Asp Val Thr Phe Ala Thr Val Lys Gly Glu Pro Val Ile Glu
        195                 200                 205

aag atc gac cat gac tgg tac gtc aac gag ttc atc ccg cgc gtc gcg        972
Lys Ile Asp His Asp Trp Tyr Val Asn Glu Phe Ile Pro Arg Val Ala
    210                 215                 220

aag cgt ggc gcc gag atc atc gag gtc cgc ggc aag tcc tcc gcc gcc       1020
Lys Arg Gly Ala Glu Ile Ile Glu Val Arg Gly Lys Ser Ser Ala Ala
225                 230                 235                 240

tcc gcc gcc tcc gcc gcg gtg gac cac atg cgt gac tgg gtc cag ggc       1068
Ser Ala Ala Ser Ala Ala Val Asp His Met Arg Asp Trp Val Gln Gly
                245                 250                 255

act gag cgg tgg gcc tcc gcc gcc ctg ccg tcc gac ggc tcc tac ggc       1116
Thr Glu Arg Trp Ala Ser Ala Ala Leu Pro Ser Asp Gly Ser Tyr Gly
            260                 265                 270

atc gac gag ggt ctc gtc gcc ggc ctg ccg acc gtc tcc cgc aac ggc       1164
Ile Asp Glu Gly Leu Val Ala Gly Leu Pro Thr Val Ser Arg Asn Gly
        275                 280                 285

tcc tgg gag atc gtc cag ggc ctc gag ctc aac gac ttc cag cgc gag       1212
Ser Trp Glu Ile Val Gln Gly Leu Glu Leu Asn Asp Phe Gln Arg Glu
    290                 295                 300

atg atc gcc cgg aac gtc gcg gag ctc aag gcc gag cgt gac gca gtc       1260
Met Ile Ala Arg Asn Val Ala Glu Leu Lys Ala Glu Arg Asp Ala Val
305                 310                 315                 320

gct gac ctg ctt cct tag cgcgtcaact cgcatccgcc gccaatcccg              1308
Ala Asp Leu Leu Pro
                325

gtagtgttca ggaacatgcg cttcgggatt gatttcggaa ccacccgtac cgtcattgcg     1368

gcggtcgacc ggggaaacta cccggtcgtc aacgtcacgg acacggacgg cgactcacgg     1428

gagtacatcc cctcggtcgt cgcgctggat ggtgaacggt tggtcggtgg ctgggaggcg     1488

ctggcggtag gtggcccgac cctcacccgc tccttcaagc gtctgctgac ctcccgcacc     1548

gtcaccgcgg agacccccgt ccggctgggc                                      1578


<210>  182
<211>  325
<212>  PRT
<213>  Corynebacterium humireducens

<400>  182
```

```
Met Thr Gln Asn Pro Val Lys Ile Ala Val Thr Gly Ala Ala Gly Asn
1               5                  10                  15

Ile Ala Tyr Ser Leu Leu Trp Arg Ile Ala Ala Gly Asp Val Tyr Gly
            20                  25                  30

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

Arg Gly Ala Glu Gly Val Ala Met Glu Leu Asn Asp Ser Ala Phe Pro
    50                  55                  60

Leu Leu Arg Asn Ile Thr Val Thr Asp Ser Ala Asp Val Ala Phe Asp
65                  70                  75                  80

Gly Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro Arg Gly Ala Gly
                85                  90                  95

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

Gln Gly Arg Ala Ile Asn Asp Arg Ala Ala Asp Asp Val Arg Val Leu
        115                 120                 125

Val Val Gly Asn Pro Ala Asn Thr Asn Ala Leu Ile Ala Gln Arg Asn
    130                 135                 140

Ala Pro Asp Val Pro Ala Glu Arg Phe Thr Ala Leu Met Arg Leu Asp
145                 150                 155                 160

His Ser Arg Ala Leu Ser Gln Leu Ala Glu Lys Leu Gly Val Leu Thr
                165                 170                 175

Thr Asp Phe Glu Asn Val Val Val Trp Gly Asn His Ser Ala Thr Gln
            180                 185                 190

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

Lys Ile Asp His Asp Trp Tyr Val Asn Glu Phe Ile Pro Arg Val Ala
    210                 215                 220

Lys Arg Gly Ala Glu Ile Ile Glu Val Arg Gly Lys Ser Ser Ala Ala
225                 230                 235                 240
```

```
Ser Ala Ala Ser Ala Ala Val Asp His Met Arg Asp Trp Val Gln Gly
                245                 250                 255

Thr Glu Arg Trp Ala Ser Ala Ala Leu Pro Ser Asp Gly Ser Tyr Gly
            260                 265                 270

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

Ser Trp Glu Ile Val Gln Gly Leu Glu Leu Asn Asp Phe Gln Arg Glu
    290                 295                 300

Met Ile Ala Arg Asn Val Ala Glu Leu Lys Ala Glu Arg Asp Ala Val
305                 310                 315                 320

Ala Asp Leu Leu Pro
                325
```

<210> 183
<211> 2100
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1800)
<223> gene murE

<400> 183

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gccggcaaga cgggtacggc ccagaaggtc gacccgcgga cgggcgcgta ctcgaactcg       60

gactactgga tcaccttcgc cggcatcgcc ccggcggatg acccgcgctt cgtcgtcgcc      120

gtcatggtcg acgagccccg cgccggcgtc gaggcgggag gcggcggtgg ccagtcctcg      180

gcgccgttgt tccgtgacat cgcgtcctgg ctgctcaacc gggacaacat cccggcgtca      240

ccgcccatgg aggacatgct gatcctccac gcccactaac ccagcccacc acggaggagt      300

atg acc atg gag acc aca gtg acc aca ctg tcc cac ctc gcc cgt atc         348
Met Thr Met Glu Thr Thr Val Thr Thr Leu Ser His Leu Ala Arg Ile
1               5                   10                  15

gcc ggg gga gag ctg acc gga tcc gtg gcc ccg gtc gtc acg tcg gtg         396
Ala Gly Gly Glu Leu Thr Gly Ser Val Ala Pro Val Val Thr Ser Val
            20                  25                  30

gag ctc gac tcc tcc cgc ctc gcg gac gag ggc gcg ctc ttc gcc gcc         444
Glu Leu Asp Ser Ser Arg Leu Ala Asp Glu Gly Ala Leu Phe Ala Ala
        35                  40                  45
```

```
gtc ccc ggc acg cgc cgc cac ggt gcg gag ttc gcg cgc ggc acg ccg        492
Val Pro Gly Thr Arg Arg His Gly Ala Glu Phe Ala Arg Gly Thr Pro
    50                  55                  60

gcc gtc gcg atc ctc acc gac gcc gcc gga aag gag ctt ctc gac gcc        540
Ala Val Ala Ile Leu Thr Asp Ala Ala Gly Lys Glu Leu Leu Asp Ala
65                  70                  75                  80

gcc ggc gac acc cgc cct gtc atc ctc gtc gat gac gtc cgc gcg gtc        588
Ala Gly Asp Thr Arg Pro Val Ile Leu Val Asp Asp Val Arg Ala Val
                85                  90                  95

ctc ggg gcc gtg gcc gcg gag atc cac ggc cac ccc tcg gag cgt ctc        636
Leu Gly Ala Val Ala Ala Glu Ile His Gly His Pro Ser Glu Arg Leu
            100                 105                 110

acc ctg ctc ggc atc acc ggc acc tcc ggg aag acg acc acc agc tac        684
Thr Leu Leu Gly Ile Thr Gly Thr Ser Gly Lys Thr Thr Thr Ser Tyr
        115                 120                 125

ctg ctc gag cag ggg ctc atg gcg gcc gac ctg aag gtc ggc ctc atc        732
Leu Leu Glu Gln Gly Leu Met Ala Ala Asp Leu Lys Val Gly Leu Ile
    130                 135                 140

ggc acg acg ggc acg cgc atc aac ggc cgt ccc gtc ccc acc gac ctc        780
Gly Thr Thr Gly Thr Arg Ile Asn Gly Arg Pro Val Pro Thr Asp Leu
145                 150                 155                 160

acg acc ccg gag gcc acg acc ctg cag ccc ctg ttc gtg cgg atg ctc        828
Thr Thr Pro Glu Ala Thr Thr Leu Gln Pro Leu Phe Val Arg Met Leu
                165                 170                 175

gcg gag ggc gtc acg cac gtg gtc atg gag gtc tcc tcc cac gcc ctg        876
Ala Glu Gly Val Thr His Val Val Met Glu Val Ser Ser His Ala Leu
            180                 185                 190

gag ctg ggc cgg gtg gcg ggc acg cgt ttc gac gtc gcc ggg ttc acc        924
Glu Leu Gly Arg Val Ala Gly Thr Arg Phe Asp Val Ala Gly Phe Thr
        195                 200                 205

aac ctc tcc cag gac cac ctc gac ttc cac ccg acg atg gag gag tac        972
Asn Leu Ser Gln Asp His Leu Asp Phe His Pro Thr Met Glu Glu Tyr
    210                 215                 220

ttc gcg gcc aag gcc cgc ttc ttc gac ccg gcg tcg ccg ctg gcc gcg       1020
Phe Ala Ala Lys Ala Arg Phe Phe Asp Pro Ala Ser Pro Leu Ala Ala
225                 230                 235                 240

gag cgg tcc gtc gtc tgc gtc gac gac gag tgg ggg cgg cgg atg gcc       1068
Glu Arg Ser Val Val Cys Val Asp Asp Glu Trp Gly Arg Arg Met Ala
                245                 250                 255

gac ctg gcc tcg gac ccg gtg acc gtc gcg acc cgc ggc gcg gag gcc       1116
Asp Leu Ala Ser Asp Pro Val Thr Val Ala Thr Arg Gly Ala Glu Ala
            260                 265                 270

gac gtc acc gcc gtc cag agc tcg ctc acg ccc acc ggc gcc cag gtc       1164
Asp Val Thr Ala Val Gln Ser Ser Leu Thr Pro Thr Gly Ala Gln Val
```

```
          275                 280                 285

atc cgg ctc acc ctg ccg gag ggg gcc gtc gag gcg gag ctg ccg ctg      1212
Ile Arg Leu Thr Leu Pro Glu Gly Ala Val Glu Ala Glu Leu Pro Leu
    290                 295                 300

ccg ggt gac ttc aac atc gcc aac gcc gcc ctg gcc acc gcc atg gcg      1260
Pro Gly Asp Phe Asn Ile Ala Asn Ala Ala Leu Ala Thr Ala Met Ala
305                 310                 315                 320

tgg gcc gtg ggc gtc gac ccg cag gcc ttc acc gcc ggt ttc ctc gac      1308
Trp Ala Val Gly Val Asp Pro Gln Ala Phe Thr Ala Gly Phe Leu Asp
                325                 330                 335

gtc gcg gtc ccc ggg cgc atg gag cgt atc gac gag ggc cag gac ttc      1356
Val Ala Val Pro Gly Arg Met Glu Arg Ile Asp Glu Gly Gln Asp Phe
            340                 345                 350

ctc gcc gtc gtc gac tac gcc cac aag ccg gcc gcc gtc gcc gcc gtc      1404
Leu Ala Val Val Asp Tyr Ala His Lys Pro Ala Ala Val Ala Ala Val
        355                 360                 365

ctc gac acc ctc cgc ggg cag gtc cgc ggc cgc ctc ggc gtg gtc gtc      1452
Leu Asp Thr Leu Arg Gly Gln Val Arg Gly Arg Leu Gly Val Val Val
    370                 375                 380

ggg gcc ggt ggt gac cgc gac gcc acc aag cgt ccc ctc atg ggg gcg      1500
Gly Ala Gly Gly Asp Arg Asp Ala Thr Lys Arg Pro Leu Met Gly Ala
385                 390                 395                 400

gag gcc gcc cac cgc gcc gac ctg gtc atc atc acc gac gac aac ccg      1548
Glu Ala Ala His Arg Ala Asp Leu Val Ile Ile Thr Asp Asp Asn Pro
                405                 410                 415

cgc agc gag gtg ccc gcc acc atc cgg gcg gcc gtg ctg cag ggg gcg      1596
Arg Ser Glu Val Pro Ala Thr Ile Arg Ala Ala Val Leu Gln Gly Ala
            420                 425                 430

gtc gac gcc ggg acg gac gcg gag atc cgc gag atc ggg gac cgc gcc      1644
Val Asp Ala Gly Thr Asp Ala Glu Ile Arg Glu Ile Gly Asp Arg Ala
        435                 440                 445

gcc gcc atc gac gcg ctg atc gag tgg gcc cgc ccg ggg gac ggc gtc      1692
Ala Ala Ile Asp Ala Leu Ile Glu Trp Ala Arg Pro Gly Asp Gly Val
    450                 455                 460

gtc gtc gcc ggc aag ggc cac gag gtc ggc cag ctg gtc aac ggc gtc      1740
Val Val Ala Gly Lys Gly His Glu Val Gly Gln Leu Val Asn Gly Val
465                 470                 475                 480

aac cac cat ttc gac gac cgg gaa gag gtc cgg cgc gca ctc aag gag      1788
Asn His His Phe Asp Asp Arg Glu Glu Val Arg Arg Ala Leu Lys Glu
                485                 490                 495

aag aag cat tga tccccctcac tctcgcggag atcgcggaca tcaccggcgg          1840
Lys Lys His

tgaactctcg cacgtgaccg acccggagac ccgggtgacc gggtccgtcg agttcgactc    1900
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ccgccgggtc accccgggcg ggctgttcct cgccctgccg ggggcgcgcg tcgacggaca 1960

cgacttcgcc gccaccgccg tcgagtccgg cgcggtcgcc gtcctggcgg cgcggccggt 2020

gggggtgccg gcggtcgtcg tgaagccgcg gggccgcagt gactccaacg ccgacatcta 2080

cgcccacgac gaggacggct 2100

<210> 184
<211> 499
<212> PRT
<213> Corynebacterium humireducens

<400> 184

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

Ala Gly Gly Glu Leu Thr Gly Ser Val Ala Pro Val Val Thr Ser Val
20 25 30

Glu Leu Asp Ser Ser Arg Leu Ala Asp Glu Gly Ala Leu Phe Ala Ala
35 40 45

Val Pro Gly Thr Arg Arg His Gly Ala Glu Phe Ala Arg Gly Thr Pro
50 55 60

Ala Val Ala Ile Leu Thr Asp Ala Ala Gly Lys Glu Leu Leu Asp Ala
65 70 75 80

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

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

Thr Leu Leu Gly Ile Thr Gly Thr Ser Gly Lys Thr Thr Thr Ser Tyr
115 120 125

Leu Leu Glu Gln Gly Leu Met Ala Ala Asp Leu Lys Val Gly Leu Ile
130 135 140

Gly Thr Thr Gly Thr Arg Ile Asn Gly Arg Pro Val Pro Thr Asp Leu
145 150 155 160

Thr Thr Pro Glu Ala Thr Thr Leu Gln Pro Leu Phe Val Arg Met Leu
165 170 175

Ala Glu Gly Val Thr His Val Val Met Glu Val Ser Ser His Ala Leu
180 185 190

Glu Leu Gly Arg Val Ala Gly Thr Arg Phe Asp Val Ala Gly Phe Thr
195 200 205

Asn Leu Ser Gln Asp His Leu Asp Phe His Pro Thr Met Glu Glu Tyr
210 215 220

Phe Ala Ala Lys Ala Arg Phe Phe Asp Pro Ala Ser Pro Leu Ala Ala
225 230 235 240

Glu Arg Ser Val Val Cys Val Asp Asp Glu Trp Gly Arg Arg Met Ala
245 250 255

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

Asp Val Thr Ala Val Gln Ser Ser Leu Thr Pro Thr Gly Ala Gln Val
275 280 285

Ile Arg Leu Thr Leu Pro Glu Gly Ala Val Glu Ala Glu Leu Pro Leu
290 295 300

Pro Gly Asp Phe Asn Ile Ala Asn Ala Ala Leu Ala Thr Ala Met Ala
305 310 315 320

Trp Ala Val Gly Val Asp Pro Gln Ala Phe Thr Ala Gly Phe Leu Asp
325 330 335

Val Ala Val Pro Gly Arg Met Glu Arg Ile Asp Glu Gly Gln Asp Phe
340 345 350

Leu Ala Val Val Asp Tyr Ala His Lys Pro Ala Ala Val Ala Ala Val
355 360 365

Leu Asp Thr Leu Arg Gly Gln Val Arg Gly Arg Leu Gly Val Val Val
370 375 380

Gly Ala Gly Gly Asp Arg Asp Ala Thr Lys Arg Pro Leu Met Gly Ala
385 390 395 400

Glu Ala Ala His Arg Ala Asp Leu Val Ile Ile Thr Asp Asp Asn Pro

405 410 415

Arg Ser Glu Val Pro Ala Thr Ile Arg Ala Ala Val Leu Gln Gly Ala
420 425 430

Val Asp Ala Gly Thr Asp Ala Glu Ile Arg Glu Ile Gly Asp Arg Ala
435 440 445

Ala Ala Ile Asp Ala Leu Ile Glu Trp Ala Arg Pro Gly Asp Gly Val
450 455 460

Val Val Ala Gly Lys Gly His Glu Val Gly Gln Leu Val Asn Gly Val
465 470 475 480

Asn His His Phe Asp Asp Arg Glu Glu Val Arg Arg Ala Leu Lys Glu
485 490 495

Lys Lys His

<210> 185
<211> 2145
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1845)
<223> gene zwf

<400> 185
cgaccctcta cgtcaccgag ctggccggcc cggagaccgt caacaccatg ccggagccga 60

ccatcgacgc cgtgctcgag cagggtggcc tccacggcga caccctgagc ggcaccgcgg 120

acgacgcgca ggccgtcttc gagcagctgg tgcaggtcgg catcgacatg gaggacgtct 180

tcgcggtgct ggagcgcgag ggcgtcgaga agttcgtgtc ctcctggtcc gagctgctcg 240

actccatgga gtcccgactg cgctagcagt cccctccccg acaggaaagg acctgagcgc 300

atg ccc ctc ccc gtg acc ggc acc gac gcc tgg atc aac ccg ctg cgg 348
Met Pro Leu Pro Val Thr Gly Thr Asp Ala Trp Ile Asn Pro Leu Arg
1 5 10 15

aac acc gtc gac aag cgg ctg ccc cgc atc gcc ggc ccc tcc ggc atg 396
Asn Thr Val Asp Lys Arg Leu Pro Arg Ile Ala Gly Pro Ser Gly Met
20 25 30

gtg atc ttc ggc gtg acc ggt gac ctg gcc cgc aag aag ctg ctc ccg 444

```
Val Ile Phe Gly Val Thr Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro
        35                  40                  45

gcc atc tac gac ctg gcc aac cgt ggc ctc ctg ccg gcc ggt ttc acc        492
Ala Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Ala Gly Phe Thr
    50                  55                  60

ctc atc ggt ttc ggc cgt cgt ccc tgg agc aaa ccc gag ttc gag gag        540
Leu Ile Gly Phe Gly Arg Arg Pro Trp Ser Lys Pro Glu Phe Glu Glu
65                  70                  75                  80

tac gtg cgg gag gcc gtc gag agc ggc gcc cgc acc gag ttc cgc gaa        588
Tyr Val Arg Glu Ala Val Glu Ser Gly Ala Arg Thr Glu Phe Arg Glu
                85                  90                  95

cac gtg tgg gag cgg ctg gcc gag ggc atg cac ttc gtc gag ggc aac        636
His Val Trp Glu Arg Leu Ala Glu Gly Met His Phe Val Glu Gly Asn
            100                 105                 110

ttc gac gac gag ggc ttc gac cgc ctc gcc gcc acc ctc gcc gag atg        684
Phe Asp Asp Glu Gly Phe Asp Arg Leu Ala Ala Thr Leu Ala Glu Met
        115                 120                 125

gac acc tcc cgc ggc acg gcg ggc aac tgg gcc ttc tac ctg tcg gtc        732
Asp Thr Ser Arg Gly Thr Ala Gly Asn Trp Ala Phe Tyr Leu Ser Val
    130                 135                 140

ccg ccg gac ttc ttc acc gcc gtc tgc cac cag ctg gag cgc tcc ggc        780
Pro Pro Asp Phe Phe Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly
145                 150                 155                 160

ctg gcg gag gcc ggt gag gag tcg tgg cgt cgc gtg atc atc gag aag        828
Leu Ala Glu Ala Gly Glu Glu Ser Trp Arg Arg Val Ile Ile Glu Lys
                165                 170                 175

ccc ttc ggc cac gac cag gac acg gcc cgg gag ctc aac cgg gtg gtc        876
Pro Phe Gly His Asp Gln Asp Thr Ala Arg Glu Leu Asn Arg Val Val
            180                 185                 190

aac gcc gtc ttc ccg gag gag tcg gtg ttc cgc atc gac cac tac ctg        924
Asn Ala Val Phe Pro Glu Glu Ser Val Phe Arg Ile Asp His Tyr Leu
        195                 200                 205

ggc aag gag acg gtg cag aac atc ctg gcg ctg cgc ttc gcc aac cag        972
Gly Lys Glu Thr Val Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln
    210                 215                 220

ctc ttc gac ccg atc tgg aac gcg cac tac gtc gac cac gtg cag atc       1020
Leu Phe Asp Pro Ile Trp Asn Ala His Tyr Val Asp His Val Gln Ile
225                 230                 235                 240

acc atg gcc gag gac atc ggt ctc ggt ggt cgg gcc ggc tac tac gac       1068
Thr Met Ala Glu Asp Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp
                245                 250                 255

ggc atc ggc gcc gcc cgc gac gtc atg cag aac cac ctc ctc cag ctc       1116
Gly Ile Gly Ala Ala Arg Asp Val Met Gln Asn His Leu Leu Gln Leu
            260                 265                 270
```

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ctg gcg ctg gtg gcc atg gag gag ccc atc gcc ttc gac ccg gct gag      1164
Leu Ala Leu Val Ala Met Glu Glu Pro Ile Ala Phe Asp Pro Ala Glu
        275                 280                 285

ctg cag gcg gag aag gtc aag gtc ctg cgc gcg acc aac ccc gtc ttc      1212
Leu Gln Ala Glu Lys Val Lys Val Leu Arg Ala Thr Asn Pro Val Phe
    290                 295                 300

ccg ctg aac aag acc acc gcc cgt ggc cag tac gcg gcg ggc tgg cag      1260
Pro Leu Asn Lys Thr Thr Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln
305                 310                 315                 320

ggc tcg cac aag gtg cgt ggc ctg cgt gag gag gag ggt ttc gac ccg      1308
Gly Ser His Lys Val Arg Gly Leu Arg Glu Glu Glu Gly Phe Asp Pro
                325                 330                 335

gac tcc acc acg gag acc tac gcc gcc tgc acc ctg gag atc aac tcc      1356
Asp Ser Thr Thr Glu Thr Tyr Ala Ala Cys Thr Leu Glu Ile Asn Ser
            340                 345                 350

cgc cgc tgg gcg ggc gtg ccc ttc tac ctg cgg acc ggc aag cgc ctg      1404
Arg Arg Trp Ala Gly Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu
        355                 360                 365

ggg cgc cgc gtc acg gag atc gcc ctc gtg ttc aag gag gcg ccg cac      1452
Gly Arg Arg Val Thr Glu Ile Ala Leu Val Phe Lys Glu Ala Pro His
    370                 375                 380

cag ccc ttc ctc gag ggg cag acg tcc tcg ctg ggg cag aac gcg atc      1500
Gln Pro Phe Leu Glu Gly Gln Thr Ser Ser Leu Gly Gln Asn Ala Ile
385                 390                 395                 400

gtc atc cgc gtc cag ccc gac gag ggc gtg ctc atg cgc ttc ggc tcc      1548
Val Ile Arg Val Gln Pro Asp Glu Gly Val Leu Met Arg Phe Gly Ser
                405                 410                 415

aag gtg ccc ggc tcc gcg atg gag gtc cgt gac gtc aac atg gac ttc      1596
Lys Val Pro Gly Ser Ala Met Glu Val Arg Asp Val Asn Met Asp Phe
            420                 425                 430

tcc tac gcg gag gcc ttc acc gag gcg tcc ccg gag gcc tat gag cgg      1644
Ser Tyr Ala Glu Ala Phe Thr Glu Ala Ser Pro Glu Ala Tyr Glu Arg
        435                 440                 445

ctc atc ctc gat gcg ctt ctc gac gag tcc tcg ctc ttc ccc acc aac      1692
Leu Ile Leu Asp Ala Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn
    450                 455                 460

gag gag gtc gag ctc tcc tgg gcg atc ctg gac ccg atc ctc gag ttc      1740
Glu Glu Val Glu Leu Ser Trp Ala Ile Leu Asp Pro Ile Leu Glu Phe
465                 470                 475                 480

tgg gct gag aag ggc cag ccc gag gag tac gag tcc ggc acc tgg ggg      1788
Trp Ala Glu Lys Gly Gln Pro Glu Glu Tyr Glu Ser Gly Thr Trp Gly
                485                 490                 495

ccc gcc tcc gcc gac cgc atg ctg gaa cgg acc ggc cgc gcc tgg cgc      1836
Pro Ala Ser Ala Asp Arg Met Leu Glu Arg Thr Gly Arg Ala Trp Arg
            500                 505                 510
```

cgc ccc tga cctggaaggg acccgacttg aagatcgaac tgccggacac 1885
Arg Pro

cgacacccgg aacatcgccg ccagcctgct cgaggcccgg gagcacaact cccagaccac 1945

cgggcgggtg ctcaccctca tcgtcgtcgc cgcgctcgac gacgacgtcg accacatcat 2005

ctccgtcacc cgcgacgcct cccacgagca ccccgcccgt gtgctggtgc tgctcaccgg 2065

ccgggaggac gctgactcgc gtctcgacgc cgaggtgcgc gtcggcggtc acgccggcgc 2125

ctcggagatg gtcatcatgc 2145

<210> 186
<211> 514
<212> PRT
<213> Corynebacterium humireducens

<400> 186

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

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

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

Ala Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Ala Gly Phe Thr
50 55 60

Leu Ile Gly Phe Gly Arg Arg Pro Trp Ser Lys Pro Glu Phe Glu Glu
65 70 75 80

Tyr Val Arg Glu Ala Val Glu Ser Gly Ala Arg Thr Glu Phe Arg Glu
85 90 95

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

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

Asp Thr Ser Arg Gly Thr Ala Gly Asn Trp Ala Phe Tyr Leu Ser Val
130 135 140

Pro Pro Asp Phe Phe Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly
145 150 155 160

Leu Ala Glu Ala Gly Glu Glu Ser Trp Arg Arg Val Ile Ile Glu Lys
165 170 175

Pro Phe Gly His Asp Gln Asp Thr Ala Arg Glu Leu Asn Arg Val Val
180 185 190

Asn Ala Val Phe Pro Glu Glu Ser Val Phe Arg Ile Asp His Tyr Leu
195 200 205

Gly Lys Glu Thr Val Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln
210 215 220

Leu Phe Asp Pro Ile Trp Asn Ala His Tyr Val Asp His Val Gln Ile
225 230 235 240

Thr Met Ala Glu Asp Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp
245 250 255

Gly Ile Gly Ala Ala Arg Asp Val Met Gln Asn His Leu Leu Gln Leu
260 265 270

Leu Ala Leu Val Ala Met Glu Glu Pro Ile Ala Phe Asp Pro Ala Glu
275 280 285

Leu Gln Ala Glu Lys Val Lys Val Leu Arg Ala Thr Asn Pro Val Phe
290 295 300

Pro Leu Asn Lys Thr Thr Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln
305 310 315 320

Gly Ser His Lys Val Arg Gly Leu Arg Glu Glu Glu Gly Phe Asp Pro
325 330 335

Asp Ser Thr Thr Glu Thr Tyr Ala Ala Cys Thr Leu Glu Ile Asn Ser
340 345 350

Arg Arg Trp Ala Gly Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu
355 360 365

Gly Arg Arg Val Thr Glu Ile Ala Leu Val Phe Lys Glu Ala Pro His
370 375 380

Gln Pro Phe Leu Glu Gly Gln Thr Ser Ser Leu Gly Gln Asn Ala Ile
385 390 395 400

Val Ile Arg Val Gln Pro Asp Glu Gly Val Leu Met Arg Phe Gly Ser
405 410 415

Lys Val Pro Gly Ser Ala Met Glu Val Arg Asp Val Asn Met Asp Phe
420 425 430

Ser Tyr Ala Glu Ala Phe Thr Glu Ala Ser Pro Glu Ala Tyr Glu Arg
435 440 445

Leu Ile Leu Asp Ala Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn
450 455 460

Glu Glu Val Glu Leu Ser Trp Ala Ile Leu Asp Pro Ile Leu Glu Phe
465 470 475 480

Trp Ala Glu Lys Gly Gln Pro Glu Glu Tyr Glu Ser Gly Thr Trp Gly
485 490 495

Pro Ala Ser Ala Asp Arg Met Leu Glu Arg Thr Gly Arg Ala Trp Arg
500 505 510

Arg Pro

<210> 187
<211> 1551
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1251)
<223> gene opcA

<400> 187
cgcgatggag gtccgtgacg tcaacatgga cttctcctac gcggaggcct tcaccgaggc 60

gtccccggag gcctatgagc ggctcatcct cgatgcgctt ctcgacgagt ccctcgctctt 120

ccccaccaac gaggaggtcg agctctcctg ggcgatcctg gacccgatcc tcgagttctg 180

ggctgagaag ggccagcccg aggagtacga gtccggcacc tgggggcccg ccctccgccga 240

ccgcatgctg gaacggaccg gccgcgcctg gcgccgcccc tgacctggaa gggacccgac 300

```
ttg aag atc gaa ctg ccg gac acc gac acc cgg aac atc gcc gcc agc        348
Leu Lys Ile Glu Leu Pro Asp Thr Asp Thr Arg Asn Ile Ala Ala Ser
1               5                  10                  15

ctg ctc gag gcc cgg gag cac aac tcc cag acc acc ggg cgg gtg ctc        396
Leu Leu Glu Ala Arg Glu His Asn Ser Gln Thr Thr Gly Arg Val Leu
            20                  25                  30

acc ctc atc gtc gtc gcc gcg ctc gac gac gac gtc gac cac atc atc        444
Thr Leu Ile Val Val Ala Ala Leu Asp Asp Asp Val Asp His Ile Ile
        35                  40                  45

tcc gtc acc cgc gac gcc tcc cac gag cac ccc gcc cgt gtg ctg gtg        492
Ser Val Thr Arg Asp Ala Ser His Glu His Pro Ala Arg Val Leu Val
    50                  55                  60

ctg ctc acc ggc cgg gag gac gct gac tcg cgt ctc gac gcc gag gtg        540
Leu Leu Thr Gly Arg Glu Asp Ala Asp Ser Arg Leu Asp Ala Glu Val
65                  70                  75                  80

cgc gtc ggc ggt cac gcc ggc gcc tcg gag atg gtc atc atg cgc atc        588
Arg Val Gly Gly His Ala Gly Ala Ser Glu Met Val Ile Met Arg Ile
                85                  90                  95

acg ggc gag atg gtc aac cac ctc gcc gcg gtg gtc acc ccc ctg ctg        636
Thr Gly Glu Met Val Asn His Leu Ala Ala Val Val Thr Pro Leu Leu
            100                 105                 110

ctg ccg gac acc ccg gtc gtc gcc tgg tgg ccg acc acc gcg ccg gag        684
Leu Pro Asp Thr Pro Val Val Ala Trp Trp Pro Thr Thr Ala Pro Glu
        115                 120                 125

aac ccc tcc ggg cat ccg ctg ggc cag ctg gcg cag cgc cgc atc acc        732
Asn Pro Ser Gly His Pro Leu Gly Gln Leu Ala Gln Arg Arg Ile Thr
    130                 135                 140

aac gcg gac cac ccg gac agt gag tcg gtc ctc cgg ctc cgc cgt gcc        780
Asn Ala Asp His Pro Asp Ser Glu Ser Val Leu Arg Leu Arg Arg Ala
145                 150                 155                 160

acc tac gcc ccc ggt gac tcc gac atg gtg tgg tcg aag atc acc gcc        828
Thr Tyr Ala Pro Gly Asp Ser Asp Met Val Trp Ser Lys Ile Thr Ala
                165                 170                 175

tgg cgc ggt atc gtc gcc tcc tcc ctg gac cgt cac ccg cac gag gac        876
Trp Arg Gly Ile Val Ala Ser Ser Leu Asp Arg His Pro His Glu Asp
            180                 185                 190

gtg gag gcc gcc gtc ctc acc ggc ccg gcg gat gag ccg cag atc gac        924
Val Glu Ala Ala Val Leu Thr Gly Pro Ala Asp Glu Pro Gln Ile Asp
        195                 200                 205

atc gcc gcc ggc tgg ctc gcc gac cgc ctc ggt gtg ccg gtc cgc cgg        972
Ile Ala Ala Gly Trp Leu Ala Asp Arg Leu Gly Val Pro Val Arg Arg
    210                 215                 220

gag gtg tgt gaa ccg ggt aac gac gcc cgg ctc ttc ccc atc cgt cgt       1020
Glu Val Cys Glu Pro Gly Asn Asp Ala Arg Leu Phe Pro Ile Arg Arg
225                 230                 235                 240
```

```
ctc aag ttc gaa cgc gcc tcc ggc ccg gtc cgc gtc gag gtg ctc gac      1068
Leu Lys Phe Glu Arg Ala Ser Gly Pro Val Arg Val Glu Val Leu Asp
                245                 250                 255

cac cgg acc gtg ctc gtc gcc ctg cca ggg cgc ccg gag tcg ctc gtc      1116
His Arg Thr Val Leu Val Ala Leu Pro Gly Arg Pro Glu Ser Leu Val
            260                 265                 270

gcc atg aac gag cgt tcc gac gcc gac tgc ctc tcc gag gaa ctg cgt      1164
Ala Met Asn Glu Arg Ser Asp Ala Asp Cys Leu Ser Glu Glu Leu Arg
        275                 280                 285

cac ctc gac ccc gat ctc gcc tac gcc aac gct ctg cgc gga ctc acc      1212
His Leu Asp Pro Asp Leu Ala Tyr Ala Asn Ala Leu Arg Gly Leu Thr
    290                 295                 300

cgt gtg aaa gga atc aat ggt cac cct gcg tcg tcc tga caccctgtcc      1261
Arg Val Lys Gly Ile Asn Gly His Pro Ala Ser Ser
305                 310                 315

accctgctcg accaggccgc cacgtcgctc atcgacgtcg tcgctgccct ccagaccacc     1321

gggggcggtg tccacgccga cggtgtggcc cgcctggtgc tcaccggcgg cggcgccggc     1381

atcggcctgc tggagcgcgt ccgtgagctc gaggacgccg actcccgcat cgactggtcc     1441

cgcgtccacg tcttcttcgg cgacgagcgc aacgtgcccg tctcccacga ggactccaac     1501

gaggggcagg cgcgtaccgc cctgctcagc cacgtcgaca tcccggaggc                1551
```

<210> 188
<211> 316
<212> PRT
<213> Corynebacterium humireducens

<400> 188

```
Leu Lys Ile Glu Leu Pro Asp Thr Asp Thr Arg Asn Ile Ala Ala Ser
1               5                   10                  15

Leu Leu Glu Ala Arg Glu His Asn Ser Gln Thr Thr Gly Arg Val Leu
            20                  25                  30

Thr Leu Ile Val Val Ala Ala Leu Asp Asp Asp Val Asp His Ile Ile
        35                  40                  45

Ser Val Thr Arg Asp Ala Ser His Glu His Pro Ala Arg Val Leu Val
    50                  55                  60

Leu Leu Thr Gly Arg Glu Asp Ala Asp Ser Arg Leu Asp Ala Glu Val
65                  70                  75                  80
```

Arg Val Gly Gly His Ala Gly Ala Ser Glu Met Val Ile Met Arg Ile
85 90 95

Thr Gly Glu Met Val Asn His Leu Ala Ala Val Val Thr Pro Leu Leu
100 105 110

Leu Pro Asp Thr Pro Val Val Ala Trp Trp Pro Thr Thr Ala Pro Glu
115 120 125

Asn Pro Ser Gly His Pro Leu Gly Gln Leu Ala Gln Arg Arg Ile Thr
130 135 140

Asn Ala Asp His Pro Asp Ser Glu Ser Val Leu Arg Leu Arg Arg Ala
145 150 155 160

Thr Tyr Ala Pro Gly Asp Ser Asp Met Val Trp Ser Lys Ile Thr Ala
165 170 175

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

Val Glu Ala Ala Val Leu Thr Gly Pro Ala Asp Glu Pro Gln Ile Asp
195 200 205

Ile Ala Ala Gly Trp Leu Ala Asp Arg Leu Gly Val Pro Val Arg Arg
210 215 220

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

Leu Lys Phe Glu Arg Ala Ser Gly Pro Val Arg Val Glu Val Leu Asp
245 250 255

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

Ala Met Asn Glu Arg Ser Asp Ala Asp Cys Leu Ser Glu Glu Leu Arg
275 280 285

His Leu Asp Pro Asp Leu Ala Tyr Ala Asn Ala Leu Arg Gly Leu Thr
290 295 300

Arg Val Lys Gly Ile Asn Gly His Pro Ala Ser Ser
305 310 315

<210> 189
<211> 2283
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1983)
<223> gene hutU (Urocanate Hydratase)

<400> 189
gctacctgtc cccggagatc gaggagtcgg tgcagctgct cacctccggg gcgctgctgg 60

aggcggtgga gggggtcgtc ggaaagctgg catgagcggg cgaatctcag atatgagact 120

aaaggggcct ccgggccctc gatcccgact gtgacctgtc ttaccgtcag aagtgtcacc 180

gacaccggcc acaccagccc ggtgctccac acccgacgat gacagccccg ggccacccgg 240

atcgcgggtg ccccggggcc ccggcctgat cggcccccac cgtagaagga gacccacccc 300

atg acc gag tcc ccg cgc acc atc cgt gcc ccg cac ggc acc gag ctc 348
Met Thr Glu Ser Pro Arg Thr Ile Arg Ala Pro His Gly Thr Glu Leu
1 5 10 15

agc gcc aag agc tgg caa acc gag gca ccc ctg cgc atg ctc atg aac 396
Ser Ala Lys Ser Trp Gln Thr Glu Ala Pro Leu Arg Met Leu Met Asn
20 25 30

aac ctc gac ccg gag gtc gcc gag cgc ccc gag gac ctc gtc gtc tac 444
Asn Leu Asp Pro Glu Val Ala Glu Arg Pro Glu Asp Leu Val Val Tyr
35 40 45

ggc ggc acc ggc cgc gcg gca cgc agc tgg gag gcc tac gac gcg atc 492
Gly Gly Thr Gly Arg Ala Ala Arg Ser Trp Glu Ala Tyr Asp Ala Ile
50 55 60

atc gag acg ctc agg gac ctc gag gag gac gag acc ctg ctc gtc cag 540
Ile Glu Thr Leu Arg Asp Leu Glu Glu Asp Glu Thr Leu Leu Val Gln
65 70 75 80

tcc ggc aag ccc gtc ggc gtc ttc cgc acc aac gtc tgg gca ccc cgc 588
Ser Gly Lys Pro Val Gly Val Phe Arg Thr Asn Val Trp Ala Pro Arg
85 90 95

gtg ctc atc gcc aac tcc aac ctc gtc ggc gac tgg gcc aac tgg ccc 636
Val Leu Ile Ala Asn Ser Asn Leu Val Gly Asp Trp Ala Asn Trp Pro
100 105 110

gag ttc cgc cgc ctc gag gcc gag ggc ctc atg atg tac ggc cag atg 684
Glu Phe Arg Arg Leu Glu Ala Glu Gly Leu Met Met Tyr Gly Gln Met
115 120 125

acc gcc ggt tcc tgg atc tac atc gcc acc cag ggc atc ctc cag ggc 732
Thr Ala Gly Ser Trp Ile Tyr Ile Ala Thr Gln Gly Ile Leu Gln Gly
130 135 140

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acc tac gag acc ttc gcc gcc gtg gcc cgc aag cgt ttc ggc ggc acc        780
Thr Tyr Glu Thr Phe Ala Ala Val Ala Arg Lys Arg Phe Gly Gly Thr
145                 150                 155                 160

ctc gcc ggc acc ctc acc ctc acc ggc ggc tgc ggc ggc atg ggc ggg        828
Leu Ala Gly Thr Leu Thr Leu Thr Gly Gly Cys Gly Gly Met Gly Gly
                165                 170                 175

gcc cag ccg ctg tcc gtc acc ctc aac ggc ggt gtc tgc ctc atc gtc        876
Ala Gln Pro Leu Ser Val Thr Leu Asn Gly Gly Val Cys Leu Ile Val
            180                 185                 190

gac gtc gac gag tcc cgg ctc agg cgt cgg cag gcc aag cgc tac ctc        924
Asp Val Asp Glu Ser Arg Leu Arg Arg Arg Gln Ala Lys Arg Tyr Leu
        195                 200                 205

gat gag gtc gcc acc gat ctc gac gac gcc gtc gcc cgc gtc agc gcc        972
Asp Glu Val Ala Thr Asp Leu Asp Asp Ala Val Ala Arg Val Ser Ala
    210                 215                 220

gcc aag gag gag aag cgt gcc ctg tcc gtc ggc cta gtg ggc aat gcc       1020
Ala Lys Glu Glu Lys Arg Ala Leu Ser Val Gly Leu Val Gly Asn Ala
225                 230                 235                 240

gcc gag gtg ttc ccc gag ctg ctg cgc cgc cac cgc gcc ggg gag atc       1068
Ala Glu Val Phe Pro Glu Leu Leu Arg Arg His Arg Ala Gly Glu Ile
                245                 250                 255

acc gtc gac gtg gtc acc gac cag acc tcc gcc cac gac ccg ctc agc       1116
Thr Val Asp Val Val Thr Asp Gln Thr Ser Ala His Asp Pro Leu Ser
            260                 265                 270

tac ctg ccc acc gag atc acc gtc gag gac tgg cag cgc gag gcc gcc       1164
Tyr Leu Pro Thr Glu Ile Thr Val Glu Asp Trp Gln Arg Glu Ala Ala
        275                 280                 285

gag gac ccc atc acc ttc acc aag aag gca cgc gag tcc atg gcc gtg       1212
Glu Asp Pro Ile Thr Phe Thr Lys Lys Ala Arg Glu Ser Met Ala Val
    290                 295                 300

cag gtc cag gcc atg gtc gag ttc cag gac gag ggc gcc gag gtc ttc       1260
Gln Val Gln Ala Met Val Glu Phe Gln Asp Glu Gly Ala Glu Val Phe
305                 310                 315                 320

gac tac ggc aac tcc atc cgc gat gag gcc cgc cac gcc ggc tac tcc       1308
Asp Tyr Gly Asn Ser Ile Arg Asp Glu Ala Arg His Ala Gly Tyr Ser
                325                 330                 335

cgc gcc ttc gag ttc ccc ggc ttc gtc ccc gcc tac atc cgg ccc ctg       1356
Arg Ala Phe Glu Phe Pro Gly Phe Val Pro Ala Tyr Ile Arg Pro Leu
            340                 345                 350

ttc tgc gag ggt ctc ggc ccc ttc cgc tgg gtg gcc ctt tcc ggc gac       1404
Phe Cys Glu Gly Leu Gly Pro Phe Arg Trp Val Ala Leu Ser Gly Asp
        355                 360                 365

ccg gag gac atc cgc gtc acc gac gag gcc gtc aag gag ctg ttc ccc       1452
Pro Glu Asp Ile Arg Val Thr Asp Glu Ala Val Lys Glu Leu Phe Pro
    370                 375                 380
```

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gac aac gag cac ctc cac cgc tgg atc gac gcg gca ggg gag tac gtc      1500
Asp Asn Glu His Leu His Arg Trp Ile Asp Ala Ala Gly Glu Tyr Val
385                 390                 395                 400

gag ttc gag ggc ctg ccg gcc cgc atc tgc tgg ctc ggc tac ggc gag      1548
Glu Phe Glu Gly Leu Pro Ala Arg Ile Cys Trp Leu Gly Tyr Gly Glu
                405                 410                 415

cgg cac aag gcg gga ctg ctg ttc aac cgt ctc gtc gcc gag ggc aag      1596
Arg His Lys Ala Gly Leu Leu Phe Asn Arg Leu Val Ala Glu Gly Lys
            420                 425                 430

gtg aag gcg ccc atc gtc atc ggc cgt gac cac ctc gac tcc ggt tcc      1644
Val Lys Ala Pro Ile Val Ile Gly Arg Asp His Leu Asp Ser Gly Ser
        435                 440                 445

gtc gcc tcc ccc tac cgg gag acc gag tcc atg ctc gac ggc tcc gac      1692
Val Ala Ser Pro Tyr Arg Glu Thr Glu Ser Met Leu Asp Gly Ser Asp
    450                 455                 460

gcc atc gcc gac tgg ccg ctg ctc aac gcc ctc acc gcc acc tcc tcc      1740
Ala Ile Ala Asp Trp Pro Leu Leu Asn Ala Leu Thr Ala Thr Ser Ser
465                 470                 475                 480

ggc gcg acc tgg gtc tcc ctg cac cac gga ggc ggc gtg ggc atc gga      1788
Gly Ala Thr Trp Val Ser Leu His His Gly Gly Gly Val Gly Ile Gly
                485                 490                 495

cgg tcc atc cac gcg ggc cag gtg tgc gtc gcc gac ggc acg gag ctg      1836
Arg Ser Ile His Ala Gly Gln Val Cys Val Ala Asp Gly Thr Glu Leu
            500                 505                 510

gcc gcc gcg aag ctc acc gcc gtg ctc acc aac gac ccg ggc atg ggc      1884
Ala Ala Ala Lys Leu Thr Ala Val Leu Thr Asn Asp Pro Gly Met Gly
        515                 520                 525

gtc atc cgc cac gtc gac gcc ggc tac gac cgt gcc cac gag gtc gcc      1932
Val Ile Arg His Val Asp Ala Gly Tyr Asp Arg Ala His Glu Val Ala
    530                 535                 540

gtc gag cgc ggg gtc cgt gtc ccc atg ccg ttc gtc agc cgc gag agg      1980
Val Glu Arg Gly Val Arg Val Pro Met Pro Phe Val Ser Arg Glu Arg
545                 550                 555                 560

tag ccatgagcac gctgttccac ggaatctccg agctgaggac cgtctccggg          2033

ctgggcacgc tcagcgacgc cgcgctcatc gtcgaccggg gccgcatcgc ctggatcggc    2093

ccgcgcgccg gggcccccgc cgccgacgcg gcggttgatc tgggcggccg ggccgtgcta    2153

cccggctggg tggactccca cacccacatg atcttcgcgg gggaccgcgc cgccgagttc    2213

gaggcccgca tgaacgggca ggactaccag gcgggcggca tcgcggtgac catgtccgcc    2273

acccgcgagg                                                          2283
```

<210> 190

<211> 560
<212> PRT
<213> Corynebacterium humireducens

<400> 190

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

Ser Ala Lys Ser Trp Gln Thr Glu Ala Pro Leu Arg Met Leu Met Asn
20 25 30

Asn Leu Asp Pro Glu Val Ala Glu Arg Pro Glu Asp Leu Val Val Tyr
35 40 45

Gly Gly Thr Gly Arg Ala Ala Arg Ser Trp Glu Ala Tyr Asp Ala Ile
50 55 60

Ile Glu Thr Leu Arg Asp Leu Glu Glu Asp Glu Thr Leu Leu Val Gln
65 70 75 80

Ser Gly Lys Pro Val Gly Val Phe Arg Thr Asn Val Trp Ala Pro Arg
85 90 95

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

Glu Phe Arg Arg Leu Glu Ala Glu Gly Leu Met Met Tyr Gly Gln Met
115 120 125

Thr Ala Gly Ser Trp Ile Tyr Ile Ala Thr Gln Gly Ile Leu Gln Gly
130 135 140

Thr Tyr Glu Thr Phe Ala Ala Val Ala Arg Lys Arg Phe Gly Gly Thr
145 150 155 160

Leu Ala Gly Thr Leu Thr Leu Thr Gly Gly Cys Gly Gly Met Gly Gly
165 170 175

Ala Gln Pro Leu Ser Val Thr Leu Asn Gly Gly Val Cys Leu Ile Val
180 185 190

Asp Val Asp Glu Ser Arg Leu Arg Arg Arg Gln Ala Lys Arg Tyr Leu
195 200 205

Asp Glu Val Ala Thr Asp Leu Asp Asp Ala Val Ala Arg Val Ser Ala

210 215 220

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

Ala Glu Val Phe Pro Glu Leu Leu Arg Arg His Arg Ala Gly Glu Ile
245 250 255

Thr Val Asp Val Val Thr Asp Gln Thr Ser Ala His Asp Pro Leu Ser
260 265 270

Tyr Leu Pro Thr Glu Ile Thr Val Glu Asp Trp Gln Arg Glu Ala Ala
275 280 285

Glu Asp Pro Ile Thr Phe Thr Lys Lys Ala Arg Glu Ser Met Ala Val
290 295 300

Gln Val Gln Ala Met Val Glu Phe Gln Asp Glu Gly Ala Glu Val Phe
305 310 315 320

Asp Tyr Gly Asn Ser Ile Arg Asp Glu Ala Arg His Ala Gly Tyr Ser
325 330 335

Arg Ala Phe Glu Phe Pro Gly Phe Val Pro Ala Tyr Ile Arg Pro Leu
340 345 350

Phe Cys Glu Gly Leu Gly Pro Phe Arg Trp Val Ala Leu Ser Gly Asp
355 360 365

Pro Glu Asp Ile Arg Val Thr Asp Glu Ala Val Lys Glu Leu Phe Pro
370 375 380

Asp Asn Glu His Leu His Arg Trp Ile Asp Ala Ala Gly Glu Tyr Val
385 390 395 400

Glu Phe Glu Gly Leu Pro Ala Arg Ile Cys Trp Leu Gly Tyr Gly Glu
405 410 415

Arg His Lys Ala Gly Leu Leu Phe Asn Arg Leu Val Ala Glu Gly Lys
420 425 430

Val Lys Ala Pro Ile Val Ile Gly Arg Asp His Leu Asp Ser Gly Ser
435 440 445

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

Ala Ile Ala Asp Trp Pro Leu Leu Asn Ala Leu Thr Ala Thr Ser Ser
465 470 475 480

Gly Ala Thr Trp Val Ser Leu His His Gly Gly Gly Val Gly Ile Gly
485 490 495

Arg Ser Ile His Ala Gly Gln Val Cys Val Ala Asp Gly Thr Glu Leu
500 505 510

Ala Ala Ala Lys Leu Thr Ala Val Leu Thr Asn Asp Pro Gly Met Gly
515 520 525

Val Ile Arg His Val Asp Ala Gly Tyr Asp Arg Ala His Glu Val Ala
530 535 540

Val Glu Arg Gly Val Arg Val Pro Met Pro Phe Val Ser Arg Glu Arg
545 550 555 560

<210> 191
<211> 1809
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1509)
<223> gene hutI (Imidazolone Propionase)

<400> 191
ctccgacgcc atcgccgact ggccgctgct caacgccctc accgccacct cctccggcgc 60

gacctgggtc tccctgcacc acggaggcgg cgtgggcatc ggacggtcca tccacgcggg 120

ccaggtgtgc gtcgccgacg gcacggagct ggccgccgcg aagctcaccg ccgtgctcac 180

caacgacccg ggcatgggcg tcatccgcca cgtcgacgcc ggctacgacc gtgcccacga 240

ggtcgccgtc gagcgcgggg tccgtgtccc catgccgttc gtcagccgcg agaggtagcc 300

atg agc acg ctg ttc cac gga atc tcc gag ctg agg acc gtc tcc ggg 348
Met Ser Thr Leu Phe His Gly Ile Ser Glu Leu Arg Thr Val Ser Gly
1 5 10 15

ctg ggc acg ctc agc gac gcc gcg ctc atc gtc gac cgg ggc cgc atc 396
Leu Gly Thr Leu Ser Asp Ala Ala Leu Ile Val Asp Arg Gly Arg Ile
20 25 30

gcc tgg atc ggc ccg cgc gcc ggg gcc ccc gcc gcc gac gcg gcg gtt 444

```
Ala Trp Ile Gly Pro Arg Ala Gly Ala Pro Ala Ala Asp Ala Ala Val
        35                  40                  45

gat ctg ggc ggc cgg gcc gtg cta ccc ggc tgg gtg gac tcc cac acc      492
Asp Leu Gly Gly Arg Ala Val Leu Pro Gly Trp Val Asp Ser His Thr
    50                  55                  60

cac atg atc ttc gcg ggg gac cgc gcc gcc gag ttc gag gcc cgc atg      540
His Met Ile Phe Ala Gly Asp Arg Ala Ala Glu Phe Glu Ala Arg Met
65                  70                  75                  80

aac ggg cag gac tac cag gcg ggc ggc atc gcg gtg acc atg tcc gcc      588
Asn Gly Gln Asp Tyr Gln Ala Gly Gly Ile Ala Val Thr Met Ser Ala
                85                  90                  95

acc cgc gag gcc ggc gcc gtc cgc ctc gag cag ctg ctg ctg cgc cgc      636
Thr Arg Glu Ala Gly Ala Val Arg Leu Glu Gln Leu Leu Leu Arg Arg
            100                 105                 110

ctg gcc gat gcg cgc gcc ggg ggc acg acc acg gtg gag acg aag acc      684
Leu Ala Asp Ala Arg Ala Gly Gly Thr Thr Thr Val Glu Thr Lys Thr
        115                 120                 125

ggc tac ggg ctc gac gtg gac tcc gag gcc ctg gcg gcc gac atc gcc      732
Gly Tyr Gly Leu Asp Val Asp Ser Glu Ala Leu Ala Ala Asp Ile Ala
    130                 135                 140

gcc cgg cac gtc gat gac gtc acc ttc ctc ggc gcg cat ctc gtg ccg      780
Ala Arg His Val Asp Asp Val Thr Phe Leu Gly Ala His Leu Val Pro
145                 150                 155                 160

ccg ggg gag gac ccg gac gag tac ctc gct ctc gtg ctc ggc gac atg      828
Pro Gly Glu Asp Pro Asp Glu Tyr Leu Ala Leu Val Leu Gly Asp Met
                165                 170                 175

ctc gac gcc gtc gcg gcc aac gtc agc tgg atc gac gtg ttc tgc gaa      876
Leu Asp Ala Val Ala Ala Asn Val Ser Trp Ile Asp Val Phe Cys Glu
            180                 185                 190

cgc ggg gcc ttc gat gag gcg gcc gcc cgc cgc gtc ctc gag gcc ggg      924
Arg Gly Ala Phe Asp Glu Ala Ala Ala Arg Arg Val Leu Glu Ala Gly
        195                 200                 205

cgg gcg cgg ggt ctg ggg ctg cgc gtg cac ggc aac cag ctc ggg cac      972
Arg Ala Arg Gly Leu Gly Leu Arg Val His Gly Asn Gln Leu Gly His
    210                 215                 220

ggt ccc gga gtg cag ctg gcg gtg gag tac ggc gcc gcc agc gtg gac     1020
Gly Pro Gly Val Gln Leu Ala Val Glu Tyr Gly Ala Ala Ser Val Asp
225                 230                 235                 240

cac gtc aac tac gtg agt gac ggt gac gtg gag gca ctc gcc tcc tcg     1068
His Val Asn Tyr Val Ser Asp Gly Asp Val Glu Ala Leu Ala Ser Ser
                245                 250                 255

gag acg gtg gcc acg gtc ctc ccc gcc tgc gac ctg tcc acg agg cag     1116
Glu Thr Val Ala Thr Val Leu Pro Ala Cys Asp Leu Ser Thr Arg Gln
            260                 265                 270
```

```
ccg ctg gcg ccg gcc cgg agg ctt ctc gac gcc ggg gtc cac ctc gcc      1164
Pro Leu Ala Pro Ala Arg Arg Leu Leu Asp Ala Gly Val His Leu Ala
        275                 280                 285

ctc gcc tcc aac ctc aac ccg ggc acg tcg tac acc tcg tcg atg gcc      1212
Leu Ala Ser Asn Leu Asn Pro Gly Thr Ser Tyr Thr Ser Ser Met Ala
    290                 295                 300

ttc tgc gtc acc acc gcg gtg ctg cag cag cac ctc acc ctc gac gag      1260
Phe Cys Val Thr Thr Ala Val Leu Gln Gln His Leu Thr Leu Asp Glu
305                 310                 315                 320

gcc atc cac gcg gcc acc gcc ggt ggg gcg cgg gcg ctg cgg cgt cac      1308
Ala Ile His Ala Ala Thr Ala Gly Gly Ala Arg Ala Leu Arg Arg His
                325                 330                 335

gac atc ggc ggc ggc gtc gac ccc cag ggc cga ccc gcc cgc ggc agc      1356
Asp Ile Gly Gly Gly Val Asp Pro Gln Gly Arg Pro Ala Arg Gly Ser
            340                 345                 350

ctc gtg gtc ggg gcc gcg gca gac ctg cac gtg ctg gac acc ccc cac      1404
Leu Val Val Gly Ala Ala Ala Asp Leu His Val Leu Asp Thr Pro His
        355                 360                 365

gcc atc gat ctg gcc tac cgg ccg ggg atg ccg ctc acg tgg cgg acc      1452
Ala Ile Asp Leu Ala Tyr Arg Pro Gly Met Pro Leu Thr Trp Arg Thr
    370                 375                 380

tac atc cag ggg gtg cag gtc cac ccg gaa ccg cag gat cag tcc gac      1500
Tyr Ile Gln Gly Val Gln Val His Pro Glu Pro Gln Asp Gln Ser Asp
385                 390                 395                 400

ggc cga tga cgcacgatct cctccacgat ccgggccgcg acccgcgcgg              1549
Gly Arg

tccggccgtc gacgtcgaga agcgggttga gttcgacgac atcgaccaga cgcagcttcc    1609

cgctgcgcgc cacggctctg acgagcgtca ggatccgtgc cagatcgacg cccaacgccg    1669

ccggcgcgct cacgccgggg gcgaccgccg cgggcaggac gtcaaggtcg atgctcaggt    1729

ggacgtccgg ggcgtcctcc aggagctttc cgacgagcgc ctcgcacccg gccgacgtca    1789

tctccgccag ctcgacgtcg                                               1809
```

<210> 192
<211> 402
<212> PRT
<213> Corynebacterium humireducens

<400> 192

```
Met Ser Thr Leu Phe His Gly Ile Ser Glu Leu Arg Thr Val Ser Gly
1               5                   10                  15

Leu Gly Thr Leu Ser Asp Ala Ala Leu Ile Val Asp Arg Gly Arg Ile
```

20 25 30

Ala Trp Ile Gly Pro Arg Ala Gly Ala Pro Ala Ala Asp Ala Ala Val
35 40 45

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

His Met Ile Phe Ala Gly Asp Arg Ala Ala Glu Phe Glu Ala Arg Met
65 70 75 80

Asn Gly Gln Asp Tyr Gln Ala Gly Gly Ile Ala Val Thr Met Ser Ala
85 90 95

Thr Arg Glu Ala Gly Ala Val Arg Leu Glu Gln Leu Leu Leu Arg Arg
100 105 110

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

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

Ala Arg His Val Asp Asp Val Thr Phe Leu Gly Ala His Leu Val Pro
145 150 155 160

Pro Gly Glu Asp Pro Asp Glu Tyr Leu Ala Leu Val Leu Gly Asp Met
165 170 175

Leu Asp Ala Val Ala Ala Asn Val Ser Trp Ile Asp Val Phe Cys Glu
180 185 190

Arg Gly Ala Phe Asp Glu Ala Ala Ala Arg Arg Val Leu Glu Ala Gly
195 200 205

Arg Ala Arg Gly Leu Gly Leu Arg Val His Gly Asn Gln Leu Gly His
210 215 220

Gly Pro Gly Val Gln Leu Ala Val Glu Tyr Gly Ala Ala Ser Val Asp
225 230 235 240

His Val Asn Tyr Val Ser Asp Gly Asp Val Glu Ala Leu Ala Ser Ser
245 250 255

Glu Thr Val Ala Thr Val Leu Pro Ala Cys Asp Leu Ser Thr Arg Gln
260 265 270

Pro Leu Ala Pro Ala Arg Arg Leu Leu Asp Ala Gly Val His Leu Ala
275 280 285

Leu Ala Ser Asn Leu Asn Pro Gly Thr Ser Tyr Thr Ser Ser Met Ala
290 295 300

Phe Cys Val Thr Thr Ala Val Leu Gln Gln His Leu Thr Leu Asp Glu
305 310 315 320

Ala Ile His Ala Ala Thr Ala Gly Gly Ala Arg Ala Leu Arg Arg His
325 330 335

Asp Ile Gly Gly Gly Val Asp Pro Gln Gly Arg Pro Ala Arg Gly Ser
340 345 350

Leu Val Val Gly Ala Ala Ala Asp Leu His Val Leu Asp Thr Pro His
355 360 365

Ala Ile Asp Leu Ala Tyr Arg Pro Gly Met Pro Leu Thr Trp Arg Thr
370 375 380

Tyr Ile Gln Gly Val Gln Val His Pro Glu Pro Gln Asp Gln Ser Asp
385 390 395 400

Gly Arg

<210> 193
<211> 2151
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1851)
<223> gene hutH (Histidine Ammonialyase)

<400> 193
ccccggcgtc gtcggtaccg gcccggaatg ccatccgtgc agctcagagc cctgacgggc 60

atctcgtatg cgagatagat tccgcgcaca ccggaaagtc tcgtaagtga gacagccgtg 120

cccttcacgg gctgtcgccg gggcgtgacg gctgacacac tgggaggaac tgcgtccggc 180

tgtcgcgcag gtcgaaccgt ccacgagtca ccgccccgga ggacaggtac cacctgtgcc 240

```
tgccccgggg ccggtgcccc ggagaaaccg ggacccacca ggaagcaggg gaagccccac      300

atg cag acc atc acc tcc cac atc cgc gtc ggc gtc gga gcg ctc agc      348
Met Gln Thr Ile Thr Ser His Ile Arg Val Gly Val Gly Ala Leu Ser
1               5                  10                  15

atc gac gag gtc gtg gct gtc gcc cgg cac gac gcc cac gtc gag atc      396
Ile Asp Glu Val Val Ala Val Ala Arg His Asp Ala His Val Glu Ile
            20                  25                  30

acc ccg gag gcg ctc gag gcc gtc gcc gcc acc cgt gcc cgc atc gag      444
Thr Pro Glu Ala Leu Glu Ala Val Ala Ala Thr Arg Ala Arg Ile Glu
        35                  40                  45

gaa ctg gcc gac cac ccg acc ccg gtg tac ggc gtg tcc acc ggt ttc      492
Glu Leu Ala Asp His Pro Thr Pro Val Tyr Gly Val Ser Thr Gly Phe
    50                  55                  60

ggc gcc ctg gcc cgc cgc tac atc ccc cag gag atg cgc ctc cag ctg      540
Gly Ala Leu Ala Arg Arg Tyr Ile Pro Gln Glu Met Arg Leu Gln Leu
65                  70                  75                  80

cag cgc agc ctc gtc cgc tcc cat gcc gcc ggc tcc ggc ccc gag gtg      588
Gln Arg Ser Leu Val Arg Ser His Ala Ala Gly Ser Gly Pro Glu Val
                85                  90                  95

gag cgc gag gtc gtc cgg gcg ctc atg ctg ctg cgc ctg tcc aca ctg      636
Glu Arg Glu Val Val Arg Ala Leu Met Leu Leu Arg Leu Ser Thr Leu
            100                 105                 110

tgc acc ggc cgt acc ggc gtg cgg ccg gtc gtc gcg gag acc tac gcc      684
Cys Thr Gly Arg Thr Gly Val Arg Pro Val Val Ala Glu Thr Tyr Ala
        115                 120                 125

gcg gtg ctc aac gcc ggc atc acc ccc gtc gtc cac gag tac ggc tcg      732
Ala Val Leu Asn Ala Gly Ile Thr Pro Val Val His Glu Tyr Gly Ser
    130                 135                 140

ctc ggc tgc tcc ggc gac ctc tcc ccg ctg gcg cac tgc gcc ctg gcg      780
Leu Gly Cys Ser Gly Asp Leu Ser Pro Leu Ala His Cys Ala Leu Ala
145                 150                 155                 160

ctg ctg ggg gag ggc gag gtc acc acc gct gac ggc cgc cgc ctg ccc      828
Leu Leu Gly Glu Gly Glu Val Thr Thr Ala Asp Gly Arg Arg Leu Pro
                165                 170                 175

gcc gcc gtc gcc ctc gcc gag cac ggc atc gag ccg ctg gtc ctg cgg      876
Ala Ala Val Ala Leu Ala Glu His Gly Ile Glu Pro Leu Val Leu Arg
            180                 185                 190

gag aag gag ggg ctg gca ctc atc aac ggc acc gac ggc atg ctg ggc      924
Glu Lys Glu Gly Leu Ala Leu Ile Asn Gly Thr Asp Gly Met Leu Gly
        195                 200                 205

atg ctg tgc ctg gcc atc gct gac ctc gag tgc ctg gcc cgc agc gcc      972
Met Leu Cys Leu Ala Ile Ala Asp Leu Glu Cys Leu Ala Arg Ser Ala
    210                 215                 220
```

```
gac atc gcc gcc gcg atg acc gtc gag gcc ctg cgg ggc acc ctc acc      1020
Asp Ile Ala Ala Ala Met Thr Val Glu Ala Leu Arg Gly Thr Leu Thr
225                 230                 235                 240

gtc ttc gcc gcg gac ctg cag gag ctg cgc ccg cac ccg ggt cag gcg      1068
Val Phe Ala Ala Asp Leu Gln Glu Leu Arg Pro His Pro Gly Gln Ala
                245                 250                 255

gcc tcc gcg gcc aac atc cgc gcc gtg gcc gag ggc tcc gcc ata ctg      1116
Ala Ser Ala Ala Asn Ile Arg Ala Val Ala Glu Gly Ser Ala Ile Leu
            260                 265                 270

cag tcc gcc acc gag gaa ttc gcc ctg acc cac gtg cag gac gcc tac      1164
Gln Ser Ala Thr Glu Glu Phe Ala Leu Thr His Val Gln Asp Ala Tyr
        275                 280                 285

tcg gtg cgg tgc gcc ccg cag gtc gcc ggt ggt ttc cgc gac acc ctg      1212
Ser Val Arg Cys Ala Pro Gln Val Ala Gly Gly Phe Arg Asp Thr Leu
    290                 295                 300

gcc cac gcc cgc ctg gtc gcc gac cgg gag ctc gcc tcc gcc gtg gac      1260
Ala His Ala Arg Leu Val Ala Asp Arg Glu Leu Ala Ser Ala Val Asp
305                 310                 315                 320

aac ccc gtg gtg gct ctc gac ggc cgc gtg acc tcc aac ggc aac ttc      1308
Asn Pro Val Val Ala Leu Asp Gly Arg Val Thr Ser Asn Gly Asn Phe
                325                 330                 335

cac ggc gcg ccc gtc ggc tac gcg ctc gac ttc ctc gcc atc gtc acc      1356
His Gly Ala Pro Val Gly Tyr Ala Leu Asp Phe Leu Ala Ile Val Thr
            340                 345                 350

gcc gac ctg gcg agc atc tcc gag cgc cgc acc gac cgg ctt ctc gac      1404
Ala Asp Leu Ala Ser Ile Ser Glu Arg Arg Thr Asp Arg Leu Leu Asp
        355                 360                 365

gtc gcc cgc agc cgc gga ctc aac gcc ttc ctc gcc gac gat ccg ggc      1452
Val Ala Arg Ser Arg Gly Leu Asn Ala Phe Leu Ala Asp Asp Pro Gly
    370                 375                 380

gtg gac tcc ggc cac atg atc gcc cag tac acg cag gcc ggg atc gtc      1500
Val Asp Ser Gly His Met Ile Ala Gln Tyr Thr Gln Ala Gly Ile Val
385                 390                 395                 400

tcc gag ctc aag cgg ctg gcc gcc ccg gcc agc gtg gac tcc atc ccc      1548
Ser Glu Leu Lys Arg Leu Ala Ala Pro Ala Ser Val Asp Ser Ile Pro
                405                 410                 415

tcc tcc gcc atg cag gag gac cac gtg tcc atg ggc tgg tcg gcc ggg      1596
Ser Ser Ala Met Gln Glu Asp His Val Ser Met Gly Trp Ser Ala Gly
            420                 425                 430

cgc aag ctg cgc cgt tcc gtc gac ggg ctg ggg cgg gtg ctc ggc gtc      1644
Arg Lys Leu Arg Arg Ser Val Asp Gly Leu Gly Arg Val Leu Gly Val
        435                 440                 445

gag gtg ctc acc gca gcc cgg gcc atc gac atg cgc gag cag gag ccc      1692
Glu Val Leu Thr Ala Ala Arg Ala Ile Asp Met Arg Glu Gln Glu Pro
    450                 455                 460
```

```
gcg ccg ggg acc cgc gcc gca ctg gac gcc ctg cgc ggc cgt gtg gag      1740
Ala Pro Gly Thr Arg Ala Ala Leu Asp Ala Leu Arg Gly Arg Val Glu
465                 470                 475                 480

ggg ccc ggc ccc gac cgc tac ctg tcc ccg gag atc gag gag tcg gtg      1788
Gly Pro Gly Pro Asp Arg Tyr Leu Ser Pro Glu Ile Glu Glu Ser Val
                485                 490                 495

cag ctg ctc acc tcc ggg gcg ctg ctg gag gcg gtg gag ggg gtc gtc      1836
Gln Leu Leu Thr Ser Gly Ala Leu Leu Glu Ala Val Glu Gly Val Val
            500                 505                 510

gga aag ctg gca tga gcgggcgaat ctcagatatg agactaaagg ggcctccggg      1891
Gly Lys Leu Ala
        515

ccctcgatcc cgactgtgac ctgtcttacc gtcagaagtg tcaccgacac cggccacacc     1951

agcccggtgc tccacacccg acgatgacag ccccgggcca cccggatcgc gggtgccccg     2011

gggccccggc ctgatcggcc cccaccgtag aaggagaccc accccatgac cgagtccccg     2071

cgcaccatcc gtgccccgca cggcaccgag ctcagcgcca agagctggca aaccgaggca     2131

cccctgcgca tgctcatgaa                                                2151
```

<210> 194
<211> 516
<212> PRT
<213> Corynebacterium humireducens

<400> 194

```
Met Gln Thr Ile Thr Ser His Ile Arg Val Gly Val Gly Ala Leu Ser
1               5                   10                  15

Ile Asp Glu Val Val Ala Val Ala Arg His Asp Ala His Val Glu Ile
            20                  25                  30

Thr Pro Glu Ala Leu Glu Ala Val Ala Ala Thr Arg Ala Arg Ile Glu
        35                  40                  45

Glu Leu Ala Asp His Pro Thr Pro Val Tyr Gly Val Ser Thr Gly Phe
    50                  55                  60

Gly Ala Leu Ala Arg Arg Tyr Ile Pro Gln Glu Met Arg Leu Gln Leu
65                  70                  75                  80

Gln Arg Ser Leu Val Arg Ser His Ala Ala Gly Ser Gly Pro Glu Val
                85                  90                  95
```

```
Glu Arg Glu Val Val Arg Ala Leu Met Leu Leu Arg Leu Ser Thr Leu
            100                 105                 110

Cys Thr Gly Arg Thr Gly Val Arg Pro Val Val Ala Glu Thr Tyr Ala
        115                 120                 125

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

Leu Gly Cys Ser Gly Asp Leu Ser Pro Leu Ala His Cys Ala Leu Ala
145                 150                 155                 160

Leu Leu Gly Glu Gly Glu Val Thr Thr Ala Asp Gly Arg Arg Leu Pro
                165                 170                 175

Ala Ala Val Ala Leu Ala Glu His Gly Ile Glu Pro Leu Val Leu Arg
            180                 185                 190

Glu Lys Glu Gly Leu Ala Leu Ile Asn Gly Thr Asp Gly Met Leu Gly
        195                 200                 205

Met Leu Cys Leu Ala Ile Ala Asp Leu Glu Cys Leu Ala Arg Ser Ala
    210                 215                 220

Asp Ile Ala Ala Ala Met Thr Val Glu Ala Leu Arg Gly Thr Leu Thr
225                 230                 235                 240

Val Phe Ala Ala Asp Leu Gln Glu Leu Arg Pro His Pro Gly Gln Ala
                245                 250                 255

Ala Ser Ala Ala Asn Ile Arg Ala Val Ala Glu Gly Ser Ala Ile Leu
            260                 265                 270

Gln Ser Ala Thr Glu Glu Phe Ala Leu Thr His Val Gln Asp Ala Tyr
        275                 280                 285

Ser Val Arg Cys Ala Pro Gln Val Ala Gly Gly Phe Arg Asp Thr Leu
    290                 295                 300

Ala His Ala Arg Leu Val Ala Asp Arg Glu Leu Ala Ser Ala Val Asp
305                 310                 315                 320

Asn Pro Val Val Ala Leu Asp Gly Arg Val Thr Ser Asn Gly Asn Phe
                325                 330                 335
```

```
His Gly Ala Pro Val Gly Tyr Ala Leu Asp Phe Leu Ala Ile Val Thr
            340                 345                 350

Ala Asp Leu Ala Ser Ile Ser Glu Arg Arg Thr Asp Arg Leu Leu Asp
        355                 360                 365

Val Ala Arg Ser Arg Gly Leu Asn Ala Phe Leu Ala Asp Asp Pro Gly
    370                 375                 380

Val Asp Ser Gly His Met Ile Ala Gln Tyr Thr Gln Ala Gly Ile Val
385                 390                 395                 400

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

Ser Ser Ala Met Gln Glu Asp His Val Ser Met Gly Trp Ser Ala Gly
            420                 425                 430

Arg Lys Leu Arg Arg Ser Val Asp Gly Leu Gly Arg Val Leu Gly Val
        435                 440                 445

Glu Val Leu Thr Ala Ala Arg Ala Ile Asp Met Arg Glu Gln Glu Pro
    450                 455                 460

Ala Pro Gly Thr Arg Ala Ala Leu Asp Ala Leu Arg Gly Arg Val Glu
465                 470                 475                 480

Gly Pro Gly Pro Asp Arg Tyr Leu Ser Pro Glu Ile Glu Glu Ser Val
                485                 490                 495

Gln Leu Leu Thr Ser Gly Ala Leu Leu Glu Ala Val Glu Gly Val Val
            500                 505                 510

Gly Lys Leu Ala
        515
```

<210> 195
<211> 1509
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1209)
<223> gene hutG (Formididoylglutamase)

<400> 195
cgagtccgta ggtgcgggtc tcggggatgc gcacgacgta gccctccgac tccatgacgg 60

cgagcaggtg gtacgtcgac gaccgggggа ggtcgagttc cgtcatgatg cgtgccgccg 120

agacgggcac gtcgatggat gagagcagcg agaggatgcg caacgtgtgt cgcgcggcgg 180

gcacctgtcc catgtcactc cttacctgtg tgtggtctgt gggtcggcgg tctcgtatgc 240

gggaccacgc tgcgtcgcag ccgggtgtgg cgggaggtcg gtggcgttat cctacggcgc 300

atg acc acc cat gaa tgg aca gga cgc gac gac ggg ccc ggg gcc ggg 348
Met Thr Thr His Glu Trp Thr Gly Arg Asp Asp Gly Pro Gly Ala Gly
1 5 10 15

cac gcc cgt tgg cac agc gtc atc acc acc acg acc gac cgg ccg ggg 396
His Ala Arg Trp His Ser Val Ile Thr Thr Thr Thr Asp Arg Pro Gly
20 25 30

gtc gcc ctc gtc ggg ttc gcc tcc gac gag ggg gtc cgc cgc aac ggt 444
Val Ala Leu Val Gly Phe Ala Ser Asp Glu Gly Val Arg Arg Asn Gly
35 40 45

ggc cgc ccc ggc gcc gcc gcc ggc ccc acg gag atc cgc cgt gcc ctg 492
Gly Arg Pro Gly Ala Ala Ala Gly Pro Thr Glu Ile Arg Arg Ala Leu
50 55 60

gcc tcc ctg gcc gtg cac acc gac gtc ccg ctt ctc gac gcc ggc acc 540
Ala Ser Leu Ala Val His Thr Asp Val Pro Leu Leu Asp Ala Gly Thr
65 70 75 80

gtc acc gtc tcc ggt acc gac ctg gag ggc ggg cac gac gca ctg tcc 588
Val Thr Val Ser Gly Thr Asp Leu Glu Gly Gly His Asp Ala Leu Ser
85 90 95

gcg cag gtg gag gag ctg acc cgc gcg ggg cac acc gtc atc gtg ctg 636
Ala Gln Val Glu Glu Leu Thr Arg Ala Gly His Thr Val Ile Val Leu
100 105 110

ggc ggt ggg cat gag acg gcg ttc ggg tcg cac cgc ggg gtg cgc cgg 684
Gly Gly Gly His Glu Thr Ala Phe Gly Ser His Arg Gly Val Arg Arg
115 120 125

gcg ctg ggg cac agt ccg gcg atc atc aac ctc gac gcc cac ttc gac 732
Ala Leu Gly His Ser Pro Ala Ile Ile Asn Leu Asp Ala His Phe Asp
130 135 140

ctg cgg gtc gcg ccg gcc ccg tcc tcg ggt acc ccg ttc cgg cag atc 780
Leu Arg Val Ala Pro Ala Pro Ser Ser Gly Thr Pro Phe Arg Gln Ile
145 150 155 160

gcg gac ctg gcc ggg gag gag ttc cgt tat gcg gtg ctg ggc atc tcg 828
Ala Asp Leu Ala Gly Glu Glu Phe Arg Tyr Ala Val Leu Gly Ile Ser
165 170 175

gtg ccc aac aac acc cgg gcg ctg ttc gac acc gcc cgg gaa ctg ggg 876
Val Pro Asn Asn Thr Arg Ala Leu Phe Asp Thr Ala Arg Glu Leu Gly
180 185 190

```
gtc cgg gtg acc acc gac gtc gag ctg gcg gag atg acg tcg gcc ggg        924
Val Arg Val Thr Thr Asp Val Glu Leu Ala Glu Met Thr Ser Ala Gly
        195                 200                 205

tgc gag gcg ctc gtc gga aag ctc ctg gag gac gcc ccg gac gtc cac        972
Cys Glu Ala Leu Val Gly Lys Leu Leu Glu Asp Ala Pro Asp Val His
    210                 215                 220

ctg agc atc gac ctt gac gtc ctg ccc gcg gcg gtc gcc ccc ggc gtg       1020
Leu Ser Ile Asp Leu Asp Val Leu Pro Ala Ala Val Ala Pro Gly Val
225                 230                 235                 240

agc gcg ccg gcg gcg ttg ggc gtc gat ctg gca cgg atc ctg acg ctc       1068
Ser Ala Pro Ala Ala Leu Gly Val Asp Leu Ala Arg Ile Leu Thr Leu
                245                 250                 255

gtc aga gcc gtg gcg cgc agc ggg aag ctg cgt ctg gtc gat gtc gtc       1116
Val Arg Ala Val Ala Arg Ser Gly Lys Leu Arg Leu Val Asp Val Val
            260                 265                 270

gaa ctc aac ccg ctt ctc gac gtc gac ggc cgg acc gcg cgg gtc gcg       1164
Glu Leu Asn Pro Leu Leu Asp Val Asp Gly Arg Thr Ala Arg Val Ala
        275                 280                 285

gcc cgg atc gtg gag gag atc gtg cgt cat cgg ccg tcg gac tga           1209
Ala Arg Ile Val Glu Glu Ile Val Arg His Arg Pro Ser Asp
    290                 295                 300

tcctgcggtt ccgggtggac ctgcaccccc tggatgtagg tccgccacgt gagcggcatc     1269

cccggccggt aggccagatc gatggcgtgg ggggtgtcca gcacgtgcag gtctgccgcg     1329

gccccgacca cgaggctgcc gcgggcgggt cggccctggg ggtcgacgcc gccgccgatg     1389

tcgtgacgcc gcagcgcccg cgccccaccg gcggtggccg cgtggatggc ctcgtcgagg     1449

gtgaggtgct gctgcagcac cgcggtggtg acgcagaagg ccatcgacga ggtgtacgac     1509
```

<210> 196
<211> 302
<212> PRT
<213> Corynebacterium humireducens

<400> 196

```
Met Thr Thr His Glu Trp Thr Gly Arg Asp Asp Gly Pro Gly Ala Gly
1               5                   10                  15

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

Val Ala Leu Val Gly Phe Ala Ser Asp Glu Gly Val Arg Arg Asn Gly
        35                  40                  45
```

Gly Arg Pro Gly Ala Ala Ala Gly Pro Thr Glu Ile Arg Arg Ala Leu
50 55 60

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

Val Thr Val Ser Gly Thr Asp Leu Glu Gly Gly His Asp Ala Leu Ser
85 90 95

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

Gly Gly Gly His Glu Thr Ala Phe Gly Ser His Arg Gly Val Arg Arg
115 120 125

Ala Leu Gly His Ser Pro Ala Ile Ile Asn Leu Asp Ala His Phe Asp
130 135 140

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

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

Val Pro Asn Asn Thr Arg Ala Leu Phe Asp Thr Ala Arg Glu Leu Gly
180 185 190

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

Cys Glu Ala Leu Val Gly Lys Leu Leu Glu Asp Ala Pro Asp Val His
210 215 220

Leu Ser Ile Asp Leu Asp Val Leu Pro Ala Ala Val Ala Pro Gly Val
225 230 235 240

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

Val Arg Ala Val Ala Arg Ser Gly Lys Leu Arg Leu Val Asp Val Val
260 265 270

Glu Leu Asn Pro Leu Leu Asp Val Asp Gly Arg Thr Ala Arg Val Ala
275 280 285

```
Ala Arg Ile Val Glu Glu Ile Val Arg His Arg Pro Ser Asp
    290                 295                 300
```

<210> 197
<211> 1767
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1467)
<223> gene sucC

<400> 197

```
gctggccggt ccggacttcc ggtacctcga tcacatcaag ccgatctacg accagcccat       60

cggtgaggcg acctggcgcg acatgtccac ctggttcacg tggcagagca ggggagaccg      120

tttcggctac ggccacctga cgtcggaact ctgcagcggt cggctcgggg agctggtgga      180

acgcttcctg gagctgtggg acgcgcccac cacggcgtag cgcctccgtc cggggcgtgt      240

ggccgcaggg tatcgccgat ccggcgtcgt gcgtgcggca acgtctatac actgcagggc      300

atg gac ctc tac gag tac cag gcc ctt gaa ctc ttc gcc gcc cac ggc        348
Met Asp Leu Tyr Glu Tyr Gln Ala Leu Glu Leu Phe Ala Ala His Gly
1               5                   10                  15

gtt ccg gtt ctg tcc gga acg gtg gct gag act ccg gcg gag gca cgc        396
Val Pro Val Leu Ser Gly Thr Val Ala Glu Thr Pro Ala Glu Ala Arg
            20                  25                  30

gcg gcg gcg gag cgg ctg ggc ggg gag tgc gtc gtc aag gcg cag gtg        444
Ala Ala Ala Glu Arg Leu Gly Gly Glu Cys Val Val Lys Ala Gln Val
        35                  40                  45

aag atc ggc ggc cgc ggc aag gcg ggc ggt gtc cgc gtc gcg gcg gcg        492
Lys Ile Gly Gly Arg Gly Lys Ala Gly Gly Val Arg Val Ala Ala Ala
    50                  55                  60

ccc gag gcg gcc gag cag gcg gcg gag gcg atc ctg ggg atg gac atc        540
Pro Glu Ala Ala Glu Gln Ala Ala Glu Ala Ile Leu Gly Met Asp Ile
65                  70                  75                  80

cgc ggg cac acg gtc gag cgg gtg ctc gtc gtg gag tgc gtg gag atc        588
Arg Gly His Thr Val Glu Arg Val Leu Val Val Glu Cys Val Glu Ile
                85                  90                  95

gag gcg gag tac tac ttc tcg ctg ctc ctc gac cgc gcg cgg cgc tcc        636
Glu Ala Glu Tyr Tyr Phe Ser Leu Leu Leu Asp Arg Ala Arg Arg Ser
            100                 105                 110

tac ctg ggg ttg ttc tcg gtg gag gga ggc gtg gac atc gag aag ctc        684
Tyr Leu Gly Leu Phe Ser Val Glu Gly Gly Val Asp Ile Glu Lys Leu
        115                 120                 125
```

```
gcc gcg gag cgg ccg gag gcg ctg gcc cgc gtg gag gtc gac ccc ctc        732
Ala Ala Glu Arg Pro Glu Ala Leu Ala Arg Val Glu Val Asp Pro Leu
    130                 135                 140

gag ggc ttc gac gcc cac gaa ctt gtc gac gcc ctc ccc gcc gac ctc        780
Glu Gly Phe Asp Ala His Glu Leu Val Asp Ala Leu Pro Ala Asp Leu
145                 150                 155                 160

cgc gac aag gtc gtc ccc gtc atc cgg cgg ctc gcc gag gtc ttc cgc        828
Arg Asp Lys Val Val Pro Val Ile Arg Arg Leu Ala Glu Val Phe Arg
                165                 170                 175

gag gag gac gcc acc ctc gtc gag gtg aac ccg ctc gtc ctc acg gtg        876
Glu Glu Asp Ala Thr Leu Val Glu Val Asn Pro Leu Val Leu Thr Val
            180                 185                 190

cag ggg gac atc atc gcc ctc gac gcg aag atc acc ctc gac gac aac        924
Gln Gly Asp Ile Ile Ala Leu Asp Ala Lys Ile Thr Leu Asp Asp Asn
        195                 200                 205

gcc gcc ttc cgt cac gac aac cgc gcg gag ctc gcc gag gcc gcc gac        972
Ala Ala Phe Arg His Asp Asn Arg Ala Glu Leu Ala Glu Ala Ala Asp
    210                 215                 220

cac ctc gac ccg atc gag cga cgc gcg agc gag cag ggg ctc aag tac       1020
His Leu Asp Pro Ile Glu Arg Arg Ala Ser Glu Gln Gly Leu Lys Tyr
225                 230                 235                 240

gtc acg ctc gag ggt tcg gtg ggc atc atc ggc aac ggc gcc ggg ctg       1068
Val Thr Leu Glu Gly Ser Val Gly Ile Ile Gly Asn Gly Ala Gly Leu
                245                 250                 255

gtc atg tcg acc ctc gac gtc gtg tcc ggg gcg ggg gag cgg cac ggc       1116
Val Met Ser Thr Leu Asp Val Val Ser Gly Ala Gly Glu Arg His Gly
            260                 265                 270

ggg cag aag ccg gcg aac ttc ctc gac atc ggc ggt ggc gcc tgc ccg       1164
Gly Gln Lys Pro Ala Asn Phe Leu Asp Ile Gly Gly Gly Ala Cys Pro
        275                 280                 285

gag acg atg acc gcg gcc ctg gag atc gtc ctc tcg gac gag cag gtg       1212
Glu Thr Met Thr Ala Ala Leu Glu Ile Val Leu Ser Asp Glu Gln Val
    290                 295                 300

cgc agc gtg ttc gtc aac gtc ttc gga ggc atc acg tcc tgc gac gcg       1260
Arg Ser Val Phe Val Asn Val Phe Gly Gly Ile Thr Ser Cys Asp Ala
305                 310                 315                 320

gtg gcc acc ggc atc gtg gag gcg ctc act cac ctc ggg gac acg gcc       1308
Val Ala Thr Gly Ile Val Glu Ala Leu Thr His Leu Gly Asp Thr Ala
                325                 330                 335

cgc aag ccg atc gtc gtg cgt ctc gac ggc aac agc gtc gac gag gga       1356
Arg Lys Pro Ile Val Val Arg Leu Asp Gly Asn Ser Val Asp Glu Gly
            340                 345                 350

cgc cgc atc ctc cgc gag tac gat cac ccc ctc gtc acc gtc gtc gac       1404
Arg Arg Ile Leu Arg Glu Tyr Asp His Pro Leu Val Thr Val Val Asp
        355                 360                 365
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gac atg gac gag gcc gcg gac cgg gtg gcg gag ctc gcc gcg gtg acc 1452
Asp Met Asp Glu Ala Ala Asp Arg Val Ala Glu Leu Ala Ala Val Thr
370 375 380

ccg agc gtc gtc tag cgaaaggcac cgacatggcg atcttcctca actccgaatc 1507
Pro Ser Val Val
385

ccgcatcatc gtccagggca tcaccgggcg tgaggggcgg gagcacaccg cccggatgct 1567

cgccgccggc gcgaacgtgg tcggcggcac caacccgaag aaggcgggcg agacggtgac 1627

ggtcggcggc cacgagctgc cggtgttcgg caccgtcgcc gacgcacgcg cggccaccga 1687

cgcgaacgtg tccgtggtgt tcgtgcctgc ccccttcgtc cgggaggcgg tctgcgaggc 1747

catcgacgcc gcgatcccgc 1767

<210> 198
<211> 388
<212> PRT
<213> Corynebacterium humireducens

<400> 198

Met Asp Leu Tyr Glu Tyr Gln Ala Leu Glu Leu Phe Ala Ala His Gly
1 5 10 15

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

Ala Ala Ala Glu Arg Leu Gly Gly Glu Cys Val Val Lys Ala Gln Val
35 40 45

Lys Ile Gly Gly Arg Gly Lys Ala Gly Gly Val Arg Val Ala Ala Ala
50 55 60

Pro Glu Ala Ala Glu Gln Ala Ala Glu Ala Ile Leu Gly Met Asp Ile
65 70 75 80

Arg Gly His Thr Val Glu Arg Val Leu Val Val Glu Cys Val Glu Ile
85 90 95

Glu Ala Glu Tyr Tyr Phe Ser Leu Leu Leu Asp Arg Ala Arg Arg Ser
100 105 110

Tyr Leu Gly Leu Phe Ser Val Glu Gly Gly Val Asp Ile Glu Lys Leu
115 120 125

Ala Ala Glu Arg Pro Glu Ala Leu Ala Arg Val Glu Val Asp Pro Leu
130 135 140

Glu Gly Phe Asp Ala His Glu Leu Val Asp Ala Leu Pro Ala Asp Leu
145 150 155 160

Arg Asp Lys Val Val Pro Val Ile Arg Arg Leu Ala Glu Val Phe Arg
165 170 175

Glu Glu Asp Ala Thr Leu Val Glu Val Asn Pro Leu Val Leu Thr Val
180 185 190

Gln Gly Asp Ile Ile Ala Leu Asp Ala Lys Ile Thr Leu Asp Asp Asn
195 200 205

Ala Ala Phe Arg His Asp Asn Arg Ala Glu Leu Ala Glu Ala Ala Asp
210 215 220

His Leu Asp Pro Ile Glu Arg Arg Ala Ser Glu Gln Gly Leu Lys Tyr
225 230 235 240

Val Thr Leu Glu Gly Ser Val Gly Ile Ile Gly Asn Gly Ala Gly Leu
245 250 255

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

Gly Gln Lys Pro Ala Asn Phe Leu Asp Ile Gly Gly Gly Ala Cys Pro
275 280 285

Glu Thr Met Thr Ala Ala Leu Glu Ile Val Leu Ser Asp Glu Gln Val
290 295 300

Arg Ser Val Phe Val Asn Val Phe Gly Gly Ile Thr Ser Cys Asp Ala
305 310 315 320

Val Ala Thr Gly Ile Val Glu Ala Leu Thr His Leu Gly Asp Thr Ala
325 330 335

Arg Lys Pro Ile Val Val Arg Leu Asp Gly Asn Ser Val Asp Glu Gly
340 345 350

Arg Arg Ile Leu Arg Glu Tyr Asp His Pro Leu Val Thr Val Val Asp
355 360 365

```
Asp Met Asp Glu Ala Ala Asp Arg Val Ala Glu Leu Ala Ala Val Thr
    370                 375                 380

Pro Ser Val Val
385

<210>  199
<211>  1455
<212>  DNA
<213>  Corynebacterium humireducens

<220>
<221>  CDS
<222>  (301)..(1155)
<223>  gene sucD

<400>  199
cctggagatc gtcctctcgg acgagcaggt gcgcagcgtg ttcgtcaacg tcttcggagg       60

catcacgtcc tgcgacgcgg tggccaccgg catcgtggag gcgctcactc acctcgggga      120

cacggcccgc aagccgatcg tcgtgcgtct cgacggcaac agcgtcgacg agggacgccg      180

catcctccgc gagtacgatc acccccctcgt caccgtcgtc gacgacatgg acgaggccgc      240

ggaccgggtg gcggagctcg ccgcggtgac cccgagcgtc gtctagcgaa aggcaccgac      300

atg gcg atc ttc ctc aac tcc gaa tcc cgc atc atc gtc cag ggc atc      348
Met Ala Ile Phe Leu Asn Ser Glu Ser Arg Ile Ile Val Gln Gly Ile
1               5                   10                  15

acc ggg cgt gag ggg cgg gag cac acc gcc cgg atg ctc gcc gcc ggc      396
Thr Gly Arg Glu Gly Arg Glu His Thr Ala Arg Met Leu Ala Ala Gly
            20                  25                  30

gcg aac gtg gtc ggc ggc acc aac ccg aag aag gcg ggc gag acg gtg      444
Ala Asn Val Val Gly Gly Thr Asn Pro Lys Lys Ala Gly Glu Thr Val
        35                  40                  45

acg gtc ggc ggc cac gag ctg ccg gtg ttc ggc acc gtc gcc gac gca      492
Thr Val Gly Gly His Glu Leu Pro Val Phe Gly Thr Val Ala Asp Ala
    50                  55                  60

cgc gcg gcc acc gac gcg aac gtg tcc gtg gtg ttc gtg cct gcc ccc      540
Arg Ala Ala Thr Asp Ala Asn Val Ser Val Val Phe Val Pro Ala Pro
65                  70                  75                  80

ttc gtc cgg gag gcg gtc tgc gag gcc atc gac gcc gcg atc ccg ctc      588
Phe Val Arg Glu Ala Val Cys Glu Ala Ile Asp Ala Ala Ile Pro Leu
                85                  90                  95

atc gtc gtc atc acc gag ggc gtg ccc gtc cgc gac acc gcc gag atg      636
Ile Val Val Ile Thr Glu Gly Val Pro Val Arg Asp Thr Ala Glu Met
            100                 105                 110
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ctg gcg cac gcg cgg acg gag gga ggc acg cgg atc atc ggc ccg aac        684
Leu Ala His Ala Arg Thr Glu Gly Gly Thr Arg Ile Ile Gly Pro Asn
        115                 120                 125

tgc ccc ggc atc atc ccc gcg gat atc agc ggc ccc ggc ccc gtg gga        732
Cys Pro Gly Ile Ile Pro Ala Asp Ile Ser Gly Pro Gly Pro Val Gly
    130                 135                 140

ctg atc tcg aag tcg ggc acg ctg acg tac cag atg atg cac gcg ctt        780
Leu Ile Ser Lys Ser Gly Thr Leu Thr Tyr Gln Met Met His Ala Leu
145                 150                 155                 160

tcc gac gtc ggc atc tcc acc gcc ctc ggc atc ggc ggc gac ccc ctc        828
Ser Asp Val Gly Ile Ser Thr Ala Leu Gly Ile Gly Gly Asp Pro Leu
                165                 170                 175

atc ggc acc gcc tac atc gac gcg ctc agc gcc ttc gag gag gac ccc        876
Ile Gly Thr Ala Tyr Ile Asp Ala Leu Ser Ala Phe Glu Glu Asp Pro
            180                 185                 190

gac acc cgg gcc atc gtc atg atc ggc gag atc ggc ggc gac gcc gag        924
Asp Thr Arg Ala Ile Val Met Ile Gly Glu Ile Gly Gly Asp Ala Glu
        195                 200                 205

gaa cgc gcc gcc gac tac atc cgg gag cac gtg acc aaa ccc gtc gtc        972
Glu Arg Ala Ala Asp Tyr Ile Arg Glu His Val Thr Lys Pro Val Val
    210                 215                 220

ggc tac gtc gcc ggg ttc acc gcc ccg gag ggc aag acc atg ggg cac       1020
Gly Tyr Val Ala Gly Phe Thr Ala Pro Glu Gly Lys Thr Met Gly His
225                 230                 235                 240

gca ggt gcc atc gtc acc ggt tcc gtc ggc acg gcg cag gcc aag aag       1068
Ala Gly Ala Ile Val Thr Gly Ser Val Gly Thr Ala Gln Ala Lys Lys
                245                 250                 255

gag gcg ctc gag gcg gcc ggt gtc cgg gtg ggc acc acg ccg acg gag       1116
Glu Ala Leu Glu Ala Ala Gly Val Arg Val Gly Thr Thr Pro Thr Glu
            260                 265                 270

acc gcg gag atc atg cgg ggg att gtc gag ggg atg tag gctgcccggg       1165
Thr Ala Glu Ile Met Arg Gly Ile Val Glu Gly Met
        275                 280

tcgcgtcggc ggcctatcat cggagcatgc tggagaccgg acgcacccac ccctggcag      1225

acatcattga cacggtcctt gccgacccga cctcgggctc cggctggtgc ctgtacacag     1285

gcccggggat gaccccgggg gagtacctcg tcgacgagta ccccgaggtc ggcgatgacg     1345

ataccgagac ctatccgccg gcggtgaggg aacgaggtct ggactatttc ctcagtggtc     1405

agatgtgcga ggacgtgatc ctcaatctgg accaccaggg atccccactt                1455
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<210> 200
<211> 284
<212> PRT
<213> Corynebacterium humireducens

<400> 200

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

Thr Gly Arg Glu Gly Arg Glu His Thr Ala Arg Met Leu Ala Ala Gly
20 25 30

Ala Asn Val Val Gly Gly Thr Asn Pro Lys Lys Ala Gly Glu Thr Val
35 40 45

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

Arg Ala Ala Thr Asp Ala Asn Val Ser Val Val Phe Val Pro Ala Pro
65 70 75 80

Phe Val Arg Glu Ala Val Cys Glu Ala Ile Asp Ala Ala Ile Pro Leu
85 90 95

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

Leu Ala His Ala Arg Thr Glu Gly Gly Thr Arg Ile Ile Gly Pro Asn
115 120 125

Cys Pro Gly Ile Ile Pro Ala Asp Ile Ser Gly Pro Gly Pro Val Gly
130 135 140

Leu Ile Ser Lys Ser Gly Thr Leu Thr Tyr Gln Met Met His Ala Leu
145 150 155 160

Ser Asp Val Gly Ile Ser Thr Ala Leu Gly Ile Gly Gly Asp Pro Leu
165 170 175

Ile Gly Thr Ala Tyr Ile Asp Ala Leu Ser Ala Phe Glu Glu Asp Pro
180 185 190

Asp Thr Arg Ala Ile Val Met Ile Gly Glu Ile Gly Gly Asp Ala Glu
195 200 205

Glu Arg Ala Ala Asp Tyr Ile Arg Glu His Val Thr Lys Pro Val Val
210 215 220

Gly Tyr Val Ala Gly Phe Thr Ala Pro Glu Gly Lys Thr Met Gly His
225 230 235 240

Ala Gly Ala Ile Val Thr Gly Ser Val Gly Thr Ala Gln Ala Lys Lys
245 250 255

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

Thr Ala Glu Ile Met Arg Gly Ile Val Glu Gly Met
275 280

<210> 201
<211> 1569
<212> DNA
<213> Corynebacterium humireducens

<220>
<221> CDS
<222> (301)..(1269)
<223> gene ddh

<400> 201
ggcgccaccc tagcgcctga gccggtttct gacacccgcg gatcctgcgg taccatctgc 60

aggcaggcgg gtacatgtgc ctgccggtgc tggagtggcg caatcggtag cgcaacggtc 120

ttgtaaaccg taggttgcga gttcaagtct cgtctccagc tctgctctcc acgaggtggg 180

gtccgggtga accggccccg cctcgttccc ttttgtggga ctcatttcta ttgactgacc 240

ggtgatgggc cgtagaatgg gcggcagcaa gcaccgtccc ccacctcaag gagtcagcac 300

atg gcc aac atc agg gtc gcg atc gtc ggt tac ggc aac ctc ggc aag 348
Met Ala Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Lys
1 5 10 15

tcc gtc gag aag ctc atc ggc cag cag ccg gac atg gag ctc gcg ggc 396
Ser Val Glu Lys Leu Ile Gly Gln Gln Pro Asp Met Glu Leu Ala Gly
20 25 30

gtg ttc tcg cgt cgc gac gca ctg gac acc ctc gac ccg gcc acc ccg 444
Val Phe Ser Arg Arg Asp Ala Leu Asp Thr Leu Asp Pro Ala Thr Pro
35 40 45

gtc ctg ccc gtc gcg gag ttc ggt gag cac acc gac aag ttc gac gtc 492
Val Leu Pro Val Ala Glu Phe Gly Glu His Thr Asp Lys Phe Asp Val
50 55 60

gcc gtc ctc tgc ctc ggc tcc gcc acc gac atc ccg gag cag gcc ccc 540
Ala Val Leu Cys Leu Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro
65 70 75 80

gag ttc atc cgc cac gcc aac acg gtc gac acc tac gac aac cac cgc 588

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Glu Phe Ile Arg His Ala Asn Thr Val Asp Thr Tyr Asp Asn His Arg
                85                  90                  95

gac atc ccg cgc cac cgc gcc gag atg gac agg gtg gcc agg gag aac      636
Asp Ile Pro Arg His Arg Ala Glu Met Asp Arg Val Ala Arg Glu Asn
            100                 105                 110

ggc acc gtc gcc atc gtc tcc acc ggc tgg gac ccg ggc atg ttc tcc      684
Gly Thr Val Ala Ile Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser
        115                 120                 125

ctc aac cgc acc atc ggc cag gcg ctc ctg ccg ggc ggc cag cag cag      732
Leu Asn Arg Thr Ile Gly Gln Ala Leu Leu Pro Gly Gly Gln Gln Gln
    130                 135                 140

acc ttc tgg ggt ccg ggc ctc tcg cag ggc cac tct gac gcg gtg cgc      780
Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Val Arg
145                 150                 155                 160

cgc gtc gcg ggc gtg aag aag ggc gtg cag tac acc atc ccc tcc ccg      828
Arg Val Ala Gly Val Lys Lys Gly Val Gln Tyr Thr Ile Pro Ser Pro
                165                 170                 175

gag gcc ctc gag gcg gcc cgc aag ggt gag tcg ggt ctc agc ggc aag      876
Glu Ala Leu Glu Ala Ala Arg Lys Gly Glu Ser Gly Leu Ser Gly Lys
            180                 185                 190

cag gcc cac ctg cgc cgc tgc ttc atc gtg gcg gac gag gcc gac cac      924
Gln Ala His Leu Arg Arg Cys Phe Ile Val Ala Asp Glu Ala Asp His
        195                 200                 205

gag cgc atc gag aac gag atc cgc acc atg ccc gac tac ttc gtc ggc      972
Glu Arg Ile Glu Asn Glu Ile Arg Thr Met Pro Asp Tyr Phe Val Gly
    210                 215                 220

tac gag gtg gag gtc aac ttc atc gac gag gcc acc ttc gac gcc gag     1020
Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ala Glu
225                 230                 235                 240

cac acc ggc atg ccg cac ggc ggg cac gtc atc acg gcg ggt gac acc     1068
His Thr Gly Met Pro His Gly Gly His Val Ile Thr Ala Gly Asp Thr
                245                 250                 255

ggc ggc tac gtc cag tcc atc gag tac aac ctc gac ctg gac cgg aac     1116
Gly Gly Tyr Val Gln Ser Ile Glu Tyr Asn Leu Asp Leu Asp Arg Asn
            260                 265                 270

ccg gac ttc acc ggt gcc gtc gcc ctg gca tac gcc cgt gcg gcc cac     1164
Pro Asp Phe Thr Gly Ala Val Ala Leu Ala Tyr Ala Arg Ala Ala His
        275                 280                 285

cgt ctg cgt gag gcg ggc cag gcc ggc gcc tac acc gtc ctc gag gtc     1212
Arg Leu Arg Glu Ala Gly Gln Ala Gly Ala Tyr Thr Val Leu Glu Val
    290                 295                 300

gcc ccg tac ctg atc tcc ccg acg ccg ctc gag gag ctc atc gcc cgc     1260
Ala Pro Tyr Leu Ile Ser Pro Thr Pro Leu Glu Glu Leu Ile Ala Arg
305                 310                 315                 320
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gac gtg tag ggtccaccac cgggatcagc aggagggcac cgaccagcag 1309
Asp Val

gaccaggccg atgccgagga tcccgaagcg gtcggtgccg cccagcagga cgaacatccc 1369

gaaggcgagc ggcgagagcc acgacacggc gcgtccggtg gtgacgtaca ggccgaagag 1429

ctggccctcc cgcccgtcgg gggcgacgcg ggagaggaac gagcgggccg ccgactgggc 1489

ggggccgacg aacaggcaca ggatgaggcc gaagatccag aacatctgcg ggccctccac 1549

gaagtagagg acgcccgcgg 1569

<210> 202
<211> 322
<212> PRT
<213> Corynebacterium humireducens

<400> 202

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

Ser Val Glu Lys Leu Ile Gly Gln Gln Pro Asp Met Glu Leu Ala Gly
20 25 30

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

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

Ala Val Leu Cys Leu Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro
65 70 75 80

Glu Phe Ile Arg His Ala Asn Thr Val Asp Thr Tyr Asp Asn His Arg
85 90 95

Asp Ile Pro Arg His Arg Ala Glu Met Asp Arg Val Ala Arg Glu Asn
100 105 110

Gly Thr Val Ala Ile Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser
115 120 125

Leu Asn Arg Thr Ile Gly Gln Ala Leu Leu Pro Gly Gly Gln Gln Gln
130 135 140

Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Val Arg

145 150 155 160

Arg Val Ala Gly Val Lys Lys Gly Val Gln Tyr Thr Ile Pro Ser Pro
165 170 175

Glu Ala Leu Glu Ala Ala Arg Lys Gly Glu Ser Gly Leu Ser Gly Lys
180 185 190

Gln Ala His Leu Arg Arg Cys Phe Ile Val Ala Asp Glu Ala Asp His
195 200 205

Glu Arg Ile Glu Asn Glu Ile Arg Thr Met Pro Asp Tyr Phe Val Gly
210 215 220

Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ala Glu
225 230 235 240

His Thr Gly Met Pro His Gly Gly His Val Ile Thr Ala Gly Asp Thr
245 250 255

Gly Gly Tyr Val Gln Ser Ile Glu Tyr Asn Leu Asp Leu Asp Arg Asn
260 265 270

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

Arg Leu Arg Glu Ala Gly Gln Ala Gly Ala Tyr Thr Val Leu Glu Val
290 295 300

Ala Pro Tyr Leu Ile Ser Pro Thr Pro Leu Glu Glu Leu Ile Ala Arg
305 310 315 320

Asp Val